Association of microbiome vs strange situation in GIMA dataset

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Correlation between Strange Situation Outcome, Mask task and IBQ-R

Table 1: Correlation matrix of Mask task and strange situation

	FacialFear	VocalDistress	BodilyFear	StartleResponse	EscapeBehavior	Strange.Average	IBQr_
FacialFear	1.00	0.99	0.90	0.78	0.57	-0.03	
VocalDistress	0.99	1.00	0.88	0.80	0.60	0.00	
BodilyFear	0.90	0.88	1.00	0.75	0.54	0.10	-
StartleResponse	0.78	0.80	0.75	1.00	0.35	0.01	
EscapeBehavior	0.57	0.60	0.54	0.35	1.00	-0.12	
Strange.Average	-0.03	0.00	0.10	0.01	-0.12	1.00	
IBQr_fear	0.05	0.13	-0.08	0.01	0.26	0.03	

Association analysis for covariates vs strange situation using linear model

Table 2: cvrt_vs_strange_yr1: Summed vs AgeAt1yrVisit, df=28

	Estimate	Std. Error	t value	Pr($>$|t|)	2.5 %	97.5 %	R2
Intercept	8.1888	3.48999	2.35	0.0263	1.0398	15.33770	0.0000
AgeAt1yrVisit	-0.0101	0.00895	-1.13	0.2685	-0.0284	0.00823	0.0421

Table 3: cvrt_vs_strange_yr1: Summed vs MAGE, df=28

	Estimate	Std. Error	t value	Pr($>$|t|)	2.5 %	97.5 %	R2
Intercept	5.255	2.1197	2.479	0.0195	0.913	9.60	0.00000
MAGE	-0.033	0.0698	-0.472	0.6403	-0.176	0.11	0.00764

Table 4: cvrt_vs_strange_yr1: Summed vs PAGE, df=28

	Estimate	Std. Error	t value	Pr($>$|t|)	2.5 %	97.5 %	R2
Intercept	5.0875	1.6307	3.120	0.00417	1.747	8.4278	0.00000
PAGE	-0.0253	0.0492	-0.514	0.61098	-0.126	0.0755	0.00904

Table 5: cvrt_vs_strange_yr1: Summed vs MEDUY, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.6872	2.612	1.412	0.169	-1.663	9.038	0.00000
MEDUY	0.0361	0.162	0.224	0.825	-0.295	0.367	0.00172

Table 6: cvrt_vs_strange_yr1: Summed vs PEDUY, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.675	1.764	4.92	3.48e-05	5.062	12.2890	0.000
PEDUY	-0.284	0.112	-2.54	1.70e-02	-0.514	-0.0548	0.182

Table 7: cvrt_vs_strange_yr1: Summed vs Income.code, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.3333	0.542	7.990	1.38e-08	3.22	5.45	0.000000
Income.code.LOW	0.0952	0.893	0.107	9.16e-01	-1.74	1.93	0.000473
Income.code.MID	-0.2424	0.784	-0.309	7.60e-01	-1.85	1.37	0.003983

Table 8: cvrt_vs_strange_yr1: Summed vs OLDERSIBLINGS, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.2857	0.495	8.6667	2.05e-09	3.27	5.30	0.00e+00
OLDERSIBLINGS	-0.0357	0.677	-0.0527	9.58e-01	-1.42	1.35	9.59e-05

Table 9: cvrt_vs_strange_yr1: Summed vs SEX, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.4	1.013	4.34	0.000167	2.32	6.48	0.000000
SEX	-0.1	0.716	-0.14	0.889984	-1.57	1.37	0.000671

Table 10: cvrt_vs_strange_yr1: Summed vs GESTAGEBIRTH, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.1500	12.2168	0.667	0.510	-16.875	33.1750	0.00000
GESTAGEBIRTH	-0.0141	0.0443	-0.318	0.753	-0.105	0.0767	0.00347

Table 11: cvrt_vs_strange_yr1: Summed vs BW, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.02341	3.065329	0.00764	0.994	-6.255633	6.30245	0.0000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
BW	0.00128	0.000922	1.39221	0.175	-0.000605	0.00317	0.0626

Table 12: cvrt_vs_strange_yr1: Summed vs MaternalInfection, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.579	0.413	11.08	9.49e-12	3.73	5.425	0.000
MaternalInfection	-0.852	0.682	-1.25	2.22e-01	-2.25	0.546	0.051

Table 13: cvrt_vs_strange_yr1: Summed vs MPSYCH, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.409	0.391	11.275	6.38e-12	3.61	5.21	0.0000
MPSYCH	-0.534	0.757	-0.705	4.86e-01	-2.09	1.02	0.0169

Table 14: cvrt_vs_strange_yr1: Summed vs VITAMINDNEO, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.421	0.422	10.482	3.37e-11	3.56	5.28	0.0000
VITAMINDNEO	-0.421	0.697	-0.605	5.50e-01	-1.85	1.01	0.0124

Table 15: cvrt_vs_strange_yr1: Summed vs PrePregBMI, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.857	0.378	10.211	1.37e-10	3.081	4.63	0.00000
PrePregBMI.Obese	1.143	1.281	0.892	3.80e-01	-1.490	3.78	0.02305
PrePregBMI.Overweight	1.810	0.801	2.258	3.25e-02	0.162	3.46	0.14861
PrePregBMI.Under	-0.857	1.772	-0.484	6.33e-01	-4.499	2.78	0.00672

Table 16: cvrt_vs_strange_yr1: Summed vs ANTIBIOTIC_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.9375	0.461	8.5460	3.69e-09	2.992	4.88	0.00e+00
ANTIBIOTIC_1yr.1	0.7548	0.688	1.0969	2.82e-01	-0.657	2.17	4.09e-02
ANTIBIOTIC_1yr.NA	0.0625	1.900	0.0329	9.74e-01	-3.835	3.96	3.68e-05

Table 17: cvrt_vs_strange_yr1: Summed vs FORMULA_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.9412	0.446	8.8421	1.86e-09	3.027	4.86	0.00e+00

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
FORMULA_1yr.1	0.8088	0.693	1.1673	2.53e-01	-0.613	2.23	4.59e-02
FORMULA_1yr.NA	0.0588	1.891	0.0311	9.75e-01	-3.821	3.94	3.26e-05

Table 18: cvrt_vs_strange_yr1: Summed vs FORMULA_6mo, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.438	0.460	9.643	2.13e-10	3.49	5.38	0.0000
FORMULA_6mo	-0.366	0.674	-0.543	5.91e-01	-1.75	1.01	0.0101

Table 19: cvrt_vs_strange_yr1: Summed vs FEVER_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.714	0.378	12.460	1.04e-12	3.94	5.491	0.00000
FEVER_1yr.1	-1.589	0.720	-2.206	3.61e-02	-3.07	-0.111	0.14459
FEVER_1yr.NA	-0.714	1.775	-0.403	6.90e-01	-4.36	2.927	0.00481

Table 20: cvrt_vs_strange_yr1: Summed vs DAYCARE, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.562	0.453	10.067	1.23e-10	3.63	5.492	0.0000
DAYCARE.1	-0.229	0.755	-0.303	7.64e-01	-1.78	1.321	0.0032
DAYCARE.NA	-1.363	0.929	-1.467	1.54e-01	-3.27	0.543	0.0748

Table 21: cvrt_vs_strange_yr1: Summed vs CURBRFEED_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.357	0.503	8.663	2.81e-09	3.33	5.39	0.0000
CURBRFEED_1yr.1	-0.157	0.699	-0.225	8.24e-01	-1.59	1.28	0.0018
CURBRFEED_1yr.NA	-0.357	1.948	-0.183	8.56e-01	-4.35	3.64	0.0012

Table 22: cvrt_vs_strange_yr1: Summed vs Milks_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.000	0.694	7.21	9.44e-08	3.58	6.42	0.00000
Milks_1yr.1	-0.955	0.796	-1.20	2.41e-01	-2.59	0.68	0.05140
Milks_1yr.NA	-1.000	1.962	-0.51	6.14e-01	-5.03	3.03	0.00929

Table 23: cvrt_vs_strange_yr1: Summed vs FrenchFries_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.727	0.552	6.754	2.98e-07	2.595	4.86	0.000000
FrenchFries_1yr.1	0.884	0.701	1.262	2.18e-01	-0.553	2.32	0.054682
FrenchFries_1yr.NA	0.273	1.912	0.143	8.88e-01	-3.650	4.20	0.000699

Table 24: cvrt_vs_strange_yr1: Summed vs SweetFoods-Drinks_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.00e+00	0.625	6.40e+00	7.35e-07	2.72	5.28	0.00e+00
SweetFoodsDrinks_1yr.1	4.00e-01	0.752	5.32e-01	5.99e-01	-1.14	1.94	1.04e-02
SweetFoodsDrinks_1yr.NA	2.34e-16	1.975	1.18e-16	1.00e+00	-4.05	4.05	5.15e-34

Table 25: cvrt_vs_strange_yr1: Summed vs PeanutButter_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.60	0.574	6.28	1.02e-06	2.423	4.78	0.0000
PeanutButter_1yr.1	1.03	0.709	1.46	1.57e-01	-0.422	2.49	0.0720
PeanutButter_1yr.NA	0.40	1.902	0.21	8.35e-01	-3.503	4.30	0.0015

Table 26: cvrt_vs_strange_yr1: Summed vs WHSTOTHER, df=22

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.50	1.23	2.853	0.00925	0.956	6.04	0.00000
WHSTOTHER.3.5 months	-0.50	2.12	-0.235	0.81614	-4.906	3.91	0.00185
WHSTOTHER.4 months	1.07	1.39	0.770	0.44933	-1.813	3.96	0.04729
WHSTOTHER.4.5 months	-0.50	2.12	-0.235	0.81614	-4.906	3.91	0.00185
WHSTOTHER.5 months	0.50	1.39	0.359	0.72268	-2.385	3.38	0.01030
WHSTOTHER.5.5 months	1.50	1.73	0.865	0.39658	-2.098	5.10	0.03224
WHSTOTHER.6 months	0.50	1.36	0.369	0.71589	-2.313	3.31	0.01209
WHSTOTHER.7 months	5.50	2.12	2.589	0.01677	1.094	9.91	0.22444

Table 27: cvrt_vs_strange_yr1: Summed vs VITAMIND_6mo, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.74	0.404	11.74	4.12e-12	3.91	5.565	0.0000
VITAMIND_6mo.1	-1.11	0.741	-1.50	1.45e-01	-2.63	0.409	0.0690
VITAMIND_6mo.NA	-1.74	1.093	-1.59	1.24e-01	-3.98	0.506	0.0775

Table 28: cvrt__vs_strange__yr1: Summed vs Cereals_6mo, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.714	0.705	6.686	3.54e-07	3.27	6.16	0.0000
Cereals_6mo.1	-0.556	0.825	-0.675	5.06e-01	-2.25	1.14	0.0206
Cereals_6mo.NA	-0.714	1.169	-0.611	5.46e-01	-3.11	1.68	0.0169

Table 29: cvrt__vs_strange__yr1: Summed vs STATE, df=15

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.00e+00	2.07	1.45e+00	0.168	-1.42	7.42	0.00e+00
STATE.22	6.67e-01	2.39	2.79e-01	0.784	-4.43	5.77	6.06e-03
STATE.23	1.50e+00	2.54	5.91e-01	0.563	-3.91	6.91	2.12e-02
STATE.24	2.00e+00	2.39	8.36e-01	0.416	-3.10	7.10	5.45e-02
STATE.26	3.74e-15	2.54	1.47e-15	1.000	-5.41	5.41	1.32e-31
STATE.27	4.18e-15	2.93	1.43e-15	1.000	-6.25	6.25	8.52e-32
STATE.29	5.00e-01	2.54	1.97e-01	0.846	-4.91	5.91	2.36e-03
STATE.33	2.00e+00	2.93	6.82e-01	0.505	-4.25	8.25	1.95e-02
STATE.35	2.00e+00	2.54	7.88e-01	0.443	-3.41	7.41	3.77e-02
STATE.38	3.11e-15	2.93	1.06e-15	1.000	-6.25	6.25	4.72e-32
STATE.39	3.00e+00	2.54	1.18e+00	0.256	-2.41	8.41	8.48e-02
STATE.40	4.08e-15	2.54	1.61e-15	1.000	-5.41	5.41	1.57e-31
STATE.41	1.00e+00	2.39	4.18e-01	0.682	-4.10	6.10	1.36e-02
STATE.73	4.00e+00	2.93	1.36e+00	0.192	-2.25	10.25	7.81e-02
STATE.NA	1.75e+00	2.32	7.55e-01	0.462	-3.19	6.69	5.36e-02

Table 30: cvrt__vs_strange__yr1: Summed vs TRAIT, df=13

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.00e+00	1.65	1.82e+00	0.0922	-0.566	6.57	0.00e+00
TRAIT.22	-6.58e-16	2.33	-2.82e-16	1.0000	-5.043	5.04	2.33e-33
TRAIT.24	-6.99e-16	2.02	-3.46e-16	1.0000	-4.367	4.37	5.09e-33
TRAIT.25	-1.30e-15	2.33	-5.57e-16	1.0000	-5.043	5.04	9.13e-33
TRAIT.26	4.50e+00	2.02	2.23e+00	0.0443	0.133	8.87	2.11e-01
TRAIT.27	6.67e-01	1.91	3.50e-01	0.7321	-3.451	4.78	6.69e-03
TRAIT.28	3.00e+00	2.02	1.48e+00	0.1616	-1.367	7.37	9.37e-02
TRAIT.29	-1.43e-15	2.33	-6.11e-16	1.0000	-5.043	5.04	1.10e-32
TRAIT.30	4.00e+00	2.02	1.98e+00	0.0694	-0.367	8.37	1.67e-01
TRAIT.32	-1.69e-15	2.33	-7.25e-16	1.0000	-5.043	5.04	1.54e-32
TRAIT.33	5.00e-01	2.02	2.47e-01	0.8085	-3.867	4.87	2.60e-03
TRAIT.36	-1.56e-15	2.33	-6.68e-16	1.0000	-5.043	5.04	1.31e-32
TRAIT.39	1.50e+00	1.85	8.13e-01	0.4309	-2.487	5.49	4.35e-02
TRAIT.48	-1.39e-15	2.33	-5.97e-16	1.0000	-5.043	5.04	1.05e-32
TRAIT.49	1.00e+00	2.33	4.28e-01	0.6754	-4.043	6.04	5.39e-03
TRAIT.52	-1.58e-15	2.33	-6.77e-16	1.0000	-5.043	5.04	1.35e-32
TRAIT.NA	1.25e+00	1.85	6.77e-01	0.5100	-2.737	5.24	3.02e-02

Table 31: cvrt_vs_strange_yr1: Summed vs NegativeLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.2500	0.966	4.3997	0.000308	2.23	6.27	0.000000
NegativeLifeEvents.1	0.0833	1.247	0.0668	0.947421	-2.53	2.69	0.000253
NegativeLifeEvents.14	-1.2500	2.160	-0.5787	0.569585	-5.77	3.27	0.011473
NegativeLifeEvents.2	0.4167	1.247	0.3341	0.741952	-2.19	3.03	0.006330
NegativeLifeEvents.26	2.7500	2.160	1.2732	0.218322	-1.77	7.27	0.055529
NegativeLifeEvents.3	0.2500	1.673	0.1494	0.882796	-3.25	3.75	0.000886
NegativeLifeEvents.4	-1.2500	1.673	-0.7471	0.464146	-4.75	2.25	0.022155
NegativeLifeEvents.5	1.7500	1.673	1.0459	0.308710	-1.75	5.25	0.043423
NegativeLifeEvents.6	-1.2500	2.160	-0.5787	0.569585	-5.77	3.27	0.011473
NegativeLifeEvents.7	-1.2500	2.160	-0.5787	0.569585	-5.77	3.27	0.011473
NegativeLifeEvents.NA	-0.7500	1.366	-0.5490	0.589394	-3.61	2.11	0.014812

Table 32: cvrt_vs_strange_yr1: Summed vs PositiveLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.50e+00	0.647	5.41e+00	3.22e-05	2.1454	4.85	0.00e+00
PositiveLifeEvents.11	-5.00e-01	1.712	-2.92e-01	7.73e-01	-4.0839	3.08	1.84e-03
PositiveLifeEvents.12	-5.00e-01	1.712	-2.92e-01	7.73e-01	-4.0839	3.08	1.84e-03
PositiveLifeEvents.25	3.50e+00	1.712	2.04e+00	5.51e-02	-0.0839	7.08	9.03e-02
PositiveLifeEvents.3	2.17e+00	0.915	2.37e+00	2.87e-02	0.2510	4.08	1.72e-01
PositiveLifeEvents.5	1.67e-01	1.121	1.49e-01	8.83e-01	-2.1796	2.51	5.72e-04
PositiveLifeEvents.6	-2.50e-01	1.023	-2.44e-01	8.10e-01	-2.3918	1.89	1.65e-03
PositiveLifeEvents.7	-5.00e-01	1.712	-2.92e-01	7.73e-01	-4.0839	3.08	1.84e-03
PositiveLifeEvents.8	2.50e+00	1.712	1.46e+00	1.61e-01	-1.0839	6.08	4.61e-02
PositiveLifeEvents.9	3.00e+00	1.294	2.32e+00	3.18e-02	0.2908	5.71	1.28e-01
PositiveLifeEvents.NA	4.30e-16	1.023	4.20e-16	1.00e+00	-2.1418	2.14	4.89e-33

Table 33: cvrt_vs_strange_yr1: Summed vs TotalLifeEvents, df=14

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.50e+00	1.36	2.57e+00	0.0223	0.577	6.42	0.00e+00
TotalLifeEvents.10	2.50e+00	1.93	1.30e+00	0.2155	-1.634	6.63	7.06e-02
TotalLifeEvents.11	5.00e-01	2.36	2.12e-01	0.8353	-4.563	5.56	1.46e-03
TotalLifeEvents.12	-5.00e-01	2.36	-2.12e-01	0.8353	-5.563	4.56	1.46e-03
TotalLifeEvents.13	-5.00e-01	2.36	-2.12e-01	0.8353	-5.563	4.56	1.46e-03
TotalLifeEvents.14	-5.00e-01	2.36	-2.12e-01	0.8353	-5.563	4.56	1.46e-03
TotalLifeEvents.15	-5.00e-01	2.36	-2.12e-01	0.8353	-5.563	4.56	1.46e-03
TotalLifeEvents.2	5.00e-01	1.93	2.59e-01	0.7991	-3.634	4.63	2.83e-03
TotalLifeEvents.27	3.50e+00	2.36	1.48e+00	0.1603	-1.563	8.56	7.17e-02
TotalLifeEvents.29	3.50e+00	2.36	1.48e+00	0.1603	-1.563	8.56	7.17e-02
TotalLifeEvents.4	-5.00e-01	2.36	-2.12e-01	0.8353	-5.563	4.56	1.46e-03
TotalLifeEvents.5	2.00e+00	1.93	1.04e+00	0.3170	-2.134	6.13	4.52e-02
TotalLifeEvents.6	1.00e+00	1.93	5.19e-01	0.6120	-3.134	5.13	1.13e-02
TotalLifeEvents.7	-2.50e-01	1.67	-1.50e-01	0.8831	-3.830	3.33	1.31e-03
TotalLifeEvents.8	1.75e+00	1.67	1.05e+00	0.3122	-1.830	5.33	6.43e-02

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
TotalLifeEvents.NA	1.54e-15	1.67	9.22e-16	1.0000	-3.580	3.58	4.97e-32

Table 34: cvrt_vs_strange_yr1: Summed vs Stranger, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.400	0.476	9.235	5.41e-10	3.42	5.38	0.00000
Stranger	-0.267	0.674	-0.396	6.95e-01	-1.65	1.11	0.00537

Table 35: cvrt_vs_strange_yr1: Average vs AgeAt1yrVisit, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.73390	1.16280	2.35	0.026	0.35201	5.11579	0.0000
AgeAt1yrVisit	-0.00338	0.00298	-1.13	0.267	-0.00949	0.00273	0.0424

Table 36: cvrt_vs_strange_yr1: Average vs MAGE, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.750	0.7064	2.478	0.0195	0.3035	3.1974	0.00000
MAGE	-0.011	0.0232	-0.471	0.6410	-0.0586	0.0367	0.00761

Table 37: cvrt_vs_strange_yr1: Average vs PAGE, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.69643	0.5434	3.122	0.00414	0.5834	2.8095	0.00000
PAGE	-0.00847	0.0164	-0.517	0.60939	-0.0421	0.0251	0.00912

Table 38: cvrt_vs_strange_yr1: Average vs MEDUY, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.2284	0.8704	1.411	0.169	-0.5545	3.011	0.00000
MEDUY	0.0121	0.0538	0.224	0.824	-0.0982	0.122	0.00173

Table 39: cvrt_vs_strange_yr1: Average vs PEDUY, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.8894	0.5880	4.91	3.51e-05	1.685	4.0939	0.000
PEDUY	-0.0947	0.0374	-2.53	1.71e-02	-0.171	-0.0182	0.181

Table 40: cvrt__vs_strange_yr1: Average vs Income.code, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.4442	0.181	7.991	1.37e-08	1.073	1.815	0.000000
Income.code.LOW	0.0315	0.298	0.106	9.16e-01	-0.579	0.642	0.000468
Income.code.MID	-0.0814	0.261	-0.312	7.58e-01	-0.618	0.455	0.004047

Table 41: cvrt__vs_strange_yr1: Average vs OLDERSIBLINGS, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.4279	0.165	8.6647	2.06e-09	1.090	1.765	0.00e+00
OLDERSIBLINGS	-0.0116	0.226	-0.0514	9.59e-01	-0.474	0.451	9.12e-05

Table 42: cvrt__vs_strange_yr1: Average vs SEX, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.4650	0.338	4.339	0.000168	0.773	2.157	0.000000
SEX	-0.0325	0.239	-0.136	0.892689	-0.522	0.457	0.000639

Table 43: cvrt__vs_strange_yr1: Average vs GESTAGEBIRTH, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.7155	4.0712	0.667	0.510	-5.624	11.0549	0.00000
GESTAGEBIRTH	-0.0047	0.0148	-0.318	0.753	-0.035	0.0256	0.00347

Table 44: cvrt__vs_strange_yr1: Average vs BW, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.007206	1.021475	0.00705	0.994	-2.085191	2.09960	0.0000
BW	0.000428	0.000307	1.39266	0.175	-0.000202	0.00106	0.0627

Table 45: cvrt__vs_strange_yr1: Average vs MaternalInfection, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.526	0.138	11.08	9.50e-12	1.24	1.808	0.000
MaternalInfection	-0.284	0.227	-1.25	2.22e-01	-0.75	0.182	0.051

Table 46: cvrt__vs_strange_yr1: Average vs MPSYCH, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.469	0.130	11.274	6.40e-12	1.202	1.736	0.0000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
MPSYCH	-0.178	0.252	-0.705	4.87e-01	-0.695	0.339	0.0168

Table 47: cvrt_vs_strange_yr1: Average vs VITAMINDNEO, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.47	0.141	10.482	3.37e-11	1.185	1.761	0.0000
VITAMINDNEO	-0.14	0.232	-0.605	5.50e-01	-0.616	0.335	0.0125

Table 48: cvrt_vs_strange_yr1: Average vs PrePregBMI, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.285	0.126	10.210	1.37e-10	1.0265	1.544	0.0000
PrePregBMI.Obese	0.380	0.427	0.890	3.82e-01	-0.4977	1.257	0.0229
PrePregBMI.Overweight	0.603	0.267	2.258	3.25e-02	0.0542	1.152	0.1487
PrePregBMI.Under	-0.285	0.590	-0.483	6.33e-01	-1.4989	0.928	0.0067

Table 49: cvrt_vs_strange_yr1: Average vs ANTIBIOTIC_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.3119	0.154	8.5451	3.69e-09	0.997	1.627	0.00e+00
ANTIBIOTIC_1yr.1	0.2520	0.229	1.0989	2.82e-01	-0.219	0.722	4.10e-02
ANTIBIOTIC_1yr.NA	0.0181	0.633	0.0286	9.77e-01	-1.281	1.317	2.78e-05

Table 50: cvrt_vs_strange_yr1: Average vs FORMULA_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.3129	0.149	8.8409	1.86e-09	1.008	1.618	0.00e+00
FORMULA_1yr.1	0.2704	0.231	1.1712	2.52e-01	-0.203	0.744	4.62e-02
FORMULA_1yr.NA	0.0171	0.630	0.0271	9.79e-01	-1.276	1.310	2.47e-05

Table 51: cvrt_vs_strange_yr1: Average vs FORMULA_6mo, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.478	0.153	9.638	2.16e-10	1.164	1.792	0.00000
FORMULA_6mo	-0.121	0.224	-0.539	5.94e-01	-0.581	0.339	0.00992

Table 52: cvrt__vs_strange_yr1: Average vs FEVER_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.571	0.126	12.461	1.04e-12	1.31	1.8296	0.00000
FEVER_1yr.1	-0.530	0.240	-2.207	3.60e-02	-1.02	-0.0372	0.14463
FEVER_1yr.NA	-0.241	0.591	-0.407	6.87e-01	-1.45	0.9723	0.00493

Table 53: cvrt__vs_strange_yr1: Average vs DAYCARE, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.5200	0.151	10.06	1.24e-10	1.210	1.830	0.00000
DAYCARE.1	-0.0756	0.252	-0.30	7.66e-01	-0.592	0.441	0.00313
DAYCARE.NA	-0.4540	0.310	-1.47	1.54e-01	-1.089	0.181	0.07482

Table 54: cvrt__vs_strange_yr1: Average vs CURBRFEED_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.4521	0.168	8.665	2.80e-09	1.108	1.796	0.00000
CURBRFEED_1yr.1	-0.0528	0.233	-0.227	8.22e-01	-0.531	0.425	0.00183
CURBRFEED_1yr.NA	-0.1221	0.649	-0.188	8.52e-01	-1.454	1.210	0.00126

Table 55: cvrt__vs_strange_yr1: Average vs Milks_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.667	0.231	7.213	9.30e-08	1.193	2.141	0.00000
Milks_1yr.1	-0.319	0.265	-1.204	2.39e-01	-0.864	0.225	0.05181
Milks_1yr.NA	-0.337	0.654	-0.516	6.10e-01	-1.678	1.004	0.00951

Table 56: cvrt__vs_strange_yr1: Average vs FrenchFries_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.2418	0.184	6.753	2.99e-07	0.864	1.619	0.000000
FrenchFries_1yr.1	0.2948	0.233	1.263	2.17e-01	-0.184	0.774	0.054805
FrenchFries_1yr.NA	0.0882	0.637	0.138	8.91e-01	-1.219	1.395	0.000658

Table 57: cvrt__vs_strange_yr1: Average vs SweetFoodsDrinks_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.33333	0.208	6.40571	7.32e-07	0.906	1.760	0.00e+00
SweetFoodsDrinks_1yr.1	0.13267	0.251	0.52931	6.01e-01	-0.382	0.647	1.03e-02
SweetFoodsDrinks_1yr.NA	-0.00333	0.658	-0.00506	9.96e-01	-1.354	1.347	9.40e-07

Table 58: cvrt_vs_strange_yr1: Average vs PeanutButter_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.200	0.191	6.278	1.02e-06	0.808	1.592	0.00000
PeanutButter_1yr.1	0.343	0.236	1.453	1.58e-01	-0.141	0.828	0.07175
PeanutButter_1yr.NA	0.130	0.634	0.205	8.39e-01	-1.171	1.431	0.00143

Table 59: cvrt_vs_strange_yr1: Average vs WHSTOTHER, df=22

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.165	0.409	2.850	0.00931	0.317	2.01	0.00000
WHSTOTHER.3.5 months	-0.165	0.708	-0.233	0.81788	-1.633	1.30	0.00182
WHSTOTHER.4 months	0.358	0.463	0.772	0.44828	-0.603	1.32	0.04745
WHSTOTHER.4.5 months	-0.165	0.708	-0.233	0.81788	-1.633	1.30	0.00182
WHSTOTHER.5 months	0.168	0.463	0.362	0.72069	-0.793	1.13	0.01044
WHSTOTHER.5.5 months	0.500	0.578	0.865	0.39641	-0.699	1.70	0.03222
WHSTOTHER.6 months	0.168	0.452	0.372	0.71309	-0.769	1.11	0.01233
WHSTOTHER.7 months	1.835	0.708	2.592	0.01665	0.367	3.30	0.22475

Table 60: cvrt_vs_strange_yr1: Average vs VITAMIND_6mo, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.578	0.134	11.74	4.12e-12	1.302	1.854	0.0000
VITAMIND_6mo.1	-0.371	0.247	-1.50	1.45e-01	-0.878	0.136	0.0691
VITAMIND_6mo.NA	-0.578	0.364	-1.59	1.24e-01	-1.326	0.169	0.0774

Table 61: cvrt_vs_strange_yr1: Average vs Cereals_6mo, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.570	0.235	6.681	3.59e-07	1.088	2.052	0.0000
Cereals_6mo.1	-0.184	0.275	-0.670	5.08e-01	-0.748	0.380	0.0203
Cereals_6mo.NA	-0.237	0.390	-0.609	5.47e-01	-1.037	0.562	0.0168

Table 62: cvrt_vs_strange_yr1: Average vs STATE, df=15

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e+00	0.691	1.45e+00	0.168	-0.472	2.47	0.00e+00
STATE.22	2.20e-01	0.797	2.76e-01	0.786	-1.480	1.92	5.94e-03
STATE.23	5.00e-01	0.846	5.91e-01	0.563	-1.303	2.30	2.12e-02
STATE.24	6.67e-01	0.797	8.36e-01	0.416	-1.033	2.37	5.46e-02
STATE.26	1.43e-15	0.846	1.70e-15	1.000	-1.803	1.80	1.75e-31
STATE.27	1.37e-15	0.977	1.40e-15	1.000	-2.082	2.08	8.26e-32
STATE.29	1.65e-01	0.846	1.95e-01	0.848	-1.638	1.97	2.31e-03
STATE.33	6.70e-01	0.977	6.86e-01	0.503	-1.412	2.75	1.97e-02
STATE.35	6.65e-01	0.846	7.86e-01	0.444	-1.138	2.47	3.75e-02

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
STATE.38	1.32e-15	0.977	1.36e-15	1.000	-2.082	2.08	7.72e-32
STATE.39	1.00e+00	0.846	1.18e+00	0.256	-0.803	2.80	8.49e-02
STATE.40	1.39e-15	0.846	1.64e-15	1.000	-1.803	1.80	1.64e-31
STATE.41	3.33e-01	0.797	4.18e-01	0.682	-1.366	2.03	1.36e-02
STATE.73	1.33e+00	0.977	1.36e+00	0.193	-0.752	3.41	7.78e-02
STATE.NA	5.83e-01	0.772	7.54e-01	0.462	-1.063	2.23	5.35e-02

Table 63: cvrt_vs_strange_yr1: Average vs TRAIT, df=13

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e+00	0.549	1.82e+00	0.0916	-0.1860	2.19	0.00e+00
TRAIT.22	-4.62e-16	0.776	-5.95e-16	1.0000	-1.6773	1.68	1.04e-32
TRAIT.24	-6.54e-16	0.672	-9.72e-16	1.0000	-1.4526	1.45	4.01e-32
TRAIT.25	-6.22e-16	0.776	-8.01e-16	1.0000	-1.6773	1.68	1.88e-32
TRAIT.26	1.50e+00	0.672	2.23e+00	0.0439	0.0474	2.95	2.11e-01
TRAIT.27	2.20e-01	0.634	3.47e-01	0.7341	-1.1495	1.59	6.57e-03
TRAIT.28	1.00e+00	0.672	1.49e+00	0.1608	-0.4526	2.45	9.39e-02
TRAIT.29	-6.27e-16	0.776	-8.08e-16	1.0000	-1.6773	1.68	1.91e-32
TRAIT.30	1.33e+00	0.672	1.99e+00	0.0686	-0.1176	2.79	1.67e-01
TRAIT.32	-7.49e-16	0.776	-9.65e-16	1.0000	-1.6773	1.68	2.73e-32
TRAIT.33	1.65e-01	0.672	2.45e-01	0.8100	-1.2876	1.62	2.56e-03
TRAIT.36	-6.07e-16	0.776	-7.81e-16	1.0000	-1.6773	1.68	1.79e-32
TRAIT.39	5.00e-01	0.614	8.15e-01	0.4300	-0.8260	1.83	4.36e-02
TRAIT.48	-6.45e-16	0.776	-8.31e-16	1.0000	-1.6773	1.68	2.02e-32
TRAIT.49	3.30e-01	0.776	4.25e-01	0.6778	-1.3473	2.01	5.29e-03
TRAIT.52	-6.08e-16	0.776	-7.83e-16	1.0000	-1.6773	1.68	1.80e-32
TRAIT.NA	4.15e-01	0.614	6.76e-01	0.5108	-0.9110	1.74	3.00e-02

Table 64: cvrt_vs_strange_yr1: Average vs NegativeLifeEvents,
df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.4175	0.322	4.4028	0.000306	0.744	2.091	0.000000
NegativeLifeEvents.1	0.0258	0.416	0.0622	0.951090	-0.844	0.896	0.000219
NegativeLifeEvents.14	-0.4175	0.720	-0.5799	0.568772	-1.924	1.089	0.011525
NegativeLifeEvents.2	0.1375	0.416	0.3308	0.744404	-0.732	1.007	0.006207
NegativeLifeEvents.26	0.9125	0.720	1.2675	0.220283	-0.594	2.419	0.055053
NegativeLifeEvents.3	0.0825	0.558	0.1479	0.883945	-1.085	1.250	0.000869
NegativeLifeEvents.4	-0.4175	0.558	-0.7487	0.463210	-1.585	0.750	0.022254
NegativeLifeEvents.5	0.5825	0.558	1.0446	0.309324	-0.585	1.750	0.043320
NegativeLifeEvents.6	-0.4175	0.720	-0.5799	0.568772	-1.924	1.089	0.011525
NegativeLifeEvents.7	-0.4175	0.720	-0.5799	0.568772	-1.924	1.089	0.011525
NegativeLifeEvents.NA	-0.2525	0.455	-0.5546	0.585660	-1.205	0.700	0.015117

Table 65: cvrt_vs_strange_yr1: Average vs PositiveLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.16667	0.216	5.40595	3.24e-05	0.7150	1.618	0.00e+00
PositiveLifeEvents.11	-0.16667	0.571	-0.29189	7.74e-01	-1.3617	1.028	1.84e-03
PositiveLifeEvents.12	-0.16667	0.571	-0.29189	7.74e-01	-1.3617	1.028	1.84e-03
PositiveLifeEvents.25	1.16333	0.571	2.03742	5.58e-02	-0.0317	2.358	8.99e-02
PositiveLifeEvents.3	0.72167	0.305	2.36454	2.89e-02	0.0829	1.360	1.72e-01
PositiveLifeEvents.5	0.05667	0.374	0.15160	8.81e-01	-0.7257	0.839	5.96e-04
PositiveLifeEvents.6	-0.08417	0.341	-0.24666	8.08e-01	-0.7984	0.630	1.69e-03
PositiveLifeEvents.7	-0.16667	0.571	-0.29189	7.74e-01	-1.3617	1.028	1.84e-03
PositiveLifeEvents.8	0.83333	0.571	1.45947	1.61e-01	-0.3617	2.028	4.61e-02
PositiveLifeEvents.9	0.99833	0.432	2.31297	3.21e-02	0.0949	1.902	1.28e-01
PositiveLifeEvents.NA	-0.00167	0.341	-0.00488	9.96e-01	-0.7159	0.713	6.61e-07

Table 66: cvrt_vs_strange_yr1: Average vs TotalLifeEvents, df=14

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.16e+00	0.454	2.57e+00	0.0224	0.191	2.14	0.00e+00
TotalLifeEvents.10	8.35e-01	0.642	1.30e+00	0.2145	-0.542	2.21	7.09e-02
TotalLifeEvents.11	1.65e-01	0.787	2.10e-01	0.8369	-1.522	1.85	1.43e-03
TotalLifeEvents.12	-1.65e-01	0.787	-2.10e-01	0.8369	-1.852	1.52	1.43e-03
TotalLifeEvents.13	-1.65e-01	0.787	-2.10e-01	0.8369	-1.852	1.52	1.43e-03
TotalLifeEvents.14	-1.65e-01	0.787	-2.10e-01	0.8369	-1.852	1.52	1.43e-03
TotalLifeEvents.15	-1.65e-01	0.787	-2.10e-01	0.8369	-1.852	1.52	1.43e-03
TotalLifeEvents.2	1.70e-01	0.642	2.65e-01	0.7951	-1.207	1.55	2.94e-03
TotalLifeEvents.27	1.17e+00	0.787	1.48e+00	0.1607	-0.522	2.85	7.15e-02
TotalLifeEvents.29	1.17e+00	0.787	1.48e+00	0.1607	-0.522	2.85	7.15e-02
TotalLifeEvents.4	-1.65e-01	0.787	-2.10e-01	0.8369	-1.852	1.52	1.43e-03
TotalLifeEvents.5	6.70e-01	0.642	1.04e+00	0.3145	-0.707	2.05	4.57e-02
TotalLifeEvents.6	3.35e-01	0.642	5.22e-01	0.6101	-1.042	1.71	1.14e-02
TotalLifeEvents.7	-8.25e-02	0.556	-1.48e-01	0.8842	-1.275	1.11	1.29e-03
TotalLifeEvents.8	5.85e-01	0.556	1.05e+00	0.3107	-0.608	1.78	6.46e-02
TotalLifeEvents.NA	3.85e-16	0.556	6.92e-16	1.0000	-1.193	1.19	2.79e-32

Table 67: cvrt_vs_strange_yr1: Average vs Stranger, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.4660	0.159	9.234	5.43e-10	1.141	1.791	0.00000
Stranger	-0.0887	0.225	-0.395	6.96e-01	-0.549	0.371	0.00535

Table 68: cvrt_vs_strange_yr1: Max vs AgeAt1yrVisit, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.24154	1.68008	1.929	0.0639	-0.1999	6.68304	0.0000
AgeAt1yrVisit	-0.00388	0.00431	-0.902	0.3749	-0.0127	0.00494	0.0273

Table 69: cvrt__vs_strange_yr1: Max vs MAGE, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.77631	1.0163	1.7478	0.0915	-0.3055	3.8582	0.00e+00
MAGE	-0.00143	0.0334	-0.0428	0.9661	-0.0699	0.0671	6.33e-05

Table 70: cvrt__vs_strange_yr1: Max vs PAGE, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.69939	0.7824	2.1719	0.0385	0.0966	3.3021	0.00e+00
PAGE	0.00105	0.0236	0.0443	0.9650	-0.0473	0.0494	6.78e-05

Table 71: cvrt__vs_strange_yr1: Max vs MEDUY, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.354	1.2206	0.29	0.774	-2.1462	2.854	0.0000
MEDUY	0.086	0.0755	1.14	0.264	-0.0686	0.241	0.0429

Table 72: cvrt__vs_strange_yr1: Max vs PEDUY, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.343	0.882	3.79	0.000735	1.536	5.149	0.000
PEDUY	-0.104	0.056	-1.85	0.074470	-0.219	0.011	0.106

Table 73: cvrt__vs_strange_yr1: Max vs Income.code, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.6667	0.256	6.502	5.70e-07	1.141	2.193	0.00000
Income.code.LOW	-0.0952	0.422	-0.226	8.23e-01	-0.962	0.771	0.00209
Income.code.MID	0.2424	0.371	0.654	5.19e-01	-0.518	1.003	0.01755

Table 74: cvrt__vs_strange_yr1: Max vs OLDERSIBLINGS, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.857	0.234	7.937	1.21e-08	1.378	2.336	0.0000
OLDERSIBLINGS	-0.232	0.320	-0.725	4.75e-01	-0.888	0.424	0.0178

Table 75: cvrt__vs_strange_yr1: Max vs SEX, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.80	0.484	3.720	0.000885	0.809	2.791	0.000000
SEX	-0.05	0.342	-0.146	0.884856	-0.751	0.651	0.000736

Table 76: cvrt_vs_strange_yr1: Max vs GESTAGEBIRTH, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.24644	5.8382	0.556	0.583	-8.7125	15.2054	0.00000
GESTAGEBIRTH	-0.00549	0.0212	-0.259	0.797	-0.0489	0.0379	0.00231

Table 77: cvrt_vs_strange_yr1: Max vs BW, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.15114	1.470818	-0.103	0.919	-3.163975	2.86169	0.0000
BW	0.00057	0.000443	1.289	0.208	-0.000336	0.00148	0.0542

Table 78: cvrt_vs_strange_yr1: Max vs MaternalInfection, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.947	0.191	10.17	6.58e-11	1.56	2.3395	0.000
MaternalInfection	-0.584	0.316	-1.85	7.54e-02	-1.23	0.0638	0.105

Table 79: cvrt_vs_strange_yr1: Max vs MPSYCH, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.818	0.186	9.784	1.56e-10	1.44	2.199	0.0000
MPSYCH	-0.318	0.360	-0.884	3.84e-01	-1.06	0.419	0.0262

Table 80: cvrt_vs_strange_yr1: Max vs VITAMINDNEO, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.684	0.202	8.331	4.59e-09	1.27	2.098	0.00000
VITAMINDNEO	0.134	0.334	0.401	6.91e-01	-0.55	0.818	0.00552

Table 81: cvrt_vs_strange_yr1: Max vs PrePregBMI, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.619	0.190	8.505	5.51e-09	1.228	2.01	0.0000
PrePregBMI.Obese	0.381	0.646	0.590	5.60e-01	-0.946	1.71	0.0112
PrePregBMI.Overweight	0.548	0.404	1.356	1.87e-01	-0.282	1.38	0.0596
PrePregBMI.Under	-0.619	0.893	-0.693	4.94e-01	-2.454	1.22	0.0153

Table 82: cvrt_vs_strange_yr1: Max vs ANTIBIOTIC_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.625	0.223	7.294	7.60e-08	1.168	2.082	0.00000
ANTIBIOTIC_1yr.1	0.221	0.333	0.665	5.12e-01	-0.462	0.904	0.01531

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
ANTIBIOTIC_1yr.NA	0.375	0.919	0.408	6.86e-01	-1.510	2.260	0.00578

Table 83: cvrt_vs_strange_yr1: Max vs FORMULA_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.647	0.217	7.602	3.55e-08	1.202	2.092	0.00000
FORMULA_1yr.1	0.186	0.337	0.553	5.85e-01	-0.505	0.877	0.01062
FORMULA_1yr.NA	0.353	0.919	0.384	7.04e-01	-1.533	2.239	0.00512

Table 84: cvrt_vs_strange_yr1: Max vs FORMULA_6mo, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.875	0.217	8.624	2.27e-09	1.430	2.320	0.0000
FORMULA_6mo	-0.304	0.318	-0.954	3.48e-01	-0.956	0.348	0.0304

Table 85: cvrt_vs_strange_yr1: Max vs FEVER_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.9524	0.177	11.0106	1.73e-11	1.59	2.316	0.00e+00
FEVER_1yr.1	-0.8274	0.338	-2.4508	2.10e-02	-1.52	-0.135	1.73e-01
FEVER_1yr.NA	0.0476	0.832	0.0573	9.55e-01	-1.66	1.754	9.46e-05

Table 86: cvrt_vs_strange_yr1: Max vs DAYCARE, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.000	0.21	9.53	3.94e-10	1.57	2.4306	0.0000
DAYCARE.1	-0.444	0.35	-1.27	2.15e-01	-1.16	0.2731	0.0511
DAYCARE.NA	-0.800	0.43	-1.86	7.38e-02	-1.68	0.0824	0.1095

Table 87: cvrt_vs_strange_yr1: Max vs CURBRFEED_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.643	0.239	6.870	2.21e-07	1.152	2.134	0.00000
CURBRFEED_1yr.1	0.157	0.332	0.473	6.40e-01	-0.525	0.839	0.00787
CURBRFEED_1yr.NA	0.357	0.926	0.386	7.03e-01	-1.543	2.257	0.00524

Table 88: cvrt_vs_strange_yr1: Max vs Milks_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.00e+00	0.334	5.99e+00	2.19e-06	1.31	2.685	0.00e+00
Milks_1yr.1	-3.64e-01	0.384	-9.48e-01	3.51e-01	-1.15	0.423	3.31e-02

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Milks_1yr.NA	-2.37e-16	0.945	-2.51e-16	1.00e+00	-1.94	1.939	2.32e-33

Table 89: cvrt_vs_strange_yr1: Max vs FrenchFries_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.455	0.263	5.536	7.25e-06	0.915	1.99	0.0000
FrenchFries_1yr.1	0.434	0.334	1.302	2.04e-01	-0.250	1.12	0.0574
FrenchFries_1yr.NA	0.545	0.910	0.599	5.54e-01	-1.322	2.41	0.0122

Table 90: cvrt_vs_strange_yr1: Max vs SweetFoodsDrinks_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.7778	0.299	5.941	2.47e-06	1.164	2.392	0.00000
SweetFoodsDrinks_1yr.1	-0.0778	0.360	-0.216	8.31e-01	-0.817	0.661	0.00172
SweetFoodsDrinks_1yr.NA	0.2222	0.946	0.235	8.16e-01	-1.719	2.164	0.00204

Table 91: cvrt_vs_strange_yr1: Max vs PeanutButter_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.500	0.279	5.375	1.11e-05	0.927	2.07	0.0000
PeanutButter_1yr.1	0.342	0.345	0.992	3.30e-01	-0.365	1.05	0.0345
PeanutButter_1yr.NA	0.500	0.926	0.540	5.93e-01	-1.399	2.40	0.0102

Table 92: cvrt_vs_strange_yr1: Max vs WHSTOTHER, df=22

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.5000	0.651	2.3054	0.031	0.151	2.85	0.000000
WHSTOTHER.3.5 months	-0.5000	1.127	-0.4437	0.662	-2.837	1.84	0.008369
WHSTOTHER.4 months	0.3571	0.738	0.4841	0.633	-1.173	1.89	0.023705
WHSTOTHER.4.5 months	-0.5000	1.127	-0.4437	0.662	-2.837	1.84	0.008369
WHSTOTHER.5 months	0.0714	0.738	0.0968	0.924	-1.459	1.60	0.000948
WHSTOTHER.5.5 months	0.5000	0.920	0.5434	0.592	-1.408	2.41	0.016161
WHSTOTHER.6 months	0.2778	0.719	0.3862	0.703	-1.214	1.77	0.016834
WHSTOTHER.7 months	1.5000	1.127	1.3310	0.197	-0.837	3.84	0.075320

Table 93: cvrt_vs_strange_yr1: Max vs VITAMIND_6mo, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.947	0.192	10.13	1.07e-10	1.55	2.342	0.000
VITAMIND_6mo.1	-0.447	0.353	-1.27	2.16e-01	-1.17	0.277	0.049
VITAMIND_6mo.NA	-0.947	0.520	-1.82	7.98e-02	-2.02	0.120	0.101

Table 94: cvrt_vs_strange_yr1: Max vs Cereals_6mo, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.857	0.338	5.501	7.95e-06	1.164	2.550	0.00000
Cereals_6mo.1	-0.120	0.395	-0.305	7.63e-01	-0.931	0.690	0.00426
Cereals_6mo.NA	-0.357	0.560	-0.638	5.29e-01	-1.506	0.792	0.01867

Table 95: cvrt_vs_strange_yr1: Max vs STATE, df=15

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e+00	0.94	1.06e+00	0.304	-1.003	3.00	0.00e+00
STATE.22	6.67e-01	1.09	6.14e-01	0.548	-1.646	2.98	2.47e-02
STATE.23	1.00e+00	1.15	8.69e-01	0.399	-1.453	3.45	3.84e-02
STATE.24	1.33e+00	1.09	1.23e+00	0.238	-0.980	3.65	9.88e-02
STATE.26	8.12e-16	1.15	7.05e-16	1.000	-2.453	2.45	2.53e-32
STATE.27	7.97e-16	1.33	6.00e-16	1.000	-2.833	2.83	1.27e-32
STATE.29	5.00e-01	1.15	4.34e-01	0.670	-1.953	2.95	9.61e-03
STATE.33	2.00e+00	1.33	1.50e+00	0.153	-0.833	4.83	7.96e-02
STATE.35	1.00e+00	1.15	8.69e-01	0.399	-1.453	3.45	3.84e-02
STATE.38	1.07e-15	1.33	8.02e-16	1.000	-2.833	2.83	2.26e-32
STATE.39	1.00e+00	1.15	8.69e-01	0.399	-1.453	3.45	3.84e-02
STATE.40	1.35e-15	1.15	1.17e-15	1.000	-2.453	2.45	6.96e-32
STATE.41	6.67e-01	1.09	6.14e-01	0.548	-1.646	2.98	2.47e-02
STATE.73	2.00e+00	1.33	1.50e+00	0.153	-0.833	4.83	7.96e-02
STATE.NA	7.50e-01	1.05	7.14e-01	0.486	-1.490	2.99	4.02e-02

Table 96: cvrt_vs_strange_yr1: Max vs TRAIT, df=13

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e+00	0.716	1.40e+00	0.1860	-0.547	2.55	0.00e+00
TRAIT.22	-4.84e-16	1.013	-4.78e-16	1.0000	-2.188	2.19	5.16e-33
TRAIT.24	-6.47e-16	0.877	-7.38e-16	1.0000	-1.895	1.89	1.79e-32
TRAIT.25	-4.53e-16	1.013	-4.47e-16	1.0000	-2.188	2.19	4.52e-33
TRAIT.26	2.00e+00	0.877	2.28e+00	0.0401	0.105	3.89	1.70e-01
TRAIT.27	6.67e-01	0.827	8.06e-01	0.4346	-1.120	2.45	2.74e-02
TRAIT.28	2.00e+00	0.877	2.28e+00	0.0401	0.105	3.89	1.70e-01
TRAIT.29	-8.27e-16	1.013	-8.17e-16	1.0000	-2.188	2.19	1.51e-32
TRAIT.30	2.00e+00	0.877	2.28e+00	0.0401	0.105	3.89	1.70e-01
TRAIT.32	-9.17e-16	1.013	-9.06e-16	1.0000	-2.188	2.19	1.86e-32
TRAIT.33	5.00e-01	0.877	5.70e-01	0.5783	-1.395	2.39	1.07e-02
TRAIT.36	-8.38e-16	1.013	-8.27e-16	1.0000	-2.188	2.19	1.55e-32
TRAIT.39	7.50e-01	0.801	9.37e-01	0.3660	-0.980	2.48	4.45e-02
TRAIT.48	-8.31e-16	1.013	-8.20e-16	1.0000	-2.188	2.19	1.52e-32
TRAIT.49	1.00e+00	1.013	9.87e-01	0.3415	-1.188	3.19	2.21e-02
TRAIT.52	0.00e+00	1.013	0.00e+00	1.0000	-2.188	2.19	0.00e+00
TRAIT.NA	7.50e-01	0.801	9.37e-01	0.3660	-0.980	2.48	4.45e-02

Table 97: cvrt__vs__strange__yr1: Max vs NegativeLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.00e+00	0.464	4.31e+00	0.000374	1.03	2.970	0.00e+00
NegativeLifeEvents.1	-3.33e-01	0.598	-5.57e-01	0.584057	-1.59	0.919	1.66e-02
NegativeLifeEvents.14	-1.00e+00	1.037	-9.65e-01	0.346823	-3.17	1.170	3.01e-02
NegativeLifeEvents.2	1.98e-17	0.598	3.30e-17	1.000000	-1.25	1.253	5.85e-35
NegativeLifeEvents.26	1.00e+00	1.037	9.65e-01	0.346823	-1.17	3.170	3.01e-02
NegativeLifeEvents.3	3.36e-16	0.803	4.18e-16	1.000000	-1.68	1.681	6.56e-33
NegativeLifeEvents.4	-1.00e+00	0.803	-1.25e+00	0.228126	-2.68	0.681	5.82e-02
NegativeLifeEvents.5	-6.45e-17	0.803	-8.03e-17	1.000000	-1.68	1.681	2.42e-34
NegativeLifeEvents.6	-1.00e+00	1.037	-9.65e-01	0.346823	-3.17	1.170	3.01e-02
NegativeLifeEvents.7	-1.00e+00	1.037	-9.65e-01	0.346823	-3.17	1.170	3.01e-02
NegativeLifeEvents.NA	-5.00e-01	0.656	-7.63e-01	0.455038	-1.87	0.872	2.70e-02

Table 98: cvrt__vs__strange__yr1: Max vs PositiveLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.3333	0.319	4.183	0.000505	0.6662	2.001	0.000000
PositiveLifeEvents.11	-0.3333	0.843	-0.395	0.697065	-2.0985	1.432	0.003450
PositiveLifeEvents.12	-0.3333	0.843	-0.395	0.697065	-2.0985	1.432	0.003450
PositiveLifeEvents.25	1.6667	0.843	1.976	0.062831	-0.0985	3.432	0.086247
PositiveLifeEvents.3	1.0000	0.451	2.218	0.038916	0.0565	1.944	0.154175
PositiveLifeEvents.5	0.3333	0.552	0.604	0.553154	-0.8222	1.489	0.009636
PositiveLifeEvents.6	-0.0833	0.504	-0.165	0.870421	-1.1382	0.972	0.000773
PositiveLifeEvents.7	-0.3333	0.843	-0.395	0.697065	-2.0985	1.432	0.003450
PositiveLifeEvents.8	1.6667	0.843	1.976	0.062831	-0.0985	3.432	0.086247
PositiveLifeEvents.9	1.1667	0.638	1.830	0.082984	-0.1677	2.501	0.081608
PositiveLifeEvents.NA	0.1667	0.504	0.331	0.744501	-0.8882	1.222	0.003093

Table 99: cvrt__vs__strange__yr1: Max vs TotalLifeEvents, df=14

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.50e+00	0.620	2.42e+00	0.0297	0.171	2.83	0.00e+00
TotalLifeEvents.10	5.00e-01	0.876	5.71e-01	0.5773	-1.379	2.38	1.36e-02
TotalLifeEvents.11	5.00e-01	1.073	4.66e-01	0.6485	-1.802	2.80	7.05e-03
TotalLifeEvents.12	-5.00e-01	1.073	-4.66e-01	0.6485	-2.802	1.80	7.05e-03
TotalLifeEvents.13	-5.00e-01	1.073	-4.66e-01	0.6485	-2.802	1.80	7.05e-03
TotalLifeEvents.14	-5.00e-01	1.073	-4.66e-01	0.6485	-2.802	1.80	7.05e-03
TotalLifeEvents.15	-5.00e-01	1.073	-4.66e-01	0.6485	-2.802	1.80	7.05e-03
TotalLifeEvents.2	1.03e-15	0.876	1.17e-15	1.0000	-1.879	1.88	5.74e-32
TotalLifeEvents.27	1.50e+00	1.073	1.40e+00	0.1840	-0.802	3.80	6.34e-02
TotalLifeEvents.29	1.50e+00	1.073	1.40e+00	0.1840	-0.802	3.80	6.34e-02
TotalLifeEvents.4	-5.00e-01	1.073	-4.66e-01	0.6485	-2.802	1.80	7.05e-03
TotalLifeEvents.5	1.50e+00	0.876	1.71e+00	0.1090	-0.379	3.38	1.23e-01
TotalLifeEvents.6	5.00e-01	0.876	5.71e-01	0.5773	-1.379	2.38	1.36e-02
TotalLifeEvents.7	-2.50e-01	0.759	-3.29e-01	0.7467	-1.878	1.38	6.32e-03
TotalLifeEvents.8	5.00e-01	0.759	6.59e-01	0.5207	-1.128	2.13	2.53e-02
TotalLifeEvents.NA	8.65e-16	0.759	1.14e-15	1.0000	-1.628	1.63	7.57e-32

Table 100: cvrt_vs_strange_yr1: Max vs Stranger, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.73e+00	0.228	7.60e+00	2.83e-08	1.266	2.201	0.00e+00
Stranger	-1.62e-16	0.323	-5.03e-16	1.00e+00	-0.661	0.661	8.71e-33

Table 101: cvrt_vs_strange_yr1: Episode3.1 vs AgeAt1yrVisit, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.97045	1.27661	2.33	0.0274	0.3554	5.58546	0.0000
AgeAt1yrVisit	-0.00413	0.00327	-1.26	0.2174	-0.0108	0.00257	0.0521

Table 102: cvrt_vs_strange_yr1: Episode3.1 vs MAGE, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.4956	0.7823	1.912	0.0662	-0.107	3.0980	0.00000
MAGE	-0.0043	0.0257	-0.167	0.8686	-0.057	0.0484	0.00096

Table 103: cvrt_vs_strange_yr1: Episode3.1 vs PAGE, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.50013	0.6020	2.492	0.0189	0.2670	2.7332	0.00000
PAGE	-0.00412	0.0182	-0.227	0.8224	-0.0413	0.0331	0.00177

Table 104: cvrt_vs_strange_yr1: Episode3.1 vs MEDUY, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.677	0.9524	0.711	0.483	-1.2740	2.628	0.0000
MEDUY	0.043	0.0589	0.730	0.471	-0.0776	0.164	0.0181

Table 105: cvrt_vs_strange_yr1: Episode3.1 vs PEDUY, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.45	0.6888	3.56	0.00135	1.04	3.8622	0.000
PEDUY	-0.07	0.0438	-1.60	0.12110	-0.16	0.0197	0.081

Table 106: cvrt_vs_strange_yr1: Episode3.1 vs Income.code, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.2500	0.196	6.388	7.66e-07	0.849	1.651	0.000000
Income.code.LOW	0.0357	0.322	0.111	9.13e-01	-0.626	0.697	0.000491

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Income.code.MID	0.2955	0.283	1.044	3.06e-01	-0.285	0.876	0.043626

Table 107: cvrt_vs_strange_yr1: Episode3.1 vs OLDERSIBLINGS, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.3571	0.182	7.4627	3.97e-08	0.985	1.730	0.000000
OLDERSIBLINGS	0.0179	0.249	0.0717	9.43e-01	-0.492	0.528	0.000177

Table 108: cvrt_vs_strange_yr1: Episode3.1 vs SEX, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.30	0.372	3.49	0.00162	0.537	2.06	0.00000
SEX	0.05	0.263	0.19	0.85081	-0.490	0.59	0.00124

Table 109: cvrt_vs_strange_yr1: Episode3.1 vs GESTAGEBIRTH, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.9801	4.4490	1.119	0.272	-4.1332	14.09	0.0000
GESTAGEBIRTH	-0.0131	0.0161	-0.813	0.423	-0.0462	0.02	0.0223

Table 110: cvrt_vs_strange_yr1: Episode3.1 vs BW, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.600473	1.156581	0.519	0.608	-1.768675	2.969621	0.0000
BW	0.000232	0.000348	0.666	0.511	-0.000481	0.000945	0.0151

Table 111: cvrt_vs_strange_yr1: Episode3.1 vs MaternalInfection, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.421	0.155	9.157	6.49e-10	1.103	1.739	0.0000
MaternalInfection	-0.148	0.256	-0.579	5.67e-01	-0.673	0.377	0.0114

Table 112: cvrt_vs_strange_yr1: Episode3.1 vs MPSYCH, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.5	0.137	10.98	1.18e-11	1.22	1.780	0.00
MPSYCH	-0.5	0.265	-1.89	6.92e-02	-1.04	0.042	0.11

Table 113: cvrt_vs_strange_yr1: Episode3.1 vs VITAMINDNEO, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.421	0.155	9.157	6.49e-10	1.103	1.739	0.0000
VITAMINDNEO	-0.148	0.256	-0.579	5.67e-01	-0.673	0.377	0.0114

Table 114: cvrt_vs_strange_yr1: Episode3.1 vs PrePregBMI, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.286	0.149	8.630	4.15e-09	0.979	1.59	0.00000
PrePregBMI.Obese	0.214	0.505	0.424	6.75e-01	-0.824	1.25	0.00596
PrePregBMI.Overweight	0.381	0.316	1.205	2.39e-01	-0.269	1.03	0.04845
PrePregBMI.Under	-0.286	0.699	-0.409	6.86e-01	-1.722	1.15	0.00549

Table 115: cvrt_vs_strange_yr1: Episode3.1 vs ANTIBI-OTIC_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.37500	0.172	7.9796	1.41e-08	1.021	1.729	0.000000
ANTIBIOTIC_1yr.1	0.00962	0.257	0.0374	9.70e-01	-0.518	0.538	0.000049
ANTIBIOTIC_1yr.NA	-0.37500	0.710	-0.5278	6.02e-01	-1.833	1.083	0.009770

Table 116: cvrt_vs_strange_yr1: Episode3.1 vs FORMULA_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.4118	0.167	8.459	4.52e-09	1.069	1.754	0.00000
FORMULA_1yr.1	-0.0784	0.259	-0.302	7.65e-01	-0.611	0.454	0.00318
FORMULA_1yr.NA	-0.4118	0.708	-0.582	5.66e-01	-1.865	1.041	0.01176

Table 117: cvrt_vs_strange_yr1: Episode3.1 vs FORMULA_6mo, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.500	0.166	9.03	8.67e-10	1.160	1.840	0.0000
FORMULA_6mo	-0.286	0.243	-1.18	2.50e-01	-0.784	0.212	0.0455

Table 118: cvrt_vs_strange_yr1: Episode3.1 vs FEVER_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.476	0.146	10.100	1.15e-10	1.176	1.78	0.0000
FEVER_1yr.1	-0.351	0.278	-1.262	2.18e-01	-0.922	0.22	0.0519

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
FEVER_1yr.NA	-0.476	0.686	-0.695	4.93e-01	-1.883	0.93	0.0157

Table 119: cvrt_vs_strange_yr1: Episode3.1 vs DAYCARE, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.500	0.167	9.00	1.29e-09	1.158	1.842	0.0000
DAYCARE.1	-0.167	0.278	-0.60	5.54e-01	-0.737	0.403	0.0124
DAYCARE.NA	-0.500	0.342	-1.46	1.55e-01	-1.201	0.201	0.0738

Table 120: cvrt_vs_strange_yr1: Episode3.1 vs CURBR-FEED_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.3571	0.184	7.371	6.28e-08	0.979	1.735	0.000000
CURBRFEED_1yr.1	0.0429	0.256	0.167	8.68e-01	-0.482	0.568	0.000991
CURBRFEED_1yr.NA	-0.3571	0.713	-0.501	6.21e-01	-1.820	1.106	0.008870

Table 121: cvrt_vs_strange_yr1: Episode3.1 vs Milks_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.4286	0.260	5.488	8.23e-06	0.894	1.963	0.00000
Milks_1yr.1	-0.0649	0.299	-0.217	8.30e-01	-0.678	0.548	0.00177
Milks_1yr.NA	-0.4286	0.736	-0.582	5.65e-01	-1.939	1.082	0.01272

Table 122: cvrt_vs_strange_yr1: Episode3.1 vs FrenchFries_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.273	0.206	6.173	1.34e-06	0.850	1.696	0.00000
FrenchFries_1yr.1	0.172	0.262	0.656	5.17e-01	-0.365	0.709	0.01533
FrenchFries_1yr.NA	-0.273	0.714	-0.382	7.06e-01	-1.738	1.193	0.00519

Table 123: cvrt_vs_strange_yr1: Episode3.1 vs SweetFoods-Drinks_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.222	0.227	5.388	1.08e-05	0.757	1.688	0.00000
SweetFoodsDrinks_1yr.1	0.228	0.273	0.834	4.12e-01	-0.333	0.788	0.02502
SweetFoodsDrinks_1yr.NA	-0.222	0.717	-0.310	7.59e-01	-1.694	1.250	0.00345

Table 124: cvrt_vs_strange_yr1: Episode3.1 vs PeanutButter_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.100	0.208	5.299	1.37e-05	0.6740	1.526	0.000000
PeanutButter_1yr.1	0.426	0.256	1.662	1.08e-01	-0.0999	0.953	0.091919
PeanutButter_1yr.NA	-0.100	0.689	-0.145	8.86e-01	-1.5128	1.313	0.000702

Table 125: cvrt_vs_strange_yr1: Episode3.1 vs WHSTOTHER, df=22

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.50e+00	0.453	3.31e+00	0.00318	0.560	2.440	0.00e+00
WHSTOTHER.3.5 months	-5.00e-01	0.785	-6.37e-01	0.53059	-2.127	1.127	1.53e-02
WHSTOTHER.4 months	7.14e-02	0.514	1.39e-01	0.89068	-0.994	1.137	1.73e-03
WHSTOTHER.4.5 months	-5.00e-01	0.785	-6.37e-01	0.53059	-2.127	1.127	1.53e-02
WHSTOTHER.5 months	-2.14e-01	0.514	-4.17e-01	0.68063	-1.280	0.851	1.56e-02
WHSTOTHER.5.5 months	-4.24e-17	0.641	-6.62e-17	1.00000	-1.329	1.329	2.12e-34
WHSTOTHER.6 months	-3.89e-01	0.501	-7.76e-01	0.44577	-1.428	0.650	6.03e-02
WHSTOTHER.7 months	1.50e+00	0.785	1.91e+00	0.06906	-0.127	3.127	1.38e-01

Table 126: cvrt_vs_strange_yr1: Episode3.1 vs VITAMIND_6mo, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.474	0.154	9.542	3.85e-10	1.157	1.791	0.0000
VITAMIND_6mo.1	-0.224	0.284	-0.788	4.37e-01	-0.806	0.358	0.0209
VITAMIND_6mo.NA	-0.474	0.418	-1.133	2.67e-01	-1.332	0.384	0.0431

Table 127: cvrt_vs_strange_yr1: Episode3.1 vs Cereals_6mo, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.571	0.253	6.202	1.25e-06	1.052	2.091	0.0000
Cereals_6mo.1	-0.203	0.296	-0.685	4.99e-01	-0.811	0.405	0.0199
Cereals_6mo.NA	-0.571	0.420	-1.360	1.85e-01	-1.434	0.291	0.0783

Table 128: cvrt_vs_strange_yr1: Episode3.1 vs STATE, df=15

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e+00	0.756	1.32e+00	0.206	-0.612	2.61	0.00e+00
STATE.22	3.33e-01	0.873	3.82e-01	0.708	-1.528	2.20	1.24e-02
STATE.23	1.53e-15	0.926	1.65e-15	1.000	-1.975	1.97	1.81e-31
STATE.24	1.00e+00	0.873	1.14e+00	0.270	-0.862	2.86	1.12e-01
STATE.26	1.61e-15	0.926	1.73e-15	1.000	-1.975	1.97	1.99e-31
STATE.27	1.61e-15	1.070	1.51e-15	1.000	-2.280	2.28	1.04e-31
STATE.29	1.25e-15	0.926	1.35e-15	1.000	-1.975	1.97	1.20e-31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
STATE.33	1.47e-15	1.070	1.37e-15	1.000	-2.280	2.28	8.60e-32
STATE.35	5.00e-01	0.926	5.40e-01	0.597	-1.475	2.47	1.93e-02
STATE.38	1.41e-15	1.070	1.32e-15	1.000	-2.280	2.28	7.96e-32
STATE.39	1.00e+00	0.926	1.08e+00	0.297	-0.975	2.97	7.72e-02
STATE.40	1.54e-15	0.926	1.66e-15	1.000	-1.975	1.97	1.83e-31
STATE.41	3.33e-01	0.873	3.82e-01	0.708	-1.528	2.20	1.24e-02
STATE.73	1.34e-15	1.070	1.25e-15	1.000	-2.280	2.28	7.16e-32
STATE.NA	7.50e-01	0.846	8.87e-01	0.389	-1.053	2.55	8.07e-02

Table 129: cvrt_vs_strange_yr1: Episode3.1 vs TRAIT, df=13

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e+00	0.630	1.59e+00	0.1367	-0.362	2.36	0.00e+00
TRAIT.22	-7.42e-16	0.892	-8.32e-16	1.0000	-1.926	1.93	2.36e-32
TRAIT.24	-9.45e-16	0.772	-1.22e-15	1.0000	-1.668	1.67	7.39e-32
TRAIT.25	-7.92e-16	0.892	-8.88e-16	1.0000	-1.926	1.93	2.69e-32
TRAIT.26	2.00e+00	0.772	2.59e+00	0.0224	0.332	3.67	3.31e-01
TRAIT.27	3.33e-01	0.728	4.58e-01	0.6546	-1.239	1.91	1.33e-02
TRAIT.28	5.00e-01	0.772	6.48e-01	0.5285	-1.168	2.17	2.07e-02
TRAIT.29	-8.70e-16	0.892	-9.76e-16	1.0000	-1.926	1.93	3.25e-32
TRAIT.30	1.00e+00	0.772	1.30e+00	0.2178	-0.668	2.67	8.29e-02
TRAIT.32	-9.03e-16	0.892	-1.01e-15	1.0000	-1.926	1.93	3.50e-32
TRAIT.33	5.00e-01	0.772	6.48e-01	0.5285	-1.168	2.17	2.07e-02
TRAIT.36	-8.52e-16	0.892	-9.56e-16	1.0000	-1.926	1.93	3.12e-32
TRAIT.39	2.50e-01	0.705	3.55e-01	0.7285	-1.273	1.77	9.62e-03
TRAIT.48	-7.62e-16	0.892	-8.55e-16	1.0000	-1.926	1.93	2.49e-32
TRAIT.49	-1.93e-15	0.892	-2.16e-15	1.0000	-1.926	1.93	1.59e-31
TRAIT.52	-1.12e-15	0.892	-1.26e-15	1.0000	-1.926	1.93	5.43e-32
TRAIT.NA	2.50e-01	0.705	3.55e-01	0.7285	-1.273	1.77	9.62e-03

Table 130: cvrt_vs_strange_yr1: Episode3.1 vs NegativeLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.50e+00	0.378	3.97e+00	0.000815	0.710	2.290	0.00e+00
NegativeLifeEvents.1	-6.02e-17	0.487	-1.23e-16	1.000000	-1.020	1.020	9.13e-34
NegativeLifeEvents.14	-5.00e-01	0.844	-5.92e-01	0.560661	-2.267	1.267	1.27e-02
NegativeLifeEvents.2	-1.67e-01	0.487	-3.42e-01	0.736149	-1.187	0.854	7.00e-03
NegativeLifeEvents.26	-5.00e-01	0.844	-5.92e-01	0.560661	-2.267	1.267	1.27e-02
NegativeLifeEvents.3	-5.00e-01	0.654	-7.65e-01	0.453901	-1.869	0.869	2.45e-02
NegativeLifeEvents.4	-5.00e-01	0.654	-7.65e-01	0.453901	-1.869	0.869	2.45e-02
NegativeLifeEvents.5	5.00e-01	0.654	7.65e-01	0.453901	-0.869	1.869	2.45e-02
NegativeLifeEvents.6	-5.00e-01	0.844	-5.92e-01	0.560661	-2.267	1.267	1.27e-02
NegativeLifeEvents.7	-5.00e-01	0.844	-5.92e-01	0.560661	-2.267	1.267	1.27e-02
NegativeLifeEvents.NA	3.53e-16	0.534	6.62e-16	1.000000	-1.118	1.118	2.27e-32

Table 131: cvrt_vs_strange_yr1: Episode3.1 vs PositiveLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e+00	0.252	3.97e+00	0.000829	0.4722	1.528	0.00e+00
PositiveLifeEvents.11	4.02e-16	0.667	6.03e-16	1.000000	-1.3965	1.396	7.79e-33
PositiveLifeEvents.12	4.03e-16	0.667	6.03e-16	1.000000	-1.3965	1.396	7.81e-33
PositiveLifeEvents.25	1.00e+00	0.667	1.50e+00	0.150366	-0.3965	2.396	4.82e-02
PositiveLifeEvents.3	5.00e-01	0.357	1.40e+00	0.177051	-0.2465	1.246	5.99e-02
PositiveLifeEvents.5	3.98e-16	0.437	9.11e-16	1.000000	-0.9142	0.914	2.13e-32
PositiveLifeEvents.6	2.50e-01	0.399	6.27e-01	0.538134	-0.5846	1.085	1.08e-02
PositiveLifeEvents.7	4.32e-16	0.667	6.48e-16	1.000000	-1.3965	1.396	9.00e-33
PositiveLifeEvents.8	2.00e+00	0.667	3.00e+00	0.007402	0.6035	3.396	1.93e-01
PositiveLifeEvents.9	1.00e+00	0.504	1.98e+00	0.062051	-0.0557	2.056	9.31e-02
PositiveLifeEvents.NA	5.00e-01	0.399	1.25e+00	0.225066	-0.3346	1.335	4.32e-02

Table 132: cvrt_vs_strange_yr1: Episode3.1 vs TotalLifeEvents, df=14

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e+00	0.543	1.84e+00	0.0867	-0.164	2.16	0.00e+00
TotalLifeEvents.10	1.00e+00	0.768	1.30e+00	0.2137	-0.646	2.65	7.48e-02
TotalLifeEvents.11	6.18e-16	0.940	6.57e-16	1.0000	-2.016	2.02	1.48e-32
TotalLifeEvents.12	6.07e-16	0.940	6.46e-16	1.0000	-2.016	2.02	1.43e-32
TotalLifeEvents.13	7.59e-16	0.940	8.07e-16	1.0000	-2.016	2.02	2.23e-32
TotalLifeEvents.14	7.40e-16	0.940	7.87e-16	1.0000	-2.016	2.02	2.12e-32
TotalLifeEvents.15	5.97e-16	0.940	6.35e-16	1.0000	-2.016	2.02	1.38e-32
TotalLifeEvents.2	5.03e-16	0.768	6.56e-16	1.0000	-1.646	1.65	1.90e-32
TotalLifeEvents.27	1.00e+00	0.940	1.06e+00	0.3055	-1.016	3.02	3.88e-02
TotalLifeEvents.29	6.11e-16	0.940	6.50e-16	1.0000	-2.016	2.02	1.45e-32
TotalLifeEvents.4	5.20e-16	0.940	5.54e-16	1.0000	-2.016	2.02	1.05e-32
TotalLifeEvents.5	5.00e-01	0.768	6.51e-01	0.5254	-1.146	2.15	1.87e-02
TotalLifeEvents.6	6.29e-16	0.768	8.20e-16	1.0000	-1.646	1.65	2.97e-32
TotalLifeEvents.7	2.50e-01	0.665	3.76e-01	0.7125	-1.176	1.68	8.69e-03
TotalLifeEvents.8	1.00e+00	0.665	1.50e+00	0.1548	-0.426	2.43	1.39e-01
TotalLifeEvents.NA	5.00e-01	0.665	7.52e-01	0.4644	-0.926	1.93	3.48e-02

Table 133: cvrt_vs_strange_yr1: Episode3.1 vs Stranger, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.533	0.17	9.02	8.89e-10	1.185	1.881	0.0000
Stranger	-0.333	0.24	-1.39	1.76e-01	-0.826	0.159	0.0622

Table 134: cvrt_vs_strange_yr1: Episode3.2 vs AgeAt1yrVisit, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.86391	1.39351	2.06	0.0493	0.00944	5.71837	0.000
AgeAt1yrVisit	-0.00377	0.00357	-1.06	0.3003	-0.01109	0.00355	0.037

Table 135: cvrt_vs_strange_yr1: Episode3.2 vs MAGE, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.8298	0.8434	2.170	0.0387	0.1022	3.5574	0.0000
MAGE	-0.0143	0.0278	-0.516	0.6098	-0.0712	0.0425	0.0091

Table 136: cvrt_vs_strange_yr1: Episode3.2 vs PAGE, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.983	0.6426	3.086	0.00453	0.6670	3.2995	0.0000
PAGE	-0.018	0.0194	-0.928	0.36155	-0.0577	0.0217	0.0288

Table 137: cvrt_vs_strange_yr1: Episode3.2 vs MEDUY, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.9387	1.0359	1.871	0.0718	-0.183	4.0606	0.00000
MEDUY	-0.0336	0.0641	-0.524	0.6041	-0.165	0.0976	0.00939

Table 138: cvrt_vs_strange_yr1: Episode3.2 vs PEDUY, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.7995	0.7313	3.83	0.000665	1.302	4.2975	0.000
PEDUY	-0.0903	0.0465	-1.94	0.062137	-0.185	0.0049	0.115

Table 139: cvrt_vs_strange_yr1: Episode3.2 vs Income.code, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.5000	0.210	7.127	1.15e-07	1.068	1.932	0.0000
Income.code.LOW	0.0714	0.347	0.206	8.38e-01	-0.640	0.783	0.0017
Income.code.MID	-0.3182	0.304	-1.046	3.05e-01	-0.943	0.306	0.0437

Table 140: cvrt_vs_strange_yr1: Episode3.2 vs OLDERSIBLINGS, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.3571	0.197	6.903	1.67e-07	0.954	1.760	0.00000
OLDERSIBLINGS	0.0804	0.269	0.298	7.68e-01	-0.471	0.632	0.00306

Table 141: cvrt_vs_strange_yr1: Episode3.2 vs SEX, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.8	0.396	4.55	9.45e-05	0.990	2.610	0.0000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
SEX	-0.3	0.280	-1.07	2.93e-01	-0.873	0.273	0.0382

Table 142: cvrt_vs_strange_yr1: Episode3.2 vs GESTAGEBIRTH, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.63816	4.8712	0.131	0.897	-9.3401	10.616	0.000000
GESTAGEBIRTH	0.00277	0.0177	0.156	0.877	-0.0334	0.039	0.000843

Table 143: cvrt_vs_strange_yr1: Episode3.2 vs BW, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.725346	1.19572	-0.607	0.5490	-3.17e+00	1.72398	0.0000
BW	0.000643	0.00036	1.788	0.0847	-9.38e-05	0.00138	0.0993

Table 144: cvrt_vs_strange_yr1: Episode3.2 vs MaternalInfection, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.526	0.164	9.29	4.81e-10	1.190	1.863	0.0000
MaternalInfection	-0.344	0.271	-1.27	2.15e-01	-0.901	0.212	0.0526

Table 145: cvrt_vs_strange_yr1: Episode3.2 vs MPSYCH, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.364	0.157	8.71	1.84e-09	1.043	1.684	0.00000
MPSYCH	0.136	0.303	0.45	6.56e-01	-0.485	0.757	0.00693

Table 146: cvrt_vs_strange_yr1: Episode3.2 vs VITAMINDNEO, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.526	0.164	9.29	4.81e-10	1.190	1.863	0.0000
VITAMINDNEO	-0.344	0.271	-1.27	2.15e-01	-0.901	0.212	0.0526

Table 147: cvrt_vs_strange_yr1: Episode3.2 vs PrePregBMI, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.19	0.143	8.298	8.85e-09	0.896	1.49	0.00000
PrePregBMI.Obese	0.81	0.487	1.664	1.08e-01	-0.191	1.81	0.07222
PrePregBMI.Overweight	0.81	0.304	2.660	1.32e-02	0.184	1.44	0.18570

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
PrePregBMI.Under	-0.19	0.673	-0.283	7.79e-01	-1.574	1.19	0.00207

Table 148: cvrt_vs_strange_yr1: Episode3.2 vs ANTIBI-OTIC_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.125	0.170	6.61	4.33e-07	0.7757	1.47	0.0000
ANTIBIOTIC_1yr.1	0.567	0.254	2.23	3.42e-02	0.0456	1.09	0.1432
ANTIBIOTIC_1yr.NA	0.875	0.702	1.25	2.23e-01	-0.5652	2.32	0.0447

Table 149: cvrt_vs_strange_yr1: Episode3.2 vs FORMULA_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.235	0.174	7.08	1.30e-07	0.877	1.593	0.0000
FORMULA_1yr.1	0.348	0.271	1.28	2.10e-01	-0.209	0.905	0.0530
FORMULA_1yr.NA	0.765	0.740	1.03	3.11e-01	-0.754	2.284	0.0344

Table 150: cvrt_vs_strange_yr1: Episode3.2 vs FORMULA_6mo, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.500	0.182	8.237	5.78e-09	1.13	1.873	0.0000
FORMULA_6mo	-0.214	0.267	-0.804	4.28e-01	-0.76	0.332	0.0218

Table 151: cvrt_vs_strange_yr1: Episode3.2 vs FEVER_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.524	0.153	9.973	1.51e-10	1.210	1.8373	0.0000
FEVER_1yr.1	-0.524	0.291	-1.801	8.30e-02	-1.121	0.0731	0.1003
FEVER_1yr.NA	0.476	0.717	0.664	5.12e-01	-0.994	1.9467	0.0137

Table 152: cvrt_vs_strange_yr1: Episode3.2 vs DAYCARE, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.375	0.185	7.436	5.34e-08	0.996	1.754	0.00000
DAYCARE.1	0.181	0.308	0.586	5.63e-01	-0.452	0.813	0.01268
DAYCARE.NA	-0.175	0.379	-0.462	6.48e-01	-0.953	0.603	0.00788

Table 153: cvrt_vs_strange_yr1: Episode3.2 vs CURBR-FEED_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.4286	0.198	7.229	8.94e-08	1.023	1.834	0.00000
CURBRFEED_1yr.1	-0.0952	0.275	-0.347	7.32e-01	-0.659	0.469	0.00419
CURBRFEED_1yr.NA	0.5714	0.765	0.747	4.62e-01	-0.999	2.142	0.01944

Table 154: cvrt_vs_strange_yr1: Episode3.2 vs Milks_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.714	0.270	6.346	8.55e-07	1.16	2.269	0.00000
Milks_1yr.1	-0.442	0.310	-1.424	1.66e-01	-1.08	0.195	0.07133
Milks_1yr.NA	0.286	0.764	0.374	7.11e-01	-1.28	1.853	0.00492

Table 155: cvrt_vs_strange_yr1: Episode3.2 vs FrenchFries_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.182	0.218	5.42	9.95e-06	0.734	1.629	0.0000
FrenchFries_1yr.1	0.318	0.277	1.15	2.61e-01	-0.250	0.886	0.0440
FrenchFries_1yr.NA	0.818	0.756	1.08	2.89e-01	-0.733	2.369	0.0391

Table 156: cvrt_vs_strange_yr1: Episode3.2 vs SweetFoods-Drinks_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.222	0.244	5.002	3.03e-05	0.721	1.724	0.0000
SweetFoodsDrinks_1yr.1	0.228	0.294	0.774	4.46e-01	-0.376	0.831	0.0209
SweetFoodsDrinks_1yr.NA	0.778	0.773	1.007	3.23e-01	-0.808	2.363	0.0354

Table 157: cvrt_vs_strange_yr1: Episode3.2 vs PeanutButter_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.100	0.225	4.89	4.04e-05	0.639	1.561	0.0000
PeanutButter_1yr.1	0.426	0.278	1.54	1.36e-01	-0.143	0.996	0.0758
PeanutButter_1yr.NA	0.900	0.745	1.21	2.38e-01	-0.629	2.429	0.0469

Table 158: cvrt_vs_strange_yr1: Episode3.2 vs WHSTOTHER, df=22

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e+00	0.500	2.00e+00	0.0578	-0.0362	2.04	0.00e+00
WHSTOTHER.3.5 months	8.47e-17	0.865	9.79e-17	1.0000	-1.7947	1.79	3.08e-34

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
WHSTOTHER.4 months	4.29e-01	0.567	7.56e-01	0.4574	-0.7464	1.60	4.38e-02
WHSTOTHER.4.5 months	3.69e-16	0.865	4.27e-16	1.0000	-1.7947	1.79	5.86e-33
WHSTOTHER.5 months	4.29e-01	0.567	7.56e-01	0.4574	-0.7464	1.60	4.38e-02
WHSTOTHER.5.5 months	1.00e+00	0.707	1.42e+00	0.1710	-0.4654	2.47	8.30e-02
WHSTOTHER.6 months	2.22e-01	0.552	4.02e-01	0.6913	-0.9233	1.37	1.38e-02
WHSTOTHER.7 months	2.00e+00	0.865	2.31e+00	0.0306	0.2053	3.79	1.72e-01

Table 159: cvrt_vs_strange_yr1: Episode3.2 vs VITAMIND_6mo, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.579	0.162	9.73	2.54e-10	1.25	1.912	0.0000
VITAMIND_6mo.1	-0.454	0.298	-1.52	1.39e-01	-1.07	0.158	0.0727
VITAMIND_6mo.NA	-0.579	0.439	-1.32	1.99e-01	-1.48	0.323	0.0544

Table 160: cvrt_vs_strange_yr1: Episode3.2 vs Cereals_6mo, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.5714	0.280	5.612	5.92e-06	0.997	2.146	0.00000
Cereals_6mo.1	-0.2556	0.328	-0.780	4.42e-01	-0.928	0.416	0.02778
Cereals_6mo.NA	-0.0714	0.464	-0.154	8.79e-01	-1.024	0.881	0.00108

Table 161: cvrt_vs_strange_yr1: Episode3.2 vs STATE, df=15

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e+00	0.796	1.26e+00	0.2281	-0.696	2.70	0.00e+00
STATE.22	3.33e-01	0.919	3.63e-01	0.7219	-1.625	2.29	1.06e-02
STATE.23	5.00e-01	0.975	5.13e-01	0.6154	-1.577	2.58	1.65e-02
STATE.24	3.33e-01	0.919	3.63e-01	0.7219	-1.625	2.29	1.06e-02
STATE.26	1.30e-15	0.975	1.33e-15	1.0000	-2.077	2.08	1.12e-31
STATE.27	1.51e-15	1.125	1.34e-15	1.0000	-2.399	2.40	7.79e-32
STATE.29	1.13e-15	0.975	1.16e-15	1.0000	-2.077	2.08	8.45e-32
STATE.33	1.22e-15	1.125	1.08e-15	1.0000	-2.399	2.40	5.07e-32
STATE.35	1.00e+00	0.975	1.03e+00	0.3212	-1.077	3.08	6.62e-02
STATE.38	1.21e-15	1.125	1.07e-15	1.0000	-2.399	2.40	5.02e-32
STATE.39	1.00e+00	0.975	1.03e+00	0.3212	-1.077	3.08	6.62e-02
STATE.40	1.24e-15	0.975	1.27e-15	1.0000	-2.077	2.08	1.01e-31
STATE.41	3.33e-01	0.919	3.63e-01	0.7219	-1.625	2.29	1.06e-02
STATE.73	2.00e+00	1.125	1.78e+00	0.0958	-0.399	4.40	1.37e-01
STATE.NA	5.00e-01	0.890	5.62e-01	0.5824	-1.396	2.40	3.07e-02

Table 162: cvrt_vs_strange_yr1: Episode3.2 vs TRAIT, df=13

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e+00	0.851	1.17e+00	0.261	-0.839	2.84	0.00e+00

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
TRAIT.22	1.85e-16	1.204	1.53e-16	1.000	-2.600	2.60	1.08e-33
TRAIT.24	-1.77e-17	1.042	-1.70e-17	1.000	-2.252	2.25	1.91e-35
TRAIT.25	7.07e-17	1.204	5.87e-17	1.000	-2.600	2.60	1.58e-34
TRAIT.26	1.50e+00	1.042	1.44e+00	0.174	-0.752	3.75	1.37e-01
TRAIT.27	3.33e-01	0.983	3.39e-01	0.740	-1.790	2.46	9.79e-03
TRAIT.28	5.00e-01	1.042	4.80e-01	0.639	-1.752	2.75	1.52e-02
TRAIT.29	1.43e-17	1.204	1.18e-17	1.000	-2.600	2.60	6.41e-36
TRAIT.30	1.00e+00	1.042	9.59e-01	0.355	-1.252	3.25	6.09e-02
TRAIT.32	1.15e-16	1.204	9.53e-17	1.000	-2.600	2.60	4.15e-34
TRAIT.33	0.00e+00	1.042	0.00e+00	1.000	-2.252	2.25	0.00e+00
TRAIT.36	0.00e+00	1.204	0.00e+00	1.000	-2.600	2.60	0.00e+00
TRAIT.39	7.50e-01	0.952	7.88e-01	0.445	-1.306	2.81	6.36e-02
TRAIT.48	2.21e-16	1.204	1.84e-16	1.000	-2.600	2.60	1.54e-33
TRAIT.49	-5.89e-16	1.204	-4.90e-16	1.000	-2.600	2.60	1.10e-32
TRAIT.52	6.08e-17	1.204	5.05e-17	1.000	-2.600	2.60	1.17e-34
TRAIT.NA	5.00e-01	0.952	5.25e-01	0.608	-1.556	2.56	2.83e-02

Table 163: cvrt_vs_strange_yr1: Episode3.2 vs NegativeLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.2500	0.361	3.460	0.00262	0.4940	2.006	0.00000
NegativeLifeEvents.1	0.0833	0.466	0.179	0.86007	-0.8927	1.059	0.00161
NegativeLifeEvents.14	-0.2500	0.808	-0.310	0.76030	-1.9406	1.441	0.00293
NegativeLifeEvents.2	0.4167	0.466	0.893	0.38277	-0.5594	1.393	0.04037
NegativeLifeEvents.26	1.7500	0.808	2.167	0.04319	0.0594	3.441	0.14340
NegativeLifeEvents.3	0.2500	0.626	0.400	0.69392	-1.0595	1.560	0.00565
NegativeLifeEvents.4	-0.2500	0.626	-0.400	0.69392	-1.5595	1.060	0.00565
NegativeLifeEvents.5	0.7500	0.626	1.199	0.24537	-0.5595	2.060	0.05086
NegativeLifeEvents.6	-0.2500	0.808	-0.310	0.76030	-1.9406	1.441	0.00293
NegativeLifeEvents.7	-0.2500	0.808	-0.310	0.76030	-1.9406	1.441	0.00293
NegativeLifeEvents.NA	-0.2500	0.511	-0.489	0.63017	-1.3192	0.819	0.01050

Table 164: cvrt_vs_strange_yr1: Episode3.2 vs PositiveLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.167	0.233	5.016	7.67e-05	0.6799	1.653	0.00000
PositiveLifeEvents.11	-0.167	0.615	-0.271	7.89e-01	-1.4546	1.121	0.00140
PositiveLifeEvents.12	-0.167	0.615	-0.271	7.89e-01	-1.4546	1.121	0.00140
PositiveLifeEvents.25	1.833	0.615	2.979	7.71e-03	0.5454	3.121	0.16982
PositiveLifeEvents.3	0.667	0.329	2.027	5.69e-02	-0.0218	1.355	0.11150
PositiveLifeEvents.5	-0.167	0.403	-0.414	6.84e-01	-1.0098	0.676	0.00392
PositiveLifeEvents.6	-0.167	0.368	-0.453	6.56e-01	-0.9364	0.603	0.00503
PositiveLifeEvents.7	-0.167	0.615	-0.271	7.89e-01	-1.4546	1.121	0.00140
PositiveLifeEvents.8	0.833	0.615	1.354	1.92e-01	-0.4546	2.121	0.03509
PositiveLifeEvents.9	1.333	0.465	2.866	9.88e-03	0.3597	2.307	0.17345
PositiveLifeEvents.NA	-0.167	0.368	-0.453	6.56e-01	-0.9364	0.603	0.00503

Table 165: cvrt_vs_strange_yr1: Episode3.2 vs TotalLifeEvents, df=14

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e+00	0.453	2.21e+00	0.0445	0.0281	1.97	0.00e+00
TotalLifeEvents.10	1.00e+00	0.641	1.56e+00	0.1410	-0.3745	2.37	7.36e-02
TotalLifeEvents.11	1.00e+00	0.785	1.27e+00	0.2234	-0.6834	2.68	3.81e-02
TotalLifeEvents.12	4.81e-16	0.785	6.13e-16	1.0000	-1.6834	1.68	8.82e-33
TotalLifeEvents.13	6.55e-16	0.785	8.34e-16	1.0000	-1.6834	1.68	1.63e-32
TotalLifeEvents.14	-1.32e-16	0.785	-1.68e-16	1.0000	-1.6834	1.68	6.63e-34
TotalLifeEvents.15	4.04e-16	0.785	5.15e-16	1.0000	-1.6834	1.68	6.22e-33
TotalLifeEvents.2	5.00e-01	0.641	7.80e-01	0.4483	-0.8745	1.87	1.84e-02
TotalLifeEvents.27	2.00e+00	0.785	2.55e+00	0.0232	0.3166	3.68	1.52e-01
TotalLifeEvents.29	2.00e+00	0.785	2.55e+00	0.0232	0.3166	3.68	1.52e-01
TotalLifeEvents.4	4.42e-16	0.785	5.63e-16	1.0000	-1.6834	1.68	7.44e-33
TotalLifeEvents.5	8.33e-16	0.641	1.30e-15	1.0000	-1.3745	1.37	5.10e-32
TotalLifeEvents.6	5.00e-01	0.641	7.80e-01	0.4483	-0.8745	1.87	1.84e-02
TotalLifeEvents.7	5.91e-16	0.555	1.07e-15	1.0000	-1.1904	1.19	4.78e-32
TotalLifeEvents.8	7.50e-01	0.555	1.35e+00	0.1980	-0.4404	1.94	7.69e-02
TotalLifeEvents.NA	6.49e-16	0.555	1.17e-15	1.0000	-1.1904	1.19	5.76e-32

Table 166: cvrt_vs_strange_yr1: Episode3.2 vs Stranger, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.467	0.189	7.744	1.95e-08	1.079	1.855	0.00000
Stranger	-0.133	0.268	-0.498	6.23e-01	-0.682	0.415	0.00847

Table 167: cvrt_vs_strange_yr1: Episode3.3 vs AgeAt1yrVisit, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.3544	1.60124	1.470	0.153	-0.9256	5.63441	0.00000
AgeAt1yrVisit	-0.0022	0.00411	-0.536	0.596	-0.0106	0.00621	0.00981

Table 168: cvrt_vs_strange_yr1: Episode3.3 vs MAGE, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.9298	0.9563	2.018	0.0533	-0.0290	3.8886	0.0000
MAGE	-0.0143	0.0315	-0.455	0.6525	-0.0788	0.0501	0.0071

Table 169: cvrt_vs_strange_yr1: Episode3.3 vs PAGE, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.60415	0.7386	2.172	0.0385	0.0911	3.1172	0.000000
PAGE	-0.00321	0.0223	-0.144	0.8865	-0.0489	0.0424	0.000716

Table 170: cvrt_vs_strange_yr1: Episode3.3 vs MEDUY, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.0715	1.1762	0.911	0.370	-1.338	3.481	0.00000
MEDUY	0.0267	0.0727	0.367	0.716	-0.122	0.176	0.00463

Table 171: cvrt_vs_strange_yr1: Episode3.3 vs PEDUY, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.424	0.8014	4.27	0.000201	1.783	5.0660	0.00
PEDUY	-0.124	0.0509	-2.44	0.021380	-0.228	-0.0198	0.17

Table 172: cvrt_vs_strange_yr1: Episode3.3 vs Income.code, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.5833	0.243	6.5082	5.61e-07	1.084	2.083	0.00e+00
Income.code.LOW	-0.0119	0.401	-0.0297	9.77e-01	-0.834	0.810	3.63e-05
Income.code.MID	-0.2197	0.352	-0.6245	5.38e-01	-0.942	0.502	1.61e-02

Table 173: cvrt_vs_strange_yr1: Episode3.3 vs OLDERSIBLINGS, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.571	0.222	7.07	1.08e-07	1.116	2.03	0.00000
OLDERSIBLINGS	-0.134	0.304	-0.44	6.63e-01	-0.757	0.49	0.00663

Table 174: cvrt_vs_strange_yr1: Episode3.3 vs SEX, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.30	0.455	2.855	0.00801	0.367	2.23	0.00000
SEX	0.15	0.322	0.466	0.64490	-0.510	0.81	0.00743

Table 175: cvrt_vs_strange_yr1: Episode3.3 vs GESTAGEBIRTH, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.53166	5.52	0.459	0.650	-8.7681	13.8314	0.00000
GESTAGEBIRTH	-0.00375	0.02	-0.187	0.853	-0.0448	0.0373	0.00121

Table 176: cvrt_vs_strange_yr1: Episode3.3 vs BW, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.148281	1.406259	0.105	0.917	-2.732309	3.02887	0.0000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
BW	0.000409	0.000423	0.967	0.342	-0.000458	0.00128	0.0312

Table 177: cvrt_vs_strange_yr1: Episode3.3 vs MaternalInfection, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.632	0.187	8.73	1.78e-09	1.249	2.015	0.0000
MaternalInfection	-0.359	0.309	-1.16	2.55e-01	-0.991	0.274	0.0445

Table 178: cvrt_vs_strange_yr1: Episode3.3 vs MPSYCH, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.55	0.177	8.724	1.79e-09	1.183	1.908	0.00000
MPSYCH	-0.17	0.343	-0.497	6.23e-01	-0.873	0.532	0.00844

Table 179: cvrt_vs_strange_yr1: Episode3.3 vs VITAMINDNEO, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.4737	0.191	7.704	2.16e-08	1.082	1.865	0.00000
VITAMINDNEO	0.0718	0.316	0.227	8.22e-01	-0.575	0.719	0.00178

Table 180: cvrt_vs_strange_yr1: Episode3.3 vs PrePregBMI, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.381	0.179	7.724	3.39e-08	1.013	1.75	0.00000
PrePregBMI.Obese	0.119	0.606	0.196	8.46e-01	-1.127	1.37	0.00123
PrePregBMI.Overweight	0.619	0.379	1.632	1.15e-01	-0.161	1.40	0.08567
PrePregBMI.Under	-0.381	0.839	-0.454	6.53e-01	-2.105	1.34	0.00653

Table 181: cvrt_vs_strange_yr1: Episode3.3 vs ANTIBIOTIC_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.438	0.210	6.852	2.32e-07	1.007	1.868	0.00000
ANTIBIOTIC_1yr.1	0.178	0.313	0.568	5.75e-01	-0.465	0.821	0.01118
ANTIBIOTIC_1yr.NA	-0.437	0.865	-0.506	6.17e-01	-2.212	1.337	0.00888

Table 182: cvrt_vs_strange_yr1: Episode3.3 vs FORMULA_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.294	0.194	6.686	3.55e-07	0.8970	1.69	0.00000
FORMULA_1yr.1	0.539	0.301	1.792	8.43e-02	-0.0782	1.16	0.10139
FORMULA_1yr.NA	-0.294	0.821	-0.358	7.23e-01	-1.9791	1.39	0.00405

Table 183: cvrt_vs_strange_yr1: Episode3.3 vs FORMULA_6mo, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.438	0.208	6.91	1.63e-07	1.01	1.863	0.00000
FORMULA_6mo	0.134	0.304	0.44	6.63e-01	-0.49	0.757	0.00663

Table 184: cvrt_vs_strange_yr1: Episode3.3 vs FEVER_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.714	0.169	10.115	1.11e-10	1.37	2.0620	0.0000
FEVER_1yr.1	-0.714	0.323	-2.214	3.55e-02	-1.38	-0.0522	0.1427
FEVER_1yr.NA	-0.714	0.795	-0.899	3.77e-01	-2.35	0.9168	0.0235

Table 185: cvrt_vs_strange_yr1: Episode3.3 vs DAYCARE, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.687	0.202	8.346	5.89e-09	1.273	2.102	0.0000
DAYCARE.1	-0.243	0.337	-0.721	4.77e-01	-0.934	0.448	0.0175
DAYCARE.NA	-0.688	0.414	-1.659	1.09e-01	-1.538	0.163	0.0924

Table 186: cvrt_vs_strange_yr1: Episode3.3 vs CURBR-FEED_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.571	0.225	6.979	1.68e-07	1.109	2.033	0.00000
CURBRFEED_1yr.1	-0.105	0.313	-0.335	7.40e-01	-0.747	0.538	0.00392
CURBRFEED_1yr.NA	-0.571	0.872	-0.655	5.18e-01	-2.361	1.218	0.01505

Table 187: cvrt_vs_strange_yr1: Episode3.3 vs Milks_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.857	0.310	5.989	2.18e-06	1.22	2.493	0.0000
Milks_1yr.1	-0.448	0.356	-1.258	2.19e-01	-1.18	0.282	0.0550
Milks_1yr.NA	-0.857	0.877	-0.977	3.37e-01	-2.66	0.943	0.0332

Table 188: cvrt_vs_strange_yr1: Episode3.3 vs FrenchFries_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.273	0.247	5.144	2.07e-05	0.765	1.78	0.00000
FrenchFries_1yr.1	0.394	0.314	1.254	2.20e-01	-0.250	1.04	0.05393
FrenchFries_1yr.NA	-0.273	0.857	-0.318	7.53e-01	-2.031	1.49	0.00347

Table 189: cvrt_vs_strange_yr1: Episode3.3 vs SweetFoods-Drinks_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.5556	0.281	5.531	7.35e-06	0.978	2.133	0.000000
SweetFoodsDrinks_1yr.1	-0.0556	0.339	-0.164	8.71e-01	-0.750	0.639	0.000981
SweetFoodsDrinks_1yr.NA	-0.5556	0.889	-0.625	5.37e-01	-2.380	1.269	0.014231

Table 190: cvrt_vs_strange_yr1: Episode3.3 vs PeanutButter_1yr, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.400	0.265	5.273	1.46e-05	0.855	1.945	0.00000
PeanutButter_1yr.1	0.179	0.328	0.546	5.90e-01	-0.494	0.852	0.01072
PeanutButter_1yr.NA	-0.400	0.881	-0.454	6.53e-01	-2.207	1.407	0.00743

Table 191: cvrt_vs_strange_yr1: Episode3.3 vs WHSTOTHER, df=22

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e+00	0.596	1.68e+00	0.1077	-0.237	2.24	0.00e+00
WHSTOTHER.3.5 months	1.41e-16	1.033	1.37e-16	1.0000	-2.142	2.14	6.43e-34
WHSTOTHER.4 months	5.71e-01	0.676	8.45e-01	0.4071	-0.831	1.97	5.85e-02
WHSTOTHER.4.5 months	-4.26e-17	1.033	-4.13e-17	1.0000	-2.142	2.14	5.86e-35
WHSTOTHER.5 months	2.86e-01	0.676	4.23e-01	0.6767	-1.116	1.69	1.46e-02
WHSTOTHER.5.5 months	5.00e-01	0.843	5.93e-01	0.5593	-1.249	2.25	1.56e-02
WHSTOTHER.6 months	6.67e-01	0.659	1.01e+00	0.3228	-0.700	2.03	9.35e-02
WHSTOTHER.7 months	2.00e+00	1.033	1.94e+00	0.0657	-0.142	4.14	1.29e-01

Table 192: cvrt_vs_strange_yr1: Episode3.3 vs VITAMIND_6mo, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.684	0.185	9.09	1.05e-09	1.30	2.064	0.0000
VITAMIND_6mo.1	-0.434	0.340	-1.28	2.13e-01	-1.13	0.264	0.0520
VITAMIND_6mo.NA	-0.684	0.502	-1.36	1.84e-01	-1.71	0.345	0.0594

Table 193: cvrt_vs_strange_yr1: Episode3.3 vs Cereals_6mo, df=27

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.5714	0.321	4.898	0.00004	0.913	2.230	0.000000
Cereals_6mo.1	-0.0977	0.375	-0.260	0.79649	-0.868	0.672	0.003173
Cereals_6mo.NA	-0.0714	0.532	-0.134	0.89419	-1.163	1.020	0.000843

Table 194: cvrt_vs_strange_yr1: Episode3.3 vs STATE, df=15

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e+00	0.869	1.15e+00	0.268	-0.853	2.85	0.00e+00
STATE.22	1.60e-15	1.004	1.60e-15	1.000	-2.139	2.14	1.90e-31
STATE.23	1.00e+00	1.065	9.39e-01	0.362	-1.269	3.27	5.09e-02
STATE.24	6.67e-01	1.004	6.64e-01	0.517	-1.473	2.81	3.27e-02
STATE.26	1.56e-15	1.065	1.46e-15	1.000	-2.269	2.27	1.24e-31
STATE.27	1.74e-15	1.229	1.41e-15	1.000	-2.620	2.62	7.95e-32
STATE.29	5.00e-01	1.065	4.70e-01	0.645	-1.769	2.77	1.27e-02
STATE.33	2.00e+00	1.229	1.63e+00	0.125	-0.620	4.62	1.05e-01
STATE.35	5.00e-01	1.065	4.70e-01	0.645	-1.769	2.77	1.27e-02
STATE.38	1.56e-15	1.229	1.27e-15	1.000	-2.620	2.62	6.38e-32
STATE.39	1.00e+00	1.065	9.39e-01	0.362	-1.269	3.27	5.09e-02
STATE.40	1.56e-15	1.065	1.47e-15	1.000	-2.269	2.27	1.24e-31
STATE.41	3.33e-01	1.004	3.32e-01	0.744	-1.806	2.47	8.18e-03
STATE.73	2.00e+00	1.229	1.63e+00	0.125	-0.620	4.62	1.05e-01
STATE.NA	5.00e-01	0.972	5.14e-01	0.614	-1.571	2.57	2.36e-02

Table 195: cvrt_vs_strange_yr1: Episode3.3 vs TRAIT, df=13

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e+00	0.679	1.47e+00	0.1648	-0.468	2.47	0.00e+00
TRAIT.22	-6.12e-16	0.961	-6.37e-16	1.0000	-2.076	2.08	1.10e-32
TRAIT.24	-6.10e-16	0.832	-7.33e-16	1.0000	-1.798	1.80	2.11e-32
TRAIT.25	-5.52e-16	0.961	-5.74e-16	1.0000	-2.076	2.08	8.94e-33
TRAIT.26	1.00e+00	0.832	1.20e+00	0.2509	-0.798	2.80	5.68e-02
TRAIT.27	-7.54e-16	0.784	-9.61e-16	1.0000	-1.695	1.69	4.66e-32
TRAIT.28	2.00e+00	0.832	2.40e+00	0.0319	0.202	3.80	2.27e-01
TRAIT.29	-7.41e-16	0.961	-7.72e-16	1.0000	-2.076	2.08	1.62e-32
TRAIT.30	2.00e+00	0.832	2.40e+00	0.0319	0.202	3.80	2.27e-01
TRAIT.32	-7.46e-16	0.961	-7.77e-16	1.0000	-2.076	2.08	1.64e-32
TRAIT.33	-2.33e-16	0.832	-2.80e-16	1.0000	-1.798	1.80	3.08e-33
TRAIT.36	-8.38e-16	0.961	-8.72e-16	1.0000	-2.076	2.08	2.06e-32
TRAIT.39	5.00e-01	0.760	6.58e-01	0.5218	-1.141	2.14	2.64e-02
TRAIT.48	-4.75e-16	0.961	-4.94e-16	1.0000	-2.076	2.08	6.63e-33
TRAIT.49	1.00e+00	0.961	1.04e+00	0.3169	-1.076	3.08	2.94e-02
TRAIT.52	-9.73e-16	0.961	-1.01e-15	1.0000	-2.076	2.08	2.78e-32
TRAIT.NA	5.00e-01	0.760	6.58e-01	0.5218	-1.141	2.14	2.64e-02

Table 196: cvrt_vs_strange_yr1: Episode3.3 vs NegativeLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.50e+00	0.427	3.52e+00	0.00231	0.607	2.393	0.00e+00
NegativeLifeEvents.1	-1.90e-16	0.551	-3.45e-16	1.00000	-1.153	1.153	6.56e-33
NegativeLifeEvents.14	-5.00e-01	0.954	-5.24e-01	0.60626	-2.497	1.497	9.15e-03
NegativeLifeEvents.2	1.67e-01	0.551	3.03e-01	0.76548	-0.986	1.319	5.05e-03
NegativeLifeEvents.26	1.50e+00	0.954	1.57e+00	0.13237	-0.497	3.497	8.23e-02
NegativeLifeEvents.3	5.00e-01	0.739	6.77e-01	0.50679	-1.047	2.047	1.77e-02
NegativeLifeEvents.4	-5.00e-01	0.739	-6.77e-01	0.50679	-2.047	1.047	1.77e-02
NegativeLifeEvents.5	5.00e-01	0.739	6.77e-01	0.50679	-1.047	2.047	1.77e-02
NegativeLifeEvents.6	-5.00e-01	0.954	-5.24e-01	0.60626	-2.497	1.497	9.15e-03
NegativeLifeEvents.7	-5.00e-01	0.954	-5.24e-01	0.60626	-2.497	1.497	9.15e-03
NegativeLifeEvents.NA	-5.00e-01	0.603	-8.29e-01	0.41756	-1.763	0.763	3.28e-02

Table 197: cvrt_vs_strange_yr1: Episode3.3 vs PositiveLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.333	0.315	4.229	0.000455	0.6734	1.99	0.00000
PositiveLifeEvents.11	-0.333	0.834	-0.400	0.693922	-2.0794	1.41	0.00432
PositiveLifeEvents.12	-0.333	0.834	-0.400	0.693922	-2.0794	1.41	0.00432
PositiveLifeEvents.25	0.667	0.834	0.799	0.434075	-1.0794	2.41	0.01728
PositiveLifeEvents.3	1.000	0.446	2.243	0.037044	0.0667	1.93	0.19310
PositiveLifeEvents.5	0.333	0.546	0.610	0.548850	-0.8097	1.48	0.01207
PositiveLifeEvents.6	-0.333	0.499	-0.669	0.511777	-1.3768	0.71	0.01550
PositiveLifeEvents.7	-0.333	0.834	-0.400	0.693922	-2.0794	1.41	0.00432
PositiveLifeEvents.8	-0.333	0.834	-0.400	0.693922	-2.0794	1.41	0.00432
PositiveLifeEvents.9	0.667	0.631	1.057	0.303683	-0.6532	1.99	0.03338
PositiveLifeEvents.NA	-0.333	0.499	-0.669	0.511777	-1.3768	0.71	0.01550

Table 198: cvrt_vs_strange_yr1: Episode3.3 vs TotalLifeEvents, df=14

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.50e+00	0.535	2.81e+00	0.0140	0.354	2.646	0.00e+00
TotalLifeEvents.10	5.00e-01	0.756	6.61e-01	0.5191	-1.121	2.121	1.71e-02
TotalLifeEvents.11	-5.00e-01	0.926	-5.40e-01	0.5976	-2.486	1.486	8.85e-03
TotalLifeEvents.12	-5.00e-01	0.926	-5.40e-01	0.5976	-2.486	1.486	8.85e-03
TotalLifeEvents.13	-5.00e-01	0.926	-5.40e-01	0.5976	-2.486	1.486	8.85e-03
TotalLifeEvents.14	-5.00e-01	0.926	-5.40e-01	0.5976	-2.486	1.486	8.85e-03
TotalLifeEvents.15	-5.00e-01	0.926	-5.40e-01	0.5976	-2.486	1.486	8.85e-03
TotalLifeEvents.2	6.57e-16	0.756	8.69e-16	1.0000	-1.621	1.621	2.95e-32
TotalLifeEvents.27	5.00e-01	0.926	5.40e-01	0.5976	-1.486	2.486	8.85e-03
TotalLifeEvents.29	1.50e+00	0.926	1.62e+00	0.1275	-0.486	3.486	7.97e-02
TotalLifeEvents.4	-5.00e-01	0.926	-5.40e-01	0.5976	-2.486	1.486	8.85e-03
TotalLifeEvents.5	1.50e+00	0.756	1.98e+00	0.0672	-0.121	3.121	1.54e-01
TotalLifeEvents.6	5.00e-01	0.756	6.61e-01	0.5191	-1.121	2.121	1.71e-02
TotalLifeEvents.7	-5.00e-01	0.655	-7.64e-01	0.4577	-1.904	0.904	3.17e-02
TotalLifeEvents.8	5.73e-16	0.655	8.76e-16	1.0000	-1.404	1.404	4.17e-32

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
TotalLifeEvents.NA	-5.00e-01	0.655		-7.64e-01	0.4577	-1.904	0.904	3.17e-02

Table 199: cvrt_vs_strange_yr1: Episode3.3 vs Stranger, df=28

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.4	0.214	6.548	4.25e-07	0.962	1.838	0.0000
Stranger	0.2	0.302	0.661	5.14e-01	-0.419	0.819	0.0149
pdf							
2							

Table 200: cvrt_vs_IBQr_yr1: IBQr_fear vs AgeAt1yrVisit, df=25

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.11637	1.9045	0.586	0.563	-2.80605	5.0388	0.0000
AgeAt1yrVisit	0.00535	0.0049	1.092	0.285	-0.00473	0.0154	0.0439

Table 201: cvrt_vs_IBQr_yr1: IBQr_fear vs MAGE, df=25

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.378	1.0753	5.93	3.43e-06	4.163	8.5926	0.000
MAGE	-0.105	0.0348	-3.01	5.96e-03	-0.176	-0.0329	0.258

Table 202: cvrt_vs_IBQr_yr1: IBQr_fear vs PAGE, df=25

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.51	0.9918	3.540	0.0016	1.4687	5.5540	0.00000
PAGE	-0.01	0.0299	-0.334	0.7408	-0.0716	0.0516	0.00428

Table 203: cvrt_vs_IBQr_yr1: IBQr_fear vs MEDUY, df=25

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.198	1.29	4.81	6.15e-05	3.542	8.8542	0.000
MEDUY	-0.189	0.08	-2.36	2.65e-02	-0.353	-0.0239	0.176

Table 204: cvrt_vs_IBQr_yr1: IBQr_fear vs PEDUY, df=25

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.5748	1.0668	4.29	0.000236	2.378	6.7720	0.0000
PEDUY	-0.0878	0.0664	-1.32	0.197823	-0.224	0.0489	0.0631

Table 205: cvrt_vs_IBQr_yr1: IBQr_fear vs Income.code, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.841	0.300	9.463	1.43e-09	2.222	3.46	0.0000
Income.code.LOW	0.760	0.481	1.578	1.28e-01	-0.234	1.75	0.0999
Income.code.MID	0.444	0.448	0.992	3.31e-01	-0.480	1.37	0.0395

Table 206: cvrt_vs_IBQr_yr1: IBQr_fear vs OLDERSIBLINGS, df=25

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.40	0.305	11.15	3.40e-11	2.77	4.028	0.0000
OLDERSIBLINGS	-0.36	0.396	-0.91	3.72e-01	-1.18	0.455	0.0308

Table 207: cvrt_vs_IBQr_yr1: IBQr_fear vs SEX, df=25

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.2427	0.595	5.449	1.17e-05	2.017	4.468	0.000000
SEX	-0.0435	0.433	-0.101	9.21e-01	-0.935	0.848	0.000388

Table 208: cvrt_vs_IBQr_yr1: IBQr_fear vs GESTAGEBIRTH, df=25

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.1343	7.3069	1.250	0.223	-5.9145	24.183	0.0000
GESTAGEBIRTH	-0.0216	0.0265	-0.814	0.423	-0.0762	0.033	0.0249

Table 209: cvrt_vs_IBQr_yr1: IBQr_fear vs BW, df=25

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.14395	1.632408	4.38	0.000188	3.7819	10.505959	0.000
BW	-0.00119	0.000489	-2.44	0.022170	-0.0022	-0.000185	0.186

Table 210: cvrt_vs_IBQr_yr1: IBQr_fear vs MaternalInfection, df=25

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.077	0.247	12.48	3.11e-12	2.569	3.58	0.0000
MaternalInfection	0.296	0.405	0.73	4.72e-01	-0.539	1.13	0.0201

Table 211: cvrt_vs_IBQr_yr1: IBQr_fear vs MPSYCH, df=25

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.148	0.229	13.730	3.80e-13	2.676	3.62	0.00000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
MPSYCH	0.146	0.450	0.325	7.48e-01	-0.781	1.07	0.00404

Table 212: cvrt_vs_IBQr_yr1: IBQr_fear vs VITAMINDNEO, df=25

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.296	0.239	13.777	3.52e-13	2.80	3.788	0.0000
VITAMINDNEO	-0.329	0.414	-0.793	4.35e-01	-1.18	0.525	0.0236

Table 213: cvrt_vs_IBQr_yr1: IBQr_fear vs PrePregBMI, df=23

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.479	0.205	16.935	1.75e-14	3.05	3.904	0.0000
PrePregBMI.Obese	-1.015	0.666	-1.525	1.41e-01	-2.39	0.362	0.0647
PrePregBMI.Overweight	-1.266	0.450	-2.812	9.89e-03	-2.20	-0.335	0.2214
PrePregBMI.Under	0.449	0.919	0.489	6.29e-01	-1.45	2.350	0.0066

Table 214: cvrt_vs_IBQr_yr1: IBQr_fear vs ANTIBIOTIC_1yr, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.428	0.262	13.09	2.02e-12	2.89	3.969	0.0000
ANTIBIOTIC_1yr.1	-0.399	0.385	-1.04	3.11e-01	-1.19	0.396	0.0367
ANTIBIOTIC_1yr.NA	-1.741	1.014	-1.72	9.90e-02	-3.83	0.352	0.1008

Table 215: cvrt_vs_IBQr_yr1: IBQr_fear vs FORMULA_1yr, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.192	0.267	11.946	1.37e-11	2.640	3.743	0.00000
FORMULA_1yr.1	0.113	0.393	0.288	7.76e-01	-0.698	0.925	0.00303
FORMULA_1yr.NA	-1.504	1.035	-1.454	1.59e-01	-3.640	0.632	0.07712

Table 216: cvrt_vs_IBQr_yr1: IBQr_fear vs FORMULA_6mo, df=25

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.009	0.270	11.151	3.40e-11	2.453	3.57	0.0000
FORMULA_6mo	0.368	0.389	0.945	3.54e-01	-0.433	1.17	0.0332

Table 217: cvrt_vs_IBQr_yr1: IBQr_fear vs FEVER_1yr, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.2224	0.230	14.036	4.57e-13	2.749	3.696	0.00000
FEVER_1yr.1	0.0799	0.442	0.181	8.58e-01	-0.833	0.993	0.00117
FEVER_1yr.NA	-1.5349	1.027	-1.495	1.48e-01	-3.654	0.584	0.08005

Table 218: cvrt_vs_IBQr_yr1: IBQr_fear vs DAYCARE, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.35	0.276	12.150	9.67e-12	2.78	3.918	0.0000
DAYCARE.1	-0.28	0.441	-0.635	5.32e-01	-1.19	0.630	0.0162
DAYCARE.NA	-0.47	0.585	-0.803	4.30e-01	-1.68	0.737	0.0260

Table 219: cvrt_vs_IBQr_yr1: IBQr_fear vs CURBRFEED_1yr, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.2753	0.289	11.335	4.03e-11	2.679	3.872	0.000000
CURBRFEED_1yr.1	-0.0583	0.394	-0.148	8.84e-01	-0.871	0.754	0.000803
CURBRFEED_1yr.NA	-1.5878	1.042	-1.524	1.41e-01	-3.738	0.562	0.085182

Table 220: cvrt_vs_IBQr_yr1: IBQr_fear vs Milks_1yr, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.2219	0.378	8.513	1.03e-08	2.441	4.003	0.00000
Milks_1yr.1	0.0301	0.443	0.068	9.46e-01	-0.884	0.944	0.00018
Milks_1yr.NA	-1.5344	1.070	-1.433	1.65e-01	-3.744	0.675	0.08000

Table 221: cvrt_vs_IBQr_yr1: IBQr_fear vs FrenchFries_1yr, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.166	0.288	10.98	7.65e-11	2.571	3.761	0.00000
FrenchFries_1yr.1	0.145	0.393	0.37	7.15e-01	-0.666	0.956	0.00504
FrenchFries_1yr.NA	-1.478	1.039	-1.42	1.68e-01	-3.623	0.667	0.07469

Table 222: cvrt_vs_IBQr_yr1: IBQr_fear vs SweetFoods-Drinks_1yr, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.536	0.347	10.20	3.34e-10	2.82	4.252	0.0000
SweetFoodsDrinks_1yr.1	-0.422	0.417	-1.01	3.21e-01	-1.28	0.438	0.0364
SweetFoodsDrinks_1yr.NA	-1.849	1.040	-1.78	8.82e-02	-4.00	0.298	0.1121

Table 223: cvrt_vs_IBQr_yr1: IBQr_fear vs PeanutButter_1yr, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.2009	0.334	9.594	1.10e-09	2.512	3.890	0.000000
PeanutButter_1yr.1	0.0658	0.413	0.159	8.75e-01	-0.786	0.917	0.000963
PeanutButter_1yr.NA	-1.5134	1.055	-1.434	1.64e-01	-3.691	0.664	0.077996

Table 224: cvrt_vs_IBQr_yr1: IBQr_fear vs WHSTOTHER, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.1875	0.802	3.9742	0.000813	1.51	4.87	0.000000
WHSTOTHER.3.5 months	-0.4732	1.389	-0.3406	0.737111	-3.38	2.43	0.006141
WHSTOTHER.4 months	0.0733	0.982	0.0746	0.941283	-1.98	2.13	0.000522
WHSTOTHER.4.5 months	0.2500	1.389	0.1800	0.859088	-2.66	3.16	0.001714
WHSTOTHER.5 months	-0.2098	0.926	-0.2266	0.823186	-2.15	1.73	0.005850
WHSTOTHER.5.5 months	-0.0670	1.134	-0.0590	0.953539	-2.44	2.31	0.000236
WHSTOTHER.6 months	0.2227	0.879	0.2535	0.802597	-1.62	2.06	0.008895
WHSTOTHER.7 months	-0.9375	1.389	-0.6749	0.507897	-3.85	1.97	0.024101

Table 225: cvrt_vs_IBQr_yr1: IBQr_fear vs VITAMIND_6mo, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.040	0.258	11.78	1.82e-11	2.508	3.57	0.0000
VITAMIND_6mo.1	0.365	0.468	0.78	4.43e-01	-0.601	1.33	0.0239
VITAMIND_6mo.NA	0.346	0.577	0.60	5.54e-01	-0.844	1.54	0.0142

Table 226: cvrt_vs_IBQr_yr1: IBQr_fear vs Cereals_6mo, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.168	0.382	8.294	1.66e-08	2.380	3.957	0.00000
Cereals_6mo.1	-0.153	0.463	-0.330	7.44e-01	-1.108	0.802	0.00557
Cereals_6mo.NA	0.555	0.592	0.938	3.57e-01	-0.666	1.777	0.04493

Table 227: cvrt_vs_IBQr_yr1: IBQr_fear vs STATE, df=12

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.0417	0.439	4.6529	0.000558	1.0856	3.00	0.00e+00
STATE.23	0.1795	0.694	0.2587	0.800246	-1.3321	1.69	8.94e-04
STATE.24	0.9210	0.621	1.4842	0.163539	-0.4310	2.27	3.39e-02
STATE.26	0.9762	0.694	1.4070	0.184784	-0.5354	2.49	2.65e-02
STATE.27	2.5833	0.878	2.9437	0.012287	0.6712	4.50	9.63e-02
STATE.29	2.2083	0.694	3.1830	0.007877	0.6967	3.72	1.35e-01
STATE.33	2.7083	0.878	3.0861	0.009430	0.7962	4.62	1.06e-01
STATE.35	1.0164	0.694	1.4650	0.168637	-0.4953	2.53	2.87e-02

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
STATE.36	2.0298	0.878	2.3129	0.039269	0.1177	3.94	5.95e-02
STATE.38	-0.0417	0.878	-0.0475	0.962912	-1.9538	1.87	2.51e-05
STATE.39	0.6771	0.694	0.9759	0.348367	-0.8346	2.19	1.27e-02
STATE.40	0.9717	0.694	1.4006	0.186655	-0.5399	2.48	2.62e-02
STATE.41	1.5655	0.694	2.2564	0.043491	0.0538	3.08	6.80e-02
STATE.73	3.0298	0.878	3.4524	0.004784	1.1177	4.94	1.32e-01
STATE.NA	1.3213	0.694	1.9045	0.081091	-0.1903	2.83	4.85e-02

Table 228: cvrt_vs_IBQr_yr1: IBQr_fear vs TRAIT, df=10

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.25	1.20	1.043	0.321	-1.419	3.92	0.00000
TRAIT.22	1.04	1.69	0.611	0.555	-2.739	4.81	0.00729
TRAIT.24	1.50	1.69	0.885	0.397	-2.275	5.28	0.01529
TRAIT.25	3.00	1.69	1.771	0.107	-0.775	6.78	0.06115
TRAIT.26	1.92	1.47	1.305	0.221	-1.354	5.18	0.04792
TRAIT.27	1.92	1.38	1.386	0.196	-1.166	5.00	0.06912
TRAIT.28	1.25	1.47	0.852	0.414	-2.019	4.52	0.02042
TRAIT.29	2.19	1.69	1.291	0.226	-1.588	5.96	0.03251
TRAIT.30	2.44	1.38	1.764	0.108	-0.642	5.52	0.11206
TRAIT.32	1.94	1.69	1.144	0.279	-1.838	5.71	0.02550
TRAIT.33	0.75	1.69	0.443	0.667	-3.025	4.53	0.00382
TRAIT.36	2.50	1.69	1.476	0.171	-1.275	6.28	0.04246
TRAIT.39	1.93	1.34	1.440	0.180	-1.056	4.91	0.08942
TRAIT.48	2.68	1.69	1.581	0.145	-1.096	6.45	0.04875
TRAIT.49	3.00	1.69	1.771	0.107	-0.775	6.78	0.06115
TRAIT.52	1.46	1.69	0.864	0.408	-2.311	5.24	0.01457
TRAIT.NA	2.55	1.47	1.741	0.112	-0.714	5.82	0.08529

Table 229: cvrt_vs_IBQr_yr1: IBQr_fear vs NegativeLifeEvents, df=25

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.9628	0.2250	13.17	9.56e-13	2.4994	3.426	0.000
NegativeLifeEvents	0.0629	0.0354	1.77	8.83e-02	-0.0101	0.136	0.108

Table 230: cvrt_vs_IBQr_yr1: IBQr_fear vs PositiveLifeEvents, df=25

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.5082	0.2731	12.85	1.64e-12	2.946	4.0706	0.0000
PositiveLifeEvents	-0.0595	0.0366	-1.63	1.16e-01	-0.135	0.0159	0.0923

Table 231: cvrt_vs_IBQr_yr1: IBQr_fear vs TotalLifeEvents, df=25

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.15068	0.3371	9.35	1.23e-09	2.4564	3.8450	0.000000
TotalLifeEvents	0.00397	0.0305	0.13	8.97e-01	-0.0588	0.0667	0.000653
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Association analysis for diversity vs strange situation or questionaire using linear model

Table 232: strange_vs_diversity_neo: Summed vs chao1, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.1006	1.1433	2.71	0.0117	0.7505	5.451	0.0000
chao1	0.0119	0.0113	1.06	0.3011	-0.0113	0.035	0.0396

Table 233: strange_vs_diversity_neo: Summed vs observed_otus, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.2167	1.1948	2.692	0.0122	0.7608	5.6727	0.0000
observed_otus	0.0176	0.0195	0.904	0.3742	-0.0225	0.0578	0.0294

Table 234: strange_vs_diversity_neo: Summed vs PD_whole_tree, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.639	1.62	1.01	0.322	-1.700	4.98	0.000
PD_whole_tree	0.542	0.33	1.64	0.112	-0.136	1.22	0.091

Table 235: strange_vs_diversity_neo: Summed vs shannon, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.3383	1.634	2.6554	0.0133	0.98	7.70	0.000000
shannon	-0.0325	0.586	-0.0554	0.9563	-1.24	1.17	0.000114

Table 236: strange_vs_diversity_neo: Summed vs wunifrac.PC.1, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.23	0.333	12.71	1.15e-12	3.546	4.91	0.000
wunifrac.PC.1	2.14	1.152	1.86	7.42e-02	-0.225	4.51	0.114

Table 237: strange_vs_diversity_neo: Summed vs wunifrac.PC.2, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.254	0.354	12.015	4.08e-12	3.53	4.98	0.00000
wunifrac.PC.2	0.622	2.557	0.243	8.10e-01	-4.63	5.88	0.00219

Table 238: strange_vs_diversity_neo: Summed vs wunifrac.PC.3, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.246	0.354	11.98	4.35e-12	3.52	4.98	0.00000
wunifrac.PC.3	0.489	2.884	0.17	8.67e-01	-5.44	6.42	0.00106

Table 239: strange_vs_diversity_neo: Summed vs wunifrac.PC.4, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.24	0.337	12.58	1.46e-12	3.55	4.93	0.0000
wunifrac.PC.4	-5.90	3.570	-1.65	1.11e-01	-13.24	1.44	0.0918

Table 240: strange_vs_diversity_neo: Average vs chao1, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.03181	0.38093	2.71	0.0118	0.24880	1.8148	0.0000
chao1	0.00397	0.00375	1.06	0.2995	-0.00374	0.0117	0.0398

Table 241: strange_vs_diversity_neo: Average vs observed_otus, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.06971	0.3981	2.69	0.0124	0.25146	1.8880	0.0000
observed_otus	0.00592	0.0065	0.91	0.3713	-0.00745	0.0193	0.0297

Table 242: strange_vs_diversity_neo: Average vs PD_whole_tree, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.542	0.541	1.00	0.326	-0.5700	1.654	0.0000
PD_whole_tree	0.181	0.110	1.65	0.111	-0.0444	0.407	0.0918

Table 243: strange_vs_diversity_neo: Average vs shannon, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.44251	0.544	2.6495	0.0135	0.323	2.562	0.00e+00
shannon	-0.00971	0.195	-0.0497	0.9607	-0.411	0.392	9.16e-05

Table 244: strange_vs_diversity_neo: Average vs wunifrac.PC.1, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.409	0.111	12.71	1.16e-12	1.1815	1.64	0.000
wunifrac.PC.1	0.714	0.384	1.86	7.42e-02	-0.0749	1.50	0.114

Table 245: strange_vs_diversity_neo: Average vs wunifrac.PC.2, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.418	0.118	12.012	4.10e-12	1.17	1.66	0.00000
wunifrac.PC.2	0.204	0.852	0.239	8.13e-01	-1.55	1.96	0.00211

Table 246: strange_vs_diversity_neo: Average vs wunifrac.PC.3, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.41	0.118	11.978	4.36e-12	1.17	1.66	0.00000
wunifrac.PC.3	0.16	0.961	0.166	8.69e-01	-1.82	2.14	0.00102

Table 247: strange_vs_diversity_neo: Average vs wunifrac.PC.4, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.41	0.112	12.57	1.48e-12	1.18	1.643	0.0000
wunifrac.PC.4	-1.96	1.190	-1.64	1.12e-01	-4.40	0.491	0.0909

Table 248: strange_vs_diversity_neo: Max vs chao1, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.4919	0.54073	2.759	0.0105	0.38042	2.6034	0.00000
chao1	0.0023	0.00533	0.432	0.6696	-0.00865	0.0132	0.00685

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Table 249: strange_vs_diversity_neo: Max vs observed_otus, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.52912	0.56273	2.717	0.0116	0.3724	2.6858	0.00000
observed_otus	0.00316	0.00919	0.344	0.7336	-0.0157	0.0221	0.00436

Table 250: strange_vs_diversity_neo: Max vs PD_whole_tree, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.033	0.781	1.322	0.198	-0.573	2.639	0.0000
PD_whole_tree	0.142	0.159	0.892	0.381	-0.185	0.468	0.0286

Table 251: strange_vs_diversity_neo: Max vs shannon, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.40	0.747	3.207	0.00354	0.860	3.93	0.0000
shannon	-0.25	0.268	-0.934	0.35869	-0.801	0.30	0.0313

Table 252: strange_vs_diversity_neo: Max vs wunifrac.PC.1, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.70	0.154	11.06	2.48e-11	1.3881	2.02	0.00
wunifrac.PC.1	1.02	0.533	1.92	6.60e-02	-0.0728	2.12	0.12

Table 253: strange_vs_diversity_neo: Max vs wunifrac.PC.2, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.720	0.163	10.521	7.29e-11	1.38	2.06	0.0000
wunifrac.PC.2	0.765	1.181	0.648	5.22e-01	-1.66	3.19	0.0153

Table 254: strange_vs_diversity_neo: Max vs wunifrac.PC.3, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.72	0.165	10.432	8.73e-11	1.38	2.06	0.00000
wunifrac.PC.3	-0.38	1.339	-0.283	7.79e-01	-3.13	2.37	0.00297

Table 255: strange_vs_diversity_neo: Max vs wunifrac.PC.4, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.71	0.159	10.78	4.36e-11	1.38	2.04	0.0000
wunifrac.PC.4	-2.38	1.681	-1.41	1.70e-01	-5.83	1.08	0.0689

Table 256: strange_vs_diversity_neo: Episode3.1 vs chao1, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.09850	0.42758	2.569	0.0163	0.21960	1.9774	0.0000
chao1	0.00267	0.00421	0.635	0.5311	-0.00598	0.0113	0.0147

Table 257: strange_vs_diversity_neo: Episode3.1 vs observed_otus, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.2636	0.44741	2.824	0.00898	0.3439	2.1832	0.00000
observed_otus	0.0016	0.00731	0.219	0.82864	-0.0134	0.0166	0.00177

Table 258: strange_vs_diversity_neo: Episode3.1 vs PD_whole_tree, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.0432	0.627	1.665	0.108	-0.245	2.331	0.00000
PD_whole_tree	0.0652	0.127	0.512	0.613	-0.196	0.327	0.00962

Table 259: strange_vs_diversity_neo: Episode3.1 vs shannon, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.101	0.584	3.6	0.00132	0.901	3.302	0.0000
shannon	-0.273	0.210	-1.3	0.20335	-0.704	0.157	0.0593

Table 260: strange_vs_diversity_neo: Episode3.1 vs wunifrac.PC.1, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.352	0.127	10.62	5.96e-11	1.091	1.61	0.0000
wunifrac.PC.1	0.523	0.441	1.19	2.46e-01	-0.383	1.43	0.0495

Table 261: strange_vs_diversity_neo: Episode3.1 vs wunifrac.PC.2, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.361	0.130	10.485	7.83e-11	1.09	1.63	0.0000
wunifrac.PC.2	0.594	0.938	0.634	5.32e-01	-1.33	2.52	0.0147

Table 262: strange_vs_diversity_neo: Episode3.1 vs wunifrac.PC.3, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.37	0.125	10.90	3.39e-11	1.11	1.626	0.0000
wunifrac.PC.3	-1.54	1.021	-1.51	1.42e-01	-3.64	0.554	0.0782

Table 263: strange_vs_diversity_neo: Episode3.1 vs wunifrac.PC.4, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.35	0.127	10.63	5.82e-11	1.09	1.62	0.0000
wunifrac.PC.4	-1.59	1.350	-1.18	2.49e-01	-4.36	1.18	0.0489

Table 264: strange_vs_diversity_neo: Episode3.2 vs chao1, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.84164	0.45535	1.85	0.076	-0.09434	1.7776	0.0000
chao1	0.00607	0.00449	1.35	0.188	-0.00315	0.0153	0.0635

Table 265: strange_vs_diversity_neo: Episode3.2 vs observed_otus, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.7934	0.47199	1.68	0.105	-0.177	1.7635	0.0000
observed_otus	0.0109	0.00771	1.41	0.171	-0.005	0.0267	0.0683

Table 266: strange_vs_diversity_neo: Episode3.2 vs PD_whole_tree, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.322	0.652	0.494	0.6254	-1.0178	1.662	0.0
PD_whole_tree	0.230	0.132	1.735	0.0945	-0.0424	0.502	0.1

Table 267: strange_vs_diversity_neo: Episode3.2 vs shannon, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.876	0.650	1.348	0.189	-0.460	2.212	0.0000
shannon	0.203	0.233	0.871	0.392	-0.276	0.682	0.0273

Table 268: strange_vs_diversity_neo: Episode3.2 vs wunifrac.PC.1, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.422	0.136	10.42	8.92e-11	1.141	1.70	0.000
wunifrac.PC.1	0.753	0.472	1.59	1.23e-01	-0.218	1.72	0.086

Table 269: strange_vs_diversity_neo: Episode3.2 vs wunifrac.PC.2, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.433	0.142	10.083	1.79e-10	1.14	1.72	0.0000
wunifrac.PC.2	0.602	1.026	0.586	5.63e-01	-1.51	2.71	0.0126

Table 270: strange_vs_diversity_neo: Episode3.2 vs wunifrac.PC.3, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.42	0.139	10.2	1.33e-10	1.13	1.70	0.0000
wunifrac.PC.3	1.47	1.128	1.3	2.04e-01	-0.85	3.79	0.0591

Table 271: strange_vs_diversity_neo: Episode3.2 vs wunifrac.PC.4, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.42	0.136	10.48	7.84e-11	1.14	1.703	0.0000
wunifrac.PC.4	-2.40	1.439	-1.67	1.07e-01	-5.36	0.555	0.0936

Table 272: strange_vs_diversity_neo: Episode3.3 vs chao1, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.16047	0.49950	2.323	0.0283	0.13374	2.1872	0.0000
chao1	0.00314	0.00492	0.638	0.5289	-0.00697	0.0133	0.0149

Table 273: strange_vs_diversity_neo: Episode3.3 vs observed_otus, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.1598	0.51946	2.233	0.0344	0.0920	2.2276	0.0000
observed_otus	0.0052	0.00849	0.613	0.5453	-0.0122	0.0226	0.0137

Table 274: strange_vs_diversity_neo: Episode3.3 vs PD_whole_tree, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.273	0.696	0.393	0.6976	-1.1571	1.704	0.000
PD_whole_tree	0.247	0.141	1.749	0.0921	-0.0433	0.538	0.102

Table 275: strange_vs_diversity_neo: Episode3.3 vs shannon, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.361	0.704	1.932	0.0643	-0.0867	2.808	0.000000
shannon	0.038	0.253	0.151	0.8815	-0.4812	0.557	0.000839

Table 276: strange_vs_diversity_neo: Episode3.3 vs wunifrac.PC.1, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.456	0.145	10.07	1.83e-10	1.159	1.75	0.0
wunifrac.PC.1	0.867	0.500	1.73	9.49e-02	-0.161	1.90	0.1

Table 277: strange_vs_diversity_neo: Episode3.3 vs wunifrac.PC.2, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.460	0.152	9.603	4.90e-10	1.15	1.77	0.00
wunifrac.PC.2	-0.574	1.098	-0.523	6.05e-01	-2.83	1.68	0.01

Table 278: strange_vs_diversity_neo: Episode3.3 vs wunifrac.PC.3, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.460	0.152	9.587	5.07e-10	1.15	1.77	0.00000
wunifrac.PC.3	0.565	1.239	0.456	6.52e-01	-1.98	3.11	0.00763

Table 279: strange_vs_diversity_neo: Episode3.3 vs wunifrac.PC.4, df=26

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.46	0.149	9.83	3.03e-10	1.16	1.77	0.0000
wunifrac.PC.4	-1.90	1.575	-1.21	2.38e-01	-5.14	1.33	0.0513

Table 280: strange_vs_diversity_neo: IBQr_fear vs chao1, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.41214	0.6618	3.65	0.00128	1.04635	3.7779	0.0000
chao1	0.00804	0.0066	1.22	0.23449	-0.00557	0.0217	0.0561

Table 281: strange_vs_diversity_neo: IBQr_fear vs observed_otus, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.4959	0.6709	3.72	0.00106	1.111	3.8805	0.0000
observed_otus	0.0119	0.0111	1.07	0.29468	-0.011	0.0347	0.0439

Table 282: strange_vs_diversity_neo: IBQr_fear vs PD_whole_tree, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.214	0.977	2.27	0.0327	0.198	4.230	0.0000
PD_whole_tree	0.203	0.201	1.01	0.3215	-0.211	0.617	0.0394

Table 283: strange_vs_diversity_neo: IBQr_fear vs shannon, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.781	0.980	1.82	0.0818	-0.242	3.80	0.0000
shannon	0.506	0.347	1.46	0.1577	-0.210	1.22	0.0784

Table 284: strange_vs_diversity_neo: IBQr_fear vs wunifrac.PC.1, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.18	0.197	16.10	2.30e-14	2.769	3.58	0.0000
wunifrac.PC.1	1.01	0.700	1.44	1.62e-01	-0.435	2.45	0.0769

Table 285: strange_vs_diversity_neo: IBQr_fear vs wunifrac.PC.2, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.18	0.187	16.98	7.06e-15	2.80	3.569	0.000
wunifrac.PC.2	-2.95	1.331	-2.22	3.64e-02	-5.69	-0.202	0.164

Table 286: strange_vs_diversity_neo: IBQr_fear vs wunifrac.PC.3, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.185	0.206	15.445	5.73e-14	2.76	3.61	0.00000
wunifrac.PC.3	-0.351	1.687	-0.208	8.37e-01	-3.83	3.13	0.00173

Table 287: strange_vs_diversity_neo: IBQr_fear vs wunifrac.PC.4, df=24

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.177	0.208	15.285	7.20e-14	2.75	3.61	0.000000
wunifrac.PC.4	0.345	2.248	0.153	8.79e-01	-4.29	4.98	0.000939

Table 288: strange_vs_diversity_yr1: Summed vs chao1, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.44099	1.5028	2.290	0.0337	0.29557	6.5864	0.000
chao1	0.00353	0.0054	0.655	0.5204	-0.00776	0.0148	0.021

Table 289: strange_vs_diversity_yr1: Summed vs observed_otus, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.14721	1.59806	1.969	0.0637	-0.1976	6.4920	0.0000
observed_otus	0.00779	0.00969	0.804	0.4316	-0.0125	0.0281	0.0313

Table 290: strange_vs_diversity_yr1: Summed vs PD_whole_tree, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.978	2.298	0.861	0.4	-2.83	6.787	0.0000
PD_whole_tree	0.239	0.224	1.065	0.3	-0.23	0.707	0.0537

Table 291: strange_vs_diversity_yr1: Summed vs shannon, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.609	2.63	0.993	0.333	-2.888	8.11	0.0000
shannon	0.411	0.60	0.685	0.502	-0.845	1.67	0.0229

Table 292: strange_vs_diversity_yr1: Summed vs wunifrac.PC.1, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.381	0.449	9.748	7.93e-09	3.44	5.32	0.00000
wunifrac.PC.1	-0.348	1.195	-0.291	7.74e-01	-2.85	2.15	0.00423

Table 293: strange_vs_diversity_yr1: Summed vs wunifrac.PC.2, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.38	0.447	9.799	7.29e-09	3.45	5.32	0.0000
wunifrac.PC.2	-1.49	2.782	-0.534	5.99e-01	-7.31	4.34	0.0141

Table 294: strange_vs_diversity_yr1: Summed vs wunifrac.PC.3, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.38	0.433	10.12	4.36e-09	3.47	5.29	0.0000
wunifrac.PC.3	-4.99	4.001	-1.25	2.27e-01	-13.37	3.38	0.0722

Table 295: strange_vs_diversity_yr1: Summed vs wunifrac.PC.4, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.38	0.427	10.27	3.43e-09	3.49	5.27	0.0000
wunifrac.PC.4	-6.84	4.636	-1.47	1.57e-01	-16.54	2.87	0.0981

Table 296: strange_vs_diversity_yr1: Average vs chao1, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.14615	0.5008	2.288	0.0337	0.09788	2.19442	0.0000
chao1	0.00118	0.0018	0.656	0.5196	-0.00258	0.00494	0.0211

Table 297: strange_vs_diversity_yr1: Average vs observed_otus, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.0482	0.53258	1.968	0.0638	-0.06649	2.16292	0.0000
observed_otus	0.0026	0.00323	0.805	0.4309	-0.00416	0.00936	0.0314

Table 298: strange_vs_diversity_yr1: Average vs PD_whole_tree, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.6587	0.7657	0.86	0.4	-0.9440	2.261	0.0000
PD_whole_tree	0.0796	0.0746	1.07	0.3	-0.0766	0.236	0.0538

Table 299: strange_vs_diversity_yr1: Average vs shannon, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.867	0.875	0.991	0.334	-0.965	2.699	0.0000
shannon	0.137	0.200	0.687	0.500	-0.281	0.556	0.0231

Table 300: strange_vs_diversity_yr1: Average vs wunifrac.PC.1, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.460	0.150	9.747	7.94e-09	1.146	1.774	0.00000
wunifrac.PC.1	-0.115	0.398	-0.289	7.76e-01	-0.949	0.719	0.00416

Table 301: strange_vs_diversity_yr1: Average vs wunifrac.PC.2, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.460	0.149	9.798	7.3e-09	1.15	1.77	0.000
wunifrac.PC.2	-0.495	0.927	-0.534	6.0e-01	-2.44	1.45	0.014

Table 302: strange_vs_diversity_yr1: Average vs wunifrac.PC.3, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.46	0.144	10.12	4.36e-09	1.16	1.76	0.0000
wunifrac.PC.3	-1.67	1.333	-1.25	2.27e-01	-4.46	1.13	0.0724

Table 303: strange_vs_diversity_yr1: Average vs wunifrac.PC.4, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.46	0.142	10.27	3.45e-09	1.16	1.758	0.0000
wunifrac.PC.4	-2.28	1.545	-1.47	1.57e-01	-5.51	0.959	0.0978

Table 304: strange_vs_diversity_yr1: Max vs chao1, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.84103	0.67760	1.24	0.230	-0.57721	2.25926	0.0000
chao1	0.00346	0.00243	1.42	0.171	-0.00163	0.00856	0.0919

Table 305: strange_vs_diversity_yr1: Max vs observed_otus, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.66941	0.71616	0.935	0.362	-0.82952	2.168	0.000
observed_otus	0.00689	0.00434	1.588	0.129	-0.00219	0.016	0.112

Table 306: strange_vs_diversity_yr1: Max vs PD_whole_tree, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.0809	1.0224	-0.0792	0.938	-2.2208	2.059	0.000
PD_whole_tree	0.1830	0.0996	1.8361	0.082	-0.0256	0.392	0.144

Table 307: strange_vs_diversity_yr1: Max vs shannon, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.240	1.195	0.201	0.843	-2.262	2.742	0.000
shannon	0.353	0.273	1.292	0.212	-0.219	0.925	0.077

Table 308: strange_vs_diversity_yr1: Max vs wunifrac.PC.1, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.762	0.208	8.454	7.32e-08	1.33	2.198	0.0000
wunifrac.PC.1	-0.401	0.554	-0.724	4.78e-01	-1.56	0.759	0.0255

Table 309: strange_vs_diversity_yr1: Max vs wunifrac.PC.2, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.762	0.21	8.37	8.44e-08	1.32	2.20	0.00000
wunifrac.PC.2	-0.524	1.31	-0.40	6.93e-01	-3.26	2.22	0.00795

Table 310: strange_vs_diversity_yr1: Max vs wunifrac.PC.3, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.76	0.205	8.59	5.71e-08	1.33	2.19	0.0000
wunifrac.PC.3	-2.05	1.895	-1.08	2.93e-01	-6.01	1.92	0.0552

Table 311: strange_vs_diversity_yr1: Max vs wunifrac.PC.4, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.76	0.20	8.81	3.88e-08	1.34	2.18	0.0000
wunifrac.PC.4	-3.23	2.17	-1.49	1.54e-01	-7.78	1.32	0.0994

Table 312: strange_vs_diversity_yr1: Episode3.1 vs chao1, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.606707	0.556	2.888	0.00942	0.44228	2.77113	0.00000
chao1	-0.000849	0.002	-0.425	0.67570	-0.00503	0.00333	0.00895

Table 313: strange_vs_diversity_yr1: Episode3.1 vs observed_otus, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.502705	0.59700	2.517	0.021	0.25317	2.75224	0.00000
observed_otus	-0.000768	0.00362	-0.212	0.834	-0.00835	0.00681	0.00225

Table 314: strange_vs_diversity_yr1: Episode3.1 vs PD_whole_tree, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.33087	0.8699	1.5299	0.143	-0.490	3.152	0.000000
PD_whole_tree	0.00497	0.0848	0.0586	0.954	-0.172	0.182	0.000172

Table 315: strange_vs_diversity_yr1: Episode3.1 vs shannon, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.6978	0.975	1.74	0.0978	-0.343	3.739	0.00000
shannon	-0.0735	0.223	-0.33	0.7452	-0.540	0.393	0.00541

Table 316: strange_vs_diversity_yr1: Episode3.1 vs wunifrac.PC.1, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.381	0.165	8.386	8.27e-08	1.036	1.73	0.0000
wunifrac.PC.1	0.211	0.438	0.483	6.35e-01	-0.705	1.13	0.0115

Table 317: strange_vs_diversity_yr1: Episode3.1 vs wunifrac.PC.2, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.381	0.163	8.48	7.00e-08	1.04	1.72	0.0000
wunifrac.PC.2	-0.821	1.014	-0.81	4.28e-01	-2.94	1.30	0.0318

Table 318: strange_vs_diversity_yr1: Episode3.1 vs wunifrac.PC.3, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.381	0.165	8.350	8.82e-08	1.03	1.73	0.00000
wunifrac.PC.3	-0.403	1.528	-0.264	7.95e-01	-3.60	2.79	0.00347

Table 319: strange_vs_diversity_yr1: Episode3.1 vs wunifrac.PC.4, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.38	0.161	8.56	6.08e-08	1.04	1.72	0.0000
wunifrac.PC.4	-1.78	1.754	-1.01	3.24e-01	-5.45	1.89	0.0488

Table 320: strange_vs_diversity_yr1: Episode3.2 vs chao1, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.06814	0.557	1.917	0.0704	-0.09794	2.23421	0.0000
chao1	0.00136	0.002	0.677	0.5063	-0.00283	0.00554	0.0224

Table 321: strange_vs_diversity_yr1: Episode3.2 vs observed_otus, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.96159	0.59248	1.62	0.121	-0.27849	2.2017	0.0000
observed_otus	0.00295	0.00359	0.82	0.422	-0.00457	0.0105	0.0326

Table 322: strange_vs_diversity_yr1: Episode3.2 vs PD_whole_tree, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.233	0.8318	0.28	0.783	-1.508	1.974	0.0000
PD_whole_tree	0.119	0.0811	1.46	0.159	-0.051	0.288	0.0969

Table 323: strange_vs_diversity_yr1: Episode3.2 vs shannon, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.916	0.979	0.936	0.361	-1.13	2.965	0.0000
shannon	0.119	0.224	0.531	0.602	-0.35	0.587	0.0139

Table 324: strange_vs_diversity_yr1: Episode3.2 vs wunifrac.PC.1, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.4286	0.167	8.552	6.14e-08	1.079	1.778	0.000000
wunifrac.PC.1	0.0523	0.444	0.118	9.08e-01	-0.878	0.982	0.000691

Table 325: strange_vs_diversity_yr1: Episode3.2 vs wunifrac.PC.2, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.429	0.166	8.618	5.45e-08	1.08	1.78	0.0000
wunifrac.PC.2	-0.576	1.032	-0.558	5.83e-01	-2.74	1.58	0.0154

Table 326: strange_vs_diversity_yr1: Episode3.2 vs wunifrac.PC.3, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.43	0.158	9.02	2.68e-08	1.10	1.760	0.000
wunifrac.PC.3	-2.16	1.463	-1.47	1.57e-01	-5.22	0.906	0.098

Table 327: strange_vs_diversity_yr1: Episode3.2 vs wunifrac.PC.4, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.43	0.153	9.34	1.57e-08	1.11	1.749	0.000
wunifrac.PC.4	-3.18	1.663	-1.91	7.09e-02	-6.66	0.299	0.155

Table 328: strange_vs_diversity_yr1: Episode3.3 vs chao1, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.76614	0.62815	1.22	0.238	-0.54860	2.08088	0.0000
chao1	0.00303	0.00226	1.34	0.195	-0.00169	0.00775	0.0826

Table 329: strange_vs_diversity_yr1: Episode3.3 vs observed_otus, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.68291	0.67003	1.02	0.321	-0.7195	2.0853	0.000
observed_otus	0.00561	0.00406	1.38	0.184	-0.0029	0.0141	0.087

Table 330: strange_vs_diversity_yr1: Episode3.3 vs PD_whole_tree, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.414	0.9866	0.42	0.679	-1.6506	2.479	0.0000
PD_whole_tree	0.115	0.0962	1.19	0.247	-0.0864	0.316	0.0666

Table 331: strange_vs_diversity_yr1: Episode3.3 vs shannon, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00511	1.090	-0.00469	0.996	-2.286	2.275	0.0000
shannon	0.36564	0.249	1.46813	0.158	-0.156	0.887	0.0973

Table 332: strange_vs_diversity_yr1: Episode3.3 vs wunifrac.PC.1, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.571	0.188	8.38	8.36e-08	1.18	1.964	0.00
wunifrac.PC.1	-0.612	0.499	-1.23	2.35e-01	-1.66	0.432	0.07

Table 333: strange_vs_diversity_yr1: Episode3.3 vs wunifrac.PC.2, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.571	0.195	8.0675	1.48e-07	1.16	1.98	0.000000
wunifrac.PC.2	-0.089	1.212	-0.0734	9.42e-01	-2.63	2.45	0.000269

Table 334: strange_vs_diversity_yr1: Episode3.3 vs wunifrac.PC.3, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.57	0.185	8.48	6.92e-08	1.18	1.96	0.0000
wunifrac.PC.3	-2.43	1.711	-1.42	1.71e-01	-6.01	1.15	0.0917

Table 335: strange_vs_diversity_yr1: Episode3.3 vs wunifrac.PC.4, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.57	0.191	8.239	1.08e-07	1.17	1.97	0.0000
wunifrac.PC.4	-1.88	2.072	-0.907	3.76e-01	-6.22	2.46	0.0395

Table 336: strange_vs_diversity_yr1: IBQr_fear vs chao1, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.62094	0.7878	4.60	0.000257	1.95875	5.28312	0.0000
chao1	-0.00227	0.0028	-0.81	0.429078	-0.00817	0.00364	0.0352

Table 337: strange_vs_diversity_yr1: IBQr_fear vs observed_otus, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.64140	0.83407	4.366	0.000421	1.8817	5.40113	0.0000
observed_otus	-0.00397	0.00504	-0.787	0.442307	-0.0146	0.00667	0.0332

Table 338: strange_vs_diversity_yr1: IBQr_fear vs PD_whole_tree, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.1768	1.23	2.588	0.0192	0.587	5.767	0.00000
PD_whole_tree	-0.0163	0.12	-0.136	0.8935	-0.269	0.236	0.00102

Table 339: strange_vs_diversity_yr1: IBQr_fear vs shannon, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.6702	1.379	1.936	0.0697	-0.240	5.581	0.00000
shannon	0.0798	0.316	0.253	0.8035	-0.586	0.746	0.00354

Table 340: strange_vs_diversity_yr1: IBQr_fear vs wunifrac.PC.1, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.01	0.244	12.349	6.48e-10	2.50	3.53	0.0000
wunifrac.PC.1	0.32	0.639	0.501	6.23e-01	-1.03	1.67	0.0138

Table 341: strange_vs_diversity_yr1: IBQr_fear vs wunifrac.PC.2, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.03	0.243	12.474	5.55e-10	2.51	3.54	0.0000
wunifrac.PC.2	-1.09	1.512	-0.719	4.82e-01	-4.28	2.10	0.0279

Table 342: strange_vs_diversity_yr1: IBQr_fear vs wunifrac.PC.3, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.00	0.241	12.429	5.87e-10	2.49	3.51	0.0000
wunifrac.PC.3	-1.76	2.163	-0.812	4.28e-01	-6.32	2.81	0.0353

Table 343: strange_vs_diversity_yr1: IBQr_fear vs wunifrac.PC.4, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.05	0.229	13.33	1.98e-10	2.57	3.54	0.000
wunifrac.PC.4	4.15	2.495	1.66	1.15e-01	-1.11	9.41	0.133

Association analysis for diversity vs strange situation or questionaire using linear mixed effect model

Table 344: diversity_vs_strange_combine_neo: strange_response VS chao1, df=52

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	0.9740112	0.3890177	2.5037710	0.0122878	0.212	1.736	0.000
chao1	0.0039606	0.0037541	1.0550143	0.2914188	-0.003	0.011	0.055

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
episodes2	0.0714286	0.1352703	0.5280432	0.5974694	-0.194	0.337	0.004
episodes3	0.1071429	0.1352703	0.7920648	0.4283229	-0.158	0.372	0.009

Table 345: diversity_vs_strange_combine_neo: strange_response VS observed_otus, df=52

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	1.0127215	0.4058487	2.4953176	0.0125844	0.217	1.808	0.000
observed_otus	0.0058832	0.0065069	0.9041477	0.3659171	-0.007	0.019	0.041
episodes2	0.0714286	0.1352703	0.5280432	0.5974694	-0.194	0.337	0.004
episodes3	0.1071429	0.1352703	0.7920648	0.4283229	-0.158	0.372	0.010

Table 346: diversity_vs_strange_combine_neo: strange_response VS PD_whole_tree, df=52

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	0.4867037	0.5469789	0.8898034	0.3735715	-0.585	1.559	0.000
PD_whole_tree	0.1806947	0.1099387	1.6435955	0.1002598	-0.035	0.396	0.117
episodes2	0.0714286	0.1352703	0.5280432	0.5974694	-0.194	0.337	0.004
episodes3	0.1071429	0.1352703	0.7920648	0.4283229	-0.158	0.372	0.009

Table 347: diversity_vs_strange_combine_neo: strange_response VS shannon, df=52

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	1.3865860	0.5501706	2.5202839	0.0117260	0.308	2.465	0.000
shannon	-0.0108180	0.1953424	-0.0553796	0.9558360	-0.394	0.372	0.000
episodes2	0.0714286	0.1352703	0.5280432	0.5974694	-0.194	0.337	0.004
episodes3	0.1071429	0.1352703	0.7920648	0.4283229	-0.158	0.372	0.010

Table 348: diversity_vs_strange_combine_neo: strange_response VS wunifrac.PC.1, df=52

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	1.3505494	0.1356560	9.9556922	0.0000000	1.085	1.616	0.000
wunifrac.PC.1	0.7142536	0.3838906	1.8605654	0.0628056	-0.038	1.467	0.142
episodes2	0.0714286	0.1352703	0.5280432	0.5974694	-0.194	0.337	0.004
episodes3	0.1071429	0.1352703	0.7920648	0.4283229	-0.158	0.372	0.009

Table 349: diversity_vs_strange_combine_neo: strange_response VS wunifrac.PC.2, df=52

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	1.3586203	0.1415333	9.5992971	0.0000000	1.081	1.636	0.000

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
wunifrac.PC.2	0.2073472	0.8524837	0.2432271	0.8078295	-1.463	1.878	0.003
episodes2	0.0714286	0.1352703	0.5280432	0.5974694	-0.194	0.337	0.004
episodes3	0.1071429	0.1352703	0.7920648	0.4283229	-0.158	0.372	0.010

Table 350: diversity_vs_strange_combine_neo: strange_response
VS wunifrac.PC.3, df=52

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	1.3559568	0.1416333	9.5737170	0.0000000	1.078	1.634	0.000
wunifrac.PC.3	0.1629746	0.9614696	0.1695057	0.8653989	-1.721	2.047	0.002
episodes2	0.0714286	0.1352703	0.5280432	0.5974694	-0.194	0.337	0.004
episodes3	0.1071429	0.1352703	0.7920648	0.4283229	-0.158	0.372	0.010

Table 351: diversity_vs_strange_combine_neo: strange_response
VS wunifrac.PC.4, df=52

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	1.3531794	0.1367836	9.8928454	0.0000000	1.085	1.621	0.000
wunifrac.PC.4	-1.9656273	1.1901437	-1.6515881	0.0986185	-4.298	0.367	0.118
episodes2	0.0714286	0.1352703	0.5280432	0.5974694	-0.194	0.337	0.004
episodes3	0.1071429	0.1352703	0.7920648	0.4283229	-0.158	0.372	0.009

Table 352: diversity_vs_strange_combine_yr1: strange_response
VS chao1, df=38

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	1.0676301	0.5089944	2.097528	0.0359468	0.070	2.065	0.000
chao1	0.0011781	0.0017989	0.654902	0.5125309	-0.002	0.005	0.035
episodes2	0.0476190	0.1562505	0.304761	0.7605482	-0.259	0.354	0.002
episodes3	0.1904762	0.1562505	1.219044	0.2228275	-0.116	0.497	0.030

Table 353: diversity_vs_strange_combine_yr1: strange_response
VS observed_otus, df=38

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	0.9697042	0.5402721	1.794844	0.0726786	-0.089	2.029	0.000
observed_otus	0.0025954	0.0032301	0.803511	0.4216795	-0.004	0.009	0.051
episodes2	0.0476190	0.1562505	0.304761	0.7605482	-0.259	0.354	0.002
episodes3	0.1904762	0.1562505	1.219044	0.2228275	-0.116	0.497	0.029

Table 354: diversity_vs_strange_combine_yr1: strange_response
VS PD_whole_tree, df=38

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	0.5799314	0.7711660	0.7520189	0.4520397	-0.932	2.091	0.000
PD_whole_tree	0.0795239	0.0746428	1.0653923	0.2866984	-0.067	0.226	0.085
episodes2	0.0476190	0.1562505	0.3047610	0.7605482	-0.259	0.354	0.002
episodes3	0.1904762	0.1562505	1.2190439	0.2228275	-0.116	0.497	0.028

Table 355: diversity_vs_strange_combine_yr1: strange_response
VS shannon, df=38

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	0.7902569	0.8800134	0.8980055	0.3691826	-0.935	2.515	0.000
shannon	0.1369971	0.2000863	0.6846899	0.4935396	-0.255	0.529	0.038
episodes2	0.0476190	0.1562505	0.3047610	0.7605482	-0.259	0.354	0.002
episodes3	0.1904762	0.1562505	1.2190439	0.2228275	-0.116	0.497	0.030

Table 356: diversity_vs_strange_combine_yr1: strange_response
VS wunifrac.PC.1, df=38

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	1.3809524	0.1748738	7.8968529	0.0000000	1.038	1.724	0.000
wunifrac.PC.1	-0.1161617	0.3984997	-0.2914975	0.7706708	-0.897	0.665	0.007
episodes2	0.0476190	0.1562505	0.3047610	0.7605482	-0.259	0.354	0.002
episodes3	0.1904762	0.1562505	1.2190439	0.2228275	-0.116	0.497	0.031

Table 357: diversity_vs_strange_combine_yr1: strange_response
VS wunifrac.PC.2, df=38

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	1.3809524	0.1742054	7.9271484	0.0000000	1.040	1.722	0.000
wunifrac.PC.2	-0.4954845	0.9273999	-0.5342727	0.5931529	-2.313	1.322	0.024
episodes2	0.0476190	0.1562505	0.3047610	0.7605482	-0.259	0.354	0.002
episodes3	0.1904762	0.1562505	1.2190439	0.2228275	-0.116	0.497	0.030

Table 358: diversity_vs_strange_combine_yr1: strange_response
VS wunifrac.PC.3, df=38

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	1.3809524	0.1702184	8.112825	0.0000000	1.047	1.715	0.000
wunifrac.PC.3	-1.6640483	1.3338193	-1.247581	0.2121843	-4.278	0.950	0.111
episodes2	0.0476190	0.1562505	0.304761	0.7605482	-0.259	0.354	0.002
episodes3	0.1904762	0.1562505	1.219044	0.2228275	-0.116	0.497	0.027

Table 359: diversity_vs_strange_combine_yr1: strange_response VS wunifrac.PC.4, df=38

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	1.3809524	0.1684215	8.199385	0.0000000	1.051	1.711	0.000
wunifrac.PC.4	-2.2790695	1.5453973	-1.474747	0.1402807	-5.308	0.750	0.144
episodes2	0.0476190	0.1562505	0.304761	0.7605482	-0.259	0.354	0.002
episodes3	0.1904762	0.1562505	1.219044	0.2228275	-0.116	0.497	0.026

Association analysis for diversity vs picrust using linear model

Table 360: diversity_vs_picrust_L1_neo: wunifrac.PC.1 vs L1.Cellular.Processes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.02e-02	9.48e-02	0.951	0.349	-1.04e-01	2.84e-01	0.0000
L1.Cellular.Processes	-4.94e-08	4.36e-08	-1.133	0.266	-1.38e-07	3.97e-08	0.0397

Table 361: diversity_vs_picrust_L1_neo: wunifrac.PC.1 vs L1.Environmental.Information.Processing, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.03e-02	8.27e-02	-0.246	0.807	-1.89e-01	1.49e-01	0.00000
L1.Environmental.Information.Processing	1.39e-09	4.37e-09	0.319	0.752	-7.53e-09	1.03e-08	0.00327

Table 362: diversity_vs_picrust_L1_neo: wunifrac.PC.1 vs L1.Genetic.Information.Processing, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.62e-02	1.13e-01	-0.232	0.818	-2.57e-01	2.05e-01	0.0000
L1.Genetic.Information.Processing	1.57e-09	6.01e-09	0.261	0.795	-1.07e-08	1.38e-08	0.0022

Table 363: diversity_vs_picrust_L1_neo: wunifrac.PC.1 vs L1.Human.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.27e-02	9.15e-02	0.138	0.891	-1.74e-01	2.00e-01	0.00000
L1.Human.Diseases	-1.74e-08	1.03e-07	-0.169	0.867	-2.28e-07	1.93e-07	0.00092

Table 364: diversity_vs_picrust_L1_neo: wunifrac.PC.1 vs L1.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.79e-02	1.00e-01	0.378	0.708	-1.67e-01	2.43e-01	0.00000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L1.Metabolism	-8.96e-10	2.02e-09	-0.444	0.661	-5.02e-09	3.23e-09	0.00631

Table 365: diversity_vs_picrust_L1_neo: wunifrac.PC.1 vs L1.None, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.04e-02	8.45e-02	0.832	0.412	-1.02e-01	2.43e-01	0.0000
L1.None	-5.83e-07	5.54e-07	-1.052	0.301	-1.72e-06	5.49e-07	0.0345

Table 366: diversity_vs_picrust_L1_neo: wunifrac.PC.1 vs L1.Organismal.Systems, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.48e-01	1.08e-01	1.37	0.182	-7.30e-02	3.68e-01	0.0000
L1.Organismal.Systems	-2.91e-07	1.88e-07	-1.55	0.132	-6.75e-07	9.32e-08	0.0717

Table 367: diversity_vs_picrust_L1_neo: wunifrac.PC.1 vs L1.Unclassified, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.18e-02	9.05e-02	0.462	0.648	-1.43e-01	2.27e-01	0.0000
L1.Unclassified	-3.18e-09	5.62e-09	-0.566	0.576	-1.47e-08	8.30e-09	0.0102

Table 368: diversity_vs_picrust_L1_neo: wunifrac.PC.2 vs L1.Cellular.Processes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.21e-03	4.56e-02	-0.0922	0.927	-9.74e-02	8.90e-02	0.000000
L1.Cellular.Processes	2.31e-09	2.10e-08	0.1098	0.913	-4.06e-08	4.52e-08	0.000389

Table 369: diversity_vs_picrust_L1_neo: wunifrac.PC.2 vs L1.Environmental.Information.Processing, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.72e-02	3.88e-02	0.443	0.661	-6.21e-02	9.65e-02	0.0000
L1.Environmental.Information.Processing	-1.18e-09	2.05e-09	-0.574	0.570	-5.37e-09	3.01e-09	0.0105

Table 370: diversity_vs_picrust_L1_neo: wunifrac.PC.2 vs L1.Genetic.Information.Processing, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.08e-02	5.34e-02	-0.203	0.841	-1.20e-01	9.82e-02	0.00000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L1.Genetic.Information.Processing	6.48e-10	2.83e-09	0.229	0.821	-5.14e-09	6.44e-09	0.00168

Table 371: diversity_vs_picrust_L1_neo: wunifrac.PC.2 vs L1.Human.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.54e-02	4.28e-02	0.594	0.557	-6.20e-02	1.13e-01	0.0000
L1.Human.Diseases	-3.50e-08	4.82e-08	-0.725	0.474	-1.33e-07	6.34e-08	0.0167

Table 372: diversity_vs_picrust_L1_neo: wunifrac.PC.2 vs L1.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.88e-02	4.73e-02	0.399	0.693	-7.77e-02	1.15e-01	0.00000
L1.Metabolism	-4.46e-10	9.52e-10	-0.468	0.643	-2.39e-09	1.50e-09	0.00701

Table 373: diversity_vs_picrust_L1_neo: wunifrac.PC.2 vs L1.None, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.08e-02	4.05e-02	-0.268	0.791	-9.35e-02	7.18e-02	0.00000
L1.None	8.99e-08	2.66e-07	0.339	0.737	-4.52e-07	6.32e-07	0.00369

Table 374: diversity_vs_picrust_L1_neo: wunifrac.PC.2 vs L1.Organismal.Systems, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.52e-02	5.21e-02	0.869	0.392	-6.11e-02	1.52e-01	0.0000
L1.Organismal.Systems	-8.93e-08	9.07e-08	-0.984	0.333	-2.74e-07	9.60e-08	0.0303

Table 375: diversity_vs_picrust_L1_neo: wunifrac.PC.2 vs L1.Unclassified, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.00e-02	4.27e-02	0.468	0.643	-6.72e-02	1.07e-01	0.0000
L1.Unclassified	-1.52e-09	2.65e-09	-0.573	0.571	-6.93e-09	3.89e-09	0.0105

Table 376: diversity_vs_picrust_L1_neo: wunifrac.PC.3 vs L1.Cellular.Processes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.99e-03	4.10e-02	-0.0971	0.923	-8.78e-02	7.98e-02	0.000000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L1.Cellular.Processes	2.18e-09	1.89e-08	0.1157	0.909	-3.64e-08	4.07e-08	0.000432

Table 377: diversity_vs_picrust_L1_neo: wunifrac.PC.3 vs L1.Environmental.Information.Processing, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.26e-02	3.43e-02	-0.951	0.349	-1.03e-01	3.74e-02	0.0000
L1.Environmental.Information.Processing	2.23e-09	1.81e-09	1.231	0.228	-1.47e-09	5.92e-09	0.0466

Table 378: diversity_vs_picrust_L1_neo: wunifrac.PC.3 vs L1.Genetic.Information.Processing, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.38e-02	4.56e-02	-1.62	0.1157	-1.67e-01	1.92e-02	0.0000
L1.Genetic.Information.Processing	4.43e-09	2.42e-09	1.83	0.0773	-5.15e-10	9.37e-09	0.0974

Table 379: diversity_vs_picrust_L1_neo: wunifrac.PC.3 vs L1.Human.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.19e-02	3.70e-02	-1.40	0.1711	-1.28e-01	2.37e-02	0.0000
L1.Human.Diseases	7.15e-08	4.17e-08	1.71	0.0969	-1.37e-08	1.57e-07	0.0866

Table 380: diversity_vs_picrust_L1_neo: wunifrac.PC.3 vs L1.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.41e-02	4.04e-02	-1.59	0.1227	-1.47e-01	1.83e-02	0.000
L1.Metabolism	1.52e-09	8.14e-10	1.86	0.0722	-1.45e-10	3.18e-09	0.101

Table 381: diversity_vs_picrust_L1_neo: wunifrac.PC.3 vs L1.None, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.48e-02	3.56e-02	-0.978	0.336	-1.08e-01	3.79e-02	0.000
L1.None	2.89e-07	2.33e-07	1.237	0.226	-1.88e-07	7.66e-07	0.047

Table 382: diversity_vs_picrust_L1_neo: wunifrac.PC.3 vs L1.Organismal.Systems, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.99e-02	4.53e-02	-1.54	0.1338	-1.62e-01	2.27e-02	0.0000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L1.Organismal.Systems	1.38e-07	7.90e-08	1.74	0.0912	-2.35e-08	2.99e-07	0.0894

Table 383: diversity_vs_picrust_L1_neo: wunifrac.PC.3 vs L1.Unclassified, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.10e-02	3.69e-02	-1.38	0.1763	-1.26e-01	2.42e-02	0.0000
L1.Unclassified	3.89e-09	2.29e-09	1.70	0.0999	-7.89e-10	8.56e-09	0.0851

Table 384: diversity_vs_picrust_L1_neo: wunifrac.PC.4 vs L1.Cellular.Processes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.89e-02	2.79e-02	-3.19	0.003357	-1.46e-01	-3.19e-02	0.000
L1.Cellular.Processes	4.87e-08	1.28e-08	3.80	0.000667	2.25e-08	7.49e-08	0.317

Table 385: diversity_vs_picrust_L1_neo: wunifrac.PC.4 vs L1.Environmental.Information.Processing, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.58e-02	2.59e-02	-2.16	0.03908	-1.09e-01	-2.98e-03	0.000
L1.Environmental.Information.Processing	3.82e-09	1.37e-09	2.80	0.00896	1.03e-09	6.60e-09	0.201

Table 386: diversity_vs_picrust_L1_neo: wunifrac.PC.4 vs L1.Genetic.Information.Processing, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.61e-02	3.55e-02	-2.42	0.0216	-1.59e-01	-1.35e-02	0.000
L1.Genetic.Information.Processing	5.16e-09	1.89e-09	2.74	0.0103	1.31e-09	9.01e-09	0.195

Table 387: diversity_vs_picrust_L1_neo: wunifrac.PC.4 vs L1.Human.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.44e-02	2.87e-02	-2.24	0.0323	-1.23e-01	-5.81e-03	0.000
L1.Human.Diseases	8.86e-08	3.23e-08	2.74	0.0101	2.27e-08	1.55e-07	0.195

Table 388: diversity_vs_picrust_L1_neo: wunifrac.PC.4 vs L1.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.18e-02	3.17e-02	-2.26	0.0311	-1.37e-01	-6.95e-03	0.000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L1.Metabolism	1.70e-09	6.39e-10	2.65	0.0126	3.91e-10	3.00e-09	0.185

Table 389: diversity_vs_picrust_L1_neo: wunifrac.PC.4 vs L1.None, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.06e-02	2.37e-02	-3.39	0.001955	-1.29e-01	-3.21e-02	0.000
L1.None	6.68e-07	1.56e-07	4.29	0.000171	3.50e-07	9.86e-07	0.373

Table 390: diversity_vs_picrust_L1_neo: wunifrac.PC.4 vs L1.Organismal.Systems, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.70e-02	3.60e-02	-2.14	0.0405	-1.50e-01	-3.54e-03	0.000
L1.Organismal.Systems	1.52e-07	6.26e-08	2.42	0.0216	2.39e-08	2.80e-07	0.159

Table 391: diversity_vs_picrust_L1_neo: wunifrac.PC.4 vs L1.Unclassified, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.94e-02	2.79e-02	-2.49	0.01856	-1.26e-01	-1.25e-02	0.000
L1.Unclassified	5.28e-09	1.73e-09	3.05	0.00473	1.75e-09	8.81e-09	0.231

Table 392: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Amino.Acid.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.60e-02	1.01e-01	0.356	0.724	-1.71e-01	2.43e-01	0.00000
L2.Amino.Acid.Metabolism	-4.39e-09	1.05e-08	-0.416	0.680	-2.59e-08	1.71e-08	0.00556

Table 393: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Biosynthesis.of.Other.Secondary.Metabolites, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.33e-01	9.97e-02	1.34	0.192	-7.04e-02	3.37e-01	0.0000
L2.Biosynthesis.of.Other.Secondary.Metabolites	-1.72e-07	1.11e-07	-1.55	0.131	-3.99e-07	5.45e-08	0.0721

Table 394: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Cancers, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.43e-02	7.93e-02	0.811	0.424	-9.77e-02	2.26e-01	0.0000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Cancers	-8.70e-07	8.14e-07	-1.069	0.294	-2.53e-06	7.93e-07	0.0355

Table 395: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Carbohydrate.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.16e-02	9.41e-02	0.442	0.662	-1.51e-01	2.34e-01	0.00000
L2.Carbohydrate.Metabolism	-4.18e-09	7.86e-09	-0.532	0.599	-2.02e-08	1.19e-08	0.00905

Table 396: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Cardiovascular.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.04025	0.05624	-0.716	0.480	-0.155104	0.07461	0.0000
L2.Cardiovascular.Diseases	0.00256	0.00157	1.624	0.115	-0.000659	0.00577	0.0784

Table 397: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Cell.Communication, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 398: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Cell.Growth.and.Death, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.42e-02	1.30e-01	-0.573	0.571	-3.39e-01	1.90e-01	0.0000
L2.Cell.Growth.and.Death	1.87e-07	2.99e-07	0.626	0.536	-4.24e-07	7.99e-07	0.0125

Table 399: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Cell.Motility, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.16e-02	7.95e-02	0.775	0.444	-1.01e-01	2.24e-01	0.0000
L2.Cell.Motility	-5.20e-08	5.09e-08	-1.021	0.315	-1.56e-07	5.19e-08	0.0326

Table 400: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Cellular.Processes.and.Signaling, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.35e-02	8.42e-02	0.635	0.530	-1.19e-01	2.25e-01	0.0000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Cellular.Processes.and.Signaling	-1.39e-08	1.72e-08	-0.808	0.425	-4.90e-08	2.12e-08	0.0206

Table 401: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Circulatory.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.45e-02	5.62e-02	0.258	0.798	-1.00e-01	0.129284	0.0000
L2.Circulatory.System	-2.35e-05	3.35e-05	-0.700	0.489	-9.19e-05	0.000045	0.0156

Table 402: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Digestive.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.49e-01	8.46e-02	1.76	0.0895	-2.43e-02	3.21e-01	0.00
L2.Digestive.System	-3.69e-06	1.71e-06	-2.15	0.0395	-7.18e-06	-1.89e-07	0.13

Table 403: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Endocrine.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.38e-01	1.11e-01	1.25	0.222	-8.78e-02	3.64e-01	0.00
L2.Endocrine.System	-6.70e-07	4.76e-07	-1.41	0.170	-1.64e-06	3.03e-07	0.06

Table 404: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Energy.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.30e-02	1.04e-01	0.414	0.682	-1.69e-01	2.55e-01	0.00000
L2.Energy.Metabolism	-8.99e-09	1.87e-08	-0.480	0.635	-4.72e-08	2.93e-08	0.00738

Table 405: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Environmental.Adaptation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.27e-02	1.03e-01	0.317	0.753	-1.78e-01	2.43e-01	0.00000
L2.Environmental.Adaptation	-2.99e-07	8.09e-07	-0.369	0.715	-1.95e-06	1.35e-06	0.00438

Table 406: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Enzyme.Families, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.22e-03	1.04e-01	0.031	0.975	-2.09e-01	2.15e-01	0.00e+00

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Enzyme.Families	-1.61e-09	4.47e-08	-0.036	0.971	-9.28e-08	8.96e-08	4.19e-05

Table 407: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Excretory.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.92e-02	6.71e-02	0.584	0.564	-9.79e-02	1.76e-01	0.0000
L2.Excretory.System	-1.55e-06	1.68e-06	-0.921	0.364	-4.99e-06	1.89e-06	0.0267

Table 408: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Folding..Sorting.and.Degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.23e-02	1.07e-01	0.209	0.836	-1.96e-01	2.40e-01	0.00000
L2.Folding..Sorting.and.Degradation	-1.07e-08	4.44e-08	-0.240	0.812	-1.01e-07	8.01e-08	0.00186

Table 409: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Genetic.Information.Processing, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.30e-02	1.02e-01	-0.127	0.900	-2.22e-01	1.96e-01	0.000000
L2.Genetic.Information.Processing	5.52e-09	3.73e-08	0.148	0.883	-7.06e-08	8.16e-08	0.000707

Table 410: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Glycan.Biosynthesis.and.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.79e-02	9.96e-02	0.983	0.333	-1.05e-01	3.01e-01	0.0000
L2.Glycan.Biosynthesis.and.Metabolism	-4.35e-08	3.78e-08	-1.149	0.260	-1.21e-07	3.38e-08	0.0408

Table 411: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Immune.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.83e-01	8.17e-02	2.24	0.0323	1.65e-02	3.50e-01	0.000
L2.Immune.System	-3.64e-06	1.33e-06	-2.75	0.0101	-6.35e-06	-9.34e-07	0.196

Table 412: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Immune.System.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.45e-02	1.17e-01	-0.638	0.528	-3.13e-01	1.64e-01	0.0000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Immune.System.Diseases	1.32e-06	1.86e-06	0.714	0.481	-2.46e-06	5.11e-06	0.0162

Table 413: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Infectious.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.55e-03	8.65e-02	0.0179	0.986	-1.75e-01	1.78e-01	0.00e+00
L2.Infectious.Diseases	-3.90e-09	1.72e-07	-0.0226	0.982	-3.56e-07	3.48e-07	1.65e-05

Table 414: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Lipid.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.70e-02	9.66e-02	0.383	0.705	-1.60e-01	2.34e-01	0.00000
L2.Lipid.Metabolism	-1.49e-08	3.26e-08	-0.456	0.652	-8.15e-08	5.18e-08	0.00665

Table 415: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Membrane.Transport, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.59e-02	8.22e-02	-0.316	0.754	-1.94e-01	1.42e-01	0.0000
L2.Membrane.Transport	2.02e-09	4.92e-09	0.410	0.685	-8.03e-09	1.21e-08	0.0054

Table 416: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Metabolic.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.6e-03	1.19e-01	-0.0302	0.976	-2.47e-01	2.40e-01	0.00e+00
L2.Metabolic.Diseases	4.2e-08	1.25e-06	0.0336	0.973	-2.51e-06	2.59e-06	3.65e-05

Table 417: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.25e-02	8.52e-02	0.616	0.543	-1.22e-01	2.26e-01	0.0000
L2.Metabolism	-2.11e-08	2.71e-08	-0.778	0.443	-7.66e-08	3.43e-08	0.0192

Table 418: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Metabolism.of.Cofactors.and.Vitamins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.05e-02	1.01e-01	0.502	0.619	-1.55e-01	2.56e-01	0.000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Metabolism.of.Cofactors.and.Vitamins	-1.35e-08	2.29e-08	-0.588	0.561	-6.03e-08	3.34e-08	0.011

Table 419: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Metabolism.of.Other.Amino.Acids, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.21e-02	9.35e-02	0.344	0.733	-1.59e-01	2.23e-01	0.00000
L2.Metabolism.of.Other.Amino.Acids	-2.18e-08	5.25e-08	-0.415	0.681	-1.29e-07	8.55e-08	0.00553

Table 420: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Metabolism.of.Terpenoids.and.Polyketides, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.05e-02	1.03e-01	0.491	0.627	-1.60e-01	2.60e-01	0.0000
L2.Metabolism.of.Terpenoids.and.Polyketides	-3.57e-08	6.26e-08	-0.570	0.573	-1.64e-07	9.22e-08	0.0104

Table 421: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Nervous.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.46e-01	1.09e-01	1.34	0.189	-7.61e-02	3.69e-01	0.0000
L2.Nervous.System	-1.96e-06	1.29e-06	-1.52	0.139	-4.59e-06	6.76e-07	0.0692

Table 422: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Neurodegenerative.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.34e-02	8.24e-02	0.284	0.778	-1.45e-01	1.92e-01	0.00000
L2.Neurodegenerative.Diseases	-2.08e-07	5.65e-07	-0.368	0.715	-1.36e-06	9.46e-07	0.00436

Table 423: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Nucleotide.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.89e-02	1.17e-01	-0.418	0.679	-2.88e-01	1.90e-01	0.00000
L2.Nucleotide.Metabolism	1.38e-08	2.95e-08	0.468	0.643	-4.65e-08	7.42e-08	0.00701

Table 424: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Poorly.Characterized, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.01e-02	9.36e-02	0.429	0.671	-1.51e-01	2.31e-01	0.00000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Poorly.Characterized	-9.01e-09	1.74e-08	-0.518	0.608	-4.46e-08	2.65e-08	0.00857

Table 425: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Replication.and.Repair, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.00e-02	1.20e-01	-0.334	0.741	-2.84e-01	2.04e-01	0.00000
L2.Replication.and.Repair	5.43e-09	1.46e-08	0.372	0.713	-2.44e-08	3.53e-08	0.00443

Table 426: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Sensory.System, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 427: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Signal.Transduction, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.78e-02	8.01e-02	0.347	0.731	-1.36e-01	1.91e-01	0.00000
L2.Signal.Transduction	-1.79e-08	3.90e-08	-0.460	0.649	-9.77e-08	6.18e-08	0.00677

Table 428: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Signaling.Molecules.and.Interaction, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.67e-02	1.28e-01	-0.756	0.455	-3.58e-01	1.64e-01	0.0000
L2.Signaling.Molecules.and.Interaction	4.51e-07	5.45e-07	0.828	0.414	-6.61e-07	1.56e-06	0.0216

Table 429: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Transcription, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.89e-02	8.84e-02	0.326	0.746	-1.52e-01	2.09e-01	0.00000
L2.Transcription	-1.13e-08	2.77e-08	-0.406	0.688	-6.79e-08	4.54e-08	0.00529

Table 430: diversity_vs_picrust_L2_neo: wunifrac.PC.1 vs L2.Translation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.48e-02	1.18e-01	-0.800	0.43	-3.37e-01	1.47e-01	0.000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Translation	2.03e-08	2.28e-08	0.891	0.38	-2.63e-08	6.69e-08	0.025

Table 431:   diversity_vs_picrust_L2_neo: wunifrac.PC.1   vs
L2.Transport.and.Catabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.245087	8.93e-02	2.74	0.01016	6.26e-02	4.28e-01	0.000
L2.Transport.and.Catabolism	-0.000001	3.15e-07	-3.19	0.00334	-1.65e-06	-3.61e-07	0.247

Table 432:   diversity_vs_picrust_L2_neo: wunifrac.PC.1   vs
L2.Xenobiotics.Biodegradation.and.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.69e-03	8.31e-02	0.0925	0.927	-1.62e-01	1.77e-01	0.0000
L2.Xenobiotics.Biodegradation.and.Metabolism	-4.60e-09	3.85e-08	-0.1196	0.906	-8.32e-08	7.40e-08	0.0004

Table 433:   diversity_vs_picrust_L2_neo: wunifrac.PC.2   vs
L2.Amino.Acid.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.35e-02	4.77e-02	0.283	0.779	-8.40e-02	1.11e-01	0.00000
L2.Amino.Acid.Metabolism	-1.65e-09	4.97e-09	-0.331	0.743	-1.18e-08	8.51e-09	0.00353

Table 434:   diversity_vs_picrust_L2_neo: wunifrac.PC.2   vs
L2.Biosynthesis.of.Other.Secondary.Metabolites, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.12e-02	4.80e-02	0.858	0.398	-5.69e-02	1.39e-01	0.000
L2.Biosynthesis.of.Other.Secondary.Metabolites	-5.33e-08	5.35e-08	-0.996	0.327	-1.63e-07	5.60e-08	0.031

Table 435:   diversity_vs_picrust_L2_neo: wunifrac.PC.2   vs
L2.Cancers, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.19e-03	3.81e-02	-0.0312	0.975	-7.90e-02	7.66e-02	0.00e+00
L2.Cancers	1.61e-08	3.91e-07	0.0411	0.967	-7.83e-07	8.15e-07	5.45e-05

Table 436:   diversity_vs_picrust_L2_neo: wunifrac.PC.2   vs
L2.Carbohydrate.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.71e-02	4.42e-02	0.614	0.544	-6.31e-02	1.17e-01	0.0000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Carbohydrate.Metabolism	-2.73e-09	3.69e-09	-0.740	0.465	-1.03e-08	4.80e-09	0.0173

Table 437: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Cardiovascular.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.24e-03	0.027644	0.0449	0.964	-0.05521	0.0577	0.000000
L2.Cardiovascular.Diseases	-7.88e-05	0.000774	-0.1019	0.920	-0.00166	0.0015	0.000335

Table 438: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Cell.Communication, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 439: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Cell.Growth.and.Death, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.97e-02	6.06e-02	-0.819	0.419	-1.74e-01	7.42e-02	0.0000
L2.Cell.Growth.and.Death	1.25e-07	1.40e-07	0.895	0.378	-1.61e-07	4.12e-07	0.0252

Table 440: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Cell.Motility, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.97e-03	3.81e-02	-0.183	0.856	-8.47e-02	7.08e-02	0.00000
L2.Cell.Motility	5.88e-09	2.44e-08	0.241	0.811	-4.39e-08	5.57e-08	0.00188

Table 441: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Cellular.Processes.and.Signaling, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.46e-02	3.97e-02	0.619	0.541	-5.65e-02	1.06e-01	0.0000
L2.Cellular.Processes.and.Signaling	-6.39e-09	8.11e-09	-0.788	0.437	-2.29e-08	1.02e-08	0.0196

Table 442: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Circulatory.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.19e-02	2.60e-02	0.459	0.650	-0.041241	6.51e-02	0.0000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Circulatory.System	-1.93e-05	1.55e-05	-1.243	0.224	-0.000051	1.24e-05	0.0475

Table 443: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Digestive.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.47e-02	4.03e-02	1.60	0.1193	-1.77e-02	1.47e-01	0.000
L2.Digestive.System	-1.61e-06	8.16e-07	-1.97	0.0585	-3.27e-06	6.13e-08	0.111

Table 444: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Endocrine.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.25e-02	5.11e-02	1.61	0.1168	-2.18e-02	1.87e-01	0.0000
L2.Endocrine.System	-4.00e-07	2.20e-07	-1.82	0.0788	-8.49e-07	4.89e-08	0.0965

Table 445: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Energy.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.65e-02	4.90e-02	0.336	0.739	-8.36e-02	1.17e-01	0.00000
L2.Energy.Metabolism	-3.44e-09	8.84e-09	-0.390	0.700	-2.15e-08	1.46e-08	0.00487

Table 446: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Environmental.Adaptation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.91e-02	4.85e-02	-0.395	0.696	-1.18e-01	7.99e-02	0.00000
L2.Environmental.Adaptation	1.75e-07	3.81e-07	0.459	0.650	-6.03e-07	9.53e-07	0.00674

Table 447: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Enzyme.Families, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.20e-02	4.88e-02	0.247	0.807	-8.76e-02	1.12e-01	0.00000
L2.Enzyme.Families	-6.02e-09	2.10e-08	-0.286	0.777	-4.90e-08	3.69e-08	0.00264

Table 448: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Excretory.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.48e-02	3.18e-02	0.465	0.645	-5.02e-02	7.98e-02	0.0000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Excretory.System	-5.85e-07	7.97e-07	-0.734	0.469	-2.21e-06	1.04e-06	0.0171

Table 449: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Folding..Sorting.and.Degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.49e-02	5.02e-02	0.297	0.769	-8.77e-02	1.17e-01	0.00000
L2.Folding..Sorting.and.Degradation	-7.14e-09	2.09e-08	-0.341	0.735	-4.99e-08	3.56e-08	0.00374

Table 450: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Genetic.Information.Processing, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.15e-03	4.82e-02	0.128	0.899	-9.23e-02	1.05e-01	0.000000
L2.Genetic.Information.Processing	-2.62e-09	1.76e-08	-0.149	0.883	-3.85e-08	3.32e-08	0.000715

Table 451: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Glycan.Biosynthesis.and.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.42e-02	4.77e-02	0.507	0.616	-7.32e-02	1.22e-01	0.0000
L2.Glycan.Biosynthesis.and.Metabolism	-1.07e-08	1.81e-08	-0.592	0.558	-4.77e-08	2.63e-08	0.0112

Table 452: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Immune.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.73e-03	4.31e-02	-0.0866	0.932	-9.17e-02	8.42e-02	0.000000
L2.Immune.System	7.41e-08	6.99e-07	0.1060	0.916	-1.35e-06	1.50e-06	0.000362

Table 453: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Immune.System.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.46e-03	5.55e-02	0.0443	0.965	-1.11e-01	1.16e-01	0.0e+00
L2.Immune.System.Diseases	-4.36e-08	8.82e-07	-0.0495	0.961	-1.84e-06	1.76e-06	7.9e-05

Table 454: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Infectious.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.97e-02	4.02e-02	0.739	0.465	-5.24e-02	1.12e-01	0.0000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Infectious.Diseases	-7.46e-08	8.01e-08	-0.932	0.359	-2.38e-07	8.89e-08	0.0272

Table 455: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Lipid.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.72e-02	4.53e-02	0.601	0.552	-6.53e-02	1.20e-01	0.0000
L2.Lipid.Metabolism	-1.10e-08	1.53e-08	-0.716	0.480	-4.22e-08	2.03e-08	0.0163

Table 456: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Membrane.Transport, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.55e-02	3.87e-02	0.400	0.692	-6.35e-02	9.44e-02	0.00000
L2.Membrane.Transport	-1.20e-09	2.31e-09	-0.519	0.607	-5.93e-09	3.53e-09	0.00863

Table 457: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Metabolic.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.60e-03	5.61e-02	-0.171	0.865	-1.24e-01	1.05e-01	0.00000
L2.Metabolic.Diseases	1.12e-07	5.88e-07	0.191	0.850	-1.09e-06	1.31e-06	0.00117

Table 458: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.40e-02	4.02e-02	0.598	0.554	-5.80e-02	1.06e-01	0.0000
L2.Metabolism	-9.68e-09	1.28e-08	-0.756	0.455	-3.58e-08	1.65e-08	0.0181

Table 459: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Metabolism.of.Cofactors.and.Vitamins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.58e-03	4.77e-02	0.0542	0.957	-9.48e-02	1.00e-01	0.00000
L2.Metabolism.of.Cofactors.and.Vitamins	-6.90e-10	1.09e-08	-0.0634	0.950	-2.29e-08	2.15e-08	0.00013

Table 460: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Metabolism.of.Other.Amino.Acids, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.37e-02	4.39e-02	0.540	0.593	-6.59e-02	1.13e-01	0.0000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Metabolism.of.Other.Amino.Acids	-1.61e-08	2.47e-08	-0.652	0.519	-6.65e-08	3.43e-08	0.0135

Table 461: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs
L2.Metabolism.of.Terpenoids.and.Polyketides, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.68e-02	4.86e-02	0.345	0.732	-8.25e-02	1.16e-01	0.00000
L2.Metabolism.of.Terpenoids.and.Polyketides	-1.19e-08	2.96e-08	-0.401	0.691	-7.23e-08	4.86e-08	0.00517

Table 462: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs
L2.Nervous.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.84e-02	5.27e-02	0.729	0.472	-6.92e-02	1.46e-01	0.0000
L2.Nervous.System	-5.14e-07	6.24e-07	-0.824	0.417	-1.79e-06	7.60e-07	0.0214

Table 463: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs
L2.Neurodegenerative.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.09e-02	3.82e-02	0.809	0.425	-4.72e-02	1.09e-01	0.0000
L2.Neurodegenerative.Diseases	-2.75e-07	2.62e-07	-1.049	0.302	-8.10e-07	2.60e-07	0.0343

Table 464: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs
L2.Nucleotide.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.92e-02	5.52e-02	-0.349	0.730	-1.32e-01	9.34e-02	0.00000
L2.Nucleotide.Metabolism	5.44e-09	1.39e-08	0.390	0.699	-2.30e-08	3.39e-08	0.00489

Table 465: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs
L2.Poorly.Characterized, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.58e-02	4.42e-02	0.358	0.723	-7.44e-02	1.06e-01	0.000
L2.Poorly.Characterized	-3.55e-09	8.21e-09	-0.433	0.668	-2.03e-08	1.32e-08	0.006

Table 466: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs
L2.Replication.and.Repair, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.31e-02	5.63e-02	-0.410	0.684	-1.38e-01	9.19e-02	0.00000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Replication.and.Repair	3.14e-09	6.88e-09	0.457	0.651	-1.09e-08	1.72e-08	0.00669

Table 467: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Sensory.System, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 468: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Signal.Transduction, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.90e-02	3.72e-02	0.779	0.442	-4.70e-02	1.05e-01	0.0000
L2.Signal.Transduction	-1.87e-08	1.81e-08	-1.032	0.310	-5.58e-08	1.83e-08	0.0332

Table 469: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Signaling.Molecules.and.Interaction, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.46e-03	6.1e-02	-0.0404	0.968	-1.27e-01	1.22e-01	0.00e+00
L2.Signaling.Molecules.and.Interaction	1.15e-08	2.6e-07	0.0443	0.965	-5.19e-07	5.42e-07	6.32e-05

Table 470: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Transcription, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.82e-02	4.16e-02	0.439	0.664	-6.67e-02	1.03e-01	0.00000
L2.Transcription	-7.11e-09	1.30e-08	-0.546	0.589	-3.37e-08	1.95e-08	0.00951

Table 471: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Translation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.00e-02	5.60e-02	-0.715	0.480	-1.54e-01	7.43e-02	0.00
L2.Translation	8.57e-09	1.08e-08	0.796	0.432	-1.34e-08	3.06e-08	0.02

Table 472: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Transport.and.Catabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.83e-02	4.58e-02	1.71	0.0977	-1.52e-02	1.72e-01	0.000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Transport.and.Catabolism	-3.21e-07	1.61e-07	-1.99	0.0562	-6.50e-07	8.99e-09	0.113

Table 473: diversity_vs_picrust_L2_neo: wunifrac.PC.2 vs L2.Xenobiotics.Biodegradation.and.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.93e-02	3.86e-02	0.759	0.454	-4.95e-02	1.08e-01	0.0000
L2.Xenobiotics.Biodegradation.and.Metabolism	-1.75e-08	1.79e-08	-0.981	0.335	-5.40e-08	1.89e-08	0.0301

Table 474: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Amino.Acid.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.91e-02	4.04e-02	-1.71	0.0976	-1.52e-01	1.34e-02	0.000
L2.Amino.Acid.Metabolism	8.42e-09	4.21e-09	2.00	0.0546	-1.77e-10	1.70e-08	0.114

Table 475: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Biosynthesis.of.Other.Secondary.Metabolites, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.78e-02	4.07e-02	-1.91	0.0655	-1.61e-01	5.33e-03	0.000
L2.Biosynthesis.of.Other.Secondary.Metabolites	1.01e-07	4.54e-08	2.22	0.0342	8.03e-09	1.93e-07	0.137

Table 476: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Cancers, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.07e-02	3.20e-02	-1.58	0.1241	-1.16e-01	1.47e-02	0.000
L2.Cancers	6.86e-07	3.29e-07	2.09	0.0456	1.43e-08	1.36e-06	0.123

Table 477: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Carbohydrate.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.26e-02	3.84e-02	-1.37	0.181	-1.31e-01	2.58e-02	0.0000
L2.Carbohydrate.Metabolism	5.29e-09	3.20e-09	1.65	0.109	-1.26e-09	1.18e-08	0.0807

Table 478: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Cardiovascular.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.001790	0.024857	0.072	0.943	-0.04897	0.05256	0.000000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Cardiovascular.Diseases	-0.000114	0.000696	-0.163	0.871	-0.00153	0.00131	0.000861

Table 479: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Cell.Communication, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 480: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Cell.Growth.and.Death, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.69e-02	5.18e-02	-1.87	0.0709	-2.03e-01	8.79e-03	0.000
L2.Cell.Growth.and.Death	2.45e-07	1.20e-07	2.05	0.0495	5.55e-10	4.89e-07	0.119

Table 481: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Cell.Motility, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.19e-02	3.41e-02	0.348	0.73	-5.78e-02	8.16e-02	0.00000
L2.Cell.Motility	-1.00e-08	2.19e-08	-0.459	0.65	-5.47e-08	3.46e-08	0.00674

Table 482: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Cellular.Processes.and.Signaling, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.38e-02	3.46e-02	-1.27	0.215	-1.15e-01	2.68e-02	0.0000
L2.Cellular.Processes.and.Signaling	1.14e-08	7.07e-09	1.61	0.117	-3.04e-09	2.58e-08	0.0774

Table 483: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Circulatory.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.63e-03	2.36e-02	-0.365	0.717	-5.69e-02	3.96e-02	0.0000
L2.Circulatory.System	1.39e-05	1.41e-05	0.990	0.330	-1.48e-05	4.27e-05	0.0306

Table 484: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Digestive.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.41e-02	3.73e-02	-1.18	0.246	-1.20e-01	3.20e-02	0.0000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Digestive.System	1.09e-06	7.54e-07	1.45	0.157	-4.46e-07	2.63e-06	0.0636

Table 485: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Endocrine.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.13e-02	4.61e-02	-1.54	0.1329	-1.66e-01	2.30e-02	0.0000
L2.Endocrine.System	3.46e-07	1.99e-07	1.74	0.0919	-5.99e-08	7.52e-07	0.0891

Table 486: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Energy.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.38e-02	4.21e-02	-1.52	0.1396	-1.50e-01	2.21e-02	0.0000
L2.Energy.Metabolism	1.33e-08	7.59e-09	1.76	0.0889	-2.16e-09	2.88e-08	0.0907

Table 487: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Environmental.Adaptation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.03e-02	4.33e-02	-0.699	0.490	-1.19e-01	5.81e-02	0.0000
L2.Environmental.Adaptation	2.77e-07	3.40e-07	0.813	0.423	-4.18e-07	9.71e-07	0.0209

Table 488: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Enzyme.Families, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.48e-02	4.24e-02	-1.29	0.206	-1.41e-01	3.18e-02	0.0000
L2.Enzyme.Families	2.74e-08	1.83e-08	1.50	0.144	-9.92e-09	6.47e-08	0.0676

Table 489: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Excretory.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.28e-02	2.73e-02	-1.2	0.2384	-8.85e-02	2.29e-02	0.000
L2.Excretory.System	1.30e-06	6.83e-07	1.9	0.0674	-9.88e-08	2.69e-06	0.104

Table 490: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Folding..Sorting.and.Degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.94e-02	4.29e-02	-1.62	0.1161	-1.57e-01	1.82e-02	0.0

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Folding..Sorting.and.Degradation	3.32e-08	1.79e-08	1.86	0.0727	-3.25e-09	6.97e-08	0.1

Table 491: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs
L2.Genetic.Information.Processing, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.42e-02	4.12e-02	-1.56	0.129	-1.48e-01	1.99e-02	0.0000
L2.Genetic.Information.Processing	2.73e-08	1.50e-08	1.82	0.079	-3.35e-09	5.79e-08	0.0964

Table 492: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs
L2.Glycan.Biosynthesis.and.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.20e-02	3.84e-02	-2.39	0.02309	-1.7e-01	-1.35e-02	0.000
L2.Glycan.Biosynthesis.and.Metabolism	4.08e-08	1.46e-08	2.80	0.00889	1.1e-08	7.06e-08	0.202

Table 493: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs
L2.Immune.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.25e-02	3.81e-02	-0.854	0.400	-1.10e-01	4.52e-02	0.000
L2.Immune.System	6.46e-07	6.18e-07	1.045	0.304	-6.16e-07	1.91e-06	0.034

Table 494: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs
L2.Immune.System.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.07e-02	4.92e-02	-0.827	0.415	-1.41e-01	5.98e-02	0.0000
L2.Immune.System.Diseases	7.24e-07	7.82e-07	0.925	0.362	-8.74e-07	2.32e-06	0.0269

Table 495: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs
L2.Infectious.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.43e-02	3.52e-02	-1.26	0.219	-1.16e-01	2.77e-02	0.0000
L2.Infectious.Diseases	1.11e-07	7.02e-08	1.58	0.124	-3.22e-08	2.54e-07	0.0748

Table 496: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs
L2.Lipid.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.47e-02	3.94e-02	-1.39	0.175	-1.35e-01	2.57e-02	0.0000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Lipid.Metabolism	2.20e-08	1.33e-08	1.66	0.108	-5.14e-09	4.91e-08	0.0812

Table 497: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Membrane.Transport, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.30e-02	3.41e-02	-0.969	0.341	-1.03e-01	3.66e-02	0.0000
L2.Membrane.Transport	2.57e-09	2.04e-09	1.259	0.218	-1.60e-09	6.73e-09	0.0486

Table 498: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Metabolic.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.34e-02	4.68e-02	-1.99	0.0553	-1.89e-01	2.25e-03	0.000
L2.Metabolic.Diseases	1.09e-06	4.91e-07	2.22	0.0339	8.86e-08	2.09e-06	0.137

Table 499: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.99e-02	3.53e-02	-1.13	0.268	-1.12e-01	3.22e-02	0.0000
L2.Metabolism	1.61e-08	1.12e-08	1.43	0.164	-6.91e-09	3.90e-08	0.0617

Table 500: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Metabolism.of.Cofactors.and.Vitamins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.04e-02	4.02e-02	-1.75	0.0899	-1.52e-01	1.16e-02	0.00
L2.Metabolism.of.Cofactors.and.Vitamins	1.88e-08	9.16e-09	2.05	0.0489	9.35e-11	3.75e-08	0.12

Table 501: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Metabolism.of.Other.Amino.Acids, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.11e-02	3.74e-02	-1.63	0.1130	-1.37e-01	1.53e-02	0.000
L2.Metabolism.of.Other.Amino.Acids	4.15e-08	2.10e-08	1.97	0.0578	-1.45e-09	8.44e-08	0.112

Table 502: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Metabolism.of.Terpenoids.and.Polyketides, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.53e-02	4.16e-02	-1.57	0.1267	-1.5e-01	1.96e-02	0.000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Metabolism.of.Terpenoids.and.Polyketides	4.62e-08	2.53e-08	1.83	0.0779	-5.5e-09	9.80e-08	0.097

Table 503: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Nervous.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.11e-02	4.41e-02	-2.07	0.0477	-1.81e-01	-1.00e-03	0.000
L2.Nervous.System	1.22e-06	5.22e-07	2.33	0.0265	1.52e-07	2.28e-06	0.149

Table 504: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Neurodegenerative.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.90e-02	3.38e-02	-1.15	0.257	-1.08e-01	3.0e-02	0.0000
L2.Neurodegenerative.Diseases	3.47e-07	2.32e-07	1.50	0.145	-1.26e-07	8.2e-07	0.0675

Table 505: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Nucleotide.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.03e-02	4.70e-02	-1.71	0.0976	-1.76e-01	1.56e-02	0.000
L2.Nucleotide.Metabolism	2.27e-08	1.19e-08	1.91	0.0653	-1.53e-09	4.69e-08	0.106

Table 506: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Poorly.Characterized, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.83e-02	3.77e-02	-1.55	0.1324	-1.35e-01	1.87e-02	0.000
L2.Poorly.Characterized	1.31e-08	7.01e-09	1.87	0.0716	-1.22e-09	2.74e-08	0.101

Table 507: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Replication.and.Repair, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.33e-02	4.80e-02	-1.74	0.0926	-1.81e-01	1.46e-02	0.000
L2.Replication.and.Repair	1.13e-08	5.86e-09	1.93	0.0627	-6.37e-10	2.33e-08	0.108

Table 508: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Sensory.System, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
	NA	NA	NA	NA	NA	NA	0

Table 509: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Signal.Transduction, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.31e-02	3.36e-02	-0.688	0.497	-9.18e-02	4.55e-02	0.000
L2.Signal.Transduction	1.49e-08	1.64e-08	0.910	0.370	-1.86e-08	4.84e-08	0.026

Table 510: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Signaling.Molecules.and.Interaction, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.38e-02	5.22e-02	-1.60	0.1191	-1.90e-01	2.29e-02	0.0000
L2.Signaling.Molecules.and.Interaction	3.91e-07	2.22e-07	1.76	0.0892	-6.35e-08	8.45e-07	0.0905

Table 511: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Transcription, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.64e-02	3.67e-02	-0.994	0.328	-1.11e-01	3.84e-02	0.0000
L2.Transcription	1.42e-08	1.15e-08	1.235	0.226	-9.28e-09	3.77e-08	0.0469

Table 512: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Translation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.54e-02	4.78e-02	-1.79	0.0841	-1.83e-01	1.22e-02	0.000
L2.Translation	1.83e-08	9.21e-09	1.99	0.0559	-4.95e-10	3.71e-08	0.113

Table 513: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Transport.and.Catabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.96e-02	4.13e-02	-1.69	0.1022	-1.54e-01	1.47e-02	0.00
L2.Transport.and.Catabolism	2.85e-07	1.45e-07	1.96	0.0594	-1.21e-08	5.82e-07	0.11

Table 514: diversity_vs_picrust_L2_neo: wunifrac.PC.3 vs L2.Xenobiotics.Biodegradation.and.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.50e-02	3.43e-02	-1.02	0.315	-1.05e-01	3.50e-02	0.0000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Xenobiotics.Biodegradation.and.Metabolism	2.09e-08	1.59e-08	1.32	0.197	-1.15e-08	5.33e-08	0.0531

Table 515: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs
L2.Amino.Acid.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.45e-02	3.18e-02	-2.34	0.0259	-1.39e-01	-9.58e-03	0.000
L2.Amino.Acid.Metabolism	9.08e-09	3.31e-09	2.74	0.0102	2.31e-09	1.58e-08	0.195

Table 516: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs
L2.Biosynthesis.of.Other.Secondary.Metabolites, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.8e-02	3.42e-02	-1.70	0.1001	-1.28e-01	1.18e-02	0.000
L2.Biosynthesis.of.Other.Secondary.Metabolites	7.5e-08	3.81e-08	1.97	0.0581	-2.74e-09	1.53e-07	0.111

Table 517: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs
L2.Cancers, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.22e-02	2.24e-02	-3.23	0.003014	-1.18e-01	-2.65e-02	0.000
L2.Cancers	9.77e-07	2.30e-07	4.25	0.000189	5.08e-07	1.45e-06	0.369

Table 518: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs
L2.Carbohydrate.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.39e-02	3.0e-02	-2.13	0.0415	-1.25e-01	-2.62e-03	0.000
L2.Carbohydrate.Metabolism	6.42e-09	2.5e-09	2.56	0.0156	1.31e-09	1.15e-08	0.175

Table 519: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs
L2.Cardiovascular.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.005891	0.020409	-0.289	0.775	-0.047571	0.03579	0.0000
L2.Cardiovascular.Diseases	0.000374	0.000571	0.655	0.517	-0.000792	0.00154	0.0136

Table 520: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs
L2.Cell.Communication, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
	NA	NA	NA	NA	NA	NA	0

Table 521: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Cell.Growth.and.Death, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.81e-02	4.22e-02	-2.09	0.0451	-1.74e-01	-2.04e-03	0.000
L2.Cell.Growth.and.Death	2.23e-07	9.74e-08	2.29	0.0295	2.37e-08	4.22e-07	0.144

Table 522: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Cell.Motility, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.93e-02	2.29e-02	-3.03	0.005038	-1.16e-01	-2.25e-02	0.000
L2.Cell.Motility	5.85e-08	1.47e-08	3.99	0.000393	2.85e-08	8.84e-08	0.339

Table 523: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Cellular.Processes.and.Signaling, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.47e-02	2.57e-02	-2.51	0.01752	-1.17e-01	-1.22e-02	0.000
L2.Cellular.Processes.and.Signaling	1.68e-08	5.26e-09	3.20	0.00324	6.09e-09	2.76e-08	0.248

Table 524: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Circulatory.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.25e-02	1.89e-02	-0.665	0.5112	-5.1e-02	2.60e-02	0.0000
L2.Circulatory.System	2.03e-05	1.12e-05	1.802	0.0816	-2.7e-06	4.32e-05	0.0948

Table 525: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Digestive.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.73e-03	3.19e-02	0.0858	0.932	-6.23e-02	6.78e-02	0.000000
L2.Digestive.System	-6.78e-08	6.44e-07	-0.1053	0.917	-1.38e-06	1.25e-06	0.000357

Table 526: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Endocrine.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.61e-02	3.93e-02	-0.919	0.366	-1.16e-01	4.42e-02	0.0000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Endocrine.System	1.75e-07	1.69e-07	1.035	0.309	-1.70e-07	5.21e-07	0.0334

Table 527: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Energy.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.02e-02	3.23e-02	-2.48	0.01904	-1.46e-01	-1.41e-02	0.00
L2.Energy.Metabolism	1.68e-08	5.84e-09	2.87	0.00742	4.84e-09	2.87e-08	0.21

Table 528: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Environmental.Adaptation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.03e-01	2.88e-02	-3.59	0.001154	-1.62e-01	-4.46e-02	0.00
L2.Environmental.Adaptation	9.44e-07	2.26e-07	4.18	0.000234	4.82e-07	1.41e-06	0.36

Table 529: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Enzyme.Families, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.77e-02	3.24e-02	-2.40	0.02281	-1.44e-01	-1.16e-02	0.0
L2.Enzyme.Families	3.89e-08	1.40e-08	2.79	0.00916	1.04e-08	6.74e-08	0.2

Table 530: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Excretory.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.24e-02	2.2e-02	-1.47	0.1506	-7.72e-02	1.25e-02	0.000
L2.Excretory.System	1.28e-06	5.5e-07	2.33	0.0269	1.56e-07	2.40e-06	0.149

Table 531: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Folding..Sorting.and.Degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.80e-02	3.36e-02	-2.32	0.0274	-1.47e-01	-9.29e-03	0.000
L2.Folding..Sorting.and.Degradation	3.73e-08	1.40e-08	2.67	0.0123	8.73e-09	6.60e-08	0.186

Table 532: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Genetic.Information.Processing, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.0e-02	3.15e-02	-2.54	0.01657	-1.44e-01	-1.56e-02	0.00

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Genetic.Information.Processing	3.4e-08	1.15e-08	2.96	0.00595	1.05e-08	5.75e-08	0.22

Table 533: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Glycan.Biosynthesis.and.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.05e-02	3.40e-02	-1.49	0.1478	-1.20e-01	1.89e-02	0.0000
L2.Glycan.Biosynthesis.and.Metabolism	2.24e-08	1.29e-08	1.74	0.0928	-3.95e-09	4.88e-08	0.0886

Table 534: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Immune.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.19e-02	2.46e-02	-3.74	7.81e-04	-1.42e-01	-4.17e-02	0.000
L2.Immune.System	1.83e-06	3.99e-07	4.57	7.76e-05	1.01e-06	2.64e-06	0.403

Table 535: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Immune.System.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.67e-02	3.81e-02	-2.01	0.0533	-1.55e-01	1.18e-03	0.00
L2.Immune.System.Diseases	1.36e-06	6.06e-07	2.25	0.0320	1.25e-07	2.60e-06	0.14

Table 536: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Infectious.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.07e-02	2.80e-02	-1.81	0.0797	-1.08e-01	6.39e-03	0.000
L2.Infectious.Diseases	1.27e-07	5.57e-08	2.29	0.0295	1.36e-08	2.41e-07	0.144

Table 537: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Lipid.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.84e-02	3.06e-02	-2.24	0.0328	-1.31e-01	-5.96e-03	0.000
L2.Lipid.Metabolism	2.75e-08	1.03e-08	2.66	0.0123	6.42e-09	4.86e-08	0.186

Table 538: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Membrane.Transport, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.42e-02	2.59e-02	-2.10	0.0446	-1.07e-01	-1.40e-03	0.000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Membrane.Transport	4.22e-09	1.55e-09	2.72	0.0106	1.06e-09	7.38e-09	0.193

Table 539: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Metabolic.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.66e-02	3.79e-02	-2.29	0.0293	-1.64e-01	-9.31e-03	0.000
L2.Metabolic.Diseases	1.01e-06	3.97e-07	2.55	0.0161	2.02e-07	1.82e-06	0.173

Table 540: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.03e-02	2.68e-02	-2.25	0.03168	-1.15e-01	-5.66e-03	0.000
L2.Metabolism	2.43e-08	8.52e-09	2.85	0.00785	6.88e-09	4.17e-08	0.208

Table 541: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Metabolism.of.Cofactors.and.Vitamins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.60e-02	3.15e-02	-2.41	0.0223	-1.4e-01	-1.16e-02	0.000
L2.Metabolism.of.Cofactors.and.Vitamins	2.03e-08	7.19e-09	2.82	0.0084	5.6e-09	3.50e-08	0.204

Table 542: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Metabolism.of.Other.Amino.Acids, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.23e-02	2.98e-02	-2.09	0.0453	-1.23e-01	-1.40e-03	0.000
L2.Metabolism.of.Other.Amino.Acids	4.23e-08	1.68e-08	2.52	0.0171	8.09e-09	7.66e-08	0.171

Table 543: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Metabolism.of.Terpenoids.and.Polyketides, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.22e-02	3.28e-02	-2.20	0.0357	-1.39e-01	-5.17e-03	0.000
L2.Metabolism.of.Terpenoids.and.Polyketides	5.11e-08	2.00e-08	2.56	0.0159	1.03e-08	9.20e-08	0.174

Table 544: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Nervous.System, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.31e-02	3.66e-02	-2.00	0.0550	-1.48e-01	1.67e-03	0.000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Nervous.System	9.79e-07	4.34e-07	2.26	0.0315	9.28e-08	1.86e-06	0.141

Table 545: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Neurodegenerative.Diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.73e-02	2.56e-02	-2.24	0.03245	-1.10e-01	-5.13e-03	0.000
L2.Neurodegenerative.Diseases	5.10e-07	1.75e-07	2.91	0.00674	1.52e-07	8.68e-07	0.215

Table 546: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Nucleotide.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.85e-02	3.79e-02	-2.07	0.0469	-1.56e-01	-1.15e-03	0.000
L2.Nucleotide.Metabolism	2.22e-08	9.57e-09	2.32	0.0274	2.65e-09	4.17e-08	0.148

Table 547: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Poorly.Characterized, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.18e-02	2.89e-02	-2.49	0.01873	-1.31e-01	-1.28e-02	0.000
L2.Poorly.Characterized	1.61e-08	5.37e-09	3.00	0.00538	5.15e-09	2.71e-08	0.225

Table 548: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Replication.and.Repair, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.11e-02	3.77e-02	-2.41	0.0221	-1.68e-01	-1.40e-02	0.000
L2.Replication.and.Repair	1.24e-08	4.61e-09	2.69	0.0117	2.97e-09	2.18e-08	0.189

Table 549: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Sensory.System, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 550: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Signal.Transduction, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.00e-02	2.41e-02	-2.48	0.01880	-1.09e-01	-1.07e-02	0.000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
L2.Signal.Transduction	3.87e-08	1.18e-08	3.29	0.00258	1.47e-08	6.27e-08	0.259

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.19e-02	4.36e-02	-1.42	0.166	-1.51e-01	2.72e-02	0.0000
L2.Signaling.Molecules.and.Interaction	2.89e-07	1.86e-07	1.55	0.131	-9.08e-08	6.68e-07	0.0722

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.55e-02	2.73e-02	-2.40	0.02271	-1.21e-01	-9.81e-03	0.000
L2.Transcription	2.55e-08	8.55e-09	2.99	0.00558	8.07e-09	4.30e-08	0.223

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.19e-02	3.86e-02	-2.12	0.0422	-1.61e-01	-3.08e-03	0.000
L2.Translation	1.76e-08	7.43e-09	2.36	0.0249	2.38e-09	3.27e-08	0.153

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.35e-03	3.62e-02	-0.231	0.819	-8.22e-02	6.55e-02	0.00000
L2.Transport.and.Catabolism	3.42e-08	1.27e-07	0.268	0.790	-2.26e-07	2.94e-07	0.00232

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.89e-02	2.56e-02	-2.30	0.0286	-1.11e-01	-6.59e-03	0.000
L2.Xenobiotics.Biodegradation.and.Metabolism	3.52e-08	1.18e-08	2.97	0.0058	1.10e-08	5.94e-08	0.222

Table 556: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation,
df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %
Intercept	-1.26e-02	5.22e-02	-0.241	0.811	-1.19e-01
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	1.49e-05	1.16e-05	1.288	0.208	-8.73e-06

Table 557: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.ABC.transporters, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.92e-02	8.03e-02	-0.239	0.813	-1.83e-01	1.45e-01	0.0000
L3.ABC.transporters	5.76e-09	1.82e-08	0.316	0.754	-3.15e-08	4.30e-08	0.0032

Table 558: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Adherens.junction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 559: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Adipocytokine.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e-01	8.32e-02	1.20	0.239	-7.00e-02	2.70e-01	0.000
L3.Adipocytokine.signaling.pathway	-2.19e-06	1.45e-06	-1.52	0.140	-5.15e-06	7.61e-07	0.069

Table 560: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.African.trypanosomiasis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.77e-02	6.67e-02	-0.714	0.481	-1.84e-01	8.87e-02	0.0000
L3.African.trypanosomiasis	6.49e-06	5.76e-06	1.125	0.270	-5.29e-06	1.83e-05	0.0392

Table 561: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Alanine..aspartate.and.glutamate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.01e-01	1.11e-01	0.908	0.371	-1.26e-01	3.28e-01	0.000
L3.Alanine..aspartate.and.glutamate.metabolism	-1.19e-07	1.16e-07	-1.026	0.313	-3.57e-07	1.18e-07	0.032

Table 562: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Aldosterone.regulated.sodium.reabsorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.0112	0.0522	-0.214	0.832	-0.118	0.0955	0.0000
L3.Aldosterone.regulated.sodium.reabsorption	0.3578	0.2955	1.211	0.235	-0.246	0.9613	0.0452

Table 563: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Alzheimer.s.disease, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.15e-02	9.57e-02	-0.225	0.823	-2.17e-01	1.74e-01	0.00000
L3.Alzheimer.s.disease	4.94e-07	1.83e-06	0.269	0.790	-3.25e-06	4.24e-06	0.00233

Table 564: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Amino.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.18e-02	7.83e-02	0.534	0.597	-1.18e-01	2.02e-01	0.0000
L3.Amino.acid.metabolism	-1.76e-07	2.46e-07	-0.717	0.479	-6.79e-07	3.26e-07	0.0163

Table 565: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Amino.acid.related.enzymes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.29e-02	1.14e-01	-0.113	0.911	-2.46e-01	2.21e-01	0.000000
L3.Amino.acid.related.enzymes	1.06e-08	8.29e-08	0.127	0.900	-1.59e-07	1.80e-07	0.000523

Table 566: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Amino.sugar.and.nucleotide.sugar.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.57e-02	1.11e-01	0.232	0.818	-2.01e-01	2.52e-01	0.00(
L3.Amino.sugar.and.nucleotide.sugar.metabolism	-1.85e-08	7.03e-08	-0.263	0.794	-1.62e-07	1.25e-07	0.00

Table 567: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Aminoacyl.tRNA.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.45e-01	1.18e-01	-1.23	0.229	-3.85e-01	9.58e-02	0.0000
L3.Aminoacyl.tRNA.biosynthesis	1.51e-07	1.10e-07	1.36	0.183	-7.50e-08	3.76e-07	0.0566

Table 568: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Aminobenzoate.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.22e-02	7.58e-02	0.161	0.874	-1.43e-01	1.67e-01	0.0000
L3.Aminobenzoate.degradation	-9.19e-08	4.12e-07	-0.223	0.825	-9.34e-07	7.50e-07	0.0016

Table 569: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Amoebiasis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.21e-01	6.02e-02	2.01	0.05395	-2.19e-03	2.44e-01	0.000
L3.Amoebiasis	-3.21e-05	1.04e-05	-3.09	0.00426	-5.33e-05	-1.09e-05	0.236

Table 570: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Amyotrophic.lateral.sclerosis..ALS., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.05e-02	6.21e-02	0.329	0.744	-1.06e-01	1.47e-01	0.0000
L3.Amyotrophic.lateral.sclerosis..ALS.	-1.13e-06	1.84e-06	-0.611	0.545	-4.89e-06	2.64e-06	0.0119

Table 571: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Antigen.processing.and.presentation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.72e-01	8.02e-02	2.14	0.0404	7.99e-03	3.36e-01	0.000
L3.Antigen.processing.and.presentation	-7.30e-06	2.75e-06	-2.65	0.0126	-1.29e-05	-1.68e-06	0.185

Table 572: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Apoptosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.07e-02	5.45e-02	-1.67	0.10604	-2.02e-01	2.05e-02	0.000
L3.Apoptosis	1.27e-05	4.10e-06	3.09	0.00429	4.30e-06	2.11e-05	0.236

Table 573: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Arachidonic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.57e-02	7.49e-02	0.210	0.835	-1.37e-01	1.69e-01	0.00000
L3.Arachidonic.acid.metabolism	-4.01e-07	1.36e-06	-0.294	0.771	-3.19e-06	2.38e-06	0.00279

Table 574: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Arginine.and.proline.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.79e-02	8.87e-02	0.991	0.330	-9.32e-02	2.69e-01	0.0000
L3.Arginine.and.proline.metabolism	-9.16e-08	7.53e-08	-1.216	0.233	-2.45e-07	6.22e-08	0.0455

Table 575: diversity_vs_picrust_L3_neo: wunifrac.PC.1
vs L3.Arrhythmogenic.right.ventricular.cardiomyopathy..ARVC.,
df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 576: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Ascorbate.and.aldarate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.54e-02	6.55e-02	0.388	0.701	-1.08e-01	1.59e-01	0.0000
L3.Ascorbate.and.aldarate.metabolism	-1.31e-07	2.02e-07	-0.645	0.524	-5.44e-07	2.83e-07	0.0132

Table 577: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Atrazine.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.87e-03	5.84e-02	0.169	0.867	-1.09e-01	1.29e-01	0.00000
L3.Atrazine.degradation	-5.90e-07	1.53e-06	-0.386	0.702	-3.71e-06	2.53e-06	0.00478

Table 578: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Bacterial.chemotaxis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.73e-02	7.56e-02	1.15	0.257	-6.71e-02	2.42e-01	0.0000
L3.Bacterial.chemotaxis	-3.19e-07	2.05e-07	-1.56	0.130	-7.39e-07	1.00e-07	0.0724

Table 579: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Bacterial.invasion.of.epithelial.cells, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.90e-03	5.57e-02	-0.124	0.902	-1.21e-01	1.07e-01	0.00000
L3.Bacterial.invasion.of.epithelial.cells	5.72e-06	1.53e-05	0.374	0.711	-2.55e-05	3.69e-05	0.00449

Table 580: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Bacterial.motility.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.15e-02	7.43e-02	0.694	0.493	-1.00e-01	2.03e-01	0.0000
L3.Bacterial.motility.proteins	-9.40e-08	9.69e-08	-0.970	0.340	-2.92e-07	1.04e-07	0.0294

Table 581: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Bacterial.secretion.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.63e-03	7.64e-02	0.0606	0.952	-1.51e-01	1.61e-01	0.000000
L3.Bacterial.secretion.system	-7.18e-09	8.60e-08	-0.0835	0.934	-1.83e-07	1.68e-07	0.000225

Table 582: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Bacterial.toxins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.76e-01	1.16e-01	-1.52	0.138	-4.13e-01	6.00e-02	0.0000
L3.Bacterial.toxins	1.33e-06	7.87e-07	1.69	0.101	-2.76e-07	2.94e-06	0.0845

Table 583: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Basal.transcription.factors, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.62e-02	5.60e-02	0.289	0.775	-9.82e-02	0.13054	0.0000
L3.Basal.transcription.factors	-1.89e-05	2.39e-05	-0.789	0.437	-6.77e-05	0.00003	0.0197

Table 584: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Base.excision.repair, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.11e-02	1.15e-01	-0.359	0.722	-2.75e-01	1.93e-01	0.00000
L3.Base.excision.repair	1.09e-07	2.69e-07	0.404	0.689	-4.41e-07	6.59e-07	0.00524

Table 585: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Benzoate.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.43e-03	7.16e-02	0.0899	0.929	-1.40e-01	1.53e-01	0.000000
L3.Benzoate.degradation	-2.54e-08	1.92e-07	-0.1327	0.895	-4.17e-07	3.66e-07	0.000567

Table 586: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Betalain.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.014396	0.055286	0.260	0.796	-0.098514	0.127306	0.0000
L3.Betalain.biosynthesis	-0.000104	0.000133	-0.781	0.441	-0.000375	0.000168	0.0193

Table 587: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Bile.secretion, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00926	0.05863	-0.158	0.876	-0.12900	0.11047	0.00000
L3.Bile.secretion	0.00136	0.00382	0.356	0.724	-0.00644	0.00916	0.00408

Table 588: diversity_vs_picrust_L3_neo: wunifrac.PC.1
vs L3.Biosynthesis.and.biodegradation.of.secondary.metabolites,
df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	1.94e-02	6.18e-02	0.314	0.755	-1.07e-01	1.46
L3.Biosynthesis.and.biodegradation.of.secondary.metabolites	-2.35e-07	3.96e-07	-0.592	0.558	-1.04e-06	5.74

Table 589: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Biosynthesis.of.12...14..and.16.membered.macrolides, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R
Intercept	-0.00154	0.0535	-0.0288	0.977	-0.111	0.108	0
L3.Biosynthesis.of.12...14..and.16.membered.macrolides	0.04933	0.3025	0.1631	0.872	-0.568	0.667	0

Table 590: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Biosynthesis.of.ansamycins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.32e-02	7.52e-02	0.442	0.662	-1.20e-01	1.87e-01	0.0000
L3.Biosynthesis.of.ansamycins	-3.17e-07	5.15e-07	-0.615	0.543	-1.37e-06	7.36e-07	0.0121

Table 591: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	9.53e-03	6.09e-02	0.156	0.877	-1.15e-01	1.34e
L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides	-1.34e-07	4.34e-07	-0.310	0.759	-1.02e-06	7.51e

Table 592: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Biosynthesis.of.type.II.polyketide.backbone, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 593: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Biosynthesis.of.type.II.polyketide.products, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.014464	0.055542	0.260	0.796	-0.098969	0.127896	0.0000
L3.Biosynthesis.of.type.II.polyketide.products	-0.000101	0.000133	-0.758	0.455	-0.000373	0.000171	0.0182

Table 594: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Biosynthesis.of.unsaturated.fatty.acids, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.60e-03	7.13e-02	0.120	0.905	-1.37e-01	1.54e-01	0.00000
L3.Biosynthesis.of.unsaturated.fatty.acids	-6.67e-08	3.74e-07	-0.178	0.860	-8.30e-07	6.96e-07	0.00103

Table 595: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Biosynthesis.of.vancomycin.group.antibiotics, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.25e-01	1.06e-01	2.12	0.0424	8.26e-03	4.41e-01	0.000
L3.Biosynthesis.of.vancomycin.group.antibiotics	-4.53e-06	1.90e-06	-2.38	0.0238	-8.41e-06	-6.46e-07	0.155

Table 596: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Biotin.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.21e-01	8.94e-02	1.35	0.187	-6.2e-02	3.03e-01	0.0000
L3.Biotin.metabolism	-9.78e-07	5.98e-07	-1.63	0.113	-2.2e-06	2.44e-07	0.0793

Table 597: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Bisphenol.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.68e-01	9.57e-02	1.76	0.0887	-2.71e-02	3.64e-01	0.00
L3.Bisphenol.degradation	-3.78e-06	1.84e-06	-2.05	0.0489	-7.54e-06	-1.86e-08	0.12

Table 598: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Bladder.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.39e-03	5.89e-02	0.159	0.875	-1.11e-01	1.30e-01	0.00000
L3.Bladder.cancer	-2.02e-06	5.76e-06	-0.352	0.727	-1.38e-05	9.73e-06	0.00398

Table 599: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Butanoate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.72e-02	8.43e-02	-0.204	0.840	-1.89e-01	1.55e-01	0.00000
L3.Butanoate.metabolism	2.69e-08	1.03e-07	0.261	0.796	-1.84e-07	2.37e-07	0.00219

Table 600: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Butirosin.and.neomycin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.85e-01	1.31e-01	1.42	0.167	-8.18e-02	4.52e-01	0.0000
L3.Butirosin.and.neomycin.biosynthesis	-3.94e-06	2.56e-06	-1.54	0.135	-9.17e-06	1.30e-06	0.0707

Table 601: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.C5.Branched.dibasic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.01e-02	1.01e-01	-0.398	0.694	-2.46e-01	1.66e-01	0.00000
L3.C5.Branched.dibasic.acid.metabolism	1.49e-07	3.20e-07	0.466	0.644	-5.05e-07	8.04e-07	0.00696

Table 602: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.CAM.ligands, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 603: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Caffeine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.039	0.0553	-0.705	0.487	-0.15196	0.074	0.0000
L3.Caffeine.metabolism	0.048	0.0283	1.693	0.101	-0.00989	0.106	0.0847

Table 604: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Calcium.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.069	0.0529	-1.30	0.20190	-0.1770	0.039	0.000
L3.Calcium.signaling.pathway	0.110	0.0393	2.81	0.00863	0.0302	0.191	0.203

Table 605: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Caprolactam.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.36e-04	6.25e-02	-0.00698	0.994	-1.28e-01	1.27e-01	0.00e+00
L3.Caprolactam.degradation	8.63e-09	6.66e-07	0.01297	0.990	-1.35e-06	1.37e-06	5.43e-06

Table 606: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Carbohydrate.digestion.and.absorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.69e-03	7.57e-02	0.0224	0.982	-1.53e-01	1.56e-01	0.00e+00
L3.Carbohydrate.digestion.and.absorption	-7.87e-08	2.53e-06	-0.0312	0.975	-5.24e-06	5.08e-06	3.13e-05

Table 607: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Carbohydrate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.71e-02	8.62e-02	0.778	0.442	-1.09e-01	2.43e-01	0.0000
L3.Carbohydrate.metabolism	-3.81e-07	3.91e-07	-0.974	0.338	-1.18e-06	4.17e-07	0.0297

Table 608: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Carbon.fixation.in.photosynthetic.organisms, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.91e-02	9.42e-02	0.521	0.606	-1.43e-01	2.41e-01	0.0000
L3.Carbon.fixation.in.photosynthetic.organisms	-9.17e-08	1.46e-07	-0.626	0.536	-3.91e-07	2.07e-07	0.0125

Table 609: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Carbon.fixation.pathways.in.prokaryotes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.96e-02	9.81e-02	0.404	0.689	-1.61e-01	2.40e-01	0.0000
L3.Carbon.fixation.pathways.in.prokaryotes	-4.60e-08	9.63e-08	-0.478	0.636	-2.43e-07	1.51e-07	0.0073

Table 610: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Cardiac.muscle.contraction, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.45e-02	5.62e-02	0.258	0.798	-1.00e-01	0.129284	0.0000
L3.Cardiac.muscle.contraction	-2.35e-05	3.35e-05	-0.700	0.489	-9.19e-05	0.000045	0.0156

Table 611: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Carotenoid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.95e-02	5.44e-02	1.28	0.2114	-4.16e-02	1.81e-01	0.000
L3.Carotenoid.biosynthesis	-2.03e-05	7.75e-06	-2.62	0.0138	-3.61e-05	-4.46e-06	0.181

Table 612: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Cell.cycle, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 613: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Cell.cycle. . . Caulobacter, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.02e-02	1.29e-01	-0.311	0.758	-3.04e-01	2.23e-01	0.00000
L3.Cell.cycle. . . Caulobacter	1.04e-07	3.06e-07	0.341	0.735	-5.20e-07	7.29e-07	0.00374

Table 614: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Cell.cycle. . . yeast, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 615: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Cell.division, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.11e-01	8.24e-02	1.35	0.1865	-5.69e-02	2.80e-01	0.0000
L3.Cell.division	-1.86e-06	1.09e-06	-1.71	0.0982	-4.08e-06	3.65e-07	0.0859

Table 616: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Cell.motility.and.secretion, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.97e-02	8.72e-02	0.226	0.823	-1.58e-01	1.98e-01	0.00000
L3.Cell.motility.and.secretion	-1.21e-07	4.25e-07	-0.283	0.779	-9.89e-07	7.48e-07	0.00259

Table 617: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Cellular.antigens, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.08e-01	8.01e-02	1.35	0.1872	-5.54e-02	2.72e-01	0.0000
L3.Cellular.antigens	-2.45e-06	1.41e-06	-1.73	0.0934	-5.33e-06	4.37e-07	0.0883

Table 618: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Chagas.disease..American.trypanosomiasis., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.01e-02	6.41e-02	-0.781	0.441	-1.81e-01	0.080841	0.0000
L3.Chagas.disease..American.trypanosomiasis.	7.39e-06	5.69e-06	1.300	0.204	-4.23e-06	0.000019	0.0517

Table 619: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Chaperones.and.folding.catalysts, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.60e-02	1.01e-01	0.357	0.723	-1.70e-01	2.42e-01	0.00000
L3.Chaperones.and.folding.catalysts	-4.19e-08	1.00e-07	-0.419	0.679	-2.46e-07	1.62e-07	0.00562

Table 620: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Chloroalkane.and.chloroalkene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.30e-02	1.04e-01	0.415	0.681	-1.69e-01	2.55e-01	0.0000
L3.Chloroalkane.and.chloroalkene.degradation	-2.64e-07	5.48e-07	-0.481	0.634	-1.38e-06	8.56e-07	0.0074

Table 621: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Chlorocyclohexane.and.chlorobenzene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	3.78e-02	6.45e-02	0.587	0.562	-9.39e-02	1.70e-01
L3.Chlorocyclohexane.and.chlorobenzene.degradation	-2.78e-06	2.82e-06	-0.986	0.332	-8.53e-06	2.98e-06

Table 622: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Cholinergic.synapse, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 623: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Chromosome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.08e-02	1.08e-01	-0.0996	0.921	-2.32e-01	2.11e-01	0.000000
L3.Chromosome	8.53e-09	7.49e-08	0.1139	0.910	-1.44e-07	1.61e-07	0.000419

Table 624: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Chronic.myeloid.leukemia, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0107	0.0566	0.189	0.851	-0.105	0.126	0.00000
L3.Chronic.myeloid.leukemia	-0.0429	0.0856	-0.501	0.620	-0.218	0.132	0.00802

Table 625: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Circadian.rhythm...plant, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00942	0.0571	-0.165	0.870	-0.1261	0.1073	0.00000
L3.Circadian.rhythm...plant	0.00655	0.0157	0.417	0.679	-0.0255	0.0386	0.00558

Table 626: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Citrate.cycle..TCA.cycle., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.49e-02	8.08e-02	0.556	0.583	-1.20e-01	2.10e-01	0.0000
L3.Citrate.cycle..TCA.cycle.	-8.19e-08	1.13e-07	-0.728	0.472	-3.12e-07	1.48e-07	0.0168

Table 627: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Clavulanic.acid.biosynthesis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 628: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Colorectal.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.04263	0.05534	-0.77	0.4471	-0.155649	0.07038	0.0000
L3.Colorectal.cancer	0.00359	0.00199	1.80	0.0817	-0.000481	0.00766	0.0947

Table 629: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Complement.and.coagulation.cascades, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 630: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Cyanoamino.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.24e-01	8.49e-02	1.46	0.1560	-4.98e-02	2.97e-01	0.0000
L3.Cyanoamino.acid.metabolism	-4.64e-07	2.58e-07	-1.80	0.0818	-9.90e-07	6.22e-08	0.0947

Table 631: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Cysteine.and.methionine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.46e-03	9.94e-02	-0.0650	0.949	-2.09e-01	1.96e-01	0.00000
L3.Cysteine.and.methionine.metabolism	7.40e-09	9.65e-08	0.0767	0.939	-1.90e-07	2.04e-07	0.00019

Table 632: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Cytochrome.P450, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.000572	0.0535	-0.0107	0.992	-0.11	0.109	0.000000
L3.Cytochrome.P450	0.018319	0.3026	0.0605	0.952	-0.60	0.636	0.000118

Table 633: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Cytokine.receptors, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 634: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Cytokine.cytokine.receptor.interaction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 635: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Cytoskeleton.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.60e-02	1.12e-01	0.410	0.685	-1.83e-01	2.75e-01	0.00000
L3.Cytoskeleton.proteins	-2.23e-07	4.81e-07	-0.464	0.646	-1.21e-06	7.59e-07	0.00689

Table 636: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Cytosolic.DNA.sensing.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 637: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.D.Alanine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.52e-01	1.05e-01	-1.44	0.160	-3.67e-01	6.34e-02	0.0000
L3.D.Alanine.metabolism	1.42e-06	8.68e-07	1.64	0.111	-3.49e-07	3.20e-06	0.0799

Table 638: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.D.Arginine.and.D.ornithine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.54e-02	5.72e-02	-0.444	0.660	-1.42e-01	9.14e-02	0.0000
L3.D.Arginine.and.D.ornithine.metabolism	6.28e-06	6.04e-06	1.039	0.307	-6.06e-06	1.86e-05	0.0337

Table 639: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.D.Glutamine.and.D.glutamate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.91e-02	1.10e-01	-0.173	0.864	-2.45e-01	2.06e-01	0.00000
L3.D.Glutamine.and.D.glutamate.metabolism	1.45e-07	7.34e-07	0.197	0.845	-1.35e-06	1.64e-06	0.00125

Table 640: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.DNA.repair.and.recombination.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.62e-02	1.18e-01	-0.477	0.637	-2.97e-01	1.85e-01	0.00000
L3.DNA.repair.and.recombination.proteins	2.34e-08	4.40e-08	0.532	0.598	-6.64e-08	1.13e-07	0.00906

Table 641: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.DNA.replication, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.00e-02	1.27e-01	-0.393	0.697	-3.10e-01	2.10e-01	0.00000
L3.DNA.replication	8.91e-08	2.07e-07	0.431	0.670	-3.33e-07	5.11e-07	0.00596

Table 642: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.DNA.replication.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.74e-02	1.24e-01	-0.141	0.889	-2.70e-01	2.35e-01	0.000000
L3.DNA.replication.proteins	1.77e-08	1.14e-07	0.155	0.877	-2.14e-07	2.50e-07	0.000779

Table 643: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Dilated.cardiomyopathy..DCM., df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 644: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Dioxin.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.62e-02	7.27e-02	-0.497	0.623	-1.85e-01	1.12e-01	0.0000
L3.Dioxin.degradation	4.17e-07	5.84e-07	0.715	0.480	-7.75e-07	1.61e-06	0.0162

Table 645: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Drug.metabolism...cytochrome.P450, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.07e-04	6.85e-02	0.0132	0.990	-1.39e-01	1.41e-01	0.00e+00
L3.Drug.metabolism...cytochrome.P450	-1.84e-08	8.87e-07	-0.0207	0.984	-1.83e-06	1.79e-06	1.38e-05

Table 646: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Drug.metabolism...other.enzymes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.34e-02	1.14e-01	0.470	0.642	-1.79e-01	2.86e-01	0.00000
L3.Drug.metabolism...other.enzymes	-1.89e-07	3.57e-07	-0.529	0.600	-9.19e-07	5.41e-07	0.00896

Table 647: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.ECM.receptor.interaction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 648: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Electron.transfer.carriers, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.88e-02	6.66e-02	-0.282	0.78	-1.55e-01	1.17e-01	0.00000
L3.Electron.transfer.carriers	3.30e-07	7.20e-07	0.458	0.65	-1.14e-06	1.80e-06	0.00672

Table 649: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Endocrine.and.other.factor.regulated.calcium.reabsorption, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 650: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Endocytosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.0302	0.0524	-0.577	0.568	-0.13720	0.0767	0.000
L3.Endocytosis	0.0285	0.0152	1.872	0.071	-0.00259	0.0595	0.102

Table 651: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Energy.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.97e-02	8.51e-02	1.17	0.251	-7.42e-02	2.74e-01	0.0000
L3.Energy.metabolism	-1.36e-07	9.28e-08	-1.46	0.155	-3.25e-07	5.40e-08	0.0644

Table 652: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	6.09e-02	9.42e-02	0.646	0.523	-1.32e-01	2.53e-0
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	-8.96e-07	1.15e-06	-0.776	0.444	-3.25e-06	1.46e-0

Table 653: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.ErbB.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 654: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Ether.lipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.89e-02	6.36e-02	0.925	0.362	-7.1e-02	1.89e-01	0.0000
L3.Ether.lipid.metabolism	-4.07e-05	2.66e-05	-1.533	0.136	-9.5e-05	1.35e-05	0.0705

Table 655: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Ethylbenzene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.55e-01	7.60e-02	2.04	0.0498	1.64e-04	3.11e-01	0.000
L3.Ethylbenzene.degradation	-5.02e-06	1.92e-06	-2.62	0.0137	-8.94e-06	-1.11e-06	0.181

Table 656: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Fat.digestion.and.absorption, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 657: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Fatty.acid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.23e-02	1.08e-01	-0.114	0.910	-2.33e-01	2.08e-01	0.000000
L3.Fatty.acid.biosynthesis	2.82e-08	2.16e-07	0.131	0.897	-4.12e-07	4.69e-07	0.000551

Table 658: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Fatty.acid.elongation.in.mitochondria, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 659: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Fatty.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.59e-03	8.06e-02	0.0197	0.984	-1.63e-01	1.66e-01	0.00e+00
L3.Fatty.acid.metabolism	-6.15e-09	2.36e-07	-0.0261	0.979	-4.88e-07	4.76e-07	2.19e-05

Table 660: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Fc.epsilon.RI.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 661: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Fc.gamma.R.mediated.phagocytosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.0302	0.0524	-0.577	0.568	-0.13720	0.0767	0.000
L3.Fc.gamma.R.mediated.phagocytosis	0.0285	0.0152	1.872	0.071	-0.00259	0.0595	0.102

Table 662: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Flagellar.assembly, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.81e-02	6.62e-02	0.274	0.786	-1.17e-01	1.53e-01	0.00000
L3.Flagellar.assembly	-1.16e-07	2.57e-07	-0.449	0.657	-6.41e-07	4.10e-07	0.00647

Table 663: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Flavone.and.flavonol.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.23e-01	5.47e-02	2.24	0.032421	1.10e-02	2.34e-01	0.000
L3.Flavone.and.flavonol.biosynthesis	-2.49e-05	6.70e-06	-3.72	0.000829	-3.86e-05	-1.12e-05	0.308

Table 664: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Flavonoid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.31e-03	0.054452	0.0975	0.923	-1.06e-01	1.17e-01	0.00000
L3.Flavonoid.biosynthesis	-4.80e-06	0.000013	-0.3705	0.714	-3.13e-05	2.17e-05	0.00441

Table 665: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Fluorobenzoate.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.25e-02	5.73e-02	0.218	0.829	-1.05e-01	1.30e-01	0.00000
L3.Fluorobenzoate.degradation	-8.34e-07	1.55e-06	-0.539	0.594	-3.99e-06	2.33e-06	0.00928

Table 666: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Focal.adhesion, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 667: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Folate.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.12e-02	1.10e-01	-0.194	0.848	-2.45e-01	2.03e-01	0.00000
L3.Folate.biosynthesis	5.65e-08	2.56e-07	0.221	0.827	-4.67e-07	5.80e-07	0.00157

Table 668: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Fructose.and.mannose.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.98e-02	8.96e-02	0.667	0.510	-1.23e-01	2.43e-01	0.0000
L3.Fructose.and.mannose.metabolism	-6.65e-08	8.11e-08	-0.820	0.419	-2.32e-07	9.91e-08	0.0212

Table 669: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Function.unknown, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.36e-03	8.05e-02	0.104	0.918	-1.56e-01	1.73e-01	0.000000
L3.Function.unknown	-6.17e-09	4.49e-08	-0.137	0.892	-9.78e-08	8.55e-08	0.000609

Table 670: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.G.protein.coupled.receptors, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 671: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.GTP.binding.proteins, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 672: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Galactose.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.67e-02	1.12e-01	0.504	0.618	-1.73e-01	2.86e-01	0.0000
L3.Galactose.metabolism	-7.46e-08	1.31e-07	-0.570	0.573	-3.42e-07	1.93e-07	0.0104

Table 673: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Gastric.acid.secretion, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 674: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.General.function.prediction.only, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.46e-02	1.01e-01	0.641	0.526	-1.41e-01	2.7e-01	0.0000
L3.General.function.prediction.only	-2.09e-08	2.78e-08	-0.750	0.459	-7.77e-08	3.6e-08	0.0178

Table 675: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Geraniol.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.23e-02	6.46e-02	0.346	0.732	-1.10e-01	1.54e-01	0.0000
L3.Geraniol.degradation	-3.09e-07	5.24e-07	-0.590	0.560	-1.38e-06	7.60e-07	0.0111

Table 676: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Germination, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.27e-02	5.81e-02	0.563	0.578	-8.60e-02	1.51e-01	0.000
L3.Germination	-8.25e-06	6.82e-06	-1.209	0.236	-2.22e-05	5.69e-06	0.045

Table 677: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Glioma, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 678: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Glutamatergic.synapse, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.46e-01	1.09e-01	1.34	0.189	-7.61e-02	3.69e-01	0.0000
L3.Glutamatergic.synapse	-1.96e-06	1.29e-06	-1.52	0.139	-4.59e-06	6.76e-07	0.0692

Table 679: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Glutathione.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.45e-02	8.34e-02	0.173	0.863	-1.56e-01	1.85e-01	0.00000
L3.Glutathione.metabolism	-5.78e-08	2.58e-07	-0.224	0.825	-5.86e-07	4.70e-07	0.00161

Table 680: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Glycan.bindng.proteins, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 681: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Glycan.biosynthesis.and.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.13e-02	6.61e-02	0.322	0.750	-1.14e-01	1.56e-01	0.00000
L3.Glycan.biosynthesis.and.metabolism	-4.05e-07	7.66e-07	-0.529	0.601	-1.97e-06	1.16e-06	0.00894

Table 682: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Glycerolipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.70e-02	9.16e-02	-0.185	0.854	-2.04e-01	1.70e-01	0.00000
L3.Glycerolipid.metabolism	4.88e-08	2.15e-07	0.226	0.822	-3.91e-07	4.89e-07	0.00165

Table 683: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Glycerophospholipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.85e-02	9.24e-02	0.309	0.76	-1.60e-01	2.17e-01	0.00000
L3.Glycerophospholipid.metabolism	-6.31e-08	1.68e-07	-0.376	0.71	-4.06e-07	2.80e-07	0.00453

Table 684: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Glycine..serine.and.threonine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.89e-02	9.79e-02	0.397	0.694	-1.61e-01	2.39e-01	0.0000
L3.Glycine..serine.and.threonine.metabolism	-5.27e-08	1.12e-07	-0.471	0.641	-2.81e-07	1.76e-07	0.0071

Table 685: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Glycolysis. . . Gluconeogenesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.25e-03	1.02e-01	-0.0904	0.929	-2.18e-01	2.00e-01	0.000000
L3.Glycolysis. . . Gluconeogenesis	8.74e-09	8.29e-08	0.1055	0.917	-1.61e-07	1.78e-07	0.000359

Table 686: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Glycosaminoglycan.biosynthesis. . . chondroitin.sulfate, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R
Intercept	-0.0138	0.0530	-0.261	0.796	-0.122	0.0944	0
L3.Glycosaminoglycan.biosynthesis. . . chondroitin.sulfate	0.0553	0.0486	1.138	0.264	-0.044	0.1546	0

Table 687: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Glycosaminoglycan.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.42e-01	6.80e-02	3.56	0.001245	1.03e-01	3.81e-01	0.000
L3.Glycosaminoglycan.degradation	-3.34e-06	7.49e-07	-4.46	0.000107	-4.87e-06	-1.81e-06	0.391

Table 688: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Glycosphingolipid.biosynthesis. . . ganglio.series, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.09e-01	6.87e-02	3.04	0.004887	6.84e-02	3.49e-01	0.(
L3.Glycosphingolipid.biosynthesis. . . ganglio.series	-4.51e-06	1.16e-06	-3.89	0.000512	-6.87e-06	-2.14e-06	0.3

Table 689: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Glycosphingolipid.biosynthesis. . . globo.series, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.08e-01	7.91e-02	2.63	0.01333	4.65e-02	3.70e-01	0.00
L3.Glycosphingolipid.biosynthesis. . . globo.series	-2.57e-06	8.01e-07	-3.21	0.00314	-4.21e-06	-9.37e-07	0.25

Table 690: diversity_vs_picrust_L3_neo: wunifrac.PC.1
vs L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series,
df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.
Intercept	9.81e-03	5.36e-02	0.183	0.856	-0.099567	0.1
L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series	-7.17e-05	9.03e-05	-0.794	0.434	-0.000256	0.0

Table 691: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Glycosylphosphatidylinositol.GPI..anchor.biosynthesis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 692: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Glycosyltransferases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e-03	9.75e-02	0.0103	0.992	-1.98e-01	2.00e-01	0.00e+00
L3.Glycosyltransferases	-2.79e-09	2.28e-07	-0.0122	0.990	-4.69e-07	4.63e-07	4.82e-06

Table 693: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Glyoxylate.and.dicarboxylate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.50e-02	7.83e-02	0.702	0.488	-1.05e-01	2.15e-01	0.0000
L3.Glyoxylate.and.dicarboxylate.metabolism	-1.18e-07	1.26e-07	-0.938	0.356	-3.75e-07	1.39e-07	0.0276

Table 694: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.GnRH.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.0302	0.0524	-0.577	0.568	-0.13720	0.0767	0.000
L3.GnRH.signaling.pathway	0.0285	0.0152	1.872	0.071	-0.00259	0.0595	0.102

Table 695: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Hedgehog.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 696: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Hematopoietic.cell.lineage, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 697: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Hepatitis.C, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 698: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Histidine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.42e-01	1.09e-01	1.30	0.205	-8.17e-02	3.65e-01	0.0000
L3.Histidine.metabolism	-2.77e-07	1.89e-07	-1.46	0.154	-6.63e-07	1.10e-07	0.0646

Table 699: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Homologous.recombination, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.20e-02	1.23e-01	-0.503	0.619	-3.14e-01	1.90e-01	0.00000
L3.Homologous.recombination	7.89e-08	1.42e-07	0.555	0.583	-2.11e-07	3.69e-07	0.00985

Table 700: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Huntington.s.disease, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.51e-02	9.19e-02	0.600	0.553	-1.33e-01	2.43e-01	0.0000
L3.Huntington.s.disease	-1.27e-06	1.74e-06	-0.729	0.472	-4.82e-06	2.29e-06	0.0168

Table 701: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Hypertrophic.cardiomyopathy..HCM., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00796	0.05456	-0.146	0.885	-0.11940	0.103	0.00000
L3.Hypertrophic.cardiomyopathy..HCM.	0.00206	0.00391	0.525	0.603	-0.00594	0.010	0.00882

Table 702: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Indole.alkaloid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.0318	0.0598	-0.531	0.599	-0.1540	0.0904	0.0000
L3.Indole.alkaloid.biosynthesis	0.0565	0.0535	1.056	0.299	-0.0528	0.1658	0.0347

Table 703: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Influenza.A, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.04263	0.05534	-0.77	0.4471	-0.155649	0.07038	0.0000
L3.Influenza.A	0.00359	0.00199	1.80	0.0817	-0.000481	0.00766	0.0947

Table 704: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Inorganic.ion.transport.and.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.13e-02	7.27e-02	0.43	0.67	-1.17e-01	1.80e-01	0.0000
L3.Inorganic.ion.transport.and.metabolism	-1.21e-07	1.95e-07	-0.62	0.54	-5.19e-07	2.77e-07	0.0122

Table 705: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Inositol.phosphate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.44e-02	6.84e-02	0.357	0.723	-1.15e-01	1.64e-01	0.00000
L3.Inositol.phosphate.metabolism	-1.90e-07	3.42e-07	-0.556	0.582	-8.88e-07	5.08e-07	0.00987

Table 706: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Insulin.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.84e-02	1.06e-01	0.363	0.719	-1.78e-01	2.55e-01	0.0000
L3.Insulin.signaling.pathway	-6.29e-07	1.50e-06	-0.418	0.679	-3.70e-06	2.44e-06	0.0056

Table 707: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Ion.channels, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.70e-02	8.97e-02	-1.08	0.288	-2.80e-01	8.62e-02	0.000
L3.Ion.channels	2.56e-06	1.94e-06	1.32	0.198	-1.41e-06	6.53e-06	0.053

Table 708: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Isoflavonoid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00582	0.05459	-0.107	0.916	-0.1173	0.1057	0.00000
L3.Isoflavonoid.biosynthesis	0.00316	0.00807	0.391	0.699	-0.0133	0.0196	0.00491

Table 709: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Isoquinoline.alkaloid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.68e-02	7.76e-02	1.12	0.273	-7.18e-02	2.45e-01	0.0000
L3.Isoquinoline.alkaloid.biosynthesis	-1.70e-06	1.15e-06	-1.48	0.150	-4.05e-06	6.48e-07	0.0659

Table 710: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Leishmaniasis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 711: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Leukocyte.transendothelial.migration, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 712: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Limonene.and.pinene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.23e-02	7.52e-02	0.429	0.671	-1.21e-01	1.86e-01	0.0000
L3.Limonene.and.pinene.degradation	-3.45e-07	5.76e-07	-0.598	0.554	-1.52e-06	8.33e-07	0.0114

Table 713: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Linoleic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.98e-01	9.83e-02	2.02	0.0528	-2.57e-03	3.99e-01	0.000
L3.Linoleic.acid.metabolism	-5.35e-06	2.31e-06	-2.32	0.0275	-1.01e-05	-6.35e-07	0.148

Table 714: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Lipid.biosynthesis.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.53e-02	1.03e-01	0.245	0.808	-1.86e-01	2.37e-01	0.0000
L3.Lipid.biosynthesis.proteins	-5.01e-08	1.76e-07	-0.284	0.778	-4.10e-07	3.10e-07	0.0026

Table 715: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Lipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.81e-03	7.66e-02	0.128	0.899	-1.47e-01	1.66e-01	0.000
L3.Lipid.metabolism	-7.59e-08	4.30e-07	-0.176	0.861	-9.55e-07	8.03e-07	0.001

Table 716: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Lipoic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.30e-01	8.60e-02	1.52	0.1399	-4.52e-02	3.06e-01	0.000
L3.Lipoic.acid.metabolism	-2.66e-06	1.43e-06	-1.86	0.0725	-5.58e-06	2.59e-07	0.101

Table 717: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Lipopolysaccharide.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.08e-02	7.15e-02	0.85	0.402	-8.52e-02	2.07e-01	0.0000
L3.Lipopolysaccharide.biosynthesis	-2.32e-07	1.89e-07	-1.22	0.231	-6.18e-07	1.55e-07	0.0461

Table 718: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Lipopolysaccharide.biosynthesis.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.84e-02	7.56e-02	0.772	0.446	-9.60e-02	2.13e-01	0.0000
L3.Lipopolysaccharide.biosynthesis.proteins	-1.34e-07	1.27e-07	-1.059	0.298	-3.93e-07	1.25e-07	0.0349

Table 719: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Long.term.depression, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 720: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Long.term.potentiation, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 721: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Lysine.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.54e-02	1.16e-01	0.220	0.828	-2.11e-01	2.62e-01	0.00000
L3.Lysine.biosynthesis	-4.07e-08	1.65e-07	-0.246	0.807	-3.78e-07	2.97e-07	0.00196

Table 722: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Lysine.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.61e-02	7.22e-02	0.500	0.621	-1.11e-01	1.84e-01	0.0000
L3.Lysine.degradation	-2.36e-07	3.26e-07	-0.723	0.475	-9.02e-07	4.30e-07	0.0166

Table 723: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Lysosome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.73e-01	6.30e-02	4.32	1.56e-04	1.44e-01	4.01e-01	0.000
L3.Lysosome	-2.76e-06	5.12e-07	-5.38	7.89e-06	-3.80e-06	-1.71e-06	0.483

Table 724:   diversity_vs_picrust_L3_neo: wunifrac.PC.1   vs
L3.MAPK.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 725:   diversity_vs_picrust_L3_neo: wunifrac.PC.1   vs
L3.MAPK.signaling.pathway. . . yeast, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.07e-01	1.08e-01	0.994	0.328	-1.13e-01	3.28e-01	0.0000
L3.MAPK.signaling.pathway. . . yeast	-2.39e-06	2.11e-06	-1.132	0.267	-6.71e-06	1.93e-06	0.0397

Table 726:   diversity_vs_picrust_L3_neo: wunifrac.PC.1   vs
L3.Measles, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 727:   diversity_vs_picrust_L3_neo: wunifrac.PC.1   vs
L3.Meiosis. . . yeast, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.74e-02	4.77e-02	-1.83	0.076612	-1.85e-01	9.93e-03	0.000
L3.Meiosis. . . yeast	2.75e-05	6.84e-06	4.03	0.000356	1.36e-05	4.15e-05	0.343

Table 728:   diversity_vs_picrust_L3_neo: wunifrac.PC.1   vs
L3.Melanogenesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.014371	0.055255	0.260	0.797	-0.098475	0.127217	0.0000
L3.Melanogenesis	-0.000104	0.000133	-0.784	0.439	-0.000375	0.000167	0.0194

Table 729:   diversity_vs_picrust_L3_neo: wunifrac.PC.1   vs
L3.Membrane.and.intracellular.structural.molecules, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.08e-02	7.70e-02	0.79	0.436	-9.64e-02	2.18e-01	0.0
L3.Membrane.and.intracellular.structural.molecules	-1.07e-07	1.01e-07	-1.07	0.295	-3.13e-07	9.83e-08	0.0

Table 730: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Metabolism.of.cofactors.and.vitamins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.30e-03	7.77e-02	0.0425	0.966	-1.55e-01	1.62e-01	0.000000
L3.Metabolism.of.cofactors.and.vitamins	-2.33e-08	4.04e-07	-0.0578	0.954	-8.47e-07	8.01e-07	0.000108

Table 731: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Metabolism.of.xenobiotics.by.cytochrome.P450, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.06e-04	6.77e-02	-0.0104	0.992	-1.39e-01	1.38e-01	0.00
L3.Metabolism.of.xenobiotics.by.cytochrome.P450	1.48e-08	8.91e-07	0.0166	0.987	-1.80e-06	1.83e-06	8.88

Table 732: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Methane.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.55e-02	1.07e-01	0.425	0.674	-1.73e-01	2.64e-01	0.00000
L3.Methane.metabolism	-4.60e-08	9.44e-08	-0.488	0.629	-2.39e-07	1.47e-07	0.00761

Table 733: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Mineral.absorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.021080	6.46e-02	-0.326	0.747	-1.53e-01	1.11e-01	0.00000
L3.Mineral.absorption	0.000012	2.16e-05	0.557	0.582	-3.21e-05	5.61e-05	0.00991

Table 734: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Mismatch.repair, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.95e-02	1.25e-01	-0.156	0.877	-2.74e-01	2.35e-01	0.000000
L3.Mismatch.repair	2.88e-08	1.67e-07	0.172	0.864	-3.13e-07	3.70e-07	0.000956

Table 735: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.N.Glycan.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.23e-01	6.24e-02	1.97	0.0582	-4.56e-03	2.5e-01	0.000
L3.N.Glycan.biosynthesis	-8.81e-06	2.99e-06	-2.94	0.0062	-1.49e-05	-2.7e-06	0.219

Table 736:   diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.NOD.like.receptor.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.89e-01	8.12e-02	2.33	0.02647	2.37e-02	3.55e-01	0.000
L3.NOD.like.receptor.signaling.pathway	-7.47e-06	2.62e-06	-2.85	0.00776	-1.28e-05	-2.12e-06	0.208

Table 737:   diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Naphthalene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.67e-02	1.08e-01	0.341	0.736	-1.83e-01	2.56e-01	0.0000
L3.Naphthalene.degradation	-2.93e-07	7.49e-07	-0.391	0.699	-1.82e-06	1.24e-06	0.0049

Table 738:   diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Neuroactive.ligand.receptor.interaction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 739:   diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Neurotrophin.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 740:   diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Nicotinate.and.nicotinamide.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.95e-03	1.05e-01	0.0187	0.985	-2.12e-01	2.16e-01	0.0e+00
L3.Nicotinate.and.nicotinamide.metabolism	-5.29e-09	2.45e-07	-0.0216	0.983	-5.05e-07	4.95e-07	1.5e-05

Table 741:   diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Nitrogen.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.00e-02	8.73e-02	0.801	0.429	-1.08e-01	2.48e-01	0.0000
L3.Nitrogen.metabolism	-1.01e-07	1.01e-07	-0.995	0.328	-3.08e-07	1.06e-07	0.0309

Table 742: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Nitrotoluene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.94e-03	7.43e-02	-0.0396	0.969	-1.55e-01	1.49e-01	0.000000
L3.Nitrotoluene.degradation	4.59e-08	8.19e-07	0.0561	0.956	-1.63e-06	1.72e-06	0.000102

Table 743: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Non.homologous.end.joining, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.81e-02	5.96e-02	0.471	0.641	-9.36e-02	1.50e-01	0.0000
L3.Non.homologous.end.joining	-2.47e-05	2.58e-05	-0.959	0.345	-7.73e-05	2.79e-05	0.0288

Table 744: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Notch.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0107	0.0566	0.189	0.851	-0.105	0.126	0.00000
L3.Notch.signaling.pathway	-0.0429	0.0856	-0.501	0.620	-0.218	0.132	0.00802

Table 745: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Novobiocin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.44e-02	9.68e-02	0.356	0.725	-1.63e-01	2.32e-01	0.00000
L3.Novobiocin.biosynthesis	-3.15e-07	7.44e-07	-0.423	0.675	-1.83e-06	1.20e-06	0.00575

Table 746: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Nucleotide.excision.repair, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.99e-02	1.32e-01	-0.755	0.456	-3.70e-01	1.70e-01	0.0000
L3.Nucleotide.excision.repair	3.29e-07	4.01e-07	0.822	0.418	-4.89e-07	1.15e-06	0.0213

Table 747: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Nucleotide.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.19e-02	6.95e-02	-0.315	0.755	-1.64e-01	1.20e-01	0.00000
L3.Nucleotide.metabolism	2.51e-07	5.21e-07	0.481	0.634	-8.13e-07	1.31e-06	0.00741

Table 748: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Olfactory.transduction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 749: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.One.carbon.pool.by.folate, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.11e-02	1.25e-01	-0.0888	0.930	-2.66e-01	2.44e-01	0.000000
L3.One.carbon.pool.by.folate	2.16e-08	2.20e-07	0.0979	0.923	-4.29e-07	4.72e-07	0.000309

Table 750: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Oocyte.meiosis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 751: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Other.glycan.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.70e-01	7.37e-02	3.67	0.000941	1.20e-01	4.21e-01	0.000
L3.Other.glycan.degradation	-9.91e-07	2.25e-07	-4.41	0.000121	-1.45e-06	-5.33e-07	0.386

Table 752: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Other.ion.coupled.transporters, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.93e-02	8.26e-02	0.476	0.637	-1.29e-01	2.08e-01	0.0000
L3.Other.ion.coupled.transporters	-2.96e-08	4.81e-08	-0.616	0.543	-1.28e-07	6.86e-08	0.0121

Table 753: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Other.transporters, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.67e-02	8.44e-02	0.672	0.507	-1.16e-01	2.29e-01	0.000
L3.Other.transporters	-2.44e-07	2.86e-07	-0.854	0.400	-8.29e-07	3.40e-07	0.023

Table 754: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Other.types.of.O.glycan.biosynthesis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 755: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Others, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.61e-02	9.64e-02	0.374	0.711	-1.61e-01	2.33e-01	0.00000
L3.Others	-3.73e-08	8.36e-08	-0.446	0.659	-2.08e-07	1.33e-07	0.00637

Table 756: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Oxidative.phosphorylation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.69e-02	1.06e-01	0.349	0.730	-1.79e-01	2.53e-01	0.00000
L3.Oxidative.phosphorylation	-4.21e-08	1.05e-07	-0.402	0.691	-2.56e-07	1.72e-07	0.00518

Table 757: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.PPAR.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.71e-02	1.11e-01	0.873	0.390	-1.30e-01	3.24e-01	0.0000
L3.PPAR.signaling.pathway	-1.28e-06	1.30e-06	-0.987	0.332	-3.94e-06	1.37e-06	0.0305

Table 758: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Pancreatic.cancer, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 759: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Pancreatic.secretion, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 760: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Pantothenate.and.CoA.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.14e-02	1.09e-01	0.105	0.917	-2.11e-01	2.34e-01	0.000000
L3.Pantothenate.and.CoA.biosynthesis	-2.20e-08	1.84e-07	-0.120	0.906	-3.98e-07	3.54e-07	0.000462

Table 761: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Parkinson.s.disease, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.42e-02	5.64e-02	0.252	0.803	-1.01e-01	1.29e-01	0.0000
L3.Parkinson.s.disease	-2.26e-05	3.35e-05	-0.672	0.506	-9.11e-05	4.59e-05	0.0144

Table 762: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Pathogenic.Escherichia.coli.infection, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.0251	0.0529	-0.474	0.639	-0.13308	0.0830	0.0000
L3.Pathogenic.Escherichia.coli.infection	0.0178	0.0111	1.603	0.119	-0.00488	0.0405	0.0765

Table 763: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Pathways.in.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.71e-02	8.24e-02	0.814	0.422	-1.01e-01	2.35e-01	0.000
L3.Pathways.in.cancer	-1.99e-06	1.90e-06	-1.045	0.304	-5.87e-06	1.90e-06	0.034

Table 764: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Penicillin.and.cephalosporin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.01e-02	8.35e-02	-0.84	0.408	-2.41e-01	1.00e-01	0.0000
L3.Penicillin.and.cephalosporin.biosynthesis	2.06e-06	1.93e-06	1.07	0.293	-1.87e-06	5.99e-06	0.0356

Table 765: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Pentose.and.glucuronate.interconversions, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.24e-02	7.21e-02	1.28	0.2099	-5.49e-02	2.40e-01	0.0000
L3.Pentose.and.glucuronate.interconversions	-1.91e-07	1.07e-07	-1.78	0.0852	-4.10e-07	2.82e-08	0.0927

Table 766: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Pentose.phosphate.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.17e-02	9.69e-02	0.533	0.598	-1.46e-01	2.50e-01	0.0000
L3.Pentose.phosphate.pathway	-6.72e-08	1.06e-07	-0.633	0.531	-2.84e-07	1.49e-07	0.0128

Table 767: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Peptidases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.41e-03	1.08e-01	0.0868	0.931	-2.12e-01	2.31e-01	0.000000
L3.Peptidases	-5.56e-09	5.59e-08	-0.0994	0.922	-1.20e-07	1.09e-07	0.000318

Table 768: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Peptidoglycan.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.06e-01	1.17e-01	-0.909	0.370	-3.45e-01	1.32e-01	0.0000
L3.Peptidoglycan.biosynthesis	1.50e-07	1.48e-07	1.015	0.318	-1.52e-07	4.51e-07	0.0321

Table 769: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Peroxisome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.15e-01	9.87e-02	1.17	0.251	-8.61e-02	3.17e-01	0.0000
L3.Peroxisome	-7.94e-07	5.81e-07	-1.37	0.182	-1.98e-06	3.92e-07	0.0569

Table 770: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Pertussis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.47e-02	5.97e-02	0.413	0.682	-9.72e-02	1.46e-01	0.0000
L3.Pertussis	-2.72e-07	3.22e-07	-0.845	0.405	-9.30e-07	3.86e-07	0.0225

Table 771: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Phagosome, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 772: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Phenylalanine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.23e-02	6.81e-02	0.622	0.539	-9.68e-02	1.81e-01	0.0000
L3.Phenylalanine.metabolism	-2.24e-07	2.34e-07	-0.959	0.345	-7.02e-07	2.54e-07	0.0288

Table 773: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-3.79e-02	1.10e-01	-0.345	0.733	-2.63e-01	1.87e-01
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis	5.68e-08	1.45e-07	0.392	0.698	-2.39e-07	3.53e-07

Table 774: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Phenylpropanoid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.79e-01	7.11e-02	2.52	0.01728	3.40e-02	3.24e-01	0.000
L3.Phenylpropanoid.biosynthesis	-1.24e-06	3.80e-07	-3.27	0.00273	-2.02e-06	-4.65e-07	0.256

Table 775: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Phosphatidylinositol.signaling.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.02e-03	1.16e-01	-0.0434	0.966	-2.41e-01	2.31e-01	0.00e+00
L3.Phosphatidylinositol.signaling.system	5.38e-08	1.10e-06	0.0487	0.961	-2.20e-06	2.31e-06	7.65e-05

Table 776: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Phosphonate.and.phosphinate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.57e-02	8.98e-02	-0.286	0.777	-2.09e-01	1.58e-01	0.000
L3.Phosphonate.and.phosphinate.metabolism	3.59e-07	1.02e-06	0.353	0.727	-1.72e-06	2.43e-06	0.004

Table 777: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Phosphotransferase.system..PTS., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.70e-02	7.61e-02	-0.355	0.725	-1.82e-01	1.28e-01	0.00000
L3.Phosphotransferase.system..PTS.	2.99e-08	6.10e-08	0.489	0.628	-9.48e-08	1.55e-07	0.00766

Table 778: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Photosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.22e-01	1.28e-01	-0.953	0.348	-3.85e-01	1.40e-01	0.0000
L3.Photosynthesis	4.30e-07	4.13e-07	1.041	0.306	-4.13e-07	1.27e-06	0.0338

Table 779: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Photosynthesis. . . antenna.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.07737	0.05383	-1.44	0.16095	-0.18730	0.0326	0.000
L3.Photosynthesis. . . antenna.proteins	0.00673	0.00234	2.88	0.00735	0.00195	0.0115	0.211

Table 780: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Photosynthesis.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.17e-01	1.26e-01	-0.926	0.362	-3.74e-01	1.41e-01	0.0000
L3.Photosynthesis.proteins	4.03e-07	3.97e-07	1.016	0.318	-4.07e-07	1.21e-06	0.0322

Table 781: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Phototransduction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 782: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Phototransduction. . . fly, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 783: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Plant.pathogen.interaction, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.27e-02	1.03e-01	0.317	0.753	-1.78e-01	2.43e-01	0.00000
L3.Plant.pathogen.interaction	-2.99e-07	8.09e-07	-0.369	0.715	-1.95e-06	1.35e-06	0.00438

Table 784: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Polycyclic.aromatic.hydrocarbon.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.90e-03	1.23e-01	-0.0235	0.981	-2.55e-01	2.49e-01	0.00e
L3.Polycyclic.aromatic.hydrocarbon.degradation	3.13e-08	1.20e-06	0.0260	0.979	-2.42e-06	2.49e-06	2.18e

Table 785: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Polyketide.sugar.unit.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.40e-01	1.07e-01	1.31	0.202	-7.88e-02	3.58e-01	0.0000
L3.Polyketide.sugar.unit.biosynthesis	-9.44e-07	6.36e-07	-1.48	0.148	-2.24e-06	3.56e-07	0.0663

Table 786: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Pores.ion.channels, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.15e-02	7.22e-02	0.99	0.330	-7.60e-02	2.19e-01	0.0000
L3.Pores.ion.channels	-1.66e-07	1.19e-07	-1.40	0.172	-4.09e-07	7.64e-08	0.0594

Table 787: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Porphyrin.and.chlorophyll.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.63e-02	8.42e-02	1.03	0.313	-8.56e-02	2.58e-01	0.0000
L3.Porphyrin.and.chlorophyll.metabolism	-1.11e-07	8.59e-08	-1.29	0.206	-2.87e-07	6.44e-08	0.0511

Table 788: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Prenyltransferases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.47e-02	1.21e-01	0.535	0.596	-1.82e-01	3.11e-01	0.0000
L3.Prenyltransferases	-2.56e-07	4.31e-07	-0.594	0.557	-1.13e-06	6.23e-07	0.0113

Table 789: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Primary.bile.acid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.11e-01	1.02e-01	1.09	0.284	-9.67e-02	3.19e-01	0.000
L3.Primary.bile.acid.biosynthesis	-5.03e-06	3.98e-06	-1.26	0.216	-1.31e-05	3.09e-06	0.049

Table 790: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Primary.immunodeficiency, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.54e-02	1.16e-01	-0.648	0.522	-3.13e-01	1.62e-01	0.0000
L3.Primary.immunodeficiency	1.34e-06	1.85e-06	0.725	0.474	-2.44e-06	5.13e-06	0.0167

Table 791: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Prion.diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.58e-03	6.28e-02	0.105	0.917	-1.22e-01	1.35e-01	0.00000
L3.Prion.diseases	-9.99e-07	5.21e-06	-0.192	0.849	-1.16e-05	9.65e-06	0.00118

Table 792: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Progesterone.mediated.oocyte.maturation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.72e-01	8.02e-02	2.14	0.0404	7.99e-03	3.36e-01	0.000
L3.Progesterone.mediated.oocyte.maturation	-7.30e-06	2.75e-06	-2.65	0.0126	-1.29e-05	-1.68e-06	0.185

Table 793: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Propanoate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.40e-05	8.96e-02	0.00105	0.999	-1.83e-01	1.83e-01	0.00e+00
L3.Propanoate.metabolism	-1.88e-10	1.45e-07	-0.00130	0.999	-2.97e-07	2.97e-07	5.42e-08

Table 794: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Prostate.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.76e-01	7.71e-02	2.29	0.02941	0.018886	3.34e-01	0.00
L3.Prostate.cancer	-6.99e-06	2.43e-06	-2.87	0.00743	-0.000012	-2.02e-06	0.21

Table 795: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Proteasome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.67e-02	1.20e-01	0.638	0.528	-1.69e-01	3.22e-01	0.0000
L3.Proteasome	-2.67e-06	3.78e-06	-0.708	0.484	-1.04e-05	5.04e-06	0.0159

Table 796: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Protein.digestion.and.absorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.92e-01	5.80e-02	3.3	0.002471	7.31e-02	3.10e-01	0.000
L3.Protein.digestion.and.absorption	-1.13e-05	2.45e-06	-4.6	0.000072	-1.62e-05	-6.26e-06	0.406

Table 797: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Protein.export, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.09e-02	1.22e-01	-0.583	0.564	-3.19e-01	1.78e-01	0.0000
L3.Protein.export	1.35e-07	2.10e-07	0.646	0.523	-2.93e-07	5.63e-07	0.0133

Table 798: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Protein.folding.and.associated.processing, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.08e-02	9.25e-02	0.225	0.823	-1.68e-01	2.10e-01	0.00000
L3.Protein.folding.and.associated.processing	-3.36e-08	1.23e-07	-0.274	0.786	-2.85e-07	2.17e-07	0.00241

Table 799: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Protein.kinases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.25e-02	8.19e-02	-0.152	0.880	-1.80e-01	1.55e-01	0.00000
L3.Protein.kinases	4.07e-08	2.05e-07	0.199	0.844	-3.77e-07	4.59e-07	0.00127

Table 800: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Protein.processing.in.endoplasmic.reticulum, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.84e-01	7.51e-02	3.78	7.02e-04	1.30e-01	4.37e-01	0.000
L3.Protein.processing.in.endoplasmic.reticulum	-6.98e-06	1.55e-06	-4.49	9.65e-05	-1.02e-05	-3.81e-06	0.395

Table 801: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Proximal.tubule.bicarbonate.reclamation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.92e-02	6.71e-02	0.584	0.564	-9.79e-02	1.76e-01	0.0000
L3.Proximal.tubule.bicarbonate.reclamation	-1.55e-06	1.68e-06	-0.921	0.364	-4.99e-06	1.89e-06	0.0267

Table 802: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Purine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.05e-02	1.14e-01	-0.444	0.66	-2.83e-01	1.82e-01	0.00000
L3.Purine.metabolism	2.54e-08	5.08e-08	0.500	0.62	-7.83e-08	1.29e-07	0.00801

Table 803: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Pyrimidine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.59e-02	1.21e-01	-0.379	0.707	-2.93e-01	2.01e-01	0.00000
L3.Pyrimidine.metabolism	2.96e-08	7.03e-08	0.421	0.677	-1.14e-07	1.73e-07	0.00569

Table 804: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Pyruvate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.26e-02	9.34e-02	0.135	0.894	-1.78e-01	2.03e-01	0.000000
L3.Pyruvate.metabolism	-1.31e-08	8.02e-08	-0.163	0.872	-1.77e-07	1.51e-07	0.000856

Table 805: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.RIG.I.like.receptor.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.62e-02	0.065362	0.248	0.806	-1.17e-01	1.5e-01	0.00000
L3.RIG.I.like.receptor.signaling.pathway	-1.13e-05	0.000027	-0.416	0.680	-6.65e-05	4.4e-05	0.00556

Table 806: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.RNA.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.72e-02	1.20e-01	0.478	0.636	-1.87e-01	3.01e-01	0.00000
L3.RNA.degradation	-1.53e-07	2.88e-07	-0.532	0.598	-7.42e-07	4.35e-07	0.00906

Table 807: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.RNA.polymerase, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.96e-01	1.14e-01	-1.71	0.0967	-4.30e-01	3.75e-02	0.000
L3.RNA.polymerase	1.36e-06	7.14e-07	1.90	0.0666	-9.89e-08	2.82e-06	0.105

Table 808: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.RNA.transport, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.40e-02	1.00e-01	-0.539	0.594	-2.58e-01	1.5e-01	0.0000
L3.RNA.transport	5.43e-07	8.58e-07	0.632	0.532	-1.21e-06	2.3e-06	0.0127

Table 809: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Regulation.of.actin.cytoskeleton, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 810: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Renal.cell.carcinoma, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.92e-02	6.50e-02	-0.602	0.551	-1.72e-01	9.37e-02	0.000
L3.Renal.cell.carcinoma	3.83e-06	3.85e-06	0.996	0.327	-4.02e-06	1.17e-05	0.031

Table 811: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Renin.angiotensin.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.013237	0.052586	-0.252	0.803	-0.120632	0.09416	0.0000
L3.Renin.angiotensin.system	0.000718	0.000596	1.205	0.238	-0.000499	0.00194	0.0447

Table 812: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Replication..recombination.and.repair.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.82e-02	1.05e-01	-0.461	0.648	-2.62e-01	1.65e-01	0.00
L3.Replication..recombination.and.repair.proteins	7.43e-08	1.40e-07	0.533	0.598	-2.11e-07	3.59e-07	0.00

Table 813: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Restriction.enzyme, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.70e-02	9.77e-02	0.788	0.437	-1.23e-01	2.77e-01	0.0000
L3.Restriction.enzyme	-5.01e-07	5.38e-07	-0.931	0.359	-1.60e-06	5.98e-07	0.0272

Table 814: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Retinol.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.70e-02	7.62e-02	-0.223	0.825	-1.73e-01	1.39e-01	0.00000
L3.Retinol.metabolism	4.68e-07	1.52e-06	0.307	0.761	-2.64e-06	3.58e-06	0.00304

Table 815: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Rheumatoid.arthritis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 816: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Riboflavin.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.99e-02	8.57e-02	0.466	0.645	-1.35e-01	2.15e-01	0.000
L3.Riboflavin.metabolism	-1.95e-07	3.31e-07	-0.588	0.561	-8.71e-07	4.81e-07	0.011

Table 817: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Ribosome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.04e-01	1.25e-01	-0.831	0.412	-3.60e-01	1.52e-01	0.0000
L3.Ribosome	5.46e-08	5.98e-08	0.914	0.368	-6.75e-08	1.77e-07	0.0262

Table 818: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Ribosome.Biogenesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.48e-02	1.07e-01	-0.605	0.550	-2.83e-01	1.54e-01	0.0000
L3.Ribosome.Biogenesis	5.35e-08	7.72e-08	0.693	0.494	-1.04e-07	2.11e-07	0.0153

Table 819: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Ribosome.biogenesis.in.eukaryotes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.44e-01	1.09e-01	-1.32	0.198	-3.68e-01	7.93e-02	0.0000
L3.Ribosome.biogenesis.in.eukaryotes	3.32e-06	2.23e-06	1.49	0.147	-1.24e-06	7.89e-06	0.0666

Table 820: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Salivary.secretion, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 821: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Secondary.bile.acid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.10e-01	1.02e-01	1.08	0.287	-9.74e-02	3.18e-01	0.0000
L3.Secondary.bile.acid.biosynthesis	-5.05e-06	4.02e-06	-1.26	0.219	-1.33e-05	3.16e-06	0.0484

Table 822: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Secretion.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.31e-02	7.71e-02	-0.170	0.866	-1.71e-01	1.44e-01	0.00000
L3.Secretion.system	1.01e-08	4.32e-08	0.233	0.817	-7.82e-08	9.83e-08	0.00175

Table 823: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Selenocompound.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.71e-03	9.90e-02	-0.0678	0.946	-2.09e-01	1.95e-01	0.000000
L3.Selenocompound.metabolism	1.90e-08	2.37e-07	0.0801	0.937	-4.65e-07	5.03e-07	0.000207

Table 824: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Sesquiterpenoid.biosynthesis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 825: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Shigellosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.01693	0.0596	-0.284	0.778	-0.1387	0.1049	0.0000
L3.Shigellosis	0.00903	0.0152	0.592	0.558	-0.0221	0.0402	0.0112

Table 826: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Signal.transduction.mechanisms, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.59e-03	9.45e-02	0.0486	0.962	-1.88e-01	1.98e-01	0.00000
L3.Signal.transduction.mechanisms	-1.07e-08	1.84e-07	-0.0585	0.954	-3.86e-07	3.65e-07	0.00011

Table 827: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Small.cell.lung.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.04263	0.05534	-0.77	0.4471	-0.155649	0.07038	0.0000
L3.Small.cell.lung.cancer	0.00359	0.00199	1.80	0.0817	-0.000481	0.00766	0.0947

Table 828: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Sphingolipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.89e-01	6.70e-02	4.30	1.64e-04	1.52e-01	4.26e-01	0.000
L3.Sphingolipid.metabolism	-1.68e-06	3.22e-07	-5.23	1.22e-05	-2.34e-06	-1.02e-06	0.469

Table 829: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Spliceosome, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 830: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Sporulation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.52e-02	7.38e-02	0.478	0.636	-1.15e-01	1.86e-01	0.0000
L3.Sporulation	-1.10e-07	1.62e-07	-0.677	0.504	-4.41e-07	2.22e-07	0.0145

Table 831: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Staphylococcus.aureus.infection, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.04e-01	5.72e-02	-1.82	0.07924	-2.21e-01	1.29e-02	0.000
L3.Staphylococcus.aureus.infection	2.45e-06	8.04e-07	3.05	0.00469	8.14e-07	4.10e-06	0.231

Table 832: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Starch.and.sucrose.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.05e-01	9.66e-02	1.09	0.286	-9.23e-02	3.02e-01	0.0000
L3.Starch.and.sucrose.metabolism	-1.19e-07	9.26e-08	-1.28	0.209	-3.08e-07	7.03e-08	0.0504

Table 833: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Steroid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.047917	0.055289	-0.867	0.3930	-1.61e-01	0.06500	0.00
L3.Steroid.biosynthesis	0.000892	0.000455	1.958	0.0595	-3.82e-05	0.00182	0.11

Table 834: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Steroid.hormone.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.05e-01	5.76e-02	1.82	0.07807	-1.26e-02	2.23e-01	0.000
L3.Steroid.hormone.biosynthesis	-6.30e-06	2.08e-06	-3.04	0.00492	-1.05e-05	-2.06e-06	0.229

Table 835: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-5.71e-03	0.056613	-0.101	0.920	-0.121325	1.10e-01
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	3.54e-06	0.000013	0.272	0.787	-0.000023	3.01e-05

Table 836: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Streptomycin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.11e-01	1.08e-01	1.03	0.314	-1.10e-01	3.31e-01	0.0000
L3.Streptomycin.biosynthesis	-4.33e-07	3.72e-07	-1.17	0.253	-1.19e-06	3.25e-07	0.0421

Table 837: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Styrene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.04e-02	5.77e-02	0.181	0.858	-1.07e-01	1.28e-01	0.00000
L3.Styrene.degradation	-3.85e-07	8.82e-07	-0.437	0.665	-2.19e-06	1.42e-06	0.00612

Table 838: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Sulfur.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.12e-02	9.57e-02	0.744	0.463	-1.24e-01	2.67e-01	0.0000
L3.Sulfur.metabolism	-2.78e-07	3.14e-07	-0.886	0.383	-9.20e-07	3.63e-07	0.0247

Table 839: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Sulfur.relay.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.80e-03	7.98e-02	0.0853	0.933	-1.56e-01	1.70e-01	0.000000
L3.Sulfur.relay.system	-2.74e-08	2.42e-07	-0.1135	0.910	-5.21e-07	4.66e-07	0.000415

Table 840: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Synthesis.and.degradation.of.ketone.bodies, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.95e-02	7.93e-02	-0.624	0.537	-2.12e-01	1.13e-01	0.0000
L3.Synthesis.and.degradation.of.ketone.bodies	1.42e-06	1.72e-06	0.827	0.415	-2.09e-06	4.93e-06	0.0216

Table 841: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Systemic.lupus.erythematosus, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.015182	0.055704	0.273	0.787	-0.098581	0.128946	0.000
L3.Systemic.lupus.erythematosus	-0.000103	0.000133	-0.774	0.445	-0.000375	0.000169	0.019

Table 842: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.TGF.beta.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 843: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Taurine.and.hypotaurine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.98e-02	1.03e-01	0.192	0.849	-1.91e-01	2.30e-01	0.00000
L3.Taurine.and.hypotaurine.metabolism	-1.87e-07	8.35e-07	-0.224	0.825	-1.89e-06	1.52e-06	0.00161

Table 844: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Terpenoid.backbone.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.80e-03	1.23e-01	0.0799	0.937	-2.41e-01	2.60e-01	0.000000
L3.Terpenoid.backbone.biosynthesis	-2.18e-08	2.47e-07	-0.0884	0.930	-5.26e-07	4.82e-07	0.000252

Table 845: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Tetracycline.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.04e-02	1.06e-01	-0.382	0.705	-2.56e-01	1.76e-01	0.00000
L3.Tetracycline.biosynthesis	3.20e-07	7.28e-07	0.440	0.663	-1.17e-06	1.81e-06	0.00619

Table 846: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Thiamine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.76e-03	1.11e-01	-0.0791	0.937	-2.35e-01	2.17e-01	0.000000
L3.Thiamine.metabolism	2.11e-08	2.35e-07	0.0899	0.929	-4.59e-07	5.01e-07	0.000261

Table 847: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Tight.junction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 848: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Toluene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.11e-02	6.16e-02	-0.342	0.735	-1.47e-01	1.05e-01	0.0000
L3.Toluene.degradation	1.86e-07	2.87e-07	0.648	0.522	-4.00e-07	7.71e-07	0.0134

Table 849: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Toxoplasmosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.04263	0.05534	-0.77	0.4471	-0.155649	0.07038	0.0000
L3.Toxoplasmosis	0.00359	0.00199	1.80	0.0817	-0.000481	0.00766	0.0947

Table 850: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Transcription.factors, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.02e-02	7.86e-02	0.130	0.898	-1.50e-01	1.71e-01	0.000000
L3.Transcription.factors	-5.81e-09	3.32e-08	-0.175	0.862	-7.37e-08	6.21e-08	0.000984

Table 851: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Transcription.machinery, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.14e-01	1.14e-01	1.87	0.0711	-1.95e-02	4.47e-01	0.000
L3.Transcription.machinery	-3.23e-07	1.56e-07	-2.07	0.0468	-6.40e-07	-4.92e-09	0.122

Table 852: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Transcription.related.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.14e-02	5.96e-02	0.191	0.850	-1.10e-01	1.33e-01	0.00000
L3.Transcription.related.proteins	-7.81e-07	1.93e-06	-0.405	0.688	-4.72e-06	3.16e-06	0.00527

Table 853: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Translation.factors, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.61e-02	1.20e-01	-0.301	0.765	-2.81e-01	2.09e-01	0.00000
L3.Translation.factors	8.16e-08	2.44e-07	0.335	0.740	-4.16e-07	5.79e-07	0.00361

Table 854: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Translation.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.70e-02	1.08e-01	-0.343	0.734	-2.57e-01	1.83e-01	0.00000
L3.Translation.proteins	4.68e-08	1.19e-07	0.393	0.697	-1.97e-07	2.91e-07	0.00495

Table 855: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Transporters, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.69e-02	8.56e-02	-0.432	0.669	-2.12e-01	1.38e-01	0.00000
L3.Transporters	5.53e-09	1.01e-08	0.546	0.589	-1.52e-08	2.62e-08	0.00952

Table 856: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	6.98e-02	8.41e-02	0.83	0.413	-0.102001	2.42e-0
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis	-6.81e-07	6.48e-07	-1.05	0.301	-0.000002	6.41e-0

Table 857: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Tryptophan.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.93e-02	6.78e-02	0.284	0.778	-1.19e-01	1.58e-01	0.00000
L3.Tryptophan.metabolism	-9.98e-08	2.22e-07	-0.449	0.656	-5.53e-07	3.54e-07	0.00647

Table 858: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Tuberculosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.53e-02	1.31e-01	-0.574	0.570	-3.43e-01	1.92e-01	0.0000
L3.Tuberculosis	6.72e-07	1.07e-06	0.627	0.536	-1.52e-06	2.86e-06	0.0125

Table 859: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Two.component.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.66e-02	7.80e-02	0.342	0.735	-1.33e-01	1.86e-01	0.00000
L3.Two.component.system	-1.89e-08	4.09e-08	-0.462	0.648	-1.02e-07	6.46e-08	0.00683

Table 860: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Type.I.diabetes.mellitus, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.20e-03	1.31e-01	-0.0321	0.975	-2.71e-01	2.63e-01	0.00e+00
L3.Type.I.diabetes.mellitus	1.02e-07	2.91e-06	0.0351	0.972	-5.85e-06	6.05e-06	3.98e-05

Table 861: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs
L3.Type.II.diabetes.mellitus, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.92e-03	1.07e-01	-0.0272	0.978	-2.22e-01	2.16e-01	0.00e+00
L3.Type.II.diabetes.mellitus	6.54e-08	2.10e-06	0.0312	0.975	-4.22e-06	4.35e-06	3.14e-05

Table 862: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Tyrosine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.49e-02	8.73e-02	0.4	0.692	-1.43e-01	2.13e-01	0.000
L3.Tyrosine.metabolism	-1.05e-07	2.11e-07	-0.5	0.621	-5.36e-07	3.25e-07	0.008

Table 863: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	4.49e-02	6.85e-02	0.655	0.518	-9.5e-02	1.85e-01
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis	-2.17e-07	2.17e-07	-1.001	0.325	-6.6e-07	2.26e-07

Table 864: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Ubiquitin.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.16e-03	6.42e-02	0.096	0.924	-1.25e-01	1.37e-01	0.000000
L3.Ubiquitin.system	-4.56e-07	2.72e-06	-0.168	0.868	-6.02e-06	5.11e-06	0.000905

Table 865: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.VEGF.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.26e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 866: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Valine..leucine.and.isoleucine.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.59e-02	1.12e-01	-0.769	0.448	-3.14e-01	1.42e-01	0.0000
L3.Valine..leucine.and.isoleucine.biosynthesis	1.36e-07	1.57e-07	0.869	0.392	-1.84e-07	4.56e-07	0.0238

Table 867: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Valine..leucine.and.isoleucine.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.58e-02	8.16e-02	0.438	0.664	-1.31e-01	2.02e-01	0.0000
L3.Valine..leucine.and.isoleucine.degradation	-1.34e-07	2.34e-07	-0.572	0.572	-6.11e-07	3.44e-07	0.0104

Table 868: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Various.types.of.N.glycan.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.032	0.0595	-0.538	0.594	-0.1535	0.0895	0.0000
L3.Various.types.of.N.glycan.biosynthesis	0.032	0.0295	1.085	0.287	-0.0283	0.0923	0.0366

Table 869: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Vascular.smooth.muscle.contraction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 870: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Vasopressin.regulated.water.reabsorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.0181	0.0538	-0.336	0.739	-0.1279	0.0918	0.0000
L3.Vasopressin.regulated.water.reabsorption	0.0724	0.0621	1.165	0.253	-0.0545	0.1992	0.0419

Table 871: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Vibrio.cholerae.infection, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0102	0.0580	0.176	0.862	-0.1083	0.1287	0.00000
L3.Vibrio.cholerae.infection	-0.0142	0.0344	-0.413	0.683	-0.0845	0.0561	0.00546

Table 872: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Vibrio.cholerae.pathogenic.cycle, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.75e-02	8.31e-02	0.451	0.655	-1.32e-01	2.07e-01	0.0000
L3.Vibrio.cholerae.pathogenic.cycle	-5.66e-07	9.74e-07	-0.581	0.565	-2.55e-06	1.42e-06	0.0108

Table 873: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Viral.myocarditis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.04263	0.05534	-0.77	0.4471	-0.155649	0.07038	0.0000
L3.Viral.myocarditis	0.00359	0.00199	1.80	0.0817	-0.000481	0.00766	0.0947

Table 874: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Vitamin.B6.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.29e-02	8.97e-02	0.924	0.363	-1.00e-01	2.66e-01	0.0000
L3.Vitamin.B6.metabolism	-5.27e-07	4.67e-07	-1.129	0.268	-1.48e-06	4.26e-07	0.0395

Table 875: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Wnt.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0107	0.0566	0.189	0.851	-0.105	0.126	0.00000
L3.Wnt.signaling.pathway	-0.0429	0.0856	-0.501	0.620	-0.218	0.132	0.00802

Table 876: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Xylene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.68e-02	7.82e-02	-0.598	0.554	-2.07e-01	1.13e-01	0.0000
L3.Xylene.degradation	7.35e-07	9.18e-07	0.802	0.429	-1.14e-06	2.61e-06	0.0203

Table 877: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.Zeatin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.25e-01	1.32e-01	0.948	0.351	-1.45e-01	3.95e-01	0.0000
L3.Zeatin.biosynthesis	-2.95e-06	2.87e-06	-1.030	0.311	-8.80e-06	2.90e-06	0.0331

Table 878: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.alpha.Linolenic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.20e-02	5.84e-02	0.205	0.839	-1.07e-01	1.31e-01	0.00000
L3.alpha.Linolenic.acid.metabolism	-9.16e-07	1.97e-06	-0.465	0.645	-4.93e-06	3.10e-06	0.00694

Table 879: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.beta.Alanine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.17e-02	7.39e-02	0.699	0.490	-9.93e-02	2.03e-01	0.0000
L3.beta.Alanine.metabolism	-2.84e-07	2.90e-07	-0.980	0.335	-8.77e-07	3.08e-07	0.0301

Table 880: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.beta.Lactam.resistance, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.49e-02	9.37e-02	-0.479	0.635	-2.36e-01	1.46e-01	0.0000
L3.beta.Lactam.resistance	2.05e-06	3.55e-06	0.578	0.568	-5.20e-06	9.31e-06	0.0107

Table 881: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.mRNA.surveillance.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 882: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.mTOR.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.25e-15	0.0518	1.21e-13	1	-0.106	0.106	0
	NA	NA	NA	NA	NA	NA	0

Table 883: diversity_vs_picrust_L3_neo: wunifrac.PC.1 vs L3.p53.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.04263	0.05534	-0.77	0.4471	-0.155649	0.07038	0.0000
L3.p53.signaling.pathway	0.00359	0.00199	1.80	0.0817	-0.000481	0.00766	0.0947

Table 884: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %
Intercept	1.66e-03	2.52e-02	0.0659	0.948	-4.98e-02
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	-1.97e-06	5.59e-06	-0.3527	0.727	-1.34e-05

Table 885: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.ABC.transporters, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.36e-02	3.78e-02	0.359	0.722	-6.36e-02	9.07e-02	0.00000
L3.ABC.transporters	-4.08e-09	8.58e-09	-0.475	0.638	-2.16e-08	1.34e-08	0.00723

Table 886: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Adherens.junction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 887: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Adipocytokine.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.48e-02	3.79e-02	1.71	0.0973	-1.25e-02	1.42e-01	0.000
L3.Adipocytokine.signaling.pathway	-1.42e-06	6.58e-07	-2.16	0.0389	-2.76e-06	-7.71e-08	0.131

Table 888: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.African.trypanosomiasis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.54e-02	2.93e-02	1.55	0.132	-1.45e-02	0.105300	0.000
L3.African.trypanosomiasis	-6.18e-06	2.53e-06	-2.44	0.021	-1.14e-05	-0.000001	0.161

Table 889: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Alanine..aspartate.and.glutamate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.19e-02	5.32e-02	0.411	0.684	-8.68e-02	1.31e-01	0.000
L3.Alanine..aspartate.and.glutamate.metabolism	-2.58e-08	5.56e-08	-0.464	0.646	-1.39e-07	8.78e-08	0.006

Table 890: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Aldosterone.regulated.sodium.reabsorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00163	0.0252	0.0648	0.949	-0.0498	0.053	0.00000
L3.Aldosterone.regulated.sodium.reabsorption	-0.05218	0.1423	-0.3667	0.716	-0.3428	0.238	0.00432

Table 891: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Alzheimer.s.disease, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.36e-02	4.51e-02	0.302	0.765	-7.85e-02	1.06e-01	0.00000
L3.Alzheimer.s.disease	-3.12e-07	8.64e-07	-0.361	0.721	-2.08e-06	1.45e-06	0.00419

Table 892: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Amino.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.68e-02	3.70e-02	0.453	0.654	-5.88e-02	9.23e-02	0.0000
L3.Amino.acid.metabolism	-7.07e-08	1.16e-07	-0.608	0.548	-3.08e-07	1.67e-07	0.0118

Table 893: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Amino.acid.related.enzymes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.78e-02	5.38e-02	-0.332	0.742	-1.28e-01	9.20e-02	0.00000
L3.Amino.acid.related.enzymes	1.46e-08	3.90e-08	0.374	0.711	-6.51e-08	9.42e-08	0.00449

Table 894: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Amino.sugar.and.nucleotide.sugar.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.26e-02	5.23e-02	0.241	0.811	-9.42e-02	1.19e-01	0.000
L3.Amino.sugar.and.nucleotide.sugar.metabolism	-9.07e-09	3.31e-08	-0.274	0.786	-7.68e-08	5.86e-08	0.002

Table 895: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Aminoacyl.tRNA.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.72e-02	5.60e-02	-1.02	0.315	-1.72e-01	5.72e-02	0.0000
L3.Aminoacyl.tRNA.biosynthesis	5.96e-08	5.25e-08	1.13	0.266	-4.77e-08	1.67e-07	0.0398

Table 896: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Aminobenzoate.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.17e-02	3.42e-02	1.22	0.232	-2.81e-02	1.11e-01	0.0000
L3.Aminobenzoate.degradation	-3.15e-07	1.86e-07	-1.69	0.101	-6.94e-07	6.49e-08	0.0846

Table 897: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Amoebiasis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.89e-02	3.22e-02	0.588	0.561	-4.68e-02	8.46e-02	0.0000
L3.Amoebiasis	-5.02e-06	5.54e-06	-0.907	0.372	-1.63e-05	6.29e-06	0.0259

Table 898: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Amyotrophic.lateral.sclerosis..ALS., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.72e-02	2.80e-02	0.971	0.3392	-3.00e-02	8.43e-02	0.0000
L3.Amyotrophic.lateral.sclerosis..ALS.	-1.50e-06	8.31e-07	-1.803	0.0815	-3.19e-06	1.99e-07	0.0949

Table 899: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Antigen.processing.and.presentation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.98e-03	4.20e-02	-0.0948	0.925	-8.97e-02	8.18e-02	0.000000
L3.Antigen.processing.and.presentation	1.69e-07	1.44e-06	0.1175	0.907	-2.77e-06	3.11e-06	0.000445

Table 900: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Apoptosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.41e-03	2.93e-02	-0.287	0.776	-6.83e-02	5.15e-02	0.00000
L3.Apoptosis	1.18e-06	2.21e-06	0.532	0.599	-3.34e-06	5.69e-06	0.00905

Table 901: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Arachidonic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.50e-02	3.48e-02	0.718	0.478	-4.60e-02	9.59e-02	0.0000
L3.Arachidonic.acid.metabolism	-6.39e-07	6.33e-07	-1.009	0.321	-1.93e-06	6.55e-07	0.0318

Table 902: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Arginine.and.proline.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.35e-02	4.25e-02	0.553	0.584	-6.33e-02	1.10e-01	0.0000
L3.Arginine.and.proline.metabolism	-2.45e-08	3.61e-08	-0.679	0.502	-9.82e-08	4.92e-08	0.0147

Table 903: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Arrhythmogenic.right.ventricular.cardiomyopathy..ARVC., df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 904: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Ascorbate.and.aldarate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.12e-02	3.04e-02	0.697	0.491	-4.09e-02	8.33e-02	0.0000
L3.Ascorbate.and.aldarate.metabolism	-1.09e-07	9.40e-08	-1.157	0.256	-3.01e-07	8.32e-08	0.0414

Table 905: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Atrazine.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.86e-02	2.65e-02	0.703	0.488	-3.55e-02	7.27e-02	0.0000
L3.Atrazine.degradation	-1.11e-06	6.93e-07	-1.605	0.119	-2.53e-06	3.03e-07	0.0768

Table 906: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Bacterial.chemotaxis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.02e-02	3.7e-02	-0.275	0.785	-8.57e-02	6.53e-02	0.00000
L3.Bacterial.chemotaxis	3.72e-08	1.0e-07	0.371	0.713	-1.68e-07	2.42e-07	0.00442

Table 907: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Bacterial.invasion.of.epithelial.cells, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.29e-03	2.62e-02	0.164	0.871	-4.92e-02	5.78e-02	0.00000
L3.Bacterial.invasion.of.epithelial.cells	-3.56e-06	7.19e-06	-0.494	0.625	-1.82e-05	1.11e-05	0.00782

Table 908: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Bacterial.motility.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.82e-03	3.55e-02	0.0795	0.937	-6.97e-02	7.54e-02	0.000000
L3.Bacterial.motility.proteins	-5.15e-09	4.64e-08	-0.1110	0.912	-9.99e-08	8.96e-08	0.000398

Table 909: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Bacterial.secretion.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.46e-02	3.55e-02	0.693	0.494	-4.79e-02	9.71e-02	0.0000
L3.Bacterial.secretion.system	-3.82e-08	3.99e-08	-0.956	0.347	-1.20e-07	4.34e-08	0.0286

Table 910: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Bacterial.toxins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.07e-02	5.53e-02	-1.28	0.210	-1.84e-01	4.21e-02	0.0000
L3.Bacterial.toxins	5.34e-07	3.76e-07	1.42	0.166	-2.34e-07	1.30e-06	0.0612

Table 911: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Basal.transcription.factors, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.25e-03	2.63e-02	-0.352	0.727	-6.29e-02	4.44e-02	0.000
L3.Basal.transcription.factors	1.08e-05	1.12e-05	0.962	0.344	-1.21e-05	3.37e-05	0.029

Table 912: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Base.excision.repair, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.83e-02	5.40e-02	-0.339	0.737	-1.29e-01	9.20e-02	0.00000
L3.Base.excision.repair	4.85e-08	1.27e-07	0.381	0.706	-2.11e-07	3.08e-07	0.00467

Table 913: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Benzoate.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.30e-02	3.36e-02	0.388	0.701	-5.55e-02	8.16e-02	0.0000
L3.Benzoate.degradation	-5.14e-08	8.99e-08	-0.572	0.572	-2.35e-07	1.32e-07	0.0104

Table 914: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Betalain.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.10e-02	2.56e-02	0.428	0.672	-0.041367	6.33e-02	0.0000
L3.Betalain.biosynthesis	-7.91e-05	6.16e-05	-1.285	0.209	-0.000205	4.67e-05	0.0505

Table 915: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Bile.secretion, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00822	0.02748	0.299	0.767	-0.04791	0.06436	0.0000
L3.Bile.secretion	-0.00121	0.00179	-0.674	0.505	-0.00486	0.00245	0.0145

Table 916: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Biosynthesis.and.biodegradation.of.secondary.metabolites, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	2.13e-02	2.83e-02	0.75	0.459	-3.66e-02	7.92
L3.Biosynthesis.and.biodegradation.of.secondary.metabolites	-2.57e-07	1.82e-07	-1.41	0.168	-6.29e-07	1.14

Table 917: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Biosynthesis.of.12. . .14..and.16.membered.macrolides, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-0.00109	0.0252	-0.0432	0.966	-0.0525	0.0504
L3.Biosynthesis.of.12. . .14..and.16.membered.macrolides	0.03479	0.1425	0.2442	0.809	-0.2562	0.3258

Table 918: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Biosynthesis.of.ansamycins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.32e-02	3.55e-02	0.372	0.713	-5.93e-02	8.57e-02	0.00000
L3.Biosynthesis.of.ansamycins	-1.26e-07	2.43e-07	-0.517	0.609	-6.23e-07	3.71e-07	0.00856

Table 919: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	2.07e-02	2.78e-02	0.745	0.462	-3.60e-02	7.74e
L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides	-2.92e-07	1.98e-07	-1.475	0.151	-6.96e-07	1.12e

Table 920: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Biosynthesis.of.type.II.polyketide.backbone, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 921: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Biosynthesis.of.type.II.polyketide.products, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.011323	2.57e-02	0.44	0.663	-0.041236	6.39e-02	0.0000
L3.Biosynthesis.of.type.II.polyketide.products	-0.000079	6.18e-05	-1.28	0.210	-0.000205	4.71e-05	0.0502

Table 922: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Biosynthesis.of.unsaturated.fatty.acids, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.99e-02	3.27e-02	0.917	0.366	-3.67e-02	9.66e-02	0.0000
L3.Biosynthesis.of.unsaturated.fatty.acids	-2.32e-07	1.71e-07	-1.358	0.184	-5.82e-07	1.17e-07	0.0562

Table 923: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Biosynthesis.of.vancomycin.group.antibiotics, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.02e-02	5.44e-02	-0.188	0.852	-1.21e-01	1.01e-01	0.0000
L3.Biosynthesis.of.vancomycin.group.antibiotics	2.06e-07	9.76e-07	0.211	0.834	-1.79e-06	2.20e-06	0.0014

Table 924: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Biotin.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.68e-03	4.40e-02	-0.152	0.880	-9.64e-02	8.31e-02	0.00000
L3.Biotin.metabolism	5.41e-08	2.94e-07	0.184	0.855	-5.47e-07	6.55e-07	0.00109

Table 925: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Bisphenol.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.69e-03	4.82e-02	-0.0765	0.940	-1.02e-01	9.47e-02	0.000000
L3.Bisphenol.degradation	8.27e-08	9.27e-07	0.0893	0.929	-1.81e-06	1.98e-06	0.000257

Table 926: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Bladder.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.03e-02	2.66e-02	0.761	0.452	-3.41e-02	7.46e-02	0.0000
L3.Bladder.cancer	-4.37e-06	2.60e-06	-1.681	0.103	-9.68e-06	9.38e-07	0.0836

Table 927: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Butanoate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.09e-02	3.95e-02	0.528	0.601	-5.98e-02	1.01e-01	0.0000
L3.Butanoate.metabolism	-3.26e-08	4.83e-08	-0.676	0.504	-1.31e-07	6.59e-08	0.0145

Table 928: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Butirosin.and.neomycin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.62e-02	6.33e-02	0.731	0.471	-8.30e-02	1.75e-01	0.0000
L3.Butirosin.and.neomycin.biosynthesis	-9.85e-07	1.24e-06	-0.793	0.434	-3.52e-06	1.55e-06	0.0199

Table 929: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.C5.Branched.dibasic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.40e-02	4.73e-02	0.506	0.617	-7.27e-02	1.21e-01	0.0000
L3.C5.Branched.dibasic.acid.metabolism	-8.94e-08	1.51e-07	-0.593	0.558	-3.97e-07	2.18e-07	0.0112

Table 930: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.CAM.ligands, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 931: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Caffeine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00363	0.0272	-0.133	0.895	-0.0593	0.052	0.0000
L3.Caffeine.metabolism	0.00447	0.0140	0.320	0.751	-0.0240	0.033	0.0033

Table 932: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Calcium.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0211	0.0268	0.788	0.437	-0.0336	0.07575	0.000
L3.Calcium.signaling.pathway	-0.0337	0.0199	-1.697	0.100	-0.0743	0.00686	0.085

Table 933: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Caprolactam.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.22e-02	2.85e-02	0.778	0.442	-3.60e-02	8.03e-02	0.0000
L3.Caprolactam.degradation	-4.39e-07	3.03e-07	-1.447	0.158	-1.06e-06	1.81e-07	0.0632

Table 934: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Carbohydrate.digestion.and.absorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.19e-02	3.47e-02	0.917	0.366	-3.91e-02	1.03e-01	0.00
L3.Carbohydrate.digestion.and.absorption	-1.48e-06	1.16e-06	-1.277	0.211	-3.85e-06	8.87e-07	0.05

Table 935: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Carbohydrate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.68e-02	3.99e-02	1.17	0.249	-3.46e-02	1.28e-01	0.0000
L3.Carbohydrate.metabolism	-2.66e-07	1.81e-07	-1.47	0.152	-6.34e-07	1.03e-07	0.0652

Table 936: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Carbon.fixation.in.photosynthetic.organisms, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.92e-02	4.45e-02	0.432	0.669	-7.17e-02	1.10e-01	0.0000
L3.Carbon.fixation.in.photosynthetic.organisms	-3.59e-08	6.91e-08	-0.519	0.608	-1.77e-07	1.05e-07	0.0086

Table 937: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Carbon.fixation.pathways.in.prokaryotes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.60e-02	4.63e-02	0.345	0.732	-7.85e-02	1.10e-01	0.00000
L3.Carbon.fixation.pathways.in.prokaryotes	-1.86e-08	4.54e-08	-0.408	0.686	-1.11e-07	7.42e-08	0.00535

Table 938: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Cardiac.muscle.contraction, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.19e-02	2.60e-02	0.459	0.650	-0.041241	6.51e-02	0.0000
L3.Cardiac.muscle.contraction	-1.93e-05	1.55e-05	-1.243	0.224	-0.000051	1.24e-05	0.0475

Table 939: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Carotenoid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.04e-04	2.84e-02	0.0318	0.975	-5.72e-02	5.90e-02	0.000000
L3.Carotenoid.biosynthesis	-2.64e-07	4.05e-06	-0.0652	0.948	-8.53e-06	8.01e-06	0.000137

Table 940: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Cell.cycle, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 941: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Cell.cycle...Caulobacter, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.05e-02	6.01e-02	-0.839	0.408	-1.73e-01	7.23e-02	0.0000
L3.Cell.cycle...Caulobacter	1.31e-07	1.42e-07	0.919	0.365	-1.60e-07	4.22e-07	0.0265

Table 942: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Cell.cycle...yeast, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 943: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Cell.division, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.95e-02	4.01e-02	0.735	0.468	-5.24e-02	1.11e-01	0.0000
L3.Cell.division	-4.92e-07	5.30e-07	-0.928	0.361	-1.57e-06	5.90e-07	0.0271

Table 944: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Cell.motility.and.secretion, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.59e-05	4.12e-02	0.00136	0.999	-8.4e-02	8.41e-02	0.00e+00
L3.Cell.motility.and.secretion	-3.41e-10	2.01e-07	-0.00170	0.999	-4.1e-07	4.09e-07	9.34e-08

Table 945: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Cellular.antigens, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.15e-02	3.69e-02	1.67	0.1055	-1.38e-02	1.37e-01	0.000
L3.Cellular.antigens	-1.39e-06	6.50e-07	-2.14	0.0404	-2.72e-06	-6.52e-08	0.129

Table 946: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Chagas.disease..American.trypanosomiasis., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.18e-02	2.83e-02	1.48	0.1506	-1.61e-02	9.97e-02	0.000
L3.Chagas.disease..American.trypanosomiasis.	-6.17e-06	2.52e-06	-2.45	0.0201	-1.13e-05	-1.04e-06	0.163

Table 947: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Chaperones.and.folding.catalysts, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.61e-02	4.73e-02	0.552	0.585	-7.05e-02	1.23e-01	0.0000
L3.Chaperones.and.folding.catalysts	-3.04e-08	4.69e-08	-0.647	0.523	-1.26e-07	6.55e-08	0.0133

Table 948: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Chloroalkane.and.chloroalkene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.30e-02	4.85e-02	0.680	0.502	-6.61e-02	1.32e-01	0.0000
L3.Chloroalkane.and.chloroalkene.degradation	-2.02e-07	2.57e-07	-0.788	0.437	-7.27e-07	3.22e-07	0.0196

Table 949: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Chlorocyclohexane.and.chlorobenzene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	3.28e-02	2.92e-02	1.12	0.2704	-2.68e-02	9.24e-02
L3.Chlorocyclohexane.and.chlorobenzene.degradation	-2.41e-06	1.28e-06	-1.89	0.0689	-5.01e-06	1.98e-07

Table 950: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Cholinergic.synapse, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 951: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Chromosome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.13e-03	5.11e-02	-0.0808	0.936	-1.09e-01	1.00e-01	0.000000
L3.Chromosome	3.26e-09	3.53e-08	0.0924	0.927	-6.88e-08	7.53e-08	0.000275

Table 952: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Chronic.myeloid.leukemia, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.012	0.0262	0.458	0.650	-0.0415	0.0654	0.0000
L3.Chronic.myeloid.leukemia	-0.048	0.0396	-1.212	0.235	-0.1288	0.0328	0.0453

Table 953: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Circadian.rhythm...plant, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00616	0.02686	0.229	0.820	-0.0487	0.0610	0.0000
L3.Circadian.rhythm...plant	-0.00428	0.00738	-0.580	0.566	-0.0194	0.0108	0.0107

Table 954: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Citrate.cycle..TCA.cycle., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.95e-02	3.78e-02	0.782	0.440	-4.76e-02	1.07e-01	0.0000
L3.Citrate.cycle..TCA.cycle.	-5.39e-08	5.26e-08	-1.025	0.314	-1.61e-07	5.35e-08	0.0328

Table 955: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Clavulanic.acid.biosynthesis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 956: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Colorectal.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00166	0.027448	-0.0606	0.952	-0.05772	0.05439	0.000000
L3.Colorectal.cancer	0.00014	0.000989	0.1417	0.888	-0.00188	0.00216	0.000648

Table 957: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Complement.and.coagulation.cascades, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 958: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Cyanoamino.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.74e-02	4.08e-02	1.16	0.254	-3.58e-02	1.31e-01	0.0000
L3.Cyanoamino.acid.metabolism	-1.78e-07	1.24e-07	-1.44	0.160	-4.30e-07	7.46e-08	0.0626

Table 959: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Cysteine.and.methionine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.07e-04	4.68e-02	0.0151	0.988	-9.50e-02	9.64e-02	0.00e+00
L3.Cysteine.and.methionine.metabolism	-8.09e-10	4.55e-08	-0.0178	0.986	-9.37e-08	9.21e-08	1.02e-05

Table 960: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Cytochrome.P450, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00416	0.0248	-0.168	0.868	-0.0549	0.0466	0.0000
L3.Cytochrome.P450	0.13323	0.1405	0.948	0.351	-0.1538	0.4203	0.0282

Table 961: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Cytokine.receptors, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 962: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Cytokine.cytokine.receptor.interaction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 963: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Cytoskeleton.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.38e-02	5.08e-02	-1.45	0.157	-1.78e-01	3.01e-02	0.00
L3.Cytoskeleton.proteins	3.58e-07	2.18e-07	1.64	0.111	-8.74e-08	8.03e-07	0.08

Table 964: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Cytosolic.DNA.sensing.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 965: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.D.Alanine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.87e-02	5.09e-02	-0.958	0.346	-1.53e-01	5.52e-02	0.0000
L3.D.Alanine.metabolism	4.57e-07	4.19e-07	1.090	0.284	-3.99e-07	1.31e-06	0.0369

Table 966: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.D.Arginine.and.D.ornithine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.89e-02	2.19e-02	-1.78	0.085140	-8.36e-02	5.72e-03	0.000
L3.D.Arginine.and.D.ornithine.metabolism	9.61e-06	2.31e-06	4.16	0.000244	4.89e-06	1.43e-05	0.359

Table 967: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.D.Glutamine.and.D.glutamate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.91e-02	5.19e-02	-0.369	0.715	-1.25e-01	8.69e-02	0.00000
L3.D.Glutamine.and.D.glutamate.metabolism	1.45e-07	3.45e-07	0.419	0.678	-5.60e-07	8.49e-07	0.00564

Table 968: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.DNA.repair.and.recombination.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.06e-02	5.57e-02	-0.370	0.714	-1.34e-01	9.31e-02	0.00000
L3.DNA.repair.and.recombination.proteins	8.58e-09	2.08e-08	0.413	0.682	-3.38e-08	5.10e-08	0.00548

Table 969: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.DNA.replication, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.82e-02	5.95e-02	-0.811	0.424	-1.70e-01	7.32e-02	0.0000
L3.DNA.replication	8.59e-08	9.65e-08	0.890	0.380	-1.11e-07	2.83e-07	0.0249

Table 970: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.DNA.replication.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.62e-02	5.82e-02	-0.278	0.783	-1.35e-01	1.03e-01	0.00000
L3.DNA.replication.proteins	1.64e-08	5.35e-08	0.307	0.761	-9.28e-08	1.26e-07	0.00303

Table 971: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Dilated.cardiomyopathy..DCM., df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 972: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Dioxin.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.61e-02	3.43e-02	0.470	0.642	-5.39e-02	8.62e-02	0.0000
L3.Dioxin.degradation	-1.86e-07	2.75e-07	-0.675	0.505	-7.48e-07	3.76e-07	0.0145

Table 973: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Drug.metabolism...cytochrome.P450, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.61e-02	3.06e-02	1.18	0.2474	-2.64e-02	9.85e-02	0.000
L3.Drug.metabolism...cytochrome.P450	-7.31e-07	3.96e-07	-1.85	0.0748	-1.54e-06	7.78e-08	0.099

Table 974: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Drug.metabolism...other.enzymes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.16e-02	5.38e-02	-0.216	0.830	-1.21e-01	9.82e-02	0.00000
L3.Drug.metabolism...other.enzymes	4.12e-08	1.69e-07	0.244	0.809	-3.04e-07	3.86e-07	0.00191

Table 975: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.ECM.receptor.interaction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 976: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Electron.transfer.carriers, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.32e-02	3.07e-02	0.756	0.455	-3.95e-02	8.6e-02	0.0000
L3.Electron.transfer.carriers	-4.08e-07	3.32e-07	-1.229	0.229	-1.09e-06	2.7e-07	0.0465

Table 977: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Endocrine.and.other.factor.regulated.calcium.reabsorption, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 978: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Endocytosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00638	0.02581	0.247	0.806	-0.0463	0.05910	0.0000
L3.Endocytosis	-0.00601	0.00749	-0.802	0.429	-0.0213	0.00929	0.0203

Table 979: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Energy.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.63e-02	4.14e-02	0.394	0.696	-6.82e-02	1.01e-01	0.00000
L3.Energy.metabolism	-2.22e-08	4.51e-08	-0.492	0.627	-1.14e-07	6.99e-08	0.00774

Table 980: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-7.39e-03	4.48e-02	-0.165	0.870	-9.89e-02	8.41e-0
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	1.09e-07	5.49e-07	0.198	0.844	-1.01e-06	1.23e-0

Table 981: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.ErbB.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 982: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Ether.lipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.49e-02	3.02e-02	-0.825	0.416	-8.66e-02	0.036762	0.0000
L3.Ether.lipid.metabolism	1.72e-05	1.26e-05	1.367	0.182	-8.52e-06	0.000043	0.0568

Table 983: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Ethylbenzene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.20e-02	3.85e-02	1.09	0.284	-3.66e-02	1.21e-01	0.0000
L3.Ethylbenzene.degradation	-1.36e-06	9.71e-07	-1.40	0.173	-3.34e-06	6.27e-07	0.0592

Table 984: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Fat.digestion.and.absorption, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 985: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Fatty.acid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.60e-03	5.09e-02	0.0511	0.960	-1.01e-01	1.07e-01	0.000000
L3.Fatty.acid.biosynthesis	-5.95e-09	1.02e-07	-0.0586	0.954	-2.14e-07	2.02e-07	0.000111

Table 986: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Fatty.acid.elongation.in.mitochondria, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 987: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Fatty.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.48e-02	3.71e-02	0.94	0.355	-4.08e-02	1.11e-01	0.0000
L3.Fatty.acid.metabolism	-1.35e-07	1.09e-07	-1.24	0.224	-3.56e-07	8.69e-08	0.0474

Table 988: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Fc.epsilon.RI.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 989: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Fc.gamma.R.mediated.phagocytosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00638	0.02581	0.247	0.806	-0.0463	0.05910	0.0000
L3.Fc.gamma.R.mediated.phagocytosis	-0.00601	0.00749	-0.802	0.429	-0.0213	0.00929	0.0203

Table 990: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Flagellar.assembly, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.93e-03	3.13e-02	-0.126	0.901	-6.78e-02	6.00e-02	0.00000
L3.Flagellar.assembly	2.51e-08	1.22e-07	0.206	0.838	-2.23e-07	2.73e-07	0.00137

Table 991: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Flavone.and.flavonol.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.24e-03	3.11e-02	0.104	0.918	-6.03e-02	6.68e-02	0.000000
L3.Flavone.and.flavonol.biosynthesis	-6.58e-07	3.81e-06	-0.172	0.864	-8.45e-06	7.13e-06	0.000958

Table 992: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Flavonoid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.31e-03	2.57e-02	0.0901	0.929	-5.01e-02	5.47e-02	0.00000
L3.Flavonoid.biosynthesis	-2.09e-06	6.11e-06	-0.3425	0.734	-1.46e-05	1.04e-05	0.00377

Table 993: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Fluorobenzoate.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.75e-02	2.60e-02	0.672	0.507	-3.56e-02	7.05e-02	0.0000
L3.Fluorobenzoate.degradation	-1.16e-06	7.01e-07	-1.661	0.107	-2.60e-06	2.67e-07	0.0817

Table 994: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Focal.adhesion, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 995: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Folate.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.93e-03	5.17e-02	0.115	0.910	-9.97e-02	1.12e-01	0.00000
L3.Folate.biosynthesis	-1.58e-08	1.21e-07	-0.131	0.897	-2.62e-07	2.31e-07	0.00055

Table 996: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Fructose.and.mannose.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.86e-02	4.25e-02	0.439	0.664	-6.82e-02	1.05e-01	0.00000
L3.Fructose.and.mannose.metabolism	-2.07e-08	3.85e-08	-0.539	0.594	-9.93e-08	5.78e-08	0.00928

Table 997: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Function.unknown, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.33e-02	3.75e-02	0.622	0.539	-5.33e-02	1.00e-01	0.0000
L3.Function.unknown	-1.72e-08	2.09e-08	-0.823	0.417	-6.00e-08	2.55e-08	0.0214

Table 998: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.G.protein.coupled.receptors, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 999: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.GTP.binding.proteins, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1000: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Galactose.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.49e-02	5.28e-02	0.661	0.513	-7.29e-02	1.43e-01	0.0000
L3.Galactose.metabolism	-4.59e-08	6.14e-08	-0.747	0.461	-1.71e-07	7.96e-08	0.0177

Table 1001: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Gastric.acid.secretion, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1002: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.General.function.prediction.only, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.56e-03	4.79e-02	0.158	0.876	-9.03e-02	1.05e-01	0.0000
L3.General.function.prediction.only	-2.44e-09	1.32e-08	-0.184	0.855	-2.95e-08	2.46e-08	0.0011

Table 1003: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Geraniol.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.90e-02	2.93e-02	0.993	0.329	-3.07e-02	8.88e-02	0.0000
L3.Geraniol.degradation	-4.02e-07	2.37e-07	-1.695	0.101	-8.86e-07	8.24e-08	0.0848

Table 1004: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Germination, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.69e-03	2.78e-02	-0.312	0.757	-6.55e-02	4.82e-02	0.0000
L3.Germination	2.19e-06	3.27e-06	0.670	0.508	-4.49e-06	8.87e-06	0.0143

Table 1005: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Glioma, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1006: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Glutamatergic.synapse, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.84e-02	5.27e-02	0.729	0.472	-6.92e-02	1.46e-01	0.0000
L3.Glutamatergic.synapse	-5.14e-07	6.24e-07	-0.824	0.417	-1.79e-06	7.60e-07	0.0214

Table 1007: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Glutathione.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.98e-02	3.87e-02	0.769	0.448	-4.93e-02	1.09e-01	0.0000
L3.Glutathione.metabolism	-1.19e-07	1.20e-07	-0.991	0.329	-3.64e-07	1.26e-07	0.0307

Table 1008: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Glycan.bindng.proteins, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1009: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Glycan.biosynthesis.and.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.00e-02	3.07e-02	0.65	0.521	-4.28e-02	8.27e-02	0.0000
L3.Glycan.biosynthesis.and.metabolism	-3.79e-07	3.56e-07	-1.07	0.295	-1.11e-06	3.47e-07	0.0354

Table 1010: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Glycerolipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.10e-03	4.32e-02	0.188	0.852	-8.00e-02	9.62e-02	0.00000
L3.Glycerolipid.metabolism	-2.33e-08	1.02e-07	-0.229	0.820	-2.31e-07	1.84e-07	0.00169

Table 1011: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Glycerophospholipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.47e-02	4.35e-02	0.339	0.737	-7.41e-02	1.04e-01	0.00000
L3.Glycerophospholipid.metabolism	-3.26e-08	7.92e-08	-0.412	0.684	-1.94e-07	1.29e-07	0.00544

Table 1012: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Glycine..serine.and.threonine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.23e-02	4.60e-02	0.485	0.631	-7.17e-02	1.16e-01	0.0000
L3.Glycine..serine.and.threonine.metabolism	-3.03e-08	5.26e-08	-0.575	0.570	-1.38e-07	7.72e-08	0.0105

Table 1013: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Glycolysis...Gluconeogenesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.83e-02	4.80e-02	0.381	0.706	-7.98e-02	1.16e-01	0.00000
L3.Glycolysis...Gluconeogenesis	-1.73e-08	3.89e-08	-0.444	0.660	-9.68e-08	6.22e-08	0.00632

Table 1014: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Glycosaminoglycan.biosynthesis...chondroitin.sulfate, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	3.77e-05	0.0255	0.00148	0.999	-0.0520	0.0521
L3.Glycosaminoglycan.biosynthesis...chondroitin.sulfate	-1.51e-04	0.0234	-0.00644	0.995	-0.0479	0.0476

Table 1015: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Glycosaminoglycan.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.71e-02	4.04e-02	0.918	0.366	-4.55e-02	1.20e-01	0.0000
L3.Glycosaminoglycan.degradation	-5.12e-07	4.46e-07	-1.148	0.260	-1.42e-06	3.99e-07	0.0408

Table 1016: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Glycosphingolipid.biosynthesis...ganglio.series, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.57e-02	3.75e-02	1.48	0.1482	-2.09e-02	1.32e-01	0.00
L3.Glycosphingolipid.biosynthesis...ganglio.series	-1.20e-06	6.33e-07	-1.90	0.0669	-2.50e-06	8.92e-08	0.10

Table 1017: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Glycosphingolipid.biosynthesis...globo.series, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.29e-02	4.01e-02	1.82	0.0789	-8.94e-03	1.55e-01	0.000
L3.Glycosphingolipid.biosynthesis...globo.series	-9.01e-07	4.06e-07	-2.22	0.0340	-1.73e-06	-7.26e-08	0.137

Table 1018: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.
Intercept	0.010808	2.40e-02	0.45	0.6561	-0.038268	5.9
L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series	-0.000079	4.05e-05	-1.95	0.0607	-0.000162	3.7

Table 1019: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Glycosylphosphatidylinositol.GPI..anchor.biosynthesis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1020: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Glycosyltransferases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.23e-02	4.59e-02	0.269	0.790	-8.14e-02	1.06e-01	0.00000
L3.Glycosyltransferases	-3.43e-08	1.07e-07	-0.320	0.751	-2.54e-07	1.85e-07	0.00329

Table 1021: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Glyoxylate.and.dicarboxylate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.11e-02	3.71e-02	0.569	0.574	-5.46e-02	9.68e-02	0.0000
L3.Glyoxylate.and.dicarboxylate.metabolism	-4.53e-08	5.96e-08	-0.759	0.453	-1.67e-07	7.64e-08	0.0183

Table 1022: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.GnRH.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00638	0.02581	0.247	0.806	-0.0463	0.05910	0.0000
L3.GnRH.signaling.pathway	-0.00601	0.00749	-0.802	0.429	-0.0213	0.00929	0.0203

Table 1023: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Hedgehog.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1024: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Hematopoietic.cell.lineage, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1025: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Hepatitis.C, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1026: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Histidine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.55e-03	5.34e-02	-0.179	0.859	-1.19e-01	9.94e-02	0.00000
L3.Histidine.metabolism	1.87e-08	9.23e-08	0.202	0.841	-1.70e-07	2.07e-07	0.00132

Table 1027: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Homologous.recombination, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.77e-02	5.79e-02	-0.650	0.520	-1.56e-01	8.06e-02	0.0000
L3.Homologous.recombination	4.79e-08	6.67e-08	0.718	0.478	-8.84e-08	1.84e-07	0.0164

Table 1028: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Huntington.s.disease, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.32e-02	4.34e-02	0.535	0.597	-6.54e-02	1.12e-01	0.0000
L3.Huntington.s.disease	-5.34e-07	8.22e-07	-0.650	0.521	-2.21e-06	1.14e-06	0.0134

Table 1029: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Hypertrophic.cardiomyopathy..HCM., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.003658	0.02572	0.142	0.888	-0.04888	0.05619	0.00000
L3.Hypertrophic.cardiomyopathy..HCM.	-0.000944	0.00185	-0.512	0.613	-0.00471	0.00282	0.00837

Table 1030: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Indole.alkaloid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00105	0.0287	0.0367	0.971	-0.0576	0.0597	0.000000
L3.Indole.alkaloid.biosynthesis	-0.00187	0.0257	-0.0729	0.942	-0.0543	0.0506	0.000171

Table 1031: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Influenza.A, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00166	0.027448	-0.0606	0.952	-0.05772	0.05439	0.000000
L3.Influenza.A	0.00014	0.000989	0.1417	0.888	-0.00188	0.00216	0.000648

Table 1032: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Inorganic.ion.transport.and.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.77e-02	3.30e-02	1.14	0.263	-2.98e-02	1.05e-01	0.00
L3.Inorganic.ion.transport.and.metabolism	-1.45e-07	8.86e-08	-1.64	0.111	-3.26e-07	3.55e-08	0.08

Table 1033: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Inositol.phosphate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.93e-02	3.13e-02	0.936	0.357	-3.46e-02	9.33e-02	0.000
L3.Inositol.phosphate.metabolism	-2.28e-07	1.57e-07	-1.456	0.156	-5.48e-07	9.18e-08	0.064

Table 1034: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Insulin.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.47e-02	4.92e-02	0.909	0.370	-5.57e-02	1.45e-01	0.0000
L3.Insulin.signaling.pathway	-7.31e-07	6.99e-07	-1.047	0.304	-2.16e-06	6.96e-07	0.0341

Table 1035: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Ion.channels, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.72e-02	4.33e-02	0.398	0.694	-7.12e-02	1.06e-01	0.00000
L3.Ion.channels	-4.55e-07	9.39e-07	-0.484	0.632	-2.37e-06	1.46e-06	0.00751

Table 1036: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Isoflavonoid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00306	0.0257	0.119	0.906	-0.04946	0.05557	0.0000
L3.Isoflavonoid.biosynthesis	-0.00166	0.0038	-0.436	0.666	-0.00943	0.00611	0.0061

Table 1037: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Isoquinoline.alkaloid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.37e-02	3.78e-02	0.362	0.720	-6.34e-02	9.08e-02	0.00000
L3.Isoquinoline.alkaloid.biosynthesis	-2.68e-07	5.60e-07	-0.479	0.635	-1.41e-06	8.75e-07	0.00736

Table 1038: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Leishmaniasis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1039: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Leukocyte.transendothelial.migration, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1040: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Limonene.and.pinene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.52e-02	3.45e-02	1.02	0.315	-3.52e-02	1.06e-01	0.0000
L3.Limonene.and.pinene.degradation	-3.76e-07	2.65e-07	-1.42	0.165	-9.17e-07	1.64e-07	0.0612

Table 1041: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Linoleic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.69e-02	5.00e-02	-0.539	0.594	-1.29e-01	7.52e-02	0.0000
L3.Linoleic.acid.metabolism	7.27e-07	1.17e-06	0.619	0.540	-1.67e-06	3.12e-06	0.0122

Table 1042: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Lipid.biosynthesis.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.80e-02	4.87e-02	0.369	0.714	-8.15e-02	1.17e-01	0.0000
L3.Lipid.biosynthesis.proteins	-3.56e-08	8.30e-08	-0.429	0.671	-2.05e-07	1.34e-07	0.0059

Table 1043: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Lipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.85e-02	3.58e-02	0.516	0.610	-5.47e-02	9.16e-02	0.000
L3.Lipid.metabolism	-1.43e-07	2.01e-07	-0.710	0.483	-5.54e-07	2.68e-07	0.016

Table 1044: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Lipoic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.63e-02	4.09e-02	1.38	0.179	-2.72e-02	1.4e-01	0.0000
L3.Lipoic.acid.metabolism	-1.15e-06	6.80e-07	-1.69	0.102	-2.54e-06	2.4e-07	0.0843

Table 1045: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Lipopolysaccharide.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.06e-03	3.45e-02	0.176	0.862	-6.44e-02	7.65e-02	0.00000
L3.Lipopolysaccharide.biosynthesis	-2.31e-08	9.13e-08	-0.253	0.802	-2.10e-07	1.63e-07	0.00206

Table 1046: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Lipopolysaccharide.biosynthesis.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.81e-02	3.60e-02	0.504	0.618	-5.54e-02	9.17e-02	0.0000
L3.Lipopolysaccharide.biosynthesis.proteins	-4.17e-08	6.04e-08	-0.691	0.495	-1.65e-07	8.17e-08	0.0152

Table 1047: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Long.term.depression, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1048: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Long.term.potentiation, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1049: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Lysine.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.89e-03	5.46e-02	-0.144	0.886	-1.19e-01	1.04e-01	0.000000
L3.Lysine.biosynthesis	1.26e-08	7.79e-08	0.162	0.872	-1.47e-07	1.72e-07	0.000848

Table 1050: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Lysine.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.23e-02	3.38e-02	0.658	0.516	-4.68e-02	9.14e-02	0.0000
L3.Lysine.degradation	-1.45e-07	1.53e-07	-0.952	0.349	-4.57e-07	1.67e-07	0.0284

Table 1051: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Lysosome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.16e-02	4.00e-02	1.29	0.207	-3.00e-02	1.33e-01	0.0000
L3.Lysosome	-5.22e-07	3.25e-07	-1.61	0.118	-1.18e-06	1.41e-07	0.0769

Table 1052: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.MAPK.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1053: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.MAPK.signaling.pathway...yeast, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.37e-03	5.19e-02	0.123	0.903	-9.96e-02	1.12e-01	0.000000
L3.MAPK.signaling.pathway...yeast	-1.42e-07	1.02e-06	-0.140	0.890	-2.22e-06	1.94e-06	0.000629

Table 1054: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Measles, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1055: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Meiosis...yeast, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.49e-02	2.72e-02	0.547	0.588	-4.07e-02	7.05e-02	0.0000
L3.Meiosis...yeast	-4.70e-06	3.91e-06	-1.201	0.239	-1.27e-05	3.29e-06	0.0445

Table 1056: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Melanogenesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.09e-02	2.56e-02	0.426	0.673	-0.041399	6.32e-02	0.0000
L3.Melanogenesis	-7.91e-05	6.16e-05	-1.284	0.209	-0.000205	4.67e-05	0.0505

Table 1057: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Membrane.and.intracellular.structural.molecules, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.84e-02	3.57e-02	1.07	0.291	-3.46e-02	1.11e-01	0.0
L3.Membrane.and.intracellular.structural.molecules	-6.78e-08	4.67e-08	-1.45	0.157	-1.63e-07	2.77e-08	0.0

Table 1058: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Metabolism.of.cofactors.and.vitamins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.77e-02	3.64e-02	0.486	0.631	-5.66e-02	9.19e-02	0.0000
L3.Metabolism.of.cofactors.and.vitamins	-1.25e-07	1.89e-07	-0.660	0.514	-5.10e-07	2.61e-07	0.0139

Table 1059: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Metabolism.of.xenobiotics.by.cytochrome.P450, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.56e-02	3.02e-02	1.18	0.2473	-2.60e-02	9.73e-02	0.00
L3.Metabolism.of.xenobiotics.by.cytochrome.P450	-7.46e-07	3.97e-07	-1.88	0.0702	-1.56e-06	6.55e-08	0.10

Table 1060: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Methane.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.16e-03	5.06e-02	0.181	0.858	-9.42e-02	1.13e-01	0.00000
L3.Methane.metabolism	-9.27e-09	4.46e-08	-0.208	0.837	-1.00e-07	8.19e-08	0.00139

Table 1061: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Mineral.absorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.07e-03	3.06e-02	0.0676	0.947	-6.04e-02	6.46e-02	0.00000
L3.Mineral.absorption	-1.18e-06	1.02e-05	-0.1154	0.909	-2.21e-05	1.97e-05	0.00043

Table 1062: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Mismatch.repair, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.50e-02	5.81e-02	-0.774	0.445	-1.64e-01	7.37e-02	0.000
L3.Mismatch.repair	6.65e-08	7.79e-08	0.853	0.400	-9.26e-08	2.26e-07	0.023

Table 1063: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.N.Glycan.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.25e-02	3.28e-02	-0.685	0.499	-8.95e-02	4.45e-02	0.0000
L3.N.Glycan.biosynthesis	1.61e-06	1.57e-06	1.024	0.314	-1.60e-06	4.83e-06	0.0327

Table 1064: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.NOD.like.receptor.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.49e-03	4.31e-02	-0.0577	0.954	-9.06e-02	8.56e-02	0.00000
L3.NOD.like.receptor.signaling.pathway	9.81e-08	1.39e-06	0.0705	0.944	-2.74e-06	2.94e-06	0.00016

Table 1065: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Naphthalene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.51e-02	4.95e-02	1.11	0.275	-4.60e-02	1.56e-01	0.0000
L3.Naphthalene.degradation	-4.40e-07	3.45e-07	-1.27	0.212	-1.14e-06	2.65e-07	0.0498

Table 1066: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Neuroactive.ligand.receptor.interaction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1067: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Neurotrophin.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1068: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Nicotinate.and.nicotinamide.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.81e-02	4.90e-02	0.574	0.570	-7.19e-02	1.28e-01	0.000
L3.Nicotinate.and.nicotinamide.metabolism	-7.61e-08	1.15e-07	-0.664	0.511	-3.10e-07	1.58e-07	0.014

Table 1069: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Nitrogen.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.02e-02	4.13e-02	0.731	0.470	-5.41e-02	1.14e-01	0.0000
L3.Nitrogen.metabolism	-4.35e-08	4.79e-08	-0.908	0.371	-1.41e-07	5.44e-08	0.0259

Table 1070: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Nitrotoluene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.93e-03	3.50e-02	-0.112	0.911	-7.54e-02	6.76e-02	0.000000
L3.Nitrotoluene.degradation	6.14e-08	3.86e-07	0.159	0.875	-7.26e-07	8.49e-07	0.000817

Table 1071: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Non.homologous.end.joining, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.42e-03	2.83e-02	0.297	0.768	-4.94e-02	6.63e-02	0.0000
L3.Non.homologous.end.joining	-7.41e-06	1.23e-05	-0.604	0.550	-3.24e-05	1.76e-05	0.0116

Table 1072: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Notch.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.012	0.0262	0.458	0.650	-0.0415	0.0654	0.0000
L3.Notch.signaling.pathway	-0.048	0.0396	-1.212	0.235	-0.1288	0.0328	0.0453

Table 1073: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Novobiocin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.24e-03	4.57e-02	-0.114	0.910	-9.86e-02	8.82e-02	0.000000
L3.Novobiocin.biosynthesis	4.79e-08	3.52e-07	0.136	0.892	-6.70e-07	7.66e-07	0.000599

Table 1074: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Nucleotide.excision.repair, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.07e-02	6.22e-02	-0.816	0.421	-1.78e-01	7.63e-02	0.0000
L3.Nucleotide.excision.repair	1.67e-07	1.88e-07	0.888	0.382	-2.18e-07	5.52e-07	0.0248

Table 1075: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Nucleotide.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.66e-02	3.25e-02	0.510	0.614	-4.99e-02	8.30e-02	0.0000
L3.Nucleotide.metabolism	-1.90e-07	2.44e-07	-0.777	0.443	-6.88e-07	3.09e-07	0.0191

Table 1076: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Olfactory.transduction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1077: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.One.carbon.pool.by.folate, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.49e-02	5.86e-02	-0.425	0.674	-1.45e-01	9.48e-02	0.00000
L3.One.carbon.pool.by.folate	4.86e-08	1.04e-07	0.469	0.642	-1.63e-07	2.60e-07	0.00705

Table 1078: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Oocyte.meiosis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1079: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Other.glycan.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.91e-02	4.27e-02	1.38	0.177	-2.81e-02	1.46e-01	0.0000
L3.Other.glycan.degradation	-2.16e-07	1.30e-07	-1.66	0.106	-4.82e-07	4.91e-08	0.0821

Table 1080: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Other.ion.coupled.transporters, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.58e-02	3.87e-02	0.668	0.509	-5.32e-02	1.05e-01	0.0000
L3.Other.ion.coupled.transporters	-1.95e-08	2.25e-08	-0.864	0.395	-6.55e-08	2.66e-08	0.0235

Table 1081: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Other.transporters, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.21e-02	3.99e-02	0.553	0.584	-5.95e-02	1.04e-01	0.0000
L3.Other.transporters	-9.52e-08	1.36e-07	-0.702	0.488	-3.72e-07	1.82e-07	0.0157

Table 1082: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Other.types.of.O.glycan.biosynthesis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1083: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Others, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.14e-02	4.54e-02	0.472	0.640	-7.12e-02	1.14e-01	0.0000
L3.Others	-2.21e-08	3.93e-08	-0.563	0.578	-1.02e-07	5.82e-08	0.0101

Table 1084: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Oxidative.phosphorylation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.37e-02	4.97e-02	0.477	0.637	-7.78e-02	1.25e-01	0.00000
L3.Oxidative.phosphorylation	-2.70e-08	4.92e-08	-0.549	0.587	-1.28e-07	7.35e-08	0.00964

Table 1085: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.PPAR.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.46e-02	4.95e-02	1.91	0.0657	-6.53e-03	1.96e-01	0.000
L3.PPAR.signaling.pathway	-1.25e-06	5.79e-07	-2.16	0.0390	-2.43e-06	-6.78e-08	0.131

Table 1086: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Pancreatic.cancer, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1087: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Pancreatic.secretion, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1088: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Pantothenate.and.CoA.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.97e-03	5.13e-02	-0.156	0.877	-1.13e-01	9.67e-02	0.00000
L3.Pantothenate.and.CoA.biosynthesis	1.54e-08	8.67e-08	0.178	0.860	-1.62e-07	1.92e-07	0.00102

Table 1089: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Parkinson.s.disease, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.22e-02	2.61e-02	0.466	0.645	-0.041171	6.55e-02	0.0000
L3.Parkinson.s.disease	-1.93e-05	1.55e-05	-1.241	0.224	-0.000051	1.24e-05	0.0473

Table 1090: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Pathogenic.Escherichia.coli.infection, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0181	0.02345	0.771	0.447	-0.0298	0.06597	0.00
L3.Pathogenic.Escherichia.coli.infection	-0.0129	0.00493	-2.609	0.014	-0.0229	-0.00279	0.18

Table 1091: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Pathways.in.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.34e-02	3.94e-02	-0.339	0.737	-9.39e-02	6.72e-02	0.00000
L3.Pathways.in.cancer	3.96e-07	9.09e-07	0.435	0.667	-1.46e-06	2.25e-06	0.00607

Table 1092: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Penicillin.and.cephalosporin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.65e-03	4.01e-02	0.116	0.908	-7.72e-02	8.65e-02	0.000000
L3.Penicillin.and.cephalosporin.biosynthesis	-1.36e-07	9.25e-07	-0.148	0.884	-2.02e-06	1.75e-06	0.000703

Table 1093: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Pentose.and.glucuronate.interconversions, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.19e-02	3.48e-02	0.915	0.368	-3.93e-02	1.03e-01	0.0000
L3.Pentose.and.glucuronate.interconversions	-6.58e-08	5.18e-08	-1.270	0.214	-1.72e-07	4.00e-08	0.0495

Table 1094: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Pentose.phosphate.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.36e-02	4.59e-02	0.297	0.769	-8.01e-02	1.07e-01	0.000
L3.Pentose.phosphate.pathway	-1.77e-08	5.02e-08	-0.353	0.727	-1.20e-07	8.48e-08	0.004

Table 1095: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Peptidases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.08e-03	5.11e-02	0.0212	0.983	-1.03e-01	1.05e-01	0.00e+00
L3.Peptidases	-6.39e-10	2.64e-08	-0.0242	0.981	-5.45e-08	5.32e-08	1.89e-05

Table 1096: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Peptidoglycan.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.00e-02	5.58e-02	-0.358	0.722	-1.34e-01	9.40e-02	0.00000
L3.Peptidoglycan.biosynthesis	2.82e-08	7.05e-08	0.400	0.692	-1.16e-07	1.72e-07	0.00513

Table 1097: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Peroxisome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.31e-02	4.53e-02	1.61	0.117	-1.94e-02	1.66e-01	0.000
L3.Peroxisome	-5.03e-07	2.67e-07	-1.89	0.069	-1.05e-06	4.16e-08	0.103

Table 1098: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Pertussis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.03e-02	2.74e-02	0.74	0.465	-3.57e-02	7.63e-02	0.0000
L3.Pertussis	-2.24e-07	1.48e-07	-1.51	0.141	-5.26e-07	7.83e-08	0.0688

Table 1099: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Phagosome, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1100: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Phenylalanine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.35e-02	3.19e-02	0.737	0.467	-4.17e-02	8.87e-02	0.00
L3.Phenylalanine.metabolism	-1.25e-07	1.10e-07	-1.137	0.265	-3.49e-07	9.93e-08	0.04

Table 1101: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	1.69e-03	5.20e-02	0.0324	0.974	-1.05e-01	1.08e-01
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis	-2.53e-09	6.85e-08	-0.0369	0.971	-1.42e-07	1.37e-07

Table 1102: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Phenylpropanoid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.41e-02	3.69e-02	1.47	0.1526	-2.12e-02	1.29e-01	0.000
L3.Phenylpropanoid.biosynthesis	-3.74e-07	1.97e-07	-1.90	0.0668	-7.76e-07	2.76e-08	0.105

Table 1103: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Phosphatidylinositol.signaling.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.53e-02	5.43e-02	0.467	0.644	-8.55e-02	1.36e-01	0.00000
L3.Phosphatidylinositol.signaling.system	-2.72e-07	5.18e-07	-0.524	0.604	-1.33e-06	7.87e-07	0.00878

Table 1104: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Phosphonate.and.phosphinate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.37e-02	4.21e-02	0.563	0.578	-6.23e-02	1.10e-01	0.0000
L3.Phosphonate.and.phosphinate.metabolism	-3.30e-07	4.76e-07	-0.694	0.493	-1.30e-06	6.42e-07	0.0153

Table 1105: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Phosphotransferase.system..PTS., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.94e-03	3.60e-02	0.137	0.892	-6.86e-02	7.85e-02	0.00000
L3.Phosphotransferase.system..PTS.	-5.47e-09	2.89e-08	-0.189	0.851	-6.44e-08	5.35e-08	0.00116

Table 1106: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Photosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.25e-02	5.99e-02	-1.21	0.235	-1.95e-01	4.98e-02	0.0000
L3.Photosynthesis	2.55e-07	1.93e-07	1.32	0.196	-1.39e-07	6.48e-07	0.0535

Table 1107: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Photosynthesis...antenna.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.02146	0.0276	0.779	0.442	-0.03483	0.077748	0.0000
L3.Photosynthesis...antenna.proteins	-0.00187	0.0012	-1.558	0.130	-0.00431	0.000581	0.0726

Table 1108: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Photosynthesis.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.17e-02	5.92e-02	-1.04	0.305	-1.83e-01	5.91e-02	0.0000
L3.Photosynthesis.proteins	2.13e-07	1.86e-07	1.14	0.261	-1.67e-07	5.93e-07	0.0405

Table 1109: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Phototransduction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1110: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Phototransduction. . . fly, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1111: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Plant.pathogen.interaction, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.91e-02	4.85e-02	-0.395	0.696	-1.18e-01	7.99e-02	0.00000
L3.Plant.pathogen.interaction	1.75e-07	3.81e-07	0.459	0.650	-6.03e-07	9.53e-07	0.00674

Table 1112: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Polycyclic.aromatic.hydrocarbon.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.26e-02	5.71e-02	-0.921	0.364	-1.69e-01	6.41e-02	0.000
L3.Polycyclic.aromatic.hydrocarbon.degradation	5.68e-07	5.57e-07	1.019	0.316	-5.70e-07	1.71e-06	0.032

Table 1113: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Polyketide.sugar.unit.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.79e-02	5.13e-02	0.934	0.358	-5.68e-02	1.53e-01	0.0000
L3.Polyketide.sugar.unit.biosynthesis	-3.24e-07	3.05e-07	-1.061	0.297	-9.47e-07	2.99e-07	0.0351

Table 1114: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Pores.ion.channels, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.03e-02	3.42e-02	0.886	0.383	-3.96e-02	1.00e-01	0.0000
L3.Pores.ion.channels	-7.05e-08	5.63e-08	-1.252	0.220	-1.86e-07	4.45e-08	0.0481

Table 1115: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Porphyrin.and.chlorophyll.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.57e-02	4.03e-02	-0.637	0.529	-1.08e-01	5.67e-02	0.0000
L3.Porphyrin.and.chlorophyll.metabolism	3.30e-08	4.12e-08	0.803	0.429	-5.10e-08	1.17e-07	0.0204

Table 1116: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Prenyltransferases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.14e-02	5.72e-02	-0.199	0.843	-1.28e-01	1.05e-01	0.00000
L3.Prenyltransferases	4.51e-08	2.04e-07	0.221	0.826	-3.71e-07	4.62e-07	0.00158

Table 1117: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Primary.bile.acid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.56e-02	4.72e-02	1.39	0.175	-3.09e-02	1.62e-01	0.0000
L3.Primary.bile.acid.biosynthesis	-2.97e-06	1.85e-06	-1.61	0.118	-6.73e-06	8.02e-07	0.0769

Table 1118: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Primary.immunodeficiency, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.63e-03	5.53e-02	0.0295	0.977	-1.11e-01	1.15e-01	0.00e+00
L3.Primary.immunodeficiency	-2.91e-08	8.82e-07	-0.0330	0.974	-1.83e-06	1.77e-06	3.51e-05

Table 1119: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Prion.diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.51e-02	2.84e-02	0.883	0.384	-3.29e-02	8.32e-02	0.0000
L3.Prion.diseases	-3.81e-06	2.36e-06	-1.616	0.117	-8.62e-06	1.01e-06	0.0777

Table 1120: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Progesterone.mediated.oocyte.maturation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.98e-03	4.20e-02	-0.0948	0.925	-8.97e-02	8.18e-02	0.000000
L3.Progesterone.mediated.oocyte.maturation	1.69e-07	1.44e-06	0.1175	0.907	-2.77e-06	3.11e-06	0.000445

Table 1121: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Propanoate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.03e-02	4.20e-02	0.483	0.632	-6.55e-02	1.06e-01	0.0000
L3.Propanoate.metabolism	-4.06e-08	6.81e-08	-0.597	0.555	-1.80e-07	9.84e-08	0.0114

Table 1122: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Prostate.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.32e-03	4.10e-02	0.179	0.859	-7.64e-02	9.11e-02	0.00000
L3.Prostate.cancer	-2.90e-07	1.29e-06	-0.224	0.824	-2.93e-06	2.35e-06	0.00162

Table 1123: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Proteasome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.87e-02	5.66e-02	0.683	0.500	-7.69e-02	1.54e-01	0.0000
L3.Proteasome	-1.35e-06	1.78e-06	-0.759	0.454	-4.98e-06	2.28e-06	0.0182

Table 1124: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Protein.digestion.and.absorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.16e-02	3.41e-02	1.22	0.2313	-2.80e-02	1.11e-01	0.0000
L3.Protein.digestion.and.absorption	-2.45e-06	1.44e-06	-1.70	0.0993	-5.38e-06	4.91e-07	0.0854

Table 1125: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Protein.export, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.40e-02	5.73e-02	-0.593	0.558	-1.51e-01	8.31e-02	0.0000
L3.Protein.export	6.48e-08	9.87e-08	0.656	0.517	-1.37e-07	2.66e-07	0.0137

Table 1126: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Protein.folding.and.associated.processing, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.34e-02	4.34e-02	0.539	0.594	-6.52e-02	1.12e-01	0.0000
L3.Protein.folding.and.associated.processing	-3.77e-08	5.76e-08	-0.655	0.518	-1.55e-07	7.99e-08	0.0136

Table 1127: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Protein.kinases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.62e-02	3.76e-02	0.961	0.344	-4.07e-02	1.13e-01	0.0000
L3.Protein.kinases	-1.18e-07	9.41e-08	-1.254	0.219	-3.10e-07	7.42e-08	0.0483

Table 1128: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Protein.processing.in.endoplasmic.reticulum, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.00e-02	4.53e-02	0.661	0.514	-6.26e-02	1.23e-01	0.0000
L3.Protein.processing.in.endoplasmic.reticulum	-7.37e-07	9.37e-07	-0.787	0.438	-2.65e-06	1.18e-06	0.0196

Table 1129: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Proximal.tubule.bicarbonate.reclamation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.48e-02	3.18e-02	0.465	0.645	-5.02e-02	7.98e-02	0.0000
L3.Proximal.tubule.bicarbonate.reclamation	-5.85e-07	7.97e-07	-0.734	0.469	-2.21e-06	1.04e-06	0.0171

Table 1130: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Purine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.20e-02	5.37e-02	-0.223	0.825	-1.22e-01	9.78e-02	0.00000
L3.Purine.metabolism	6.03e-09	2.40e-08	0.251	0.803	-4.30e-08	5.51e-08	0.00203

Table 1131: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Pyrimidine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.99e-02	5.69e-02	-0.524	0.604	-1.46e-01	8.64e-02	0.0000
L3.Pyrimidine.metabolism	1.92e-08	3.31e-08	0.582	0.565	-4.83e-08	8.68e-08	0.0108

Table 1132: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Pyruvate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.20e-02	4.38e-02	0.502	0.619	-6.75e-02	1.11e-01	0.0000
L3.Pyruvate.metabolism	-2.28e-08	3.76e-08	-0.607	0.548	-9.96e-08	5.39e-08	0.0118

Table 1133: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.RIG.I.like.receptor.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.55e-03	3.09e-02	-0.147	0.884	-6.76e-02	5.85e-02	0.00000
L3.RIG.I.like.receptor.signaling.pathway	3.16e-06	1.28e-05	0.247	0.806	-2.29e-05	2.92e-05	0.00197

Table 1134: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.RNA.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.36e-03	5.66e-02	0.0947	0.925	-1.10e-01	1.21e-01	0.000000
L3.RNA.degradation	-1.44e-08	1.36e-07	-0.1053	0.917	-2.93e-07	2.64e-07	0.000358

Table 1135: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.RNA.polymerase, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.38e-02	5.56e-02	-1.15	0.260	-1.77e-01	4.98e-02	0.0000
L3.RNA.polymerase	4.42e-07	3.47e-07	1.27	0.212	-2.67e-07	1.15e-06	0.0498

Table 1136: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.RNA.transport, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.54e-03	4.75e-02	0.159	0.875	-8.94e-02	1.04e-01	0.00000
L3.RNA.transport	-7.58e-08	4.07e-07	-0.186	0.854	-9.07e-07	7.55e-07	0.00112

Table 1137: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Regulation.of.actin.cytoskeleton, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1138: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Renal.cell.carcinoma, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.37e-02	3.09e-02	-0.442	0.661	-7.67e-02	4.94e-02	0.000
L3.Renal.cell.carcinoma	1.34e-06	1.83e-06	0.732	0.470	-2.39e-06	5.07e-06	0.017

Table 1139: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Renin.angiotensin.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.002242	0.025303	0.0886	0.930	-0.049433	0.053917	0.00000
L3.Renin.angiotensin.system	-0.000122	0.000287	-0.4241	0.675	-0.000707	0.000464	0.00577

Table 1140: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Replication..recombination.and.repair.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.95e-03	4.95e-02	0.0393	0.969	-9.92e-02	1.03e-01	0.00
L3.Replication..recombination.and.repair.proteins	-3.00e-09	6.61e-08	-0.0454	0.964	-1.38e-07	1.32e-07	6.66

Table 1141: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Restriction.enzyme, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.01e-02	4.65e-02	0.432	0.669	-7.49e-02	1.15e-01	0.00000
L3.Restriction.enzyme	-1.31e-07	2.56e-07	-0.510	0.614	-6.54e-07	3.93e-07	0.00833

Table 1142: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Retinol.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.71e-02	3.40e-02	1.39	0.1759	-2.23e-02	1.16e-01	0.000
L3.Retinol.metabolism	-1.30e-06	6.79e-07	-1.91	0.0652	-2.68e-06	8.70e-08	0.106

Table 1143: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Rheumatoid.arthritis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1144: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Riboflavin.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.11e-02	4.05e-02	0.273	0.786	-7.17e-02	9.39e-02	0.00000
L3.Riboflavin.metabolism	-5.41e-08	1.57e-07	-0.346	0.732	-3.74e-07	2.66e-07	0.00384

Table 1145: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Ribosome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.56e-02	5.88e-02	-0.945	0.352	-1.76e-01	6.45e-02	0.0000
L3.Ribosome	2.91e-08	2.81e-08	1.039	0.307	-2.82e-08	8.65e-08	0.0336

Table 1146: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Ribosome.Biogenesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.57e-02	5.08e-02	-0.310	0.759	-1.19e-01	8.80e-02	0.00000
L3.Ribosome.Biogenesis	1.30e-08	3.66e-08	0.355	0.725	-6.17e-08	8.77e-08	0.00404

Table 1147: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Ribosome.biogenesis.in.eukaryotes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.11e-03	5.34e-02	0.133	0.895	-1.02e-01	1.16e-01	0.000000
L3.Ribosome.biogenesis.in.eukaryotes	-1.64e-07	1.09e-06	-0.150	0.882	-2.39e-06	2.06e-06	0.000729

Table 1148: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Salivary.secretion, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1149: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Secondary.bile.acid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.58e-02	4.71e-02	1.40	0.173	-3.04e-02	1.62e-01	0.0000
L3.Secondary.bile.acid.biosynthesis	-3.01e-06	1.86e-06	-1.62	0.116	-6.82e-06	7.91e-07	0.0779

Table 1150: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Secretion.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.26e-02	3.59e-02	0.630	0.534	-5.08e-02	9.60e-02	0.0000
L3.Secretion.system	-1.73e-08	2.01e-08	-0.861	0.396	-5.85e-08	2.38e-08	0.0234

Table 1151: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Selenocompound.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.13e-02	4.66e-02	0.243	0.810	-8.38e-02	1.06e-01	0.00000
L3.Selenocompound.metabolism	-3.20e-08	1.12e-07	-0.287	0.776	-2.60e-07	1.96e-07	0.00265

Table 1152: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Sesquiterpenoid.biosynthesis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1153: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Shigellosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0259	0.02650	0.977	0.3365	-0.0282	8.00e-02	0.000
L3.Shigellosis	-0.0138	0.00677	-2.039	0.0504	-0.0276	2.52e-05	0.118

Table 1154: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Signal.transduction.mechanisms, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.84e-03	4.45e-02	0.199	0.844	-8.21e-02	9.97e-02	0.00000
L3.Signal.transduction.mechanisms	-2.07e-08	8.66e-08	-0.239	0.813	-1.97e-07	1.56e-07	0.00184

Table 1155: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Small.cell.lung.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00166	0.027448	-0.0606	0.952	-0.05772	0.05439	0.000000
L3.Small.cell.lung.cancer	0.00014	0.000989	0.1417	0.888	-0.00188	0.00216	0.000648

Table 1156: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Sphingolipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.73e-02	4.11e-02	1.64	0.1119	-1.66e-02	1.51e-01	0.000
L3.Sphingolipid.metabolism	-3.92e-07	1.97e-07	-1.99	0.0558	-7.94e-07	1.03e-08	0.113

Table 1157: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Spliceosome, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1158: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Sporulation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.24e-02	3.33e-02	-1.27	0.2129	-1.10e-01	2.56e-02	0.0000
L3.Sporulation	1.32e-07	7.32e-08	1.80	0.0814	-1.75e-08	2.81e-07	0.0949

Table 1159: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Staphylococcus.aureus.infection, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.01e-02	3.07e-02	-0.329	0.745	-7.28e-02	5.26e-02	0.00000
L3.Staphylococcus.aureus.infection	2.39e-07	4.32e-07	0.553	0.585	-6.43e-07	1.12e-06	0.00976

Table 1160: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Starch.and.sucrose.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.85e-02	4.56e-02	1.06	0.296	-4.46e-02	1.42e-01	0.0000
L3.Starch.and.sucrose.metabolism	-5.48e-08	4.37e-08	-1.25	0.219	-1.44e-07	3.44e-08	0.0483

Table 1161: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Steroid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.94e-03	0.027628	-0.143	0.887	-0.060369	0.052479	0.00000
L3.Steroid.biosynthesis	7.34e-05	0.000228	0.323	0.749	-0.000391	0.000538	0.00335

Table 1162: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Steroid.hormone.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.91e-02	2.87e-02	1.36	0.1830	-1.95e-02	9.77e-02	0.000
L3.Steroid.hormone.biosynthesis	-2.34e-06	1.03e-06	-2.27	0.0307	-4.46e-06	-2.33e-07	0.142

Table 1163: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	1.65e-03	2.67e-02	0.0618	0.951	-5.29e-02	5.62e-02
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	-1.02e-06	6.14e-06	-0.1668	0.869	-1.36e-05	1.15e-05

Table 1164: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Streptomycin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.81e-02	5.06e-02	1.15	0.260	-4.52e-02	1.61e-01	0.0000
L3.Streptomycin.biosynthesis	-2.28e-07	1.74e-07	-1.31	0.201	-5.83e-07	1.28e-07	0.0522

Table 1165: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Styrene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.76e-02	2.61e-02	0.673	0.506	-3.58e-02	7.10e-02	0.0000
L3.Styrene.degradation	-6.49e-07	4.00e-07	-1.625	0.115	-1.47e-06	1.67e-07	0.0785

Table 1166: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Sulfur.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.28e-02	4.51e-02	0.728	0.472	-5.93e-02	1.25e-01	0.0000
L3.Sulfur.metabolism	-1.28e-07	1.48e-07	-0.867	0.393	-4.31e-07	1.74e-07	0.0237

Table 1167: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Sulfur.relay.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.80e-02	3.74e-02	0.481	0.634	-5.83e-02	9.43e-02	0.0000
L3.Sulfur.relay.system	-7.24e-08	1.13e-07	-0.641	0.527	-3.03e-07	1.59e-07	0.0131

Table 1168: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Synthesis.and.degradation.of.ketone.bodies, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.27e-02	3.77e-02	-0.337	0.738	-8.97e-02	6.43e-02	0.0000
L3.Synthesis.and.degradation.of.ketone.bodies	3.65e-07	8.16e-07	0.447	0.658	-1.30e-06	2.03e-06	0.0064

Table 1169: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Systemic.lupus.erythematosus, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.11e-02	2.59e-02	0.429	0.671	-0.041765	6.40e-02	0.0000
L3.Systemic.lupus.erythematosus	-7.54e-05	6.19e-05	-1.218	0.233	-0.000202	5.11e-05	0.0456

Table 1170: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.TGF.beta.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1171: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Taurine.and.hypotaurine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.07e-02	4.84e-02	0.428	0.672	-7.81e-02	1.20e-01	0.00000
L3.Taurine.and.hypotaurine.metabolism	-1.96e-07	3.92e-07	-0.498	0.622	-9.97e-07	6.06e-07	0.00794

Table 1172: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Terpenoid.backbone.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.37e-02	5.68e-02	-0.946	0.352	-1.70e-01	6.22e-02	0.0000
L3.Terpenoid.backbone.biosynthesis	1.20e-07	1.14e-07	1.048	0.303	-1.14e-07	3.53e-07	0.0342

Table 1173: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs
L3.Tetracycline.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.24e-03	5.00e-02	-0.0249	0.980	-1.03e-01	1.01e-01	0.00e+00
L3.Tetracycline.biosynthesis	9.87e-09	3.44e-07	0.0287	0.977	-6.93e-07	7.13e-07	2.65e-05

Table 1174: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Thiamine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.07e-03	5.22e-02	0.0397	0.969	-1.05e-01	1.09e-01	0.00e+00
L3.Thiamine.metabolism	-5.00e-09	1.11e-07	-0.0451	0.964	-2.31e-07	2.21e-07	6.57e-05

Table 1175: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Tight.junction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1176: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Toluene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.78e-02	2.86e-02	0.624	0.538	-4.05e-02	7.61e-02	0.0000
L3.Toluene.degradation	-1.57e-07	1.33e-07	-1.181	0.247	-4.29e-07	1.15e-07	0.0431

Table 1177: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Toxoplasmosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00166	0.027448	-0.0606	0.952	-0.05772	0.05439	0.000000
L3.Toxoplasmosis	0.00014	0.000989	0.1417	0.888	-0.00188	0.00216	0.000648

Table 1178: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Transcription.factors, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.87e-02	3.68e-02	0.507	0.616	-5.65e-02	9.38e-02	0.0000
L3.Transcription.factors	-1.06e-08	1.56e-08	-0.683	0.500	-4.24e-08	2.12e-08	0.0148

Table 1179: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Transcription.machinery, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.34e-03	5.76e-02	0.128	0.899	-1.10e-01	1.25e-01	0.000000
L3.Transcription.machinery	-1.11e-08	7.84e-08	-0.141	0.889	-1.71e-07	1.49e-07	0.000644

Table 1180: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Transcription.related.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.04e-02	2.70e-02	0.756	0.455	-3.47e-02	7.56e-02	0.0000
L3.Transcription.related.proteins	-1.40e-06	8.75e-07	-1.603	0.119	-3.19e-06	3.84e-07	0.0766

Table 1181: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Translation.factors, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.99e-02	5.61e-02	-0.712	0.482	-1.54e-01	7.45e-02	0.0000
L3.Translation.factors	9.03e-08	1.14e-07	0.793	0.434	-1.42e-07	3.23e-07	0.0199

Table 1182: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Translation.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.78e-02	5.08e-02	-0.350	0.729	-1.22e-01	8.60e-02	0.00000
L3.Translation.proteins	2.25e-08	5.62e-08	0.401	0.691	-9.23e-08	1.37e-07	0.00516

Table 1183: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Transporters, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.48e-02	4.04e-02	0.365	0.717	-6.77e-02	9.72e-02	0.00000
L3.Transporters	-2.21e-09	4.78e-09	-0.462	0.647	-1.20e-08	7.56e-09	0.00684

Table 1184: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	9.64e-03	4.03e-02	0.239	0.813	-7.27e-02	9.2e-02
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis	-9.40e-08	3.10e-07	-0.303	0.764	-7.28e-07	5.4e-07

Table 1185: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Tryptophan.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.39e-02	3.13e-02	0.763	0.452	-4.01e-02	8.78e-02	0.0000
L3.Tryptophan.metabolism	-1.24e-07	1.03e-07	-1.205	0.238	-3.33e-07	8.59e-08	0.0447

Table 1186: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Tuberculosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.30e-02	6.20e-02	-0.371	0.713	-1.50e-01	1.04e-01	0.00000
L3.Tuberculosis	2.06e-07	5.07e-07	0.405	0.688	-8.31e-07	1.24e-06	0.00527

Table 1187: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Two.component.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.83e-02	3.62e-02	0.783	0.440	-4.56e-02	1.02e-01	0.0000
L3.Two.component.system	-2.01e-08	1.90e-08	-1.058	0.298	-5.88e-08	1.87e-08	0.0349

Table 1188: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Type.I.diabetes.mellitus, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.95e-02	6.14e-02	-0.318	0.753	-1.45e-01	1.06e-01	0.00000
L3.Type.I.diabetes.mellitus	4.76e-07	1.37e-06	0.347	0.731	-2.32e-06	3.27e-06	0.00387

Table 1189: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Type.II.diabetes.mellitus, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.10e-03	5.06e-02	-0.0613	0.951	-1.06e-01	1.00e-01	0.00000
L3.Type.II.diabetes.mellitus	6.96e-08	9.88e-07	0.0704	0.944	-1.95e-06	2.09e-06	0.00016

Table 1190: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Tyrosine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.47e-02	4.09e-02	0.604	0.550	-5.88e-02	1.08e-01	0.0000
L3.Tyrosine.metabolism	-7.47e-08	9.89e-08	-0.756	0.456	-2.77e-07	1.27e-07	0.0181

Table 1191: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	2.73e-02	3.19e-02	0.856	0.399	-3.79e-02	9.25e-02
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis	-1.32e-07	1.01e-07	-1.308	0.201	-3.39e-07	7.43e-08

Table 1192: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Ubiquitin.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.57e-02	2.81e-02	1.27	0.213	-2.16e-02	9.30e-02	0.000
L3.Ubiquitin.system	-2.64e-06	1.19e-06	-2.22	0.034	-5.07e-06	-2.13e-07	0.137

Table 1193: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.VEGF.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1194: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Valine..leucine.and.isoleucine.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.35e-04	5.33e-02	0.00817	0.994	-1.08e-01	1.09e-01	0.00e+0
L3.Valine..leucine.and.isoleucine.biosynthesis	-6.90e-10	7.47e-08	-0.00923	0.993	-1.53e-07	1.52e-07	2.75e-0

Table 1195: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Valine..leucine.and.isoleucine.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.24e-02	3.83e-02	0.585	0.563	-5.58e-02	1.01e-01	0.0000
L3.Valine..leucine.and.isoleucine.degradation	-8.38e-08	1.10e-07	-0.763	0.451	-3.08e-07	1.40e-07	0.0185

Table 1196: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Various.types.of.N.glycan.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.0274	0.0267	-1.02	0.3143	-0.082009	0.0273	0.000
L3.Various.types.of.N.glycan.biosynthesis	0.0274	0.0133	2.06	0.0479	0.000274	0.0545	0.121

Table 1197: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Vascular.smooth.muscle.contraction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1198: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Vasopressin.regulated.water.reabsorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00532	0.0257	-0.207	0.837	-0.0578	0.0472	0.0000
L3.Vasopressin.regulated.water.reabsorption	0.02128	0.0297	0.717	0.479	-0.0393	0.0819	0.0163

Table 1199: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Vibrio.cholerae.infection, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0129	0.0269	0.48	0.635	-0.0420	0.0678	0.0000
L3.Vibrio.cholerae.infection	-0.0179	0.0159	-1.13	0.269	-0.0505	0.0146	0.0392

Table 1200: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Vibrio.cholerae.pathogenic.cycle, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.38e-02	3.86e-02	0.875	0.388	-4.50e-02	1.13e-01	0.0000
L3.Vibrio.cholerae.pathogenic.cycle	-5.10e-07	4.52e-07	-1.128	0.268	-1.43e-06	4.13e-07	0.0394

Table 1201: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Viral.myocarditis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00166	0.027448	-0.0606	0.952	-0.05772	0.05439	0.000000
L3.Viral.myocarditis	0.00014	0.000989	0.1417	0.888	-0.00188	0.00216	0.000648

Table 1202: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Vitamin.B6.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.50e-02	4.20e-02	1.07	0.293	-4.08e-02	1.31e-01	0.0000
L3.Vitamin.B6.metabolism	-2.86e-07	2.18e-07	-1.31	0.201	-7.32e-07	1.60e-07	0.0523

Table 1203: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Wnt.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.012	0.0262	0.458	0.650	-0.0415	0.0654	0.0000
L3.Wnt.signaling.pathway	-0.048	0.0396	-1.212	0.235	-0.1288	0.0328	0.0453

Table 1204: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Xylene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.54e-02	3.71e-02	0.417	0.680	-6.03e-02	9.11e-02	0.00000
L3.Xylene.degradation	-2.43e-07	4.35e-07	-0.558	0.581	-1.13e-06	6.45e-07	0.00996

Table 1205: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.Zeatin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.44e-02	6.32e-02	-0.386	0.702	-1.53e-01	1.05e-01	0.00000
L3.Zeatin.biosynthesis	5.75e-07	1.37e-06	0.420	0.678	-2.22e-06	3.37e-06	0.00566

Table 1206: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.alpha.Linolenic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.94e-02	2.64e-02	0.735	0.468	-3.46e-02	7.34e-02	0.0000
L3.alpha.Linolenic.acid.metabolism	-1.49e-06	8.90e-07	-1.671	0.105	-3.31e-06	3.30e-07	0.0826

Table 1207: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.beta.Alanine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.38e-02	3.49e-02	0.683	0.500	-4.74e-02	9.50e-02	0.0000
L3.beta.Alanine.metabolism	-1.31e-07	1.37e-07	-0.958	0.346	-4.10e-07	1.48e-07	0.0288

Table 1208: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.beta.Lactam.resistance, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.83e-03	4.44e-02	-0.109	0.914	-9.55e-02	8.58e-02	0.000000
L3.beta.Lactam.resistance	2.21e-07	1.68e-06	0.131	0.896	-3.22e-06	3.66e-06	0.000555

Table 1209: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.mRNA.surveillance.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1210: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.mTOR.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	2.19e-14	0.0244	8.96e-13	1	-0.0498	0.0498	0
	NA	NA	NA	NA	NA	NA	0

Table 1211: diversity_vs_picrust_L3_neo: wunifrac.PC.2 vs L3.p53.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00166	0.027448	-0.0606	0.952	-0.05772	0.05439	0.000000
L3.p53.signaling.pathway	0.00014	0.000989	0.1417	0.888	-0.00188	0.00216	0.000648

Table 1212: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %
Intercept	3.83e-03	2.24e-02	0.171	0.865	-4.19e-02
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	-4.54e-06	4.97e-06	-0.914	0.368	-1.47e-05

Table 1213: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.ABC.transporters, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.26e-02	3.32e-02	-0.983	0.333	-1.00e-01	3.51e-02	0.0000
L3.ABC.transporters	9.80e-09	7.54e-09	1.301	0.203	-5.59e-09	2.52e-08	0.0518

Table 1214: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Adherens.junction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1215: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Adipocytokine.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.73e-02	3.50e-02	-1.35	0.1863	-1.19e-01	2.41e-02	0.0000
L3.Adipocytokine.signaling.pathway	1.04e-06	6.07e-07	1.71	0.0983	-2.04e-07	2.28e-06	0.0859

Table 1216: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.African.trypanosomiasis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.84e-02	2.84e-02	-0.648	0.522	-7.64e-02	3.96e-02	0.0000
L3.African.trypanosomiasis	2.50e-06	2.45e-06	1.021	0.316	-2.51e-06	7.51e-06	0.0325

Table 1217: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Alanine..aspartate.and.glutamate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.94e-02	4.51e-02	-1.76	0.0889	-1.72e-01	1.28e-02	0.000
L3.Alanine..aspartate.and.glutamate.metabolism	9.38e-08	4.72e-08	1.99	0.0562	-2.65e-09	1.90e-07	0.113

Table 1218: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Aldosterone.regulated.sodium.reabsorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00376	0.0223	0.168	0.867	-0.0419	0.0494	0.0000
L3.Aldosterone.regulated.sodium.reabsorption	-0.12039	0.1264	-0.952	0.348	-0.3785	0.1378	0.0284

Table 1219: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Alzheimer.s.disease, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.21e-02	3.83e-02	-1.62	0.1154	-1.40e-01	1.61e-02	0.000
L3.Alzheimer.s.disease	1.42e-06	7.34e-07	1.94	0.0617	-7.45e-08	2.92e-06	0.108

Table 1220: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Amino.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.81e-02	3.21e-02	-1.19	0.245	-1.04e-01	2.75e-02	0.0000
L3.Amino.acid.metabolism	1.61e-07	1.01e-07	1.59	0.122	-4.53e-08	3.67e-07	0.0757

Table 1221: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Amino.acid.related.enzymes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.55e-02	4.52e-02	-1.89	0.0679	-1.78e-01	6.70e-03	0.000
L3.Amino.acid.related.enzymes	6.99e-08	3.28e-08	2.13	0.0412	2.99e-09	1.37e-07	0.128

Table 1222: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Amino.sugar.and.nucleotide.sugar.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.40e-02	4.45e-02	-1.66	0.1069	-1.65e-01	1.69e-02	0.000
L3.Amino.sugar.and.nucleotide.sugar.metabolism	5.33e-08	2.82e-08	1.89	0.0687	-4.35e-09	1.11e-07	0.10

Table 1223: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Aminoacyl.tRNA.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.52e-02	4.85e-02	-1.76	0.0890	-1.84e-01	1.38e-02	0.000
L3.Aminoacyl.tRNA.biosynthesis	8.86e-08	4.54e-08	1.95	0.0605	-4.16e-09	1.81e-07	0.109

Table 1224: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Aminobenzoate.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.79e-02	3.14e-02	-0.89	0.381	-9.20e-02	3.62e-02	0.0000
L3.Aminobenzoate.degradation	2.11e-07	1.71e-07	1.24	0.226	-1.38e-07	5.59e-07	0.0469

Table 1225: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Amoebiasis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.40e-02	2.85e-02	-0.839	0.408	-8.22e-02	3.43e-02	0.0000
L3.Amoebiasis	6.36e-06	4.92e-06	1.294	0.206	-3.68e-06	1.64e-05	0.0513

Table 1226: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Amyotrophic.lateral.sclerosis..ALS., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.07e-02	2.56e-02	-0.808	0.425	-7.28e-02	3.15e-02	0.0000
L3.Amyotrophic.lateral.sclerosis..ALS.	1.14e-06	7.59e-07	1.500	0.144	-4.11e-07	2.69e-06	0.0677

Table 1227: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Antigen.processing.and.presentation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.14e-02	3.71e-02	-0.846	0.404	-1.07e-01	4.44e-02	0.0000
L3.Antigen.processing.and.presentation	1.33e-06	1.27e-06	1.049	0.303	-1.26e-06	3.93e-06	0.0343

Table 1228: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Apoptosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.0e-03	0.026498	0.0756	0.940	-5.21e-02	5.61e-02	0.000000
L3.Apoptosis	-2.8e-07	0.000002	-0.1402	0.889	-4.36e-06	3.80e-06	0.000634

Table 1229: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Arachidonic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.60e-02	3.15e-02	-0.506	0.617	-8.03e-02	4.84e-02	0.000
L3.Arachidonic.acid.metabolism	4.08e-07	5.74e-07	0.711	0.483	-7.65e-07	1.58e-06	0.016

Table 1230: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Arginine.and.proline.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.44e-02	3.65e-02	-1.49	0.1471	-1.29e-01	2.02e-02	0.0000
L3.Arginine.and.proline.metabolism	5.66e-08	3.10e-08	1.83	0.0778	-6.70e-09	1.20e-07	0.0971

Table 1231: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Arrhythmogenic.right.ventricular.cardiomyopathy..ARVC., df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1232: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Ascorbate.and.aldarate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.44e-02	2.70e-02	-0.904	0.373	-7.95e-02	3.07e-02	0.0000
L3.Ascorbate.and.aldarate.metabolism	1.25e-07	8.33e-08	1.501	0.144	-4.51e-08	2.95e-07	0.0678

Table 1233: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Atrazine.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.12e-02	2.44e-02	-0.459	0.650	-6.10e-02	3.86e-02	0.0000
L3.Atrazine.degradation	6.69e-07	6.38e-07	1.049	0.303	-6.34e-07	1.97e-06	0.0343

Table 1234: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Bacterial.chemotaxis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.47e-02	3.28e-02	0.754	0.456	-4.22e-02	9.16e-02	0.0000
L3.Bacterial.chemotaxis	-9.04e-08	8.90e-08	-1.016	0.318	-2.72e-07	9.13e-08	0.0322

Table 1235: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Bacterial.invasion.of.epithelial.cells, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.28e-03	2.37e-02	0.0541	0.957	-4.70e-02	4.96e-02	0.000000
L3.Bacterial.invasion.of.epithelial.cells	-1.06e-06	6.49e-06	-0.1632	0.871	-1.43e-05	1.22e-05	0.000858

Table 1236: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Bacterial.motility.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.67e-03	3.19e-02	0.240	0.812	-5.75e-02	7.28e-02	0.00000
L3.Bacterial.motility.proteins	-1.40e-08	4.17e-08	-0.336	0.739	-9.90e-08	7.11e-08	0.00362

Table 1237: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Bacterial.secretion.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.65e-02	3.11e-02	-1.17	0.250	-1.00e-01	2.70e-02	0.0000
L3.Bacterial.secretion.system	5.66e-08	3.50e-08	1.62	0.116	-1.48e-08	1.28e-07	0.0779

Table 1238: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Bacterial.toxins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.08e-02	4.99e-02	-1.22	0.232	-1.63e-01	4.11e-02	0.0000
L3.Bacterial.toxins	4.59e-07	3.39e-07	1.35	0.186	-2.34e-07	1.15e-06	0.0558

Table 1239: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Basal.transcription.factors, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.38e-02	2.30e-02	0.602	0.552	-3.31e-02	6.08e-02	0.0000
L3.Basal.transcription.factors	-1.61e-05	9.81e-06	-1.645	0.110	-3.62e-05	3.89e-06	0.0803

Table 1240: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Base.excision.repair, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.29e-02	4.56e-02	-1.82	0.0792	-1.76e-01	1.03e-02	0.000
L3.Base.excision.repair	2.19e-07	1.07e-07	2.04	0.0498	2.50e-10	4.39e-07	0.119

Table 1241: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Benzoate.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.25e-02	2.91e-02	-1.12	0.273	-9.18e-02	2.69e-02	0.0000
L3.Benzoate.degradation	1.28e-07	7.78e-08	1.65	0.110	-3.06e-08	2.87e-07	0.0807

Table 1242: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Betalain.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.008185	2.32e-02	-0.352	0.727	-5.57e-02	0.039292	0.0000
L3.Betalain.biosynthesis	0.000059	5.59e-05	1.057	0.299	-5.51e-05	0.000173	0.0348

Table 1243: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Bile.secretion, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.002937	0.02488	0.118	0.907	-0.04787	0.05375	0.00000
L3.Bile.secretion	-0.000431	0.00162	-0.266	0.792	-0.00374	0.00288	0.00228

Table 1244: diversity_vs_picrust_L3_neo: wunifrac.PC.3
vs L3.Biosynthesis.and.biodegradation.of.secondary.metabolites,
df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	-2.05e-02	2.54e-02	-0.806	0.426	-7.23e-02	3.14
L3.Biosynthesis.and.biodegradation.of.secondary.metabolites	2.47e-07	1.63e-07	1.520	0.139	-8.50e-08	5.80

Table 1245: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Biosynthesis.of.12...14..and.16.membered.macrolides, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	0.00222	0.0226	0.0985	0.922	-0.0439	0.0483
L3.Biosynthesis.of.12...14..and.16.membered.macrolides	-0.07112	0.1276	-0.5572	0.582	-0.3318	0.1895

Table 1246: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Biosynthesis.of.ansamycins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.97e-02	3.12e-02	-0.954	0.348	-9.34e-02	3.39e-02	0.0000
L3.Biosynthesis.of.ansamycins	2.84e-07	2.14e-07	1.328	0.194	-1.53e-07	7.20e-07	0.0538

Table 1247: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	-1.72e-02	2.51e-02	-0.685	0.498	-6.85e-02	3.41e
L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides	2.43e-07	1.79e-07	1.358	0.185	-1.22e-07	6.08e

Table 1248: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Biosynthesis.of.type.II.polyketide.backbone, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1249: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Biosynthesis.of.type.II.polyketide.products, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.47e-03	0.023341	-0.363	0.719	-5.61e-02	0.039199	0.0000
L3.Biosynthesis.of.type.II.polyketide.products	5.91e-05	0.000056	1.056	0.300	-5.53e-05	0.000174	0.0347

Table 1250: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Biosynthesis.of.unsaturated.fatty.acids, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.59e-02	2.94e-02	-0.879	0.386	-8.60e-02	3.42e-02	0.0000
L3.Biosynthesis.of.unsaturated.fatty.acids	2.01e-07	1.54e-07	1.302	0.203	-1.14e-07	5.16e-07	0.0519

Table 1251: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Biosynthesis.of.vancomycin.group.antibiotics, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.76e-02	4.70e-02	-1.44	0.161	-1.64e-01	2.83e-02	0.0000
L3.Biosynthesis.of.vancomycin.group.antibiotics	1.36e-06	8.43e-07	1.62	0.116	-3.59e-07	3.08e-06	0.0777

Table 1252: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Biotin.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.90e-02	3.43e-02	-2.59	0.01458	-1.59e-01	-1.89e-02	0.000
L3.Biotin.metabolism	7.21e-07	2.30e-07	3.14	0.00377	2.52e-07	1.19e-06	0.241

Table 1253: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Bisphenol.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.37e-02	4.18e-02	-1.28	0.209	-1.39e-01	3.17e-02	0.0000
L3.Bisphenol.degradation	1.20e-06	8.04e-07	1.50	0.145	-4.38e-07	2.85e-06	0.0675

Table 1254: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Bladder.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.18e-02	2.46e-02	-0.481	0.634	-6.20e-02	3.84e-02	0.0000
L3.Bladder.cancer	2.55e-06	2.40e-06	1.062	0.297	-2.35e-06	7.45e-06	0.0351

Table 1255: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Butanoate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.80e-02	3.52e-02	-0.797	0.432	-9.99e-02	4.38e-02	0.0000
L3.Butanoate.metabolism	4.38e-08	4.30e-08	1.020	0.316	-4.40e-08	1.32e-07	0.0324

Table 1256: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Butirosin.and.neomycin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.70e-02	5.42e-02	-1.79	0.0837	-2.08e-01	1.37e-02	0.000
L3.Butirosin.and.neomycin.biosynthesis	2.06e-06	1.06e-06	1.94	0.0617	-1.07e-07	4.24e-06	0.108

Table 1257: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.C5.Branched.dibasic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.21e-02	4.07e-02	-1.53	0.1375	-1.45e-01	2.10e-02	0.0000
L3.C5.Branched.dibasic.acid.metabolism	2.32e-07	1.30e-07	1.79	0.0839	-3.30e-08	4.96e-07	0.0935

Table 1258: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.CAM.ligands, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1259: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Caffeine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00334	0.0245	0.136	0.892	-0.0467	0.0534	0.00000
L3.Caffeine.metabolism	-0.00412	0.0126	-0.328	0.745	-0.0297	0.0215	0.00346

Table 1260: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Calcium.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00804	0.0250	0.322	0.750	-0.0430	0.0591	0.0000
L3.Calcium.signaling.pathway	-0.01287	0.0186	-0.693	0.494	-0.0508	0.0251	0.0153

Table 1261: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Caprolactam.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.89e-02	2.57e-02	-0.736	0.467	-7.14e-02	3.36e-02	0.000
L3.Caprolactam.degradation	3.75e-07	2.74e-07	1.368	0.181	-1.84e-07	9.34e-07	0.057

Table 1262: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Carbohydrate.digestion.and.absorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.41e-02	3.19e-02	-0.442	0.661	-7.92e-02	5.10e-02	0.0000
L3.Carbohydrate.digestion.and.absorption	6.55e-07	1.06e-06	0.616	0.543	-1.52e-06	2.83e-06	0.0121

Table 1263: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Carbohydrate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.80e-02	3.61e-02	-1.05	0.301	-1.12e-01	3.57e-02	0.000
L3.Carbohydrate.metabolism	2.15e-07	1.64e-07	1.32	0.198	-1.19e-07	5.49e-07	0.053

Table 1264: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Carbon.fixation.in.photosynthetic.organisms, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.27e-02	3.78e-02	-1.66	0.1076	-1.40e-01	1.45e-02	0.000
L3.Carbon.fixation.in.photosynthetic.organisms	1.17e-07	5.87e-08	1.99	0.0553	-2.81e-09	2.37e-07	0.114

Table 1265: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Carbon.fixation.pathways.in.prokaryotes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.24e-02	4.02e-02	-1.30	0.202	-1.34e-01	2.97e-02	0.0000
L3.Carbon.fixation.pathways.in.prokaryotes	6.08e-08	3.94e-08	1.54	0.133	-1.97e-08	1.41e-07	0.0713

Table 1266: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Cardiac.muscle.contraction, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.63e-03	2.36e-02	-0.365	0.717	-5.69e-02	3.96e-02	0.0000
L3.Cardiac.muscle.contraction	1.39e-05	1.41e-05	0.990	0.330	-1.48e-05	4.27e-05	0.0306

Table 1267: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Carotenoid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.90e-03	2.53e-02	0.391	0.698	-4.18e-02	6.16e-02	0.0000
L3.Carotenoid.biosynthesis	-2.89e-06	3.60e-06	-0.802	0.429	-1.03e-05	4.47e-06	0.0203

Table 1268: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Cell.cycle, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1269: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Cell.cycle...Caulobacter, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.95e-02	5.11e-02	-1.95	0.0609	-2.04e-01	4.83e-03	0.000
L3.Cell.cycle...Caulobacter	2.58e-07	1.21e-07	2.13	0.0413	1.09e-08	5.05e-07	0.128

Table 1270: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Cell.cycle...yeast, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1271: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Cell.division, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.79e-02	3.55e-02	-1.07	0.294	-1.10e-01	3.46e-02	0.0000
L3.Cell.division	6.32e-07	4.69e-07	1.35	0.188	-3.26e-07	1.59e-06	0.0553

Table 1272: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Cell.motility.and.secretion, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.97e-02	3.34e-02	-2.09	0.0455	-1.38e-01	-1.50e-03	0.000
L3.Cell.motility.and.secretion	4.26e-07	1.63e-07	2.62	0.0138	9.34e-08	7.59e-07	0.181

Table 1273: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Cellular.antigens, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.50e-02	3.4e-02	-1.32	0.1957	-1.14e-01	2.44e-02	0.0000
L3.Cellular.antigens	1.02e-06	6.0e-07	1.70	0.0997	-2.06e-07	2.24e-06	0.0852

Table 1274: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Chagas.disease..American.trypanosomiasis., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.89e-02	2.73e-02	-0.693	0.494	-7.48e-02	3.69e-02	0.0000
L3.Chagas.disease..American.trypanosomiasis.	2.80e-06	2.43e-06	1.153	0.258	-2.16e-06	7.75e-06	0.0411

Table 1275: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Chaperones.and.folding.catalysts, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.36e-02	4.06e-02	-1.57	0.1280	-1.47e-01	1.94e-02	0.0000
L3.Chaperones.and.folding.catalysts	7.39e-08	4.03e-08	1.83	0.0766	-8.41e-09	1.56e-07	0.0978

Table 1276: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Chloroalkane.and.chloroalkene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.45e-02	4.38e-02	-0.559	0.581	-1.14e-01	6.50e-02	0.0000
L3.Chloroalkane.and.chloroalkene.degradation	1.50e-07	2.32e-07	0.648	0.522	-3.23e-07	6.23e-07	0.0134

Table 1277: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Chlorocyclohexane.and.chlorobenzene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-1.15e-02	2.76e-02	-0.416	0.68	-6.77e-02	4.48e-02
L3.Chlorocyclohexane.and.chlorobenzene.degradation	8.42e-07	1.20e-06	0.700	0.49	-1.62e-06	3.30e-06

Table 1278: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Cholinergic.synapse, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1279: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Chromosome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.90e-02	4.37e-02	-1.58	0.1245	-1.58e-01	2.02e-02	0.0000
L3.Chromosome	5.45e-08	3.01e-08	1.81	0.0807	-7.08e-09	1.16e-07	0.0953

Table 1280: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Chronic.myeloid.leukemia, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00799	0.0238	-0.336	0.739	-0.0566	0.0406	0.0000
L3.Chronic.myeloid.leukemia	0.03197	0.0360	0.888	0.381	-0.0415	0.1055	0.0248

Table 1281: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Circadian.rhythm...plant, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00716	0.02407	0.298	0.768	-0.0420	0.05632	0.000
L3.Circadian.rhythm...plant	-0.00498	0.00661	-0.753	0.457	-0.0185	0.00852	0.018

Table 1282: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Citrate.cycle..TCA.cycle., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.72e-02	3.34e-02	-1.11	0.274	-1.05e-01	3.10e-02	0.0000
L3.Citrate.cycle..TCA.cycle.	6.79e-08	4.65e-08	1.46	0.155	-2.71e-08	1.63e-07	0.0643

Table 1283: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Clavulanic.acid.biosynthesis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1284: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Colorectal.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.01e-03	0.024692	-0.0407	0.968	-0.05143	0.0494	0.000000
L3.Colorectal.cancer	8.47e-05	0.000889	0.0952	0.925	-0.00173	0.0019	0.000292

Table 1285: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Complement.and.coagulation.cascades, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1286: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Cyanoamino.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.70e-02	3.56e-02	-1.60	0.120	-1.30e-01	1.58e-02	0.000
L3.Cyanoamino.acid.metabolism	2.14e-07	1.08e-07	1.98	0.057	-6.78e-09	4.35e-07	0.112

Table 1287: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Cysteine.and.methionine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.96e-02	3.94e-02	-1.77	0.0873	-1.50e-01	1.08e-02	0.000
L3.Cysteine.and.methionine.metabolism	7.97e-08	3.82e-08	2.08	0.0458	1.59e-09	1.58e-07	0.123

Table 1288: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Cytochrome.P450, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00289	0.0225	0.128	0.899	-0.043	0.0488	0.0000
L3.Cytochrome.P450	-0.09233	0.1272	-0.726	0.474	-0.352	0.1674	0.0167

Table 1289: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Cytokine.receptors, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1290: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Cytokine.cytokine.receptor.interaction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1291: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Cytoskeleton.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.18e-02	4.60e-02	-1.34	0.189	-1.56e-01	3.22e-02	0.0000
L3.Cytoskeleton.proteins	2.99e-07	1.97e-07	1.52	0.139	-1.03e-07	7.02e-07	0.0693

Table 1292: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Cytosolic.DNA.sensing.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1293: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.D.Alanine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.80e-02	4.45e-02	-1.53	0.1369	-1.59e-01	2.29e-02	0.000
L3.D.Alanine.metabolism	6.37e-07	3.66e-07	1.74	0.0921	-1.11e-07	1.38e-06	0.089

Table 1294: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.D.Arginine.and.D.ornithine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.29e-02	2.03e-02	-1.62	0.115424	-7.44e-02	8.55e-03	0.000
L3.D.Arginine.and.D.ornithine.metabolism	8.13e-06	2.14e-06	3.79	0.000677	3.75e-06	1.25e-05	0.317

Table 1295: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.D.Glutamine.and.D.glutamate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.69e-02	4.32e-02	-2.01	0.0534	-1.75e-01	1.37e-03	0.000
L3.D.Glutamine.and.D.glutamate.metabolism	6.57e-07	2.87e-07	2.29	0.0294	7.03e-08	1.24e-06	0.144

Table 1296: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.DNA.repair.and.recombination.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.19e-02	4.74e-02	-1.73	0.0939	-1.79e-01	1.48e-02	0.000
L3.DNA.repair.and.recombination.proteins	3.41e-08	1.77e-08	1.93	0.0629	-1.96e-09	7.02e-08	0.107

Table 1297: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.DNA.replication, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.54e-02	5.07e-02	-1.88	0.0695	-1.99e-01	8.11e-03	0.000
L3.DNA.replication	1.70e-07	8.23e-08	2.07	0.0476	1.93e-09	3.38e-07	0.121

Table 1298: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.DNA.replication.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.70e-02	4.94e-02	-1.76	0.0884	-1.88e-01	1.39e-02	0.000
L3.DNA.replication.proteins	8.84e-08	4.54e-08	1.95	0.0610	-4.34e-09	1.81e-07	0.109

Table 1299: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Dilated.cardiomyopathy..DCM., df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1300: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Dioxin.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.62e-02	3.03e-02	-0.865	0.394	-8.81e-02	3.57e-02	0.0000
L3.Dioxin.degradation	3.02e-07	2.43e-07	1.243	0.224	-1.95e-07	7.99e-07	0.0475

Table 1301: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Drug.metabolism...cytochrome.P450, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.68e-02	2.86e-02	-0.588	0.561	-7.53e-02	4.16e-02	0.0000
L3.Drug.metabolism...cytochrome.P450	3.41e-07	3.71e-07	0.920	0.365	-4.16e-07	1.10e-06	0.0266

Table 1302: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Drug.metabolism...other.enzymes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.86e-02	4.56e-02	-1.72	0.0956	-1.72e-01	1.47e-02	0.000
L3.Drug.metabolism...other.enzymes	2.78e-07	1.43e-07	1.94	0.0619	-1.48e-08	5.71e-07	0.108

Table 1303: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.ECM.receptor.interaction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1304: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Electron.transfer.carriers, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.37e-02	2.80e-02	-0.489	0.629	-7.09e-02	4.35e-02	0.0000
L3.Electron.transfer.carriers	2.41e-07	3.03e-07	0.794	0.433	-3.78e-07	8.60e-07	0.0199

Table 1305: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Endocrine.and.other.factor.regulated.calcium.reabsorption, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1306: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Endocytosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0110	0.02254	0.489	0.628	-0.0350	0.05706	0.0000
L3.Endocytosis	-0.0104	0.00654	-1.587	0.123	-0.0237	0.00298	0.0751

Table 1307: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Energy.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.16e-02	3.61e-02	-1.15	0.258	-1.15e-01	3.21e-02	0.0000
L3.Energy.metabolism	5.66e-08	3.94e-08	1.44	0.161	-2.38e-08	1.37e-07	0.0625

Table 1308: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-0.068137	3.75e-02	-1.82	0.079	-1.45e-01	8.39e-(
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	0.000001	4.59e-07	2.18	0.037	6.47e-08	1.94e-(

Table 1309: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.ErbB.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1310: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Ether.lipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.56e-02	2.69e-02	0.95	0.350	-2.94e-02	8.05e-02	0.000
L3.Ether.lipid.metabolism	-1.77e-05	1.12e-05	-1.57	0.126	-4.06e-05	5.27e-06	0.074

Table 1311: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Ethylbenzene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.09e-02	3.50e-02	-0.882	0.385	-1.02e-01	4.06e-02	0.0000
L3.Ethylbenzene.degradation	9.97e-07	8.82e-07	1.130	0.268	-8.05e-07	2.80e-06	0.0395

Table 1312: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Fat.digestion.and.absorption, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1313: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Fatty.acid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.54e-02	4.43e-02	-1.25	0.221	-1.46e-01	3.50e-02	0.0000
L3.Fatty.acid.biosynthesis	1.27e-07	8.85e-08	1.43	0.162	-5.39e-08	3.07e-07	0.0621

Table 1314: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Fatty.acid.elongation.in.mitochondria, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1315: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Fatty.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.16e-02	3.33e-02	-0.948	0.351	-9.96e-02	3.65e-02	0.0000
L3.Fatty.acid.metabolism	1.22e-07	9.76e-08	1.252	0.220	-7.72e-08	3.21e-07	0.0481

Table 1316: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Fc.epsilon.RI.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1317: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Fc.gamma.R.mediated.phagocytosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0110	0.02254	0.489	0.628	-0.0350	0.05706	0.0000
L3.Fc.gamma.R.mediated.phagocytosis	-0.0104	0.00654	-1.587	0.123	-0.0237	0.00298	0.0751

Table 1318: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Flagellar.assembly, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.68e-02	2.77e-02	0.605	0.550	-3.98e-02	7.33e-02	0.0000
L3.Flagellar.assembly	-1.07e-07	1.08e-07	-0.993	0.329	-3.27e-07	1.13e-07	0.0308

Table 1319: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Flavone.and.flavonol.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.74e-03	2.79e-02	0.277	0.784	-4.93e-02	6.47e-02	0.00000
L3.Flavone.and.flavonol.biosynthesis	-1.57e-06	3.42e-06	-0.459	0.649	-8.55e-06	5.41e-06	0.00676

Table 1320: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Flavonoid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.25e-03	2.29e-02	-0.185	0.854	-5.11e-02	0.042621	0.0000
L3.Flavonoid.biosynthesis	3.84e-06	5.46e-06	0.703	0.487	-7.32e-06	0.000015	0.0157

Table 1321: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Fluorobenzoate.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.28e-02	2.37e-02	-0.538	0.595	-6.12e-02	3.57e-02	0.0000
L3.Fluorobenzoate.degradation	8.50e-07	6.40e-07	1.328	0.194	-4.57e-07	2.16e-06	0.0538

Table 1322: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Focal.adhesion, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1323: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Folate.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.10e-02	4.34e-02	-1.87	0.0718	-1.70e-01	7.64e-03	0.000
L3.Folate.biosynthesis	2.15e-07	1.01e-07	2.13	0.0418	8.56e-09	4.22e-07	0.127

Table 1324: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Fructose.and.mannose.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.66e-02	3.70e-02	-1.26	0.217	-1.22e-01	2.89e-02	0.0000
L3.Fructose.and.mannose.metabolism	5.18e-08	3.34e-08	1.55	0.132	-1.65e-08	1.20e-07	0.0719

Table 1325: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Function.unknown, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.21e-02	3.26e-02	-1.29	0.2066	-1.09e-01	2.45e-02	0.0000
L3.Function.unknown	3.10e-08	1.82e-08	1.71	0.0982	-6.10e-09	6.81e-08	0.0859

Table 1326: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.G.protein.coupled.receptors, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1327: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.GTP.binding.proteins, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1328: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Galactose.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.61e-02	4.60e-02	-1.44	0.161	-1.60e-01	2.78e-02	0.0000
L3.Galactose.metabolism	8.68e-08	5.35e-08	1.62	0.115	-2.24e-08	1.96e-07	0.0784

Table 1329: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Gastric.acid.secretion, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1330: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.General.function.prediction.only, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.72e-02	4.07e-02	-1.65	0.1088	-1.50e-01	1.58e-02	0.000
L3.General.function.prediction.only	2.17e-08	1.12e-08	1.93	0.0629	-1.24e-09	4.46e-08	0.107

Table 1331: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Geraniol.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.48e-02	2.64e-02	-0.938	0.356	-7.88e-02	2.92e-02	0.0000
L3.Geraniol.degradation	3.43e-07	2.14e-07	1.600	0.120	-9.47e-08	7.81e-07	0.0763

Table 1332: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Germination, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.72e-02	2.43e-02	0.709	0.484	-3.24e-02	6.69e-02	0.0000
L3.Germination	-4.34e-06	2.85e-06	-1.522	0.139	-1.02e-05	1.49e-06	0.0695

Table 1333: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Glioma, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1334: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Glutamatergic.synapse, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.11e-02	4.41e-02	-2.07	0.0477	-1.81e-01	-1.00e-03	0.000
L3.Glutamatergic.synapse	1.22e-06	5.22e-07	2.33	0.0265	1.52e-07	2.28e-06	0.149

Table 1335: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Glutathione.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.09e-02	3.40e-02	-1.20	0.239	-1.1e-01	2.86e-02	0.0000
L3.Glutathione.metabolism	1.64e-07	1.06e-07	1.55	0.132	-5.2e-08	3.79e-07	0.0719

Table 1336: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Glycan.bindng.proteins, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1337: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Glycan.biosynthesis.and.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.08e-02	2.75e-02	-0.756	0.455	-7.68e-02	3.53e-02	0.0000
L3.Glycan.biosynthesis.and.metabolism	3.95e-07	3.18e-07	1.241	0.224	-2.55e-07	1.04e-06	0.0473

Table 1338: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Glycerolipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.63e-02	3.80e-02	-0.955	0.347	-1.14e-01	4.13e-02	0.0000
L3.Glycerolipid.metabolism	1.04e-07	8.94e-08	1.167	0.253	-7.83e-08	2.87e-07	0.0421

Table 1339: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Glycerophospholipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.72e-02	3.78e-02	-1.25	0.222	-1.24e-01	3.01e-02	0.000
L3.Glycerophospholipid.metabolism	1.04e-07	6.88e-08	1.52	0.140	-3.62e-08	2.45e-07	0.069

Table 1340: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Glycine..serine.and.threonine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.68e-02	3.91e-02	-1.71	0.0976	-1.47e-01	1.30e-02	0.000
L3.Glycine..serine.and.threonine.metabolism	9.04e-08	4.47e-08	2.03	0.0518	-7.54e-10	1.82e-07	0.117

Table 1341: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Glycolysis. . . Gluconeogenesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.88e-02	4.15e-02	-1.42	0.167	-1.44e-01	2.60e-02	0.0000
L3.Glycolysis. . . Gluconeogenesis	5.56e-08	3.36e-08	1.65	0.109	-1.32e-08	1.24e-07	0.0808

Table 1342: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Glycosaminoglycan.biosynthesis. . . chondroitin.sulfate, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-0.00396	0.0227	-0.175	0.863	-0.0504	0.0424
L3.Glycosaminoglycan.biosynthesis. . . chondroitin.sulfate	0.01586	0.0208	0.761	0.453	-0.0267	0.0584

Table 1343: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Glycosaminoglycan.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.36e-02	3.42e-02	-1.86	0.0725	-1.33e-01	6.17e-03	0.000
L3.Glycosaminoglycan.degradation	8.78e-07	3.77e-07	2.33	0.0268	1.08e-07	1.65e-06	0.149

Table 1344: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Glycosphingolipid.biosynthesis. . . ganglio.series, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.41e-02	3.24e-02	-1.98	0.0572	-1.30e-01	2.1e-03	0.000
L3.Glycosphingolipid.biosynthesis. . . ganglio.series	1.39e-06	5.47e-07	2.53	0.0168	2.69e-07	2.5e-06	0.172

Table 1345: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Glycosphingolipid.biosynthesis. . . globo.series, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.49e-02	3.61e-02	-1.8	0.0823	-1.39e-01	8.84e-03	0.000
L3.Glycosphingolipid.biosynthesis. . . globo.series	8.02e-07	3.65e-07	2.2	0.0360	5.58e-08	1.55e-06	0.135

Table 1346: diversity_vs_picrust_L3_neo: wunifrac.PC.3
vs L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series,
df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	-1.00e-02	2.15e-02	-0.466	0.6446	-5.40e-02	0.03
L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series	7.33e-05	3.63e-05	2.019	0.0525	-8.37e-07	0.00

Table 1347: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Glycosylphosphatidylinositol.GPI..anchor.biosynthesis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1348: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Glycosyltransferases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.87e-02	3.86e-02	-1.78	0.0851	-1.47e-01	1.01e-02	0.000
L3.Glycosyltransferases	1.91e-07	9.03e-08	2.12	0.0428	6.62e-09	3.75e-07	0.126

Table 1349: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Glyoxylate.and.dicarboxylate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.30e-02	3.20e-02	-1.34	0.189	-1.08e-01	2.24e-02	0.000
L3.Glyoxylate.and.dicarboxylate.metabolism	9.22e-08	5.14e-08	1.79	0.083	-1.28e-08	1.97e-07	0.094

Table 1350: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.GnRH.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0110	0.02254	0.489	0.628	-0.0350	0.05706	0.0000
L3.GnRH.signaling.pathway	-0.0104	0.00654	-1.587	0.123	-0.0237	0.00298	0.0751

Table 1351: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Hedgehog.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1352: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Hematopoietic.cell.lineage, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1353: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Hepatitis.C, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1354: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Histidine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.09e-02	4.42e-02	-2.06	0.0486	-1.81e-01	-5.81e-04	0.000
L3.Histidine.metabolism	1.78e-07	7.65e-08	2.32	0.0272	2.13e-08	3.34e-07	0.148

Table 1355: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Homologous.recombination, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.01e-02	4.93e-02	-1.83	0.0777	-1.91e-01	1.06e-02	0.000
L3.Homologous.recombination	1.15e-07	5.68e-08	2.02	0.0526	-1.38e-09	2.31e-07	0.116

Table 1356: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Huntington.s.disease, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.38e-02	3.86e-02	-0.877	0.387	-1.13e-01	4.49e-02	0.0000
L3.Huntington.s.disease	7.79e-07	7.30e-07	1.066	0.295	-7.13e-07	2.27e-06	0.0354

Table 1357: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Hypertrophic.cardiomyopathy..HCM., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.003679	0.02311	0.159	0.875	-0.04352	0.05088	0.0000
L3.Hypertrophic.cardiomyopathy..HCM.	-0.000949	0.00166	-0.573	0.571	-0.00434	0.00244	0.0105

Table 1358: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Indole.alkaloid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00726	0.0257	-0.282	0.780	-0.0597	0.0452	0.0000
L3.Indole.alkaloid.biosynthesis	0.01290	0.0230	0.561	0.579	-0.0340	0.0598	0.0101

Table 1359: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Influenza.A, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.01e-03	0.024692	-0.0407	0.968	-0.05143	0.0494	0.000000
L3.Influenza.A	8.47e-05	0.000889	0.0952	0.925	-0.00173	0.0019	0.000292

Table 1360: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Inorganic.ion.transport.and.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.96e-02	3.00e-02	-0.985	0.333	-9.09e-02	3.18e-02	0.0000
L3.Inorganic.ion.transport.and.metabolism	1.14e-07	8.05e-08	1.418	0.166	-5.02e-08	2.79e-07	0.0609

Table 1361: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Inositol.phosphate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.58e-02	2.82e-02	-0.915	0.367	-8.34e-02	3.18e-02	0.0000
L3.Inositol.phosphate.metabolism	2.01e-07	1.41e-07	1.423	0.165	-8.73e-08	4.89e-07	0.0613

Table 1362: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Insulin.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.80e-02	4.39e-02	-1.09	0.283	-1.38e-01	4.17e-02	0.0000
L3.Insulin.signaling.pathway	7.85e-07	6.24e-07	1.26	0.218	-4.89e-07	2.06e-06	0.0486

Table 1363: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Ion.channels, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.22e-02	3.88e-02	-0.573	0.571	-1.01e-01	5.7e-02	0.0000
L3.Ion.channels	5.87e-07	8.41e-07	0.698	0.491	-1.13e-06	2.3e-06	0.0155

Table 1364: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Isoflavonoid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00299	0.02312	0.130	0.898	-0.04421	0.05020	0.00000
L3.Isoflavonoid.biosynthesis	-0.00162	0.00342	-0.475	0.638	-0.00861	0.00536	0.00722

Table 1365: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Isoquinoline.alkaloid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.87e-02	3.20e-02	-1.52	0.1389	-1.14e-01	1.67e-02	0.000
L3.Isoquinoline.alkaloid.biosynthesis	9.54e-07	4.74e-07	2.01	0.0534	-1.47e-08	1.92e-06	0.115

Table 1366: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Leishmaniasis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1367: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Leukocyte.transendothelial.migration, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1368: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Limonene.and.pinene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.55e-02	3.14e-02	-0.81	0.424	-8.96e-02	3.87e-02	0.0000
L3.Limonene.and.pinene.degradation	2.72e-07	2.41e-07	1.13	0.268	-2.20e-07	7.64e-07	0.0395

Table 1369: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Linoleic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.07e-02	0.042766	-1.65	0.1088	-1.58e-01	1.67e-02	0.000
L3.Linoleic.acid.metabolism	1.91e-06	0.000001	1.90	0.0671	-1.43e-07	3.96e-06	0.104

Table 1370: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Lipid.biosynthesis.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.99e-02	4.14e-02	-1.69	0.1016	-1.54e-01	1.46e-02	0.00
L3.Lipid.biosynthesis.proteins	1.38e-07	7.05e-08	1.96	0.0592	-5.72e-09	2.82e-07	0.11

Table 1371: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Lipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.19e-02	3.15e-02	-1.01	0.319	-9.62e-02	3.24e-02	0.0000
L3.Lipid.metabolism	2.47e-07	1.77e-07	1.40	0.173	-1.14e-07	6.08e-07	0.0592

Table 1372: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Lipoic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.45e-02	3.72e-02	-1.20	0.241	-1.20e-01	3.15e-02	0.000
L3.Lipoic.acid.metabolism	9.07e-07	6.18e-07	1.47	0.153	-3.55e-07	2.17e-06	0.065

Table 1373: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Lipopolysaccharide.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.73e-02	2.72e-02	-2.11	0.04345	-1.13e-01	-1.80e-03	0.000
L3.Lipopolysaccharide.biosynthesis	2.18e-07	7.19e-08	3.03	0.00495	7.13e-08	3.65e-07	0.229

Table 1374: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Lipopolysaccharide.biosynthesis.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.03e-02	2.89e-02	-2.08	0.04568	-1.19e-01	-1.24e-03	0.000
L3.Lipopolysaccharide.biosynthesis.proteins	1.39e-07	4.86e-08	2.86	0.00767	3.96e-08	2.38e-07	0.209

Table 1375: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Long.term.depression, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1376: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Long.term.potentiation, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1377: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Lysine.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.38e-02	4.61e-02	-1.82	0.0788	-1.78e-01	1.02e-02	0.000
L3.Lysine.biosynthesis	1.34e-07	6.57e-08	2.04	0.0500	2.12e-11	2.68e-07	0.119

Table 1378: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Lysine.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.15e-02	2.98e-02	-1.06	0.298	-9.22e-02	2.93e-02	0.0000
L3.Lysine.degradation	2.06e-07	1.34e-07	1.53	0.136	-6.87e-08	4.80e-07	0.0703

Table 1379: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Lysosome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.87e-02	3.58e-02	-1.36	0.184	-1.22e-01	2.45e-02	0.0000
L3.Lysosome	4.92e-07	2.91e-07	1.69	0.101	-1.02e-07	1.09e-06	0.0846

Table 1380: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.MAPK.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1381: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.MAPK.signaling.pathway...yeast, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.10e-01	4.07e-02	-2.71	0.01101	-1.93e-01	-2.72e-02	0.000
L3.MAPK.signaling.pathway...yeast	2.46e-06	7.98e-07	3.09	0.00434	8.32e-07	4.09e-06	0.235

Table 1382: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Measles, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1383: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Meiosis...yeast, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.01e-03	2.48e-02	0.363	0.719	-4.17e-02	5.97e-02	0.0000
L3.Meiosis...yeast	-2.84e-06	3.56e-06	-0.797	0.432	-1.01e-05	4.43e-06	0.0201

Table 1384: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Melanogenesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.13e-03	2.32e-02	-0.35	0.729	-5.56e-02	0.039323	0.0000
L3.Melanogenesis	5.89e-05	5.59e-05	1.05	0.300	-5.52e-05	0.000173	0.0346

Table 1385: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Membrane.and.intracellular.structural.molecules, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.45e-02	3.14e-02	-1.42	0.1664	-1.09e-01	1.96e-02	0.0
L3.Membrane.and.intracellular.structural.molecules	7.86e-08	4.11e-08	1.91	0.0652	-5.28e-09	1.62e-07	0.

Table 1386: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Metabolism.of.cofactors.and.vitamins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.08e-02	3.20e-02	-0.962	0.344	-9.62e-02	3.46e-02	0.0000
L3.Metabolism.of.cofactors.and.vitamins	2.18e-07	1.66e-07	1.308	0.201	-1.22e-07	5.58e-07	0.0523

Table 1387: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Metabolism.of.xenobiotics.by.cytochrome.P450, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.75e-02	2.82e-02	-0.621	0.539	-7.52e-02	4.01e-02	0.00
L3.Metabolism.of.xenobiotics.by.cytochrome.P450	3.67e-07	3.72e-07	0.989	0.331	-3.92e-07	1.13e-06	0.03

Table 1388: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Methane.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.05e-02	4.38e-02	-1.38	0.177	-1.50e-01	2.89e-02	0.000
L3.Methane.metabolism	6.12e-08	3.86e-08	1.59	0.123	-1.76e-08	1.40e-07	0.075

Table 1389: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Mineral.absorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.90e-02	2.60e-02	1.12	0.273	-2.41e-02	8.22e-02	0.000
L3.Mineral.absorption	-1.66e-05	8.69e-06	-1.91	0.066	-3.43e-05	1.17e-06	0.105

Table 1390: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Mismatch.repair, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.30e-02	5.02e-02	-1.65	0.1087	-1.85e-01	1.95e-02	0.0000
L3.Mismatch.repair	1.23e-07	6.73e-08	1.82	0.0782	-1.47e-08	2.60e-07	0.0969

Table 1391: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.N.Glycan.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.68e-02	2.72e-02	-1.72	0.0949	-1.02e-01	8.63e-03	0.000
L3.N.Glycan.biosynthesis	3.36e-06	1.30e-06	2.58	0.0151	6.98e-07	6.02e-06	0.177

Table 1392: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.NOD.like.receptor.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.48e-02	3.80e-02	-0.915	0.367	-1.12e-01	4.28e-02	0.0000
L3.NOD.like.receptor.signaling.pathway	1.37e-06	1.23e-06	1.119	0.272	-1.13e-06	3.88e-06	0.0388

Table 1393: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Naphthalene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.23e-02	4.49e-02	-0.943	0.353	-1.34e-01	4.93e-02	0.0000
L3.Naphthalene.degradation	3.37e-07	3.12e-07	1.080	0.289	-3.01e-07	9.75e-07	0.0363

Table 1394: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Neuroactive.ligand.receptor.interaction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1395: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Neurotrophin.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1396: diversity__vs__picrust__L3__neo: wunifrac.PC.3 vs
L3.Nicotinate.and.nicotinamide.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.78e-02	4.27e-02	-1.35	0.186	-1.45e-01	2.93e-02	0.0000
L3.Nicotinate.and.nicotinamide.metabolism	1.56e-07	9.98e-08	1.57	0.127	-4.74e-08	3.60e-07	0.0734

Table 1397: diversity__vs__picrust__L3__neo: wunifrac.PC.3 vs
L3.Nitrogen.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.92e-02	3.59e-02	-1.37	0.1809	-1.23e-01	2.42e-02	0.0000
L3.Nitrogen.metabolism	7.10e-08	4.17e-08	1.70	0.0992	-1.42e-08	1.56e-07	0.0854

Table 1398: diversity__vs__picrust__L3__neo: wunifrac.PC.3 vs
L3.Nitrotoluene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.53e-02	3.13e-02	-0.491	0.627	-7.92e-02	4.85e-02	0.0000
L3.Nitrotoluene.degradation	2.40e-07	3.44e-07	0.696	0.492	-4.64e-07	9.43e-07	0.0154

Table 1399: diversity__vs__picrust__L3__neo: wunifrac.PC.3 vs
L3.Non.homologous.end.joining, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.06e-03	2.56e-02	0.0803	0.937	-5.03e-02	5.44e-02	0.000000
L3.Non.homologous.end.joining	-1.81e-06	1.11e-05	-0.1632	0.871	-2.45e-05	2.08e-05	0.000859

Table 1400: diversity__vs__picrust__L3__neo: wunifrac.PC.3 vs
L3.Notch.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00799	0.0238	-0.336	0.739	-0.0566	0.0406	0.0000
L3.Notch.signaling.pathway	0.03197	0.0360	0.888	0.381	-0.0415	0.1055	0.0248

Table 1401: diversity__vs__picrust__L3__neo: wunifrac.PC.3 vs
L3.Novobiocin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.77e-02	3.84e-02	-1.76	0.0885	-1.46e-01	1.08e-02	0.000
L3.Novobiocin.biosynthesis	6.19e-07	2.95e-07	2.10	0.0446	1.58e-08	1.22e-06	0.124

Table 1402: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Nucleotide.excision.repair, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.81e-02	5.39e-02	-1.63	0.1126	-1.98e-01	2.20e-02	0.0000
L3.Nucleotide.excision.repair	2.90e-07	1.63e-07	1.78	0.0855	-4.31e-08	6.24e-07	0.0926

Table 1403: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Nucleotide.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.69e-02	2.86e-02	-0.941	0.354	-8.53e-02	3.15e-02	0.0000
L3.Nucleotide.metabolism	3.08e-07	2.14e-07	1.435	0.162	-1.30e-07	7.46e-07	0.0623

Table 1404: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Olfactory.transduction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1405: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.One.carbon.pool.by.folate, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.02e-01	4.87e-02	-2.10	0.0439	-2.02e-01	-3.00e-03	0.000
L3.One.carbon.pool.by.folate	2.00e-07	8.61e-08	2.32	0.0273	2.39e-08	3.75e-07	0.148

Table 1406: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Oocyte.meiosis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1407: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Other.glycan.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.62e-02	3.82e-02	-1.47	0.1514	-1.34e-01	2.18e-02	0.0000
L3.Other.glycan.degradation	2.06e-07	1.16e-07	1.77	0.0867	-3.15e-08	4.44e-07	0.0919

Table 1408: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Other.ion.coupled.transporters, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.57e-02	3.35e-02	-1.36	0.1833	-1.14e-01	2.28e-02	0.000
L3.Other.ion.coupled.transporters	3.44e-08	1.95e-08	1.76	0.0884	-5.49e-09	7.43e-08	0.091

Table 1409: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Other.transporters, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.32e-02	3.48e-02	-1.24	0.224	-1.14e-01	2.79e-02	0.0000
L3.Other.transporters	1.86e-07	1.18e-07	1.58	0.125	-5.50e-08	4.27e-07	0.0742

Table 1410: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Other.types.of.O.glycan.biosynthesis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1411: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Others, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.31e-02	3.99e-02	-1.08	0.289	-1.25e-01	3.84e-02	0.0000
L3.Others	4.45e-08	3.46e-08	1.29	0.208	-2.62e-08	1.15e-07	0.0507

Table 1412: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Oxidative.phosphorylation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.76e-02	4.33e-02	-1.33	0.193	-1.46e-01	3.07e-02	0.0000
L3.Oxidative.phosphorylation	6.58e-08	4.28e-08	1.53	0.135	-2.17e-08	1.53e-07	0.0706

Table 1413: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.PPAR.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.34e-02	4.61e-02	-1.38	0.179	-1.58e-01	3.07e-02	0.0000
L3.PPAR.signaling.pathway	8.38e-07	5.39e-07	1.56	0.130	-2.62e-07	1.94e-06	0.0724

Table 1414: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Pancreatic.cancer, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1415: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Pancreatic.secretion, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1416: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Pantothenate.and.CoA.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.60e-02	4.33e-02	-1.76	0.0895	-1.65e-01	1.24e-02	0.000
L3.Pantothenate.and.CoA.biosynthesis	1.47e-07	7.32e-08	2.01	0.0540	-2.71e-09	2.96e-07	0.115

Table 1417: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Parkinson.s.disease, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.008821	2.37e-02	-0.372	0.712	-5.72e-02	3.96e-02	0.0000
L3.Parkinson.s.disease	0.000014	1.41e-05	0.992	0.329	-1.48e-05	4.28e-05	0.0308

Table 1418: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Pathogenic.Escherichia.coli.infection, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00276	0.0233	0.118	0.907	-0.0448	0.05035	0.00000
L3.Pathogenic.Escherichia.coli.infection	-0.00196	0.0049	-0.401	0.691	-0.0120	0.00804	0.00515

Table 1419: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Pathways.in.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.44e-02	3.32e-02	-1.64	0.112	-1.22e-01	1.35e-02	0.000
L3.Pathways.in.cancer	1.61e-06	7.66e-07	2.10	0.044	4.61e-08	3.17e-06	0.125

Table 1420: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Penicillin.and.cephalosporin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.25e-02	3.47e-02	-1.23	0.230	-1.13e-01	2.83e-02	0.0000
L3.Penicillin.and.cephalosporin.biosynthesis	1.25e-06	8.00e-07	1.56	0.129	-3.86e-07	2.88e-06	0.0728

Table 1421: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Pentose.and.glucuronate.interconversions, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.12e-02	3.12e-02	-1.00	0.325	-9.49e-02	3.24e-02	0.0000
L3.Pentose.and.glucuronate.interconversions	6.45e-08	4.64e-08	1.39	0.174	-3.02e-08	1.59e-07	0.0588

Table 1422: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Pentose.phosphate.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.92e-02	3.93e-02	-1.50	0.1430	-1.39e-01	2.12e-02	0.0000
L3.Pentose.phosphate.pathway	7.69e-08	4.30e-08	1.79	0.0841	-1.10e-08	1.65e-07	0.0934

Table 1423: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Peptidases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.23e-02	4.41e-02	-1.41	0.167	-1.52e-01	2.76e-02	0.000
L3.Peptidases	3.68e-08	2.27e-08	1.62	0.116	-9.63e-09	8.33e-08	0.078

Table 1424: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Peptidoglycan.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.74e-02	4.84e-02	-1.39	0.174	-1.66e-01	3.15e-02	0.0000
L3.Peptidoglycan.biosynthesis	9.50e-08	6.12e-08	1.55	0.131	-3.00e-08	2.20e-07	0.0722

Table 1425: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Peroxisome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.21e-02	4.10e-02	-1.51	0.1405	-1.46e-01	2.17e-02	0.0000
L3.Peroxisome	4.27e-07	2.41e-07	1.77	0.0869	-6.58e-08	9.21e-07	0.0918

Table 1426: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Pertussis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.9e-02	2.46e-02	-0.775	0.445	-6.93e-02	3.12e-02	0.0000
L3.Pertussis	2.1e-07	1.33e-07	1.584	0.124	-6.08e-08	4.81e-07	0.0749

Table 1427: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Phagosome, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1428: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Phenylalanine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.92e-02	2.81e-02	-1.04	0.307	-8.67e-02	2.83e-02	0.0000
L3.Phenylalanine.metabolism	1.55e-07	9.67e-08	1.60	0.120	-4.26e-08	3.52e-07	0.0764

Table 1429: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-8.94e-02	4.30e-02	-2.08	0.0461	-1.77e-01	-1.65e-03
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis	1.34e-07	5.66e-08	2.37	0.0246	1.84e-08	2.49e-07

Table 1430: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Phenylpropanoid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.15e-02	3.29e-02	-1.56	0.1285	-1.19e-01	1.58e-02	0.000
L3.Phenylpropanoid.biosynthesis	3.56e-07	1.76e-07	2.03	0.0517	-2.87e-09	7.15e-07	0.117

Table 1431: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Phosphatidylinositol.signaling.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.29e-02	4.78e-02	-1.11	0.277	-1.51e-01	4.47e-02	0.0000
L3.Phosphatidylinositol.signaling.system	5.68e-07	4.57e-07	1.24	0.223	-3.65e-07	1.50e-06	0.0475

Table 1432: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Phosphonate.and.phosphinate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.80e-02	3.49e-02	-1.95	0.0609	-1.39e-01	3.31e-03	0.000
L3.Phosphonate.and.phosphinate.metabolism	9.49e-07	3.95e-07	2.40	0.0227	1.42e-07	1.76e-06	0.157

Table 1433: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Phosphotransferase.system..PTS., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.10e-02	3.20e-02	-0.656	0.517	-8.63e-02	4.43e-02	0.0000
L3.Phosphotransferase.system..PTS.	2.32e-08	2.56e-08	0.905	0.373	-2.92e-08	7.55e-08	0.0257

Table 1434: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Photosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.31e-02	5.22e-02	-1.78	0.0848	-2.0e-01	1.36e-02	0.000
L3.Photosynthesis	3.27e-07	1.68e-07	1.95	0.0609	-1.6e-08	6.70e-07	0.109

Table 1435: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Photosynthesis...antenna.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.010736	0.02547	0.421	0.676	-0.04129	0.06276	0.0000
L3.Photosynthesis...antenna.proteins	-0.000934	0.00111	-0.843	0.406	-0.00319	0.00133	0.0224

Table 1436: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Photosynthesis.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.93e-02	5.13e-02	-1.74	0.0920	-1.94e-01	1.55e-02	0.000
L3.Photosynthesis.proteins	3.08e-07	1.62e-07	1.91	0.0659	-2.16e-08	6.38e-07	0.105

Table 1437: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Phototransduction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1438: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Phototransduction...fly, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1439: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Plant.pathogen.interaction, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.03e-02	4.33e-02	-0.699	0.490	-1.19e-01	5.81e-02	0.0000
L3.Plant.pathogen.interaction	2.77e-07	3.40e-07	0.813	0.422	-4.18e-07	9.71e-07	0.0209

Table 1440: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Polycyclic.aromatic.hydrocarbon.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.39e-02	4.87e-02	-1.93	0.0633	-1.93e-01	5.53e-03	0.000
L3.Polycyclic.aromatic.hydrocarbon.degradation	1.01e-06	4.75e-07	2.13	0.0412	4.31e-08	1.98e-06	0.128

Table 1441: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Polyketide.sugar.unit.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.09e-02	4.52e-02	-1.35	0.188	-1.53e-01	3.15e-02	0.0000
L3.Polyketide.sugar.unit.biosynthesis	4.12e-07	2.69e-07	1.53	0.136	-1.38e-07	9.62e-07	0.0703

Table 1442: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Pores.ion.channels, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.19e-02	2.97e-02	-1.41	0.1682	-1.03e-01	1.87e-02	0.000
L3.Pores.ion.channels	9.75e-08	4.88e-08	2.00	0.0552	-2.29e-09	1.97e-07	0.114

Table 1443: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Porphyrin.and.chlorophyll.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.80e-02	3.50e-02	-1.37	0.1801	-1.19e-01	2.34e-02	0.0000
L3.Porphyrin.and.chlorophyll.metabolism	6.17e-08	3.57e-08	1.73	0.0938	-1.11e-08	1.35e-07	0.0881

Table 1444: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Prenyltransferases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.97e-02	4.74e-02	-2.11	0.0437	-1.96e-01	-2.99e-03	0.00
L3.Prenyltransferases	3.94e-07	1.69e-07	2.34	0.0264	4.96e-08	7.39e-07	0.15

Table 1445: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Primary.bile.acid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.65e-02	4.03e-02	-2.14	0.0402	-1.69e-01	-4.11e-03	0.000
L3.Primary.bile.acid.biosynthesis	3.91e-06	1.58e-06	2.48	0.0189	6.94e-07	7.13e-06	0.166

Table 1446: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Primary.immunodeficiency, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.00e-02	4.91e-02	-0.814	0.422	-1.40e-01	6.03e-02	0.0000
L3.Primary.immunodeficiency	7.13e-07	7.82e-07	0.911	0.369	-8.85e-07	2.31e-06	0.0261

Table 1447: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Prion.diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.14e-02	2.64e-02	-0.433	0.668	-6.53e-02	4.25e-02	0.0000
L3.Prion.diseases	1.73e-06	2.19e-06	0.793	0.434	-2.73e-06	6.20e-06	0.0199

Table 1448: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Progesterone.mediated.oocyte.maturation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.14e-02	3.71e-02	-0.846	0.404	-1.07e-01	4.44e-02	0.0000
L3.Progesterone.mediated.oocyte.maturation	1.33e-06	1.27e-06	1.049	0.303	-1.26e-06	3.93e-06	0.0343

Table 1449: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Propanoate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.49e-02	3.66e-02	-1.23	0.23	-1.20e-01	2.99e-02	0.0000
L3.Propanoate.metabolism	8.99e-08	5.94e-08	1.51	0.14	-3.13e-08	2.11e-07	0.0689

Table 1450: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Prostate.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.86e-02	3.58e-02	-1.08	0.291	-1.12e-01	3.46e-02	0.0000
L3.Prostate.cancer	1.53e-06	1.13e-06	1.35	0.187	-7.82e-07	3.84e-06	0.0556

Table 1451: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Proteasome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.63e-02	5.01e-02	-1.12	0.270	-1.59e-01	4.60e-02	0.0000
L3.Proteasome	1.96e-06	1.57e-06	1.25	0.222	-1.25e-06	5.18e-06	0.0478

Table 1452: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Protein.digestion.and.absorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.44e-02	3.00e-02	-1.48	0.1495	-1.06e-01	1.69e-02	0.00
L3.Protein.digestion.and.absorption	2.61e-06	1.27e-06	2.06	0.0483	2.13e-08	5.20e-06	0.12

Table 1453: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Protein.export, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.84e-02	4.88e-02	-1.81	0.0800	-1.88e-01	1.12e-02	0.000
L3.Protein.export	1.69e-07	8.40e-08	2.01	0.0539	-2.99e-09	3.40e-07	0.115

Table 1454: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Protein.folding.and.associated.processing, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.68e-02	3.72e-02	-1.53	0.1376	-1.33e-01	1.92e-02	0.0000
L3.Protein.folding.and.associated.processing	9.16e-08	4.94e-08	1.85	0.0736	-9.30e-09	1.93e-07	0.0998

Table 1455: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Protein.kinases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.51e-02	3.42e-02	-0.734	0.468	-9.50e-02	4.47e-02	0.0000
L3.Protein.kinases	8.20e-08	8.55e-08	0.959	0.345	-9.27e-08	2.57e-07	0.0288

Table 1456: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Protein.processing.in.endoplasmic.reticulum, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.46e-02	4.00e-02	-1.11	0.274	-1.26e-01	3.71e-02	0.0000
L3.Protein.processing.in.endoplasmic.reticulum	1.10e-06	8.28e-07	1.33	0.195	-5.92e-07	2.79e-06	0.0537

Table 1457: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Proximal.tubule.bicarbonate.reclamation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.28e-02	2.73e-02	-1.2	0.2384	-8.85e-02	2.29e-02	0.000
L3.Proximal.tubule.bicarbonate.reclamation	1.30e-06	6.83e-07	1.9	0.0674	-9.88e-08	2.69e-06	0.104

Table 1458: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Purine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.82e-02	4.56e-02	-1.71	0.0968	-1.71e-01	1.5e-02	0.000
L3.Purine.metabolism	3.94e-08	2.04e-08	1.93	0.0628	-2.24e-09	8.1e-08	0.108

Table 1459: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Pyrimidine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.25e-02	4.87e-02	-1.69	0.101	-1.82e-01	1.70e-02	0.000
L3.Pyrimidine.metabolism	5.32e-08	2.83e-08	1.88	0.070	-4.63e-09	1.11e-07	0.102

Table 1460: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Pyruvate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.27e-02	3.79e-02	-1.39	0.174	-1.30e-01	2.47e-02	0.0000
L3.Pyruvate.metabolism	5.47e-08	3.25e-08	1.68	0.103	-1.17e-08	1.21e-07	0.0838

Table 1461: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.RIG.I.like.receptor.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.60e-03	2.77e-02	0.274	0.786	-4.90e-02	6.42e-02	0.0000
L3.RIG.I.like.receptor.signaling.pathway	-5.28e-06	1.15e-05	-0.461	0.648	-2.87e-05	1.81e-05	0.0068

Table 1462: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.RNA.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.64e-02	4.70e-02	-2.05	0.0491	-1.92e-01	-3.84e-04	0.000
L3.RNA.degradation	2.58e-07	1.13e-07	2.28	0.0298	2.71e-08	4.90e-07	0.144

Table 1463: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.RNA.polymerase, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.35e-02	4.91e-02	-1.49	0.145	-1.74e-01	2.69e-02	0.0000
L3.RNA.polymerase	5.09e-07	3.07e-07	1.66	0.107	-1.17e-07	1.14e-06	0.0816

Table 1464: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.RNA.transport, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.50e-02	4.24e-02	-0.591	0.559	-1.12e-01	6.15e-02	0.0000
L3.RNA.transport	2.52e-07	3.63e-07	0.693	0.494	-4.90e-07	9.94e-07	0.0152

Table 1465: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Regulation.of.actin.cytoskeleton, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1466: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Renal.cell.carcinoma, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.48e-02	2.45e-02	-1.83	0.0776	-9.50e-02	5.27e-03	0.000
L3.Renal.cell.carcinoma	4.39e-06	1.45e-06	3.02	0.0051	1.42e-06	7.35e-06	0.228

Table 1467: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Renin.angiotensin.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.004502	0.022485	0.200	0.843	-0.041418	0.050422	0.0000
L3.Renin.angiotensin.system	-0.000244	0.000255	-0.958	0.346	-0.000765	0.000276	0.0288

Table 1468: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Replication..recombination.and.repair.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.45e-02	4.30e-02	-1.27	0.215	-1.42e-01	3.34e-02	0.00
L3.Replication..recombination.and.repair.proteins	8.40e-08	5.74e-08	1.46	0.154	-3.33e-08	2.01e-07	0.06

Table 1469: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Restriction.enzyme, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.82e-02	3.85e-02	-2.03	0.0511	-1.57e-01	4.07e-04	0.000
L3.Restriction.enzyme	5.08e-07	2.12e-07	2.40	0.0229	7.54e-08	9.41e-07	0.156

Table 1470: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Retinol.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.79e-02	3.21e-02	-0.557	0.581	-8.33e-02	4.76e-02	0.0000
L3.Retinol.metabolism	4.93e-07	6.40e-07	0.770	0.447	-8.15e-07	1.80e-06	0.0188

Table 1471: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Rheumatoid.arthritis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1472: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Riboflavin.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.97e-02	3.47e-02	-1.43	0.1624	-1.21e-01	2.12e-02	0.0000
L3.Riboflavin.metabolism	2.43e-07	1.34e-07	1.81	0.0804	-3.12e-08	5.16e-07	0.0955

Table 1473: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Ribosome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.36e-02	5.05e-02	-1.85	0.0735	-1.97e-01	9.48e-03	0.000
L3.Ribosome	4.91e-08	2.41e-08	2.04	0.0505	-1.12e-10	9.82e-08	0.118

Table 1474: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Ribosome.Biogenesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.22e-02	4.32e-02	-1.67	0.1051	-1.60e-01	1.60e-02	0.000
L3.Ribosome.Biogenesis	5.96e-08	3.11e-08	1.91	0.0652	-3.99e-09	1.23e-07	0.106

Table 1475: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Ribosome.biogenesis.in.eukaryotes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.11e-02	4.58e-02	-1.55	0.1309	-1.65e-01	2.24e-02	0.0000
L3.Ribosome.biogenesis.in.eukaryotes	1.64e-06	9.35e-07	1.75	0.0897	-2.70e-07	3.55e-06	0.0902

Table 1476: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Salivary.secretion, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1477: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Secondary.bile.acid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.80e-02	4.01e-02	-2.19	0.0361	-1.70e-01	-6.09e-03	0.000
L3.Secondary.bile.acid.biosynthesis	4.03e-06	1.58e-06	2.54	0.0164	7.93e-07	7.27e-06	0.173

Table 1478: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Secretion.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.09e-02	3.18e-02	-0.973	0.338	-9.59e-02	3.40e-02	0.0000
L3.Secretion.system	2.37e-08	1.78e-08	1.331	0.193	-1.27e-08	6.01e-08	0.0541

Table 1479: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Selenocompound.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.36e-02	3.97e-02	-1.60	0.1192	-1.45e-01	1.74e-02	0.000
L3.Selenocompound.metabolism	1.80e-07	9.50e-08	1.89	0.0679	-1.41e-08	3.74e-07	0.104

Table 1480: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Sesquiterpenoid.biosynthesis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1481: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Shigellosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00250	0.02541	-0.0985	0.922	-0.0544	0.0494	0.00000
L3.Shigellosis	0.00134	0.00649	0.2056	0.839	-0.0119	0.0146	0.00136

Table 1482: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Signal.transduction.mechanisms, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.50e-02	3.88e-02	-1.16	0.256	-1.24e-01	3.43e-02	0.000
L3.Signal.transduction.mechanisms	1.05e-07	7.55e-08	1.39	0.173	-4.89e-08	2.60e-07	0.059

Table 1483: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Small.cell.lung.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.01e-03	0.024692	-0.0407	0.968	-0.05143	0.0494	0.000000
L3.Small.cell.lung.cancer	8.47e-05	0.000889	0.0952	0.925	-0.00173	0.0019	0.000292

Table 1484: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Sphingolipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.05e-02	3.69e-02	-1.64	0.112	-1.36e-01	1.50e-02	0.000
L3.Sphingolipid.metabolism	3.52e-07	1.77e-07	1.99	0.056	-9.55e-09	7.14e-07	0.113

Table 1485: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Spliceosome, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1486: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Sporulation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.06e-02	3.11e-02	0.665	0.511	-4.28e-02	8.41e-02	0.0000
L3.Sporulation	-6.43e-08	6.83e-08	-0.941	0.354	-2.04e-07	7.52e-08	0.0278

Table 1487: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Staphylococcus.aureus.infection, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.95e-03	2.77e-02	0.215	0.831	-5.06e-02	6.25e-02	0.00000
L3.Staphylococcus.aureus.infection	-1.41e-07	3.89e-07	-0.361	0.721	-9.35e-07	6.54e-07	0.00419

Table 1488: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Starch.and.sucrose.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.37e-02	4.04e-02	-1.33	0.194	-1.36e-01	2.89e-02	0.0000
L3.Starch.and.sucrose.metabolism	6.08e-08	3.88e-08	1.57	0.127	-1.84e-08	1.40e-07	0.0735

Table 1489: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Steroid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.002740	0.024867	0.110	0.913	-0.048046	0.053525	0.000
L3.Steroid.biosynthesis	-0.000051	0.000205	-0.249	0.805	-0.000469	0.000367	0.002

Table 1490: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Steroid.hormone.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.55e-02	2.43e-02	-1.88	0.07035	-9.51e-02	4.02e-03	0.000
L3.Steroid.hormone.biosynthesis	2.73e-06	8.74e-07	3.12	0.00395	9.45e-07	4.52e-06	0.239

Table 1491: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	2.35e-03	2.40e-02	0.0978	0.923	-4.67e-02	5.14e-02
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	-1.46e-06	5.52e-06	-0.2641	0.794	-1.27e-05	9.82e-06

Table 1492: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Streptomycin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.97e-02	4.45e-02	-1.57	0.1274	-1.61e-01	2.11e-02	0.0000
L3.Streptomycin.biosynthesis	2.73e-07	1.53e-07	1.78	0.0845	-3.95e-08	5.86e-07	0.0931

Table 1493: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Styrene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.12e-02	2.40e-02	-0.467	0.644	-6.03e-02	3.78e-02	0.0000
L3.Styrene.degradation	4.14e-07	3.67e-07	1.127	0.269	-3.36e-07	1.16e-06	0.0394

Table 1494: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Sulfur.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.81e-02	3.83e-02	-1.78	0.0856	-1.46e-01	1.02e-02	0.000
L3.Sulfur.metabolism	2.66e-07	1.26e-07	2.12	0.0427	9.40e-09	5.23e-07	0.126

Table 1495: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Sulfur.relay.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.78e-02	3.31e-02	-0.839	0.408	-9.55e-02	3.99e-02	0.0000
L3.Sulfur.relay.system	1.12e-07	1.00e-07	1.117	0.273	-9.28e-08	3.17e-07	0.0387

Table 1496: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Synthesis.and.degradation.of.ketone.bodies, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.18e-02	3.31e-02	-0.958	0.346	-9.94e-02	3.59e-02	0.0000
L3.Synthesis.and.degradation.of.ketone.bodies	9.11e-07	7.18e-07	1.270	0.214	-5.54e-07	2.38e-06	0.0494

Table 1497: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Systemic.lupus.erythematosus, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.11e-03	2.35e-02	-0.345	0.732	-5.61e-02	0.03984	0.0000
L3.Systemic.lupus.erythematosus	5.51e-05	5.62e-05	0.981	0.335	-5.96e-05	0.00017	0.0301

Table 1498: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.TGF.beta.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1499: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Taurine.and.hypotaurine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.10e-02	4.02e-02	-2.02	0.0528	-1.63e-01	1.03e-03	0.000
L3.Taurine.and.hypotaurine.metabolism	7.64e-07	3.26e-07	2.35	0.0258	9.89e-08	1.43e-06	0.151

Table 1500: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Terpenoid.backbone.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.60e-02	4.83e-02	-1.99	0.0558	-1.95e-01	2.54e-03	0.000
L3.Terpenoid.backbone.biosynthesis	2.14e-07	9.71e-08	2.20	0.0354	1.56e-08	4.12e-07	0.135

Table 1501: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Tetracycline.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.8e-03	4.5e-02	-0.107	0.916	-9.66e-02	8.7e-02	0.000000
L3.Tetracycline.biosynthesis	3.8e-08	3.1e-07	0.123	0.903	-5.94e-07	6.7e-07	0.000487

Table 1502: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Thiamine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.86e-02	4.47e-02	-1.53	0.1357	-1.60e-01	2.28e-02	0.0000
L3.Thiamine.metabolism	1.66e-07	9.50e-08	1.74	0.0916	-2.84e-08	3.60e-07	0.0893

Table 1503: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Tight.junction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1504: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Toluene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.65e-03	2.63e-02	-0.101	0.920	-5.63e-02	5.10e-02	0.00000
L3.Toluene.degradation	2.34e-08	1.22e-07	0.191	0.849	-2.26e-07	2.73e-07	0.00118

Table 1505: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Toxoplasmosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.01e-03	0.024692	-0.0407	0.968	-0.05143	0.0494	0.000000
L3.Toxoplasmosis	8.47e-05	0.000889	0.0952	0.925	-0.00173	0.0019	0.000292

Table 1506: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Transcription.factors, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.58e-02	3.27e-02	-0.787	0.437	-9.27e-02	4.11e-02	0.000
L3.Transcription.factors	1.47e-08	1.38e-08	1.060	0.298	-1.36e-08	4.29e-08	0.035

Table 1507: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Transcription.machinery, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.80e-02	4.93e-02	-1.58	0.1242	-1.79e-01	2.27e-02	0.0000
L3.Transcription.machinery	1.18e-07	6.72e-08	1.75	0.0899	-1.94e-08	2.55e-07	0.0902

Table 1508: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Transcription.related.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.34e-02	2.48e-02	-0.541	0.592	-6.40e-02	3.72e-02	0.0000
L3.Transcription.related.proteins	9.21e-07	8.02e-07	1.148	0.260	-7.18e-07	2.56e-06	0.0408

Table 1509: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Translation.factors, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.49e-02	4.72e-02	-2.01	0.0531	-1.91e-01	1.36e-03	0.000
L3.Translation.factors	2.15e-07	9.58e-08	2.24	0.0327	1.89e-08	4.10e-07	0.139

Table 1510: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Translation.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.07e-02	4.34e-02	-1.63	0.114	-1.59e-01	1.79e-02	0.000
L3.Translation.proteins	8.95e-08	4.80e-08	1.86	0.072	-8.52e-09	1.88e-07	0.101

Table 1511: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Transporters, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.43e-02	3.56e-02	-0.965	0.342	-1.07e-01	3.83e-02	0.0000
L3.Transporters	5.14e-09	4.21e-09	1.220	0.232	-3.47e-09	1.38e-08	0.0458

Table 1512: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-5.31e-02	3.42e-02	-1.55	0.1306	-1.23e-01	1.67e-02
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis	5.18e-07	2.63e-07	1.97	0.0581	-1.89e-08	1.06e-06

Table 1513: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Tryptophan.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.36e-02	2.80e-02	-0.842	0.406	-8.08e-02	3.36e-02	0.000
L3.Tryptophan.metabolism	1.22e-07	9.18e-08	1.331	0.193	-6.53e-08	3.10e-07	0.054

Table 1514: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Tuberculosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.43e-02	5.27e-02	-1.79	0.0834	-2.02e-01	1.32e-02	0.00
L3.Tuberculosis	8.42e-07	4.31e-07	1.95	0.0602	-3.83e-08	1.72e-06	0.11

Table 1515: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Two.component.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.07e-02	3.28e-02	-0.631	0.533	-8.76e-02	4.62e-02	0.000
L3.Two.component.system	1.47e-08	1.72e-08	0.854	0.400	-2.04e-08	4.97e-08	0.023

Table 1516: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Type.I.diabetes.mellitus, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.31e-01	4.88e-02	-2.68	0.01189	-2.31e-01	-3.11e-02	0.000
L3.Type.I.diabetes.mellitus	3.19e-06	1.09e-06	2.93	0.00648	9.63e-07	5.41e-06	0.216

Table 1517: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Type.II.diabetes.mellitus, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.34e-02	4.35e-02	-1.46	0.155	-1.52e-01	2.54e-02	0.0000
L3.Type.II.diabetes.mellitus	1.42e-06	8.50e-07	1.67	0.105	-3.14e-07	3.16e-06	0.0828

Table 1518: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Tyrosine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.45e-02	3.57e-02	-1.24	0.223	-1.17e-01	2.85e-02	0.0000
L3.Tyrosine.metabolism	1.34e-07	8.63e-08	1.56	0.130	-4.20e-08	3.11e-07	0.0724

Table 1519: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-3.74e-02	2.76e-02	-1.35	0.1858	-9.38e-02	1.9e-02
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis	1.81e-07	8.74e-08	2.07	0.0472	2.37e-09	3.6e-07

Table 1520: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Ubiquitin.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.40e-02	2.61e-02	-0.919	0.365	-7.74e-02	2.94e-02	0.0000
L3.Ubiquitin.system	1.78e-06	1.11e-06	1.605	0.119	-4.85e-07	4.04e-06	0.0767

Table 1521: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.VEGF.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1522: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Valine..leucine.and.isoleucine.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.04e-02	4.57e-02	-1.54	0.1337	-1.64e-01	2.29e-02	0.0000
L3.Valine..leucine.and.isoleucine.biosynthesis	1.12e-07	6.40e-08	1.74	0.0918	-1.92e-08	2.42e-07	0.0892

Table 1523: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Valine..leucine.and.isoleucine.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.25e-02	3.33e-02	-1.28	0.212	-1.1e-01	2.55e-02	0.0000
L3.Valine..leucine.and.isoleucine.degradation	1.59e-07	9.54e-08	1.66	0.106	-3.6e-08	3.54e-07	0.0821

Table 1524: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Various.types.of.N.glycan.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00594	0.0256	-0.232	0.818	-0.0583	0.0464	0.00000
L3.Various.types.of.N.glycan.biosynthesis	0.00594	0.0127	0.468	0.643	-0.0200	0.0319	0.00701

Table 1525: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Vascular.smooth.muscle.contraction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1526: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Vasopressin.regulated.water.reabsorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00119	0.0233	-0.0509	0.960	-0.0488	0.0464	0.000
L3.Vasopressin.regulated.water.reabsorption	0.00474	0.0269	0.1762	0.861	-0.0502	0.0597	0.001

Table 1527: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.Vibrio.cholerae.infection, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00701	0.0245	-0.286	0.777	-0.0570	0.0430	0.0000
L3.Vibrio.cholerae.infection	0.00976	0.0145	0.672	0.507	-0.0199	0.0394	0.0143

Table 1528: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Vibrio.cholerae.pathogenic.cycle, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.74e-02	3.52e-02	-0.494	0.625	-8.92e-02	5.45e-02	0.0000
L3.Vibrio.cholerae.pathogenic.cycle	2.62e-07	4.12e-07	0.637	0.529	-5.80e-07	1.10e-06	0.0129

Table 1529: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Viral.myocarditis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.01e-03	0.024692	-0.0407	0.968	-0.05143	0.0494	0.000000
L3.Viral.myocarditis	8.47e-05	0.000889	0.0952	0.925	-0.00173	0.0019	0.000292

Table 1530: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Vitamin.B6.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.02e-02	3.64e-02	-1.65	0.1093	-1.35e-01	1.43e-02	0.000
L3.Vitamin.B6.metabolism	3.82e-07	1.90e-07	2.02	0.0527	-4.84e-09	7.69e-07	0.116

Table 1531: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Wnt.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00799	0.0238	-0.336	0.739	-0.0566	0.0406	0.0000
L3.Wnt.signaling.pathway	0.03197	0.0360	0.888	0.381	-0.0415	0.1055	0.0248

Table 1532: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Xylene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.33e-02	3.30e-02	-0.706	0.485	-9.08e-02	4.41e-02	0.0000
L3.Xylene.degradation	3.67e-07	3.87e-07	0.947	0.351	-4.24e-07	1.16e-06	0.0281

Table 1533: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs
L3.Zeatin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.29e-01	5.1e-02	-2.53	0.0170	-2.33e-01	-2.47e-02	0.000
L3.Zeatin.biosynthesis	3.04e-06	1.1e-06	2.75	0.0101	7.79e-07	5.29e-06	0.196

Table 1534: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.alpha.Linolenic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.39e-02	2.42e-02	-0.576	0.569	-6.33e-02	3.54e-02	0.0000
L3.alpha.Linolenic.acid.metabolism	1.07e-06	8.14e-07	1.310	0.200	-5.96e-07	2.73e-06	0.0525

Table 1535: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.beta.Alanine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.41e-02	3.06e-02	-1.11	0.274	-9.67e-02	2.84e-02	0.0000
L3.beta.Alanine.metabolism	1.88e-07	1.20e-07	1.56	0.128	-5.75e-08	4.33e-07	0.0731

Table 1536: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.beta.Lactam.resistance, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.11e-02	3.67e-02	-1.93	0.0627	-1.46e-01	4.00e-03	0.000
L3.beta.Lactam.resistance	3.25e-06	1.39e-06	2.33	0.0266	4.03e-07	6.09e-06	0.149

Table 1537: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.mRNA.surveillance.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1538: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.mTOR.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-1.38e-14	0.022	-6.26e-13	1	-0.0448	0.0448	0
	NA	NA	NA	NA	NA	NA	0

Table 1539: diversity_vs_picrust_L3_neo: wunifrac.PC.3 vs L3.p53.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.01e-03	0.024692	-0.0407	0.968	-0.05143	0.0494	0.000000
L3.p53.signaling.pathway	8.47e-05	0.000889	0.0952	0.925	-0.00173	0.0019	0.000292

Table 1540: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation,
df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %
Intercept	-5.12e-03	1.81e-02	-0.283	0.779	-4.21e-02
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	6.07e-06	4.01e-06	1.513	0.141	-2.13e-06

Table 1541: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.ABC.transporters, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.49e-02	2.49e-02	-2.21	0.03510	-1.06e-01	-4.1e-03	0.000
L3.ABC.transporters	1.65e-08	5.65e-09	2.92	0.00659	4.96e-09	2.8e-08	0.216

Table 1542: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Adherens.junction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1543: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Adipocytokine.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.99e-02	2.99e-02	0.664	0.512	-4.12e-02	8.10e-02	0.0000
L3.Adipocytokine.signaling.pathway	-4.35e-07	5.20e-07	-0.838	0.409	-1.50e-06	6.26e-07	0.0221

Table 1544: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.African.trypanosomiasis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.86e-02	2.33e-02	-0.80	0.430	-6.61e-02	2.89e-02	0.0000
L3.African.trypanosomiasis	2.53e-06	2.01e-06	1.26	0.217	-1.57e-06	6.64e-06	0.0488

Table 1545: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Alanine..aspartate.and.glutamate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.89e-02	3.52e-02	-2.53	0.01701	-1.61e-01	-1.71e-02	0.00
L3.Alanine..aspartate.and.glutamate.metabolism	1.05e-07	3.68e-08	2.85	0.00775	2.99e-08	1.80e-07	0.20

Table 1546: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Aldosterone.regulated.sodium.reabsorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00503	0.018	-0.279	0.782	-0.0418	0.0318	0.0000
L3.Aldosterone.regulated.sodium.reabsorption	0.16092	0.102	1.579	0.125	-0.0472	0.3690	0.0745

Table 1547: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Alzheimer.s.disease, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.27e-02	3.07e-02	-2.04	0.0499	-1.25e-01	-3.60e-05	0.000
L3.Alzheimer.s.disease	1.44e-06	5.88e-07	2.45	0.0205	2.37e-07	2.64e-06	0.162

Table 1548: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Amino.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.82e-02	2.50e-02	-1.93	0.0633	-9.93e-02	2.84e-03	0.000
L3.Amino.acid.metabolism	2.03e-07	7.86e-08	2.59	0.0147	4.30e-08	3.64e-07	0.178

Table 1549: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Amino.acid.related.enzymes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.50e-02	3.60e-02	-2.36	0.0250	-1.59e-01	-1.14e-02	0.000
L3.Amino.acid.related.enzymes	6.95e-08	2.61e-08	2.66	0.0125	1.61e-08	1.23e-07	0.186

Table 1550: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Amino.sugar.and.nucleotide.sugar.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.59e-02	3.64e-02	-1.81	0.0806	-1.40e-01	8.52e-03	0.00
L3.Amino.sugar.and.nucleotide.sugar.metabolism	4.74e-08	2.31e-08	2.05	0.0488	2.72e-10	9.46e-08	0.12

Table 1551: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Aminoacyl.tRNA.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.76e-02	3.95e-02	-1.96	0.0588	-1.58e-01	3.08e-03	0.000
L3.Aminoacyl.tRNA.biosynthesis	8.08e-08	3.70e-08	2.18	0.0372	5.11e-09	1.56e-07	0.133

Table 1552: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Aminobenzoate.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.01e-02	2.46e-02	-1.63	0.1132	-9.03e-02	1.01e-02	0.000
L3.Aminobenzoate.degradation	3.03e-07	1.34e-07	2.27	0.0308	2.99e-08	5.76e-07	0.142

Table 1553: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Amoebiasis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.01e-03	2.42e-02	0.290	0.774	-4.23e-02	5.63e-02	0.00000
L3.Amoebiasis	-1.86e-06	4.16e-06	-0.448	0.658	-1.04e-05	6.63e-06	0.00642

Table 1554: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Amyotrophic.lateral.sclerosis..ALS., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.67e-02	1.99e-02	-1.34	0.1901	-6.74e-02	1.40e-02	0.000
L3.Amyotrophic.lateral.sclerosis..ALS.	1.47e-06	5.92e-07	2.49	0.0186	2.64e-07	2.68e-06	0.167

Table 1555: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Antigen.processing.and.presentation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.93e-02	2.38e-02	-3.75	7.46e-04	-1.38e-01	-4.07e-02	0.000
L3.Antigen.processing.and.presentation	3.80e-06	8.16e-07	4.65	6.19e-05	2.13e-06	5.46e-06	0.411

Table 1556: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Apoptosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.40e-02	2.03e-02	1.18	0.2465	-1.75e-02	6.56e-02	0.000
L3.Apoptosis	-3.36e-06	1.53e-06	-2.19	0.0363	-6.49e-06	-2.29e-07	0.134

Table 1557: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Arachidonic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.13e-02	2.40e-02	-1.72	0.0958	-9.04e-02	7.76e-03	0.000
L3.Arachidonic.acid.metabolism	1.06e-06	4.38e-07	2.42	0.0220	1.63e-07	1.95e-06	0.158

Table 1558: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Arginine.and.proline.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.87e-02	2.79e-02	-2.47	0.01954	-1.26e-01	-1.18e-02	0.000
L3.Arginine.and.proline.metabolism	7.16e-08	2.36e-08	3.03	0.00503	2.33e-08	1.20e-07	0.228

Table 1559: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Arrhythmogenic.right.ventricular.cardiomyopathy..ARVC., df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1560: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Ascorbate.and.aldarate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.21e-02	2.10e-02	-1.53	0.1362	-7.49e-02	1.07e-02	0.000
L3.Ascorbate.and.aldarate.metabolism	1.65e-07	6.48e-08	2.54	0.0164	3.24e-08	2.97e-07	0.173

Table 1561: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Atrazine.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.0e-02	1.87e-02	-1.07	0.2939	-5.83e-02	1.83e-02	0.000
L3.Atrazine.degradation	1.2e-06	4.90e-07	2.44	0.0208	1.95e-07	2.20e-06	0.161

Table 1562: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Bacterial.chemotaxis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.82e-02	2.49e-02	-1.94	0.0622	-9.89e-02	2.62e-03	0.00
L3.Bacterial.chemotaxis	1.76e-07	6.75e-08	2.61	0.0140	3.83e-08	3.14e-07	0.18

Table 1563: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Bacterial.invasion.of.epithelial.cells, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.11e-02	1.86e-02	-0.599	0.5535	-4.91e-02	2.68e-02	0.0000
L3.Bacterial.invasion.of.epithelial.cells	9.22e-06	5.10e-06	1.807	0.0808	-1.20e-06	1.96e-05	0.0953

Table 1564: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Bacterial.motility.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.28e-02	2.10e-02	-2.99	0.005595	-1.06e-01	-1.98e-02	0.000
L3.Bacterial.motility.proteins	1.14e-07	2.74e-08	4.17	0.000239	5.84e-08	1.70e-07	0.359

Table 1565: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Bacterial.secretion.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.30e-02	2.45e-02	-1.76	0.0894	-9.31e-02	7.03e-03	0.000
L3.Bacterial.secretion.system	6.67e-08	2.76e-08	2.42	0.0217	1.04e-08	1.23e-07	0.159

Table 1566: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Bacterial.toxins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.23e-02	4.05e-02	-1.54	0.135	-1.45e-01	2.04e-02	0.000
L3.Bacterial.toxins	4.71e-07	2.76e-07	1.71	0.098	-9.22e-08	1.03e-06	0.086

Table 1567: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Basal.transcription.factors, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.47e-03	1.98e-02	-0.125	0.901	-4.29e-02	3.79e-02	0.00000
L3.Basal.transcription.factors	2.89e-06	8.45e-06	0.341	0.735	-1.44e-05	2.01e-05	0.00375

Table 1568: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Base.excision.repair, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.54e-02	3.62e-02	-2.36	0.0250	-1.59e-01	-1.15e-02	0.000
L3.Base.excision.repair	2.26e-07	8.52e-08	2.66	0.0126	5.23e-08	4.00e-07	0.185

Table 1569: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Benzoate.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.35e-02	2.22e-02	-1.96	0.0591	-8.88e-02	1.78e-03	0.000
L3.Benzoate.degradation	1.72e-07	5.94e-08	2.90	0.0070	5.07e-08	2.93e-07	0.213

Table 1570: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Betalain.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.08e-02	1.87e-02	-0.577	0.5685	-0.048867	0.027348	0.0000
L3.Betalain.biosynthesis	7.76e-05	4.49e-05	1.730	0.0938	-0.000014	0.000169	0.0881

Table 1571: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Bile.secretion, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.01732	0.01931	-0.897	0.3771	-0.056760	0.02213	0.000
L3.Bile.secretion	0.00254	0.00126	2.021	0.0523	-0.000027	0.00511	0.116

Table 1572: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Biosynthesis.and.biodegradation.of.secondary.metabolites, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	-2.21e-02	2.04e-02	-1.09	0.2861	-6.38e-02	1.95
L3.Biosynthesis.and.biodegradation.of.secondary.metabolites	2.68e-07	1.31e-07	2.05	0.0495	6.05e-10	5.35

Table 1573: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Biosynthesis.of.12. . .14..and.16.membered.macrolides, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	
Intercept	-0.00231	0.0186	-0.124	0.902	-0.0403	0.0357	
L3.Biosynthesis.of.12. . .14..and.16.membered.macrolides	0.07393	0.1052	0.703	0.488	-0.1409	0.2887	

Table 1574: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Biosynthesis.of.ansamycins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.06e-02	2.32e-02	-2.18	0.03691	-9.80e-02	-3.29e-03	0.00
L3.Biosynthesis.of.ansamycins	4.83e-07	1.59e-07	3.04	0.00487	1.59e-07	8.07e-07	0.23

Table 1575: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	-1.90e-02	2.02e-02	-0.939	0.3552	-6.03e-02	2.23e
L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides	2.68e-07	1.44e-07	1.861	0.0726	-2.62e-08	5.63e

Table 1576: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Biosynthesis.of.type.II.polyketide.backbone, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1577: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Biosynthesis.of.type.II.polyketide.products, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.11e-02	0.018734	-0.595	0.5562	-0.049408	0.02711	0.0000
L3.Biosynthesis.of.type.II.polyketide.products	7.78e-05	0.000045	1.731	0.0937	-0.000014	0.00017	0.0882

Table 1578: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Biosynthesis.of.unsaturated.fatty.acids, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.81e-02	2.28e-02	-1.67	0.105	-8.47e-02	8.41e-03	0.000
L3.Biosynthesis.of.unsaturated.fatty.acids	2.96e-07	1.19e-07	2.48	0.019	5.21e-08	5.40e-07	0.165

Table 1579: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Biosynthesis.of.vancomycin.group.antibiotics, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.44e-02	4.04e-02	-0.357	0.724	-9.69e-02	6.80e-02	0.0000
L3.Biosynthesis.of.vancomycin.group.antibiotics	2.90e-07	7.24e-07	0.401	0.691	-1.19e-06	1.77e-06	0.0051

Table 1580: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Biotin.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.27e-02	2.96e-02	-2.12	0.0425	-1.23e-01	-2.27e-03	0.000
L3.Biotin.metabolism	5.09e-07	1.98e-07	2.57	0.0155	1.04e-07	9.13e-07	0.175

Table 1581: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Bisphenol.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.57e-02	3.08e-02	-2.78	0.00932	-1.49e-01	-2.27e-02	0.000
L3.Bisphenol.degradation	1.92e-06	5.93e-07	3.24	0.00290	7.12e-07	3.13e-06	0.253

Table 1582: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Bladder.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.39e-02	1.83e-02	-1.31	0.20133	-6.13e-02	1.35e-02	0.000
L3.Bladder.cancer	5.16e-06	1.79e-06	2.89	0.00717	1.51e-06	8.81e-06	0.212

Table 1583: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Butanoate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.80e-02	2.49e-02	-2.73	0.01055	-1.19e-01	-1.71e-02	0.000
L3.Butanoate.metabolism	1.06e-07	3.05e-08	3.49	0.00151	4.41e-08	1.69e-07	0.282

Table 1584: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Butirosin.and.neomycin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.91e-02	4.65e-02	-1.06	0.299	-1.44e-01	4.59e-02	0.0000
L3.Butirosin.and.neomycin.biosynthesis	1.05e-06	9.13e-07	1.15	0.261	-8.18e-07	2.91e-06	0.0407

Table 1585: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.C5.Branched.dibasic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.98e-02	3.38e-02	-1.47	0.1508	-1.19e-01	1.92e-02	0.0000
L3.C5.Branched.dibasic.acid.metabolism	1.86e-07	1.07e-07	1.73	0.0943	-3.38e-08	4.05e-07	0.0878

Table 1586: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.CAM.ligands, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1587: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Caffeine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00380	0.0202	0.188	0.852	-0.0375	0.0451	0.00000
L3.Caffeine.metabolism	-0.00468	0.0104	-0.452	0.655	-0.0258	0.0165	0.00654

Table 1588: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Calcium.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00395	0.0208	-0.190	0.851	-0.0464	0.0385	0.00000
L3.Calcium.signaling.pathway	0.00631	0.0154	0.409	0.685	-0.0252	0.0378	0.00537

Table 1589: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Caprolactam.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.66e-02	1.99e-02	-1.33	0.1928	-6.73e-02	1.42e-02	0.000
L3.Caprolactam.degradation	5.26e-07	2.12e-07	2.48	0.0192	9.22e-08	9.60e-07	0.165

Table 1590: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Carbohydrate.digestion.and.absorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.93e-02	2.61e-02	-0.74	0.465	-7.25e-02	3.39e-02	0.0000
L3.Carbohydrate.digestion.and.absorption	8.96e-07	8.70e-07	1.03	0.311	-8.80e-07	2.67e-06	0.0331

Table 1591: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Carbohydrate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.82e-02	3.00e-02	-0.939	0.355	-8.94e-02	3.31e-02	0.0000
L3.Carbohydrate.metabolism	1.60e-07	1.36e-07	1.174	0.249	-1.18e-07	4.37e-07	0.0426

Table 1592: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Carbon.fixation.in.photosynthetic.organisms, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.4e-02	3.01e-02	-2.13	0.0418	-1.26e-01	-2.55e-03	0.000
L3.Carbon.fixation.in.photosynthetic.organisms	1.2e-07	4.68e-08	2.56	0.0158	2.41e-08	2.15e-07	0.174

Table 1593: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Carbon.fixation.pathways.in.prokaryotes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.11e-02	2.97e-02	-2.73	0.01049	-1.42e-01	-2.04e-02	0.000
L3.Carbon.fixation.pathways.in.prokaryotes	9.43e-08	2.92e-08	3.23	0.00299	3.47e-08	1.54e-07	0.252

Table 1594: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Cardiac.muscle.contraction, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.25e-02	1.89e-02	-0.665	0.5112	-5.1e-02	2.60e-02	0.0000
L3.Cardiac.muscle.contraction	2.03e-05	1.12e-05	1.802	0.0816	-2.7e-06	4.32e-05	0.0948

Table 1595: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Carotenoid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.37e-03	0.021074	0.208	0.837	-3.87e-02	4.74e-02	0.0000
L3.Carotenoid.biosynthesis	-1.28e-06	0.000003	-0.425	0.674	-7.41e-06	4.85e-06	0.0058

Table 1596: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Cell.cycle, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1597: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Cell.cycle. . . Caulobacter, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.53e-02	4.11e-02	-2.32	0.0274	-1.79e-01	-1.13e-02	0.000
L3.Cell.cycle. . . Caulobacter	2.47e-07	9.74e-08	2.54	0.0166	4.83e-08	4.46e-07	0.172

Table 1598: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Cell.cycle. . . yeast, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1599: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Cell.division, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.82e-02	2.58e-02	-2.64	0.01299	-1.21e-01	-1.55e-02	0.000
L3.Cell.division	1.14e-06	3.41e-07	3.33	0.00229	4.41e-07	1.83e-06	0.264

Table 1600: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Cell.motility.and.secretion, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.31e-02	2.70e-02	-2.34	0.02616	-1.18e-01	-8.02e-03	0.000
L3.Cell.motility.and.secretion	3.86e-07	1.32e-07	2.93	0.00639	1.17e-07	6.54e-07	0.217

Table 1601: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Cellular.antigens, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.33e-02	2.93e-02	-0.453	0.654	-7.30e-02	4.65e-02	0.0000
L3.Cellular.antigens	3.00e-07	5.16e-07	0.582	0.565	-7.54e-07	1.35e-06	0.0108

Table 1602: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Chagas.disease..American.trypanosomiasis., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.53e-02	2.26e-02	-0.676	0.504	-6.15e-02	3.09e-02	0.0000
L3.Chagas.disease..American.trypanosomiasis.	2.26e-06	2.01e-06	1.124	0.270	-1.84e-06	6.36e-06	0.0392

Table 1603: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Chaperones.and.folding.catalysts, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.07e-02	3.20e-02	-2.21	0.0350	-1.36e-01	-5.31e-03	0.000
L3.Chaperones.and.folding.catalysts	8.22e-08	3.18e-08	2.59	0.0148	1.73e-08	1.47e-07	0.178

Table 1604: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Chloroalkane.and.chloroalkene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.63e-02	3.27e-02	-2.34	0.0264	-1.43e-01	-9.58e-03	0.000
L3.Chloroalkane.and.chloroalkene.degradation	4.68e-07	1.73e-07	2.71	0.0111	1.15e-07	8.21e-07	0.191

Table 1605: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Chlorocyclohexane.and.chlorobenzene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-3.64e-02	2.01e-02	-1.82	0.0791	-7.74e-02	4.50e-03
L3.Chlorocyclohexane.and.chlorobenzene.degradation	2.68e-06	8.76e-07	3.05	0.0047	8.87e-07	4.47e-06

Table 1606: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Cholinergic.synapse, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1607: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Chromosome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.01e-02	3.30e-02	-2.73	0.01056	-1.58e-01	-2.26e-02	0.000
L3.Chromosome	7.11e-08	2.28e-08	3.12	0.00398	2.46e-08	1.18e-07	0.239

Table 1608: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Chronic.myeloid.leukemia, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.0158	0.0184	-0.856	0.3986	-0.05338	0.0218	0.000
L3.Chronic.myeloid.leukemia	0.0631	0.0278	2.266	0.0308	0.00622	0.1199	0.142

Table 1609: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Circadian.rhythm...plant, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.01237	0.01925	-0.643	0.525	-0.05169	0.0269	0.0000
L3.Circadian.rhythm...plant	0.00861	0.00529	1.628	0.114	-0.00219	0.0194	0.0787

Table 1610: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Citrate.cycle..TCA.cycle., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.31e-02	2.56e-02	-2.07	0.0467	-1.05e-01	-8.34e-04	0.000
L3.Citrate.cycle..TCA.cycle.	9.69e-08	3.56e-08	2.72	0.0108	2.41e-08	1.70e-07	0.192

Table 1611: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Clavulanic.acid.biosynthesis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1612: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Colorectal.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.002361	0.020387	0.116	0.909	-0.0393	0.0440	0.00000
L3.Colorectal.cancer	-0.000199	0.000734	-0.271	0.788	-0.0017	0.0013	0.00236

Table 1613: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Complement.and.coagulation.cascades, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1614: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Cyanoamino.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.39e-02	2.89e-02	-1.87	0.0714	-1.13e-01	5.00e-03	0.000
L3.Cyanoamino.acid.metabolism	2.02e-07	8.76e-08	2.31	0.0278	2.37e-08	3.81e-07	0.147

Table 1615: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Cysteine.and.methionine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.37e-02	3.10e-02	-2.38	0.0240	-1.37e-01	-1.04e-02	0.000
L3.Cysteine.and.methionine.metabolism	8.43e-08	3.01e-08	2.80	0.0088	2.29e-08	1.46e-07	0.202

Table 1616: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Cytochrome.P450, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.000318	0.0187	-0.017	0.987	-0.0386	0.038	0.000000
L3.Cytochrome.P450	0.010175	0.1060	0.096	0.924	-0.2064	0.227	0.000297

Table 1617: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Cytokine.receptors, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1618: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Cytokine.cytokine.receptor.interaction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1619: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Cytoskeleton.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.15e-01	3.15e-02	-3.66	0.000953	-1.80e-01	-5.10e-02	0.000
L3.Cytoskeleton.proteins	5.59e-07	1.35e-07	4.15	0.000256	2.84e-07	8.34e-07	0.357

Table 1620: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Cytosolic.DNA.sensing.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1621: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.D.Alanine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.54e-02	3.68e-02	-1.51	0.1426	-1.31e-01	1.98e-02	0.0000
L3.D.Alanine.metabolism	5.19e-07	3.03e-07	1.71	0.0967	-9.93e-08	1.14e-06	0.0866

Table 1622: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.D.Arginine.and.D.ornithine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.43e-03	2.03e-02	-0.268	0.791	-4.68e-02	3.60e-02	0.0000
L3.D.Arginine.and.D.ornithine.metabolism	1.34e-06	2.14e-06	0.626	0.536	-3.03e-06	5.71e-06	0.0125

Table 1623: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.D.Glutamine.and.D.glutamate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.76e-02	3.52e-02	-2.21	0.0352	-1.49e-01	-5.76e-03	0.000
L3.D.Glutamine.and.D.glutamate.metabolism	5.87e-07	2.34e-07	2.51	0.0177	1.09e-07	1.06e-06	0.169

Table 1624: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.DNA.repair.and.recombination.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.56e-02	3.77e-02	-2.27	0.0305	-1.62e-01	-8.63e-03	0.000
L3.DNA.repair.and.recombination.proteins	3.56e-08	1.40e-08	2.54	0.0167	6.93e-09	6.43e-08	0.172

Table 1625: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.DNA.replication, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.86e-02	4.11e-02	-2.16	0.0393	-1.73e-01	-4.64e-03	0.000
L3.DNA.replication	1.58e-07	6.67e-08	2.37	0.0247	2.15e-08	2.94e-07	0.153

Table 1626: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.DNA.replication.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.53e-02	3.88e-02	-2.46	0.0201	-1.75e-01	-1.6e-02	0.000
L3.DNA.replication.proteins	9.69e-08	3.57e-08	2.71	0.0109	2.40e-08	1.7e-07	0.192

Table 1627: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Dilated.cardiomyopathy..DCM., df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1628: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Dioxin.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.33e-02	2.42e-02	-1.38	0.1784	-8.26e-02	1.61e-02	0.000
L3.Dioxin.degradation	3.84e-07	1.94e-07	1.98	0.0569	-1.21e-08	7.80e-07	0.112

Table 1629: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Drug.metabolism...cytochrome.P450, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.74e-02	2.27e-02	-1.21	0.2368	-7.37e-02	1.89e-02	0.000
L3.Drug.metabolism...cytochrome.P450	5.55e-07	2.94e-07	1.89	0.0686	-4.51e-08	1.15e-06	0.103

Table 1630: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Drug.metabolism...other.enzymes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.67e-02	3.68e-02	-2.08	0.0457	-1.52e-01	-1.57e-03	0.000
L3.Drug.metabolism...other.enzymes	2.72e-07	1.16e-07	2.35	0.0256	3.55e-08	5.08e-07	0.151

Table 1631: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.ECM.receptor.interaction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1632: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Electron.transfer.carriers, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.01e-02	2.16e-02	-1.39	0.1746	-7.43e-02	1.41e-02	0.000
L3.Electron.transfer.carriers	5.29e-07	2.34e-07	2.26	0.0313	5.09e-08	1.01e-06	0.141

Table 1633: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Endocrine.and.other.factor.regulated.calcium.reabsorption, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1634: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Endocytosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00406	0.01925	0.211	0.835	-0.0352	0.04336	0.0000
L3.Endocytosis	-0.00382	0.00558	-0.683	0.500	-0.0152	0.00759	0.0148

Table 1635: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Energy.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.23e-02	2.61e-02	-2.77	0.00962	-1.26e-01	-1.89e-02	0.000
L3.Energy.metabolism	9.83e-08	2.85e-08	3.45	0.00169	4.01e-08	1.56e-07	0.277

Table 1636: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-7.84e-02	2.86e-02	-2.74	0.01019	-1.37e-01	-2.00e-0
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	1.15e-06	3.50e-07	3.29	0.00255	4.38e-07	1.87e-0

Table 1637: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.ErbB.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1638: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Ether.lipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.56e-03	2.30e-02	-0.328	0.745	-5.46e-02	3.95e-02	0.00000
L3.Ether.lipid.metabolism	5.23e-06	9.62e-06	0.544	0.590	-1.44e-05	2.49e-05	0.00946

Table 1639: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Ethylbenzene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.48e-02	2.38e-02	-3.14	0.003750	-1.23e-01	-2.62e-02	0.000
L3.Ethylbenzene.degradation	2.42e-06	6.00e-07	4.03	0.000356	1.19e-06	3.64e-06	0.343

Table 1640: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Fat.digestion.and.absorption, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1641: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Fatty.acid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.92e-02	3.50e-02	-1.98	0.0569	-1.41e-01	2.18e-03	0.000
L3.Fatty.acid.biosynthesis	1.58e-07	6.98e-08	2.27	0.0307	1.58e-08	3.01e-07	0.142

Table 1642: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Fatty.acid.elongation.in.mitochondria, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1643: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Fatty.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.23e-02	2.53e-02	-2.07	0.0474	-1.04e-01	-6.49e-04	0.000
L3.Fatty.acid.metabolism	2.02e-07	7.40e-08	2.73	0.0105	5.10e-08	3.53e-07	0.194

Table 1644: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Fc.epsilon.RI.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1645: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Fc.gamma.R.mediated.phagocytosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00406	0.01925	0.211	0.835	-0.0352	0.04336	0.0000
L3.Fc.gamma.R.mediated.phagocytosis	-0.00382	0.00558	-0.683	0.500	-0.0152	0.00759	0.0148

Table 1646: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Flagellar.assembly, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.93e-02	2.01e-02	-1.96	0.05994	-8.03e-02	1.75e-03	0.000
L3.Flagellar.assembly	2.50e-07	7.81e-08	3.21	0.00318	9.10e-08	4.10e-07	0.249

Table 1647: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Flavone.and.flavonol.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.50e-03	2.31e-02	-0.282	0.780	-5.36e-02	4.06e-02	0.00000
L3.Flavone.and.flavonol.biosynthesis	1.32e-06	2.83e-06	0.467	0.644	-4.45e-06	7.09e-06	0.00698

Table 1648: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Flavonoid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.88e-03	1.83e-02	-0.43	0.670	-4.53e-02	0.029551	0.0000
L3.Flavonoid.biosynthesis	7.13e-06	4.36e-06	1.63	0.113	-1.78e-06	0.000016	0.0793

Table 1649: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Fluorobenzoate.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.70e-02	1.87e-02	-0.914	0.3681	-5.51e-02	2.10e-02	0.000
L3.Fluorobenzoate.degradation	1.14e-06	5.03e-07	2.258	0.0314	1.08e-07	2.16e-06	0.141

Table 1650: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Focal.adhesion, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1651: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Folate.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.47e-02	3.60e-02	-1.80	0.0825	-1.38e-01	8.86e-03	0.000
L3.Folate.biosynthesis	1.72e-07	8.41e-08	2.05	0.0495	4.15e-10	3.44e-07	0.119

Table 1652: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Fructose.and.mannose.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.17e-02	2.86e-02	-2.16	0.0391	-1.20e-01	-3.30e-03	0.000
L3.Fructose.and.mannose.metabolism	6.86e-08	2.59e-08	2.65	0.0127	1.57e-08	1.21e-07	0.185

Table 1653: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Function.unknown, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.09e-02	2.54e-02	-2.01	0.0538	-1.03e-01	8.86e-04	0.000
L3.Function.unknown	3.76e-08	1.42e-08	2.65	0.0126	8.66e-09	6.65e-08	0.185

Table 1654: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.G.protein.coupled.receptors, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1655: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.GTP.binding.proteins, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1656: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Galactose.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.51e-02	3.85e-02	-1.17	0.251	-1.24e-01	3.36e-02	0.0000
L3.Galactose.metabolism	5.92e-08	4.48e-08	1.32	0.196	-3.23e-08	1.51e-07	0.0534

Table 1657: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Gastric.acid.secretion, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1658: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.General.function.prediction.only, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.34e-02	3.09e-02	-2.70	0.01122	-1.46e-01	-2.04e-02	0.000
L3.General.function.prediction.only	2.69e-08	8.53e-09	3.16	0.00361	9.52e-09	4.44e-08	0.243

Table 1659: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Geraniol.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.98e-02	2.08e-02	-1.43	0.1621	-7.23e-02	1.27e-02	0.000
L3.Geraniol.degradation	4.12e-07	1.68e-07	2.45	0.0205	6.81e-08	7.56e-07	0.162

Table 1660: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Germination, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.02e-03	2.08e-02	-0.0489	0.961	-4.36e-02	4.16e-02	0.000000
L3.Germination	2.57e-07	2.45e-06	0.1051	0.917	-4.74e-06	5.26e-06	0.000356

Table 1661: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Glioma, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1662: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Glutamatergic.synapse, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.31e-02	3.66e-02	-2.00	0.0550	-1.48e-01	1.67e-03	0.000
L3.Glutamatergic.synapse	9.79e-07	4.34e-07	2.26	0.0315	9.28e-08	1.86e-06	0.141

Table 1663: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Glutathione.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.44e-02	2.73e-02	-1.63	0.1142	-1.00e-01	1.13e-02	0.000
L3.Glutathione.metabolism	1.77e-07	8.46e-08	2.10	0.0445	4.62e-09	3.50e-07	0.124

Table 1664: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Glycan.bindng.proteins, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1665: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Glycan.biosynthesis.and.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.29e-02	1.94e-02	-2.21	0.03452	-8.25e-02	-3.34e-03	0.000
L3.Glycan.biosynthesis.and.metabolism	8.16e-07	2.25e-07	3.64	0.00103	3.58e-07	1.28e-06	0.299

Table 1666: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Glycerolipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.08e-02	2.80e-02	-2.53	0.01677	-1.28e-01	-1.37e-02	0.000
L3.Glycerolipid.metabolism	2.04e-07	6.58e-08	3.09	0.00424	6.92e-08	3.38e-07	0.236

Table 1667: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Glycerophospholipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.74e-02	2.75e-02	-2.82	0.00853	-1.34e-01	-2.13e-02	0.000
L3.Glycerophospholipid.metabolism	1.71e-07	5.01e-08	3.42	0.00181	6.91e-08	2.74e-07	0.274

Table 1668: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Glycine..serine.and.threonine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.08e-02	3.18e-02	-1.91	0.0656	-1.26e-01	4.18e-03	0.000
L3.Glycine..serine.and.threonine.metabolism	8.23e-08	3.64e-08	2.26	0.0310	8.05e-09	1.57e-07	0.142

Table 1669: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Glycolysis. . . Gluconeogenesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.77e-02	3.28e-02	-2.06	0.0480	-1.35e-01	-6.43e-04	0.000
L3.Glycolysis. . . Gluconeogenesis	6.40e-08	2.66e-08	2.41	0.0225	9.65e-09	1.18e-07	0.157

Table 1670: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Glycosaminoglycan.biosynthesis. . . chondroitin.sulfate, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	0.00555	0.0184	0.301	0.766	-0.0321	0.0432
L3.Glycosaminoglycan.biosynthesis. . . chondroitin.sulfate	-0.02218	0.0169	-1.311	0.200	-0.0567	0.0124

Table 1671: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Glycosaminoglycan.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.74e-03	3.07e-02	-0.122	0.904	-6.64e-02	5.89e-02	0.000000
L3.Glycosaminoglycan.degradation	5.16e-08	3.38e-07	0.152	0.880	-6.39e-07	7.43e-07	0.000749

Table 1672: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Glycosphingolipid.biosynthesis. . . ganglio.series, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.45e-02	2.90e-02	0.847	0.404	-3.46e-02	8.36e-02	0.00
L3.Glycosphingolipid.biosynthesis. . . ganglio.series	-5.30e-07	4.88e-07	-1.084	0.287	-1.53e-06	4.68e-07	0.03

Table 1673: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Glycosphingolipid.biosynthesis. . . globo.series, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.27e-03	3.21e-02	0.133	0.895	-6.14e-02	6.99e-02	0.000
L3.Glycosphingolipid.biosynthesis. . . globo.series	-5.27e-08	3.25e-07	-0.162	0.872	-7.17e-07	6.12e-07	0.000

Table 1674: diversity_vs_picrust_L3_neo: wunifrac.PC.4
vs L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series,
df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.
Intercept	-0.002052	1.89e-02	-0.109	0.914	-4.06e-02	3.6
L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series	0.000015	3.19e-05	0.471	0.641	-5.01e-05	8.0

Table 1675: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Glycosylphosphatidylinositol.GPI..anchor.biosynthesis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1676: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Glycosyltransferases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.83e-02	3.25e-02	-1.48	0.1480	-1.15e-01	1.81e-02	0.0000
L3.Glycosyltransferases	1.34e-07	7.61e-08	1.76	0.0879	-2.12e-08	2.90e-07	0.0912

Table 1677: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Glyoxylate.and.dicarboxylate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.77e-02	2.40e-02	-2.41	0.02255	-1.07e-01	-8.71e-03	0.00
L3.Glyoxylate.and.dicarboxylate.metabolism	1.24e-07	3.86e-08	3.21	0.00313	4.52e-08	2.03e-07	0.25

Table 1678: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.GnRH.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00406	0.01925	0.211	0.835	-0.0352	0.04336	0.0000
L3.GnRH.signaling.pathway	-0.00382	0.00558	-0.683	0.500	-0.0152	0.00759	0.0148

Table 1679: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Hedgehog.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1680: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Hematopoietic.cell.lineage, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1681: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Hepatitis.C, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1682: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Histidine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.00e-02	3.51e-02	-2.57	0.01549	-1.62e-01	-1.84e-02	0.000
L3.Histidine.metabolism	1.76e-07	6.07e-08	2.90	0.00693	5.20e-08	3.00e-07	0.213

Table 1683: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Homologous.recombination, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.85e-02	3.96e-02	-2.23	0.0330	-1.69e-01	-7.61e-03	0.000
L3.Homologous.recombination	1.13e-07	4.56e-08	2.47	0.0195	1.94e-08	2.06e-07	0.164

Table 1684: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Huntington.s.disease, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.79e-02	2.88e-02	-2.36	0.02489	-1.27e-01	-9.18e-03	0.00
L3.Huntington.s.disease	1.56e-06	5.45e-07	2.87	0.00746	4.51e-07	2.68e-06	0.21

Table 1685: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Hypertrophic.cardiomyopathy..HCM., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.01102	0.01779	-0.619	0.5403	-0.047353	0.02531	0.000
L3.Hypertrophic.cardiomyopathy..HCM.	0.00284	0.00128	2.229	0.0335	0.000238	0.00545	0.138

Table 1686: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Indole.alkaloid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00988	0.0210	-0.469	0.642	-0.0529	0.0331	0.0000
L3.Indole.alkaloid.biosynthesis	0.01756	0.0188	0.933	0.358	-0.0209	0.0560	0.0273

Table 1687: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Influenza.A, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.002361	0.020387	0.116	0.909	-0.0393	0.0440	0.00000
L3.Influenza.A	-0.000199	0.000734	-0.271	0.788	-0.0017	0.0013	0.00236

Table 1688: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Inorganic.ion.transport.and.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.64e-02	2.38e-02	-1.53	0.1360	-8.50e-02	1.21e-02	0.000
L3.Inorganic.ion.transport.and.metabolism	1.41e-07	6.38e-08	2.21	0.0352	1.04e-08	2.71e-07	0.136

Table 1689: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Inositol.phosphate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.92e-02	2.26e-02	-1.29	0.2066	-7.54e-02	1.70e-02	0.000
L3.Inositol.phosphate.metabolism	2.27e-07	1.13e-07	2.01	0.0537	-3.84e-09	4.58e-07	0.115

Table 1690: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Insulin.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.56e-02	3.60e-02	-1.27	0.215	-1.19e-01	2.79e-02	0.0000
L3.Insulin.signaling.pathway	7.45e-07	5.11e-07	1.46	0.155	-2.99e-07	1.79e-06	0.0642

Table 1691: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Ion.channels, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.82e-02	3.21e-02	-0.568	0.574	-8.37e-02	4.73e-02	0.0000
L3.Ion.channels	4.81e-07	6.95e-07	0.692	0.494	-9.39e-07	1.90e-06	0.0152

Table 1692: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Isoflavonoid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.01030	0.01789	-0.576	0.5690	-0.046845	0.0262	0.000
L3.Isoflavonoid.biosynthesis	0.00559	0.00265	2.112	0.0432	0.000184	0.0110	0.126

Table 1693: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Isoquinoline.alkaloid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.34e-02	2.51e-02	-2.13	0.04147	-1.05e-01	-2.20e-03	0.000
L3.Isoquinoline.alkaloid.biosynthesis	1.05e-06	3.71e-07	2.82	0.00847	2.88e-07	1.81e-06	0.204

Table 1694: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Leishmaniasis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1695: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Leukocyte.transendothelial.migration, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1696: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Limonene.and.pinene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.53e-02	2.25e-02	-2.46	0.01996	-1.01e-01	-9.35e-03	0.000
L3.Limonene.and.pinene.degradation	5.90e-07	1.72e-07	3.42	0.00181	2.38e-07	9.42e-07	0.274

Table 1697: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Linoleic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.90e-02	3.35e-02	-2.35	0.0253	-1.47e-01	-1.05e-02	0.000
L3.Linoleic.acid.metabolism	2.13e-06	7.87e-07	2.71	0.0111	5.22e-07	3.74e-06	0.191

Table 1698: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Lipid.biosynthesis.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.53e-02	3.36e-02	-1.95	0.0612	-1.34e-01	3.26e-03	0.000
L3.Lipid.biosynthesis.proteins	1.29e-07	5.72e-08	2.26	0.0313	1.24e-08	2.46e-07	0.141

Table 1699: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Lipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.77e-02	2.40e-02	-1.99	0.0562	-9.68e-02	1.34e-03	0.000
L3.Lipid.metabolism	3.69e-07	1.35e-07	2.73	0.0104	9.35e-08	6.45e-07	0.194

Table 1700: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Lipoic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.17e-02	3.14e-02	-0.691	0.495	-8.59e-02	4.25e-02	0.0000
L3.Lipoic.acid.metabolism	4.43e-07	5.23e-07	0.848	0.403	-6.24e-07	1.51e-06	0.0227

Table 1701: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Lipopolysaccharide.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.00e-02	2.34e-02	-1.71	0.0982	-8.78e-02	7.86e-03	0.000
L3.Lipopolysaccharide.biosynthesis	1.52e-07	6.20e-08	2.46	0.0201	2.56e-08	2.79e-07	0.163

Table 1702: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Lipopolysaccharide.biosynthesis.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.24e-02	2.48e-02	-1.71	0.0977	-9.30e-02	8.25e-03	0.000
L3.Lipopolysaccharide.biosynthesis.proteins	9.75e-08	4.16e-08	2.34	0.0259	1.25e-08	1.83e-07	0.151

Table 1703: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Long.term.depression, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1704: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Long.term.potentiation, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1705: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Lysine.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.07e-02	3.61e-02	-2.51	0.01770	-1.64e-01	-1.69e-02	0.000
L3.Lysine.biosynthesis	1.45e-07	5.15e-08	2.82	0.00849	4.00e-08	2.51e-07	0.204

Table 1706: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Lysine.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.85e-02	2.21e-02	-2.20	0.03587	-9.36e-02	-3.42e-03	0.000
L3.Lysine.degradation	3.17e-07	9.97e-08	3.18	0.00342	1.13e-07	5.20e-07	0.246

Table 1707: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Lysosome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.98e-02	3.06e-02	0.646	0.523	-4.28e-02	8.24e-02	0.0000
L3.Lysosome	-2.00e-07	2.49e-07	-0.804	0.428	-7.08e-07	3.08e-07	0.0204

Table 1708: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.MAPK.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1709: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.MAPK.signaling.pathway. . . yeast, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.31e-02	3.63e-02	-1.74	0.0924	-1.37e-01	1.10e-02	0.000
L3.MAPK.signaling.pathway. . . yeast	1.41e-06	7.12e-07	1.98	0.0570	-4.48e-08	2.86e-06	0.112

Table 1710: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Measles, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1711: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Meiosis. . . yeast, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.80e-03	2.05e-02	0.331	0.743	-3.52e-02	4.88e-02	0.0000
L3.Meiosis. . . yeast	-2.14e-06	2.95e-06	-0.726	0.473	-8.17e-06	3.88e-06	0.0167

Table 1712: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Melanogenesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.07e-02	1.87e-02	-0.573	0.5708	-4.88e-02	0.027405	0.0000
L3.Melanogenesis	7.74e-05	4.48e-05	1.727	0.0945	-1.41e-05	0.000169	0.0878

Table 1713: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Membrane.and.intracellular.structural.molecules, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.42e-02	2.52e-02	-1.75	0.0900	-9.57e-02	7.32e-03	0.0
L3.Membrane.and.intracellular.structural.molecules	7.80e-08	3.30e-08	2.36	0.0247	1.06e-08	1.45e-07	0.1

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Table 1714: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Metabolism.of.cofactors.and.vitamins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.14e-02	2.40e-02	-2.14	0.04070	-1.01e-01	-2.32e-03	0.000
L3.Metabolism.of.cofactors.and.vitamins	3.63e-07	1.25e-07	2.91	0.00677	1.08e-07	6.18e-07	0.214

Table 1715: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Metabolism.of.xenobiotics.by.cytochrome.P450, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.58e-02	2.25e-02	-1.15	0.2606	-7.18e-02	2.02e-02	0.00
L3.Metabolism.of.xenobiotics.by.cytochrome.P450	5.40e-07	2.96e-07	1.82	0.0781	-6.45e-08	1.15e-06	0.09

Table 1716: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Methane.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.00e-02	3.37e-02	-2.37	0.0243	-1.49e-01	-1.11e-02	0.000
L3.Methane.metabolism	8.09e-08	2.97e-08	2.72	0.0107	2.02e-08	1.42e-07	0.193

Table 1717: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Mineral.absorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.17e-03	2.27e-02	-0.184	0.856	-5.06e-02	4.22e-02	0.00000
L3.Mineral.absorption	2.38e-06	7.59e-06	0.314	0.756	-1.31e-05	1.79e-05	0.00316

Table 1718: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Mismatch.repair, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.63e-02	3.92e-02	-2.46	0.020	-1.76e-01	-1.63e-02	0.000
L3.Mismatch.repair	1.42e-07	5.25e-08	2.71	0.011	3.51e-08	2.50e-07	0.192

Table 1719: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.N.Glycan.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.59e-03	2.48e-02	0.266	0.792	-4.4e-02	5.71e-02	0.00000
L3.N.Glycan.biosynthesis	-4.72e-07	1.19e-06	-0.398	0.694	-2.9e-06	1.95e-06	0.00508

Table 1720: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.NOD.like.receptor.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.84e-02	2.53e-02	-3.50	0.001491	-1.40e-01	-3.68e-02	0.000
L3.NOD.like.receptor.signaling.pathway	3.49e-06	8.15e-07	4.27	0.000179	1.82e-06	5.15e-06	0.371

Table 1721: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Naphthalene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.49e-02	3.44e-02	-2.18	0.0374	-1.45e-01	-4.68e-03	0.000
L3.Naphthalene.degradation	5.98e-07	2.39e-07	2.50	0.0183	1.09e-07	1.09e-06	0.167

Table 1722: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Neuroactive.ligand.receptor.interaction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1723: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Neurotrophin.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1724: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Nicotinate.and.nicotinamide.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.85e-02	3.27e-02	-2.40	0.0229	-1.45e-01	-1.17e-02	0.000
L3.Nicotinate.and.nicotinamide.metabolism	2.12e-07	7.65e-08	2.78	0.0094	5.61e-08	3.69e-07	0.199

Table 1725: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Nitrogen.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.89e-02	2.81e-02	-2.1	0.0446	-1.16e-01	-1.51e-03	0.000
L3.Nitrogen.metabolism	8.49e-08	3.26e-08	2.6	0.0142	1.83e-08	1.52e-07	0.179

Table 1726: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Nitrotoluene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.53e-02	1.98e-02	-3.30	2.52e-03	-1.06e-01	-2.49e-02	0.000
L3.Nitrotoluene.degradation	1.02e-06	2.18e-07	4.67	5.88e-05	5.74e-07	1.47e-06	0.413

Table 1727: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Non.homologous.end.joining, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.50e-02	2.04e-02	-0.736	0.467	-5.68e-02	2.67e-02	0.0000
L3.Non.homologous.end.joining	1.32e-05	8.84e-06	1.498	0.145	-4.81e-06	3.13e-05	0.0675

Table 1728: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Notch.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.0158	0.0184	-0.856	0.3986	-0.05338	0.0218	0.000
L3.Notch.signaling.pathway	0.0631	0.0278	2.266	0.0308	0.00622	0.1199	0.142

Table 1729: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Novobiocin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.32e-02	2.88e-02	-2.89	0.00713	-1.42e-01	-2.44e-02	0.000
L3.Novobiocin.biosynthesis	7.61e-07	2.21e-07	3.44	0.00174	3.09e-07	1.21e-06	0.276

Table 1730: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Nucleotide.excision.repair, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.32e-02	4.3e-02	-2.17	0.0383	-1.81e-01	-5.35e-03	0.000
L3.Nucleotide.excision.repair	3.07e-07	1.3e-07	2.36	0.0251	4.11e-08	5.73e-07	0.152

Table 1731: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Nucleotide.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.47e-02	2.24e-02	-1.55	0.1326	-8.05e-02	1.11e-02	0.000
L3.Nucleotide.metabolism	3.97e-07	1.68e-07	2.36	0.0251	5.32e-08	7.41e-07	0.152

Table 1732: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Olfactory.transduction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1733: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.One.carbon.pool.by.folate, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.13e-02	4.13e-02	-1.73	0.0945	-1.56e-01	1.30e-02	0.000
L3.One.carbon.pool.by.folate	1.39e-07	7.30e-08	1.90	0.0665	-1.01e-08	2.88e-07	0.105

Table 1734: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Oocyte.meiosis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1735: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Other.glycan.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.84e-02	3.26e-02	0.873	0.390	-3.81e-02	9.50e-02	0.0000
L3.Other.glycan.degradation	-1.04e-07	9.92e-08	-1.050	0.302	-3.07e-07	9.85e-08	0.0343

Table 1736: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Other.ion.coupled.transporters, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.07e-02	2.53e-02	-2.39	0.02307	-1.12e-01	-8.94e-03	0.000
L3.Other.ion.coupled.transporters	4.57e-08	1.48e-08	3.10	0.00423	1.56e-08	7.59e-08	0.236

Table 1737: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Other.transporters, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.92e-02	2.53e-02	-2.74	0.01021	-1.21e-01	-1.77e-02	0.000
L3.Other.transporters	2.98e-07	8.57e-08	3.48	0.00155	1.23e-07	4.74e-07	0.281

Table 1738: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Other.types.of.O.glycan.biosynthesis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1739: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Others, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.87e-02	3.04e-02	-2.26	0.0312	-1.31e-01	-6.63e-03	0.00
L3.Others	7.11e-08	2.64e-08	2.69	0.0114	1.72e-08	1.25e-07	0.19

Table 1740: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Oxidative.phosphorylation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.72e-02	3.23e-02	-2.70	0.01125	-1.53e-01	-2.13e-02	0.000
L3.Oxidative.phosphorylation	9.95e-08	3.20e-08	3.11	0.00405	3.42e-08	1.65e-07	0.238

Table 1741: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.PPAR.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.37e-02	3.93e-02	-0.603	0.551	-1.04e-01	5.65e-02	0.0000
L3.PPAR.signaling.pathway	3.13e-07	4.59e-07	0.681	0.501	-6.25e-07	1.25e-06	0.0148

Table 1742: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Pancreatic.cancer, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1743: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Pancreatic.secretion, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1744: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Pantothenate.and.CoA.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.48e-02	3.48e-02	-2.15	0.0397	-1.46e-01	-3.78e-03	0.000
L3.Pantothenate.and.CoA.biosynthesis	1.45e-07	5.88e-08	2.46	0.0200	2.44e-08	2.65e-07	0.163

Table 1745: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Parkinson.s.disease, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.28e-02	1.89e-02	-0.675	0.5051	-5.14e-02	2.59e-02	0.0000
L3.Parkinson.s.disease	2.02e-05	1.12e-05	1.798	0.0822	-2.75e-06	4.32e-05	0.0944

Table 1746: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Pathogenic.Escherichia.coli.infection, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00541	0.019	-0.284	0.778	-0.04426	0.0334	0.000
L3.Pathogenic.Escherichia.coli.infection	0.00385	0.004	0.963	0.343	-0.00431	0.0120	0.029

Table 1747: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Pathways.in.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.03e-02	2.26e-02	-3.56	1.27e-03	-1.26e-01	-3.42e-02	0.000
L3.Pathways.in.cancer	2.38e-06	5.21e-07	4.57	7.84e-05	1.32e-06	3.44e-06	0.402

Table 1748: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Penicillin.and.cephalosporin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.76e-03	2.97e-02	0.295	0.77	-5.19e-02	6.95e-02	0.00000
L3.Penicillin.and.cephalosporin.biosynthesis	-2.58e-07	6.86e-07	-0.375	0.71	-1.66e-06	1.14e-06	0.00453

Table 1749: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Pentose.and.glucuronate.interconversions, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.27e-02	2.43e-02	-1.76	0.0886	-9.23e-02	6.85e-03	0.000
L3.Pentose.and.glucuronate.interconversions	8.83e-08	3.61e-08	2.44	0.0206	1.45e-08	1.62e-07	0.162

Table 1750: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Pentose.phosphate.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.21e-02	3.04e-02	-2.37	0.02441	-1.34e-01	-9.97e-03	0.000
L3.Pentose.phosphate.pathway	9.37e-08	3.33e-08	2.82	0.00853	2.57e-08	1.62e-07	0.204

Table 1751: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Peptidases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.45e-02	3.36e-02	-2.51	0.01758	-1.53e-01	-1.58e-02	0.000
L3.Peptidases	4.99e-08	1.74e-08	2.88	0.00736	1.45e-08	8.53e-08	0.211

Table 1752: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Peptidoglycan.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.54e-02	3.94e-02	-1.66	0.1072	-1.46e-01	1.50e-02	0.0000
L3.Peptidoglycan.biosynthesis	9.23e-08	4.98e-08	1.85	0.0738	-9.45e-09	1.94e-07	0.0997

Table 1753: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Peroxisome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.37e-02	3.49e-02	-0.965	0.342	-1.05e-01	3.76e-02	0.0000
L3.Peroxisome	2.32e-07	2.05e-07	1.127	0.268	-1.88e-07	6.51e-07	0.0394

Table 1754: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Pertussis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.16e-02	1.96e-02	-1.10	0.2783	-6.15e-02	1.83e-02	0.000
L3.Pertussis	2.38e-07	1.06e-07	2.26	0.0314	2.27e-08	4.54e-07	0.141

Table 1755: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Phagosome, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1756: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Phenylalanine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.09e-02	2.13e-02	-1.92	0.06443	-8.45e-02	2.61e-03	0.000
L3.Phenylalanine.metabolism	2.17e-07	7.32e-08	2.96	0.00594	6.73e-08	3.66e-07	0.221

Table 1757: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-6.36e-02	3.63e-02	-1.75	0.0902	-1.38e-01	1.06e-02
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis	9.54e-08	4.79e-08	1.99	0.0555	-2.40e-09	1.93e-07

Table 1758: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Phenylpropanoid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.20e-02	2.8e-02	-1.14	0.261	-8.92e-02	2.51e-02	0.0000
L3.Phenylpropanoid.biosynthesis	2.22e-07	1.5e-07	1.48	0.148	-8.36e-08	5.27e-07	0.0663

Table 1759: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Phosphatidylinositol.signaling.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.76e-02	3.88e-02	-1.49	0.148	-1.37e-01	2.16e-02	0.0000
L3.Phosphatidylinositol.signaling.system	6.18e-07	3.70e-07	1.67	0.105	-1.38e-07	1.37e-06	0.0825

Table 1760: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Phosphonate.and.phosphinate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.57e-02	2.89e-02	-1.93	0.0636	-1.15e-01	3.36e-03	0.000
L3.Phosphonate.and.phosphinate.metabolism	7.77e-07	3.27e-07	2.38	0.0241	1.09e-07	1.45e-06	0.154

Table 1761: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Phosphotransferase.system..PTS., df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.11e-02	2.35e-02	-2.17	0.03781	-9.9e-02	-3.07e-03	0.000
L3.Phosphotransferase.system..PTS.	5.65e-08	1.88e-08	3.00	0.00542	1.8e-08	9.49e-08	0.225

Table 1762: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Photosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.21e-02	4.28e-02	-1.92	0.0647	-1.69e-01	5.31e-03	0.000
L3.Photosynthesis	2.88e-07	1.38e-07	2.10	0.0447	7.35e-09	5.69e-07	0.124

Table 1763: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Photosynthesis. . . antenna.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.006158	0.021183	-0.291	0.773	-0.04942	0.03710	0.0000
L3.Photosynthesis. . . antenna.proteins	0.000535	0.000921	0.582	0.565	-0.00134	0.00242	0.0108

Table 1764: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Photosynthesis.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.55e-02	4.15e-02	-2.06	0.0484	-1.7e-01	-6.21e-04	0.000
L3.Photosynthesis.proteins	2.95e-07	1.31e-07	2.26	0.0315	2.8e-08	5.62e-07	0.141

Table 1765: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Phototransduction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1766: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Phototransduction. . . fly, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1767: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Plant.pathogen.interaction, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.03e-01	2.88e-02	-3.59	0.001154	-1.62e-01	-4.46e-02	0.00
L3.Plant.pathogen.interaction	9.44e-07	2.26e-07	4.18	0.000234	4.82e-07	1.41e-06	0.36

Table 1768: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Polycyclic.aromatic.hydrocarbon.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.61e-02	4.04e-02	-1.88	0.0693	-1.59e-01	6.40e-03	0.000
L3.Polycyclic.aromatic.hydrocarbon.degradation	8.20e-07	3.94e-07	2.08	0.0459	1.61e-08	1.62e-06	0.123

Table 1769: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Polyketide.sugar.unit.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.53e-02	3.87e-02	0.394	0.696	-6.37e-02	9.43e-02	0.00000
L3.Polyketide.sugar.unit.biosynthesis	-1.03e-07	2.30e-07	-0.448	0.657	-5.74e-07	3.67e-07	0.00644

Table 1770: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Pores.ion.channels, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.86e-02	2.41e-02	-1.60	0.1202	-8.79e-02	1.07e-02	0.000
L3.Pores.ion.channels	8.98e-08	3.97e-08	2.26	0.0312	8.66e-09	1.71e-07	0.141

Table 1771: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Porphyrin.and.chlorophyll.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.06e-02	2.56e-02	-2.76	0.00977	-1.23e-01	-1.83e-02	0.000
L3.Porphyrin.and.chlorophyll.metabolism	9.08e-08	2.61e-08	3.48	0.00156	3.75e-08	1.44e-07	0.281

Table 1772: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Prenyltransferases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.01e-02	3.85e-02	-2.34	0.0259	-1.69e-01	-1.16e-02	0.000
L3.Prenyltransferases	3.56e-07	1.37e-07	2.60	0.0143	7.65e-08	6.36e-07	0.179

Table 1773: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Primary.bile.acid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.30e-02	3.63e-02	-0.634	0.531	-9.71e-02	5.11e-02	0.0000
L3.Primary.bile.acid.biosynthesis	1.04e-06	1.42e-06	0.734	0.468	-1.85e-06	3.93e-06	0.0171

Table 1774: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Primary.immunodeficiency, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.56e-02	3.81e-02	-1.98	0.0565	-1.54e-01	2.24e-03	0.000
L3.Primary.immunodeficiency	1.35e-06	6.07e-07	2.22	0.0342	1.07e-07	2.59e-06	0.137

Table 1775: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Prion.diseases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.78e-02	1.81e-02	-2.10	0.0446	-7.47e-02	-9.8e-04	0.000
L3.Prion.diseases	5.74e-06	1.50e-06	3.83	0.0006	2.68e-06	8.8e-06	0.322

Table 1776: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Progesterone.mediated.oocyte.maturation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.93e-02	2.38e-02	-3.75	7.46e-04	-1.38e-01	-4.07e-02	0.000
L3.Progesterone.mediated.oocyte.maturation	3.80e-06	8.16e-07	4.65	6.19e-05	2.13e-06	5.46e-06	0.411

Table 1777: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Propanoate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.30e-02	2.80e-02	-2.25	0.03188	-1.20e-01	-5.84e-03	0.0
L3.Propanoate.metabolism	1.26e-07	4.54e-08	2.78	0.00927	3.35e-08	2.19e-07	0.2

Table 1778: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Prostate.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.63e-02	2.50e-02	-3.05	0.004729	-1.27e-01	-2.52e-02	0.000
L3.Prostate.cancer	3.02e-06	7.89e-07	3.83	0.000605	1.41e-06	4.64e-06	0.321

Table 1779: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Proteasome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.08e-01	3.63e-02	-2.98	0.00563	-1.83e-01	-3.42e-02	0.000
L3.Proteasome	3.78e-06	1.14e-06	3.31	0.00242	1.45e-06	6.11e-06	0.261

Table 1780: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Protein.digestion.and.absorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.88e-02	2.55e-02	1.13	0.268	-2.33e-02	8.09e-02	0.0000
L3.Protein.digestion.and.absorption	-1.69e-06	1.08e-06	-1.57	0.126	-3.89e-06	5.05e-07	0.0739

Table 1781: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Protein.export, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.32e-02	4.03e-02	-1.82	0.0793	-1.56e-01	9.10e-03	0.000
L3.Protein.export	1.40e-07	6.94e-08	2.01	0.0533	-2.11e-09	2.81e-07	0.115

Table 1782: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Protein.folding.and.associated.processing, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.03e-02	2.96e-02	-2.04	0.0505	-1.21e-01	1.52e-04	0.000
L3.Protein.folding.and.associated.processing	9.73e-08	3.93e-08	2.48	0.0192	1.70e-08	1.78e-07	0.165

Table 1783: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Protein.kinases, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.54e-02	2.66e-02	-1.71	0.0983	-9.97e-02	8.94e-03	0.000
L3.Protein.kinases	1.48e-07	6.65e-08	2.23	0.0336	1.23e-08	2.84e-07	0.138

Table 1784: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Protein.processing.in.endoplasmic.reticulum, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.27e-02	3.21e-02	-1.64	0.1105	-1.18e-01	1.27e-02	0.00
L3.Protein.processing.in.endoplasmic.reticulum	1.30e-06	6.63e-07	1.96	0.0597	-5.65e-08	2.65e-06	0.11

Table 1785: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Proximal.tubule.bicarbonate.reclamation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.24e-02	2.2e-02	-1.47	0.1506	-7.72e-02	1.25e-02	0.000
L3.Proximal.tubule.bicarbonate.reclamation	1.28e-06	5.5e-07	2.33	0.0269	1.56e-07	2.40e-06	0.149

Table 1786: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Purine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.65e-02	3.68e-02	-2.08	0.0460	-1.52e-01	-1.46e-03	0.000
L3.Purine.metabolism	3.85e-08	1.64e-08	2.35	0.0257	5.00e-09	7.21e-08	0.151

Table 1787: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Pyrimidine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.05e-02	3.93e-02	-2.05	0.0496	-1.61e-01	-1.61e-04	0.000
L3.Pyrimidine.metabolism	5.19e-08	2.28e-08	2.27	0.0305	5.22e-09	9.85e-08	0.143

Table 1788: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Pyruvate.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.79e-02	3.02e-02	-1.92	0.0645	-1.19e-01	3.71e-03	0.000
L3.Pyruvate.metabolism	6.01e-08	2.59e-08	2.32	0.0272	7.25e-09	1.13e-07	0.148

Table 1789: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.RIG.I.like.receptor.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.35e-02	2.18e-02	-1.08	0.2902	-6.80e-02	2.11e-02	0.0000
L3.RIG.I.like.receptor.signaling.pathway	1.63e-05	9.02e-06	1.81	0.0807	-2.12e-06	3.47e-05	0.0954

Table 1790: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.RNA.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.56e-02	3.83e-02	-2.24	0.0330	-1.64e-01	-7.40e-03	0.000
L3.RNA.degradation	2.30e-07	9.23e-08	2.49	0.0187	4.11e-08	4.18e-07	0.166

Table 1791: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.RNA.polymerase, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.27e-02	4.05e-02	-1.55	0.1323	-1.45e-01	2.01e-02	0.0000
L3.RNA.polymerase	4.34e-07	2.53e-07	1.72	0.0961	-8.20e-08	9.50e-07	0.0869

Table 1792: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.RNA.transport, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.26e-02	3.27e-02	-1.91	0.0651	-1.29e-01	4.17e-03	0.00
L3.RNA.transport	6.29e-07	2.80e-07	2.25	0.0323	5.69e-08	1.20e-06	0.14

Table 1793: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Regulation.of.actin.cytoskeleton, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1794: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Renal.cell.carcinoma, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.57e-02	2.05e-02	-1.74	0.09175	-7.76e-02	6.16e-03	0.000
L3.Renal.cell.carcinoma	3.49e-06	1.21e-06	2.88	0.00726	1.02e-06	5.97e-06	0.211

Table 1795: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Renin.angiotensin.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.006548	0.017978	-0.364	0.7183	-0.043264	0.030168	0.0000
L3.Renin.angiotensin.system	0.000355	0.000204	1.743	0.0916	-0.000061	0.000771	0.0893

Table 1796: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Replication..recombination.and.repair.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.86e-02	3.04e-02	-3.25	0.002854	-1.61e-01	-3.66e-02	0.0
L3.Replication..recombination.and.repair.proteins	1.52e-07	4.05e-08	3.75	0.000746	6.94e-08	2.35e-07	0.3

Table 1797: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Restriction.enzyme, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.16e-02	3.36e-02	-1.24	0.225	-1.10e-01	2.69e-02	0.0000
L3.Restriction.enzyme	2.70e-07	1.85e-07	1.46	0.154	-1.07e-07	6.48e-07	0.0646

Table 1798: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Retinol.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.18e-02	2.62e-02	-0.834	0.411	-7.53e-02	3.16e-02	0.000
L3.Retinol.metabolism	6.02e-07	5.23e-07	1.152	0.258	-4.66e-07	1.67e-06	0.041

Table 1799: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Rheumatoid.arthritis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1800: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Riboflavin.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.81e-02	2.58e-02	-2.64	0.01295	-1.21e-01	-1.55e-02	0.000
L3.Riboflavin.metabolism	3.33e-07	9.96e-08	3.34	0.00226	1.29e-07	5.36e-07	0.264

Table 1801: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Ribosome, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.02e-02	4.15e-02	-1.93	0.0628	-1.65e-01	4.57e-03	0.000
L3.Ribosome	4.20e-08	1.98e-08	2.12	0.0421	1.60e-09	8.25e-08	0.127

Table 1802: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Ribosome.Biogenesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.86e-02	3.41e-02	-2.31	0.0281	-1.48e-01	-9.02e-03	0.000
L3.Ribosome.Biogenesis	6.49e-08	2.45e-08	2.64	0.0129	1.47e-08	1.15e-07	0.184

Table 1803: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Ribosome.biogenesis.in.eukaryotes, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.01e-02	3.70e-02	-1.89	0.0679	-1.46e-01	5.48e-03	0.000
L3.Ribosome.biogenesis.in.eukaryotes	1.62e-06	7.56e-07	2.14	0.0407	7.30e-08	3.16e-06	0.129

Table 1804: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Salivary.secretion, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1805: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Secondary.bile.acid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.10e-02	3.63e-02	-0.580	0.566	-9.51e-02	5.30e-02	0.0000
L3.Secondary.bile.acid.biosynthesis	9.63e-07	1.43e-06	0.672	0.507	-1.96e-06	3.89e-06	0.0143

Table 1806: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Secretion.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.67e-02	2.44e-02	-1.92	0.0649	-9.65e-02	3.07e-03	0.000
L3.Secretion.system	3.58e-08	1.37e-08	2.62	0.0136	7.92e-09	6.37e-08	0.181

Table 1807: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Selenocompound.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.73e-02	3.15e-02	-2.14	0.0408	-1.32e-01	-3.01e-03	0.000
L3.Selenocompound.metabolism	1.91e-07	7.55e-08	2.52	0.0171	3.64e-08	3.45e-07	0.171

Table 1808: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Sesquiterpenoid.biosynthesis, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1809: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Shigellosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.0256	0.01862	-1.37	0.17975	-0.06362	0.0125	0.00
L3.Shigellosis	0.0136	0.00476	2.87	0.00752	0.00392	0.0234	0.21

Table 1810: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Signal.transduction.mechanisms, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.65e-02	2.85e-02	-2.68	0.01180	-1.35e-01	-1.82e-02	0.000
L3.Signal.transduction.mechanisms	1.79e-07	5.55e-08	3.23	0.00301	6.58e-08	2.92e-07	0.252

Table 1811: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Small.cell.lung.cancer, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.002361	0.020387	0.116	0.909	-0.0393	0.0440	0.00000
L3.Small.cell.lung.cancer	-0.000199	0.000734	-0.271	0.788	-0.0017	0.0013	0.00236

Table 1812: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Sphingolipid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.05e-03	3.25e-02	0.186	0.853	-6.02e-02	7.23e-02	0.00000
L3.Sphingolipid.metabolism	-3.52e-08	1.56e-07	-0.226	0.822	-3.53e-07	2.83e-07	0.00165

Table 1813: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Spliceosome, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1814: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Sporulation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.39e-02	2.20e-02	-2.45	0.02022	-9.89e-02	-9.02e-03	0.00
L3.Sporulation	1.68e-07	4.84e-08	3.47	0.00158	6.93e-08	2.67e-07	0.28

Table 1815: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Staphylococcus.aureus.infection, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.20e-02	2.19e-02	1.01	0.323	-2.27e-02	6.68e-02	0.0000
L3.Staphylococcus.aureus.infection	-5.21e-07	3.08e-07	-1.69	0.101	-1.15e-06	1.08e-07	0.0844

Table 1816: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Starch.and.sucrose.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.84e-02	3.24e-02	-1.80	0.0817	-1.25e-01	7.81e-03	0.000
L3.Starch.and.sucrose.metabolism	6.60e-08	3.11e-08	2.13	0.0419	2.58e-09	1.29e-07	0.127

Table 1817: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Steroid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.20e-05	0.020574	0.00253	0.998	-0.041967	0.042071	0.00e+00
L3.Steroid.biosynthesis	-9.69e-07	0.000169	-0.00571	0.995	-0.000347	0.000345	1.05e-06

Table 1818: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Steroid.hormone.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.24e-02	2.28e-02	-0.545	0.590	-5.89e-02	3.41e-02	0.0000
L3.Steroid.hormone.biosynthesis	7.44e-07	8.21e-07	0.906	0.372	-9.32e-07	2.42e-06	0.0258

Table 1819: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-8.15e-03	1.95e-02	-0.419	0.678	-4.79e-02	3.16e-02
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	5.06e-06	4.47e-06	1.132	0.267	-4.07e-06	1.42e-05

Table 1820: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Streptomycin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.86e-02	3.85e-02	-0.483	0.633	-9.71e-02	6.00e-02	0.00000
L3.Streptomycin.biosynthesis	7.27e-08	1.32e-07	0.549	0.587	-1.98e-07	3.43e-07	0.00964

Table 1821: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Styrene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.79e-02	1.87e-02	-0.96	0.3447	-5.60e-02	2.02e-02	0.000
L3.Styrene.degradation	6.62e-07	2.85e-07	2.32	0.0274	7.89e-08	1.24e-06	0.148

Table 1822: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Sulfur.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.00e-02	3.14e-02	-1.91	0.0654	-1.24e-01	4.06e-03	0.000
L3.Sulfur.metabolism	2.34e-07	1.03e-07	2.28	0.0300	2.43e-08	4.45e-07	0.143

Table 1823: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Sulfur.relay.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.95e-02	2.39e-02	-2.49	0.01865	-1.08e-01	-1.07e-02	0.000
L3.Sulfur.relay.system	2.40e-07	7.24e-08	3.31	0.00243	9.18e-08	3.88e-07	0.261

Table 1824: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Synthesis.and.degradation.of.ketone.bodies, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.78e-02	2.44e-02	-2.37	0.02431	-1.08e-01	-8.04e-03	0.000
L3.Synthesis.and.degradation.of.ketone.bodies	1.66e-06	5.28e-07	3.14	0.00375	5.81e-07	2.74e-06	0.242

Table 1825: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Systemic.lupus.erythematosus, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.18e-02	1.87e-02	-0.627	0.5351	-5.00e-02	0.026522	0.0000
L3.Systemic.lupus.erythematosus	7.99e-05	4.48e-05	1.782	0.0849	-1.17e-05	0.000171	0.0929

Table 1826: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.TGF.beta.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1827: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Taurine.and.hypotaurine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.03e-02	3.45e-02	-1.46	0.155	-1.21e-01	2.02e-02	0.0000
L3.Taurine.and.hypotaurine.metabolism	4.74e-07	2.80e-07	1.70	0.100	-9.72e-08	1.05e-06	0.0848

Table 1828: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Terpenoid.backbone.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.41e-02	3.86e-02	-2.44	0.0208	-1.73e-01	-1.53e-02	0.000
L3.Terpenoid.backbone.biosynthesis	2.10e-07	7.76e-08	2.70	0.0112	5.12e-08	3.68e-07	0.191

Table 1829: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Tetracycline.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.44e-02	3.37e-02	-2.21	0.0352	-1.43e-01	-5.52e-03	0.000
L3.Tetracycline.biosynthesis	5.90e-07	2.32e-07	2.54	0.0165	1.16e-07	1.06e-06	0.172

Table 1830: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Thiamine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.60e-02	3.45e-02	-2.50	0.01830	-1.56e-01	-1.56e-02	0.000
L3.Thiamine.metabolism	2.08e-07	7.32e-08	2.84	0.00809	5.81e-08	3.57e-07	0.206

Table 1831: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Tight.junction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1832: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Toluene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.65e-02	1.97e-02	-1.35	0.188	-6.67e-02	1.37e-02	0.000
L3.Toluene.degradation	2.34e-07	9.17e-08	2.55	0.016	4.69e-08	4.21e-07	0.174

Table 1833: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Toxoplasmosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.002361	0.020387	0.116	0.909	-0.0393	0.0440	0.00000
L3.Toxoplasmosis	-0.000199	0.000734	-0.271	0.788	-0.0017	0.0013	0.00236

Table 1834: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Transcription.factors, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.29e-02	2.43e-02	-2.18	0.03745	-1.03e-01	-3.28e-03	0.000
L3.Transcription.factors	3.01e-08	1.03e-08	2.93	0.00641	9.13e-09	5.11e-08	0.217

Table 1835: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Transcription.machinery, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.29e-02	3.85e-02	-2.42	0.0220	-1.71e-01	-1.44e-02	0.000
L3.Transcription.machinery	1.40e-07	5.24e-08	2.68	0.0119	3.33e-08	2.47e-07	0.188

Table 1836: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Transcription.related.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.42e-02	1.87e-02	-1.29	0.2064	-6.24e-02	1.4e-02	0.000
L3.Transcription.related.proteins	1.66e-06	6.06e-07	2.74	0.0103	4.22e-07	2.9e-06	0.195

Table 1837: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Translation.factors, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.81e-02	3.81e-02	-2.31	0.0278	-1.66e-01	-1.03e-02	0.000
L3.Translation.factors	1.99e-07	7.74e-08	2.57	0.0153	4.11e-08	3.57e-07	0.176

Table 1838: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Translation.proteins, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.44e-02	3.35e-02	-2.51	0.01750	-1.53e-01	-1.58e-02	0.000
L3.Translation.proteins	1.07e-07	3.71e-08	2.88	0.00729	3.10e-08	1.83e-07	0.211

Table 1839: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Transporters, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.58e-02	2.72e-02	-2.05	0.0491	-1.11e-01	-2.28e-04	0.000
L3.Transporters	8.37e-09	3.23e-09	2.59	0.0145	1.78e-09	1.50e-08	0.178

Table 1840: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-7.67e-02	2.42e-02	-3.17	0.003515	-1.26e-01	-2.73e-0
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis	7.48e-07	1.86e-07	4.02	0.000365	3.68e-07	1.13e-0

Table 1841: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Tryptophan.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.57e-02	2.15e-02	-1.66	0.1069	-7.96e-02	8.17e-03	0.000
L3.Tryptophan.metabolism	1.85e-07	7.04e-08	2.63	0.0135	4.11e-08	3.29e-07	0.182

Table 1842: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Tuberculosis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.62e-02	4.37e-02	-1.75	0.0910	-1.65e-01	1.29e-02	0.000
L3.Tuberculosis	6.80e-07	3.57e-07	1.90	0.0664	-4.91e-08	1.41e-06	0.105

Table 1843: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Two.component.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.79e-02	2.34e-02	-2.47	0.01921	-1.06e-01	-1.01e-02	0.000
L3.Two.component.system	4.10e-08	1.23e-08	3.35	0.00222	1.60e-08	6.61e-08	0.265

Table 1844: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Type.I.diabetes.mellitus, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.77e-02	4.37e-02	-1.55	0.132	-1.57e-01	2.16e-02	0.0000
L3.Type.I.diabetes.mellitus	1.65e-06	9.76e-07	1.69	0.101	-3.43e-07	3.64e-06	0.0844

Table 1845: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Type.II.diabetes.mellitus, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.089075	3.26e-02	-2.73	0.01052	-1.56e-01	-2.24e-02	0.00
L3.Type.II.diabetes.mellitus	0.000002	6.38e-07	3.13	0.00386	6.95e-07	3.30e-06	0.24

Table 1846: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Tyrosine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.11e-02	2.74e-02	-2.24	0.03298	-1.17e-01	-5.29e-03	0.000
L3.Tyrosine.metabolism	1.85e-07	6.61e-08	2.80	0.00893	4.98e-08	3.20e-07	0.201

Table 1847: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-3.21e-02	2.27e-02	-1.41	0.1675	-7.85e-02	1.42e-02
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis	1.55e-07	7.19e-08	2.16	0.0388	8.58e-09	3.02e-07

Table 1848: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Ubiquitin.system, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.38e-02	2.21e-02	-0.627	0.536	-5.89e-02	3.12e-02	0.0000
L3.Ubiquitin.system	1.02e-06	9.36e-07	1.094	0.283	-8.88e-07	2.94e-06	0.0372

Table 1849: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.VEGF.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1850: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Valine..leucine.and.isoleucine.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.51e-02	3.79e-02	-1.45	0.157	-1.33e-01	2.24e-02	0.0000
L3.Valine..leucine.and.isoleucine.biosynthesis	8.73e-08	5.32e-08	1.64	0.111	-2.14e-08	1.96e-07	0.0799

Table 1851: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Valine..leucine.and.isoleucine.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.30e-02	2.58e-02	-2.05	0.049	-1.06e-01	-2.40e-04	0.000
L3.Valine..leucine.and.isoleucine.degradation	1.98e-07	7.40e-08	2.68	0.012	4.69e-08	3.49e-07	0.188

Table 1852: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Various.types.of.N.glycan.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00901	0.0210	0.429	0.671	-0.0339	0.0519	0.0000
L3.Various.types.of.N.glycan.biosynthesis	-0.00901	0.0104	-0.865	0.394	-0.0303	0.0123	0.0236

Table 1853: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Vascular.smooth.muscle.contraction, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1854: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Vasopressin.regulated.water.reabsorption, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00334	0.0192	0.174	0.863	-0.0358	0.0425	0.0000
L3.Vasopressin.regulated.water.reabsorption	-0.01336	0.0221	-0.604	0.550	-0.0585	0.0318	0.0116

Table 1855: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Vibrio.cholerae.infection, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.0198	0.0186	-1.07	0.295	-0.05767	0.0181	0.000
L3.Vibrio.cholerae.infection	0.0275	0.0110	2.50	0.018	0.00506	0.0500	0.168

Table 1856: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Vibrio.cholerae.pathogenic.cycle, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.75e-02	2.46e-02	-2.75	0.01006	-1.18e-01	-1.73e-02	0.000
L3.Vibrio.cholerae.pathogenic.cycle	1.02e-06	2.88e-07	3.54	0.00133	4.31e-07	1.61e-06	0.288

Table 1857: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs
L3.Viral.myocarditis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.002361	0.020387	0.116	0.909	-0.0393	0.0440	0.00000
L3.Viral.myocarditis	-0.000199	0.000734	-0.271	0.788	-0.0017	0.0013	0.00236

Table 1858: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Vitamin.B6.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.10e-02	3.00e-02	-1.70	0.0995	-1.12e-01	1.03e-02	0.000
L3.Vitamin.B6.metabolism	3.24e-07	1.56e-07	2.08	0.0464	5.47e-09	6.43e-07	0.122

Table 1859: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Wnt.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.0158	0.0184	-0.856	0.3986	-0.05338	0.0218	0.000
L3.Wnt.signaling.pathway	0.0631	0.0278	2.266	0.0308	0.00622	0.1199	0.142

Table 1860: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Xylene.degradation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.43e-02	2.55e-02	-1.74	0.0927	-9.63e-02	7.79e-03	0.000
L3.Xylene.degradation	6.96e-07	2.99e-07	2.33	0.0268	8.56e-08	1.31e-06	0.149

Table 1861: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.Zeatin.biosynthesis, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.08e-02	4.55e-02	-1.33	0.192	-1.54e-01	3.22e-02	0.0000
L3.Zeatin.biosynthesis	1.43e-06	9.88e-07	1.45	0.157	-5.85e-07	3.45e-06	0.0635

Table 1862: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.alpha.Linolenic.acid.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.05e-02	1.87e-02	-1.09	0.2829	-5.87e-02	1.77e-02	0.000
L3.alpha.Linolenic.acid.metabolism	1.57e-06	6.30e-07	2.49	0.0187	2.80e-07	2.85e-06	0.166

Table 1863: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.beta.Alanine.metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.16e-02	2.28e-02	-2.27	0.03081	-9.81e-02	-5.10e-03	0.000
L3.beta.Alanine.metabolism	2.84e-07	8.93e-08	3.18	0.00342	1.01e-07	4.66e-07	0.246

Table 1864: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.beta.Lactam.resistance, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.68e-03	3.30e-02	0.112	0.912	-6.37e-02	7.11e-02	0.000000
L3.beta.Lactam.resistance	-1.68e-07	1.25e-06	-0.135	0.894	-2.72e-06	2.39e-06	0.000584

Table 1865: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.mRNA.surveillance.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1866: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.mTOR.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	-5.97e-14	0.0181	-3.29e-12	1	-0.037	0.037	0
	NA	NA	NA	NA	NA	NA	0

Table 1867: diversity_vs_picrust_L3_neo: wunifrac.PC.4 vs L3.p53.signaling.pathway, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.002361	0.020387	0.116	0.909	-0.0393	0.0440	0.00000
L3.p53.signaling.pathway	-0.000199	0.000734	-0.271	0.788	-0.0017	0.0013	0.00236

Table 1868: diversity_vs_picrust_L1_yr1: wunifrac.PC.1 vs L1.Cellular.Processes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.16e-02	1.60e-01	0.447	0.660	-2.63e-01	4.06e-01	0.0000
L1.Cellular.Processes	-4.11e-08	7.76e-08	-0.529	0.603	-2.04e-07	1.21e-07	0.0138

Table 1869: diversity_vs_picrust_L1_yr1: wunifrac.PC.1 vs L1.Environmental.Information.Processing, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.39e-01	1.61e-01	0.863	0.399	-1.98e-01	4.76e-01	0.0000
L1.Environmental.Information.Processing	-1.54e-08	1.53e-08	-1.012	0.324	-4.74e-08	1.65e-08	0.0487

Table 1870: diversity_vs_picrust_L1_yr1: wunifrac.PC.1 vs
L1.Genetic.Information.Processing, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.04e-02	1.89e-01	0.478	0.638	-3.05e-01	4.86e-01	0.0000
L1.Genetic.Information.Processing	-7.32e-09	1.36e-08	-0.537	0.598	-3.59e-08	2.12e-08	0.0142

Table 1871: diversity_vs_picrust_L1_yr1: wunifrac.PC.1 vs
L1.Human.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.39e-02	1.93e-01	0.228	0.822	-3.59e-01	4.47e-01	0.00000
L1.Human.Diseases	-9.87e-08	3.88e-07	-0.255	0.802	-9.10e-07	7.13e-07	0.00323

Table 1872: diversity_vs_picrust_L1_yr1: wunifrac.PC.1 vs
L1.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.40e-02	1.95e-01	0.328	0.746	-3.44e-01	4.72e-01	0.00000
L1.Metabolism	-2.05e-09	5.61e-09	-0.366	0.719	-1.38e-08	9.69e-09	0.00665

Table 1873: diversity_vs_picrust_L1_yr1: wunifrac.PC.1 vs
L1.None, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.50e-01	1.64e-01	0.912	0.373	-1.94e-01	4.94e-01	0.0000
L1.None	-1.15e-06	1.09e-06	-1.060	0.303	-3.43e-06	1.12e-06	0.0531

Table 1874: diversity_vs_picrust_L1_yr1: wunifrac.PC.1 vs
L1.Organismal.Systems, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.74e-02	1.97e-01	-0.342	0.736	-4.80e-01	3.46e-01	0.00000
L1.Organismal.Systems	1.44e-07	3.80e-07	0.379	0.709	-6.51e-07	9.39e-07	0.00715

Table 1875: diversity_vs_picrust_L1_yr1: wunifrac.PC.1 vs
L1.Unclassified, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.38e-02	1.93e-01	0.382	0.707	-3.31e-01	4.79e-01	0.000
L1.Unclassified	-8.08e-09	1.90e-08	-0.426	0.675	-4.77e-08	3.16e-08	0.009

Table 1876: diversity_vs_picrust_L1_yr1: wunifrac.PC.2 vs L1.Cellular.Processes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.47e-02	6.58e-02	1.13	0.271	-6.31e-02	2.13e-01	0.0000
L1.Cellular.Processes	-4.29e-08	3.19e-08	-1.34	0.195	-1.10e-07	2.39e-08	0.0828

Table 1877: diversity_vs_picrust_L1_yr1: wunifrac.PC.2 vs L1.Environmental.Information.Processing, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e-01	6.53e-02	1.54	0.1406	-3.63e-02	2.37e-01	0.00
L1.Environmental.Information.Processing	-1.12e-08	6.19e-09	-1.80	0.0874	-2.41e-08	1.80e-09	0.14

Table 1878: diversity_vs_picrust_L1_yr1: wunifrac.PC.2 vs L1.Genetic.Information.Processing, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.22e-02	7.86e-02	1.05	0.309	-8.23e-02	2.47e-01	0.0000
L1.Genetic.Information.Processing	-6.65e-09	5.67e-09	-1.17	0.255	-1.85e-08	5.22e-09	0.0643

Table 1879: diversity_vs_picrust_L1_yr1: wunifrac.PC.2 vs L1.Human.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.33e-02	8.09e-02	0.783	0.443	-1.06e-01	2.33e-01	0.0000
L1.Human.Diseases	-1.42e-07	1.63e-07	-0.875	0.393	-4.83e-07	1.98e-07	0.0369

Table 1880: diversity_vs_picrust_L1_yr1: wunifrac.PC.2 vs L1.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.5e-02	8.14e-02	0.921	0.368	-9.54e-02	2.45e-01	0.00
L1.Metabolism	-2.4e-09	2.34e-09	-1.026	0.318	-7.31e-09	2.50e-09	0.05

Table 1881: diversity_vs_picrust_L1_yr1: wunifrac.PC.2 vs L1.None, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.23e-02	6.8e-02	1.36	0.191	-5.01e-02	2.35e-01	0.00
L1.None	-7.09e-07	4.5e-07	-1.58	0.132	-1.65e-06	2.32e-07	0.11

Table 1882: diversity_vs_picrust_L1_yr1: wunifrac.PC.2 vs L1.Organismal.Systems, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.71e-02	8.41e-02	0.441	0.664	-1.39e-01	2.13e-01	0.0000
L1.Organismal.Systems	-7.93e-08	1.62e-07	-0.489	0.630	-4.18e-07	2.60e-07	0.0118

Table 1883: diversity_vs_picrust_L1_yr1: wunifrac.PC.2 vs L1.Unclassified, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.07e-02	8.04e-02	1.00	0.329	-8.77e-02	2.49e-01	0.0000
L1.Unclassified	-8.82e-09	7.88e-09	-1.12	0.277	-2.53e-08	7.68e-09	0.0589

Table 1884: diversity_vs_picrust_L1_yr1: wunifrac.PC.3 vs L1.Cellular.Processes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.51e-02	4.59e-02	0.546	0.591	-7.1e-02	1.21e-01	0.0000
L1.Cellular.Processes	-1.44e-08	2.23e-08	-0.646	0.526	-6.1e-08	3.22e-08	0.0205

Table 1885: diversity_vs_picrust_L1_yr1: wunifrac.PC.3 vs L1.Environmental.Information.Processing, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.09e-02	4.73e-02	0.442	0.664	-7.80e-02	1.20e-01	0.0000
L1.Environmental.Information.Processing	-2.32e-09	4.48e-09	-0.518	0.611	-1.17e-08	7.05e-09	0.0132

Table 1886: diversity_vs_picrust_L1_yr1: wunifrac.PC.3 vs L1.Genetic.Information.Processing, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.83e-02	5.43e-02	0.520	0.609	-8.55e-02	1.42e-01	0.0000
L1.Genetic.Information.Processing	-2.29e-09	3.92e-09	-0.584	0.566	-1.05e-08	5.92e-09	0.0167

Table 1887: diversity_vs_picrust_L1_yr1: wunifrac.PC.3 vs L1.Human.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.49e-02	5.48e-02	0.636	0.533	-7.99e-02	1.50e-01	0.0000
L1.Human.Diseases	-7.84e-08	1.10e-07	-0.711	0.486	-3.09e-07	1.53e-07	0.0246

Table 1888: diversity_vs_picrust_L1_yr1: wunifrac.PC.3 vs L1.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.87e-02	5.59e-02	0.513	0.614	-8.83e-02	1.46e-01	0.0000
L1.Metabolism	-9.18e-10	1.61e-09	-0.571	0.574	-4.28e-09	2.45e-09	0.0161

Table 1889: diversity_vs_picrust_L1_yr1: wunifrac.PC.3 vs L1.None, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.81e-02	4.85e-02	0.374	0.713	-8.34e-02	1.20e-01	0.00000
L1.None	-1.39e-07	3.20e-07	-0.435	0.669	-8.10e-07	5.31e-07	0.00936

Table 1890: diversity_vs_picrust_L1_yr1: wunifrac.PC.3 vs L1.Organismal.Systems, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.65e-02	5.63e-02	0.649	0.524	-8.12e-02	1.54e-01	0.0000
L1.Organismal.Systems	-7.81e-08	1.08e-07	-0.721	0.480	-3.05e-07	1.49e-07	0.0253

Table 1891: diversity_vs_picrust_L1_yr1: wunifrac.PC.3 vs L1.Unclassified, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.09e-02	5.54e-02	0.558	0.583	-8.50e-02	1.47e-01	0.000
L1.Unclassified	-3.38e-09	5.43e-09	-0.623	0.541	-1.47e-08	7.98e-09	0.019

Table 1892: diversity_vs_picrust_L1_yr1: wunifrac.PC.4 vs L1.Cellular.Processes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.19e-03	3.94e-02	-0.0555	0.956	-8.48e-02	8.04e-02	0.000000
L1.Cellular.Processes	1.26e-09	1.91e-08	0.0657	0.948	-3.88e-08	4.13e-08	0.000216

Table 1893: diversity_vs_picrust_L1_yr1: wunifrac.PC.4 vs L1.Environmental.Information.Processing, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.53e-02	4.03e-02	-0.381	0.708	-9.96e-02	6.89e-02	0.00000
L1.Environmental.Information.Processing	1.70e-09	3.81e-09	0.446	0.660	-6.28e-09	9.69e-09	0.00987

Table 1894: diversity_vs_picrust_L1_yr1: wunifrac.PC.4 vs
L1.Genetic.Information.Processing, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.71e-04	4.66e-02	0.0144	0.989	-9.69e-02	9.83e-02	0.0e+00
L1.Genetic.Information.Processing	-5.43e-11	3.36e-09	-0.0162	0.987	-7.09e-09	6.99e-09	1.3e-05

Table 1895: diversity_vs_picrust_L1_yr1: wunifrac.PC.4 vs
L1.Human.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.10e-03	4.73e-02	-0.0655	0.948	-1.02e-01	9.58e-02	0.000000
L1.Human.Diseases	6.96e-09	9.51e-08	0.0732	0.942	-1.92e-07	2.06e-07	0.000268

Table 1896: diversity_vs_picrust_L1_yr1: wunifrac.PC.4 vs
L1.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.49e-03	4.79e-02	-0.0938	0.926	-1.05e-01	9.58e-02	0.000000
L1.Metabolism	1.44e-10	1.38e-09	0.1045	0.918	-2.74e-09	3.03e-09	0.000546

Table 1897: diversity_vs_picrust_L1_yr1: wunifrac.PC.4 vs
L1.None, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.63e-03	4.14e-02	-0.208	0.837	-9.52e-02	7.80e-02	0.00000
L1.None	6.62e-08	2.73e-07	0.242	0.811	-5.06e-07	6.38e-07	0.00293

Table 1898: diversity_vs_picrust_L1_yr1: wunifrac.PC.4 vs
L1.Organismal.Systems, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.89e-02	4.82e-02	0.391	0.700	-8.21e-02	1.20e-01	0.00000
L1.Organismal.Systems	-4.03e-08	9.29e-08	-0.434	0.669	-2.35e-07	1.54e-07	0.00934

Table 1899: diversity_vs_picrust_L1_yr1: wunifrac.PC.4 vs
L1.Unclassified, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.19e-03	4.75e-02	-0.172	0.865	-1.08e-01	9.13e-02	0.00000
L1.Unclassified	8.95e-10	4.66e-09	0.192	0.850	-8.85e-09	1.06e-08	0.00184

Table 1900: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Amino.Acid.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.30e-02	1.92e-01	0.432	0.670	-3.19e-01	4.84e-01	0.0000
L2.Amino.Acid.Metabolism	-1.33e-08	2.75e-08	-0.483	0.634	-7.08e-08	4.42e-08	0.0115

Table 1901: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Biosynthesis.of.Other.Secondary.Metabolites, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.24e-02	1.92e-01	0.0644	0.949	-3.90e-01	4.15e-01	0.0000
L2.Biosynthesis.of.Other.Secondary.Metabolites	-1.86e-08	2.58e-07	-0.0721	0.943	-5.59e-07	5.22e-07	0.0002

Table 1902: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Cancers, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.40e-02	1.82e-01	0.187	0.854	-3.47e-01	4.15e-01	0.00000
L2.Cancers	-5.42e-07	2.56e-06	-0.212	0.834	-5.89e-06	4.81e-06	0.00224

Table 1903: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Carbohydrate.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.99e-02	1.91e-01	0.261	0.797	-3.50e-01	4.50e-01	0.00000
L2.Carbohydrate.Metabolism	-6.91e-09	2.36e-08	-0.292	0.773	-5.64e-08	4.26e-08	0.00425

Table 1904: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Cardiovascular.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.38e-03	8.81e-02	-0.0724	0.943	-0.190867	0.178105	0.00000
L2.Cardiovascular.Diseases	2.27e-05	6.86e-05	0.3302	0.745	-0.000121	0.000166	0.00542

Table 1905: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Cell.Communication, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 1906: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Cell.Growth.and.Death, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.00e-02	1.90e-01	0.420	0.679	-3.18e-01	4.78e-01	0.000
L2.Cell.Growth.and.Death	-2.55e-07	5.41e-07	-0.471	0.643	-1.39e-06	8.78e-07	0.011

Table 1907: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Cell.Motility, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.30e-02	1.43e-01	0.581	0.568	-2.16e-01	3.82e-01	0.0000
L2.Cell.Motility	-6.86e-08	9.47e-08	-0.724	0.478	-2.67e-07	1.30e-07	0.0255

Table 1908: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Cellular.Processes.and.Signaling, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.21e-02	1.96e-01	0.265	0.794	-3.59e-01	4.63e-01	0.00000
L2.Cellular.Processes.and.Signaling	-1.88e-08	6.38e-08	-0.295	0.771	-1.52e-07	1.15e-07	0.00434

Table 1909: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Circulatory.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.61e-03	0.088597	-0.0746	0.941	-1.92e-01	1.79e-01	0.00000
L2.Circulatory.System	7.16e-06	0.000023	0.3119	0.759	-4.09e-05	5.52e-05	0.00484

Table 1910: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Digestive.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.12e-01	1.77e-01	-1.76	0.0943	-6.84e-01	5.88e-02	0.000
L2.Digestive.System	1.13e-05	5.78e-06	1.96	0.0642	-7.39e-07	2.34e-05	0.162

Table 1911: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Endocrine.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.92e-02	1.99e-01	-0.499	0.623	-5.15e-01	3.17e-01	0.0000
L2.Endocrine.System	5.03e-07	9.10e-07	0.553	0.587	-1.40e-06	2.41e-06	0.0151

Table 1912: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Energy.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.40e-02	1.91e-01	0.388	0.703	-3.26e-01	4.74e-01	0.00000
L2.Energy.Metabolism	-1.91e-08	4.40e-08	-0.434	0.669	-1.11e-07	7.30e-08	0.00933

Table 1913: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Environmental.Adaptation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.18e-02	1.73e-01	0.416	0.682	-2.89e-01	4.33e-01	0.0000
L2.Environmental.Adaptation	-7.25e-07	1.51e-06	-0.479	0.637	-3.89e-06	2.44e-06	0.0114

Table 1914: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Enzyme.Families, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.99e-02	1.91e-01	0.419	0.680	-3.19e-01	4.79e-01	0.0000
L2.Enzyme.Families	-5.74e-08	1.22e-07	-0.469	0.645	-3.14e-07	1.99e-07	0.0109

Table 1915: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Excretory.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.61e-01	1.40e-01	-1.86	0.0786	-5.54e-01	3.28e-02	0.000
L2.Excretory.System	1.87e-05	8.42e-06	2.22	0.0386	1.09e-06	3.63e-05	0.198

Table 1916: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Folding..Sorting.and.Degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.87e-02	1.99e-01	0.245	0.809	-3.67e-01	4.65e-01	0.00000
L2.Folding..Sorting.and.Degradation	-3.12e-08	1.15e-07	-0.272	0.789	-2.72e-07	2.09e-07	0.00368

Table 1917: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Genetic.Information.Processing, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.16e-01	1.89e-01	0.613	0.547	-2.80e-01	5.11e-01	0.000
L2.Genetic.Information.Processing	-7.09e-08	1.03e-07	-0.686	0.501	-2.87e-07	1.45e-07	0.023

Table 1918: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs
L2.Glycan.Biosynthesis.and.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.21e-01	2.21e-01	-0.548	0.590	-5.84e-01	3.42e-01	0.0000
L2.Glycan.Biosynthesis.and.Metabolism	7.48e-08	1.26e-07	0.594	0.559	-1.89e-07	3.38e-07	0.0174

Table 1919: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs
L2.Immune.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.35e-03	1.95e-01	0.0377	0.970	-4.01e-01	4.16e-01	0.00e+00
L2.Immune.System	-1.31e-07	3.12e-06	-0.0420	0.967	-6.66e-06	6.39e-06	8.82e-05

Table 1920: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs
L2.Immune.System.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.59e-02	1.88e-01	0.190	0.851	-3.58e-01	4.30e-01	0.00000
L2.Immune.System.Diseases	-1.16e-06	5.39e-06	-0.214	0.833	-1.24e-05	1.01e-05	0.00229

Table 1921: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs
L2.Infectious.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.78e-02	1.95e-01	0.245	0.809	-3.60e-01	4.56e-01	0.00000
L2.Infectious.Diseases	-2.10e-07	7.70e-07	-0.273	0.788	-1.82e-06	1.40e-06	0.00372

Table 1922: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs
L2.Lipid.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.82e-02	1.92e-01	0.199	0.845	-3.64e-01	4.40e-01	0.00000
L2.Lipid.Metabolism	-2.10e-08	9.43e-08	-0.222	0.826	-2.18e-07	1.76e-07	0.00247

Table 1923: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs
L2.Membrane.Transport, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.43e-01	1.58e-01	0.903	0.378	-1.88e-01	4.74e-01	0.0000
L2.Membrane.Transport	-1.82e-08	1.71e-08	-1.064	0.301	-5.39e-08	1.76e-08	0.0536

Table 1924: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Metabolic.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.17e-02	1.99e-01	-0.0586	0.954	-4.28e-01	4.05e-01	0.000000
L2.Metabolic.Diseases	1.87e-07	2.87e-06	0.0650	0.949	-5.83e-06	6.20e-06	0.000211

Table 1925: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.13e-02	1.94e-01	0.368	0.717	-3.35e-01	4.77e-01	0.00000
L2.Metabolism	-4.40e-08	1.07e-07	-0.410	0.686	-2.68e-07	1.80e-07	0.00834

Table 1926: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Metabolism.of.Cofactors.and.Vitamins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.33e-02	1.97e-01	0.473	0.641	-3.19e-01	5.06e-01	0.0000
L2.Metabolism.of.Cofactors.and.Vitamins	-3.31e-08	6.29e-08	-0.526	0.605	-1.65e-07	9.86e-08	0.0136

Table 1927: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Metabolism.of.Other.Amino.Acids, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.36e-02	1.97e-01	0.272	0.789	-3.59e-01	4.66e-01	0.00000
L2.Metabolism.of.Other.Amino.Acids	-5.48e-08	1.81e-07	-0.302	0.766	-4.34e-07	3.25e-07	0.00455

Table 1928: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Metabolism.of.Terpenoids.and.Polyketides, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.77e-02	2.01e-01	0.337	0.740	-3.53e-01	4.89e-01	0.00000
L2.Metabolism.of.Terpenoids.and.Polyketides	-6.65e-08	1.78e-07	-0.373	0.714	-4.40e-07	3.07e-07	0.00689

Table 1929: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs L2.Nervous.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.88e-02	1.92e-01	-0.461	0.650	-4.92e-01	3.14e-01	0.0000
L2.Nervous.System	1.22e-06	2.37e-06	0.515	0.613	-3.75e-06	6.19e-06	0.0131

Table 1930: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs
L2.Neurodegenerative.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.51e-02	1.71e-01	0.439	0.666	-2.83e-01	4.33e-01	0.0000
L2.Neurodegenerative.Diseases	-1.23e-06	2.43e-06	-0.507	0.618	-6.32e-06	3.86e-06	0.0127

Table 1931: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs
L2.Nucleotide.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.39e-02	1.95e-01	0.481	0.636	-3.15e-01	5.02e-01	0.0000
L2.Nucleotide.Metabolism	-3.71e-08	6.93e-08	-0.535	0.599	-1.82e-07	1.08e-07	0.0141

Table 1932: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs
L2.Poorly.Characterized, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.03e-02	1.92e-01	0.366	0.718	-3.32e-01	4.72e-01	0.00000
L2.Poorly.Characterized	-2.25e-08	5.49e-08	-0.410	0.687	-1.37e-07	9.25e-08	0.00832

Table 1933: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs
L2.Replication.and.Repair, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.08e-02	1.92e-01	0.420	0.679	-3.22e-01	4.83e-01	0.0000
L2.Replication.and.Repair	-1.47e-08	3.13e-08	-0.469	0.644	-8.01e-08	5.07e-08	0.0109

Table 1934: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs
L2.Sensory.System, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 1935: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs
L2.Signal.Transduction, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.01e-01	1.74e-01	0.580	0.569	-2.64e-01	4.66e-01	0.0000
L2.Signal.Transduction	-9.81e-08	1.47e-07	-0.665	0.514	-4.07e-07	2.11e-07	0.0216

Table 1936: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs
L2.Signaling.Molecules.and.Interaction, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.13e-01	2.26e-01	-0.498	0.624	-5.86e-01	3.61e-01	0.0000
L2.Signaling.Molecules.and.Interaction	9.76e-07	1.81e-06	0.538	0.597	-2.82e-06	4.77e-06	0.0143

Table 1937: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs
L2.Transcription, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.15e-01	1.77e-01	0.650	0.523	-2.56e-01	4.87e-01	0.0000
L2.Transcription	-6.24e-08	8.43e-08	-0.741	0.468	-2.39e-07	1.14e-07	0.0267

Table 1938: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs
L2.Translation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.04e-01	1.85e-01	0.562	0.581	-2.83e-01	4.91e-01	0.0000
L2.Translation	-3.02e-08	4.77e-08	-0.633	0.534	-1.30e-07	6.96e-08	0.0197

Table 1939: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs
L2.Transport.and.Catabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.68e-01	1.99e-01	-1.34	0.195	-6.85e-01	1.49e-01	0.000
L2.Transport.and.Catabolism	1.24e-06	8.38e-07	1.47	0.157	-5.19e-07	2.99e-06	0.098

Table 1940: diversity_vs_picrust_L2_yr1: wunifrac.PC.1 vs
L2.Xenobiotics.Biodegradation.and.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.07e-01	1.85e-01	0.578	0.570	-2.80e-01	4.93e-01	0.0000
L2.Xenobiotics.Biodegradation.and.Metabolism	-1.05e-07	1.61e-07	-0.651	0.523	-4.43e-07	2.33e-07	0.0208

Table 1941: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs
L2.Amino.Acid.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.87e-02	8.00e-02	0.984	0.337	-8.87e-02	2.46e-01	0.000
L2.Amino.Acid.Metabolism	-1.26e-08	1.15e-08	-1.100	0.285	-3.66e-08	1.14e-08	0.057

Table 1942: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs
L2.Biosynthesis.of.Other.Secondary.Metabolites, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.74e-02	8.09e-02	0.709	0.487	-1.12e-01	2.27e-01	0.0000
L2.Biosynthesis.of.Other.Secondary.Metabolites	-8.62e-08	1.09e-07	-0.793	0.437	-3.14e-07	1.41e-07	0.0305

Table 1943: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs
L2.Cancers, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.18e-02	7.72e-02	0.542	0.594	-1.20e-01	2.03e-01	0.0000
L2.Cancers	-6.66e-07	1.08e-06	-0.615	0.546	-2.93e-06	1.60e-06	0.0185

Table 1944: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs
L2.Carbohydrate.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.69e-02	7.95e-02	0.968	0.345	-8.94e-02	2.43e-01	0.0000
L2.Carbohydrate.Metabolism	-1.07e-08	9.83e-09	-1.084	0.292	-3.12e-08	9.92e-09	0.0555

Table 1945: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs
L2.Cardiovascular.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.41e-04	3.78e-02	0.00373	0.997	-7.89e-02	7.92e-02	0.00e+00
L2.Cardiovascular.Diseases	-5.00e-07	2.94e-05	-0.01700	0.987	-6.21e-05	6.11e-05	1.44e-05

Table 1946: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs
L2.Cell.Communication, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 1947: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs
L2.Cell.Growth.and.Death, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.48e-02	7.96e-02	0.94	0.359	-9.18e-02	2.41e-01	0.0000
L2.Cell.Growth.and.Death	-2.38e-07	2.26e-07	-1.05	0.306	-7.11e-07	2.35e-07	0.0525

Table 1948: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Cell.Motility, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.54e-02	5.80e-02	1.30	0.209	-4.59e-02	1.97e-01	0.000
L2.Cell.Motility	-6.23e-08	3.85e-08	-1.62	0.122	-1.43e-07	1.82e-08	0.116

Table 1949: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Cellular.Processes.and.Signaling, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.96e-02	8.16e-02	0.975	0.342	-9.12e-02	2.50e-01	0.0000
L2.Cellular.Processes.and.Signaling	-2.88e-08	2.65e-08	-1.085	0.291	-8.43e-08	2.67e-08	0.0556

Table 1950: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Circulatory.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.45e-04	3.80e-02	0.00909	0.993	-0.079121	7.98e-02	0.00e+00
L2.Circulatory.System	-3.74e-07	9.84e-06	-0.03798	0.970	-0.000021	2.02e-05	7.21e-05

Table 1951: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Digestive.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.36e-01	7.56e-02	-1.80	0.0881	-2.94e-01	2.23e-02	0.000
L2.Digestive.System	4.93e-06	2.46e-06	2.01	0.0593	-2.14e-07	1.01e-05	0.168

Table 1952: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Endocrine.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.05e-03	8.57e-02	0.0939	0.926	-1.71e-01	1.87e-01	0.000000
L2.Endocrine.System	-4.08e-08	3.92e-07	-0.1041	0.918	-8.61e-07	7.79e-07	0.000541

Table 1953: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Energy.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.00e-02	7.94e-02	1.01	0.326	-8.62e-02	2.46e-01	0.0000
L2.Energy.Metabolism	-2.07e-08	1.83e-08	-1.13	0.273	-5.90e-08	1.77e-08	0.0598

Table 1954: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Environmental.Adaptation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.71e-02	7.05e-02	1.23	0.232	-6.06e-02	2.35e-01	0.0000
L2.Environmental.Adaptation	-8.79e-07	6.18e-07	-1.42	0.171	-2.17e-06	4.15e-07	0.0919

Table 1955: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Enzyme.Families, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.39e-02	7.92e-02	1.06	0.302	-8.18e-02	2.5e-01	0.0000
L2.Enzyme.Families	-6.03e-08	5.08e-08	-1.19	0.250	-1.67e-07	4.6e-08	0.0658

Table 1956: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Excretory.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.19e-03	6.72e-02	-0.0623	0.951	-1.45e-01	1.37e-01	0.000000
L2.Excretory.System	3.01e-07	4.04e-06	0.0745	0.941	-8.15e-06	8.75e-06	0.000277

Table 1957: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Folding..Sorting.and.Degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.04e-02	8.32e-02	0.845	0.408	-1.04e-01	2.45e-01	0.0000
L2.Folding..Sorting.and.Degradation	-4.51e-08	4.81e-08	-0.938	0.360	-1.46e-07	5.56e-08	0.0421

Table 1958: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Genetic.Information.Processing, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.65e-02	7.86e-02	1.10	0.285	-7.81e-02	2.51e-01	0.0000
L2.Genetic.Information.Processing	-5.30e-08	4.30e-08	-1.23	0.233	-1.43e-07	3.70e-08	0.0706

Table 1959: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Glycan.Biosynthesis.and.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.29e-02	9.53e-02	-0.136	0.894	-2.12e-01	1.87e-01	0.00000
L2.Glycan.Biosynthesis.and.Metabolism	7.98e-09	5.43e-08	0.147	0.885	-1.06e-07	1.22e-07	0.00108

Table 1960: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Immune.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.26e-02	8.27e-02	0.516	0.612	-1.30e-01	2.16e-01	0.0000
L2.Immune.System	-7.60e-07	1.32e-06	-0.575	0.572	-3.52e-06	2.01e-06	0.0163

Table 1961: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Immune.System.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.46e-02	7.97e-02	0.560	0.582	-1.22e-01	2.12e-01	0.0000
L2.Immune.System.Diseases	-1.44e-06	2.28e-06	-0.629	0.537	-6.22e-06	3.34e-06	0.0194

Table 1962: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Infectious.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.62e-02	8.06e-02	1.07	0.298	-8.24e-02	2.55e-01	0.0000
L2.Infectious.Diseases	-3.79e-07	3.18e-07	-1.19	0.248	-1.05e-06	2.87e-07	0.0664

Table 1963: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Lipid.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.06e-02	8.02e-02	0.880	0.390	-9.73e-02	2.39e-01	0.0000
L2.Lipid.Metabolism	-3.87e-08	3.94e-08	-0.984	0.337	-1.21e-07	4.36e-08	0.0462

Table 1964: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Membrane.Transport, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.01e-01	6.40e-02	1.58	0.1307	-3.29e-02	2.35e-01	0.000
L2.Membrane.Transport	-1.29e-08	6.91e-09	-1.86	0.0782	-2.73e-08	1.60e-09	0.148

Table 1965: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Metabolic.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.75e-02	8.34e-02	0.810	0.428	-1.07e-01	2.42e-01	0.0000
L2.Metabolic.Diseases	-1.08e-06	1.20e-06	-0.898	0.380	-3.60e-06	1.44e-06	0.0388

Table 1966: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.32e-02	8.11e-02	0.902	0.378	-9.66e-02	2.43e-01	0.0000
L2.Metabolism	-4.51e-08	4.49e-08	-1.006	0.327	-1.39e-07	4.88e-08	0.0482

Table 1967: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Metabolism.of.Cofactors.and.Vitamins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.69e-02	8.25e-02	0.932	0.363	-9.58e-02	2.50e-01	0.0000
L2.Metabolism.of.Cofactors.and.Vitamins	-2.73e-08	2.64e-08	-1.035	0.314	-8.25e-08	2.79e-08	0.0509

Table 1968: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Metabolism.of.Other.Amino.Acids, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.40e-02	8.23e-02	0.898	0.380	-9.84e-02	2.46e-01	0.0000
L2.Metabolism.of.Other.Amino.Acids	-7.56e-08	7.58e-08	-0.998	0.331	-2.34e-07	8.29e-08	0.0475

Table 1969: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Metabolism.of.Terpenoids.and.Polyketides, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.95e-02	8.45e-02	0.823	0.421	-1.07e-01	2.46e-01	0.0000
L2.Metabolism.of.Terpenoids.and.Polyketides	-6.82e-08	7.49e-08	-0.910	0.374	-2.25e-07	8.86e-08	0.0398

Table 1970: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Nervous.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.81e-02	8.10e-02	0.841	0.411	-1.01e-01	2.38e-01	0.0000
L2.Nervous.System	-9.39e-07	9.99e-07	-0.939	0.359	-3.03e-06	1.15e-06	0.0423

Table 1971: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Neurodegenerative.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.11e-03	7.36e-02	0.124	0.903	-1.45e-01	1.63e-01	0.00000
L2.Neurodegenerative.Diseases	-1.50e-07	1.05e-06	-0.143	0.888	-2.34e-06	2.04e-06	0.00102

Table 1972: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Nucleotide.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.01e-02	8.15e-02	0.983	0.338	-9.05e-02	2.51e-01	0.0000
L2.Nucleotide.Metabolism	-3.17e-08	2.90e-08	-1.094	0.288	-9.23e-08	2.89e-08	0.0564

Table 1973: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Poorly.Characterized, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.13e-02	7.97e-02	1.02	0.321	-8.56e-02	2.48e-01	0.0000
L2.Poorly.Characterized	-2.60e-08	2.28e-08	-1.14	0.268	-7.38e-08	2.17e-08	0.0611

Table 1974: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Replication.and.Repair, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.94e-02	8.01e-02	0.99	0.334	-8.84e-02	2.47e-01	0.0000
L2.Replication.and.Repair	-1.44e-08	1.30e-08	-1.11	0.282	-4.17e-08	1.29e-08	0.0577

Table 1975: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Sensory.System, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 1976: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Signal.Transduction, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.65e-02	7.18e-02	1.20	0.243	-6.38e-02	2.37e-01	0.0000
L2.Signal.Transduction	-8.40e-08	6.08e-08	-1.38	0.183	-2.11e-07	4.33e-08	0.0871

Table 1977: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs L2.Signaling.Molecules.and.Interaction, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.57e-02	9.72e-02	0.265	0.794	-1.78e-01	2.29e-01	0.00000
L2.Signaling.Molecules.and.Interaction	-2.23e-07	7.80e-07	-0.286	0.778	-1.85e-06	1.41e-06	0.00407

Table 1978: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs
L2.Transcription, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.41e-02	7.29e-02	1.29	0.212	-5.84e-02	2.47e-01	0.0000
L2.Transcription	-5.10e-08	3.46e-08	-1.47	0.157	-1.23e-07	2.15e-08	0.0978

Table 1979: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs
L2.Translation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.21e-02	7.70e-02	1.07	0.300	-7.92e-02	2.43e-01	0.0000
L2.Translation	-2.38e-08	1.98e-08	-1.20	0.245	-6.54e-08	1.77e-08	0.0672

Table 1980: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs
L2.Transport.and.Catabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.28e-02	8.68e-02	-1.07	0.299	-2.74e-01	8.89e-02	0.0000
L2.Transport.and.Catabolism	4.28e-07	3.65e-07	1.17	0.256	-3.37e-07	1.19e-06	0.0642

Table 1981: diversity_vs_picrust_L2_yr1: wunifrac.PC.2 vs
L2.Xenobiotics.Biodegradation.and.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.13e-02	7.70e-02	1.06	0.304	-7.99e-02	2.43e-01	0.0000
L2.Xenobiotics.Biodegradation.and.Metabolism	-8.00e-08	6.72e-08	-1.19	0.249	-2.21e-07	6.07e-08	0.0661

Table 1982: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs
L2.Amino.Acid.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.60e-02	5.52e-02	0.472	0.642	-8.94e-02	1.41e-01	0.0000
L2.Amino.Acid.Metabolism	-4.17e-09	7.90e-09	-0.527	0.604	-2.07e-08	1.24e-08	0.0137

Table 1983: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs
L2.Biosynthesis.of.Other.Secondary.Metabolites, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.49e-02	5.46e-02	0.638	0.531	-7.95e-02	1.49e-01	0.0000
L2.Biosynthesis.of.Other.Secondary.Metabolites	-5.24e-08	7.34e-08	-0.714	0.484	-2.06e-07	1.01e-07	0.0249

Table 1984: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Cancers, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.48e-02	5.12e-02	0.875	0.393	-6.24e-02	1.52e-01	0.000
L2.Cancers	-7.13e-07	7.18e-07	-0.993	0.333	-2.22e-06	7.90e-07	0.047

Table 1985: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Carbohydrate.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.79e-02	5.47e-02	0.510	0.616	-8.65e-02	1.42e-01	0.0000
L2.Carbohydrate.Metabolism	-3.87e-09	6.76e-09	-0.571	0.574	-1.80e-08	1.03e-08	0.0161

Table 1986: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Cardiovascular.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.005338	2.48e-02	0.215	0.832	-4.66e-02	5.73e-02	0.0000
L2.Cardiovascular.Diseases	-0.000019	1.93e-05	-0.981	0.339	-5.94e-05	2.15e-05	0.0459

Table 1987: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Cell.Communication, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 1988: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Cell.Growth.and.Death, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.95e-02	5.46e-02	0.540	0.595	-8.48e-02	1.44e-01	0.000
L2.Cell.Growth.and.Death	-9.38e-08	1.55e-07	-0.605	0.552	-4.19e-07	2.31e-07	0.018

Table 1989: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Cell.Motility, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.15e-02	4.12e-02	0.523	0.607	-6.47e-02	1.08e-01	0.0000
L2.Cell.Motility	-1.78e-08	2.73e-08	-0.651	0.523	-7.50e-08	3.94e-08	0.0207

Table 1990: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs
L2.Cellular.Processes.and.Signaling, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.03e-02	5.61e-02	0.541	0.595	-8.71e-02	1.48e-01	0.0000
L2.Cellular.Processes.and.Signaling	-1.10e-08	1.82e-08	-0.602	0.555	-4.91e-08	2.72e-08	0.0178

Table 1991: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs
L2.Circulatory.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.10e-03	2.49e-02	0.245	0.809	-4.60e-02	5.82e-02	0.0000
L2.Circulatory.System	-6.61e-06	6.45e-06	-1.025	0.318	-2.01e-05	6.89e-06	0.0499

Table 1992: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs
L2.Digestive.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.80e-03	5.60e-02	0.139	0.891	-1.09e-01	1.25e-01	0.00000
L2.Digestive.System	-2.83e-07	1.82e-06	-0.156	0.878	-4.10e-06	3.53e-06	0.00121

Table 1993: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs
L2.Endocrine.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.87e-02	5.69e-02	0.681	0.504	-8.03e-02	1.58e-01	0.0000
L2.Endocrine.System	-1.96e-07	2.60e-07	-0.755	0.460	-7.41e-07	3.48e-07	0.0277

Table 1994: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs
L2.Energy.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.80e-02	5.48e-02	0.511	0.616	-8.67e-02	1.43e-01	0.0000
L2.Energy.Metabolism	-7.22e-09	1.26e-08	-0.571	0.574	-3.37e-08	1.92e-08	0.0161

Table 1995: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs
L2.Environmental.Adaptation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.88e-02	4.94e-02	0.583	0.567	-7.46e-02	1.32e-01	0.0000
L2.Environmental.Adaptation	-2.91e-07	4.33e-07	-0.672	0.510	-1.20e-06	6.15e-07	0.0221

Table 1996: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Enzyme.Families, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.75e-02	5.48e-02	0.501	0.622	-8.72e-02	1.42e-01	0.0000
L2.Enzyme.Families	-1.97e-08	3.52e-08	-0.561	0.581	-9.33e-08	5.39e-08	0.0155

Table 1997: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Excretory.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.61e-02	4.35e-02	1.06	0.302	-4.49e-02	1.37e-01	0.0000
L2.Excretory.System	-3.31e-06	2.61e-06	-1.27	0.220	-8.78e-06	2.16e-06	0.0743

Table 1998: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Folding..Sorting.and.Degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.13e-02	5.68e-02	0.552	0.588	-8.75e-02	1.50e-01	0.0000
L2.Folding..Sorting.and.Degradation	-2.01e-08	3.28e-08	-0.612	0.548	-8.88e-08	4.86e-08	0.0184

Table 1999: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Genetic.Information.Processing, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.75e-02	5.46e-02	0.504	0.620	-8.67e-02	1.42e-01	0.0000
L2.Genetic.Information.Processing	-1.69e-08	2.99e-08	-0.564	0.579	-7.94e-08	4.57e-08	0.0157

Table 2000: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Glycan.Biosynthesis.and.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.38e-02	6.37e-02	0.530	0.602	-9.96e-02	1.67e-01	0.0000
L2.Glycan.Biosynthesis.and.Metabolism	-2.08e-08	3.62e-08	-0.574	0.572	-9.67e-08	5.50e-08	0.0162

Table 2001: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Immune.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.59e-02	5.58e-02	0.464	0.648	-9.08e-02	1.43e-01	0.0000
L2.Immune.System	-4.61e-07	8.91e-07	-0.518	0.611	-2.33e-06	1.40e-06	0.0132

Table 2002: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Immune.System.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.35e-02	5.39e-02	0.436	0.668	-8.94e-02	1.36e-01	0.0000
L2.Immune.System.Diseases	-7.57e-07	1.54e-06	-0.490	0.630	-3.99e-06	2.48e-06	0.0119

Table 2003: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Infectious.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.77e-02	5.58e-02	0.497	0.625	-8.91e-02	1.45e-01	0.0000
L2.Infectious.Diseases	-1.22e-07	2.20e-07	-0.554	0.586	-5.83e-07	3.39e-07	0.0151

Table 2004: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Lipid.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.76e-02	5.45e-02	0.690	0.499	-7.65e-02	1.52e-01	0.0000
L2.Lipid.Metabolism	-2.07e-08	2.68e-08	-0.772	0.450	-7.67e-08	3.54e-08	0.0289

Table 2005: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Membrane.Transport, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.96e-02	4.66e-02	0.420	0.679	-7.8e-02	1.17e-01	0.0000
L2.Membrane.Transport	-2.49e-09	5.03e-09	-0.495	0.626	-1.3e-08	8.04e-09	0.0121

Table 2006: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Metabolic.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.56e-02	5.66e-02	0.629	0.537	-8.29e-02	1.54e-01	0.0000
L2.Metabolic.Diseases	-5.71e-07	8.17e-07	-0.698	0.493	-2.28e-06	1.14e-06	0.0238

Table 2007: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.65e-02	5.53e-02	0.660	0.517	-7.92e-02	1.52e-01	0.0000
L2.Metabolism	-2.25e-08	3.06e-08	-0.736	0.471	-8.65e-08	4.15e-08	0.0264

Table 2008: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Metabolism.of.Cofactors.and.Vitamins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.40e-02	5.68e-02	0.423	0.677	-9.49e-02	1.43e-01	0.0000
L2.Metabolism.of.Cofactors.and.Vitamins	-8.51e-09	1.81e-08	-0.469	0.644	-4.65e-08	2.95e-08	0.0109

Table 2009: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Metabolism.of.Other.Amino.Acids, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.39e-02	5.62e-02	0.603	0.554	-8.38e-02	1.52e-01	0.0000
L2.Metabolism.of.Other.Amino.Acids	-3.46e-08	5.17e-08	-0.670	0.511	-1.43e-07	7.36e-08	0.0219

Table 2010: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Metabolism.of.Terpenoids.and.Polyketides, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.62e-02	5.77e-02	0.453	0.656	-9.47e-02	1.47e-01	0.0000
L2.Metabolism.of.Terpenoids.and.Polyketides	-2.57e-08	5.12e-08	-0.501	0.622	-1.33e-07	8.15e-08	0.0124

Table 2011: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Nervous.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.05e-02	5.52e-02	0.553	0.587	-8.51e-02	1.46e-01	0.0000
L2.Nervous.System	-4.21e-07	6.81e-07	-0.617	0.544	-1.85e-06	1.01e-06	0.0187

Table 2012: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Neurodegenerative.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.91e-02	4.85e-02	0.805	0.431	-6.25e-02	1.41e-01	0.0000
L2.Neurodegenerative.Diseases	-6.41e-07	6.89e-07	-0.930	0.364	-2.08e-06	8.02e-07	0.0415

Table 2013: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Nucleotide.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.66e-02	5.62e-02	0.473	0.642	-9.10e-02	1.44e-01	0.0000
L2.Nucleotide.Metabolism	-1.05e-08	2.00e-08	-0.526	0.605	-5.23e-08	3.13e-08	0.0136

Table 2014: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Poorly.Characterized, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.01e-02	5.50e-02	0.547	0.591	-8.50e-02	1.45e-01	0.0000
L2.Poorly.Characterized	-9.62e-09	1.57e-08	-0.611	0.548	-4.25e-08	2.33e-08	0.0183

Table 2015: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Replication.and.Repair, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.82e-02	5.52e-02	0.511	0.615	-8.73e-02	1.44e-01	0.000
L2.Replication.and.Repair	-5.12e-09	8.97e-09	-0.571	0.575	-2.39e-08	1.37e-08	0.016

Table 2016: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Sensory.System, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2017: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Signal.Transduction, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.12e-02	5.01e-02	0.623	0.541	-7.36e-02	1.36e-01	0.0000
L2.Signal.Transduction	-3.03e-08	4.24e-08	-0.715	0.484	-1.19e-07	5.84e-08	0.0249

Table 2018: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Signaling.Molecules.and.Interaction, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.32e-02	6.55e-02	0.202	0.842	-1.24e-01	1.50e-01	0.00000
L2.Signaling.Molecules.and.Interaction	-1.15e-07	5.25e-07	-0.218	0.830	-1.21e-06	9.85e-07	0.00238

Table 2019: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Transcription, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.17e-02	5.15e-02	0.421	0.678	-8.61e-02	1.29e-01	0.0000
L2.Transcription	-1.17e-08	2.45e-08	-0.480	0.637	-6.29e-08	3.95e-08	0.0114

Table 2020: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Translation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.04e-02	5.32e-02	0.572	0.574	-8.10e-02	1.42e-01	0.0000
L2.Translation	-8.83e-09	1.37e-08	-0.644	0.527	-3.75e-08	1.99e-08	0.0203

Table 2021: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Transport.and.Catabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.82e-02	6.04e-02	0.301	0.767	-1.08e-01	1.45e-01	0.00000
L2.Transport.and.Catabolism	-8.39e-08	2.54e-07	-0.330	0.745	-6.15e-07	4.48e-07	0.00542

Table 2022: diversity_vs_picrust_L2_yr1: wunifrac.PC.3 vs L2.Xenobiotics.Biodegradation.and.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.06e-02	5.32e-02	0.575	0.572	-8.07e-02	1.42e-01	0.0000
L2.Xenobiotics.Biodegradation.and.Metabolism	-3.01e-08	4.64e-08	-0.649	0.524	-1.27e-07	6.71e-08	0.0206

Table 2023: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Amino.Acid.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.11e-04	4.72e-02	0.00871	0.993	-9.85e-02	9.93e-02	0.00e+00
L2.Amino.Acid.Metabolism	-6.58e-11	6.76e-09	-0.00973	0.992	-1.42e-08	1.41e-08	4.74e-06

Table 2024: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Biosynthesis.of.Other.Secondary.Metabolites, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.66e-02	4.69e-02	-0.353	0.728	-1.15e-01	8.16e-02	0.0000
L2.Biosynthesis.of.Other.Secondary.Metabolites	2.49e-08	6.30e-08	0.395	0.697	-1.07e-07	1.57e-07	0.0077

Table 2025: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Cancers, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.44e-03	4.46e-02	-0.167	0.869	-1.01e-01	8.59e-02	0.00000
L2.Cancers	1.19e-07	6.26e-07	0.189	0.852	-1.19e-06	1.43e-06	0.00179

Table 2026: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Carbohydrate.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.52e-03	4.69e-02	-0.161	0.874	-1.06e-01	9.05e-02	0.00000
L2.Carbohydrate.Metabolism	1.04e-09	5.80e-09	0.180	0.859	-1.11e-08	1.32e-08	0.00161

Table 2027: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Cardiovascular.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.35e-03	2.12e-02	0.206	0.839	-3.99e-02	0.048629	0.0000
L2.Cardiovascular.Diseases	-1.54e-05	1.65e-05	-0.938	0.360	-4.99e-05	0.000019	0.0421

Table 2028: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Cell.Communication, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 2029: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Cell.Growth.and.Death, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.34e-03	4.69e-02	-0.050	0.961	-1.00e-01	9.58e-02	0.000000
L2.Cell.Growth.and.Death	7.46e-09	1.33e-07	0.056	0.956	-2.71e-07	2.86e-07	0.000157

Table 2030: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Cell.Motility, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.75e-03	3.54e-02	-0.0777	0.939	-7.69e-02	7.14e-02	0.000000
L2.Cell.Motility	2.27e-09	2.35e-08	0.0968	0.924	-4.69e-08	5.15e-08	0.000468

Table 2031: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Cellular.Processes.and.Signaling, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.02e-02	4.81e-02	-0.212	0.834	-1.11e-01	9.04e-02	0.00000
L2.Cellular.Processes.and.Signaling	3.68e-09	1.56e-08	0.236	0.816	-2.90e-08	3.64e-08	0.00277

Table 2032: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Circulatory.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.69e-03	2.13e-02	0.221	0.828	-3.98e-02	4.92e-02	0.0000
L2.Circulatory.System	-5.08e-06	5.51e-06	-0.922	0.368	-1.66e-05	6.45e-06	0.0408

Table 2033: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Digestive.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.24e-02	4.73e-02	-0.474	0.641	-1.21e-01	7.65e-02	0.0000
L2.Digestive.System	8.15e-07	1.54e-06	0.529	0.603	-2.41e-06	4.04e-06	0.0138

Table 2034: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Endocrine.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.25e-02	4.87e-02	0.462	0.649	-7.95e-02	1.25e-01	0.0000
L2.Endocrine.System	-1.14e-07	2.23e-07	-0.512	0.615	-5.81e-07	3.52e-07	0.0129

Table 2035: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Energy.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.36e-03	4.70e-02	-0.114	0.91	-1.04e-01	9.29e-02	0.000000
L2.Energy.Metabolism	1.38e-09	1.08e-08	0.128	0.90	-2.13e-08	2.40e-08	0.000816

Table 2036: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Environmental.Adaptation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.27e-03	4.24e-02	0.171	0.866	-8.16e-02	9.61e-02	0.00000
L2.Environmental.Adaptation	-7.34e-08	3.72e-07	-0.197	0.846	-8.52e-07	7.05e-07	0.00194

Table 2037: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Enzyme.Families, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.76e-03	4.70e-02	-0.0800	0.937	-1.02e-01	9.46e-02	0.000000
L2.Enzyme.Families	2.70e-09	3.01e-08	0.0896	0.930	-6.04e-08	6.58e-08	0.000401

Table 2038: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Excretory.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.90e-02	3.61e-02	1.36	0.191	-2.66e-02	1.25e-01	0.000
L2.Excretory.System	-3.52e-06	2.17e-06	-1.62	0.121	-8.05e-06	1.02e-06	0.116

Table 2039: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Folding..Sorting.and.Degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.82e-04	4.88e-02	0.0201	0.984	-1.01e-01	1.03e-01	0.0e+00
L2.Folding..Sorting.and.Degradation	-6.30e-10	2.82e-08	-0.0223	0.982	-5.96e-08	5.83e-08	2.5e-05

Table 2040: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Genetic.Information.Processing, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.13e-04	4.68e-02	0.00669	0.995	-9.76e-02	9.82e-02	0.00e+00
L2.Genetic.Information.Processing	-1.92e-10	2.56e-08	-0.00749	0.994	-5.38e-08	5.34e-08	2.81e-06

Table 2041: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Glycan.Biosynthesis.and.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.11e-02	5.46e-02	-0.203	0.841	-1.25e-01	1.03e-01	0.00000
L2.Glycan.Biosynthesis.and.Metabolism	6.84e-09	3.11e-08	0.220	0.828	-5.82e-08	7.18e-08	0.00242

Table 2042: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Immune.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.55e-02	4.76e-02	0.326	0.748	-8.41e-02	1.15e-01	0.00000
L2.Immune.System	-2.76e-07	7.61e-07	-0.364	0.720	-1.87e-06	1.32e-06	0.00656

Table 2043: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Immune.System.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.89e-02	4.55e-02	-0.635	0.533	-1.24e-01	6.64e-02	0.0000
L2.Immune.System.Diseases	9.31e-07	1.30e-06	0.714	0.484	-1.80e-06	3.66e-06	0.0248

Table 2044: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Infectious.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.22e-04	4.78e-02	0.0193	0.985	-9.92e-02	1.01e-01	0.00e+00
L2.Infectious.Diseases	-4.06e-09	1.89e-07	-0.0215	0.983	-3.99e-07	3.91e-07	2.31e-05

Table 2045: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Lipid.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.13e-03	4.71e-02	-0.0241	0.981	-9.97e-02	9.75e-02	0.00e+00
L2.Lipid.Metabolism	6.22e-10	2.31e-08	0.0269	0.979	-4.77e-08	4.90e-08	3.63e-05

Table 2046: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Membrane.Transport, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.59e-02	3.96e-02	-0.401	0.693	-9.89e-02	6.71e-02	0.000
L2.Membrane.Transport	2.02e-09	4.28e-09	0.473	0.642	-6.93e-09	1.10e-08	0.011

Table 2047: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Metabolic.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.29e-03	4.88e-02	-0.0264	0.979	-1.03e-01	1.01e-01	0.0e+00
L2.Metabolic.Diseases	2.06e-08	7.04e-07	0.0293	0.977	-1.45e-06	1.49e-06	4.3e-05

Table 2048: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.71e-03	4.76e-02	-0.204	0.841	-1.09e-01	9.00e-02	0.00000
L2.Metabolism	5.99e-09	2.63e-08	0.227	0.823	-4.91e-08	6.11e-08	0.00258

Table 2049: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Metabolism.of.Cofactors.and.Vitamins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.45e-03	4.85e-02	-0.133	0.896	-1.08e-01	9.52e-02	0.00000
L2.Metabolism.of.Cofactors.and.Vitamins	2.29e-09	1.55e-08	0.147	0.884	-3.02e-08	3.48e-08	0.00109

Table 2050: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Metabolism.of.Other.Amino.Acids, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.87e-03	4.83e-02	-0.184	0.856	-1.1e-01	9.23e-02	0.00000
L2.Metabolism.of.Other.Amino.Acids	9.07e-09	4.45e-08	0.204	0.841	-8.4e-08	1.02e-07	0.00208

Table 2051: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Metabolism.of.Terpenoids.and.Polyketides, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.20e-04	4.94e-02	0.00242	0.998	-1.03e-01	1.04e-01	0.0e+0
L2.Metabolism.of.Terpenoids.and.Polyketides	-1.18e-10	4.38e-08	-0.00268	0.998	-9.19e-08	9.16e-08	3.6e-07

Table 2052: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Nervous.System, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.19e-02	4.71e-02	0.464	0.648	-7.68e-02	1.20e-01	0.0000
L2.Nervous.System	-3.01e-07	5.81e-07	-0.518	0.610	-1.52e-06	9.15e-07	0.0132

Table 2053: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Neurodegenerative.Diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.35e-03	4.22e-02	-0.0321	0.975	-8.96e-02	8.69e-02	0.00e+00
L2.Neurodegenerative.Diseases	2.22e-08	5.99e-07	0.0371	0.971	-1.23e-06	1.28e-06	6.88e-05

Table 2054: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Nucleotide.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.61e-03	4.81e-02	-0.0751	0.941	-1.04e-01	9.71e-02	0.000000
L2.Nucleotide.Metabolism	1.43e-09	1.71e-08	0.0835	0.934	-3.44e-08	3.72e-08	0.000349

Table 2055: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Poorly.Characterized, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.02e-02	4.71e-02	-0.216	0.832	-1.09e-01	8.85e-02	0.0000
L2.Poorly.Characterized	3.25e-09	1.35e-08	0.241	0.812	-2.50e-08	3.15e-08	0.0029

Table 2056: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Replication.and.Repair, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.39e-03	4.74e-02	0.0504	0.960	-9.67e-02	1.01e-01	0.000000
L2.Replication.and.Repair	-4.33e-10	7.70e-09	-0.0563	0.956	-1.65e-08	1.57e-08	0.000158

Table 2057: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Sensory.System, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 2058: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Signal.Transduction, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.27e-03	4.31e-02	-0.215	0.832	-9.94e-02	8.09e-02	0.00000
L2.Signal.Transduction	8.99e-09	3.65e-08	0.247	0.808	-6.73e-08	8.53e-08	0.00303

Table 2059: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Signaling.Molecules.and.Interaction, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.89e-03	5.58e-02	0.0339	0.973	-1.15e-01	1.19e-01	0.0e+00
L2.Signaling.Molecules.and.Interaction	-1.64e-08	4.47e-07	-0.0366	0.971	-9.53e-07	9.20e-07	6.7e-05

Table 2060: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Transcription, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.43e-03	4.40e-02	-0.0551	0.957	-9.46e-02	8.97e-02	0.000000
L2.Transcription	1.31e-09	2.09e-08	0.0628	0.951	-4.25e-08	4.51e-08	0.000197

Table 2061: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Translation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.45e-04	4.58e-02	-0.00318	0.997	-9.59e-02	9.56e-02	0.00e+00
L2.Translation	4.22e-11	1.18e-08	0.00358	0.997	-2.46e-08	2.47e-08	6.42e-07

Table 2062: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Transport.and.Catabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.12e-02	5.14e-02	0.218	0.830	-9.64e-02	1.19e-01	0.00000
L2.Transport.and.Catabolism	-5.17e-08	2.16e-07	-0.239	0.814	-5.04e-07	4.01e-07	0.00285

Table 2063: diversity_vs_picrust_L2_yr1: wunifrac.PC.4 vs L2.Xenobiotics.Biodegradation.and.Metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.95e-03	4.57e-02	0.0645	0.949	-9.28e-02	9.87e-02	0.0000
L2.Xenobiotics.Biodegradation.and.Metabolism	-2.90e-09	3.99e-08	-0.0728	0.943	-8.64e-08	8.06e-08	0.0002

Table 2064: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %
Intercept	9.81e-03	9.93e-02	0.0988	0.922	-0.197956
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	-1.42e-05	7.15e-05	-0.1989	0.844	-0.000164

Table 2065: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.ABC.transporters, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.54e-01	1.54e-01	1.00	0.329	-1.68e-01	4.77e-01	0.0000
L3.ABC.transporters	-7.01e-08	5.89e-08	-1.19	0.249	-1.93e-07	5.32e-08	0.0661

Table 2066: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Adherens.junction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2067: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Adipocytokine.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.35e-01	1.84e-01	-1.27	0.218	-6.20e-01	1.51e-01	0.0000
L3.Adipocytokine.signaling.pathway	5.15e-06	3.62e-06	1.42	0.171	-2.42e-06	1.27e-05	0.0921

Table 2068:   diversity_vs_picrust_L3_yr1:   wunifrac.PC.1 vs
L3.African.trypanosomiasis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.129253	1.09e-01	1.19	0.2485	-0.097979	3.56e-01	0.000
L3.African.trypanosomiasis	-0.000173	9.84e-05	-1.76	0.0944	-0.000379	3.28e-05	0.134

Table 2069:   diversity_vs_picrust_L3_yr1:   wunifrac.PC.1 vs
L3.Alanine..aspartate.and.glutamate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.47e-03	2.01e-01	-0.0123	0.990	-4.23e-01	4.18e-01	0.00
L3.Alanine..aspartate.and.glutamate.metabolism	3.42e-09	2.52e-07	0.0136	0.989	-5.23e-07	5.30e-07	9.24

Table 2070:   diversity_vs_picrust_L3_yr1:   wunifrac.PC.1 vs
L3.Aldosterone.regulated.sodium.reabsorption, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2071:   diversity_vs_picrust_L3_yr1:   wunifrac.PC.1 vs
L3.Alzheimer.s.disease, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.2e-02	1.69e-01	0.307	0.762	-3.03e-01	4.07e-01	0.00000
L3.Alzheimer.s.disease	-1.8e-06	5.06e-06	-0.356	0.725	-1.24e-05	8.78e-06	0.00631

Table 2072:   diversity_vs_picrust_L3_yr1:   wunifrac.PC.1 vs
L3.Amino.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.43e-01	1.72e-01	0.834	0.415	-2.17e-01	5.03e-01	0.0000
L3.Amino.acid.metabolism	-9.89e-07	1.03e-06	-0.957	0.351	-3.15e-06	1.18e-06	0.0437

Table 2073:   diversity_vs_picrust_L3_yr1:   wunifrac.PC.1 vs
L3.Amino.acid.related.enzymes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.16e-02	1.90e-01	0.481	0.636	-3.07e-01	4.90e-01	0.0000
L3.Amino.acid.related.enzymes	-9.79e-08	1.82e-07	-0.539	0.596	-4.78e-07	2.83e-07	0.0143

Table 2074: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Amino.sugar.and.nucleotide.sugar.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.47e-03	1.96e-01	-0.0381	0.970	-4.18e-01	4.03e-01	0e+
L3.Amino.sugar.and.nucleotide.sugar.metabolism	7.61e-09	1.79e-07	0.0424	0.967	-3.68e-07	3.83e-07	9e-0

Table 2075: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Aminoacyl.tRNA.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.09e-01	1.77e-01	0.613	0.547	-2.62e-01	4.79e-01	0.0000
L3.Aminoacyl.tRNA.biosynthesis	-1.52e-07	2.17e-07	-0.700	0.492	-6.07e-07	3.03e-07	0.0239

Table 2076: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Aminobenzoate.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.74e-02	2.0e-01	0.0873	0.931	-4.00e-01	4.35e-01	0.000000
L3.Aminobenzoate.degradation	-2.52e-07	2.6e-06	-0.0968	0.924	-5.69e-06	5.19e-06	0.000468

Table 2077: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Amoebiasis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.94e-03	1.31e-01	0.0300	0.976	-2.71e-01	2.79e-01	0.00e+00
L3.Amoebiasis	-5.07e-07	1.27e-05	-0.0398	0.969	-2.72e-05	2.61e-05	7.94e-05

Table 2078: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Amyotrophic.lateral.sclerosis..ALS., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.12e-02	1.44e-01	0.495	0.626	-2.30e-01	3.72e-01	0.0000
L3.Amyotrophic.lateral.sclerosis..ALS.	-7.77e-06	1.26e-05	-0.616	0.546	-3.42e-05	1.86e-05	0.0186

Table 2079: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Antigen.processing.and.presentation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.4e-02	1.88e-01	0.181	0.858	-3.59e-01	0.427577	0.00000
L3.Antigen.processing.and.presentation	-1.3e-06	6.37e-06	-0.204	0.841	-1.46e-05	0.000012	0.00207

Table 2080: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Apoptosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.020299	9.65e-02	-0.210	0.836	-0.222280	0.181682	0.0000
L3.Apoptosis	0.000029	6.33e-05	0.459	0.651	-0.000103	0.000161	0.0104

Table 2081: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Arachidonic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.07e-02	2.14e-01	-0.237	0.816	-4.99e-01	3.98e-01	0.00000
L3.Arachidonic.acid.metabolism	4.60e-06	1.78e-05	0.258	0.799	-3.27e-05	4.19e-05	0.00332

Table 2082: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Arginine.and.proline.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.89e-02	1.92e-01	0.412	0.685	-3.22e-01	4.80e-01	0.0000
L3.Arginine.and.proline.metabolism	-9.51e-08	2.06e-07	-0.461	0.650	-5.27e-07	3.37e-07	0.0105

Table 2083: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Arrhythmogenic.right.ventricular.cardiomyopathy..ARVC., df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2084: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Ascorbate.and.aldarate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.21e-02	1.74e-01	0.528	0.604	-2.73e-01	4.57e-01	0.000
L3.Ascorbate.and.aldarate.metabolism	-1.26e-06	2.08e-06	-0.606	0.552	-5.62e-06	3.10e-06	0.018

Table 2085: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Atrazine.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.52e-01	1.20e-01	1.27	0.218	-9.80e-02	4.03e-01	0.000
L3.Atrazine.degradation	-1.19e-05	6.93e-06	-1.72	0.102	-2.64e-05	2.60e-06	0.129

Table 2086: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Bacterial.chemotaxis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.30e-01	1.41e-01	0.923	0.368	-1.65e-01	4.24e-01	0.0000
L3.Bacterial.chemotaxis	-4.52e-07	3.94e-07	-1.145	0.266	-1.28e-06	3.73e-07	0.0616

Table 2087: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Bacterial.invasion.of.epithelial.cells, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.118145	0.104284	1.13	0.2713	-0.100124	3.36e-01	0.000
L3.Bacterial.invasion.of.epithelial.cells	-0.000328	0.000186	-1.76	0.0937	-0.000717	6.11e-05	0.135

Table 2088: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Bacterial.motility.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.50e-02	1.37e-01	0.549	0.590	-2.11e-01	3.61e-01	0.000
L3.Bacterial.motility.proteins	-1.54e-07	2.19e-07	-0.702	0.491	-6.13e-07	3.05e-07	0.024

Table 2089: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Bacterial.secretion.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.7e-02	1.94e-01	0.396	0.696	-3.30e-01	4.84e-01	0.00000
L3.Bacterial.secretion.system	-2.2e-07	4.99e-07	-0.442	0.664	-1.26e-06	8.24e-07	0.00965

Table 2090: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Bacterial.toxins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.54e-02	1.96e-01	0.130	0.898	-3.86e-01	4.36e-01	0.00000
L3.Bacterial.toxins	-3.29e-07	2.28e-06	-0.144	0.887	-5.10e-06	4.44e-06	0.00104

Table 2091: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Basal.transcription.factors, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.030263	0.094588	-0.320	0.753	-0.228238	0.16771	0.000
L3.Basal.transcription.factors	0.000109	0.000149	0.731	0.474	-0.000202	0.00042	0.026

Table 2092: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Base.excision.repair, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.38e-02	1.85e-01	0.508	0.617	-2.93e-01	4.80e-01	0.0000
L3.Base.excision.repair	-3.47e-07	6.06e-07	-0.573	0.573	-1.62e-06	9.21e-07	0.0161

Table 2093: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Benzoate.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.28e-01	1.74e-01	0.735	0.471	-2.37e-01	4.93e-01	0.0000
L3.Benzoate.degradation	-1.03e-06	1.23e-06	-0.841	0.411	-3.60e-06	1.54e-06	0.0341

Table 2094: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Betalain.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.002279	0.09223	0.0247	0.981	-0.1908	0.1953	0.000000
L3.Betalain.biosynthesis	-0.000352	0.00505	-0.0697	0.945	-0.0109	0.0102	0.000243

Table 2095: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Bile.secretion, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0306	0.0823	0.371	0.715	-0.142	0.203	0.000
L3.Bile.secretion	-0.6418	0.3773	-1.701	0.105	-1.431	0.148	0.126

Table 2096: diversity_vs_picrust_L3_yr1: wunifrac.PC.1
vs L3.Biosynthesis.and.biodegradation.of.secondary.metabolites,
df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	3.39e-02	1.92e-01	0.177	0.862	-3.67e-01	4.35
L3.Biosynthesis.and.biodegradation.of.secondary.metabolites	-7.88e-07	3.98e-06	-0.198	0.845	-9.13e-06	7.55

Table 2097: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Biosynthesis.of.12. . . 14..and.16.membered.macrolides, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2098: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Biosynthesis.of.ansamycins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.13e-02	1.73e-01	0.469	0.644	-2.81e-01	4.44e-01	0.0000
L3.Biosynthesis.of.ansamycins	-1.05e-06	1.94e-06	-0.540	0.596	-5.11e-06	3.02e-06	0.0144

Table 2099: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	-6.71e-02	0.224042	-0.299	0.768	-5.36e-01	4.02e
L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides	5.82e-06	0.000018	0.324	0.749	-3.18e-05	4.34e

Table 2100: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Biosynthesis.of.type.II.polyketide.backbone, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2101: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Biosynthesis.of.type.II.polyketide.products, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.006218	0.09306	0.0668	0.947	-0.1886	0.20099	0.00000
L3.Biosynthesis.of.type.II.polyketide.products	-0.000865	0.00488	-0.1770	0.861	-0.0111	0.00936	0.00156

Table 2102: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Biosynthesis.of.unsaturated.fatty.acids, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.18e-01	1.75e-01	0.673	0.509	-2.48e-01	4.84e-01	0.0000
L3.Biosynthesis.of.unsaturated.fatty.acids	-1.72e-06	2.23e-06	-0.769	0.451	-6.38e-06	2.95e-06	0.0287

Table 2103: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Biosynthesis.of.vancomycin.group.antibiotics, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.79e-02	2.16e-01	0.129	0.899	-4.24e-01	4.80e-01	0.0000
L3.Biosynthesis.of.vancomycin.group.antibiotics	-6.12e-07	4.35e-06	-0.141	0.889	-9.71e-06	8.48e-06	0.0009

Table 2104: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Biotin.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.20e-02	1.89e-01	0.381	0.708	-3.24e-01	4.68e-01	0.00000
L3.Biotin.metabolism	-6.52e-07	1.52e-06	-0.427	0.674	-3.84e-06	2.54e-06	0.00905

Table 2105: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Bisphenol.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.32e-02	1.84e-01	0.126	0.901	-3.62e-01	4.08e-01	0.00000
L3.Bisphenol.degradation	-3.82e-07	2.68e-06	-0.143	0.888	-5.99e-06	5.23e-06	0.00102

Table 2106: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Bladder.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.048542	0.107259	0.453	0.656	-0.17595	0.273038	0.0000
L3.Bladder.cancer	-0.000298	0.000401	-0.742	0.467	-0.00114	0.000542	0.0268

Table 2107: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Butanoate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.01e-01	1.85e-01	0.547	0.590	-2.85e-01	4.87e-01	0.0000
L3.Butanoate.metabolism	-2.50e-07	4.04e-07	-0.617	0.544	-1.10e-06	5.96e-07	0.0187

Table 2108: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Butirosin.and.neomycin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.69e-02	1.76e-01	-0.0962	0.924	-3.85e-01	3.51e-01	0.000000
L3.Butirosin.and.neomycin.biosynthesis	3.49e-07	3.16e-06	0.1104	0.913	-6.26e-06	6.96e-06	0.000609

Table 2109: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.C5.Branched.dibasic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.24e-01	1.70e-01	0.726	0.477	-2.33e-01	4.80e-01	0.0000
L3.C5.Branched.dibasic.acid.metabolism	-5.77e-07	6.89e-07	-0.837	0.413	-2.02e-06	8.65e-07	0.0338

Table 2110: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.CAM.ligands, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2111: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Caffeine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.035178	0.092760	0.379	0.709	-0.15897	0.229328	0.0000
L3.Caffeine.metabolism	-0.000385	0.000421	-0.914	0.372	-0.00127	0.000496	0.0401

Table 2112: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Calcium.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.01163	0.09112	0.128	0.900	-0.1791	0.2024	0.00000
L3.Calcium.signaling.pathway	-0.00284	0.00741	-0.383	0.706	-0.0184	0.0127	0.00729

Table 2113: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Caprolactam.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.98e-01	1.43e-01	1.39	0.181	-1.00e-01	4.97e-01	0.000
L3.Caprolactam.degradation	-2.89e-05	1.72e-05	-1.68	0.109	-6.48e-05	7.06e-06	0.124

Table 2114: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Carbohydrate.digestion.and.absorption, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.26e-02	1.53e-01	0.54	0.596	-2.38e-01	4.03e-01	0.0000
L3.Carbohydrate.digestion.and.absorption	-9.86e-06	1.52e-05	-0.65	0.523	-4.16e-05	2.19e-05	0.0207

Table 2115: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Carbohydrate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.90e-02	1.84e-01	0.103	0.919	-3.67e-01	4.05e-01	0.000000
L3.Carbohydrate.metabolism	-1.42e-07	1.22e-06	-0.117	0.908	-2.69e-06	2.40e-06	0.000679

Table 2116: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Carbon.fixation.in.photosynthetic.organisms, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.81e-02	1.94e-01	0.196	0.847	-3.69e-01	4.45e-01	0.0000
L3.Carbon.fixation.in.photosynthetic.organisms	-8.98e-08	4.11e-07	-0.219	0.829	-9.50e-07	7.70e-07	0.0023

Table 2117: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Carbon.fixation.pathways.in.prokaryotes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.47e-02	2.04e-01	0.121	0.905	-4.02e-01	4.52e-01	0.000000
L3.Carbon.fixation.pathways.in.prokaryotes	-3.80e-08	2.85e-07	-0.133	0.895	-6.35e-07	5.59e-07	0.000888

Table 2118: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Cardiac.muscle.contraction, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.61e-03	0.088597	-0.0746	0.941	-1.92e-01	1.79e-01	0.00000
L3.Cardiac.muscle.contraction	7.16e-06	0.000023	0.3119	0.759	-4.09e-05	5.52e-05	0.00484

Table 2119: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Carotenoid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.268823	8.61e-02	3.12	0.005607	0.088628	4.49e-01	0.000
L3.Carotenoid.biosynthesis	-0.000166	3.76e-05	-4.40	0.000306	-0.000244	-8.68e-05	0.492

Table 2120: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Cell.cycle, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2121: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Cell.cycle...Caulobacter, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.18e-02	1.91e-01	0.428	0.674	-3.19e-01	4.82e-01	0.0000
L3.Cell.cycle...Caulobacter	-2.62e-07	5.49e-07	-0.478	0.638	-1.41e-06	8.86e-07	0.0113

Table 2122: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Cell.cycle...yeast, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2123: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Cell.division, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.97e-02	1.88e-01	0.318	0.754	-3.33e-01	4.53e-01	0.00000
L3.Cell.division	-1.11e-06	3.11e-06	-0.357	0.725	-7.62e-06	5.40e-06	0.00635

Table 2124: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Cell.motility.and.secretion, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.23e-02	2.04e-01	0.207	0.838	-3.85e-01	4.70e-01	0.0000
L3.Cell.motility.and.secretion	-3.74e-07	1.64e-06	-0.228	0.822	-3.80e-06	3.05e-06	0.0026

Table 2125: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Cellular.antigens, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.32e-01	1.59e-01	-2.08	0.0510	-6.65e-01	1.62e-03	0.000
L3.Cellular.antigens	1.14e-05	4.83e-06	2.37	0.0286	1.33e-06	2.16e-05	0.219

Table 2126: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Chagas.disease..American.trypanosomiasis., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.118775	0.105564	1.13	0.275	-0.102174	3.40e-01	0.00
L3.Chagas.disease..American.trypanosomiasis.	-0.000185	0.000107	-1.73	0.100	-0.000408	3.88e-05	0.13

Table 2127: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Chaperones.and.folding.catalysts, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.34e-02	2.03e-01	0.0661	0.948	-4.11e-01	4.38e-01	0.000000
L3.Chaperones.and.folding.catalysts	-2.09e-08	2.86e-07	-0.0730	0.943	-6.20e-07	5.78e-07	0.000266

Table 2128: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Chloroalkane.and.chloroalkene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.62e-01	1.63e-01	0.993	0.333	-1.79e-01	5.03e-01	0.0000
L3.Chloroalkane.and.chloroalkene.degradation	-1.43e-06	1.24e-06	-1.156	0.262	-4.02e-06	1.16e-06	0.0627

Table 2129: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Chlorocyclohexane.and.chlorobenzene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	2.07e-01	1.19e-01	1.74	0.0975	-4.16e-02	4.56e-01
L3.Chlorocyclohexane.and.chlorobenzene.degradation	-2.87e-05	1.26e-05	-2.28	0.0346	-5.51e-05	-2.31e-06

Table 2130: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Cholinergic.synapse, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2131: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Chromosome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.27e-02	1.90e-01	0.383	0.706	-3.24e-01	4.70e-01	0.00000
L3.Chromosome	-7.42e-08	1.73e-07	-0.430	0.672	-4.35e-07	2.87e-07	0.00915

Table 2132: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Chronic.myeloid.leukemia, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2133: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Circadian.rhythm...plant, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.035626	0.092822	0.384	0.705	-0.15865	0.229904	0.0000
L3.Circadian.rhythm...plant	-0.000388	0.000421	-0.921	0.369	-0.00127	0.000494	0.0407

Table 2134: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Citrate.cycle..TCA.cycle., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.39e-02	2.08e-01	-0.163	0.872	-4.69e-01	4.01e-01	0.0000
L3.Citrate.cycle..TCA.cycle.	8.42e-08	4.70e-07	0.179	0.860	-9.00e-07	1.07e-06	0.0016

Table 2135: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Clavulanic.acid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0198	0.0859	0.23	0.820	-0.16	0.200	0.0000
L3.Clavulanic.acid.biosynthesis	-0.2078	0.1968	-1.06	0.304	-0.62	0.204	0.0528

Table 2136: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Colorectal.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.38e-03	8.81e-02	-0.0724	0.943	-0.190852	0.178096	0.00000
L3.Colorectal.cancer	2.27e-05	6.86e-05	0.3304	0.745	-0.000121	0.000166	0.00543

Table 2137: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Complement.and.coagulation.cascades, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2138: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Cyanoamino.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.21e-02	1.75e-01	0.126	0.901	-3.45e-01	3.89e-01	0.00000
L3.Cyanoamino.acid.metabolism	-9.31e-08	6.44e-07	-0.145	0.887	-1.44e-06	1.26e-06	0.00104

Table 2139: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Cysteine.and.methionine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.51e-02	1.91e-01	0.499	0.624	-3.04e-01	4.94e-01	0.0000
L3.Cysteine.and.methionine.metabolism	-1.57e-07	2.81e-07	-0.558	0.583	-7.45e-07	4.31e-07	0.0153

Table 2140: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Cytochrome.P450, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2141: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Cytokine.receptors, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2142: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Cytokine.cytokine.receptor.interaction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2143: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Cytoskeleton.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.74e-02	1.71e-01	0.453	0.656	-2.80e-01	4.35e-01	0.0000
L3.Cytoskeleton.proteins	-3.15e-07	6.02e-07	-0.524	0.607	-1.58e-06	9.45e-07	0.0135

Table 2144: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Cytosolic.DNA.sensing.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2145: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.D.Alanine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.27e-01	1.85e-01	0.687	0.500	-2.60e-01	5.15e-01	0.000
L3.D.Alanine.metabolism	-1.95e-06	2.52e-06	-0.773	0.449	-7.22e-06	3.32e-06	0.029

Table 2146: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.D.Arginine.and.D.ornithine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.7e-01	1.18e-01	1.44	0.1661	-0.076947	4.17e-01	0.000
L3.D.Arginine.and.D.ornithine.metabolism	-5.2e-05	2.68e-05	-1.94	0.0678	-0.000108	4.19e-06	0.158

Table 2147: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.D.Glutamine.and.D.glutamate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.86e-02	2.02e-01	0.142	0.889	-3.93e-01	4.51e-01	0.00000
L3.D.Glutamine.and.D.glutamate.metabolism	-3.04e-07	1.94e-06	-0.157	0.877	-4.36e-06	3.75e-06	0.00123

Table 2148: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.DNA.repair.and.recombination.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.35e-02	1.92e-01	0.487	0.632	-3.08e-01	4.95e-01	0.0000
L3.DNA.repair.and.recombination.proteins	-5.36e-08	9.84e-08	-0.544	0.593	-2.60e-07	1.52e-07	0.0146

Table 2149: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.DNA.replication, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.50e-02	1.99e-01	0.378	0.71	-3.40e-01	4.91e-01	0.00000
L3.DNA.replication	-1.85e-07	4.40e-07	-0.419	0.68	-1.11e-06	7.37e-07	0.00871

Table 2150: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.DNA.replication.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.11e-02	1.97e-01	0.311	0.759	-3.5e-01	4.72e-01	0.00000
L3.DNA.replication.proteins	-7.94e-08	2.30e-07	-0.346	0.733	-5.6e-07	4.01e-07	0.00594

Table 2151: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Dilated.cardiomyopathy..DCM., df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2152: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Dioxin.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.02e-01	1.43e-01	0.715	0.483	-1.96e-01	4.00e-01	0.0000
L3.Dioxin.degradation	-3.10e-06	3.49e-06	-0.888	0.386	-1.04e-05	4.21e-06	0.0379

Table 2153: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Drug.metabolism...cytochrome.P450, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.15e-02	0.164541	-0.0698	0.945	-3.56e-01	3.33e-01	0.000000
L3.Drug.metabolism...cytochrome.P450	9.83e-07	0.000012	0.0820	0.936	-2.41e-05	2.61e-05	0.000336

Table 2154: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Drug.metabolism...other.enzymes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.25e-02	2.04e-01	0.257	0.80	-3.75e-01	4.8e-01	0.000
L3.Drug.metabolism...other.enzymes	-2.51e-07	8.86e-07	-0.283	0.78	-2.11e-06	1.6e-06	0.004

Table 2155: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.ECM.receptor.interaction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2156: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Electron.transfer.carriers, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.77e-01	1.24e-01	1.43	0.1695	-8.26e-02	4.37e-01	0.000
L3.Electron.transfer.carriers	-1.68e-05	9.04e-06	-1.86	0.0789	-3.57e-05	2.13e-06	0.147

Table 2157: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Endocrine.and.other.factor.regulated.calcium.reabsorption, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2158: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Endocytosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0177	0.0891	0.198	0.845	-0.169	0.204	0.0000
L3.Endocytosis	-0.1237	0.1827	-0.677	0.507	-0.506	0.259	0.0224

Table 2159: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Energy.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.15e-02	2.01e-01	0.207	0.839	-3.79e-01	4.62e-01	0.00000
L3.Energy.metabolism	-7.37e-08	3.22e-07	-0.229	0.822	-7.48e-07	6.01e-07	0.00261

Table 2160: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	1.13e-01	1.74e-01	0.648	0.525	-2.52e-01	4.77e-0
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	-1.91e-06	2.57e-06	-0.743	0.467	-7.30e-06	3.48e-0

Table 2161: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.ErbB.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2162: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Ether.lipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.13e-01	1.19e-01	0.948	0.355	-0.136128	3.62e-01	0.0000
L3.Ether.lipid.metabolism	-9.08e-05	6.89e-05	-1.318	0.203	-0.000235	5.34e-05	0.0799

Table 2163: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Ethylbenzene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.22e-02	1.89e-01	-0.382	0.707	-4.69e-01	3.24e-01	0.00000
L3.Ethylbenzene.degradation	2.93e-06	6.84e-06	0.428	0.673	-1.14e-05	1.72e-05	0.00908

Table 2164: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Fat.digestion.and.absorption, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2165: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Fatty.acid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.96e-02	1.92e-01	0.311	0.759	-3.42e-01	4.61e-01	0.00000
L3.Fatty.acid.biosynthesis	-1.92e-07	5.53e-07	-0.348	0.732	-1.35e-06	9.65e-07	0.00601

Table 2166: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Fatty.acid.elongation.in.mitochondria, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.034913	0.092730	0.377	0.711	-0.15917	0.228999	0.0000
L3.Fatty.acid.elongation.in.mitochondria	-0.000383	0.000421	-0.910	0.374	-0.00126	0.000498	0.0398

Table 2167: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Fatty.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.17e-01	1.90e-01	0.613	0.547	-2.82e-01	5.15e-01	0.0000
L3.Fatty.acid.metabolism	-9.06e-07	1.32e-06	-0.685	0.501	-3.68e-06	1.86e-06	0.0229

Table 2168: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Fc.epsilon.RI.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2169: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Fc.gamma.R.mediated.phagocytosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0177	0.0891	0.198	0.845	-0.169	0.204	0.0000
L3.Fc.gamma.R.mediated.phagocytosis	-0.1237	0.1827	-0.677	0.507	-0.506	0.259	0.0224

Table 2170: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Flagellar.assembly, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.67e-02	1.29e-01	0.284	0.779	-2.33e-01	3.07e-01	0.00000
L3.Flagellar.assembly	-1.93e-07	5.07e-07	-0.381	0.707	-1.25e-06	8.68e-07	0.00721

Table 2171: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Flavone.and.flavonol.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.78e-02	1.61e-01	0.483	0.635	-2.60e-01	4.15e-01	0.0000
L3.Flavone.and.flavonol.biosynthesis	-1.29e-05	2.26e-05	-0.569	0.576	-6.03e-05	3.45e-05	0.0159

Table 2172: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Flavonoid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.17e-02	1.17e-01	0.781	0.445	-0.154144	3.37e-01	0.0000
L3.Flavonoid.biosynthesis	-7.61e-05	6.85e-05	-1.111	0.280	-0.000219	6.72e-05	0.0581

Table 2173: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Fluorobenzoate.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.117028	0.112039	1.04	0.309	-0.117473	3.52e-01	0.000
L3.Fluorobenzoate.degradation	-0.000222	0.000146	-1.52	0.145	-0.000528	8.36e-05	0.104

Table 2174: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Focal.adhesion, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2175: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Folate.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.74e-02	2.11e-01	0.225	0.824	-3.93e-01	4.88e-01	0.00000
L3.Folate.biosynthesis	-1.99e-07	8.08e-07	-0.247	0.808	-1.89e-06	1.49e-06	0.00304

Table 2176: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Fructose.and.mannose.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.61e-02	1.84e-01	0.251	0.805	-3.39e-01	4.31e-01	0.00000
L3.Fructose.and.mannose.metabolism	-6.90e-08	2.43e-07	-0.284	0.780	-5.78e-07	4.40e-07	0.00401

Table 2177: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Function.unknown, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.18e-02	1.86e-01	0.386	0.704	-3.18e-01	4.61e-01	0.00000
L3.Function.unknown	-9.13e-08	2.10e-07	-0.435	0.668	-5.31e-07	3.48e-07	0.00938

Table 2178: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.G.protein.coupled.receptors, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0230	0.0962	0.239	0.814	-0.178	0.2243	0.0000
L3.G.protein.coupled.receptors	-0.0172	0.0329	-0.525	0.606	-0.086	0.0515	0.0136

Table 2179: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.GTP.binding.proteins, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2180: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Galactose.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.95e-03	1.91e-01	-0.0259	0.980	-4.04e-01	3.94e-01	0.00e+00
L3.Galactose.metabolism	8.56e-09	2.94e-07	0.0291	0.977	-6.07e-07	6.24e-07	4.23e-05

Table 2181: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Gastric.acid.secretion, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2182: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.General.function.prediction.only, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.93e-02	1.94e-01	0.358	0.724	-3.36e-01	4.74e-01	0.0000
L3.General.function.prediction.only	-2.96e-08	7.42e-08	-0.399	0.694	-1.85e-07	1.26e-07	0.0079

Table 2183: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Geraniol.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.38e-01	1.98e-01	-1.71	0.1039	-7.52e-01	7.62e-02	0.000
L3.Geraniol.degradation	1.69e-05	9.07e-06	1.86	0.0778	-2.07e-06	3.59e-05	0.148

Table 2184: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Germination, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.15e-01	1.30e-01	0.879	0.390	-1.58e-01	3.87e-01	0.0000
L3.Germination	-4.55e-06	3.98e-06	-1.144	0.267	-1.29e-05	3.77e-06	0.0614

Table 2185: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Glioma, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2186: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Glutamatergic.synapse, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.88e-02	1.92e-01	-0.461	0.650	-4.92e-01	3.14e-01	0.0000
L3.Glutamatergic.synapse	1.22e-06	2.37e-06	0.515	0.613	-3.75e-06	6.19e-06	0.0131

Table 2187: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Glutathione.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.16e-03	2.32e-01	0.0179	0.986	-4.82e-01	4.90e-01	0.00e+00
L3.Glutathione.metabolism	-3.59e-08	1.86e-06	-0.0193	0.985	-3.93e-06	3.86e-06	1.87e-05

Table 2188: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Glycan.bindng.proteins, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2189: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Glycan.biosynthesis.and.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.74e-02	1.76e-01	-0.552	0.588	-4.67e-01	2.72e-01	0.0000
L3.Glycan.biosynthesis.and.metabolism	6.12e-06	9.71e-06	0.630	0.536	-1.42e-05	2.65e-05	0.0195

Table 2190: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Glycerolipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.07e-01	1.65e-01	0.648	0.525	-2.38e-01	4.52e-01	0.0000
L3.Glycerolipid.metabolism	-4.40e-07	5.83e-07	-0.756	0.459	-1.66e-06	7.79e-07	0.0278

Table 2191: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Glycerophospholipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.65e-02	1.77e-01	0.489	0.630	-2.84e-01	4.57e-01	0.0000
L3.Glycerophospholipid.metabolism	-2.50e-07	4.48e-07	-0.559	0.583	-1.19e-06	6.86e-07	0.0154

Table 2192: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Glycine..serine.and.threonine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.04e-01	2.00e-01	0.519	0.610	-3.14e-01	5.21e-01	0.0000
L3.Glycine..serine.and.threonine.metabolism	-1.91e-07	3.33e-07	-0.574	0.573	-8.88e-07	5.06e-07	0.0162

Table 2193: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Glycolysis...Gluconeogenesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.52e-02	1.87e-01	0.401	0.693	-3.17e-01	4.67e-01	0.0000
L3.Glycolysis...Gluconeogenesis	-1.05e-07	2.33e-07	-0.451	0.657	-5.93e-07	3.83e-07	0.0101

Table 2194: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Glycosaminoglycan.biosynthesis. . . chondroitin.sulfate, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	0.00515	0.0884	0.0583	0.954	-0.1798	0.1901
L3.Glycosaminoglycan.biosynthesis. . . chondroitin.sulfate	-0.00387	0.0150	-0.2578	0.799	-0.0352	0.0275

Table 2195: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Glycosaminoglycan.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.91e-01	1.33e-01	-2.94	0.00839	-6.69e-01	-1.13e-01	0.000
L3.Glycosaminoglycan.degradation	5.94e-06	1.74e-06	3.42	0.00287	2.30e-06	9.57e-06	0.369

Table 2196: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Glycosphingolipid.biosynthesis. . . ganglio.series, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.67e-01	1.16e-01	-3.17	0.00509	-6.1e-01	-1.24e-01	0.00
L3.Glycosphingolipid.biosynthesis. . . ganglio.series	8.19e-06	2.15e-06	3.82	0.00116	3.7e-06	1.27e-05	0.42

Table 2197: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Glycosphingolipid.biosynthesis. . . globo.series, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.31e-01	1.72e-01	-1.92	0.0694	-6.91e-01	2.9e-02	0.000
L3.Glycosphingolipid.biosynthesis. . . globo.series	3.60e-06	1.67e-06	2.15	0.0442	1.03e-07	7.1e-06	0.188

Table 2198: diversity_vs_picrust_L3_yr1: wunifrac.PC.1
vs L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series,
df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	-0.05642	0.084461	-0.668	0.5122	-2.33e-01	0.12
L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series	0.00028	0.000147	1.899	0.0728	-2.85e-05	0.00

Table 2199: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Glycosylphosphatidylinositol.GPI..anchor.biosynthesis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2200: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Glycosyltransferases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.86e-02	2.15e-01	0.226	0.824	-4.01e-01	4.99e-01	0.00000
L3.Glycosyltransferases	-2.24e-07	9.07e-07	-0.246	0.808	-2.12e-06	1.67e-06	0.00303

Table 2201: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Glyoxylate.and.dicarboxylate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.43e-02	1.90e-01	0.391	0.700	-3.23e-01	4.72e-01	0.00000
L3.Glyoxylate.and.dicarboxylate.metabolism	-2.09e-07	4.76e-07	-0.439	0.666	-1.21e-06	7.88e-07	0.00952

Table 2202: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.GnRH.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0177	0.0891	0.198	0.845	-0.169	0.204	0.0000
L3.GnRH.signaling.pathway	-0.1237	0.1827	-0.677	0.507	-0.506	0.259	0.0224

Table 2203: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Hedgehog.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2204: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Hematopoietic.cell.lineage, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2205: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Hepatitis.C, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2206: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Histidine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.30e-02	1.96e-01	0.168	0.868	-3.77e-01	4.43e-01	0.00000
L3.Histidine.metabolism	-7.82e-08	4.17e-07	-0.187	0.853	-9.52e-07	7.95e-07	0.00175

Table 2207: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Homologous.recombination, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.04e-02	1.95e-01	0.362	0.722	-3.37e-01	4.78e-01	0.00000
L3.Homologous.recombination	-1.22e-07	3.03e-07	-0.403	0.692	-7.57e-07	5.13e-07	0.00805

Table 2208: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Huntington.s.disease, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.79e-02	1.77e-01	0.326	0.748	-3.14e-01	0.429408	0.0000
L3.Huntington.s.disease	-3.26e-06	8.74e-06	-0.373	0.713	-2.16e-05	0.000015	0.0069

Table 2209: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Hypertrophic.cardiomyopathy..HCM., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00424	0.0883	0.048	0.962	-0.180	0.189	0.00000
L3.Hypertrophic.cardiomyopathy..HCM.	-0.01272	0.0578	-0.220	0.828	-0.134	0.108	0.00242

Table 2210: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Indole.alkaloid.biosynthesis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2211: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Influenza.A, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.38e-03	8.81e-02	-0.0724	0.943	-0.190852	0.178096	0.00000
L3.Influenza.A	2.27e-05	6.86e-05	0.3304	0.745	-0.000121	0.000166	0.00543

Table 2212: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Inorganic.ion.transport.and.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.33e-02	1.93e-01	-0.224	0.825	-4.47e-01	3.61e-01	0.00000
L3.Inorganic.ion.transport.and.metabolism	3.48e-07	1.39e-06	0.251	0.805	-2.56e-06	3.25e-06	0.00313

Table 2213: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Inositol.phosphate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.29e-02	1.98e-01	0.116	0.909	-3.92e-01	4.38e-01	0.000000
L3.Inositol.phosphate.metabolism	-3.68e-07	2.87e-06	-0.128	0.899	-6.37e-06	5.64e-06	0.000823

Table 2214: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Insulin.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.31e-02	1.74e-01	-0.0751	0.941	-3.77e-01	3.51e-01	0.000000
L3.Insulin.signaling.pathway	2.40e-07	2.77e-06	0.0865	0.932	-5.56e-06	6.04e-06	0.000374

Table 2215: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Ion.channels, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.76e-02	2.05e-01	0.428	0.674	-3.41e-01	5.16e-01	0.000
L3.Ion.channels	-9.62e-06	2.04e-05	-0.471	0.643	-5.24e-05	3.31e-05	0.011

Table 2216: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Isoflavonoid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00533	0.0901	-0.0591	0.953	-0.194	0.183	0.00000
L3.Isoflavonoid.biosynthesis	0.03729	0.1847	0.2019	0.842	-0.349	0.424	0.00203

Table 2217: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Isoquinoline.alkaloid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.48e-03	2.25e-01	0.0244	0.981	-4.65e-01	4.76e-01	0.00e+00
L3.Isoquinoline.alkaloid.biosynthesis	-1.46e-07	5.53e-06	-0.0264	0.979	-1.17e-05	1.14e-05	3.48e-05

Table 2218: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Leishmaniasis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2219: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Leukocyte.transendothelial.migration, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2220: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Limonene.and.pinene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.66e-01	1.87e-01	0.885	0.387	-2.26e-01	5.58e-01	0.0000
L3.Limonene.and.pinene.degradation	-3.65e-06	3.69e-06	-0.990	0.335	-1.14e-05	4.07e-06	0.0467

Table 2221: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Linoleic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.92e-03	1.83e-01	-0.0432	0.966	-3.92e-01	3.76e-01	0.00000
L3.Linoleic.acid.metabolism	1.53e-07	3.13e-06	0.0490	0.961	-6.39e-06	6.70e-06	0.00012

Table 2222: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Lipid.biosynthesis.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.94e-02	1.98e-01	0.148	0.884	-3.86e-01	4.45e-01	0.00000
L3.Lipid.biosynthesis.proteins	-7.89e-08	4.80e-07	-0.164	0.871	-1.08e-06	9.26e-07	0.00135

Table 2223: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Lipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.52e-02	1.69e-01	0.504	0.620	-2.69e-01	4.39e-01	0.0000
L3.Lipid.metabolism	-9.97e-07	1.71e-06	-0.584	0.566	-4.57e-06	2.58e-06	0.0168

Table 2224: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Lipoic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.58e-01	1.71e-01	-1.51	0.148	-6.16e-01	1.00e-01	0.000
L3.Lipoic.acid.metabolism	1.09e-05	6.37e-06	1.71	0.104	-2.45e-06	2.42e-05	0.127

Table 2225: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Lipopolysaccharide.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.42e-01	1.99e-01	-0.715	0.483	-5.59e-01	2.74e-01	0.0000
L3.Lipopolysaccharide.biosynthesis	9.03e-07	1.14e-06	0.791	0.439	-1.49e-06	3.29e-06	0.0303

Table 2226: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Lipopolysaccharide.biosynthesis.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.45e-01	2.13e-01	-0.679	0.505	-5.91e-01	3.01e-01	0.0000
L3.Lipopolysaccharide.biosynthesis.proteins	6.10e-07	8.24e-07	0.741	0.468	-1.11e-06	2.33e-06	0.0267

Table 2227: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Long.term.depression, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2228: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Long.term.potentiation, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2229: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Lysine.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.07e-01	1.81e-01	0.593	0.56	-2.72e-01	4.86e-01	0.0000
L3.Lysine.biosynthesis	-1.96e-07	2.91e-07	-0.672	0.51	-8.06e-07	4.14e-07	0.0221

Table 2230: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Lysine.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.66e-01	1.96e-01	0.849	0.406	-2.43e-01	5.76e-01	0.0000
L3.Lysine.degradation	-2.23e-06	2.37e-06	-0.941	0.358	-7.18e-06	2.73e-06	0.0424

Table 2231: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Lysosome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.56e-01	1.60e-01	-2.22	0.0386	-6.91e-01	-2.07e-02	0.00
L3.Lysosome	3.50e-06	1.39e-06	2.51	0.0211	5.86e-07	6.42e-06	0.24

Table 2232: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.MAPK.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2233: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.MAPK.signaling.pathway. . . yeast, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.32e-02	2.06e-01	-0.355	0.726	-5.05e-01	3.58e-01	0.00000
L3.MAPK.signaling.pathway. . . yeast	2.32e-06	5.94e-06	0.391	0.700	-1.01e-05	1.47e-05	0.00757

Table 2234: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Measles, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2235: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Meiosis. . . yeast, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.17e-02	9.64e-02	0.122	0.904	-1.90e-01	2.13e-01	0.00000
L3.Meiosis. . . yeast	-7.01e-06	2.59e-05	-0.271	0.789	-6.12e-05	4.71e-05	0.00366

Table 2236: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Melanogenesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.002279	0.09223	0.0247	0.981	-0.1908	0.1953	0.000000
L3.Melanogenesis	-0.000352	0.00505	-0.0697	0.945	-0.0109	0.0102	0.000243

Table 2237: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Membrane.and.intracellular.structural.molecules, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.49e-01	2.09e-01	-1.2	0.247	-6.86e-01	1.87e-01	0.0
L3.Membrane.and.intracellular.structural.molecules	6.89e-07	5.29e-07	1.3	0.209	-4.19e-07	1.80e-06	0.0

Table 2238: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Metabolism.of.cofactors.and.vitamins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.37e-01	1.65e-01	0.828	0.418	-2.09e-01	4.83e-01	0.0000
L3.Metabolism.of.cofactors.and.vitamins	-1.95e-06	2.02e-06	-0.962	0.348	-6.19e-06	2.29e-06	0.0442

Table 2239: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Metabolism.of.xenobiotics.by.cytochrome.P450, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.44e-02	0.163127	-0.0881	0.931	-3.56e-01	3.27e-01	0.00
L3.Metabolism.of.xenobiotics.by.cytochrome.P450	1.25e-06	0.000012	0.1038	0.918	-2.39e-05	2.64e-05	0.00

Table 2240: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Methane.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.09e-01	1.81e-01	0.603	0.553	-2.70e-01	4.88e-01	0.0000
L3.Methane.metabolism	-1.30e-07	1.90e-07	-0.684	0.502	-5.27e-07	2.67e-07	0.0228

Table 2241: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Mineral.absorption, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.40e-02	1.23e-01	-0.114	0.911	-0.271700	0.243711	0.00000
L3.Mineral.absorption	8.37e-06	5.26e-05	0.159	0.875	-0.000102	0.000118	0.00126

Table 2242: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Mismatch.repair, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.32e-02	1.91e-01	0.435	0.668	-3.17e-01	4.83e-01	0.0000
L3.Mismatch.repair	-1.62e-07	3.32e-07	-0.487	0.632	-8.57e-07	5.33e-07	0.0117

Table 2243: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.N.Glycan.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.05e-01	1.94e-01	0.543	0.593	-3.00e-01	5.11e-01	0.000
L3.N.Glycan.biosynthesis	-6.61e-06	1.09e-05	-0.605	0.552	-2.95e-05	1.63e-05	0.018

Table 2244: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.NOD.like.receptor.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.14e-02	1.96e-01	-0.313	0.758	-4.72e-01	3.49e-01	0.00000
L3.NOD.like.receptor.signaling.pathway	2.15e-06	6.19e-06	0.348	0.732	-1.08e-05	1.51e-05	0.00602

Table 2245: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Naphthalene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.58e-02	1.93e-01	0.0820	0.936	-3.89e-01	4.20e-01	0.000000
L3.Naphthalene.degradation	-1.97e-07	2.16e-06	-0.0916	0.928	-4.71e-06	4.31e-06	0.000419

Table 2246: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Neuroactive.ligand.receptor.interaction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2247: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Neurotrophin.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2248: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Nicotinate.and.nicotinamide.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.27e-02	1.92e-01	0.378	0.709	-3.30e-01	4.75e-01	0.00000
L3.Nicotinate.and.nicotinamide.metabolism	-2.76e-07	6.54e-07	-0.423	0.677	-1.65e-06	1.09e-06	0.00885

Table 2249: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Nitrogen.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.53e-02	2.06e-01	0.365	0.719	-3.56e-01	5.06e-01	0.00000
L3.Nitrogen.metabolism	-1.56e-07	3.87e-07	-0.402	0.692	-9.65e-07	6.54e-07	0.00802

Table 2250: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Nitrotoluene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.56e-01	1.36e-01	1.15	0.264	-1.28e-01	4.41e-01	0.0000
L3.Nitrotoluene.degradation	-2.41e-06	1.67e-06	-1.44	0.165	-5.90e-06	1.08e-06	0.0943

Table 2251: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Non.homologous.end.joining, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.79e-02	1.25e-01	0.465	0.647	-2.03e-01	3.19e-01	0.00
L3.Non.homologous.end.joining	-1.84e-05	2.88e-05	-0.638	0.531	-7.86e-05	4.19e-05	0.02

Table 2252: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Notch.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2253: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Novobiocin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.01e-02	1.92e-01	0.470	0.644	-3.11e-01	4.92e-01	0.0000
L3.Novobiocin.biosynthesis	-1.05e-06	1.99e-06	-0.525	0.606	-5.22e-06	3.13e-06	0.0136

Table 2254: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Nucleotide.excision.repair, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.82e-02	1.86e-01	0.475	0.640	-3.00e-01	4.76e-01	0.0000
L3.Nucleotide.excision.repair	-3.62e-07	6.76e-07	-0.536	0.598	-1.78e-06	1.05e-06	0.0141

Table 2255: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Nucleotide.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.51e-01	1.47e-01	1.03	0.316	-1.56e-01	4.59e-01	0.0000
L3.Nucleotide.metabolism	-5.45e-06	4.37e-06	-1.25	0.227	-1.46e-05	3.70e-06	0.0722

Table 2256: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Olfactory.transduction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2257: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.One.carbon.pool.by.folate, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.96e-02	2.03e-01	0.194	0.848	-3.86e-01	4.65e-01	0.0000
L3.One.carbon.pool.by.folate	-1.01e-07	4.69e-07	-0.215	0.832	-1.08e-06	8.81e-07	0.0023

Table 2258: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Oocyte.meiosis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2259: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Other.glycan.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.73e-01	1.96e-01	-1.39	0.181	-6.84e-01	1.38e-01	0.000
L3.Other.glycan.degradation	9.66e-07	6.32e-07	1.53	0.143	-3.58e-07	2.29e-06	0.104

Table 2260: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Other.ion.coupled.transporters, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.88e-02	2.06e-01	0.188	0.853	-3.93e-01	4.70e-01	0.00000
L3.Other.ion.coupled.transporters	-4.39e-08	2.12e-07	-0.207	0.838	-4.87e-07	3.99e-07	0.00214

Table 2261: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Other.transporters, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.53e-02	1.94e-01	0.182	0.858	-3.71e-01	4.41e-01	0.00000
L3.Other.transporters	-2.00e-07	9.86e-07	-0.203	0.841	-2.26e-06	1.86e-06	0.00206

Table 2262: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Other.types.of.O.glycan.biosynthesis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2263: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Others, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.27e-02	1.91e-01	0.433	0.670	-3.17e-01	4.82e-01	0.0000
L3.Others	-1.35e-07	2.77e-07	-0.485	0.633	-7.15e-07	4.46e-07	0.0116

Table 2264: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Oxidative.phosphorylation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.81e-02	1.91e-01	0.305	0.764	-3.41e-01	4.58e-01	0.00000
L3.Oxidative.phosphorylation	-7.80e-08	2.28e-07	-0.341	0.737	-5.56e-07	4.00e-07	0.00579

Table 2265: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.PPAR.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.22e-01	2.05e-01	-0.595	0.559	-5.52e-01	3.08e-01	0.0000
L3.PPAR.signaling.pathway	1.72e-06	2.63e-06	0.654	0.521	-3.78e-06	7.22e-06	0.0209

Table 2266: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Pancreatic.cancer, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2267: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Pancreatic.secretion, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2268: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Pantothenate.and.CoA.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.67e-02	1.84e-01	0.472	0.642	-2.98e-01	4.71e-01	0.000
L3.Pantothenate.and.CoA.biosynthesis	-2.11e-07	3.96e-07	-0.533	0.600	-1.04e-06	6.18e-07	0.014

Table 2269: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Parkinson.s.disease, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.56e-03	8.85e-02	-0.0741	0.942	-1.92e-01	1.79e-01	0.00000
L3.Parkinson.s.disease	5.43e-06	1.72e-05	0.3156	0.756	-3.06e-05	4.14e-05	0.00496

Table 2270: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Pathogenic.Escherichia.coli.infection, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2271: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Pathways.in.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.14e-02	1.83e-01	0.282	0.781	-3.31e-01	4.34e-01	0.00000
L3.Pathways.in.cancer	-1.70e-06	5.33e-06	-0.319	0.753	-1.29e-05	9.46e-06	0.00507

Table 2272: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Penicillin.and.cephalosporin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.08e-01	1.76e-01	-1.19	0.250	-5.76e-01	0.15949	0.0000
L3.Penicillin.and.cephalosporin.biosynthesis	1.17e-05	8.74e-06	1.34	0.195	-6.56e-06	0.00003	0.0826

Table 2273: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Pentose.and.glucuronate.interconversions, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.94e-02	1.95e-01	0.0993	0.922	-3.89e-01	4.28e-01	0.000000
L3.Pentose.and.glucuronate.interconversions	-4.50e-08	4.07e-07	-0.1107	0.913	-8.97e-07	8.07e-07	0.000612

Table 2274: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Pentose.phosphate.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.16e-02	1.85e-01	0.440	0.665	-3.06e-01	4.70e-01	0.0000
L3.Pentose.phosphate.pathway	-1.37e-07	2.76e-07	-0.496	0.626	-7.15e-07	4.41e-07	0.0122

Table 2275: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Peptidases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.84e-02	1.95e-01	0.351	0.729	-3.40e-01	4.76e-01	0.00000
L3.Peptidases	-5.72e-08	1.46e-07	-0.391	0.700	-3.64e-07	2.49e-07	0.00759

Table 2276: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Peptidoglycan.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.10e-01	1.86e-01	0.593	0.560	-2.79e-01	4.99e-01	0.0000
L3.Peptidoglycan.biosynthesis	-2.17e-07	3.25e-07	-0.668	0.512	-8.98e-07	4.64e-07	0.0218

Table 2277: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Peroxisome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.26e-02	2.11e-01	-0.345	0.734	-5.13e-01	3.68e-01	0.00000
L3.Peroxisome	6.30e-07	1.67e-06	0.378	0.710	-2.86e-06	4.12e-06	0.00708

Table 2278: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Pertussis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.79e-01	1.86e-01	-1.50	0.150	-6.69e-01	1.10e-01	0.000
L3.Pertussis	1.52e-05	9.14e-06	1.66	0.112	-3.91e-06	3.43e-05	0.122

Table 2279: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Phagosome, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2280: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Phenylalanine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.12e-02	2.00e-01	-0.106	0.917	-4.39e-01	3.97e-01	0.000000
L3.Phenylalanine.metabolism	1.75e-07	1.49e-06	0.118	0.908	-2.95e-06	3.30e-06	0.000691

Table 2281: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	9.18e-02	1.82e-01	0.504	0.620	-2.89e-01	4.73e-01
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis	-1.67e-07	2.93e-07	-0.571	0.575	-7.81e-07	4.47e-07

Table 2282: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Phenylpropanoid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.73e-02	1.60e-01	0.170	0.866	-3.08e-01	3.63e-01	0.00000
L3.Phenylpropanoid.biosynthesis	-1.83e-07	9.04e-07	-0.202	0.842	-2.07e-06	1.71e-06	0.00204

Table 2283: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Phosphatidylinositol.signaling.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.10e-02	2.07e-01	0.0529	0.958	-4.23e-01	4.45e-01	0.000000
L3.Phosphatidylinositol.signaling.system	-1.91e-07	3.29e-06	-0.0581	0.954	-7.07e-06	6.69e-06	0.000169

Table 2284: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Phosphonate.and.phosphinate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.05e-02	1.87e-01	-0.376	0.711	-4.62e-01	3.21e-01	0.00000
L3.Phosphonate.and.phosphinate.metabolism	1.62e-06	3.82e-06	0.424	0.677	-6.38e-06	9.62e-06	0.00889

Table 2285: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Phosphotransferase.system..PTS., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.20e-01	1.33e-01	0.907	0.376	-1.57e-01	3.98e-01	0.0000
L3.Phosphotransferase.system..PTS.	-4.84e-07	4.15e-07	-1.166	0.258	-1.35e-06	3.85e-07	0.0636

Table 2286: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Photosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e-01	1.66e-01	0.605	0.552	-2.47e-01	4.48e-01	0.0000
L3.Photosynthesis	-3.72e-07	5.28e-07	-0.705	0.490	-1.48e-06	7.34e-07	0.0242

Table 2287: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Photosynthesis. . .antenna.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.012162	0.091149	0.133	0.895	-0.17862	0.202940	0.00000
L3.Photosynthesis. . .antenna.proteins	-0.000174	0.000436	-0.398	0.695	-0.00109	0.000739	0.00788

Table 2288: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Photosynthesis.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.01e-01	1.66e-01	0.608	0.550	-2.46e-01	4.48e-01	0.0000
L3.Photosynthesis.proteins	-3.72e-07	5.25e-07	-0.708	0.487	-1.47e-06	7.27e-07	0.0245

Table 2289: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Phototransduction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2290: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Phototransduction. . . fly, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2291: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Plant.pathogen.interaction, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.13e-02	1.72e-01	0.413	0.684	-2.90e-01	4.32e-01	0.0000
L3.Plant.pathogen.interaction	-7.21e-07	1.51e-06	-0.476	0.639	-3.89e-06	2.45e-06	0.0112

Table 2292: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Polycyclic.aromatic.hydrocarbon.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.04e-02	1.86e-01	0.324	0.749	-3.29e-01	4.50e-01	0.000
L3.Polycyclic.aromatic.hydrocarbon.degradation	-8.65e-07	2.37e-06	-0.365	0.719	-5.82e-06	4.09e-06	0.006

Table 2293: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Polyketide.sugar.unit.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.28e-02	2.06e-01	-0.0618	0.951	-4.45e-01	4.19e-01	0.000000
L3.Polyketide.sugar.unit.biosynthesis	8.76e-08	1.29e-06	0.0681	0.946	-2.61e-06	2.78e-06	0.000232

Table 2294: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Pores.ion.channels, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.15e-01	2.17e-01	-1.46	0.162	-7.69e-01	1.38e-01	0.00
L3.Pores.ion.channels	1.33e-06	8.51e-07	1.57	0.133	-4.46e-07	3.12e-06	0.11

Table 2295: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Porphyrin.and.chlorophyll.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.83e-01	1.75e-01	1.05	0.308	-1.83e-01	5.48e-01	0.0000
L3.Porphyrin.and.chlorophyll.metabolism	-2.75e-07	2.31e-07	-1.19	0.248	-7.59e-07	2.09e-07	0.0662

Table 2296: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Prenyltransferases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.01e-02	2.04e-01	0.147	0.884	-3.97e-01	4.57e-01	0.00000
L3.Prenyltransferases	-1.56e-07	9.57e-07	-0.163	0.872	-2.16e-06	1.85e-06	0.00132

Table 2297: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Primary.bile.acid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.60e-01	1.66e-01	-0.968	0.345	-5.07e-01	1.86e-01	0.0000
L3.Primary.bile.acid.biosynthesis	5.79e-06	5.17e-06	1.121	0.276	-5.02e-06	1.66e-05	0.0591

Table 2298: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Primary.immunodeficiency, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.36e-02	1.88e-01	0.179	0.860	-3.59e-01	4.26e-01	0.00000
L3.Primary.immunodeficiency	-1.09e-06	5.39e-06	-0.202	0.842	-1.24e-05	1.02e-05	0.00203

Table 2299: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Prion.diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.74e-01	1.24e-01	1.40	0.1765	-0.085220	4.32e-01	0.000
L3.Prion.diseases	-4.48e-05	2.44e-05	-1.83	0.0825	-0.000096	6.36e-06	0.144

Table 2300: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Progesterone.mediated.oocyte.maturation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.4e-02	1.88e-01	0.181	0.858	-3.59e-01	0.427577	0.00000
L3.Progesterone.mediated.oocyte.maturation	-1.3e-06	6.37e-06	-0.204	0.841	-1.46e-05	0.000012	0.00207

Table 2301: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Propanoate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.39e-01	1.88e-01	0.738	0.469	-2.54e-01	5.32e-01	0.0000
L3.Propanoate.metabolism	-4.50e-07	5.44e-07	-0.827	0.418	-1.59e-06	6.88e-07	0.0331

Table 2302: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Prostate.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.43e-03	1.91e-01	-0.00749	0.994	-4.01e-01	3.99e-01	0.00e+00
L3.Prostate.cancer	5.08e-08	6.05e-06	0.00840	0.993	-1.26e-05	1.27e-05	3.53e-06

Table 2303: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Proteasome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.01e-02	1.85e-01	0.271	0.790	-3.38e-01	4.38e-01	0.00000
L3.Proteasome	-1.85e-06	6.05e-06	-0.306	0.763	-1.45e-05	1.08e-05	0.00465

Table 2304: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Protein.digestion.and.absorption, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.46e-01	1.32e-01	-2.62	0.01674	-6.23e-01	-7.00e-02	0.000
L3.Protein.digestion.and.absorption	1.98e-05	6.40e-06	3.10	0.00592	6.43e-06	3.32e-05	0.324

Table 2305: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Protein.export, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.13e-02	1.94e-01	0.419	0.680	-3.25e-01	4.87e-01	0.0000
L3.Protein.export	-2.16e-07	4.62e-07	-0.467	0.646	-1.18e-06	7.51e-07	0.0108

Table 2306: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Protein.folding.and.associated.processing, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.32e-01	1.94e-01	0.677	0.506	-2.75e-01	5.38e-01	0.0000
L3.Protein.folding.and.associated.processing	-3.23e-07	4.29e-07	-0.753	0.461	-1.22e-06	5.75e-07	0.0276

Table 2307: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Protein.kinases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.24e-01	1.67e-01	0.744	0.466	-2.25e-01	4.73e-01	0.0000
L3.Protein.kinases	-6.32e-07	7.32e-07	-0.863	0.399	-2.16e-06	9.01e-07	0.0359

Table 2308: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Protein.processing.in.endoplasmic.reticulum, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.12e-01	2.13e-01	-0.998	0.331	-6.57e-01	2.33e-01	0.0000
L3.Protein.processing.in.endoplasmic.reticulum	5.05e-06	4.65e-06	1.086	0.291	-4.69e-06	1.48e-05	0.0557

Table 2309: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Proximal.tubule.bicarbonate.reclamation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.61e-01	1.40e-01	-1.86	0.0786	-5.54e-01	3.28e-02	0.000
L3.Proximal.tubule.bicarbonate.reclamation	1.87e-05	8.42e-06	2.22	0.0386	1.09e-06	3.63e-05	0.198

Table 2310: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Purine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.97e-02	1.94e-01	0.513	0.614	-3.07e-01	5.07e-01	0.0000
L3.Purine.metabolism	-7.20e-08	1.26e-07	-0.571	0.575	-3.36e-07	1.92e-07	0.0161

Table 2311: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Pyrimidine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.61e-02	1.96e-01	0.441	0.664	-3.23e-01	4.95e-01	0.0000
L3.Pyrimidine.metabolism	-7.52e-08	1.53e-07	-0.490	0.630	-3.96e-07	2.46e-07	0.0119

Table 2312: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Pyruvate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.54e-02	1.90e-01	0.344	0.735	-3.33e-01	4.64e-01	0.00000
L3.Pyruvate.metabolism	-9.73e-08	2.52e-07	-0.385	0.704	-6.26e-07	4.31e-07	0.00738

Table 2313: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.RIG.I.like.receptor.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.143151	9.95e-02	1.44	0.1665	-0.065122	3.51e-01	0.000
L3.RIG.I.like.receptor.signaling.pathway	-0.000107	4.75e-05	-2.25	0.0362	-0.000206	-7.65e-06	0.203

Table 2314: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.RNA.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.74e-02	2.01e-01	0.335	0.741	-3.54e-01	4.89e-01	0.00000
L3.RNA.degradation	-2.22e-07	5.99e-07	-0.370	0.715	-1.48e-06	1.03e-06	0.00681

Table 2315: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.RNA.polymerase, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.48e-01	1.89e-01	0.783	0.443	-2.48e-01	5.44e-01	0.0000
L3.RNA.polymerase	-1.57e-06	1.79e-06	-0.875	0.393	-5.31e-06	2.18e-06	0.0369

Table 2316: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.RNA.transport, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.15e-01	1.65e-01	0.695	0.496	-2.31e-01	4.61e-01	0.0000
L3.RNA.transport	-1.32e-06	1.62e-06	-0.809	0.428	-4.72e-06	2.09e-06	0.0317

Table 2317: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Regulation.of.actin.cytoskeleton, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2318: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Renal.cell.carcinoma, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.23e-01	1.42e-01	0.865	0.398	-1.74e-01	4.19e-01	0.0000
L3.Renal.cell.carcinoma	-3.34e-05	3.12e-05	-1.072	0.297	-9.87e-05	3.19e-05	0.0543

Table 2319: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Renin.angiotensin.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0136	0.0895	0.152	0.881	-0.1737	0.2009	0.0000
L3.Renin.angiotensin.system	-0.0190	0.0364	-0.522	0.608	-0.0952	0.0572	0.0134

Table 2320: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Replication..recombination.and.repair.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.42e-01	1.75e-01	0.810	0.428	-2.25e-01	5.09e-01	0.00
L3.Replication..recombination.and.repair.proteins	-2.96e-07	3.20e-07	-0.924	0.367	-9.67e-07	3.75e-07	0.04

Table 2321: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Restriction.enzyme, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.23e-01	1.97e-01	-1.13	0.272	-6.34e-01	1.89e-01	0.0000
L3.Restriction.enzyme	1.92e-06	1.54e-06	1.25	0.227	-1.30e-06	5.15e-06	0.0723

Table 2322: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Retinol.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.34e-01	1.66e-01	-0.811	0.427	-4.81e-01	2.13e-01	0.0000
L3.Retinol.metabolism	9.09e-06	9.65e-06	0.942	0.358	-1.11e-05	2.93e-05	0.0425

Table 2323: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Rheumatoid.arthritis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2324: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Riboflavin.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.30e-02	2.06e-01	0.160	0.875	-3.99e-01	4.65e-01	0.00000
L3.Riboflavin.metabolism	-2.22e-07	1.26e-06	-0.176	0.862	-2.86e-06	2.42e-06	0.00155

Table 2325: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Ribosome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.66e-02	1.89e-01	0.510	0.616	-3.00e-01	4.93e-01	0.0000
L3.Ribosome	-6.77e-08	1.18e-07	-0.572	0.574	-3.15e-07	1.80e-07	0.0161

Table 2326: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Ribosome.Biogenesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.11e-01	1.83e-01	0.607	0.551	-2.72e-01	4.94e-01	0.000
L3.Ribosome.Biogenesis	-1.29e-07	1.89e-07	-0.686	0.501	-5.25e-07	2.66e-07	0.023

Table 2327: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Ribosome.biogenesis.in.eukaryotes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.36e-02	1.83e-01	0.510	0.616	-2.90e-01	4.77e-01	0.0000
L3.Ribosome.biogenesis.in.eukaryotes	-3.23e-06	5.59e-06	-0.577	0.571	-1.49e-05	8.48e-06	0.0164

Table 2328: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Salivary.secretion, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2329: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Secondary.bile.acid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.76e-01	1.66e-01	-1.06	0.302	-5.24e-01	1.72e-01	0.0000
L3.Secondary.bile.acid.biosynthesis	6.54e-06	5.34e-06	1.22	0.236	-4.63e-06	1.77e-05	0.0698

Table 2330: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Secretion.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.04e-02	1.70e-01	0.531	0.602	-2.66e-01	4.47e-01	0.0000
L3.Secretion.system	-1.38e-07	2.25e-07	-0.613	0.547	-6.09e-07	3.33e-07	0.0185

Table 2331: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Selenocompound.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.09e-01	1.88e-01	0.581	0.568	-2.84e-01	5.02e-01	0.0000
L3.Selenocompound.metabolism	-4.66e-07	7.14e-07	-0.652	0.522	-1.96e-06	1.03e-06	0.0208

Table 2332: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Sesquiterpenoid.biosynthesis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2333: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Shigellosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.0191	0.0925	-0.207	0.838	-0.2128	0.1746	0.0000
L3.Shigellosis	0.0100	0.0185	0.543	0.593	-0.0287	0.0487	0.0145

Table 2334: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Signal.transduction.mechanisms, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.56e-01	1.70e-01	0.915	0.372	-2.00e-01	5.11e-01	0.0000
L3.Signal.transduction.mechanisms	-5.28e-07	5.02e-07	-1.052	0.306	-1.58e-06	5.23e-07	0.0524

Table 2335: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Small.cell.lung.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.38e-03	8.81e-02	-0.0724	0.943	-0.190852	0.178096	0.00000
L3.Small.cell.lung.cancer	2.27e-05	6.86e-05	0.3304	0.745	-0.000121	0.000166	0.00543

Table 2336: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Sphingolipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.99e-01	1.92e-01	-1.03	0.314	-6.01e-01	2.03e-01	0.0000
L3.Sphingolipid.metabolism	9.81e-07	8.54e-07	1.15	0.265	-8.06e-07	2.77e-06	0.0619

Table 2337: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Spliceosome, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2338: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Sporulation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.30e-01	1.38e-01	0.938	0.360	-1.59e-01	4.19e-01	0.0000
L3.Sporulation	-2.67e-07	2.27e-07	-1.176	0.254	-7.43e-07	2.08e-07	0.0647

Table 2339: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Staphylococcus.aureus.infection, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.49e-01	1.19e-01	1.25	0.227	-1.00e-01	3.97e-01	0.000
L3.Staphylococcus.aureus.infection	-4.37e-05	2.58e-05	-1.70	0.106	-9.77e-05	1.02e-05	0.126

Table 2340: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Starch.and.sucrose.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.24e-02	1.78e-01	0.182	0.858	-3.41e-01	4.05e-01	0.00000
L3.Starch.and.sucrose.metabolism	-4.29e-08	2.07e-07	-0.208	0.838	-4.76e-07	3.90e-07	0.00215

Table 2341: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Steroid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.036509	0.09315	0.392	0.699	-0.158455	0.231473	0.000
L3.Steroid.biosynthesis	-0.000129	0.00014	-0.925	0.367	-0.000422	0.000163	0.041

Table 2342: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Steroid.hormone.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.70e-01	1.13e-01	-2.40	0.02684	-5.06e-01	-3.45e-02	0.000
L3.Steroid.hormone.biosynthesis	1.71e-05	5.57e-06	3.08	0.00621	5.48e-06	2.88e-05	0.321

Table 2343: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	0.049055	0.103429	0.474	0.641	-0.16742	0.265535
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	-0.000167	0.000202	-0.827	0.418	-0.00059	0.000256

Table 2344: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Streptomycin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.97e-02	2.02e-01	-0.147	0.885	-4.53e-01	3.94e-01	0.00000
L3.Streptomycin.biosynthesis	1.34e-07	8.23e-07	0.163	0.873	-1.59e-06	1.86e-06	0.00132

Table 2345: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Styrene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.48e-01	1.30e-01	1.13	0.272	-1.25e-01	4.21e-01	0.0000
L3.Styrene.degradation	-1.21e-05	8.31e-06	-1.45	0.162	-2.95e-05	5.31e-06	0.0956

Table 2346: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Sulfur.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.91e-02	2.0e-01	0.0955	0.925	-4.00e-01	4.38e-01	0.000000
L3.Sulfur.metabolism	-1.02e-07	9.6e-07	-0.1058	0.917	-2.11e-06	1.91e-06	0.000559

Table 2347: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Sulfur.relay.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.07e-01	1.71e-01	0.624	0.540	-2.51e-01	4.65e-01	0.0000
L3.Sulfur.relay.system	-6.52e-07	9.07e-07	-0.720	0.481	-2.55e-06	1.25e-06	0.0252

Table 2348: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Synthesis.and.degradation.of.ketone.bodies, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.29e-01	1.56e-01	0.828	0.418	-1.97e-01	4.55e-01	0.0000
L3.Synthesis.and.degradation.of.ketone.bodies	-8.45e-06	8.59e-06	-0.984	0.338	-2.64e-05	9.53e-06	0.0461

Table 2349: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Systemic.lupus.erythematosus, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.046538	0.096294	0.483	0.634	-0.15501	0.248083	0.0000
L3.Systemic.lupus.erythematosus	-0.000413	0.000417	-0.992	0.334	-0.00129	0.000459	0.0469

Table 2350: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.TGF.beta.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2351: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Taurine.and.hypotaurine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.94e-02	2.16e-01	-0.275	0.786	-5.11e-01	3.92e-01	0.00000
L3.Taurine.and.hypotaurine.metabolism	8.63e-07	2.87e-06	0.300	0.767	-5.15e-06	6.88e-06	0.00449

Table 2352: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Terpenoid.backbone.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.01e-01	1.96e-01	0.517	0.611	-3.09e-01	5.12e-01	0.0000
L3.Terpenoid.backbone.biosynthesis	-2.87e-07	5.00e-07	-0.574	0.573	-1.33e-06	7.60e-07	0.0162

Table 2353: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Tetracycline.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.06e-01	1.70e-01	0.625	0.539	-2.50e-01	4.63e-01	0.0000
L3.Tetracycline.biosynthesis	-1.18e-06	1.63e-06	-0.722	0.479	-4.59e-06	2.23e-06	0.0254

Table 2354: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Thiamine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.08e-02	1.89e-01	0.480	0.636	-3.05e-01	4.87e-01	0.0000
L3.Thiamine.metabolism	-2.83e-07	5.26e-07	-0.539	0.596	-1.38e-06	8.17e-07	0.0143

Table 2355: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Tight.junction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2356: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Toluene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.3e-03	1.49e-01	0.0424	0.967	-3.05e-01	3.17e-01	0.000000
L3.Toluene.degradation	-8.6e-08	1.65e-06	-0.0521	0.959	-3.54e-06	3.37e-06	0.000135

Table 2357: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Toxoplasmosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.38e-03	8.81e-02	-0.0724	0.943	-0.190852	0.178096	0.00000
L3.Toxoplasmosis	2.27e-05	6.86e-05	0.3304	0.745	-0.000121	0.000166	0.00543

Table 2358: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Transcription.factors, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.41e-01	1.61e-01	0.873	0.393	-1.97e-01	4.79e-01	0.0000
L3.Transcription.factors	-1.31e-07	1.29e-07	-1.023	0.319	-4.01e-07	1.38e-07	0.0497

Table 2359: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Transcription.machinery, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.58e-02	1.99e-01	0.129	0.899	-3.92e-01	4.43e-01	0.00000
L3.Transcription.machinery	-3.79e-08	2.64e-07	-0.143	0.888	-5.91e-07	5.15e-07	0.00103

Table 2360: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Transcription.related.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.06e-02	1.08e-01	0.283	0.781	-1.96e-01	2.57e-01	0.0000
L3.Transcription.related.proteins	-1.46e-05	3.15e-05	-0.463	0.648	-8.06e-05	5.14e-05	0.0106

Table 2361: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Translation.factors, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.44e-02	1.95e-01	0.485	0.634	-3.13e-01	5.02e-01	0.0000
L3.Translation.factors	-2.87e-07	5.32e-07	-0.539	0.596	-1.40e-06	8.27e-07	0.0143

Table 2362: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Translation.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.11e-01	1.89e-01	0.586	0.565	-2.85e-01	5.06e-01	0.0000
L3.Translation.proteins	-2.01e-07	3.07e-07	-0.657	0.519	-8.43e-07	4.41e-07	0.0211

Table 2363: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Transporters, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.42e-01	1.56e-01	0.91	0.374	-1.85e-01	4.70e-01	0.0000
L3.Transporters	-3.23e-08	3.00e-08	-1.08	0.295	-9.51e-08	3.05e-08	0.0548

Table 2364: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	4.06e-02	2.00e-01	0.203	0.841	-3.79e-01	4.60e-01
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis	-5.36e-07	2.39e-06	-0.225	0.825	-5.53e-06	4.46e-06

Table 2365: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Tryptophan.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.10e-01	1.76e-01	1.20	0.247	-1.58e-01	5.78e-01	0.0000
L3.Tryptophan.metabolism	-2.83e-06	2.09e-06	-1.35	0.192	-7.22e-06	1.55e-06	0.0839

Table 2366: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Tuberculosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.43e-02	1.88e-01	0.235	0.817	-3.5e-01	4.39e-01	0.00000
L3.Tuberculosis	-4.71e-07	1.78e-06	-0.264	0.794	-4.2e-06	3.26e-06	0.00348

Table 2367: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Two.component.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.06e-01	1.71e-01	0.622	0.541	-2.51e-01	4.63e-01	0.0000
L3.Two.component.system	-1.13e-07	1.57e-07	-0.718	0.481	-4.41e-07	2.16e-07	0.0251

Table 2368: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Type.I.diabetes.mellitus, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.48e-02	1.98e-01	-0.429	0.673	-4.99e-01	3.29e-01	0.0000
L3.Type.I.diabetes.mellitus	2.53e-06	5.31e-06	0.476	0.640	-8.59e-06	1.37e-05	0.0112

Table 2369: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Type.II.diabetes.mellitus, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.96e-02	1.94e-01	0.358	0.724	-0.336660	4.76e-01	0.00000
L3.Type.II.diabetes.mellitus	-2.41e-06	6.02e-06	-0.400	0.694	-0.000015	1.02e-05	0.00793

Table 2370: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Tyrosine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.48e-02	1.90e-01	0.445	0.661	-3.14e-01	4.83e-01	0.0000
L3.Tyrosine.metabolism	-4.21e-07	8.43e-07	-0.499	0.624	-2.19e-06	1.34e-06	0.0123

Table 2371: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-1.62e-01	2.24e-01	-0.721	0.480	-6.31e-01	3.08e-01
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis	1.60e-06	2.05e-06	0.779	0.446	-2.69e-06	5.88e-06

Table 2372: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Ubiquitin.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.56e-01	1.25e-01	-2.86	0.01005	-6.17e-01	-0.095454	0.000
L3.Ubiquitin.system	6.34e-05	1.86e-05	3.41	0.00294	2.45e-05	0.000102	0.368

Table 2373: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.VEGF.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2374: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Valine..leucine.and.isoleucine.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.08e-01	1.75e-01	0.619	0.543	-2.58e-01	4.75e-01	0.0000
L3.Valine..leucine.and.isoleucine.biosynthesis	-2.21e-07	3.13e-07	-0.708	0.487	-8.75e-07	4.33e-07	0.0245

Table 2375: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Valine..leucine.and.isoleucine.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.19e-01	2.22e-01	0.536	0.598	-3.46e-01	5.84e-01	0.0000
L3.Valine..leucine.and.isoleucine.degradation	-9.02e-07	1.55e-06	-0.581	0.568	-4.15e-06	2.35e-06	0.0166

Table 2376: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Various.types.of.N.glycan.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.02166	0.09537	0.227	0.823	-0.17797	0.22128	0.0000
L3.Various.types.of.N.glycan.biosynthesis	-0.00169	0.00328	-0.516	0.612	-0.00855	0.00517	0.0131

Table 2377: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Vascular.smooth.muscle.contraction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2378: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Vasopressin.regulated.water.reabsorption, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.0253	0.0896	-0.282	0.781	-0.213	0.162	0.0000
L3.Vasopressin.regulated.water.reabsorption	0.1063	0.1238	0.858	0.401	-0.153	0.365	0.0355

Table 2379: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs
L3.Vibrio.cholerae.infection, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0208	0.0889	0.234	0.818	-0.165	0.2068	0.0000
L3.Vibrio.cholerae.infection	-0.0436	0.0554	-0.787	0.441	-0.160	0.0724	0.0301

Table 2380: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Vibrio.cholerae.pathogenic.cycle, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.70e-03	1.89e-01	-0.0143	0.989	-3.99e-01	3.93e-01	0.00e+00
L3.Vibrio.cholerae.pathogenic.cycle	6.39e-08	3.99e-06	0.0160	0.987	-8.28e-06	8.41e-06	1.29e-05

Table 2381: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Viral.myocarditis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.38e-03	8.81e-02	-0.0724	0.943	-0.190852	0.178096	0.00000
L3.Viral.myocarditis	2.27e-05	6.86e-05	0.3304	0.745	-0.000121	0.000166	0.00543

Table 2382: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Vitamin.B6.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.43e-03	2.02e-01	-0.0269	0.979	-4.28e-01	4.18e-01	0.00e+00
L3.Vitamin.B6.metabolism	4.15e-08	1.39e-06	0.0297	0.977	-2.88e-06	2.96e-06	4.42e-05

Table 2383: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Wnt.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2384: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Xylene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.20e-02	1.39e-01	0.662	0.516	-1.99e-01	3.83e-01	0.0000
L3.Xylene.degradation	-3.01e-06	3.61e-06	-0.835	0.414	-1.06e-05	4.54e-06	0.0337

Table 2385: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.Zeatin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.41e-02	2.12e-01	-0.161	0.874	-4.78e-01	4.10e-01	0.00000
L3.Zeatin.biosynthesis	9.75e-07	5.53e-06	0.176	0.862	-1.06e-05	1.26e-05	0.00155

Table 2386: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.alpha.Linolenic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.22e-02	1.23e-01	-0.262	0.796	-0.289568	0.225087	0.00000
L3.alpha.Linolenic.acid.metabolism	2.58e-05	7.03e-05	0.367	0.718	-0.000121	0.000173	0.00668

Table 2387: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.beta.Alanine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.88e-02	1.92e-01	0.411	0.686	-3.23e-01	4.80e-01	0.0000
L3.beta.Alanine.metabolism	-6.82e-07	1.49e-06	-0.459	0.651	-3.79e-06	2.43e-06	0.0104

Table 2388: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.beta.Lactam.resistance, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.12e-02	1.59e-01	0.134	0.895	-3.12e-01	3.54e-01	0.00000
L3.beta.Lactam.resistance	-1.05e-06	6.60e-06	-0.159	0.875	-1.49e-05	1.28e-05	0.00126

Table 2389: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.mRNA.surveillance.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2390: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.mTOR.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	1.29e-13	0.0841	1.53e-12	1	-0.175	0.175	0
	NA	NA	NA	NA	NA	NA	0

Table 2391: diversity_vs_picrust_L3_yr1: wunifrac.PC.1 vs L3.p53.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.38e-03	8.81e-02	-0.0724	0.943	-0.190852	0.178096	0.00000
L3.p53.signaling.pathway	2.27e-05	6.86e-05	0.3304	0.745	-0.000121	0.000166	0.00543

Table 2392: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %
Intercept	3.02e-04	4.25e-02	0.00711	0.994	-8.86e-0
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	-4.38e-07	3.06e-05	-0.01432	0.989	-6.45e-0

Table 2393: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.ABC.transporters, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.03e-01	6.23e-02	1.65	0.1159	-2.78e-02	2.33e-01	0.000
L3.ABC.transporters	-4.66e-08	2.38e-08	-1.96	0.0652	-9.64e-08	3.23e-09	0.161

Table 2394: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Adherens.junction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2395: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Adipocytokine.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.97e-02	7.95e-02	-1.13	0.273	-2.56e-01	7.67e-02	0.0000
L3.Adipocytokine.signaling.pathway	1.97e-06	1.56e-06	1.26	0.223	-1.30e-06	5.24e-06	0.0736

Table 2396: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.African.trypanosomiasis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.077480	4.26e-02	1.82	0.0847	-0.011668	0.166628	0.000
L3.African.trypanosomiasis	-0.000104	3.86e-05	-2.69	0.0145	-0.000185	-0.000023	0.266

Table 2397: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Alanine..aspartate.and.glutamate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.99e-02	8.46e-02	0.708	0.487	-1.17e-01	2.37e-01	0.000
L3.Alanine..aspartate.and.glutamate.metabolism	-8.30e-08	1.06e-07	-0.784	0.443	-3.04e-07	1.39e-07	0.029

Table 2398: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Aldosterone.regulated.sodium.reabsorption, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2399: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Alzheimer.s.disease, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.41e-02	7.12e-02	0.759	0.457	-9.50e-02	2.03e-01	0.0000
L3.Alzheimer.s.disease	-1.87e-06	2.13e-06	-0.881	0.389	-6.32e-06	2.58e-06	0.0373

Table 2400: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Amino.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.82e-02	7.07e-02	1.39	0.181	-4.97e-02	2.46e-01	0.000
L3.Amino.acid.metabolism	-6.78e-07	4.25e-07	-1.59	0.127	-1.57e-06	2.12e-07	0.113

Table 2401: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Amino.acid.related.enzymes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.88e-02	7.95e-02	0.991	0.334	-8.76e-02	2.45e-01	0.000
L3.Amino.acid.related.enzymes	-8.42e-08	7.59e-08	-1.110	0.281	-2.43e-07	7.46e-08	0.058

Table 2402: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Amino.sugar.and.nucleotide.sugar.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.39e-02	8.17e-02	0.904	0.377	-9.71e-02	2.45e-01	0.000
L3.Amino.sugar.and.nucleotide.sugar.metabolism	-7.52e-08	7.47e-08	-1.007	0.327	-2.32e-07	8.12e-08	0.048

Table 2403: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Aminoacyl.tRNA.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.38e-02	7.34e-02	1.14	0.267	-6.97e-02	2.37e-01	0.0000
L3.Aminoacyl.tRNA.biosynthesis	-1.18e-07	9.02e-08	-1.30	0.208	-3.06e-07	7.12e-08	0.0783

Table 2404: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Aminobenzoate.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.49e-02	8.42e-02	0.652	0.522	-1.21e-01	2.31e-01	0.0000
L3.Aminobenzoate.degradation	-7.92e-07	1.10e-06	-0.723	0.478	-3.09e-06	1.50e-06	0.0255

Table 2405: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Amoebiasis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.18e-02	5.29e-02	1.17	0.257	-4.88e-02	1.72e-01	0.000
L3.Amoebiasis	-7.96e-06	5.13e-06	-1.55	0.137	-1.87e-05	2.78e-06	0.107

Table 2406: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Amyotrophic.lateral.sclerosis..ALS., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.69e-02	6.19e-02	-0.273	0.787	-1.47e-01	1.13e-01	0.00000
L3.Amyotrophic.lateral.sclerosis..ALS.	1.85e-06	5.43e-06	0.340	0.738	-9.52e-06	1.32e-05	0.00574

Table 2407: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Antigen.processing.and.presentation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.78e-02	7.95e-02	0.601	0.555	-1.19e-01	2.14e-01	0.0000
L3.Antigen.processing.and.presentation	-1.82e-06	2.69e-06	-0.676	0.507	-7.45e-06	3.81e-06	0.0224

Table 2408: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Apoptosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.54e-03	4.13e-02	0.183	0.857	-7.89e-02	9.40e-02	0.00000
L3.Apoptosis	-1.08e-05	2.71e-05	-0.399	0.695	-6.75e-05	4.59e-05	0.00788

Table 2409: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Arachidonic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.86e-02	8.83e-02	-1.12	0.278	-2.83e-01	8.63e-02	0.0000
L3.Arachidonic.acid.metabolism	8.96e-06	7.35e-06	1.22	0.238	-6.42e-06	2.43e-05	0.0692

Table 2410: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Arginine.and.proline.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.48e-02	8.01e-02	0.935	0.362	-9.27e-02	2.42e-01	0.0000
L3.Arginine.and.proline.metabolism	-9.02e-08	8.63e-08	-1.045	0.309	-2.71e-07	9.04e-08	0.0518

Table 2411: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Arrhythmogenic.right.ventricular.cardiomyopathy..ARVC., df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2412: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Ascorbate.and.aldarate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.73e-02	7.31e-02	0.921	0.369	-8.57e-02	2.20e-01	0.0000
L3.Ascorbate.and.aldarate.metabolism	-9.22e-07	8.73e-07	-1.056	0.304	-2.75e-06	9.06e-07	0.0528

Table 2413: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Atrazine.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.41e-02	4.84e-02	1.74	0.0985	-1.72e-02	1.85e-01	0.000
L3.Atrazine.degradation	-6.57e-06	2.80e-06	-2.34	0.0302	-1.24e-05	-7.00e-07	0.215

Table 2414: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Bacterial.chemotaxis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.84e-02	5.80e-02	1.35	0.192	-4.30e-02	2.00e-01	0.000
L3.Bacterial.chemotaxis	-2.73e-07	1.63e-07	-1.68	0.110	-6.13e-07	6.75e-08	0.123

Table 2415: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Bacterial.invasion.of.epithelial.cells, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.086090	3.70e-02	2.33	0.0311	0.008717	0.163463	0.000
L3.Bacterial.invasion.of.epithelial.cells	-0.000239	6.59e-05	-3.63	0.0018	-0.000377	-0.000101	0.397

Table 2416: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Bacterial.motility.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.01e-02	5.55e-02	1.26	0.222	-4.6e-02	1.86e-01	0.000
L3.Bacterial.motility.proteins	-1.44e-07	8.90e-08	-1.62	0.123	-3.3e-07	4.25e-08	0.115

Table 2417: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Bacterial.secretion.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.36e-02	8.14e-02	0.905	0.377	-9.67e-02	2.44e-01	0.0000
L3.Bacterial.secretion.system	-2.10e-07	2.09e-07	-1.008	0.326	-6.47e-07	2.26e-07	0.0484

Table 2418: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Bacterial.toxins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.74e-02	8.1e-02	1.08	0.294	-8.21e-02	2.57e-01	0.0000
L3.Bacterial.toxins	-1.13e-06	9.4e-07	-1.20	0.244	-3.10e-06	8.39e-07	0.0673

Table 2419: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Basal.transcription.factors, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.24e-03	4.10e-02	0.0303	0.976	-0.084556	0.08704	0.00000
L3.Basal.transcription.factors	-4.46e-06	6.44e-05	-0.0693	0.946	-0.000139	0.00013	0.00024

Table 2420: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Base.excision.repair, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.37e-02	7.66e-02	1.09	0.289	-7.67e-02	2.44e-01	0.0000
L3.Base.excision.repair	-3.10e-07	2.51e-07	-1.23	0.233	-8.36e-07	2.17e-07	0.0705

Table 2421: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Benzoate.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.72e-02	7.24e-02	1.20	0.243	-6.44e-02	2.39e-01	0.0000
L3.Benzoate.degradation	-7.02e-07	5.10e-07	-1.38	0.184	-1.77e-06	3.65e-07	0.0866

Table 2422: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Betalain.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.01742	0.03778	0.461	0.650	-0.06167	0.09650	0.0000
L3.Betalain.biosynthesis	-0.00269	0.00207	-1.300	0.209	-0.00702	0.00164	0.0779

Table 2423: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Bile.secretion, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00654	0.0371	-0.176	0.862	-0.0843	0.0712	0.0000
L3.Bile.secretion	0.13726	0.1702	0.806	0.430	-0.2190	0.4935	0.0315

Table 2424: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Biosynthesis.and.biodegradation.of.secondary.metabolites, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	1.00e-01	7.79e-02	1.28	0.214	-6.30e-02	2.63
L3.Biosynthesis.and.biodegradation.of.secondary.metabolites	-2.33e-06	1.62e-06	-1.44	0.167	-5.72e-06	1.06

Table 2425: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Biosynthesis.of.12...14..and.16.membered.macrolides, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2426: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Biosynthesis.of.ansamycins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.66e-02	7.01e-02	1.38	0.184	-5.02e-02	2.43e-01	0.000
L3.Biosynthesis.of.ansamycins	-1.25e-06	7.86e-07	-1.58	0.130	-2.89e-06	4.00e-07	0.112

Table 2427: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	-3.65e-02	9.56e-02	-0.381	0.707	-2.37e-01	1.64e
L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides	3.17e-06	7.67e-06	0.413	0.684	-1.29e-05	1.92e

Table 2428: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Biosynthesis.of.type.II.polyketide.backbone, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2429: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Biosynthesis.of.type.II.polyketide.products, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.02241	0.03741	0.599	0.556	-0.05589	0.100704	0.000
L3.Biosynthesis.of.type.II.polyketide.products	-0.00312	0.00196	-1.587	0.129	-0.00723	0.000994	0.112

Table 2430: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Biosynthesis.of.unsaturated.fatty.acids, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.05e-01	7.07e-02	1.49	0.153	-4.26e-02	2.53e-01	0.000
L3.Biosynthesis.of.unsaturated.fatty.acids	-1.54e-06	9.01e-07	-1.70	0.105	-3.42e-06	3.50e-07	0.127

Table 2431: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Biosynthesis.of.vancomycin.group.antibiotics, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.69e-02	9.16e-02	0.512	0.615	-1.45e-01	2.39e-01	0.0000
L3.Biosynthesis.of.vancomycin.group.antibiotics	-1.03e-06	1.84e-06	-0.558	0.583	-4.89e-06	2.83e-06	0.0153

Table 2432: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Biotin.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.25e-02	7.90e-02	0.917	0.371	-9.29e-02	2.38e-01	0.0000
L3.Biotin.metabolism	-6.56e-07	6.37e-07	-1.029	0.316	-1.99e-06	6.78e-07	0.0503

Table 2433: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Bisphenol.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.83e-02	7.66e-02	0.892	0.383	-9.20e-02	2.29e-01	0.0000
L3.Bisphenol.degradation	-1.13e-06	1.12e-06	-1.010	0.325	-3.46e-06	1.21e-06	0.0485

Table 2434: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Bladder.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.079030	0.035758	2.21	0.0396	0.004188	0.153872	0.000
L3.Bladder.cancer	-0.000485	0.000134	-3.63	0.0018	-0.000764	-0.000205	0.397

Table 2435: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Butanoate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.14e-02	7.69e-02	1.06	0.303	-7.94e-02	2.42e-01	0.0000
L3.Butanoate.metabolism	-2.01e-07	1.68e-07	-1.20	0.247	-5.53e-07	1.51e-07	0.0667

Table 2436: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Butirosin.and.neomycin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.32e-02	7.38e-02	0.721	0.480	-1.01e-01	2.08e-01	0.0000
L3.Butirosin.and.neomycin.biosynthesis	-1.10e-06	1.33e-06	-0.827	0.418	-3.87e-06	1.68e-06	0.0331

Table 2437: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.C5.Branched.dibasic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.09e-02	7.02e-02	1.29	0.211	-5.60e-02	2.38e-01	0.0
L3.C5.Branched.dibasic.acid.metabolism	-4.23e-07	2.84e-07	-1.49	0.152	-1.02e-06	1.70e-07	0.1

Table 2438: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.CAM.ligands, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2439: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Caffeine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.003471	0.040469	-0.0858	0.933	-0.088173	0.081230	0.00000
L3.Caffeine.metabolism	0.000038	0.000184	0.2068	0.838	-0.000347	0.000423	0.00213

Table 2440: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Calcium.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.001561	0.03909	0.0399	0.969	-0.08025	0.08337	0.000000
L3.Calcium.signaling.pathway	-0.000381	0.00318	-0.1199	0.906	-0.00704	0.00628	0.000718

Table 2441: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Caprolactam.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.12e-01	5.76e-02	1.94	0.0675	-8.87e-03	2.32e-01	0.000
L3.Caprolactam.degradation	-1.63e-05	6.92e-06	-2.35	0.0299	-3.07e-05	-1.76e-06	0.216

Table 2442: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Carbohydrate.digestion.and.absorption, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.68e-02	6.57e-02	-0.408	0.688	-1.64e-01	1.11e-01	0.0000
L3.Carbohydrate.digestion.and.absorption	3.20e-06	6.51e-06	0.491	0.629	-1.04e-05	1.68e-05	0.0119

Table 2443: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Carbohydrate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.64e-02	7.75e-02	0.728	0.475	-1.06e-01	2.19e-01	0.0000
L3.Carbohydrate.metabolism	-4.21e-07	5.11e-07	-0.824	0.420	-1.49e-06	6.49e-07	0.0328

Table 2444: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Carbon.fixation.in.photosynthetic.organisms, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.21e-02	8.11e-02	0.889	0.385	-9.77e-02	2.42e-01	0.0000
L3.Carbon.fixation.in.photosynthetic.organisms	-1.70e-07	1.71e-07	-0.992	0.334	-5.29e-07	1.89e-07	0.0469

Table 2445: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Carbon.fixation.pathways.in.prokaryotes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.32e-02	8.62e-02	0.617	0.545	-1.27e-01	2.34e-01	0.0000
L3.Carbon.fixation.pathways.in.prokaryotes	-8.20e-08	1.20e-07	-0.681	0.504	-3.34e-07	1.70e-07	0.0226

Table 2446: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Cardiac.muscle.contraction, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.45e-04	3.80e-02	0.00909	0.993	-0.079121	7.98e-02	0.00e+00
L3.Cardiac.muscle.contraction	-3.74e-07	9.84e-06	-0.03798	0.970	-0.000021	2.02e-05	7.21e-05

Table 2447: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Carotenoid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.67e-02	5.01e-02	-0.932	0.363	-0.151478	5.81e-02	0.0000
L3.Carotenoid.biosynthesis	2.87e-05	2.19e-05	1.314	0.205	-0.000017	7.45e-05	0.0794

Table 2448: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Cell.cycle, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2449: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Cell.cycle...Caulobacter, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.52e-02	7.99e-02	0.941	0.359	-9.21e-02	2.43e-01	0.0000
L3.Cell.cycle...Caulobacter	-2.41e-07	2.29e-07	-1.053	0.306	-7.21e-07	2.39e-07	0.0525

Table 2450: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Cell.cycle...yeast, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2451: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Cell.division, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.43e-02	7.76e-02	1.09	0.291	-7.81e-02	2.47e-01	0.0000
L3.Cell.division	-1.57e-06	1.28e-06	-1.22	0.237	-4.26e-06	1.12e-06	0.0695

Table 2452: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Cell.motility.and.secretion, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.17e-02	8.60e-02	0.717	0.482	-1.18e-01	2.42e-01	0.0000
L3.Cell.motility.and.secretion	-5.45e-07	6.89e-07	-0.791	0.439	-1.99e-06	8.98e-07	0.0303

Table 2453: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Cellular.antigens, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.43e-01	6.79e-02	-2.11	0.0487	-2.85e-01	-8.87e-04	0.000
L3.Cellular.antigens	4.94e-06	2.06e-06	2.39	0.0271	6.22e-07	9.25e-06	0.223

Table 2454: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Chagas.disease..American.trypanosomiasis., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.074601	4.08e-02	1.83	0.0832	-0.010796	1.60e-01	0.000
L3.Chagas.disease..American.trypanosomiasis.	-0.000116	4.13e-05	-2.81	0.0112	-0.000202	-2.96e-05	0.283

Table 2455: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Chaperones.and.folding.catalysts, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.26e-02	8.52e-02	0.735	0.471	-1.16e-01	2.41e-01	0.0000
L3.Chaperones.and.folding.catalysts	-9.77e-08	1.20e-07	-0.812	0.427	-3.50e-07	1.54e-07	0.0319

Table 2456: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Chloroalkane.and.chloroalkene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.79e-02	6.90e-02	1.13	0.273	-6.65e-02	2.22e-01	0.0000
L3.Chloroalkane.and.chloroalkene.degradation	-6.88e-07	5.24e-07	-1.31	0.204	-1.78e-06	4.08e-07	0.0795

Table 2457: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Chlorocyclohexane.and.chlorobenzene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	6.42e-02	5.40e-02	1.19	0.249	-4.88e-02	1.77e-01
L3.Chlorocyclohexane.and.chlorobenzene.degradation	-8.90e-06	5.73e-06	-1.55	0.137	-2.09e-05	3.09e-06

Table 2458: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Cholinergic.synapse, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2459: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Chromosome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.21e-02	7.87e-02	1.04	0.310	-8.26e-02	2.47e-01	0.0000
L3.Chromosome	-8.38e-08	7.16e-08	-1.17	0.256	-2.34e-07	6.61e-08	0.0641

Table 2460: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Chronic.myeloid.leukemia, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2461: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Circadian.rhythm...plant, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.41e-03	0.040510	-0.0843	0.934	-0.088203	0.081374	0.00000
L3.Circadian.rhythm...plant	3.72e-05	0.000184	0.2023	0.842	-0.000348	0.000422	0.00204

Table 2462: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Citrate.cycle..TCA.cycle., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.97e-02	8.88e-02	0.222	0.827	-1.66e-01	2.05e-01	0.00000
L3.Citrate.cycle..TCA.cycle.	-4.89e-08	2.01e-07	-0.244	0.810	-4.69e-07	3.72e-07	0.00296

Table 2463: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Clavulanic.acid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0167	0.0335	0.498	0.6245	-0.0534	0.0867	0.000
L3.Clavulanic.acid.biosynthesis	-0.1749	0.0767	-2.280	0.0343	-0.3354	-0.0143	0.206

Table 2464: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Colorectal.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.39e-04	3.78e-02	0.00369	0.997	-7.89e-02	7.92e-02	0.00e+00
L3.Colorectal.cancer	-4.95e-07	2.94e-05	-0.01683	0.987	-6.21e-05	6.11e-05	1.42e-05

Table 2465: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Complement.and.coagulation.cascades, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2466: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Cyanoamino.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.14e-02	7.43e-02	0.557	0.584	-1.14e-01	1.97e-01	0.0000
L3.Cyanoamino.acid.metabolism	-1.74e-07	2.73e-07	-0.640	0.530	-7.45e-07	3.96e-07	0.0201

Table 2467: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Cysteine.and.methionine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.12e-02	7.87e-02	1.16	0.261	-7.36e-02	2.56e-01	0.0000
L3.Cysteine.and.methionine.metabolism	-1.50e-07	1.16e-07	-1.30	0.210	-3.93e-07	9.24e-08	0.0775

Table 2468: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Cytochrome.P450, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2469: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Cytokine.receptors, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2470: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Cytokine.cytokine.receptor.interaction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2471: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Cytoskeleton.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.64e-02	6.99e-02	1.24	0.231	-5.98e-02	2.33e-01	0.0000
L3.Cytoskeleton.proteins	-3.52e-07	2.46e-07	-1.43	0.169	-8.68e-07	1.63e-07	0.0928

Table 2472: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Cytosolic.DNA.sensing.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2473: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.D.Alanine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.73e-02	7.72e-02	1.13	0.272	-7.42e-02	2.49e-01	0.000
L3.D.Alanine.metabolism	-1.34e-06	1.05e-06	-1.27	0.218	-3.53e-06	8.60e-07	0.075

Table 2474: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.D.Arginine.and.D.ornithine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.03e-02	5.37e-02	0.75	0.462	-7.21e-02	1.53e-01	0.0000
L3.D.Arginine.and.D.ornithine.metabolism	-1.23e-05	1.22e-05	-1.01	0.326	-3.79e-05	1.33e-05	0.0484

Table 2475: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.D.Glutamine.and.D.glutamate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.77e-02	8.40e-02	0.926	0.366	-9.80e-02	2.53e-01	0.0000
L3.D.Glutamine.and.D.glutamate.metabolism	-8.26e-07	8.06e-07	-1.024	0.319	-2.51e-06	8.62e-07	0.0498

Table 2476: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.DNA.repair.and.recombination.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.02e-02	8.01e-02	1.00	0.329	-8.74e-02	2.48e-01	0.0000
L3.DNA.repair.and.recombination.proteins	-4.59e-08	4.11e-08	-1.12	0.277	-1.32e-07	4.00e-08	0.0589

Table 2477: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.DNA.replication, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.10e-02	8.33e-02	0.852	0.405	-1.03e-01	2.45e-01	0.0000
L3.DNA.replication	-1.75e-07	1.85e-07	-0.945	0.357	-5.61e-07	2.12e-07	0.0427

Table 2478: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.DNA.replication.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.65e-02	8.20e-02	0.933	0.363	-9.51e-02	2.48e-01	0.000
L3.DNA.replication.proteins	-9.94e-08	9.58e-08	-1.037	0.313	-3.00e-07	1.01e-07	0.051

Table 2479: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Dilated.cardiomyopathy..DCM., df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2480: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Dioxin.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.67e-02	5.71e-02	1.52	0.1452	-3.28e-02	2.06e-01	0.000
L3.Dioxin.degradation	-2.64e-06	1.40e-06	-1.89	0.0746	-5.56e-06	2.89e-07	0.151

Table 2481: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Drug.metabolism...cytochrome.P450, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.02e-03	7.03e-02	0.0145	0.989	-1.46e-01	1.48e-01	0.00e+00
L3.Drug.metabolism...cytochrome.P450	-8.74e-08	5.13e-06	-0.0170	0.987	-1.08e-05	1.06e-05	1.45e-05

Table 2482: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Drug.metabolism...other.enzymes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.24e-02	8.65e-02	0.606	0.552	-1.29e-01	2.33e-01	0.0000
L3.Drug.metabolism...other.enzymes	-2.51e-07	3.75e-07	-0.668	0.512	-1.04e-06	5.35e-07	0.0218

Table 2483: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.ECM.receptor.interaction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2484: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Electron.transfer.carriers, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.63e-02	5.42e-02	1.22	0.236	-4.71e-02	1.80e-01	0.000
L3.Electron.transfer.carriers	-6.27e-06	3.94e-06	-1.59	0.128	-1.45e-05	1.98e-06	0.112

Table 2485: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Endocrine.and.other.factor.regulated.calcium.reabsorption, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2486: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Endocytosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0118	0.0374	0.315	0.756	-0.0665	0.0901	0.0000
L3.Endocytosis	-0.0826	0.0767	-1.077	0.295	-0.2432	0.0779	0.0548

Table 2487: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Energy.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.31e-02	8.49e-02	0.625	0.539	-1.25e-01	2.31e-01	0.0000
L3.Energy.metabolism	-9.43e-08	1.36e-07	-0.692	0.497	-3.80e-07	1.91e-07	0.0234

Table 2488: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	9.58e-02	7.12e-02	1.35	0.194	-5.32e-02	2.45e-0
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	-1.62e-06	1.05e-06	-1.54	0.140	-3.83e-06	5.80e-0

Table 2489: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.ErbB.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2490: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Ether.lipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.44e-02	5.29e-02	0.272	0.788	-9.63e-02	1.25e-01	0.0000
L3.Ether.lipid.metabolism	-1.16e-05	3.07e-05	-0.378	0.709	-7.58e-05	5.26e-05	0.0071

Table 2491: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Ethylbenzene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.51e-02	8.12e-02	-0.186	0.855	-1.85e-01	1.55e-01	0.00000
L3.Ethylbenzene.degradation	6.11e-07	2.93e-06	0.208	0.837	-5.53e-06	6.75e-06	0.00216

Table 2492: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Fat.digestion.and.absorption, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2493: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Fatty.acid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.34e-02	8.00e-02	0.917	0.370	-9.41e-02	2.41e-01	0.00
L3.Fatty.acid.biosynthesis	-2.37e-07	2.31e-07	-1.026	0.318	-7.20e-07	2.46e-07	0.05

Table 2494: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Fatty.acid.elongation.in.mitochondria, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.49e-03	0.040447	-0.0862	0.932	-0.088143	0.081168	0.00000
L3.Fatty.acid.elongation.in.mitochondria	3.83e-05	0.000184	0.2084	0.837	-0.000346	0.000423	0.00217

Table 2495: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Fatty.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.80e-02	7.99e-02	0.976	0.341	-8.92e-02	2.45e-01	0.0000
L3.Fatty.acid.metabolism	-6.06e-07	5.55e-07	-1.092	0.289	-1.77e-06	5.56e-07	0.0563

Table 2496: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Fc.epsilon.RI.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2497: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Fc.gamma.R.mediated.phagocytosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0118	0.0374	0.315	0.756	-0.0665	0.0901	0.0000
L3.Fc.gamma.R.mediated.phagocytosis	-0.0826	0.0767	-1.077	0.295	-0.2432	0.0779	0.0548

Table 2498: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Flagellar.assembly, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.13e-02	5.21e-02	1.18	0.254	-4.78e-02	1.70e-01	0.00
L3.Flagellar.assembly	-3.23e-07	2.05e-07	-1.58	0.132	-7.51e-07	1.06e-07	0.11

Table 2499: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Flavone.and.flavonol.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.46e-02	6.89e-02	-0.503	0.621	-1.79e-01	1.1e-01	0.0000
L3.Flavone.and.flavonol.biosynthesis	5.73e-06	9.67e-06	0.593	0.560	-1.45e-05	2.6e-05	0.0173

Table 2500: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Flavonoid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.027714	5.10e-02	0.543	0.593	-7.91e-02	1.34e-01	0.000
L3.Flavonoid.biosynthesis	-0.000023	2.97e-05	-0.773	0.449	-8.52e-05	3.92e-05	0.029

Table 2501: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Fluorobenzoate.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.077733	4.36e-02	1.78	0.0904	-0.013468	1.69e-01	0.000
L3.Fluorobenzoate.degradation	-0.000148	5.68e-05	-2.60	0.0177	-0.000267	-2.87e-05	0.252

Table 2502: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Focal.adhesion, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2503: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Folate.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.49e-02	8.87e-02	0.732	0.473	-1.21e-01	2.50e-01	0.0000
L3.Folate.biosynthesis	-2.73e-07	3.40e-07	-0.802	0.432	-9.85e-07	4.39e-07	0.0312

Table 2504: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Fructose.and.mannose.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.79e-02	7.62e-02	1.02	0.319	-8.15e-02	2.37e-01	0.0000
L3.Fructose.and.mannose.metabolism	-1.17e-07	1.01e-07	-1.16	0.261	-3.27e-07	9.42e-08	0.0628

Table 2505: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Function.unknown, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.87e-02	7.66e-02	1.16	0.261	-7.15e-02	2.49e-01	0.0000
L3.Function.unknown	-1.13e-07	8.64e-08	-1.31	0.207	-2.94e-07	6.79e-08	0.0786

Table 2506: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.G.protein.coupled.receptors, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0229	0.0398	0.575	0.572	-0.0604	0.1061	0.0000
L3.G.protein.coupled.receptors	-0.0171	0.0136	-1.262	0.222	-0.0456	0.0113	0.0737

Table 2507: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.GTP.binding.proteins, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2508: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Galactose.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.57e-02	7.98e-02	0.823	0.421	-1.01e-01	2.33e-01	0.0000
L3.Galactose.metabolism	-1.13e-07	1.23e-07	-0.922	0.368	-3.71e-07	1.44e-07	0.0408

Table 2509: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Gastric.acid.secretion, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2510: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.General.function.prediction.only, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.80e-02	8.07e-02	0.967	0.346	-9.08e-02	2.47e-01	0.000
L3.General.function.prediction.only	-3.33e-08	3.09e-08	-1.079	0.294	-9.80e-08	3.13e-08	0.055

Table 2511: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Geraniol.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.37e-02	9.06e-02	-0.703	0.490	-2.53e-01	1.26e-01	0.0000
L3.Geraniol.degradation	3.19e-06	4.15e-06	0.768	0.452	-5.50e-06	1.19e-05	0.0286

Table 2512: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Germination, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.32e-02	5.04e-02	1.85	0.0802	-1.23e-02	1.99e-01	0.000
L3.Germination	-3.70e-06	1.54e-06	-2.41	0.0265	-6.92e-06	-4.81e-07	0.224

Table 2513: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Glioma, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2514: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Glutamatergic.synapse, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.81e-02	8.10e-02	0.841	0.411	-1.01e-01	2.38e-01	0.0000
L3.Glutamatergic.synapse	-9.39e-07	9.99e-07	-0.939	0.359	-3.03e-06	1.15e-06	0.0423

Table 2515: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Glutathione.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.37e-02	9.90e-02	0.240	0.813	-1.84e-01	2.31e-01	0.00000
L3.Glutathione.metabolism	-2.05e-07	7.94e-07	-0.258	0.799	-1.87e-06	1.46e-06	0.00332

Table 2516: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Glycan.bindng.proteins, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2517: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Glycan.biosynthesis.and.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.08e-02	7.58e-02	-0.406	0.689	-1.89e-01	1.28e-01	0.0000
L3.Glycan.biosynthesis.and.metabolism	1.94e-06	4.17e-06	0.464	0.648	-6.80e-06	1.07e-05	0.0106

Table 2518: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Glycerolipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.74e-02	6.76e-02	1.29	0.212	-5.41e-02	2.29e-01	0.000
L3.Glycerolipid.metabolism	-3.60e-07	2.39e-07	-1.51	0.148	-8.60e-07	1.40e-07	0.102

Table 2519: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Glycerophospholipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.79e-02	7.26e-02	1.21	0.241	-6.41e-02	2.40e-01	0.0000
L3.Glycerophospholipid.metabolism	-2.54e-07	1.84e-07	-1.38	0.183	-6.39e-07	1.31e-07	0.0873

Table 2520: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Glycine..serine.and.threonine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.29e-02	8.41e-02	0.867	0.397	-1.03e-01	2.49e-01	0.000
L3.Glycine..serine.and.threonine.metabolism	-1.34e-07	1.40e-07	-0.959	0.349	-4.28e-07	1.59e-07	0.044

Table 2521: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Glycolysis...Gluconeogenesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.36e-02	7.75e-02	1.08	0.295	-7.87e-02	2.46e-01	0.0000
L3.Glycolysis...Gluconeogenesis	-1.17e-07	9.65e-08	-1.21	0.240	-3.19e-07	8.50e-08	0.0685

Table 2522: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Glycosaminoglycan.biosynthesis...chondroitin.sulfate, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	0.00162	0.03781	0.0429	0.966	-0.0775	0.0808
L3.Glycosaminoglycan.biosynthesis...chondroitin.sulfate	-0.00122	0.00641	-0.1897	0.852	-0.0146	0.0122

Table 2523: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Glycosaminoglycan.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.12e-01	6.58e-02	-1.70	0.1054	-2.50e-01	2.58e-02	0.000
L3.Glycosaminoglycan.degradation	1.70e-06	8.59e-07	1.98	0.0627	-9.95e-08	3.50e-06	0.164

Table 2524: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Glycosphingolipid.biosynthesis. . . ganglio.series, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.93e-02	5.99e-02	-1.66	0.114	-2.25e-01	2.61e-02	0.00
L3.Glycosphingolipid.biosynthesis. . . ganglio.series	2.22e-06	1.11e-06	2.00	0.060	-1.03e-07	4.54e-06	0.16

Table 2525: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Glycosphingolipid.biosynthesis. . . globo.series, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.88e-02	8.14e-02	-0.477	0.639	-2.09e-01	1.31e-01	0.000
L3.Glycosphingolipid.biosynthesis. . . globo.series	4.23e-07	7.92e-07	0.534	0.600	-1.23e-06	2.08e-06	0.014

Table 2526: diversity_vs_picrust_L3_yr1: wunifrac.PC.2
vs L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series,
df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.
Intercept	-5.96e-04	3.94e-02	-0.0151	0.988	-0.083019	0.0
L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series	2.95e-06	6.86e-05	0.0430	0.966	-0.000141	0.0

Table 2527: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Glycosylphosphatidylinositol.GPI..anchor.biosynthesis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2528: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Glycosyltransferases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.79e-02	9.05e-02	0.750	0.462	-1.21e-01	2.57e-01	0.0000
L3.Glycosyltransferases	-3.12e-07	3.82e-07	-0.819	0.423	-1.11e-06	4.86e-07	0.0325

Table 2529: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Glyoxylate.and.dicarboxylate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.41e-02	7.87e-02	1.07	0.299	-8.07e-02	2.49e-01	0.0000
L3.Glyoxylate.and.dicarboxylate.metabolism	-2.36e-07	1.97e-07	-1.20	0.246	-6.49e-07	1.77e-07	0.0668

Table 2530: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.GnRH.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0118	0.0374	0.315	0.756	-0.0665	0.0901	0.0000
L3.GnRH.signaling.pathway	-0.0826	0.0767	-1.077	0.295	-0.2432	0.0779	0.0548

Table 2531: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Hedgehog.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2532: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Hematopoietic.cell.lineage, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2533: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Hepatitis.C, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2534: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Histidine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.62e-02	8.27e-02	0.680	0.505	-1.17e-01	2.29e-01	0.0000
L3.Histidine.metabolism	-1.33e-07	1.76e-07	-0.757	0.458	-5.01e-07	2.35e-07	0.0279

Table 2535: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Homologous.recombination, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.31e-02	8.15e-02	0.897	0.381	-9.75e-02	2.44e-01	0.0000
L3.Homologous.recombination	-1.27e-07	1.27e-07	-0.999	0.330	-3.92e-07	1.39e-07	0.0476

Table 2536: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Huntington.s.disease, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.92e-02	7.45e-02	-0.795	0.437	-2.15e-01	0.096781	0.0000
L3.Huntington.s.disease	3.33e-06	3.67e-06	0.908	0.375	-4.35e-06	0.000011	0.0396

Table 2537: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Hypertrophic.cardiomyopathy..HCM., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00112	0.0378	0.0296	0.977	-0.0779	0.0801	0.000000
L3.Hypertrophic.cardiomyopathy..HCM.	-0.00335	0.0247	-0.1355	0.894	-0.0551	0.0484	0.000918

Table 2538: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Indole.alkaloid.biosynthesis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2539: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Influenza.A, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.39e-04	3.78e-02	0.00369	0.997	-7.89e-02	7.92e-02	0.00e+00
L3.Influenza.A	-4.95e-07	2.94e-05	-0.01683	0.987	-6.21e-05	6.11e-05	1.42e-05

Table 2540: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Inorganic.ion.transport.and.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.83e-02	8.13e-02	0.718	0.482	-1.12e-01	2.28e-01	0.0000
L3.Inorganic.ion.transport.and.metabolism	-4.69e-07	5.84e-07	-0.802	0.432	-1.69e-06	7.54e-07	0.0312

Table 2541: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Inositol.phosphate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.69e-02	8.43e-02	0.438	0.666	-1.39e-01	2.13e-01	0.0000
L3.Inositol.phosphate.metabolism	-5.93e-07	1.22e-06	-0.487	0.632	-3.14e-06	1.96e-06	0.0117

Table 2542: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Insulin.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.78e-02	7.27e-02	0.794	0.437	-9.45e-02	2.10e-01	0.0000
L3.Insulin.signaling.pathway	-1.06e-06	1.16e-06	-0.915	0.372	-3.49e-06	1.37e-06	0.0402

Table 2543: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Ion.channels, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.94e-02	8.72e-02	0.567	0.578	-1.33e-01	2.32e-01	0.0000
L3.Ion.channels	-5.42e-06	8.69e-06	-0.624	0.540	-2.36e-05	1.28e-05	0.0191

Table 2544: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Isoflavonoid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00083	0.0385	0.0215	0.983	-0.0799	0.0815	0.00000
L3.Isoflavonoid.biosynthesis	-0.00581	0.0790	-0.0735	0.942	-0.1712	0.1595	0.00027

Table 2545: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Isoquinoline.alkaloid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.93e-02	9.56e-02	0.411	0.686	-1.61e-01	2.39e-01	0.00000
L3.Isoquinoline.alkaloid.biosynthesis	-1.05e-06	2.35e-06	-0.445	0.661	-5.96e-06	3.87e-06	0.00982

Table 2546: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Leishmaniasis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2547: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Leukocyte.transendothelial.migration, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2548: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Limonene.and.pinene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.97e-02	8.07e-02	0.740	0.468	-1.09e-01	2.29e-01	0.0000
L3.Limonene.and.pinene.degradation	-1.32e-06	1.59e-06	-0.828	0.418	-4.64e-06	2.01e-06	0.0332

Table 2549: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Linoleic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.88e-02	7.63e-02	0.902	0.378	-9.09e-02	2.28e-01	0.0000
L3.Linoleic.acid.metabolism	-1.33e-06	1.30e-06	-1.022	0.320	-4.05e-06	1.39e-06	0.0496

Table 2550: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Lipid.biosynthesis.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.50e-02	8.37e-02	0.657	0.519	-1.20e-01	2.30e-01	0.0000
L3.Lipid.biosynthesis.proteins	-1.48e-07	2.03e-07	-0.729	0.475	-5.72e-07	2.76e-07	0.0259

Table 2551: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Lipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.01e-01	6.78e-02	1.48	0.155	-4.14e-02	2.43e-01	0.000
L3.Lipid.metabolism	-1.18e-06	6.85e-07	-1.72	0.102	-2.61e-06	2.56e-07	0.129

Table 2552: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Lipoic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.26e-01	7.14e-02	-1.76	0.0940	-2.75e-01	2.36e-02	0.000
L3.Lipoic.acid.metabolism	5.31e-06	2.66e-06	2.00	0.0604	-2.56e-07	1.09e-05	0.166

Table 2553: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Lipopolysaccharide.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.24e-01	8.06e-02	-1.54	0.139	-2.93e-01	4.42e-02	0.000
L3.Lipopolysaccharide.biosynthesis	7.88e-07	4.62e-07	1.71	0.104	-1.78e-07	1.76e-06	0.127

Table 2554: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Lipopolysaccharide.biosynthesis.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.99e-02	8.96e-02	-1.00	0.328	-2.78e-01	9.76e-02	0.0000
L3.Lipopolysaccharide.biosynthesis.proteins	3.79e-07	3.46e-07	1.09	0.287	-3.46e-07	1.10e-06	0.0565

Table 2555: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Long.term.depression, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2556: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Long.term.potentiation, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2557: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Lysine.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.60e-02	7.50e-02	1.15	0.266	-7.11e-02	2.43e-01	0.0000
L3.Lysine.biosynthesis	-1.57e-07	1.21e-07	-1.30	0.210	-4.10e-07	9.59e-08	0.0778

Table 2558: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Lysine.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.05e-02	0.083098	0.969	0.345	-9.34e-02	2.54e-01	0.0000
L3.Lysine.degradation	-1.08e-06	0.000001	-1.074	0.296	-3.18e-06	1.02e-06	0.0545

Table 2559: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Lysosome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.22e-01	7.23e-02	-1.69	0.1082	-2.73e-01	2.95e-02	0.000
L3.Lysosome	1.20e-06	6.30e-07	1.91	0.0718	-1.18e-07	2.52e-06	0.154

Table 2560: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.MAPK.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2561: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.MAPK.signaling.pathway. . . yeast, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.42e-02	8.84e-02	0.160	0.874	-1.71e-01	1.99e-01	0.00000
L3.MAPK.signaling.pathway. . . yeast	-4.49e-07	2.55e-06	-0.176	0.862	-5.78e-06	4.88e-06	0.00155

Table 2562: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Measles, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2563: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Meiosis. . . yeast, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.87e-03	4.1e-02	0.241	0.812	-7.59e-02	9.56e-02	0.0000
L3.Meiosis. . . yeast	-5.89e-06	1.1e-05	-0.536	0.598	-2.89e-05	1.71e-05	0.0142

Table 2564: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Melanogenesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.01742	0.03778	0.461	0.650	-0.06167	0.09650	0.0000
L3.Melanogenesis	-0.00269	0.00207	-1.300	0.209	-0.00702	0.00164	0.0779

Table 2565: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Membrane.and.intracellular.structural.molecules, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.14e-02	9.31e-02	-0.123	0.904	-2.06e-01	1.83e-01	0.0
L3.Membrane.and.intracellular.structural.molecules	3.15e-08	2.36e-07	0.134	0.895	-4.62e-07	5.25e-07	0.0

Table 2566: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Metabolism.of.cofactors.and.vitamins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.68e-02	6.76e-02	1.43	0.168	-4.47e-02	2.38e-01	0.000
L3.Metabolism.of.cofactors.and.vitamins	-1.38e-06	8.28e-07	-1.66	0.113	-3.11e-06	3.56e-07	0.122

Table 2567: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Metabolism.of.xenobiotics.by.cytochrome.P450, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.87e-04	6.97e-02	0.00554	0.996	-1.46e-01	1.46e-01	0.0
L3.Metabolism.of.xenobiotics.by.cytochrome.P450	-3.35e-08	5.13e-06	-0.00653	0.995	-1.08e-05	1.07e-05	2.1

Table 2568: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Methane.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.22e-02	7.46e-02	1.24	0.232	-6.40e-02	2.48e-01	0.0000
L3.Methane.metabolism	-1.09e-07	7.81e-08	-1.40	0.178	-2.73e-07	5.41e-08	0.0893

Table 2569: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Mineral.absorption, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.33e-02	5.08e-02	0.853	0.404	-6.30e-02	1.50e-01	0.0000
L3.Mineral.absorption	-2.59e-05	2.17e-05	-1.195	0.247	-7.13e-05	1.95e-05	0.0666

Table 2570: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Mismatch.repair, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.08e-02	7.95e-02	1.02	0.322	-8.56e-02	2.47e-01	0.0000
L3.Mismatch.repair	-1.57e-07	1.38e-07	-1.14	0.270	-4.46e-07	1.32e-07	0.0607

Table 2571: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.N.Glycan.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.33e-04	8.36e-02	-0.0112	0.991	-1.76e-01	1.74e-01	0.00e+00
L3.N.Glycan.biosynthesis	5.86e-08	4.71e-06	0.0124	0.990	-9.81e-06	9.93e-06	7.73e-06

Table 2572: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.NOD.like.receptor.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.29e-02	8.35e-02	0.514	0.613	-1.32e-01	0.217582	0.0000
L3.NOD.like.receptor.signaling.pathway	-1.50e-06	2.63e-06	-0.572	0.574	-7.01e-06	0.000004	0.0161

Table 2573: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Naphthalene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.61e-02	8.21e-02	0.440	0.665	-1.36e-01	2.08e-01	0.0000
L3.Naphthalene.degradation	-4.50e-07	9.16e-07	-0.491	0.629	-2.37e-06	1.47e-06	0.0119

Table 2574: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Neuroactive.ligand.receptor.interaction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2575: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Neurotrophin.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2576: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Nicotinate.and.nicotinamide.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.06e-02	8.06e-02	0.875	0.392	-9.81e-02	2.39e-01	0.0000
L3.Nicotinate.and.nicotinamide.metabolism	-2.68e-07	2.74e-07	-0.978	0.340	-8.42e-07	3.06e-07	0.0457

Table 2577: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Nitrogen.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.47e-02	8.69e-02	0.744	0.466	-1.17e-01	2.47e-01	0.0000
L3.Nitrogen.metabolism	-1.34e-07	1.63e-07	-0.819	0.423	-4.75e-07	2.08e-07	0.0324

Table 2578: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Nitrotoluene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.78e-02	5.43e-02	1.80	0.0877	-1.59e-02	2.12e-01	0.000
L3.Nitrotoluene.degradation	-1.51e-06	6.67e-07	-2.26	0.0360	-2.90e-06	-1.09e-07	0.203

Table 2579: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Non.homologous.end.joining, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.20e-02	5.12e-02	1.02	0.323	-5.52e-02	1.59e-01	0.0000
L3.Non.homologous.end.joining	-1.65e-05	1.18e-05	-1.39	0.179	-4.13e-05	8.28e-06	0.0886

Table 2580: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Notch.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2581: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Novobiocin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.31e-02	7.98e-02	1.04	0.311	-8.4e-02	2.50e-01	0.0000
L3.Novobiocin.biosynthesis	-9.65e-07	8.30e-07	-1.16	0.259	-2.7e-06	7.72e-07	0.0633

Table 2582: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Nucleotide.excision.repair, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.35e-02	7.69e-02	1.08	0.292	-7.76e-02	2.44e-01	0.0000
L3.Nucleotide.excision.repair	-3.43e-07	2.80e-07	-1.22	0.236	-9.30e-07	2.44e-07	0.0696

Table 2583: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Nucleotide.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.110790	5.76e-02	1.92	0.0695	-9.73e-03	2.31e-01	0.000
L3.Nucleotide.metabolism	-0.000004	1.71e-06	-2.33	0.0309	-7.58e-06	-4.08e-07	0.214

Table 2584: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Olfactory.transduction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2585: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.One.carbon.pool.by.folate, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.95e-02	8.58e-02	0.694	0.496	-1.20e-01	2.39e-01	0.0000
L3.One.carbon.pool.by.folate	-1.51e-07	1.98e-07	-0.766	0.453	-5.65e-07	2.62e-07	0.0285

Table 2586: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Oocyte.meiosis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2587: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Other.glycan.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.40e-02	8.7e-02	-0.851	0.405	-2.56e-01	1.08e-01	0.0000
L3.Other.glycan.degradation	2.62e-07	2.8e-07	0.935	0.362	-3.24e-07	8.48e-07	0.0419

Table 2588: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Other.ion.coupled.transporters, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.41e-02	8.67e-02	0.739	0.469	-1.17e-01	2.46e-01	0.000
L3.Other.ion.coupled.transporters	-7.25e-08	8.91e-08	-0.814	0.426	-2.59e-07	1.14e-07	0.032

Table 2589: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Other.transporters, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.81e-02	8.12e-02	0.839	0.412	-1.02e-01	2.38e-01	0.000
L3.Other.transporters	-3.86e-07	4.12e-07	-0.936	0.361	-1.25e-06	4.77e-07	0.042

Table 2590: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Other.types.of.O.glycan.biosynthesis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2591: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Others, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.16e-02	8.00e-02	0.895	0.382	-9.58e-02	2.39e-01	0.0000
L3.Others	-1.17e-07	1.16e-07	-1.002	0.329	-3.60e-07	1.27e-07	0.0478

Table 2592: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Oxidative.phosphorylation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.38e-02	7.96e-02	0.928	0.365	-9.27e-02	2.4e-01	0.0000
L3.Oxidative.phosphorylation	-9.90e-08	9.53e-08	-1.039	0.312	-2.98e-07	1.0e-07	0.0512

Table 2593: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.PPAR.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.50e-04	8.88e-02	0.00845	0.993	-1.85e-01	1.87e-01	0.00e+00
L3.PPAR.signaling.pathway	-1.06e-08	1.14e-06	-0.00929	0.993	-2.39e-06	2.37e-06	4.32e-06

Table 2594: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Pancreatic.cancer, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2595: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Pancreatic.secretion, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2596: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Pantothenate.and.CoA.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.03e-02	7.56e-02	1.20	0.247	-6.79e-02	2.49e-01	0.0000
L3.Pantothenate.and.CoA.biosynthesis	-2.20e-07	1.63e-07	-1.35	0.193	-5.61e-07	1.21e-07	0.0836

Table 2597: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Parkinson.s.disease, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.94e-04	3.79e-02	0.00774	0.994	-7.91e-02	7.97e-02	0.00e+00
L3.Parkinson.s.disease	-2.43e-07	7.37e-06	-0.03299	0.974	-1.57e-05	1.52e-05	5.44e-05

Table 2598: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Pathogenic.Escherichia.coli.infection, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2599: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Pathways.in.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.84e-02	7.72e-02	0.627	0.538	-1.13e-01	2.10e-01	0.0000
L3.Pathways.in.cancer	-1.60e-06	2.26e-06	-0.711	0.486	-6.33e-06	3.12e-06	0.0247

Table 2600: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Penicillin.and.cephalosporin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.92e-02	7.58e-02	1.04	0.309	-7.95e-02	2.38e-01	0.0000
L3.Penicillin.and.cephalosporin.biosynthesis	-4.46e-06	3.77e-06	-1.18	0.251	-1.24e-05	3.43e-06	0.0654

Table 2601: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Pentose.and.glucuronate.interconversions, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.80e-02	8.21e-02	0.706	0.489	-1.14e-01	2.30e-01	0.0000
L3.Pentose.and.glucuronate.interconversions	-1.35e-07	1.71e-07	-0.787	0.441	-4.93e-07	2.24e-07	0.0301

Table 2602: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Pentose.phosphate.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.19e-02	7.69e-02	1.07	0.300	-7.90e-02	2.43e-01	0.0000
L3.Pentose.phosphate.pathway	-1.38e-07	1.14e-07	-1.20	0.244	-3.77e-07	1.02e-07	0.0674

Table 2603: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Peptidases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.96e-02	8.11e-02	0.982	0.339	-9.02e-02	2.49e-01	0.0000
L3.Peptidases	-6.66e-08	6.09e-08	-1.093	0.288	-1.94e-07	6.09e-08	0.0564

Table 2604: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Peptidoglycan.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.69e-02	7.71e-02	1.13	0.274	-7.45e-02	2.48e-01	0.0000
L3.Peptidoglycan.biosynthesis	-1.71e-07	1.35e-07	-1.27	0.220	-4.54e-07	1.11e-07	0.0745

Table 2605: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Peroxisome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.66e-02	9.01e-02	-0.296	0.771	-2.15e-01	1.62e-01	0.00000
L3.Peroxisome	2.31e-07	7.13e-07	0.324	0.749	-1.26e-06	1.72e-06	0.00522

Table 2606: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Pertussis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.42e-02	8.24e-02	-1.02	0.320	-2.57e-01	8.82e-02	0.0000
L3.Pertussis	4.59e-06	4.05e-06	1.13	0.271	-3.88e-06	1.31e-05	0.0604

Table 2607: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Phagosome, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2608: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Phenylalanine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.61e-02	8.46e-02	0.544	0.593	-1.31e-01	2.23e-01	0.0000
L3.Phenylalanine.metabolism	-3.81e-07	6.32e-07	-0.604	0.553	-1.70e-06	9.41e-07	0.0179

Table 2609: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	9.18e-02	7.48e-02	1.23	0.235	-6.48e-02	2.48e-01
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis	-1.67e-07	1.20e-07	-1.39	0.181	-4.20e-07	8.47e-08

Table 2610: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Phenylpropanoid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.76e-02	6.82e-02	0.404	0.691	-1.15e-01	1.7e-01	0.0000
L3.Phenylpropanoid.biosynthesis	-1.84e-07	3.84e-07	-0.479	0.637	-9.89e-07	6.2e-07	0.0114

Table 2611: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Phosphatidylinositol.signaling.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.05e-02	8.83e-02	0.346	0.734	-1.54e-01	2.15e-01	0.00000
L3.Phosphatidylinositol.signaling.system	-5.32e-07	1.40e-06	-0.380	0.708	-3.46e-06	2.40e-06	0.00717

Table 2612: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Phosphonate.and.phosphinate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.59e-02	7.80e-02	0.973	0.343	-8.74e-02	2.39e-01	0.0000
L3.Phosphonate.and.phosphinate.metabolism	-1.74e-06	1.59e-06	-1.095	0.287	-5.08e-06	1.59e-06	0.0565

Table 2613: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Phosphotransferase.system..PTS., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.96e-02	5.24e-02	1.71	0.1033	-2.00e-02	1.99e-01	0.000
L3.Phosphotransferase.system..PTS.	-3.61e-07	1.64e-07	-2.20	0.0404	-7.04e-07	-1.75e-08	0.195

Table 2614: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Photosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.43e-02	6.73e-02	1.40	0.177	-4.65e-02	2.35e-01	0.000
L3.Photosynthesis	-3.50e-07	2.14e-07	-1.63	0.119	-7.98e-07	9.87e-08	0.118

Table 2615: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Photosynthesis...antenna.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00140	0.039113	0.0359	0.972	-0.080462	0.083267	0.000000
L3.Photosynthesis...antenna.proteins	-0.00002	0.000187	-0.1071	0.916	-0.000412	0.000372	0.000573

Table 2616: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Photosynthesis.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.40e-02	6.73e-02	1.40	0.178	-4.68e-02	2.35e-01	0.000
L3.Photosynthesis.proteins	-3.47e-07	2.13e-07	-1.63	0.120	-7.92e-07	9.90e-08	0.117

Table 2617: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Phototransduction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2618: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Phototransduction...fly, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2619: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Plant.pathogen.interaction, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.71e-02	7.05e-02	1.24	0.232	-6.05e-02	2.35e-01	0.000
L3.Plant.pathogen.interaction	-8.80e-07	6.18e-07	-1.42	0.171	-2.17e-06	4.14e-07	0.092

Table 2620: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Polycyclic.aromatic.hydrocarbon.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.26e-02	7.76e-02	0.935	0.362	-8.99e-02	2.35e-01	0.000
L3.Polycyclic.aromatic.hydrocarbon.degradation	-1.04e-06	9.88e-07	-1.054	0.305	-3.11e-06	1.03e-06	0.052

Table 2621: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Polyketide.sugar.unit.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.35e-02	8.68e-02	0.732	0.473	-1.18e-01	2.45e-01	0.0000
L3.Polyketide.sugar.unit.biosynthesis	-4.36e-07	5.41e-07	-0.805	0.431	-1.57e-06	6.97e-07	0.0314

Table 2622: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Pores.ion.channels, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.90e-02	9.59e-02	-0.928	0.365	-2.90e-01	1.12e-01	0.0000
L3.Pores.ion.channels	3.77e-07	3.77e-07	1.000	0.330	-4.12e-07	1.17e-06	0.0477

Table 2623: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Porphyrin.and.chlorophyll.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.94e-02	7.37e-02	1.21	0.240	-6.49e-02	2.44e-01	0.000
L3.Porphyrin.and.chlorophyll.metabolism	-1.35e-07	9.77e-08	-1.38	0.184	-3.39e-07	6.96e-08	0.087

Table 2624: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Prenyltransferases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.69e-02	8.65e-02	0.542	0.594	-1.34e-01	2.28e-01	0.0000
L3.Prenyltransferases	-2.43e-07	4.06e-07	-0.598	0.557	-1.09e-06	6.06e-07	0.0176

Table 2625: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Primary.bile.acid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.11e-02	7.06e-02	1.01	0.327	-7.67e-02	2.19e-01	0.0000
L3.Primary.bile.acid.biosynthesis	-2.57e-06	2.20e-06	-1.17	0.258	-7.18e-06	2.04e-06	0.0636

Table 2626: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Primary.immunodeficiency, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.44e-02	7.95e-02	0.559	0.583	-1.22e-01	2.11e-01	0.0000
L3.Primary.immunodeficiency	-1.44e-06	2.28e-06	-0.629	0.537	-6.21e-06	3.34e-06	0.0194

Table 2627: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Prion.diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.65e-02	5.71e-02	0.290	0.775	-1.03e-01	1.36e-01	0.0000
L3.Prion.diseases	-4.27e-06	1.13e-05	-0.378	0.709	-2.79e-05	1.94e-05	0.0071

Table 2628: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Progesterone.mediated.oocyte.maturation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.78e-02	7.95e-02	0.601	0.555	-1.19e-01	2.14e-01	0.0000
L3.Progesterone.mediated.oocyte.maturation	-1.82e-06	2.69e-06	-0.676	0.507	-7.45e-06	3.81e-06	0.0224

Table 2629: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Propanoate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.65e-02	7.87e-02	1.10	0.285	-7.81e-02	2.51e-01	0.0000
L3.Propanoate.metabolism	-2.81e-07	2.28e-07	-1.23	0.233	-7.57e-07	1.96e-07	0.0706

Table 2630: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Prostate.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.23e-02	8.13e-02	0.397	0.696	-1.38e-01	2.02e-01	0.0000
L3.Prostate.cancer	-1.15e-06	2.57e-06	-0.445	0.661	-6.53e-06	4.24e-06	0.0098

Table 2631: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Proteasome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.7e-02	7.80e-02	0.731	0.474	-1.06e-01	2.20e-01	0.0000
L3.Proteasome	-2.1e-06	2.55e-06	-0.825	0.420	-7.44e-06	3.23e-06	0.0329

Table 2632: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Protein.digestion.and.absorption, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.28e-01	6.00e-02	-2.13	0.0463	-2.53e-01	-2.31e-03	0.000
L3.Protein.digestion.and.absorption	7.32e-06	2.91e-06	2.52	0.0209	1.23e-06	1.34e-05	0.241

Table 2633: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Protein.export, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.34e-02	8.13e-02	0.904	0.377	-9.66e-02	2.43e-01	0.0000
L3.Protein.export	-1.95e-07	1.93e-07	-1.007	0.326	-6.00e-07	2.10e-07	0.0483

Table 2634: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Protein.folding.and.associated.processing, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.28e-02	8.22e-02	0.886	0.387	-9.93e-02	2.45e-01	0.0000
L3.Protein.folding.and.associated.processing	-1.79e-07	1.82e-07	-0.985	0.337	-5.59e-07	2.01e-07	0.0462

Table 2635: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Protein.kinases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.72e-02	6.80e-02	1.43	0.169	-4.50e-02	2.39e-01	0.000
L3.Protein.kinases	-4.95e-07	2.98e-07	-1.66	0.113	-1.12e-06	1.29e-07	0.121

Table 2636: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Protein.processing.in.endoplasmic.reticulum, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.71e-02	9.30e-02	-0.507	0.618	-2.42e-01	1.47e-01	0.000
L3.Protein.processing.in.endoplasmic.reticulum	1.12e-06	2.03e-06	0.552	0.588	-3.13e-06	5.38e-06	0.015

Table 2637: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Proximal.tubule.bicarbonate.reclamation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.19e-03	6.72e-02	-0.0623	0.951	-1.45e-01	1.37e-01	0.000000
L3.Proximal.tubule.bicarbonate.reclamation	3.01e-07	4.04e-06	0.0745	0.941	-8.15e-06	8.75e-06	0.000277

Table 2638: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Purine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.32e-02	8.11e-02	1.03	0.318	-8.65e-02	2.53e-01	0.0000
L3.Purine.metabolism	-6.01e-08	5.26e-08	-1.14	0.267	-1.70e-07	5.00e-08	0.0613

Table 2639: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Pyrimidine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.59e-02	8.18e-02	0.927	0.365	-9.54e-02	2.47e-01	0.0000
L3.Pyrimidine.metabolism	-6.63e-08	6.42e-08	-1.032	0.315	-2.01e-07	6.82e-08	0.0505

Table 2640: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Pyruvate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.59e-02	7.86e-02	1.09	0.288	-7.86e-02	2.50e-01	0.0000
L3.Pyruvate.metabolism	-1.28e-07	1.04e-07	-1.22	0.236	-3.46e-07	9.05e-08	0.0698

Table 2641: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.RIG.I.like.receptor.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.19e-02	4.72e-02	-0.463	0.649	-1.21e-01	7.70e-02	0.0000
L3.RIG.I.like.receptor.signaling.pathway	1.64e-05	2.25e-05	0.726	0.477	-3.08e-05	6.35e-05	0.0257

Table 2642: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.RNA.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.13e-02	8.49e-02	0.722	0.479	-1.16e-01	2.39e-01	0.0000
L3.RNA.degradation	-2.02e-07	2.53e-07	-0.798	0.435	-7.31e-07	3.27e-07	0.0309

Table 2643: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.RNA.polymerase, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.43e-02	7.88e-02	1.20	0.246	-7.07e-02	2.59e-01	0.0000
L3.RNA.polymerase	-9.98e-07	7.46e-07	-1.34	0.197	-2.56e-06	5.64e-07	0.0821

Table 2644: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.RNA.transport, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.70e-02	6.70e-02	1.45	0.164	-4.32e-02	2.37e-01	0.000
L3.RNA.transport	-1.11e-06	6.59e-07	-1.69	0.108	-2.49e-06	2.67e-07	0.125

Table 2645: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Regulation.of.actin.cytoskeleton, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2646: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Renal.cell.carcinoma, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.23e-02	6.12e-02	0.690	0.498	-8.59e-02	1.70e-01	0.0000
L3.Renal.cell.carcinoma	-1.15e-05	1.35e-05	-0.856	0.403	-3.97e-05	1.67e-05	0.0353

Table 2647: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Renin.angiotensin.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00481	0.0383	0.125	0.901	-0.0754	0.0851	0.00000
L3.Renin.angiotensin.system	-0.00674	0.0156	-0.432	0.671	-0.0394	0.0259	0.00925

Table 2648: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Replication..recombination.and.repair.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.65e-02	7.23e-02	1.33	0.198	-5.48e-02	2.48e-01	0.00
L3.Replication..recombination.and.repair.proteins	-2.01e-07	1.32e-07	-1.52	0.144	-4.78e-07	7.54e-08	0.10

Table 2649: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Restriction.enzyme, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.36e-03	8.74e-02	0.0270	0.979	-1.81e-01	1.85e-01	0.00e+00
L3.Restriction.enzyme	-2.04e-08	6.85e-07	-0.0297	0.977	-1.45e-06	1.41e-06	4.42e-05

Table 2650: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Retinol.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.29e-02	7.20e-02	-0.457	0.653	-1.84e-01	0.117747	0.0000
L3.Retinol.metabolism	2.22e-06	4.19e-06	0.531	0.602	-6.55e-06	0.000011	0.0139

Table 2651: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Rheumatoid.arthritis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2652: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Riboflavin.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.33e-02	8.58e-02	0.971	0.344	-9.62e-02	2.63e-01	0.000
L3.Riboflavin.metabolism	-5.61e-07	5.25e-07	-1.069	0.299	-1.66e-06	5.37e-07	0.054

Table 2653: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Ribosome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.65e-02	7.92e-02	0.965	0.346	-8.94e-02	2.42e-01	0.0000
L3.Ribosome	-5.36e-08	4.95e-08	-1.082	0.293	-1.57e-07	5.01e-08	0.0553

Table 2654: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Ribosome.Biogenesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.78e-02	7.58e-02	1.16	0.261	-7.09e-02	2.46e-01	0.0000
L3.Ribosome.Biogenesis	-1.02e-07	7.82e-08	-1.31	0.207	-2.66e-07	6.14e-08	0.0788

Table 2655: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Ribosome.biogenesis.in.eukaryotes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.81e-02	7.64e-02	1.02	0.320	-8.19e-02	2.38e-01	0.0000
L3.Ribosome.biogenesis.in.eukaryotes	-2.69e-06	2.33e-06	-1.16	0.262	-7.57e-06	2.19e-06	0.0625

Table 2656: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Salivary.secretion, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2657: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Secondary.bile.acid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.75e-02	7.16e-02	0.942	0.358	-8.24e-02	2.17e-01	0.0000
L3.Secondary.bile.acid.biosynthesis	-2.50e-06	2.30e-06	-1.088	0.290	-7.31e-06	2.31e-06	0.0558

Table 2658: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Secretion.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.03e-02	6.96e-02	1.3	0.21	-5.53e-02	2.36e-01	0.000
L3.Secretion.system	-1.38e-07	9.18e-08	-1.5	0.15	-3.30e-07	5.44e-08	0.101

Table 2659: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Selenocompound.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.40e-02	7.75e-02	1.21	0.240	-6.82e-02	2.56e-01	0.0000
L3.Selenocompound.metabolism	-4.01e-07	2.95e-07	-1.36	0.189	-1.02e-06	2.15e-07	0.0849

Table 2660: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Sesquiterpenoid.biosynthesis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2661: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Shigellosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.01144	0.03927	0.291	0.774	-0.0707	0.0936	0.0000
L3.Shigellosis	-0.00601	0.00785	-0.766	0.453	-0.0224	0.0104	0.0285

Table 2662: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Signal.transduction.mechanisms, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.53e-02	7.04e-02	1.35	0.192	-5.20e-02	2.43e-01	0.000
L3.Signal.transduction.mechanisms	-3.23e-07	2.08e-07	-1.56	0.136	-7.58e-07	1.11e-07	0.108

Table 2663: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Small.cell.lung.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.39e-04	3.78e-02	0.00369	0.997	-7.89e-02	7.92e-02	0.00e+00
L3.Small.cell.lung.cancer	-4.95e-07	2.94e-05	-0.01683	0.987	-6.21e-05	6.11e-05	1.42e-05

Table 2664: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Sphingolipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.63e-02	8.44e-02	-0.430	0.672	-2.13e-01	1.40e-01	0.0000
L3.Sphingolipid.metabolism	1.79e-07	3.75e-07	0.477	0.639	-6.06e-07	9.64e-07	0.0113

Table 2665: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Spliceosome, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2666: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Sporulation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.38e-02	5.49e-02	1.71	0.1036	-2.10e-02	2.09e-01	0.000
L3.Sporulation	-1.93e-07	9.03e-08	-2.14	0.0453	-3.82e-07	-4.53e-09	0.187

Table 2667: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Staphylococcus.aureus.infection, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.81e-02	5.32e-02	0.716	0.483	-7.33e-02	1.49e-01	0.0000
L3.Staphylococcus.aureus.infection	-1.12e-05	1.15e-05	-0.972	0.343	-3.54e-05	1.29e-05	0.0451

Table 2668: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Starch.and.sucrose.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.91e-02	7.41e-02	0.933	0.362	-8.59e-02	2.24e-01	0.0000
L3.Starch.and.sucrose.metabolism	-9.16e-08	8.59e-08	-1.066	0.300	-2.72e-07	8.82e-08	0.0538

Table 2669: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Steroid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.54e-03	0.040658	-0.0872	0.931	-0.088643	0.08155	0.00000
L3.Steroid.biosynthesis	1.25e-05	0.000061	0.2057	0.839	-0.000115	0.00014	0.00211

Table 2670: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Steroid.hormone.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.85e-02	5.42e-02	-1.45	0.164	-1.92e-01	3.50e-02	0.000
L3.Steroid.hormone.biosynthesis	4.98e-06	2.68e-06	1.86	0.079	-6.35e-07	1.06e-05	0.147

Table 2671: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	0.030132	4.34e-02	0.695	0.495	-0.06061	1.21e-01
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	-0.000103	8.47e-05	-1.212	0.240	-0.00028	7.46e-05

Table 2672: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Streptomycin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.77e-02	8.53e-02	0.677	0.507	-1.21e-01	2.36e-01	0.0000
L3.Streptomycin.biosynthesis	-2.60e-07	3.47e-07	-0.748	0.464	-9.86e-07	4.67e-07	0.0272

Table 2673: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Styrene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.74e-02	5.13e-02	1.90	0.0728	-9.94e-03	2.05e-01	0.000
L3.Styrene.degradation	-7.97e-06	3.27e-06	-2.44	0.0247	-1.48e-05	-1.13e-06	0.229

Table 2674: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Sulfur.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.07e-02	8.43e-02	0.721	0.480	-1.16e-01	2.37e-01	0.0000
L3.Sulfur.metabolism	-3.23e-07	4.04e-07	-0.798	0.435	-1.17e-06	5.23e-07	0.0309

Table 2675: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Sulfur.relay.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.06e-01	6.85e-02	1.55	0.137	-3.69e-02	2.50e-01	0.000
L3.Sulfur.relay.system	-6.51e-07	3.63e-07	-1.79	0.089	-1.41e-06	1.09e-07	0.138

Table 2676: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Synthesis.and.degradation.of.ketone.bodies, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.60e-02	6.51e-02	1.17	0.257	-6.02e-02	2.12e-01	0.0000
L3.Synthesis.and.degradation.of.ketone.bodies	-4.98e-06	3.59e-06	-1.39	0.181	-1.25e-05	2.53e-06	0.0878

Table 2677: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Systemic.lupus.erythematosus, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.15e-03	0.042211	-0.0271	0.979	-0.089493	0.087202	0.000000
L3.Systemic.lupus.erythematosus	1.02e-05	0.000183	0.0557	0.956	-0.000372	0.000392	0.000155

Table 2678: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.TGF.beta.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2679: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Taurine.and.hypotaurine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.68e-02	9.13e-02	0.622	0.541	-1.34e-01	2.48e-01	0.0000
L3.Taurine.and.hypotaurine.metabolism	-8.25e-07	1.22e-06	-0.678	0.506	-3.37e-06	1.72e-06	0.0225

Table 2680: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Terpenoid.backbone.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.10e-02	8.26e-02	0.859	0.401	-1.02e-01	2.44e-01	0.0000
L3.Terpenoid.backbone.biosynthesis	-2.01e-07	2.11e-07	-0.955	0.352	-6.42e-07	2.40e-07	0.0436

Table 2681: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Tetracycline.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.23e-02	6.95e-02	1.33	0.200	-5.33e-02	2.38e-01	0.000
L3.Tetracycline.biosynthesis	-1.02e-06	6.66e-07	-1.53	0.142	-2.41e-06	3.73e-07	0.105

Table 2682: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Thiamine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.62e-02	7.84e-02	1.10	0.285	-7.78e-02	2.50e-01	0.0000
L3.Thiamine.metabolism	-2.69e-07	2.18e-07	-1.23	0.232	-7.25e-07	1.87e-07	0.0707

Table 2683: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Tight.junction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2684: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Toluene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.38e-02	6.34e-02	0.218	0.830	-1.19e-01	1.47e-01	0.00000
L3.Toluene.degradation	-1.89e-07	7.05e-07	-0.267	0.792	-1.66e-06	1.29e-06	0.00356

Table 2685: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Toxoplasmosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.39e-04	3.78e-02	0.00369	0.997	-7.89e-02	7.92e-02	0.00e+00
L3.Toxoplasmosis	-4.95e-07	2.94e-05	-0.01683	0.987	-6.21e-05	6.11e-05	1.42e-05

Table 2686: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Transcription.factors, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.01e-01	6.55e-02	1.54	0.1399	-3.62e-02	2.38e-01	0.00
L3.Transcription.factors	-9.41e-08	5.22e-08	-1.80	0.0871	-2.03e-07	1.51e-08	0.14

Table 2687: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Transcription.machinery, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.09e-02	8.39e-02	0.726	0.476	-1.15e-01	2.36e-01	0.0000
L3.Transcription.machinery	-8.95e-08	1.11e-07	-0.805	0.431	-3.22e-07	1.43e-07	0.0314

Table 2688: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Transcription.related.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.20e-02	4.22e-02	1.23	0.2333	-3.64e-02	1.40e-01	0.000
L3.Transcription.related.proteins	-2.48e-05	1.23e-05	-2.02	0.0579	-5.06e-05	9.18e-07	0.169

Table 2689: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Translation.factors, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.49e-02	8.17e-02	0.917	0.371	-9.61e-02	2.46e-01	0.0000
L3.Translation.factors	-2.28e-07	2.23e-07	-1.021	0.320	-6.95e-07	2.39e-07	0.0495

Table 2690: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Translation.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.24e-02	7.88e-02	1.05	0.309	-8.25e-02	2.47e-01	0.0000
L3.Translation.proteins	-1.50e-07	1.28e-07	-1.17	0.256	-4.18e-07	1.18e-07	0.0643

Table 2691: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Transporters, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.96e-02	6.34e-02	1.57	0.1326	-3.31e-02	2.32e-01	0.000
L3.Transporters	-2.26e-08	1.22e-08	-1.86	0.0784	-4.80e-08	2.83e-09	0.147

Table 2692: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	5.94e-02	8.44e-02	0.704	0.490	-1.17e-01	2.36e-01
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis	-7.84e-07	1.01e-06	-0.779	0.445	-2.89e-06	1.32e-06

Table 2693: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Tryptophan.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.00e-02	7.58e-02	1.05	0.305	-7.87e-02	2.39e-01	0.0000
L3.Tryptophan.metabolism	-1.08e-06	9.04e-07	-1.19	0.247	-2.97e-06	8.13e-07	0.0666

Table 2694: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Tuberculosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.72e-02	7.88e-02	0.853	0.404	-9.77e-02	2.32e-01	0.0000
L3.Tuberculosis	-7.14e-07	7.45e-07	-0.959	0.350	-2.27e-06	8.45e-07	0.0439

Table 2695: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Two.component.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.84e-02	7.01e-02	1.26	0.222	-5.82e-02	2.35e-01	0.0000
L3.Two.component.system	-9.39e-08	6.45e-08	-1.46	0.162	-2.29e-07	4.11e-08	0.0959

Table 2696: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Type.I.diabetes.mellitus, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.10e-02	8.40e-02	0.607	0.551	-1.25e-01	2.27e-01	0.0000
L3.Type.I.diabetes.mellitus	-1.52e-06	2.26e-06	-0.674	0.509	-6.25e-06	3.21e-06	0.0222

Table 2697: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Type.II.diabetes.mellitus, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.20e-02	8.06e-02	1.02	0.322	-8.68e-02	2.51e-01	0.0000
L3.Type.II.diabetes.mellitus	-2.83e-06	2.50e-06	-1.13	0.271	-8.07e-06	2.40e-06	0.0604

Table 2698: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Tyrosine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.08e-02	7.98e-02	0.887	0.386	-9.63e-02	2.38e-01	0.000
L3.Tyrosine.metabolism	-3.51e-07	3.54e-07	-0.993	0.333	-1.09e-06	3.89e-07	0.047

Table 2699: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-1.06e-01	9.39e-02	-1.12	0.275	-3.02e-01	9.09e-02
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis	1.04e-06	8.57e-07	1.21	0.239	-7.53e-07	2.83e-06

Table 2700: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Ubiquitin.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.31e-02	6.37e-02	-1.30	0.208	-2.16e-01	5.03e-02	0.000
L3.Ubiquitin.system	1.48e-05	9.50e-06	1.55	0.137	-5.12e-06	3.47e-05	0.108

Table 2701: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.VEGF.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2702: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Valine..leucine.and.isoleucine.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.29e-02	7.19e-02	1.29	0.212	-5.75e-02	2.43e-01	0.0000
L3.Valine..leucine.and.isoleucine.biosynthesis	-1.90e-07	1.28e-07	-1.48	0.156	-4.58e-07	7.87e-08	0.0985

Table 2703: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Valine..leucine.and.isoleucine.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.40e-02	9.56e-02	0.250	0.805	-1.76e-01	2.24e-01	0.00000
L3.Valine..leucine.and.isoleucine.degradation	-1.81e-07	6.69e-07	-0.271	0.789	-1.58e-06	1.22e-06	0.00367

Table 2704: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Various.types.of.N.glycan.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.01339	0.04046	-0.331	0.744	-0.09806	0.07129	0.0000
L3.Various.types.of.N.glycan.biosynthesis	0.00104	0.00139	0.752	0.461	-0.00186	0.00395	0.0275

Table 2705: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Vascular.smooth.muscle.contraction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2706: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Vasopressin.regulated.water.reabsorption, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.000173	0.0390	0.00444	0.997	-0.0815	0.0819	0.0e+00
L3.Vasopressin.regulated.water.reabsorption	-0.000728	0.0539	-0.01349	0.989	-0.1136	0.1122	9.1e-06

Table 2707: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Vibrio.cholerae.infection, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0172	0.0362	0.476	0.640	-0.0586	0.0931	0.000
L3.Vibrio.cholerae.infection	-0.0362	0.0226	-1.603	0.125	-0.0835	0.0111	0.114

Table 2708: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Vibrio.cholerae.pathogenic.cycle, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.06e-02	7.74e-02	1.17	0.256	-7.14e-02	2.53e-01	0.0000
L3.Vibrio.cholerae.pathogenic.cycle	-2.15e-06	1.63e-06	-1.32	0.204	-5.56e-06	1.27e-06	0.0796

Table 2709: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.Viral.myocarditis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.39e-04	3.78e-02	0.00369	0.997	-7.89e-02	7.92e-02	0.00e+00
L3.Viral.myocarditis	-4.95e-07	2.94e-05	-0.01683	0.987	-6.21e-05	6.11e-05	1.42e-05

Table 2710: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Vitamin.B6.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.20e-02	8.60e-02	0.372	0.714	-1.48e-01	2.12e-01	0.00000
L3.Vitamin.B6.metabolism	-2.44e-07	5.94e-07	-0.411	0.686	-1.49e-06	9.98e-07	0.00838

Table 2711: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Wnt.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2712: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Xylene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.03e-02	5.58e-02	1.44	0.1665	-3.65e-02	1.97e-01	0.000
L3.Xylene.degradation	-2.63e-06	1.45e-06	-1.81	0.0854	-5.67e-06	4.04e-07	0.141

Table 2713: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.Zeatin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.71e-02	9.06e-02	0.189	0.852	-1.73e-01	2.07e-01	0.00000
L3.Zeatin.biosynthesis	-4.89e-07	2.36e-06	-0.207	0.838	-5.44e-06	4.46e-06	0.00213

Table 2714: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.alpha.Linolenic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.48e-02	4.70e-02	1.59	0.1279	-0.023546	1.73e-01	0.000
L3.alpha.Linolenic.acid.metabolism	-5.98e-05	2.68e-05	-2.23	0.0383	-0.000116	-3.57e-06	0.199

Table 2715: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs L3.beta.Alanine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.87e-02	7.85e-02	1.26	0.224	-6.56e-02	2.63e-01	0.00
L3.beta.Alanine.metabolism	-8.55e-07	6.08e-07	-1.41	0.176	-2.13e-06	4.18e-07	0.09

Table 2716: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.beta.Lactam.resistance, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.00e-01	6.23e-02	1.61	0.1230	-2.98e-02	2.31e-01	0.000
L3.beta.Lactam.resistance	-4.96e-06	2.58e-06	-1.92	0.0699	-1.04e-05	4.45e-07	0.156

Table 2717: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.mRNA.surveillance.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2718: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.mTOR.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	8.5e-14	0.0359	2.37e-12	1	-0.075	0.075	0
	NA	NA	NA	NA	NA	NA	0

Table 2719: diversity_vs_picrust_L3_yr1: wunifrac.PC.2 vs
L3.p53.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.39e-04	3.78e-02	0.00369	0.997	-7.89e-02	7.92e-02	0.00e+00
L3.p53.signaling.pathway	-4.95e-07	2.94e-05	-0.01683	0.987	-6.21e-05	6.11e-05	1.42e-05

Table 2720: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation,
df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %
Intercept	0.026875	2.58e-02	1.04	0.3101	-2.71e-02
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	-0.000039	1.86e-05	-2.10	0.0494	-7.78e-05

Table 2721: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.ABC.transporters, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.78e-02	4.57e-02	0.389	0.702	-7.79e-02	1.13e-01	0.0000
L3.ABC.transporters	-8.07e-09	1.75e-08	-0.462	0.650	-4.47e-08	2.85e-08	0.0105

Table 2722: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Adherens.junction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2723: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Adipocytokine.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.35e-02	5.51e-02	0.609	0.550	-0.081690	1.49e-01	0.0000
L3.Adipocytokine.signaling.pathway	-7.37e-07	1.08e-06	-0.681	0.504	-0.000003	1.53e-06	0.0226

Table 2724: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.African.trypanosomiasis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.02e-02	3.21e-02	0.94	0.359	-0.037027	9.74e-02	0.0000
L3.African.trypanosomiasis	-4.05e-05	2.91e-05	-1.39	0.181	-0.000101	2.05e-05	0.0881

Table 2725: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Alanine..aspartate.and.glutamate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.83e-02	5.74e-02	0.493	0.627	-9.18e-02	1.48e-01	0.000
L3.Alanine..aspartate.and.glutamate.metabolism	-3.92e-08	7.18e-08	-0.546	0.591	-1.90e-07	1.11e-07	0.014

Table 2726: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Aldosterone.regulated.sodium.reabsorption, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2727: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Alzheimer.s.disease, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.68e-02	4.84e-02	0.553	0.586	-7.45e-02	1.28e-01	0.0000
L3.Alzheimer.s.disease	-9.28e-07	1.44e-06	-0.642	0.528	-3.95e-06	2.10e-06	0.0202

Table 2728: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Amino.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.38e-03	5.06e-02	0.165	0.870	-9.76e-02	1.14e-01	0.0000
L3.Amino.acid.metabolism	-5.78e-08	3.04e-07	-0.190	0.851	-6.95e-07	5.79e-07	0.0018

Table 2729: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Amino.acid.related.enzymes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.69e-02	5.48e-02	0.491	0.629	-8.78e-02	1.42e-01	0.0000
L3.Amino.acid.related.enzymes	-2.87e-08	5.23e-08	-0.549	0.589	-1.38e-07	8.07e-08	0.0149

Table 2730: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Amino.sugar.and.nucleotide.sugar.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.95e-02	5.62e-02	0.347	0.732	-9.82e-02	1.37e-01	0.000
L3.Amino.sugar.and.nucleotide.sugar.metabolism	-1.99e-08	5.14e-08	-0.386	0.703	-1.28e-07	8.78e-08	0.007

Table 2731: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Aminoacyl.tRNA.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.03e-02	5.10e-02	0.595	0.559	-7.64e-02	1.37e-01	0.0000
L3.Aminoacyl.tRNA.biosynthesis	-4.25e-08	6.26e-08	-0.678	0.506	-1.74e-07	8.86e-08	0.0225

Table 2732: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Aminobenzoate.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.44e-02	5.71e-02	0.427	0.674	-9.52e-02	1.44e-01	0.0000
L3.Aminobenzoate.degradation	-3.52e-07	7.44e-07	-0.474	0.641	-1.91e-06	1.20e-06	0.0111

Table 2733: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Amoebiasis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.10e-02	3.66e-02	0.848	0.407	-4.56e-02	1.08e-01	0.0000
L3.Amoebiasis	-3.99e-06	3.55e-06	-1.125	0.275	-1.14e-05	3.44e-06	0.0595

Table 2734: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Amyotrophic.lateral.sclerosis..ALS., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.88e-02	4.1e-02	0.703	0.491	-5.70e-02	1.15e-01	0.0000
L3.Amyotrophic.lateral.sclerosis..ALS.	-3.14e-06	3.6e-06	-0.873	0.393	-1.07e-05	4.39e-06	0.0367

Table 2735: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Antigen.processing.and.presentation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.83e-02	5.37e-02	0.527	0.605	-8.41e-02	1.41e-01	0.0000
L3.Antigen.processing.and.presentation	-1.08e-06	1.82e-06	-0.592	0.561	-4.88e-06	2.73e-06	0.0172

Table 2736: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Apoptosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.55e-02	2.68e-02	0.576	0.572	-4.07e-02	7.16e-02	0.0000
L3.Apoptosis	-2.21e-05	1.76e-05	-1.256	0.224	-5.89e-05	1.47e-05	0.0731

Table 2737: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Arachidonic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.00e-02	6.16e-02	0.324	0.749	-1.09e-01	1.49e-01	0.00000
L3.Arachidonic.acid.metabolism	-1.81e-06	5.12e-06	-0.354	0.727	-1.25e-05	8.91e-06	0.00623

Table 2738: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Arginine.and.proline.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.11e-02	5.52e-02	0.383	0.706	-9.44e-02	1.37e-01	0.00000
L3.Arginine.and.proline.metabolism	-2.55e-08	5.95e-08	-0.428	0.673	-1.50e-07	9.90e-08	0.00908

Table 2739: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Arrhythmogenic.right.ventricular.cardiomyopathy..ARVC., df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2740: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Ascorbate.and.aldarate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.33e-02	5.03e-02	0.463	0.648	-8.20e-02	1.29e-01	0.0000
L3.Ascorbate.and.aldarate.metabolism	-3.19e-07	6.01e-07	-0.532	0.601	-1.58e-06	9.38e-07	0.0139

Table 2741: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Atrazine.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.54e-03	3.70e-02	0.0417	0.967	-7.59e-02	7.90e-02	0.000000
L3.Atrazine.degradation	-1.20e-07	2.14e-06	-0.0562	0.956	-4.61e-06	4.36e-06	0.000158

Table 2742: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Bacterial.chemotaxis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.56e-02	4.16e-02	0.376	0.711	-7.15e-02	1.03e-01	0.0000
L3.Bacterial.chemotaxis	-5.44e-08	1.17e-07	-0.467	0.646	-2.99e-07	1.90e-07	0.0108

Table 2743: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Bacterial.invasion.of.epithelial.cells, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.16e-02	3.21e-02	0.362	0.721	-0.055594	7.89e-02	0.0000
L3.Bacterial.invasion.of.epithelial.cells	-3.23e-05	5.73e-05	-0.564	0.579	-0.000152	8.76e-05	0.0157

Table 2744: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Bacterial.motility.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.22e-02	3.93e-02	0.565	0.579	-6.00e-02	1.04e-01	0.0000
L3.Bacterial.motility.proteins	-4.56e-08	6.31e-08	-0.723	0.479	-1.78e-07	8.64e-08	0.0254

Table 2745: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Bacterial.secretion.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.96e-02	5.53e-02	0.716	0.483	-7.62e-02	1.55e-01	0.0000
L3.Bacterial.secretion.system	-1.13e-07	1.42e-07	-0.798	0.435	-4.10e-07	1.84e-07	0.0308

Table 2746: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Bacterial.toxins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.37e-02	5.64e-02	0.243	0.811	-1.04e-01	1.32e-01	0.00000
L3.Bacterial.toxins	-1.77e-07	6.56e-07	-0.270	0.790	-1.55e-06	1.20e-06	0.00363

Table 2747: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Basal.transcription.factors, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.05e-02	2.71e-02	0.388	0.702	-0.046117	6.71e-02	0.0000
L3.Basal.transcription.factors	-3.78e-05	4.25e-05	-0.888	0.386	-0.000127	5.13e-05	0.0379

Table 2748: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Base.excision.repair, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.39e-02	5.33e-02	0.449	0.659	-8.76e-02	1.35e-01	0.0000
L3.Base.excision.repair	-8.85e-08	1.75e-07	-0.506	0.618	-4.54e-07	2.77e-07	0.0127

Table 2749: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Benzoate.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.14e-02	5.08e-02	0.42	0.679	-8.51e-02	1.28e-01	0.0000
L3.Benzoate.degradation	-1.72e-07	3.58e-07	-0.48	0.636	-9.21e-07	5.77e-07	0.0114

Table 2750: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Betalain.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00694	0.02617	-0.265	0.794	-0.06172	0.04783	0.0000
L3.Betalain.biosynthesis	0.00107	0.00143	0.748	0.464	-0.00193	0.00407	0.0272

Table 2751: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Bile.secretion, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00434	0.025	-0.173	0.864	-0.0567	0.048	0.0000
L3.Bile.secretion	0.09114	0.115	0.795	0.437	-0.1489	0.331	0.0306

Table 2752: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Biosynthesis.and.biodegradation.of.secondary.metabolites, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	2.19e-02	5.50e-02	0.399	0.694	-9.31e-02	1.37
L3.Biosynthesis.and.biodegradation.of.secondary.metabolites	-5.10e-07	1.14e-06	-0.446	0.660	-2.90e-06	1.88

Table 2753: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Biosynthesis.of.12...14..and.16.membered.macrolides, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2754: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Biosynthesis.of.ansamycins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.47e-02	5.01e-02	0.294	0.772	-9.02e-02	1.20e-01	0.00000
L3.Biosynthesis.of.ansamycins	-1.90e-07	5.62e-07	-0.338	0.739	-1.36e-06	9.86e-07	0.00567

Table 2755: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	-1.77e-02	6.45e-02	-0.275	0.786	-1.53e-01	1.17e
L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides	1.54e-06	5.17e-06	0.298	0.769	-9.29e-06	1.24e

Table 2756: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Biosynthesis.of.type.II.polyketide.backbone, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2757: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Biosynthesis.of.type.II.polyketide.products, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.007009	0.02647	-0.265	0.794	-0.06241	0.04839	0.000
L3.Biosynthesis.of.type.II.polyketide.products	0.000975	0.00139	0.701	0.491	-0.00193	0.00388	0.024

Table 2758: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Biosynthesis.of.unsaturated.fatty.acids, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.93e-02	5.05e-02	0.579	0.569	-7.65e-02	1.35e-01	0.0000
L3.Biosynthesis.of.unsaturated.fatty.acids	-4.27e-07	6.44e-07	-0.663	0.515	-1.78e-06	9.22e-07	0.0215

Table 2759: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Biosynthesis.of.vancomycin.group.antibiotics, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.07e-02	6.20e-02	0.334	0.742	-1.09e-01	1.50e-01	0.0000
L3.Biosynthesis.of.vancomycin.group.antibiotics	-4.55e-07	1.25e-06	-0.365	0.719	-3.07e-06	2.16e-06	0.0066

Table 2760: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Biotin.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.05e-02	5.44e-02	0.377	0.710	-9.34e-02	1.34e-01	0.00000
L3.Biotin.metabolism	-1.86e-07	4.39e-07	-0.423	0.677	-1.10e-06	7.33e-07	0.00887

Table 2761: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Bisphenol.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.21e-02	5.26e-02	0.420	0.679	-8.80e-02	1.32e-01	0.0000
L3.Bisphenol.degradation	-3.65e-07	7.67e-07	-0.476	0.640	-1.97e-06	1.24e-06	0.0112

Table 2762: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Bladder.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.11e-03	0.031300	0.0993	0.922	-0.062403	0.068619	0.00000
L3.Bladder.cancer	-1.91e-05	0.000117	-0.1629	0.872	-0.000264	0.000226	0.00132

Table 2763: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Butanoate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.48e-02	5.29e-02	0.659	0.518	-7.59e-02	1.46e-01	0.0000
L3.Butanoate.metabolism	-8.61e-08	1.16e-07	-0.743	0.467	-3.29e-07	1.56e-07	0.0269

Table 2764: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Butirosin.and.neomycin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.73e-02	4.97e-02	0.752	0.461	-6.66e-02	1.41e-01	0.0000
L3.Butirosin.and.neomycin.biosynthesis	-7.70e-07	8.92e-07	-0.863	0.399	-2.64e-06	1.10e-06	0.0359

Table 2765: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.C5.Branched.dibasic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.65e-02	4.95e-02	0.535	0.599	-7.70e-02	1.30e-01	0.0000
L3.C5.Branched.dibasic.acid.metabolism	-1.23e-07	2.00e-07	-0.617	0.545	-5.42e-07	2.95e-07	0.0187

Table 2766: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.CAM.ligands, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2767: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Caffeine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.91e-03	0.027264	-0.0699	0.945	-0.058972	0.05516	0.00000
L3.Caffeine.metabolism	2.09e-05	0.000124	0.1687	0.868	-0.000238	0.00028	0.00142

Table 2768: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Calcium.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00504	0.02610	0.193	0.849	-0.04959	0.05968	0.0000
L3.Calcium.signaling.pathway	-0.00123	0.00212	-0.580	0.569	-0.00568	0.00321	0.0165

Table 2769: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Caprolactam.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.57e-02	4.29e-02	0.832	0.416	-0.054129	1.26e-01	0.0000
L3.Caprolactam.degradation	-5.20e-06	5.16e-06	-1.007	0.327	-0.000016	5.60e-06	0.0483

Table 2770: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Carbohydrate.digestion.and.absorption, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.28e-02	4.29e-02	0.997	0.331	-0.047070	1.33e-01	0.0000
L3.Carbohydrate.digestion.and.absorption	-5.11e-06	4.25e-06	-1.201	0.245	-0.000014	3.80e-06	0.0672

Table 2771: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Carbohydrate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.93e-02	5.16e-02	0.956	0.351	-5.86e-02	1.57e-01	0.0000
L3.Carbohydrate.metabolism	-3.68e-07	3.40e-07	-1.081	0.293	-1.08e-06	3.44e-07	0.0552

Table 2772: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Carbon.fixation.in.photosynthetic.organisms, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.38e-02	5.57e-02	0.427	0.674	-9.28e-02	1.4e-01	0.0000
L3.Carbon.fixation.in.photosynthetic.organisms	-5.60e-08	1.18e-07	-0.476	0.640	-3.02e-07	1.9e-07	0.0112

Table 2773: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Carbon.fixation.pathways.in.prokaryotes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.07e-02	5.79e-02	0.703	0.491	-8.04e-02	1.62e-01	0.0000
L3.Carbon.fixation.pathways.in.prokaryotes	-6.27e-08	8.09e-08	-0.776	0.448	-2.32e-07	1.07e-07	0.0292

Table 2774: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Cardiac.muscle.contraction, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.10e-03	2.49e-02	0.245	0.809	-4.60e-02	5.82e-02	0.0000
L3.Cardiac.muscle.contraction	-6.61e-06	6.45e-06	-1.025	0.318	-2.01e-05	6.89e-06	0.0499

Table 2775: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Carotenoid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.41e-03	3.52e-02	-0.182	0.857	-8.00e-02	6.72e-02	0.00000
L3.Carotenoid.biosynthesis	3.95e-06	1.54e-05	0.257	0.800	-2.82e-05	3.61e-05	0.00329

Table 2776: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Cell.cycle, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2777: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Cell.cycle. . . Caulobacter, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.67e-02	5.50e-02	0.485	0.633	-8.84e-02	1.42e-01	0.0000
L3.Cell.cycle. . . Caulobacter	-8.55e-08	1.58e-07	-0.543	0.594	-4.16e-07	2.44e-07	0.0145

Table 2778: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Cell.cycle. . . yeast, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2779: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Cell.division, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.96e-02	5.40e-02	0.362	0.721	-9.35e-02	1.33e-01	0.00000
L3.Cell.division	-3.64e-07	8.95e-07	-0.407	0.688	-2.24e-06	1.51e-06	0.00822

Table 2780: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Cell.motility.and.secretion, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.07e-02	5.80e-02	0.702	0.491	-8.06e-02	1.62e-01	0.0000
L3.Cell.motility.and.secretion	-3.60e-07	4.65e-07	-0.775	0.448	-1.33e-06	6.12e-07	0.0291

Table 2781: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Cellular.antigens, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.52e-03	5.21e-02	-0.106	0.917	-1.15e-01	1.04e-01	0.000000
L3.Cellular.antigens	1.91e-07	1.58e-06	0.120	0.905	-3.12e-06	3.50e-06	0.000724

Table 2782: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Chagas.disease..American.trypanosomiasis., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.25e-02	0.030621	1.06	0.302	-0.031601	9.66e-02	0.000
L3.Chagas.disease..American.trypanosomiasis.	-5.05e-05	0.000031	-1.63	0.119	-0.000115	1.43e-05	0.117

Table 2783: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Chaperones.and.folding.catalysts, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.07e-02	5.79e-02	0.530	0.602	-9.04e-02	1.52e-01	0.0000
L3.Chaperones.and.folding.catalysts	-4.78e-08	8.17e-08	-0.586	0.565	-2.19e-07	1.23e-07	0.0169

Table 2784: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Chloroalkane.and.chloroalkene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.09e-02	4.82e-02	0.433	0.67	-8.0e-02	1.22e-01	0.0000
L3.Chloroalkane.and.chloroalkene.degradation	-1.84e-07	3.66e-07	-0.504	0.62	-9.5e-07	5.81e-07	0.0125

Table 2785: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Chlorocyclohexane.and.chlorobenzene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	4.78e-03	3.86e-02	0.124	0.903	-7.60e-02	8.55e-02
L3.Chlorocyclohexane.and.chlorobenzene.degradation	-6.63e-07	4.09e-06	-0.162	0.873	-9.23e-06	7.90e-06

Table 2786: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Cholinergic.synapse, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2787: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Chromosome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.83e-02	5.44e-02	0.520	0.609	-8.55e-02	1.42e-01	0.0000
L3.Chromosome	-2.89e-08	4.95e-08	-0.583	0.566	-1.32e-07	7.47e-08	0.0167

Table 2788: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Chronic.myeloid.leukemia, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2789: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Circadian.rhythm...plant, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.91e-03	0.027291	-0.0702	0.945	-0.059035	0.05521	0.00000
L3.Circadian.rhythm...plant	2.09e-05	0.000124	0.1684	0.868	-0.000238	0.00028	0.00142

Table 2790: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Citrate.cycle..TCA.cycle., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.63e-02	5.82e-02	0.968	0.345	-6.54e-02	1.78e-01	0.0000
L3.Citrate.cycle..TCA.cycle.	-1.40e-07	1.32e-07	-1.064	0.301	-4.16e-07	1.35e-07	0.0536

Table 2791: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Clavulanic.acid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00177	0.0254	0.0696	0.945	-0.0513	0.0549	0.00000
L3.Clavulanic.acid.biosynthesis	-0.01853	0.0581	-0.3188	0.753	-0.1402	0.1031	0.00506

Table 2792: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Colorectal.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.32e-03	2.48e-02	0.214	0.832	-4.66e-02	5.73e-02	0.0000
L3.Colorectal.cancer	-1.89e-05	1.93e-05	-0.979	0.340	-5.94e-05	2.15e-05	0.0458

Table 2793: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Complement.and.coagulation.cascades, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2794: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Cyanoamino.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.09e-02	4.94e-02	0.829	0.417	-6.24e-02	1.44e-01	0.0000
L3.Cyanoamino.acid.metabolism	-1.73e-07	1.81e-07	-0.952	0.353	-5.52e-07	2.07e-07	0.0433

Table 2795: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Cysteine.and.methionine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.88e-02	5.48e-02	0.525	0.605	-8.60e-02	1.44e-01	0.000
L3.Cysteine.and.methionine.metabolism	-4.75e-08	8.08e-08	-0.588	0.563	-2.17e-07	1.22e-07	0.017

Table 2796: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Cytochrome.P450, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2797: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Cytokine.receptors, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2798: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Cytokine.cytokine.receptor.interaction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2799: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Cytoskeleton.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.26e-02	4.92e-02	0.460	0.651	-8.03e-02	1.25e-01	0.0000
L3.Cytoskeleton.proteins	-9.21e-08	1.73e-07	-0.532	0.601	-4.55e-07	2.71e-07	0.0139

Table 2800: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Cytosolic.DNA.sensing.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2801: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.D.Alanine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.53e-02	5.38e-02	0.471	0.643	-8.72e-02	1.38e-01	0.0000
L3.D.Alanine.metabolism	-3.88e-07	7.31e-07	-0.530	0.602	-1.92e-06	1.14e-06	0.0139

Table 2802: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.D.Arginine.and.D.ornithine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.18e-03	3.71e-02	-0.0319	0.975	-7.89e-02	7.65e-02	0.0e+00
L3.D.Arginine.and.D.ornithine.metabolism	3.63e-07	8.45e-06	0.0429	0.966	-1.73e-05	1.81e-05	9.2e-05

Table 2803: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.D.Glutamine.and.D.glutamate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.68e-02	5.73e-02	0.642	0.528	-8.32e-02	1.57e-01	0.0000
L3.D.Glutamine.and.D.glutamate.metabolism	-3.91e-07	5.51e-07	-0.710	0.486	-1.54e-06	7.61e-07	0.0246

Table 2804: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.DNA.repair.and.recombination.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.91e-02	5.52e-02	0.527	0.604	-8.64e-02	1.45e-01	0.000
L3.DNA.repair.and.recombination.proteins	-1.67e-08	2.83e-08	-0.589	0.563	-7.59e-08	4.26e-08	0.017

Table 2805: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.DNA.replication, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.71e-02	5.70e-02	0.475	0.640	-9.22e-02	1.46e-01	0.0000
L3.DNA.replication	-6.66e-08	1.26e-07	-0.527	0.605	-3.31e-07	1.98e-07	0.0137

Table 2806: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.DNA.replication.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.46e-02	5.64e-02	0.436	0.668	-9.35e-02	1.43e-01	0.0000
L3.DNA.replication.proteins	-3.20e-08	6.59e-08	-0.485	0.633	-1.70e-07	1.06e-07	0.0116

Table 2807: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Dilated.cardiomyopathy..DCM., df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2808: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Dioxin.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.4e-02	4.13e-02	0.581	0.568	-6.25e-02	1.10e-01	0.0000
L3.Dioxin.degradation	-7.3e-07	1.01e-06	-0.721	0.480	-2.85e-06	1.39e-06	0.0253

Table 2809: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Drug.metabolism...cytochrome.P450, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.50e-02	4.50e-02	1.22	0.237	-3.92e-02	1.49e-01	0.0000
L3.Drug.metabolism...cytochrome.P450	-4.71e-06	3.28e-06	-1.44	0.168	-1.16e-05	2.16e-06	0.0934

Table 2810: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Drug.metabolism...other.enzymes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.27e-02	5.88e-02	0.216	0.831	-1.10e-01	1.36e-01	0.00000
L3.Drug.metabolism...other.enzymes	-6.07e-08	2.55e-07	-0.238	0.815	-5.95e-07	4.73e-07	0.00282

Table 2811: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.ECM.receptor.interaction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2812: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Electron.transfer.carriers, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.91e-02	3.84e-02	0.497	0.625	-6.13e-02	9.95e-02	0.0000
L3.Electron.transfer.carriers	-1.81e-06	2.80e-06	-0.646	0.526	-7.66e-06	4.05e-06	0.0204

Table 2813: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Endocrine.and.other.factor.regulated.calcium.reabsorption, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2814: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Endocytosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00798	0.0252	0.317	0.755	-0.0448	0.0607	0.0000
L3.Endocytosis	-0.05584	0.0516	-1.081	0.293	-0.1639	0.0523	0.0552

Table 2815: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Energy.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.91e-02	5.74e-02	0.507	0.618	-9.10e-02	1.49e-01	0.0000
L3.Energy.metabolism	-5.17e-08	9.22e-08	-0.561	0.581	-2.45e-07	1.41e-07	0.0155

Table 2816: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	1.81e-02	5.06e-02	0.358	0.724	-8.78e-02	1.24e-0
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	-3.07e-07	7.48e-07	-0.410	0.686	-1.87e-06	1.26e-0

Table 2817: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.ErbB.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2818: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Ether.lipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.16e-03	3.58e-02	0.0326	0.974	-7.37e-02	7.60e-02	0.000000
L3.Ether.lipid.metabolism	-9.38e-07	2.07e-05	-0.0452	0.964	-4.43e-05	4.24e-05	0.000102

Table 2819: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Ethylbenzene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.52e-02	5.46e-02	0.279	0.783	-9.91e-02	1.30e-01	0.00000
L3.Ethylbenzene.degradation	-6.18e-07	1.97e-06	-0.313	0.758	-4.75e-06	3.51e-06	0.00488

Table 2820: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Fat.digestion.and.absorption, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2821: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Fatty.acid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.09e-02	5.44e-02	0.753	0.461	-7.29e-02	1.55e-01	0.0000
L3.Fatty.acid.biosynthesis	-1.32e-07	1.57e-07	-0.842	0.410	-4.60e-07	1.96e-07	0.0343

Table 2822: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Fatty.acid.elongation.in.mitochondria, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.90e-03	0.027250	-0.0699	0.945	-0.058939	0.05513	0.00000
L3.Fatty.acid.elongation.in.mitochondria	2.09e-05	0.000124	0.1690	0.868	-0.000238	0.00028	0.00143

Table 2823: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Fatty.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.73e-02	5.50e-02	0.495	0.626	-8.80e-02	1.42e-01	0.0000
L3.Fatty.acid.metabolism	-2.12e-07	3.82e-07	-0.554	0.586	-1.01e-06	5.89e-07	0.0151

Table 2824: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Fc.epsilon.RI.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2825: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Fc.gamma.R.mediated.phagocytosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00798	0.0252	0.317	0.755	-0.0448	0.0607	0.0000
L3.Fc.gamma.R.mediated.phagocytosis	-0.05584	0.0516	-1.081	0.293	-0.1639	0.0523	0.0552

Table 2826: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Flagellar.assembly, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.10e-02	3.67e-02	0.573	0.573	-5.58e-02	9.79e-02	0.0000
L3.Flagellar.assembly	-1.11e-07	1.44e-07	-0.768	0.452	-4.13e-07	1.91e-07	0.0286

Table 2827: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Flavone.and.flavonol.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.17e-03	4.68e-02	-0.0464	0.963	-1.00e-01	9.58e-02	0.00000
L3.Flavone.and.flavonol.biosynthesis	3.60e-07	6.57e-06	0.0548	0.957	-1.34e-05	1.41e-05	0.00015

Table 2828: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Flavonoid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.51e-02	3.45e-02	0.437	0.667	-5.72e-02	8.74e-02	0.000
L3.Flavonoid.biosynthesis	-1.25e-05	2.01e-05	-0.622	0.541	-5.47e-05	2.96e-05	0.019

Table 2829: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Fluorobenzoate.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.58e-03	3.41e-02	-0.164	0.872	-7.70e-02	0.065809	0.00000
L3.Fluorobenzoate.degradation	1.06e-05	4.45e-05	0.238	0.814	-8.25e-05	0.000104	0.00283

Table 2830: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Focal.adhesion, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2831: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Folate.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.57e-02	6.04e-02	0.426	0.675	-1.01e-01	1.52e-01	0.0000
L3.Folate.biosynthesis	-1.08e-07	2.32e-07	-0.466	0.646	-5.93e-07	3.77e-07	0.0108

Table 2832: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Fructose.and.mannose.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.56e-02	5.29e-02	0.295	0.771	-9.51e-02	1.26e-01	0.00000
L3.Fructose.and.mannose.metabolism	-2.33e-08	6.99e-08	-0.334	0.742	-1.70e-07	1.23e-07	0.00554

Table 2833: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Function.unknown, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.80e-02	5.29e-02	0.719	0.481	-7.27e-02	1.49e-01	0.0000
L3.Function.unknown	-4.84e-08	5.97e-08	-0.810	0.428	-1.73e-07	7.66e-08	0.0318

Table 2834: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.G.protein.coupled.receptors, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00206	0.02787	0.074	0.942	-0.0563	0.0604	0.00000
L3.G.protein.coupled.receptors	-0.00155	0.00952	-0.162	0.873	-0.0215	0.0184	0.00132

Table 2835: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.GTP.binding.proteins, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

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Table 2836: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Galactose.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.67e-02	5.41e-02	0.679	0.506	-7.65e-02	1.50e-01	0.0000
L3.Galactose.metabolism	-6.35e-08	8.35e-08	-0.761	0.456	-2.38e-07	1.11e-07	0.0281

Table 2837: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Gastric.acid.secretion, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2838: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.General.function.prediction.only, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.69e-02	5.55e-02	0.484	0.634	-8.94e-02	1.43e-01	0.0000
L3.General.function.prediction.only	-1.15e-08	2.13e-08	-0.540	0.595	-5.60e-08	3.30e-08	0.0144

Table 2839: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Geraniol.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.93e-02	6.18e-02	0.313	0.758	-1.10e-01	1.49e-01	0.00000
L3.Geraniol.degradation	-9.66e-07	2.83e-06	-0.341	0.737	-6.89e-06	4.96e-06	0.00579

Table 2840: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Germination, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.10e-02	3.87e-02	0.285	0.778	-6.99e-02	9.19e-02	0.00000
L3.Germination	-4.38e-07	1.18e-06	-0.371	0.714	-2.91e-06	2.03e-06	0.00685

Table 2841: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Glioma, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2842: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Glutamatergic.synapse, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.05e-02	5.52e-02	0.553	0.587	-8.51e-02	1.46e-01	0.0000
L3.Glutamatergic.synapse	-4.21e-07	6.81e-07	-0.617	0.544	-1.85e-06	1.01e-06	0.0187

Table 2843: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Glutathione.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.73e-02	6.62e-02	0.564	0.579	-1.01e-01	1.76e-01	0.0000
L3.Glutathione.metabolism	-3.22e-07	5.30e-07	-0.608	0.551	-1.43e-06	7.88e-07	0.0181

Table 2844: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Glycan.bindng.proteins, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2845: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Glycan.biosynthesis.and.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.41e-02	4.75e-02	1.56	0.1354	-2.53e-02	1.74e-01	0.000
L3.Glycan.biosynthesis.and.metabolism	-4.66e-06	2.62e-06	-1.78	0.0908	-1.01e-05	8.14e-07	0.137

Table 2846: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Glycerolipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.38e-02	4.73e-02	0.713	0.484	-6.53e-02	1.33e-01	0.0000
L3.Glycerolipid.metabolism	-1.39e-07	1.67e-07	-0.832	0.416	-4.89e-07	2.11e-07	0.0335

Table 2847: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Glycerophospholipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.84e-02	5.08e-02	0.559	0.583	-7.79e-02	1.35e-01	0.00
L3.Glycerophospholipid.metabolism	-8.20e-08	1.29e-07	-0.638	0.531	-3.51e-07	1.87e-07	0.02

Table 2848: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Glycine..serine.and.threonine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.94e-02	5.78e-02	0.335	0.741	-1.02e-01	1.40e-01	0.00000
L3.Glycine..serine.and.threonine.metabolism	-3.57e-08	9.63e-08	-0.371	0.715	-2.37e-07	1.66e-07	0.00682

Table 2849: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Glycolysis. . . Gluconeogenesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.45e-02	5.38e-02	0.455	0.654	-8.82e-02	1.37e-01	0.0000
L3.Glycolysis. . . Gluconeogenesis	-3.43e-08	6.70e-08	-0.511	0.615	-1.74e-07	1.06e-07	0.0129

Table 2850: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Glycosaminoglycan.biosynthesis. . . chondroitin.sulfate, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	0.00563	0.02484	0.227	0.823	-0.0464	0.0576
L3.Glycosaminoglycan.biosynthesis. . . chondroitin.sulfate	-0.00422	0.00421	-1.002	0.329	-0.0130	0.0046

Table 2851: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Glycosaminoglycan.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.85e-03	4.86e-02	-0.0792	0.938	-1.06e-01	9.80e-02	0.000000
L3.Glycosaminoglycan.degradation	5.85e-08	6.35e-07	0.0921	0.928	-1.27e-06	1.39e-06	0.000424

Table 2852: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Glycosphingolipid.biosynthesis. . . ganglio.series, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.30e-03	4.43e-02	-0.187	0.854	-1.01e-01	8.45e-02	0.00
L3.Glycosphingolipid.biosynthesis. . . ganglio.series	1.85e-07	8.20e-07	0.226	0.824	-1.53e-06	1.90e-06	0.00

Table 2853: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Glycosphingolipid.biosynthesis. . . globo.series, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.72e-02	5.48e-02	0.497	0.625	-8.74e-02	1.42e-01	0.000
L3.Glycosphingolipid.biosynthesis. . . globo.series	-2.97e-07	5.33e-07	-0.557	0.584	-1.41e-06	8.19e-07	0.015

Table 2854: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Glycosphingolipid.biosynthesis...lacto.and.neolacto.series, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	-5.93e-03	2.62e-02	-0.226	0.824	-6.08e-02	0.04
L3.Glycosphingolipid.biosynthesis...lacto.and.neolacto.series	2.94e-05	4.57e-05	0.642	0.528	-6.63e-05	0.00

Table 2855: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Glycosylphosphatidylinositol.GPI..anchor.biosynthesis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2856: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Glycosyltransferases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.33e-02	6.14e-02	0.543	0.594	-9.52e-02	1.62e-01	0.0000
L3.Glycosyltransferases	-1.53e-07	2.59e-07	-0.592	0.561	-6.96e-07	3.89e-07	0.0172

Table 2857: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Glyoxylate.and.dicarboxylate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.53e-02	5.46e-02	0.463	0.649	-8.90e-02	1.40e-01	0.0000
L3.Glyoxylate.and.dicarboxylate.metabolism	-7.09e-08	1.37e-07	-0.518	0.610	-3.57e-07	2.15e-07	0.0133

Table 2858: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.GnRH.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00798	0.0252	0.317	0.755	-0.0448	0.0607	0.0000
L3.GnRH.signaling.pathway	-0.05584	0.0516	-1.081	0.293	-0.1639	0.0523	0.0552

Table 2859: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Hedgehog.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2860: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Hematopoietic.cell.lineage, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2861: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Hepatitis.C, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2862: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Histidine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.06e-02	5.60e-02	0.546	0.591	-8.66e-02	1.48e-01	0.0000
L3.Histidine.metabolism	-7.24e-08	1.19e-07	-0.608	0.550	-3.22e-07	1.77e-07	0.0181

Table 2863: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Homologous.recombination, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.06e-02	5.57e-02	0.550	0.589	-8.60e-02	1.47e-01	0.0000
L3.Homologous.recombination	-5.32e-08	8.68e-08	-0.612	0.548	-2.35e-07	1.29e-07	0.0184

Table 2864: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Huntington.s.disease, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.03e-02	5.02e-02	0.804	0.432	-6.47e-02	1.45e-01	0.0000
L3.Huntington.s.disease	-2.27e-06	2.47e-06	-0.918	0.370	-7.44e-06	2.90e-06	0.0405

Table 2865: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Hypertrophic.cardiomyopathy..HCM., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0055	0.0248	0.222	0.827	-0.0464	0.0574	0.0000
L3.Hypertrophic.cardiomyopathy..HCM.	-0.0165	0.0162	-1.017	0.322	-0.0504	0.0175	0.0492

Table 2866: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Indole.alkaloid.biosynthesis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2867: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Influenza.A, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.32e-03	2.48e-02	0.214	0.832	-4.66e-02	5.73e-02	0.0000
L3.Influenza.A	-1.89e-05	1.93e-05	-0.979	0.340	-5.94e-05	2.15e-05	0.0458

Table 2868: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Inorganic.ion.transport.and.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.37e-02	5.45e-02	0.801	0.433	-7.04e-02	1.58e-01	0.0000
L3.Inorganic.ion.transport.and.metabolism	-3.51e-07	3.92e-07	-0.895	0.382	-1.17e-06	4.70e-07	0.0385

Table 2869: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Inositol.phosphate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.32e-02	5.68e-02	0.409	0.687	-9.57e-02	1.42e-01	0.0000
L3.Inositol.phosphate.metabolism	-3.73e-07	8.22e-07	-0.454	0.655	-2.09e-06	1.35e-06	0.0102

Table 2870: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Insulin.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.97e-02	4.89e-02	0.810	0.428	-6.28e-02	1.42e-01	0.0000
L3.Insulin.signaling.pathway	-7.28e-07	7.80e-07	-0.933	0.363	-2.36e-06	9.05e-07	0.0417

Table 2871: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Ion.channels, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.54e-02	5.89e-02	0.431	0.671	-9.80e-02	1.49e-01	0.0000
L3.Ion.channels	-2.79e-06	5.88e-06	-0.474	0.641	-1.51e-05	9.51e-06	0.0111

Table 2872: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Isoflavonoid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0101	0.0247	0.407	0.689	-0.0417	0.0618	0.0000
L3.Isoflavonoid.biosynthesis	-0.0704	0.0507	-1.389	0.181	-0.1765	0.0357	0.0879

Table 2873: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Isoquinoline.alkaloid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.61e-03	6.47e-02	0.133	0.896	-1.27e-01	1.44e-01	0.00000
L3.Isoquinoline.alkaloid.biosynthesis	-2.29e-07	1.59e-06	-0.144	0.887	-3.56e-06	3.10e-06	0.00104

Table 2874: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Leishmaniasis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2875: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Leukocyte.transendothelial.migration, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2876: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Limonene.and.pinene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.18e-02	5.50e-02	0.396	0.697	-9.34e-02	1.37e-01	0.00000
L3.Limonene.and.pinene.degradation	-4.80e-07	1.08e-06	-0.443	0.663	-2.75e-06	1.79e-06	0.00971

Table 2877: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Linoleic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.1e-02	5.22e-02	0.595	0.559	-7.81e-02	1.40e-01	0.0000
L3.Linoleic.acid.metabolism	-6.0e-07	8.90e-07	-0.674	0.508	-2.46e-06	1.26e-06	0.0222

Table 2878: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Lipid.biosynthesis.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.24e-02	5.62e-02	0.756	0.459	-7.51e-02	1.6e-01	0.000
L3.Lipid.biosynthesis.proteins	-1.14e-07	1.36e-07	-0.839	0.412	-3.98e-07	1.7e-07	0.034

Table 2879: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Lipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.47e-02	4.82e-02	0.720	0.481	-6.62e-02	1.36e-01	0.0000
L3.Lipid.metabolism	-4.06e-07	4.87e-07	-0.834	0.415	-1.43e-06	6.13e-07	0.0336

Table 2880: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Lipoic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.67e-02	5.27e-02	0.317	0.755	-9.36e-02	1.27e-01	0.00000
L3.Lipoic.acid.metabolism	-7.04e-07	1.96e-06	-0.359	0.724	-4.81e-06	3.40e-06	0.00639

Table 2881: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Lipopolysaccharide.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.41e-02	5.76e-02	0.592	0.561	-8.65e-02	1.55e-01	0.000
L3.Lipopolysaccharide.biosynthesis	-2.16e-07	3.30e-07	-0.654	0.521	-9.08e-07	4.75e-07	0.021

Table 2882: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Lipopolysaccharide.biosynthesis.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.54e-02	6.16e-02	0.574	0.572	-9.35e-02	1.64e-01	0.0000
L3.Lipopolysaccharide.biosynthesis.proteins	-1.49e-07	2.38e-07	-0.626	0.538	-6.47e-07	3.49e-07	0.0192

Table 2883: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Long.term.depression, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2884: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Long.term.potentiation, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2885: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Lysine.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.17e-02	5.24e-02	0.414	0.683	-8.80e-02	1.31e-01	0.0000
L3.Lysine.biosynthesis	-3.96e-08	8.44e-08	-0.470	0.644	-2.16e-07	1.37e-07	0.0109

Table 2886: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Lysine.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.81e-02	5.72e-02	0.492	0.629	-9.16e-02	1.48e-01	0.0000
L3.Lysine.degradation	-3.77e-07	6.92e-07	-0.545	0.592	-1.82e-06	1.07e-06	0.0146

Table 2887: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Lysosome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.54e-03	5.32e-02	0.0478	0.962	-1.09e-01	1.14e-01	0.000000
L3.Lysosome	-2.50e-08	4.63e-07	-0.0541	0.957	-9.94e-07	9.44e-07	0.000146

Table 2888: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.MAPK.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2889: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.MAPK.signaling.pathway...yeast, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.13e-03	5.96e-02	-0.0357	0.972	-1.27e-01	1.23e-01	0.00e+00
L3.MAPK.signaling.pathway...yeast	6.74e-08	1.72e-06	0.0393	0.969	-3.52e-06	3.66e-06	7.72e-05

Table 2890: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Measles, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2891: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Meiosis...yeast, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.030108	2.32e-02	1.30	0.20926	-0.018378	7.86e-02	0.000
L3.Meiosis...yeast	-0.000018	6.22e-06	-2.89	0.00937	-0.000031	-4.96e-06	0.295

Table 2892: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Melanogenesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00694	0.02617	-0.265	0.794	-0.06172	0.04783	0.0000
L3.Melanogenesis	0.00107	0.00143	0.748	0.464	-0.00193	0.00407	0.0272

Table 2893: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Membrane.and.intracellular.structural.molecules, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.92e-02	6.19e-02	0.632	0.535	-9.04e-02	1.69e-01	0.0
L3.Membrane.and.intracellular.structural.molecules	-1.08e-07	1.57e-07	-0.689	0.499	-4.37e-07	2.20e-07	0.0

Table 2894: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Metabolism.of.cofactors.and.vitamins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.19e-02	4.80e-02	0.664	0.515	-6.86e-02	1.32e-01	0.0000
L3.Metabolism.of.cofactors.and.vitamins	-4.53e-07	5.88e-07	-0.771	0.450	-1.68e-06	7.77e-07	0.0289

Table 2895: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Metabolism.of.xenobiotics.by.cytochrome.P450, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.48e-02	4.46e-02	1.23	0.234	-3.85e-02	1.48e-01	0.00
L3.Metabolism.of.xenobiotics.by.cytochrome.P450	-4.75e-06	3.28e-06	-1.45	0.164	-1.16e-05	2.11e-06	0.09

Table 2896: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Methane.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.87e-02	5.26e-02	0.357	0.725	-9.13e-02	1.29e-01	0.0000
L3.Methane.metabolism	-2.22e-08	5.50e-08	-0.404	0.691	-1.37e-07	9.29e-08	0.0081

Table 2897: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Mineral.absorption, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.84e-03	3.54e-02	-0.137	0.893	-7.90e-02	6.93e-02	0.00000
L3.Mineral.absorption	2.89e-06	1.51e-05	0.191	0.850	-2.88e-05	3.46e-05	0.00183

Table 2898: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Mismatch.repair, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.76e-02	5.49e-02	0.504	0.620	-8.72e-02	1.42e-01	0.0000
L3.Mismatch.repair	-5.38e-08	9.54e-08	-0.564	0.579	-2.53e-07	1.46e-07	0.0157

Table 2899: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.N.Glycan.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.35e-02	5.60e-02	-0.419	0.680	-1.41e-01	9.37e-02	0.0000
L3.N.Glycan.biosynthesis	1.48e-06	3.16e-06	0.467	0.646	-5.13e-06	8.08e-06	0.0108

Table 2900: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.NOD.like.receptor.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.54e-02	5.63e-02	0.452	0.657	-9.24e-02	1.43e-01	0.0000
L3.NOD.like.receptor.signaling.pathway	-8.92e-07	1.78e-06	-0.502	0.621	-4.61e-06	2.82e-06	0.0125

Table 2901: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Naphthalene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.62e-02	5.52e-02	0.474	0.641	-8.94e-02	1.42e-01	0.0000
L3.Naphthalene.degradation	-3.27e-07	6.16e-07	-0.530	0.602	-1.62e-06	9.63e-07	0.0139

Table 2902: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Neuroactive.ligand.receptor.interaction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2903: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Neurotrophin.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2904: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Nicotinate.and.nicotinamide.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.23e-02	5.50e-02	0.588	0.564	-8.28e-02	1.47e-01	0.0000
L3.Nicotinate.and.nicotinamide.metabolism	-1.23e-07	1.87e-07	-0.657	0.519	-5.14e-07	2.69e-07	0.0211

Table 2905: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Nitrogen.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.95e-02	5.91e-02	0.499	0.624	-9.42e-02	1.53e-01	0.0000
L3.Nitrogen.metabolism	-6.09e-08	1.11e-07	-0.549	0.590	-2.93e-07	1.71e-07	0.0148

Table 2906: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Nitrotoluene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.67e-02	4.09e-02	0.409	0.687	-6.89e-02	1.02e-01	0.000
L3.Nitrotoluene.degradation	-2.58e-07	5.03e-07	-0.512	0.614	-1.31e-06	7.94e-07	0.013

Table 2907: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Non.homologous.end.joining, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.64e-02	3.59e-02	0.458	0.652	-5.86e-02	9.15e-02	0.0000
L3.Non.homologous.end.joining	-5.22e-06	8.29e-06	-0.629	0.537	-2.26e-05	1.21e-05	0.0194

Table 2908: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Notch.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2909: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Novobiocin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.80e-02	5.52e-02	0.507	0.618	-8.75e-02	1.43e-01	0.0000
L3.Novobiocin.biosynthesis	-3.25e-07	5.73e-07	-0.567	0.577	-1.53e-06	8.75e-07	0.0158

Table 2910: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Nucleotide.excision.repair, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.29e-02	5.31e-02	0.619	0.543	-7.83e-02	1.44e-01	0.0000
L3.Nucleotide.excision.repair	-1.35e-07	1.94e-07	-0.698	0.494	-5.41e-07	2.70e-07	0.0238

Table 2911: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Nucleotide.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.09e-02	4.31e-02	0.717	0.482	-5.93e-02	1.21e-01	0.0000
L3.Nucleotide.metabolism	-1.12e-06	1.28e-06	-0.869	0.396	-3.80e-06	1.57e-06	0.0364

Table 2912: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Olfactory.transduction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2913: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.One.carbon.pool.by.folate, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.64e-02	5.83e-02	0.454	0.655	-9.55e-02	1.48e-01	0.0000
L3.One.carbon.pool.by.folate	-6.73e-08	1.34e-07	-0.501	0.622	-3.48e-07	2.14e-07	0.0124

Table 2914: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Oocyte.meiosis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2915: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Other.glycan.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.40e-02	5.96e-02	0.402	0.692	-1.01e-01	1.49e-01	0.00000
L3.Other.glycan.degradation	-8.48e-08	1.92e-07	-0.442	0.663	-4.86e-07	3.17e-07	0.00968

Table 2916: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Other.ion.coupled.transporters, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.32e-02	5.88e-02	0.564	0.579	-8.99e-02	1.56e-01	0.0000
L3.Other.ion.coupled.transporters	-3.75e-08	6.04e-08	-0.621	0.542	-1.64e-07	8.89e-08	0.0189

Table 2917: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Other.transporters, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.48e-02	5.52e-02	0.631	0.535	-8.07e-02	1.50e-01	0.0000
L3.Other.transporters	-1.98e-07	2.80e-07	-0.705	0.490	-7.85e-07	3.89e-07	0.0242

Table 2918: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Other.types.of.O.glycan.biosynthesis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2919: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Others, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.02e-02	5.43e-02	0.740	0.468	-7.35e-02	1.54e-01	0.0000
L3.Others	-6.54e-08	7.90e-08	-0.828	0.418	-2.31e-07	9.99e-08	0.0332

Table 2920: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Oxidative.phosphorylation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.25e-02	5.45e-02	0.596	0.558	-8.15e-02	1.46e-01	0.0000
L3.Oxidative.phosphorylation	-4.35e-08	6.52e-08	-0.668	0.512	-1.80e-07	9.29e-08	0.0218

Table 2921: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.PPAR.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.08e-02	5.93e-02	0.520	0.609	-9.32e-02	1.55e-01	0.0000
L3.PPAR.signaling.pathway	-4.33e-07	7.58e-07	-0.572	0.574	-2.02e-06	1.15e-06	0.0161

Table 2922: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Pancreatic.cancer, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2923: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Pancreatic.secretion, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2924: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Pantothenate.and.CoA.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.3e-02	5.30e-02	0.434	0.669	-8.79e-02	1.34e-01	0.0000
L3.Pantothenate.and.CoA.biosynthesis	-5.6e-08	1.14e-07	-0.491	0.629	-2.95e-07	1.83e-07	0.0119

Table 2925: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Parkinson.s.disease, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.93e-03	2.49e-02	0.238	0.814	-0.046132	5.80e-02	0.0000
L3.Parkinson.s.disease	-4.91e-06	4.84e-06	-1.016	0.322	-0.000015	5.21e-06	0.0491

Table 2926: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Pathogenic.Escherichia.coli.infection, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2927: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Pathways.in.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.83e-02	5.18e-02	0.740	0.468	-7.00e-02	1.47e-01	0.000
L3.Pathways.in.cancer	-1.27e-06	1.51e-06	-0.839	0.412	-4.43e-06	1.90e-06	0.034

Table 2928: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Penicillin.and.cephalosporin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.3e-02	5.26e-02	0.437	0.667	-8.71e-02	1.33e-01	0.0000
L3.Penicillin.and.cephalosporin.biosynthesis	-1.3e-06	2.62e-06	-0.495	0.626	-6.77e-06	4.18e-06	0.0121

Table 2929: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Pentose.and.glucuronate.interconversions, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.18e-02	5.59e-02	0.390	0.701	-9.53e-02	1.39e-01	0.00000
L3.Pentose.and.glucuronate.interconversions	-5.07e-08	1.17e-07	-0.435	0.669	-2.95e-07	1.93e-07	0.00936

Table 2930: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Pentose.phosphate.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.04e-02	5.35e-02	0.382	0.707	-9.15e-02	1.32e-01	0.00000
L3.Pentose.phosphate.pathway	-3.43e-08	7.96e-08	-0.431	0.672	-2.01e-07	1.32e-07	0.00919

Table 2931: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Peptidases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.90e-02	5.59e-02	0.518	0.61	-8.79e-02	1.46e-01	0.0000
L3.Peptidases	-2.42e-08	4.19e-08	-0.578	0.57	-1.12e-07	6.35e-08	0.0164

Table 2932: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Peptidoglycan.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.77e-02	5.36e-02	0.517	0.611	-8.45e-02	1.40e-01	0.0000
L3.Peptidoglycan.biosynthesis	-5.47e-08	9.39e-08	-0.582	0.567	-2.51e-07	1.42e-07	0.0167

Table 2933: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Peroxisome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.15e-02	6.03e-02	0.522	0.608	-9.48e-02	1.58e-01	0.0000
L3.Peroxisome	-2.73e-07	4.78e-07	-0.571	0.574	-1.27e-06	7.27e-07	0.0161

Table 2934: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Pertussis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.12e-02	5.68e-02	-0.55	0.589	-1.50e-01	8.76e-02	0.0000
L3.Pertussis	1.70e-06	2.79e-06	0.61	0.549	-4.14e-06	7.54e-06	0.0183

Table 2935: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Phagosome, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2936: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Phenylalanine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.32e-02	5.65e-02	0.765	0.454	-7.50e-02	1.61e-01	0.0000
L3.Phenylalanine.metabolism	-3.58e-07	4.22e-07	-0.848	0.407	-1.24e-06	5.25e-07	0.0347

Table 2937: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	2.68e-02	5.24e-02	0.511	0.615	-8.29e-02	1.36e-01
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis	-4.89e-08	8.44e-08	-0.579	0.570	-2.26e-07	1.28e-07

Table 2938: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Phenylpropanoid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.03e-02	4.49e-02	0.898	0.381	-5.36e-02	1.34e-01	0.0000
L3.Phenylpropanoid.biosynthesis	-2.69e-07	2.53e-07	-1.064	0.300	-7.99e-07	2.60e-07	0.0536

Table 2939: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Phosphatidylinositol.signaling.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.26e-02	5.87e-02	0.725	0.477	-8.03e-02	1.65e-01	0.0000
L3.Phosphatidylinositol.signaling.system	-7.42e-07	9.31e-07	-0.797	0.435	-2.69e-06	1.21e-06	0.0308

Table 2940: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Phosphonate.and.phosphinate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.20e-02	5.25e-02	0.991	0.334	-5.79e-02	1.62e-01	0.0000
L3.Phosphonate.and.phosphinate.metabolism	-1.19e-06	1.07e-06	-1.114	0.279	-3.44e-06	1.05e-06	0.0585

Table 2941: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Phosphotransferase.system..PTS., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.01e-03	3.95e-02	0.178	0.861	-7.56e-02	8.96e-02	0.0000
L3.Phosphotransferase.system..PTS.	-2.82e-08	1.23e-07	-0.228	0.822	-2.87e-07	2.30e-07	0.0026

Table 2942: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Photosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.15e-02	4.81e-02	0.446	0.660	-7.91e-02	1.22e-01	0.0000
L3.Photosynthesis	-7.96e-08	1.53e-07	-0.520	0.609	-4.00e-07	2.41e-07	0.0133

Table 2943: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Photosynthesis...antenna.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.13e-03	0.026113	0.197	0.846	-0.049522	0.059789	0.0000
L3.Photosynthesis...antenna.proteins	-7.33e-05	0.000125	-0.587	0.564	-0.000335	0.000188	0.0169

Table 2944: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Photosynthesis.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.19e-02	4.80e-02	0.456	0.654	-7.86e-02	1.22e-01	0.0000
L3.Photosynthesis.proteins	-8.06e-08	1.52e-07	-0.531	0.602	-3.99e-07	2.37e-07	0.0139

Table 2945: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Phototransduction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2946: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Phototransduction...fly, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2947: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Plant.pathogen.interaction, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.88e-02	4.94e-02	0.584	0.566	-7.45e-02	1.32e-01	0.0000
L3.Plant.pathogen.interaction	-2.91e-07	4.33e-07	-0.673	0.509	-1.20e-06	6.15e-07	0.0221

Table 2948: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Polycyclic.aromatic.hydrocarbon.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.75e-02	5.33e-02	0.517	0.611	-8.41e-02	1.39e-01	0.000
L3.Polycyclic.aromatic.hydrocarbon.degradation	-3.95e-07	6.78e-07	-0.582	0.567	-1.81e-06	1.02e-06	0.016

Table 2949: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Polyketide.sugar.unit.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.63e-02	5.91e-02	0.445	0.661	-9.73e-02	1.50e-01	0.0000
L3.Polyketide.sugar.unit.biosynthesis	-1.80e-07	3.68e-07	-0.490	0.630	-9.52e-07	5.91e-07	0.0119

Table 2950: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Pores.ion.channels, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.16e-02	6.58e-02	0.481	0.636	-1.06e-01	1.69e-01	0.0000
L3.Pores.ion.channels	-1.34e-07	2.58e-07	-0.518	0.610	-6.75e-07	4.07e-07	0.0133

Table 2951: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Porphyrin.and.chlorophyll.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.23e-02	5.20e-02	0.237	0.815	-9.65e-02	1.21e-01	0.00000
L3.Porphyrin.and.chlorophyll.metabolism	-1.86e-08	6.88e-08	-0.270	0.790	-1.63e-07	1.26e-07	0.00363

Table 2952: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Prenyltransferases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.29e-02	5.82e-02	0.565	0.579	-8.89e-02	1.55e-01	0.000
L3.Prenyltransferases	-1.70e-07	2.73e-07	-0.623	0.541	-7.42e-07	4.01e-07	0.019

Table 2953: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Primary.bile.acid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.74e-02	4.87e-02	0.562	0.581	-7.46e-02	1.29e-01	0.0000
L3.Primary.bile.acid.biosynthesis	-9.88e-07	1.52e-06	-0.651	0.523	-4.17e-06	2.19e-06	0.0207

Table 2954: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Primary.immunodeficiency, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.33e-02	5.37e-02	0.434	0.669	-8.91e-02	1.36e-01	0.0000
L3.Primary.immunodeficiency	-7.54e-07	1.54e-06	-0.488	0.631	-3.98e-06	2.48e-06	0.0118

Table 2955: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Prion.diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.51e-02	3.83e-02	0.395	0.698	-6.51e-02	0.095394	0.0000
L3.Prion.diseases	-3.91e-06	7.58e-06	-0.515	0.612	-1.98e-05	0.000012	0.0131

Table 2956: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Progesterone.mediated.oocyte.maturation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.83e-02	5.37e-02	0.527	0.605	-8.41e-02	1.41e-01	0.0000
L3.Progesterone.mediated.oocyte.maturation	-1.08e-06	1.82e-06	-0.592	0.561	-4.88e-06	2.73e-06	0.0172

Table 2957: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Propanoate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.95e-02	5.45e-02	0.542	0.594	-8.46e-02	1.44e-01	0.0000
L3.Propanoate.metabolism	-9.58e-08	1.58e-07	-0.607	0.551	-4.26e-07	2.35e-07	0.0181

Table 2958: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Prostate.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.39e-02	5.38e-02	0.816	0.424	-6.87e-02	1.57e-01	0.0000
L3.Prostate.cancer	-1.56e-06	1.71e-06	-0.915	0.372	-5.13e-06	2.01e-06	0.0402

Table 2959: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Proteasome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.44e-02	5.27e-02	0.653	0.522	-7.59e-02	1.45e-01	0.0000
L3.Proteasome	-1.27e-06	1.72e-06	-0.738	0.470	-4.87e-06	2.33e-06	0.0265

Table 2960: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Protein.digestion.and.absorption, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.47e-02	4.65e-02	-0.316	0.756	-1.12e-01	8.26e-02	0.00000
L3.Protein.digestion.and.absorption	8.40e-07	2.25e-06	0.373	0.713	-3.87e-06	5.55e-06	0.00691

Table 2961: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Protein.export, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.43e-02	5.55e-02	0.619	0.543	-8.18e-02	1.50e-01	0.0000
L3.Protein.export	-9.12e-08	1.32e-07	-0.690	0.498	-3.68e-07	1.85e-07	0.0233

Table 2962: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Protein.folding.and.associated.processing, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.70e-02	5.64e-02	0.478	0.638	-9.10e-02	1.45e-01	0.0000
L3.Protein.folding.and.associated.processing	-6.62e-08	1.25e-07	-0.532	0.601	-3.27e-07	1.94e-07	0.0139

Table 2963: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Protein.kinases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.95e-02	4.87e-02	0.401	0.693	-8.24e-02	1.21e-01	0.0000
L3.Protein.kinases	-9.95e-08	2.14e-07	-0.466	0.647	-5.47e-07	3.48e-07	0.0107

Table 2964: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Protein.processing.in.endoplasmic.reticulum, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.22e-02	6.30e-02	0.194	0.848	-1.20e-01	1.44e-01	0.0000
L3.Protein.processing.in.endoplasmic.reticulum	-2.91e-07	1.38e-06	-0.211	0.835	-3.18e-06	2.59e-06	0.0022

Table 2965: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Proximal.tubule.bicarbonate.reclamation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.61e-02	4.35e-02	1.06	0.302	-4.49e-02	1.37e-01	0.0000
L3.Proximal.tubule.bicarbonate.reclamation	-3.31e-06	2.61e-06	-1.27	0.220	-8.78e-06	2.16e-06	0.0743

Table 2966: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Purine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.64e-02	5.60e-02	0.470	0.643	-9.09e-02	1.44e-01	0.0000
L3.Purine.metabolism	-1.90e-08	3.64e-08	-0.524	0.606	-9.52e-08	5.71e-08	0.0135

Table 2967: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Pyrimidine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.66e-02	5.62e-02	0.474	0.641	-9.11e-02	1.44e-01	0.0000
L3.Pyrimidine.metabolism	-2.33e-08	4.41e-08	-0.527	0.604	-1.16e-07	6.91e-08	0.0137

Table 2968: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Pyruvate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.53e-02	5.46e-02	0.463	0.649	-8.90e-02	1.40e-01	0.0000
L3.Pyruvate.metabolism	-3.76e-08	7.25e-08	-0.519	0.610	-1.89e-07	1.14e-07	0.0133

Table 2969: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.RIG.I.like.receptor.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.41e-03	3.21e-02	-0.262	0.796	-7.56e-02	5.88e-02	0.00000
L3.RIG.I.like.receptor.signaling.pathway	6.29e-06	1.53e-05	0.410	0.686	-2.58e-05	3.84e-05	0.00835

Table 2970: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.RNA.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.79e-02	5.77e-02	0.484	0.634	-9.28e-02	1.49e-01	0.0000
L3.RNA.degradation	-9.20e-08	1.72e-07	-0.536	0.598	-4.52e-07	2.68e-07	0.0141

Table 2971: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.RNA.polymerase, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.16e-02	5.53e-02	0.391	0.700	-9.41e-02	1.37e-01	0.00000
L3.RNA.polymerase	-2.28e-07	5.23e-07	-0.437	0.667	-1.32e-06	8.66e-07	0.00945

Table 2972: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.RNA.transport, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.05e-02	4.81e-02	0.426	0.675	-8.01e-02	1.21e-01	0.0000
L3.RNA.transport	-2.35e-07	4.73e-07	-0.496	0.625	-1.22e-06	7.55e-07	0.0122

Table 2973: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Regulation.of.actin.cytoskeleton, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2974: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Renal.cell.carcinoma, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.24e-02	3.93e-02	1.33	0.198	-2.99e-02	1.35e-01	0.00
L3.Renal.cell.carcinoma	-1.43e-05	8.65e-06	-1.65	0.115	-3.24e-05	3.82e-06	0.12

Table 2975: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Renin.angiotensin.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00798	0.0252	0.317	0.755	-0.0447	0.0607	0.0000
L3.Renin.angiotensin.system	-0.01117	0.0102	-1.092	0.289	-0.0326	0.0102	0.0563

Table 2976: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Replication..recombination.and.repair.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.17e-02	5.12e-02	0.424	0.676	-8.55e-02	1.29e-01	0.00
L3.Replication..recombination.and.repair.proteins	-4.53e-08	9.37e-08	-0.484	0.634	-2.41e-07	1.51e-07	0.01

Table 2977: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Restriction.enzyme, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.46e-02	5.85e-02	0.420	0.679	-9.79e-02	1.47e-01	0.0000
L3.Restriction.enzyme	-2.13e-07	4.59e-07	-0.464	0.648	-1.17e-06	7.48e-07	0.0106

Table 2978: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Retinol.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.07e-02	4.51e-02	1.57	0.1333	-2.36e-02	1.65e-01	0.000
L3.Retinol.metabolism	-4.78e-06	2.62e-06	-1.82	0.0844	-1.03e-05	7.13e-07	0.142

Table 2979: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Rheumatoid.arthritis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2980: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Riboflavin.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.13e-02	5.92e-02	0.360	0.723	-1.03e-01	1.45e-01	0.00000
L3.Riboflavin.metabolism	-1.43e-07	3.62e-07	-0.396	0.697	-9.02e-07	6.15e-07	0.00777

Table 2981: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Ribosome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.09e-02	5.44e-02	0.567	0.577	-8.30e-02	1.45e-01	0.0000
L3.Ribosome	-2.16e-08	3.40e-08	-0.636	0.533	-9.28e-08	4.95e-08	0.0198

Table 2982: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Ribosome.Biogenesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.04e-02	5.27e-02	0.576	0.571	-8.00e-02	1.41e-01	0.0000
L3.Ribosome.Biogenesis	-3.54e-08	5.44e-08	-0.651	0.523	-1.49e-07	7.85e-08	0.0208

Table 2983: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Ribosome.biogenesis.in.eukaryotes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.14e-02	5.22e-02	0.794	0.437	-6.77e-02	1.51e-01	0.0000
L3.Ribosome.biogenesis.in.eukaryotes	-1.43e-06	1.59e-06	-0.898	0.380	-4.76e-06	1.90e-06	0.0388

Table 2984: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Salivary.secretion, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2985: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Secondary.bile.acid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.92e-02	4.91e-02	0.595	0.559	-7.35e-02	1.32e-01	0.000
L3.Secondary.bile.acid.biosynthesis	-1.08e-06	1.58e-06	-0.687	0.500	-4.38e-06	2.22e-06	0.023

Table 2986: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Secretion.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.59e-02	4.86e-02	0.739	0.469	-6.58e-02	1.38e-01	0.0000
L3.Secretion.system	-5.48e-08	6.42e-08	-0.854	0.404	-1.89e-07	7.95e-08	0.0352

Table 2987: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Selenocompound.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.18e-02	5.44e-02	0.400	0.694	-9.21e-02	1.36e-01	0.00000
L3.Selenocompound.metabolism	-9.28e-08	2.07e-07	-0.449	0.658	-5.26e-07	3.40e-07	0.00999

Table 2988: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Sesquiterpenoid.biosynthesis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2989: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Shigellosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.01165	0.02591	-0.45	0.658	-0.06589	0.0426	0.0000
L3.Shigellosis	0.00612	0.00518	1.18	0.252	-0.00472	0.0170	0.0653

Table 2990: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Signal.transduction.mechanisms, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.97e-02	5.01e-02	0.394	0.698	-8.51e-02	1.25e-01	0.0000
L3.Signal.transduction.mechanisms	-6.69e-08	1.48e-07	-0.452	0.656	-3.76e-07	2.43e-07	0.0101

Table 2991: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Small.cell.lung.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.32e-03	2.48e-02	0.214	0.832	-4.66e-02	5.73e-02	0.0000
L3.Small.cell.lung.cancer	-1.89e-05	1.93e-05	-0.979	0.340	-5.94e-05	2.15e-05	0.0458

Table 2992: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Sphingolipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.96e-02	5.63e-02	0.704	0.490	-7.82e-02	1.57e-01	0.0000
L3.Sphingolipid.metabolism	-1.96e-07	2.50e-07	-0.782	0.444	-7.19e-07	3.28e-07	0.0297

Table 2993: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Spliceosome, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 2994: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Sporulation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.29e-02	4.10e-02	0.314	0.757	-7.30e-02	9.87e-02	0.00000
L3.Sporulation	-2.66e-08	6.75e-08	-0.394	0.698	-1.68e-07	1.15e-07	0.00769

Table 2995: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Staphylococcus.aureus.infection, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.013569	3.65e-02	0.372	0.714	-6.28e-02	8.99e-02	0.0000
L3.Staphylococcus.aureus.infection	-0.000004	7.91e-06	-0.505	0.619	-2.06e-05	1.26e-05	0.0126

Table 2996: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Starch.and.sucrose.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.36e-02	5.06e-02	0.664	0.515	-7.23e-02	1.40e-01	0.000
L3.Starch.and.sucrose.metabolism	-4.45e-08	5.87e-08	-0.759	0.457	-1.67e-07	7.83e-08	0.028

Table 2997: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Steroid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.70e-03	2.74e-02	-0.0619	0.951	-0.05904	0.055645	0.00000
L3.Steroid.biosynthesis	6.01e-06	4.11e-05	0.1461	0.885	-0.00008	0.000092	0.00107

Table 2998: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Steroid.hormone.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.79e-04	3.97e-02	0.00450	0.996	-8.28e-02	8.32e-02	0.00e+00
L3.Steroid.hormone.biosynthesis	-1.13e-08	1.96e-06	-0.00577	0.995	-4.12e-06	4.10e-06	1.67e-06

Table 2999: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	3.99e-03	3.03e-02	0.132	0.897	-0.059357	0.06733
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	-1.36e-05	5.91e-05	-0.230	0.821	-0.000137	0.00011

Table 3000: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Streptomycin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.17e-02	5.77e-02	0.549	0.589	-8.91e-02	1.52e-01	0.0000
L3.Streptomycin.biosynthesis	-1.43e-07	2.35e-07	-0.607	0.551	-6.34e-07	3.49e-07	0.0181

Table 3001: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Styrene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.74e-03	3.96e-02	0.0438	0.965	-8.11e-02	8.46e-02	0.000000
L3.Styrene.degradation	-1.42e-07	2.52e-06	-0.0563	0.956	-5.42e-06	5.14e-06	0.000159

Table 3002: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Sulfur.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.22e-02	5.71e-02	0.564	0.579	-8.73e-02	1.52e-01	0.0000
L3.Sulfur.metabolism	-1.71e-07	2.74e-07	-0.625	0.539	-7.44e-07	4.02e-07	0.0192

Table 3003: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Sulfur.relay.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.98e-02	4.93e-02	0.605	0.552	-7.33e-02	1.33e-01	0.0000
L3.Sulfur.relay.system	-1.82e-07	2.61e-07	-0.698	0.494	-7.29e-07	3.64e-07	0.0238

Table 3004: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Synthesis.and.degradation.of.ketone.bodies, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.01e-03	4.60e-02	0.0655	0.948	-9.32e-02	9.93e-02	0.00000
L3.Synthesis.and.degradation.of.ketone.bodies	-1.97e-07	2.53e-06	-0.0779	0.939	-5.50e-06	5.11e-06	0.00030

Table 3005: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Systemic.lupus.erythematosus, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.06e-03	0.028425	0.0373	0.971	-0.058434	0.060554	0.000000
L3.Systemic.lupus.erythematosus	-9.41e-06	0.000123	-0.0765	0.940	-0.000267	0.000248	0.000293

Table 3006: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.TGF.beta.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 3007: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Taurine.and.hypotaurine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.71e-02	6.18e-02	0.439	0.666	-1.02e-01	1.57e-01	0.0000
L3.Taurine.and.hypotaurine.metabolism	-3.94e-07	8.24e-07	-0.478	0.638	-2.12e-06	1.33e-06	0.0113

Table 3008: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Terpenoid.backbone.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.30e-02	5.67e-02	0.406	0.689	-9.56e-02	1.42e-01	0.0000
L3.Terpenoid.backbone.biosynthesis	-6.51e-08	1.44e-07	-0.451	0.657	-3.67e-07	2.37e-07	0.0101

Table 3009: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs
L3.Tetracycline.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.80e-02	4.91e-02	0.570	0.575	-7.48e-02	1.31e-01	0.0000
L3.Tetracycline.biosynthesis	-3.09e-07	4.70e-07	-0.658	0.518	-1.29e-06	6.74e-07	0.0212

Table 3010: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Thiamine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.20e-02	5.45e-02	0.403	0.691	-9.22e-02	1.36e-01	0.0000
L3.Thiamine.metabolism	-6.86e-08	1.52e-07	-0.452	0.656	-3.86e-07	2.49e-07	0.0101

Table 3011: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Tight.junction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 3012: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Toluene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.87e-02	3.95e-02	1.49	0.1536	-2.39e-02	1.41e-01	0.000
L3.Toluene.degradation	-8.01e-07	4.39e-07	-1.83	0.0837	-1.72e-06	1.18e-07	0.143

Table 3013: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Toxoplasmosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.32e-03	2.48e-02	0.214	0.832	-4.66e-02	5.73e-02	0.0000
L3.Toxoplasmosis	-1.89e-05	1.93e-05	-0.979	0.340	-5.94e-05	2.15e-05	0.0458

Table 3014: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Transcription.factors, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.79e-02	4.75e-02	0.377	0.710	-8.14e-02	1.17e-01	0.00000
L3.Transcription.factors	-1.67e-08	3.78e-08	-0.442	0.663	-9.59e-08	6.25e-08	0.00967

Table 3015: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Transcription.machinery, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.75e-02	5.70e-02	0.483	0.635	-9.18e-02	1.47e-01	0.0000
L3.Transcription.machinery	-4.05e-08	7.56e-08	-0.535	0.599	-1.99e-07	1.18e-07	0.0141

Table 3016: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Transcription.related.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.50e-02	2.64e-02	1.70	0.1045	-1.02e-02	1.00e-01	0.000
L3.Transcription.related.proteins	-2.15e-05	7.68e-06	-2.79	0.0116	-3.76e-05	-5.39e-06	0.281

Table 3017: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Translation.factors, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.97e-02	5.60e-02	0.531	0.601	-8.74e-02	1.47e-01	0.0000
L3.Translation.factors	-9.05e-08	1.53e-07	-0.591	0.561	-4.11e-07	2.30e-07	0.0172

Table 3018: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Translation.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.12e-02	5.44e-02	0.575	0.572	-8.26e-02	1.45e-01	0.0000
L3.Translation.proteins	-5.69e-08	8.83e-08	-0.644	0.527	-2.42e-07	1.28e-07	0.0203

Table 3019: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Transporters, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.78e-02	4.61e-02	0.385	0.704	-7.88e-02	1.14e-01	0.0000
L3.Transporters	-4.03e-09	8.85e-09	-0.456	0.654	-2.26e-08	1.45e-08	0.0103

Table 3020: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	2.68e-02	5.73e-02	0.467	0.646	-9.33e-02	1.47e-01
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis	-3.53e-07	6.83e-07	-0.517	0.611	-1.78e-06	1.08e-06

Table 3021: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Tryptophan.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.58e-02	5.25e-02	0.490	0.630	-8.42e-02	1.36e-01	0.0000
L3.Tryptophan.metabolism	-3.48e-07	6.26e-07	-0.555	0.585	-1.66e-06	9.63e-07	0.0152

Table 3022: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Tuberculosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.35e-02	5.37e-02	0.624	0.540	-7.89e-02	1.46e-01	0.000
L3.Tuberculosis	-3.56e-07	5.07e-07	-0.701	0.492	-1.42e-06	7.06e-07	0.024

Table 3023: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Two.component.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.08e-02	4.91e-02	0.628	0.537	-7.19e-02	1.34e-01	0.0000
L3.Two.component.system	-3.28e-08	4.52e-08	-0.725	0.477	-1.27e-07	6.18e-08	0.0256

Table 3024: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Type.I.diabetes.mellitus, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.06e-02	5.63e-02	0.721	0.480	-7.73e-02	1.58e-01	0.000
L3.Type.I.diabetes.mellitus	-1.21e-06	1.51e-06	-0.800	0.433	-4.38e-06	1.96e-06	0.031

Table 3025: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Type.II.diabetes.mellitus, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.82e-02	5.56e-02	0.506	0.619	-8.83e-02	1.45e-01	0.0000
L3.Type.II.diabetes.mellitus	-9.74e-07	1.73e-06	-0.564	0.579	-4.59e-06	2.64e-06	0.0157

Table 3026: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Tyrosine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.69e-02	5.47e-02	0.491	0.629	-8.77e-02	1.41e-01	0.0000
L3.Tyrosine.metabolism	-1.33e-07	2.42e-07	-0.550	0.589	-6.41e-07	3.74e-07	0.0149

Table 3027: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	2.94e-02	6.52e-02	0.451	0.657	-1.07e-01	1.66e-01
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis	-2.90e-07	5.95e-07	-0.487	0.632	-1.54e-06	9.56e-07

Table 3028: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Ubiquitin.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.17e-02	4.52e-02	-0.481	0.636	-1.16e-01	0.072836	0.0000
L3.Ubiquitin.system	3.86e-06	6.74e-06	0.573	0.573	-1.02e-05	0.000018	0.0162

Table 3029: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.VEGF.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 3030: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Valine..leucine.and.isoleucine.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.49e-02	5.07e-02	0.491	0.629	-8.12e-02	1.31e-01	0.0000
L3.Valine..leucine.and.isoleucine.biosynthesis	-5.07e-08	9.04e-08	-0.561	0.581	-2.40e-07	1.38e-07	0.0155

Table 3031: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Valine..leucine.and.isoleucine.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.98e-02	6.43e-02	0.308	0.761	-1.15e-01	1.54e-01	0.00000
L3.Valine..leucine.and.isoleucine.degradation	-1.50e-07	4.50e-07	-0.334	0.742	-1.09e-06	7.91e-07	0.00554

Table 3032: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Various.types.of.N.glycan.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.01391	0.026679	0.522	0.608	-0.0419	0.069754	0.0000
L3.Various.types.of.N.glycan.biosynthesis	-0.00109	0.000916	-1.185	0.250	-0.0030	0.000832	0.0656

Table 3033: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Vascular.smooth.muscle.contraction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 3034: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Vasopressin.regulated.water.reabsorption, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00475	0.0261	0.182	0.857	-0.0498	0.0593	0.0000
L3.Vasopressin.regulated.water.reabsorption	-0.01995	0.0360	-0.554	0.586	-0.0954	0.0555	0.0151

Table 3035: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Vibrio.cholerae.infection, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.000607	0.0260	0.0234	0.982	-0.0538	0.0550	0.000000
L3.Vibrio.cholerae.infection	-0.001275	0.0162	-0.0787	0.938	-0.0352	0.0327	0.000309

Table 3036: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Vibrio.cholerae.pathogenic.cycle, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.34e-02	5.44e-02	0.247	0.808	-1.00e-01	1.27e-01	0.00000
L3.Vibrio.cholerae.pathogenic.cycle	-3.18e-07	1.15e-06	-0.277	0.785	-2.72e-06	2.08e-06	0.00383

Table 3037: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Viral.myocarditis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.32e-03	2.48e-02	0.214	0.832	-4.66e-02	5.73e-02	0.0000
L3.Viral.myocarditis	-1.89e-05	1.93e-05	-0.979	0.340	-5.94e-05	2.15e-05	0.0458

Table 3038: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Vitamin.B6.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.66e-02	5.74e-02	0.637	0.531	-8.36e-02	1.57e-01	0.0000
L3.Vitamin.B6.metabolism	-2.79e-07	3.96e-07	-0.705	0.489	-1.11e-06	5.50e-07	0.0242

Table 3039: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Wnt.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 3040: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Xylene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.95e-02	4.03e-02	0.485	0.634	-6.49e-02	1.04e-01	0.0000
L3.Xylene.degradation	-6.40e-07	1.05e-06	-0.611	0.548	-2.83e-06	1.55e-06	0.0183

Table 3041: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.Zeatin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.77e-02	6.07e-02	0.456	0.653	-9.93e-02	1.55e-01	0.0000
L3.Zeatin.biosynthesis	-7.91e-07	1.58e-06	-0.499	0.623	-4.11e-06	2.52e-06	0.0123

Table 3042: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.alpha.Linolenic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.21e-02	3.53e-02	0.344	0.735	-6.17e-02	8.60e-02	0.0000
L3.alpha.Linolenic.acid.metabolism	-9.71e-06	2.02e-05	-0.481	0.636	-5.19e-05	3.25e-05	0.0114

Table 3043: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.beta.Alanine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.82e-02	5.54e-02	0.328	0.747	-9.77e-02	1.34e-01	0.00000
L3.beta.Alanine.metabolism	-1.57e-07	4.29e-07	-0.367	0.718	-1.05e-06	7.40e-07	0.00667

Table 3044: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.beta.Lactam.resistance, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.25e-03	4.58e-02	0.0273	0.979	-9.46e-02	9.71e-02	0.00e+00
L3.beta.Lactam.resistance	-6.17e-08	1.90e-06	-0.0324	0.974	-4.04e-06	3.92e-06	5.26e-05

Table 3045: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.mRNA.surveillance.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 3046: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.mTOR.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	4.77e-15	0.0242	1.97e-13	1	-0.0505	0.0505	0
	NA	NA	NA	NA	NA	NA	0

Table 3047: diversity_vs_picrust_L3_yr1: wunifrac.PC.3 vs L3.p53.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.32e-03	2.48e-02	0.214	0.832	-4.66e-02	5.73e-02	0.0000
L3.p53.signaling.pathway	-1.89e-05	1.93e-05	-0.979	0.340	-5.94e-05	2.15e-05	0.0458

Table 3048: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %
Intercept	-2.95e-03	2.43e-02	-0.121	0.905	-5.38e-02
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	4.28e-06	1.75e-05	0.244	0.810	-3.23e-05

Table 3049: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.ABC.transporters, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.80e-02	3.88e-02	-0.464	0.648	-9.92e-02	6.32e-02	0.000
L3.ABC.transporters	8.17e-09	1.48e-08	0.551	0.588	-2.29e-08	3.92e-08	0.015

Table 3050: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Adherens.junction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3051: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Adipocytokine.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.73e-02	4.69e-02	0.583	0.567	-7.08e-02	1.25e-01	0.0000
L3.Adipocytokine.signaling.pathway	-6.00e-07	9.21e-07	-0.652	0.523	-2.53e-06	1.33e-06	0.0208

Table 3052: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.African.trypanosomiasis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.41e-02	2.62e-02	-1.30	0.2098	-8.90e-02	2.09e-02	0.000
L3.African.trypanosomiasis	4.57e-05	2.38e-05	1.92	0.0701	-4.13e-06	9.54e-05	0.156

Table 3053: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Alanine..aspartate.and.glutamate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.93e-03	4.92e-02	0.161	0.874	-9.5e-02	1.11e-01	0.0000
L3.Alanine..aspartate.and.glutamate.metabolism	-1.10e-08	6.15e-08	-0.179	0.860	-1.4e-07	1.18e-07	0.0015

Table 3054: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Aldosterone.regulated.sodium.reabsorption, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3055: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Alzheimer.s.disease, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.76e-02	4.14e-02	0.426	0.675	-6.89e-02	1.04e-01	0.0000
L3.Alzheimer.s.disease	-6.10e-07	1.23e-06	-0.494	0.627	-3.19e-06	1.97e-06	0.0121

Table 3056: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Amino.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.14e-02	4.27e-02	-0.501	0.622	-1.11e-01	6.80e-02	0.0000
L3.Amino.acid.metabolism	1.48e-07	2.57e-07	0.574	0.573	-3.90e-07	6.85e-07	0.0162

Table 3057: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Amino.acid.related.enzymes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.30e-03	4.70e-02	0.0277	0.978	-9.70e-02	9.96e-02	0.00e+00
L3.Amino.acid.related.enzymes	-1.39e-09	4.48e-08	-0.0310	0.976	-9.52e-08	9.24e-08	4.82e-05

Table 3058: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Amino.sugar.and.nucleotide.sugar.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.32e-02	4.79e-02	-0.276	0.785	-1.13e-01	8.70e-02	0.000
L3.Amino.sugar.and.nucleotide.sugar.metabolism	1.35e-08	4.38e-08	0.307	0.762	-7.82e-08	1.05e-07	0.004

Table 3059: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Aminoacyl.tRNA.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.20e-03	4.38e-02	-0.0729	0.943	-9.50e-02	8.86e-02	0.000000
L3.Aminoacyl.tRNA.biosynthesis	4.48e-09	5.39e-08	0.0832	0.935	-1.08e-07	1.17e-07	0.000346

Table 3060: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Aminobenzoate.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.30e-02	4.88e-02	0.267	0.793	-8.91e-02	1.15e-01	0.00000
L3.Aminobenzoate.degradation	-1.88e-07	6.35e-07	-0.296	0.771	-1.52e-06	1.14e-06	0.00435

Table 3061: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Amoebiasis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.55e-02	2.90e-02	-1.57	0.1327	-1.06e-01	1.51e-02	0.000
L3.Amoebiasis	5.86e-06	2.81e-06	2.08	0.0509	-2.55e-08	1.17e-05	0.178

Table 3062: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Amyotrophic.lateral.sclerosis..ALS., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.36e-02	3.33e-02	-1.31	0.206	-1.13e-01	2.61e-02	0.000
L3.Amyotrophic.lateral.sclerosis..ALS.	4.76e-06	2.92e-06	1.63	0.120	-1.36e-06	1.09e-05	0.117

Table 3063: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Antigen.processing.and.presentation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.77e-03	4.60e-02	0.169	0.868	-8.86e-02	1.04e-01	0.0000
L3.Antigen.processing.and.presentation	-2.96e-07	1.56e-06	-0.190	0.851	-3.56e-06	2.97e-06	0.0018

Table 3064:   diversity_vs_picrust_L3_yr1:   wunifrac.PC.4 vs
L3.Apoptosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.70e-02	2.22e-02	0.767	0.452	-2.94e-02	6.34e-02	0.000
L3.Apoptosis	-2.43e-05	1.45e-05	-1.674	0.111	-5.48e-05	6.10e-06	0.123

Table 3065:   diversity_vs_picrust_L3_yr1:   wunifrac.PC.4 vs
L3.Arachidonic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.98e-02	5.16e-02	0.772	0.449	-6.81e-02	1.48e-01	0.0000
L3.Arachidonic.acid.metabolism	-3.62e-06	4.29e-06	-0.843	0.409	-1.26e-05	5.36e-06	0.0343

Table 3066:   diversity_vs_picrust_L3_yr1:   wunifrac.PC.4 vs
L3.Arginine.and.proline.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.34e-03	4.71e-02	0.113	0.911	-9.33e-02	1.04e-01	0.000000
L3.Arginine.and.proline.metabolism	-6.44e-09	5.08e-08	-0.127	0.900	-1.13e-07	9.99e-08	0.000804

Table   3067:   diversity_vs_picrust_L3_yr1:   wunifrac.PC.4
vs   L3.Arrhythmogenic.right.ventricular.cardiomyopathy..ARVC.,
df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3068:   diversity_vs_picrust_L3_yr1:   wunifrac.PC.4 vs
L3.Ascorbate.and.aldarate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.61e-02	4.05e-02	-1.38	0.182	-1.41e-01	2.87e-02	0.000
L3.Ascorbate.and.aldarate.metabolism	7.68e-07	4.84e-07	1.59	0.129	-2.44e-07	1.78e-06	0.112

Table 3069:   diversity_vs_picrust_L3_yr1:   wunifrac.PC.4 vs
L3.Atrazine.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.52e-02	3.11e-02	-0.489	0.630	-8.04e-02	4.99e-02	0.0000
L3.Atrazine.degradation	1.19e-06	1.80e-06	0.660	0.517	-2.58e-06	4.96e-06	0.0213

Table 3070: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Bacterial.chemotaxis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.06e-03	3.55e-02	-0.227	0.823	-8.24e-02	6.63e-02	0.00000
L3.Bacterial.chemotaxis	2.80e-08	9.96e-08	0.282	0.781	-1.80e-07	2.36e-07	0.00395

Table 3071: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Bacterial.invasion.of.epithelial.cells, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.1e-02	0.025221	-1.23	0.234	-8.38e-02	0.02182	0.000
L3.Bacterial.invasion.of.epithelial.cells	8.6e-05	0.000045	1.91	0.071	-8.13e-06	0.00018	0.155

Table 3072: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Bacterial.motility.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.45e-03	3.39e-02	-0.102	0.920	-7.43e-02	6.74e-02	0.000000
L3.Bacterial.motility.proteins	7.08e-09	5.43e-08	0.130	0.898	-1.07e-07	1.21e-07	0.000848

Table 3073: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Bacterial.secretion.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.87e-03	4.78e-02	0.186	0.855	-9.11e-02	1.09e-01	0.00000
L3.Bacterial.secretion.system	-2.54e-08	1.23e-07	-0.207	0.838	-2.82e-07	2.31e-07	0.00214

Table 3074: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Bacterial.toxins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.12e-02	4.80e-02	-0.233	0.818	-1.12e-01	8.93e-02	0.00000
L3.Bacterial.toxins	1.45e-07	5.58e-07	0.260	0.798	-1.02e-06	1.31e-06	0.00336

Table 3075: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Basal.transcription.factors, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.007780	2.31e-02	0.336	0.740	-0.040615	5.62e-02	0.0000
L3.Basal.transcription.factors	-0.000028	3.63e-05	-0.769	0.451	-0.000104	4.81e-05	0.0287

Table 3076: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Base.excision.repair, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.37e-03	4.56e-02	-0.184	0.856	-1.04e-01	8.70e-02	0.00000
L3.Base.excision.repair	3.10e-08	1.49e-07	0.207	0.838	-2.82e-07	3.44e-07	0.00214

Table 3077: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Benzoate.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.18e-02	4.27e-02	0.746	0.465	-5.75e-02	1.21e-01	0.0000
L3.Benzoate.degradation	-2.56e-07	3.00e-07	-0.853	0.404	-8.85e-07	3.72e-07	0.0351

Table 3078: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Betalain.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.01253	0.02108	-0.595	0.559	-0.05664	0.03158	0.000
L3.Betalain.biosynthesis	0.00194	0.00115	1.677	0.110	-0.00048	0.00435	0.123

Table 3079: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Bile.secretion, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00153	0.0216	-0.0707	0.944	-0.0467	0.0436	0.00000
L3.Bile.secretion	0.03203	0.0989	0.3240	0.750	-0.1749	0.2390	0.00522

Table 3080: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Biosynthesis.and.biodegradation.of.secondary.metabolites, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	3.12e-03	4.70e-02	0.0664	0.948	-9.52e-02	1.01
L3.Biosynthesis.and.biodegradation.of.secondary.metabolites	-7.26e-08	9.76e-07	-0.0743	0.942	-2.12e-06	1.97

Table 3081: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Biosynthesis.of.12...14..and.16.membered.macrolides, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3082: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Biosynthesis.of.ansamycins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.26e-02	4.26e-02	-0.296	0.771	-1.02e-01	7.66e-02	0.00000
L3.Biosynthesis.of.ansamycins	1.62e-07	4.77e-07	0.340	0.738	-8.37e-07	1.16e-06	0.00575

Table 3083: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	-3.16e-02	5.44e-02	-0.580	0.569	-1.45e-01	8.24e
L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides	2.74e-06	4.36e-06	0.628	0.538	-6.39e-06	1.19e

Table 3084: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Biosynthesis.of.type.II.polyketide.backbone, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3085: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Biosynthesis.of.type.II.polyketide.products, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.01279	0.02143	-0.597	0.558	-0.057654	0.03206	0.000
L3.Biosynthesis.of.type.II.polyketide.products	0.00178	0.00113	1.582	0.130	-0.000575	0.00413	0.111

Table 3086: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Biosynthesis.of.unsaturated.fatty.acids, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.46e-02	4.33e-02	-0.337	0.740	-1.05e-01	7.61e-02	0.00000
L3.Biosynthesis.of.unsaturated.fatty.acids	2.13e-07	5.52e-07	0.385	0.704	-9.43e-07	1.37e-06	0.00737

Table 3087: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Biosynthesis.of.vancomycin.group.antibiotics, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.44e-02	5.28e-02	-0.273	0.788	-1.25e-01	9.61e-02	0.0000
L3.Biosynthesis.of.vancomycin.group.antibiotics	3.16e-07	1.06e-06	0.297	0.769	-1.91e-06	2.54e-06	0.0044

Table 3088: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Biotin.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.93e-02	4.54e-02	-0.866	0.397	-1.34e-01	5.57e-02	0.0000
L3.Biotin.metabolism	3.56e-07	3.66e-07	0.972	0.343	-4.10e-07	1.12e-06	0.0451

Table 3089: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Bisphenol.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.86e-03	4.50e-02	-0.153	0.880	-1.01e-01	8.73e-02	0.00000
L3.Bisphenol.degradation	1.13e-07	6.56e-07	0.173	0.865	-1.26e-06	1.49e-06	0.00149

Table 3090: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Bladder.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.028620	2.44e-02	-1.17	0.2546	-7.96e-02	0.022369	0.000
L3.Bladder.cancer	0.000175	9.11e-05	1.93	0.0691	-1.51e-05	0.000366	0.157

Table 3091: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Butanoate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.42e-02	4.52e-02	0.535	0.599	-7.04e-02	1.19e-01	0.0000
L3.Butanoate.metabolism	-5.98e-08	9.90e-08	-0.604	0.553	-2.67e-07	1.47e-07	0.0179

Table 3092: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Butirosin.and.neomycin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.93e-03	4.30e-02	-0.068	0.947	-9.30e-02	8.72e-02	0.000000
L3.Butirosin.and.neomycin.biosynthesis	6.03e-08	7.73e-07	0.078	0.939	-1.56e-06	1.68e-06	0.000304

Table 3093: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.C5.Branched.dibasic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.39e-02	4.23e-02	-0.328	0.747	-1.02e-01	7.47e-02	0.00000
L3.C5.Branched.dibasic.acid.metabolism	6.46e-08	1.71e-07	0.378	0.710	-2.93e-07	4.23e-07	0.00708

Table 3094: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.CAM.ligands, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3095: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Caffeine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.68e-03	0.023184	0.0724	0.943	-0.046846	0.050204	0.00000
L3.Caffeine.metabolism	-1.84e-05	0.000105	-0.1746	0.863	-0.000239	0.000202	0.00152

Table 3096: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Calcium.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00722	0.02183	0.331	0.745	-0.03848	0.05292	0.0000
L3.Calcium.signaling.pathway	-0.00176	0.00178	-0.992	0.334	-0.00548	0.00196	0.0469

Table 3097: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Caprolactam.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.31e-02	3.44e-02	-1.54	0.1397	-1.25e-01	1.90e-02	0.000
L3.Caprolactam.degradation	7.73e-06	4.14e-06	1.87	0.0776	-9.40e-07	1.64e-05	0.148

Table 3098: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Carbohydrate.digestion.and.absorption, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.26e-02	3.50e-02	-1.51	0.1487	-1.26e-01	2.05e-02	0.000
L3.Carbohydrate.digestion.and.absorption	6.28e-06	3.46e-06	1.81	0.0856	-9.69e-07	1.35e-05	0.141

Table 3099: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Carbohydrate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.06e-02	4.49e-02	-0.458	0.652	-1.14e-01	7.33e-02	0.0000
L3.Carbohydrate.metabolism	1.53e-07	2.96e-07	0.518	0.610	-4.66e-07	7.72e-07	0.0133

Table 3100: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Carbon.fixation.in.photosynthetic.organisms, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.04e-03	4.76e-02	-0.0428	0.966	-1.02e-01	9.77e-02	0.0000
L3.Carbon.fixation.in.photosynthetic.organisms	4.81e-09	1.01e-07	0.0477	0.962	-2.06e-07	2.16e-07	0.0001

Table 3101: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Carbon.fixation.pathways.in.prokaryotes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.15e-02	4.99e-02	0.230	0.821	-9.29e-02	1.16e-01	0.00000
L3.Carbon.fixation.pathways.in.prokaryotes	-1.77e-08	6.97e-08	-0.254	0.802	-1.64e-07	1.28e-07	0.00321

Table 3102: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Cardiac.muscle.contraction, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.69e-03	2.13e-02	0.221	0.828	-3.98e-02	4.92e-02	0.0000
L3.Cardiac.muscle.contraction	-5.08e-06	5.51e-06	-0.922	0.368	-1.66e-05	6.45e-06	0.0408

Table 3103: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Carotenoid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.67e-02	2.95e-02	-0.566	0.578	-7.83e-02	4.50e-02	0.0000
L3.Carotenoid.biosynthesis	1.03e-05	1.29e-05	0.798	0.435	-1.67e-05	3.72e-05	0.0309

Table 3104: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Cell.cycle, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3105: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Cell.cycle...Caulobacter, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.42e-03	4.71e-02	-0.0515	0.959	-1.01e-01	9.62e-02	0.000000
L3.Cell.cycle...Caulobacter	7.78e-09	1.35e-07	0.0576	0.955	-2.75e-07	2.91e-07	0.000166

Table 3106: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Cell.cycle...yeast, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3107: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Cell.division, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.55e-02	4.57e-02	-0.559	0.583	-1.21e-01	7.01e-02	0.0000
L3.Cell.division	4.75e-07	7.56e-07	0.628	0.537	-1.11e-06	2.06e-06	0.0194

Table 3108: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Cell.motility.and.secretion, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.43e-02	4.93e-02	-0.694	0.496	-1.37e-01	6.90e-02	0.0000
L3.Cell.motility.and.secretion	3.03e-07	3.95e-07	0.766	0.453	-5.24e-07	1.13e-06	0.0285

Table 3109: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Cellular.antigens, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.35e-02	4.29e-02	1.02	0.323	-4.62e-02	1.33e-01	0.0000
L3.Cellular.antigens	-1.50e-06	1.30e-06	-1.15	0.262	-4.23e-06	1.22e-06	0.0625

Table 3110: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Chagas.disease..American.trypanosomiasis., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.08e-02	2.56e-02	-1.20	0.2440	-8.44e-02	0.022796	0.000
L3.Chagas.disease..American.trypanosomiasis.	4.78e-05	2.59e-05	1.85	0.0802	-6.34e-06	0.000102	0.146

Table 3111: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Chaperones.and.folding.catalysts, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.23e-03	4.96e-02	0.105	0.917	-9.86e-02	1.09e-01	0.000000
L3.Chaperones.and.folding.catalysts	-8.16e-09	7.01e-08	-0.116	0.909	-1.55e-07	1.39e-07	0.000677

Table 3112: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Chloroalkane.and.chloroalkene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.00e-02	4.09e-02	-0.488	0.631	-1.06e-01	6.57e-02	0.0000
L3.Chloroalkane.and.chloroalkene.degradation	1.76e-07	3.11e-07	0.568	0.576	-4.73e-07	8.26e-07	0.0159

Table 3113: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Chlorocyclohexane.and.chlorobenzene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-4.09e-02	3.05e-02	-1.34	0.1947	-1.05e-01	2.28e-02
L3.Chlorocyclohexane.and.chlorobenzene.degradation	5.67e-06	3.23e-06	1.76	0.0953	-1.09e-06	1.24e-05

Table 3114: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Cholinergic.synapse, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3115: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Chromosome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.61e-03	4.67e-02	0.0346	0.973	-9.60e-02	9.93e-02	0.00e+00
L3.Chromosome	-1.65e-09	4.24e-08	-0.0388	0.969	-9.05e-08	8.72e-08	7.52e-05

Table 3116: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Chronic.myeloid.leukemia, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3117: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Circadian.rhythm…plant, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.71e-03	0.023206	0.0738	0.942	-0.046857	0.050285	0.00000
L3.Circadian.rhythm…plant	-1.87e-05	0.000105	-0.1772	0.861	-0.000239	0.000202	0.00157

Table 3118: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Citrate.cycle..TCA.cycle., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.21e-03	5.09e-02	0.102	0.920	-1.01e-01	1.12e-01	0.000000
L3.Citrate.cycle..TCA.cycle.	-1.30e-08	1.15e-07	-0.112	0.912	-2.54e-07	2.28e-07	0.000632

Table 3119: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Clavulanic.acid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.0030	0.0214	0.140	0.890	-0.0418	0.0478	0.0000
L3.Clavulanic.acid.biosynthesis	-0.0315	0.0490	-0.642	0.529	-0.1341	0.0712	0.0202

Table 3120: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Colorectal.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.34e-03	2.12e-02	0.205	0.84	-3.99e-02	0.048620	0.0000
L3.Colorectal.cancer	-1.54e-05	1.65e-05	-0.937	0.36	-4.99e-05	0.000019	0.0421

Table 3121: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Complement.and.coagulation.cascades, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3122: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Cyanoamino.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.51e-02	4.25e-02	-0.592	0.561	-1.14e-01	6.37e-02	0.0000
L3.Cyanoamino.acid.metabolism	1.06e-07	1.56e-07	0.680	0.505	-2.20e-07	4.32e-07	0.0226

Table 3123: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Cysteine.and.methionine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.4e-03	4.70e-02	-0.115	0.910	-1.04e-01	9.30e-02	0.000000
L3.Cysteine.and.methionine.metabolism	8.9e-09	6.93e-08	0.129	0.899	-1.36e-07	1.54e-07	0.000825

Table 3124: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Cytochrome.P450, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3125: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Cytokine.receptors, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3126: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Cytokine.cytokine.receptor.interaction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3127: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Cytoskeleton.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.13e-02	4.20e-02	0.269	0.791	-7.66e-02	9.92e-02	0.00000
L3.Cytoskeleton.proteins	-4.61e-08	1.48e-07	-0.311	0.759	-3.56e-07	2.64e-07	0.00482

Table 3128: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Cytosolic.DNA.sensing.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3129: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.D.Alanine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.91e-02	4.58e-02	0.418	0.681	-7.67e-02	1.15e-01	0.0000
L3.D.Alanine.metabolism	-2.93e-07	6.22e-07	-0.470	0.644	-1.60e-06	1.01e-06	0.0109

Table 3130: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.D.Arginine.and.D.ornithine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.20e-02	2.72e-02	-1.91	0.0711	-1.09e-01	4.93e-03	0.000
L3.D.Arginine.and.D.ornithine.metabolism	1.59e-05	6.19e-06	2.57	0.0187	2.96e-06	2.89e-05	0.248

Table 3131: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.D.Glutamine.and.D.glutamate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.09e-02	4.93e-02	0.222	0.827	-9.23e-02	1.14e-01	0.000
L3.D.Glutamine.and.D.glutamate.metabolism	-1.16e-07	4.74e-07	-0.246	0.809	-1.11e-06	8.75e-07	0.003

Table 3132: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.DNA.repair.and.recombination.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.45e-03	4.73e-02	0.0306	0.976	-9.76e-02	1.01e-01	0.00e+00
L3.DNA.repair.and.recombination.proteins	-8.29e-10	2.43e-08	-0.0341	0.973	-5.17e-08	5.00e-08	5.83e-05

Table 3133: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.DNA.replication, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.01e-03	4.88e-02	0.0821	0.935	-9.82e-02	1.06e-01	0.000000
L3.DNA.replication	-9.86e-09	1.08e-07	-0.0911	0.928	-2.37e-07	2.17e-07	0.000415

Table 3134: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.DNA.replication.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.01e-02	4.82e-02	0.210	0.836	-9.07e-02	1.11e-01	0.00000
L3.DNA.replication.proteins	-1.32e-08	5.63e-08	-0.234	0.818	-1.31e-07	1.05e-07	0.00272

Table 3135: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Dilated.cardiomyopathy..DCM., df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3136: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Dioxin.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.77e-03	3.56e-02	0.0777	0.939	-7.17e-02	7.73e-02	0.000000
L3.Dioxin.degradation	-8.42e-08	8.72e-07	-0.0965	0.924	-1.91e-06	1.74e-06	0.000465

Table 3137: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Drug.metabolism...cytochrome.P450, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.40e-02	4.01e-02	0.348	0.732	-7.00e-02	9.79e-02	0.00000
L3.Drug.metabolism...cytochrome.P450	-1.19e-06	2.92e-06	-0.408	0.688	-7.31e-06	4.93e-06	0.00827

Table 3138: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Drug.metabolism...other.enzymes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.55e-02	4.99e-02	0.311	0.759	-8.90e-02	1.20e-01	0.00000
L3.Drug.metabolism...other.enzymes	-7.43e-08	2.17e-07	-0.343	0.736	-5.28e-07	3.79e-07	0.00584

Table 3139: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.ECM.receptor.interaction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3140: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Electron.transfer.carriers, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.32e-02	3.15e-02	-1.05	0.305	-9.92e-02	3.28e-02	0.0000
L3.Electron.transfer.carriers	3.14e-06	2.29e-06	1.37	0.187	-1.66e-06	7.94e-06	0.0858

Table 3141: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Endocrine.and.other.factor.regulated.calcium.reabsorption, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3142: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Endocytosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00398	0.0219	0.182	0.857	-0.0418	0.0497	0.000
L3.Endocytosis	-0.02788	0.0448	-0.622	0.541	-0.1216	0.0659	0.019

Table 3143: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Energy.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.25e-02	4.91e-02	0.254	0.803	-9.03e-02	1.15e-01	0.00000
L3.Energy.metabolism	-2.21e-08	7.88e-08	-0.281	0.782	-1.87e-07	1.43e-07	0.00392

Table 3144: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-1.13e-02	4.32e-02	-0.261	0.797	-1.02e-01	7.90e-0
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	1.91e-07	6.38e-07	0.300	0.768	-1.14e-06	1.53e-0

Table 3145: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.ErbB.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3146: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Ether.lipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.91e-02	2.61e-02	-1.88	0.075	-1.04e-01	5.46e-03	0.000
L3.Ether.lipid.metabolism	3.95e-05	1.51e-05	2.62	0.017	7.91e-06	7.12e-05	0.255

Table 3147: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Ethylbenzene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.38e-02	4.45e-02	1.21	0.241	-3.93e-02	1.47e-01	0.0000
L3.Ethylbenzene.degradation	-2.18e-06	1.61e-06	-1.36	0.191	-5.54e-06	1.18e-06	0.0843

Table 3148: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Fat.digestion.and.absorption, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3149: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Fatty.acid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.08e-02	4.70e-02	0.230	0.82	-8.76e-02	1.09e-01	0.0000
L3.Fatty.acid.biosynthesis	-3.49e-08	1.36e-07	-0.258	0.80	-3.19e-07	2.49e-07	0.0033

Table 3150: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Fatty.acid.elongation.in.mitochondria, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.67e-03	0.023172	0.072	0.943	-0.046831	0.050168	0.00000
L3.Fatty.acid.elongation.in.mitochondria	-1.83e-05	0.000105	-0.174	0.864	-0.000239	0.000202	0.00151

Table 3151: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Fatty.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.87e-02	4.69e-02	0.398	0.695	-7.96e-02	1.17e-01	0.00000
L3.Fatty.acid.metabolism	-1.45e-07	3.26e-07	-0.445	0.661	-8.28e-07	5.37e-07	0.00981

Table 3152: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Fc.epsilon.RI.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3153: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Fc.gamma.R.mediated.phagocytosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00398	0.0219	0.182	0.857	-0.0418	0.0497	0.000
L3.Fc.gamma.R.mediated.phagocytosis	-0.02788	0.0448	-0.622	0.541	-0.1216	0.0659	0.019

Table 3154: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Flagellar.assembly, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.93e-03	3.17e-02	-0.0925	0.927	-6.93e-02	6.34e-02	0.000000
L3.Flagellar.assembly	1.54e-08	1.25e-07	0.1239	0.903	-2.45e-07	2.76e-07	0.000767

Table 3155: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Flavone.and.flavonol.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.17e-03	3.98e-02	-0.105	0.918	-0.087457	7.91e-02	0.000000
L3.Flavone.and.flavonol.biosynthesis	6.90e-07	5.59e-06	0.124	0.903	-0.000011	1.24e-05	0.000762

Table 3156: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Flavonoid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.56e-03	2.95e-02	-0.324	0.75	-7.13e-02	5.22e-02	0.0000
L3.Flavonoid.biosynthesis	7.93e-06	1.72e-05	0.461	0.65	-2.81e-05	4.39e-05	0.0105

Table 3157: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Fluorobenzoate.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.82e-02	2.75e-02	-1.03	0.317	-8.57e-02	0.029292	0.000
L3.Fluorobenzoate.degradation	5.36e-05	3.58e-05	1.50	0.151	-2.14e-05	0.000129	0.101

Table 3158: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Focal.adhesion, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3159: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Folate.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.57e-02	5.15e-02	-0.305	0.764	-1.23e-01	9.21e-02	0.00000
L3.Folate.biosynthesis	6.60e-08	1.98e-07	0.334	0.742	-3.47e-07	4.79e-07	0.00555

Table 3160: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Fructose.and.mannose.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.96e-02	4.48e-02	-0.436	0.668	-1.13e-01	7.43e-02	0.000
L3.Fructose.and.mannose.metabolism	2.93e-08	5.93e-08	0.493	0.627	-9.48e-08	1.53e-07	0.012

Table 3161: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Function.unknown, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.10e-02	4.54e-02	-0.463	0.649	-1.16e-01	7.41e-02	0.0000
L3.Function.unknown	2.68e-08	5.13e-08	0.522	0.608	-8.05e-08	1.34e-07	0.0134

Table 3162: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.G.protein.coupled.receptors, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00743	0.0234	-0.317	0.754	-0.0564	0.0416	0.0000
L3.G.protein.coupled.receptors	0.00557	0.0080	0.697	0.494	-0.0112	0.0223	0.0237

Table 3163: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.GTP.binding.proteins, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3164: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Galactose.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.57e-02	4.65e-02	-0.337	0.74	-1.13e-01	8.17e-02	0.00000
L3.Galactose.metabolism	2.71e-08	7.18e-08	0.378	0.71	-1.23e-07	1.77e-07	0.00709

Table 3165: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Gastric.acid.secretion, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3166: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.General.function.prediction.only, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.05e-03	4.76e-02	-0.127	0.900	-1.06e-01	9.35e-02	0.00000
L3.General.function.prediction.only	2.59e-09	1.82e-08	0.142	0.889	-3.55e-08	4.07e-08	0.00101

Table 3167: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Geraniol.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.70e-02	5.22e-02	-0.517	0.611	-1.36e-01	8.23e-02	0.0000
L3.Geraniol.degradation	1.35e-06	2.39e-06	0.565	0.579	-3.66e-06	6.36e-06	0.0157

Table 3168: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Germination, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.28e-02	0.032769	-0.389	0.701	-8.13e-02	5.58e-02	0.0000
L3.Germination	5.07e-07	0.000001	0.507	0.618	-1.59e-06	2.60e-06	0.0127

Table 3169: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Glioma, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3170: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Glutamatergic.synapse, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.19e-02	4.71e-02	0.464	0.648	-7.68e-02	1.20e-01	0.0000
L3.Glutamatergic.synapse	-3.01e-07	5.81e-07	-0.518	0.610	-1.52e-06	9.15e-07	0.0132

Table 3171: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Glutathione.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.89e-02	5.64e-02	0.512	0.615	-8.91e-02	1.47e-01	0.000
L3.Glutathione.metabolism	-2.49e-07	4.52e-07	-0.551	0.588	-1.19e-06	6.96e-07	0.015

Table 3172: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Glycan.bindng.proteins, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3173: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Glycan.biosynthesis.and.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.14e-02	4.35e-02	-0.263	0.796	-1.03e-01	7.97e-02	0.00000
L3.Glycan.biosynthesis.and.metabolism	7.19e-07	2.40e-06	0.300	0.767	-4.30e-06	5.74e-06	0.00448

Table 3174: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Glycerolipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.57e-02	4.08e-02	-0.386	0.704	-1.01e-01	6.96e-02	0.00
L3.Glycerolipid.metabolism	6.48e-08	1.44e-07	0.450	0.658	-2.37e-07	3.66e-07	0.01

Table 3175: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Glycerophospholipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.84e-03	4.36e-02	-0.111	0.913	-9.61e-02	8.65e-02	0.000000
L3.Glycerophospholipid.metabolism	1.40e-08	1.10e-07	0.127	0.901	-2.17e-07	2.45e-07	0.000802

Table 3176: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Glycine..serine.and.threonine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.03e-03	4.93e-02	-0.0614	0.952	-1.06e-01	1.00e-01	0.000000
L3.Glycine..serine.and.threonine.metabolism	5.58e-09	8.22e-08	0.0679	0.947	-1.66e-07	1.78e-07	0.000231

Table 3177: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Glycolysis...Gluconeogenesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.25e-03	4.61e-02	0.0272	0.979	-9.52e-02	9.77e-02	0.00e+00
L3.Glycolysis...Gluconeogenesis	-1.76e-09	5.74e-08	-0.0306	0.976	-1.22e-07	1.18e-07	4.68e-05

Table 3178: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Glycosaminoglycan.biosynthesis. . . chondroitin.sulfate, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	0.00154	0.02162	0.0711	0.944	-0.04371	0.04679
L3.Glycosaminoglycan.biosynthesis. . . chondroitin.sulfate	-0.00115	0.00367	-0.3145	0.757	-0.00883	0.00652

Table 3179: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Glycosaminoglycan.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.44e-02	4.12e-02	0.351	0.730	-7.18e-02	1.01e-01	0.00000
L3.Glycosaminoglycan.degradation	-2.19e-07	5.38e-07	-0.408	0.688	-1.34e-06	9.06e-07	0.00824

Table 3180: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Glycosphingolipid.biosynthesis. . . ganglio.series, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.51e-02	3.75e-02	0.402	0.692	-6.34e-02	9.36e-02	0.00
L3.Glycosphingolipid.biosynthesis. . . ganglio.series	-3.36e-07	6.94e-07	-0.485	0.633	-1.79e-06	1.12e-06	0.01

Table 3181: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Glycosphingolipid.biosynthesis. . . globo.series, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-8.61e-03	4.69e-02	-0.184	0.856	-1.07e-01	8.95e-02	0.000
L3.Glycosphingolipid.biosynthesis. . . globo.series	9.38e-08	4.56e-07	0.206	0.839	-8.61e-07	1.05e-06	0.002

Table 3182: diversity_vs_picrust_L3_yr1: wunifrac.PC.4
vs L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series,
df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5
Intercept	-9.83e-03	2.16e-02	-0.454	0.655	-5.51e-02	0.03
L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series	4.87e-05	3.77e-05	1.292	0.212	-3.02e-05	0.00

Table 3183: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Glycosylphosphatidylinositol.GPI..anchor.biosynthesis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3184: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Glycosyltransferases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.02e-02	5.25e-02	-0.386	0.704	-1.3e-01	8.96e-02	0.00000
L3.Glycosyltransferases	9.32e-08	2.21e-07	0.421	0.679	-3.7e-07	5.56e-07	0.00878

Table 3185: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Glyoxylate.and.dicarboxylate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.82e-03	4.67e-02	-0.210	0.836	-1.08e-01	8.79e-02	0.00000
L3.Glyoxylate.and.dicarboxylate.metabolism	2.76e-08	1.17e-07	0.236	0.816	-2.17e-07	2.72e-07	0.00277

Table 3186: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.GnRH.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00398	0.0219	0.182	0.857	-0.0418	0.0497	0.000
L3.GnRH.signaling.pathway	-0.02788	0.0448	-0.622	0.541	-0.1216	0.0659	0.019

Table 3187: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Hedgehog.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3188: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Hematopoietic.cell.lineage, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3189: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Hepatitis.C, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3190: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Histidine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.55e-03	4.80e-02	0.0739	0.942	-9.70e-02	1.04e-01	0.000000
L3.Histidine.metabolism	-8.41e-09	1.02e-07	-0.0823	0.935	-2.22e-07	2.06e-07	0.000338

Table 3191: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Homologous.recombination, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.62e-03	4.78e-02	0.138	0.891	-9.35e-02	1.07e-01	0.00000
L3.Homologous.recombination	-1.15e-08	7.45e-08	-0.154	0.879	-1.67e-07	1.44e-07	0.00119

Table 3192: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Huntington.s.disease, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.98e-03	4.36e-02	-0.0454	0.964	-9.33e-02	8.93e-02	0.000000
L3.Huntington.s.disease	1.11e-07	2.15e-06	0.0519	0.959	-4.38e-06	4.61e-06	0.000135

Table 3193: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Hypertrophic.cardiomyopathy..HCM., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00169	0.0216	0.0783	0.938	-0.0434	0.0468	0.00000
L3.Hypertrophic.cardiomyopathy..HCM.	-0.00506	0.0141	-0.3587	0.724	-0.0346	0.0245	0.00639

Table 3194: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Indole.alkaloid.biosynthesis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3195: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Influenza.A, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.34e-03	2.12e-02	0.205	0.84	-3.99e-02	0.048620	0.0000
L3.Influenza.A	-1.54e-05	1.65e-05	-0.937	0.36	-4.99e-05	0.000019	0.0421

Table 3196: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Inorganic.ion.transport.and.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.56e-02	4.64e-02	-0.766	0.453	-1.33e-01	6.16e-02	0.0000
L3.Inorganic.ion.transport.and.metabolism	2.86e-07	3.34e-07	0.855	0.403	-4.13e-07	9.84e-07	0.0353

Table 3197: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Inositol.phosphate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.39e-03	4.86e-02	0.0492	0.961	-9.93e-02	1.04e-01	0.000000
L3.Inositol.phosphate.metabolism	-3.84e-08	7.02e-07	-0.0546	0.957	-1.51e-06	1.43e-06	0.000149

Table 3198: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Insulin.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.31e-03	4.26e-02	0.101	0.920	-8.47e-02	9.34e-02	0.000000
L3.Insulin.signaling.pathway	-7.92e-08	6.78e-07	-0.117	0.908	-1.50e-06	1.34e-06	0.000681

Table 3199: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Ion.channels, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.51e-02	4.77e-02	-1.37	0.188	-1.65e-01	3.46e-02	0.000
L3.Ion.channels	7.15e-06	4.75e-06	1.50	0.149	-2.80e-06	1.71e-05	0.102

Table 3200: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Isoflavonoid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00646	0.0215	0.30	0.767	-0.0385	0.0514	0.00
L3.Isoflavonoid.biosynthesis	-0.04519	0.0440	-1.03	0.318	-0.1374	0.0470	0.05

Table 3201: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Isoquinoline.alkaloid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.51e-02	5.49e-02	0.274	0.787	-9.99e-02	1.30e-01	0.00000
L3.Isoquinoline.alkaloid.biosynthesis	-4.01e-07	1.35e-06	-0.297	0.770	-3.23e-06	2.42e-06	0.00439

Table 3202: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Leishmaniasis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3203: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Leukocyte.transendothelial.migration, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3204: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Limonene.and.pinene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.47e-02	4.69e-02	0.314	0.757	-8.34e-02	1.13e-01	0.00000
L3.Limonene.and.pinene.degradation	-3.24e-07	9.23e-07	-0.351	0.729	-2.26e-06	1.61e-06	0.00612

Table 3205: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Linoleic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.49e-02	4.47e-02	-0.333	0.743	-1.08e-01	7.87e-02	0.00000
L3.Linoleic.acid.metabolism	2.87e-07	7.63e-07	0.377	0.710	-1.31e-06	1.88e-06	0.00706

Table 3206: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Lipid.biosynthesis.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.98e-03	4.86e-02	0.205	0.839	-9.17e-02	1.12e-01	0.00000
L3.Lipid.biosynthesis.proteins	-2.68e-08	1.18e-07	-0.228	0.822	-2.73e-07	2.19e-07	0.00259

Table 3207: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Lipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.77e-03	4.17e-02	-0.186	0.854	-9.51e-02	7.95e-02	0.00000
L3.Lipid.metabolism	9.09e-08	4.21e-07	0.216	0.831	-7.90e-07	9.72e-07	0.00233

Table 3208: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Lipoic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.76e-03	4.50e-02	-0.128	0.899	-9.98e-02	8.83e-02	0.00000
L3.Lipoic.acid.metabolism	2.43e-07	1.67e-06	0.145	0.886	-3.26e-06	3.75e-06	0.00105

Table 3209: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Lipopolysaccharide.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.36e-02	4.88e-02	-0.689	0.499	-1.36e-01	6.86e-02	0.0000
L3.Lipopolysaccharide.biosynthesis	2.13e-07	2.80e-07	0.761	0.456	-3.73e-07	7.99e-07	0.0281

Table 3210: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Lipopolysaccharide.biosynthesis.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.89e-02	5.24e-02	-0.552	0.587	-1.39e-01	8.08e-02	0.0000
L3.Lipopolysaccharide.biosynthesis.proteins	1.22e-07	2.03e-07	0.602	0.554	-3.02e-07	5.46e-07	0.0178

Table 3211: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Long.term.depression, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3212: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Long.term.potentiation, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3213: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Lysine.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.53e-03	4.48e-02	-0.0565	0.956	-9.64e-02	9.13e-02	0.000000
L3.Lysine.biosynthesis	4.62e-09	7.21e-08	0.0640	0.950	-1.46e-07	1.56e-07	0.000205

Table 3214: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Lysine.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.62e-03	4.90e-02	0.156	0.878	-9.49e-02	1.10e-01	0.00000
L3.Lysine.degradation	-1.02e-07	5.92e-07	-0.172	0.865	-1.34e-06	1.14e-06	0.00148

Table 3215: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Lysosome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.78e-03	4.51e-02	0.217	0.831	-8.47e-02	1.04e-01	0.00000
L3.Lysosome	-9.63e-08	3.93e-07	-0.245	0.809	-9.19e-07	7.27e-07	0.00299

Table 3216: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.MAPK.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3217: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.MAPK.signaling.pathway...yeast, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.44e-03	5.07e-02	-0.0680	0.946	-1.09e-01	1.03e-01	0.00000
L3.MAPK.signaling.pathway...yeast	1.09e-07	1.46e-06	0.0748	0.941	-2.95e-06	3.16e-06	0.00028

Table 3218: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Measles, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3219: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Meiosis...yeast, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.01e-02	2.31e-02	-0.437	0.667	-5.84e-02	0.038214	0.000
L3.Meiosis...yeast	6.02e-06	6.19e-06	0.971	0.344	-6.95e-06	0.000019	0.045

Table 3220: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Melanogenesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.01253	0.02108	-0.595	0.559	-0.05664	0.03158	0.000
L3.Melanogenesis	0.00194	0.00115	1.677	0.110	-0.00048	0.00435	0.123

Table 3221: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Membrane.and.intracellular.structural.molecules, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.40e-02	5.32e-02	-0.264	0.795	-1.25e-01	9.73e-02	0.0
L3.Membrane.and.intracellular.structural.molecules	3.87e-08	1.35e-07	0.287	0.777	-2.44e-07	3.21e-07	0.0

Table 3222: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Metabolism.of.cofactors.and.vitamins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.40e-02	3.98e-02	-1.11	0.282	-1.27e-01	3.92e-02	0.0000
L3.Metabolism.of.cofactors.and.vitamins	6.26e-07	4.87e-07	1.29	0.214	-3.93e-07	1.64e-06	0.0764

Table 3223: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Metabolism.of.xenobiotics.by.cytochrome.P450, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.45e-02	3.98e-02	0.366	0.718	-6.87e-02	9.77e-02	0.00
L3.Metabolism.of.xenobiotics.by.cytochrome.P450	-1.26e-06	2.92e-06	-0.431	0.671	-7.38e-06	4.86e-06	0.00

Table 3224: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Methane.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.20e-03	4.49e-02	-0.138	0.891	-1.00e-01	8.77e-02	0.00000
L3.Methane.metabolism	7.36e-09	4.70e-08	0.157	0.877	-9.09e-08	1.06e-07	0.00123

Table 3225: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Mineral.absorption, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.99e-02	2.56e-02	-1.95	0.0658	-1.03e-01	3.59e-03	0.000
L3.Mineral.absorption	2.98e-05	1.09e-05	2.73	0.0132	6.99e-06	5.27e-05	0.272

Table 3226: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Mismatch.repair, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.40e-03	4.70e-02	0.0297	0.977	-9.71e-02	9.99e-02	0.00e+00
L3.Mismatch.repair	-2.71e-09	8.18e-08	-0.0332	0.974	-1.74e-07	1.68e-07	5.51e-05

Table 3227: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.N.Glycan.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.96e-02	4.45e-02	-1.57	0.1339	-1.63e-01	2.34e-02	0.000
L3.N.Glycan.biosynthesis	4.37e-06	2.51e-06	1.74	0.0972	-8.74e-07	9.62e-06	0.132

Table 3228: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.NOD.like.receptor.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.23e-02	4.79e-02	0.466	0.646	-7.79e-02	1.23e-01	0.0000
L3.NOD.like.receptor.signaling.pathway	-7.83e-07	1.51e-06	-0.519	0.610	-3.94e-06	2.38e-06	0.0133

Table 3229: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Naphthalene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.65e-02	4.68e-02	0.566	0.578	-7.15e-02	1.25e-01	0.0000
L3.Naphthalene.degradation	-3.30e-07	5.22e-07	-0.632	0.535	-1.42e-06	7.63e-07	0.0196

Table 3230: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Neuroactive.ligand.receptor.interaction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3231: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Neurotrophin.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3232: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Nicotinate.and.nicotinamide.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.64e-03	4.73e-02	-0.0771	0.939	-1.03e-01	9.54e-02	0.000000
L3.Nicotinate.and.nicotinamide.metabolism	1.39e-08	1.61e-07	0.0861	0.932	-3.23e-07	3.51e-07	0.000371

Table 3233: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Nitrogen.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.75e-02	5.04e-02	-0.347	0.732	-1.23e-01	8.80e-02	0.00000
L3.Nitrogen.metabolism	3.62e-08	9.48e-08	0.382	0.707	-1.62e-07	2.35e-07	0.00725

Table 3234: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Nitrotoluene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.67e-02	3.47e-02	-0.482	0.635	-8.94e-02	5.59e-02	0.0000
L3.Nitrotoluene.degradation	2.58e-07	4.26e-07	0.604	0.553	-6.35e-07	1.15e-06	0.0179

Table 3235: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Non.homologous.end.joining, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.96e-02	2.44e-02	-2.44	0.02452	-1.11e-01	-8.54e-03	0.00
L3.Non.homologous.end.joining	1.89e-05	5.65e-06	3.35	0.00333	7.12e-06	3.08e-05	0.36

Table 3236: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Notch.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3237: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Novobiocin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.53e-03	4.73e-02	0.0958	0.925	-9.44e-02	1.04e-01	0.000000
L3.Novobiocin.biosynthesis	-5.26e-08	4.92e-07	-0.1070	0.916	-1.08e-06	9.76e-07	0.000572

Table 3238: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Nucleotide.excision.repair, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.74e-03	4.57e-02	-0.104	0.919	-1.0e-01	9.10e-02	0.00000
L3.Nucleotide.excision.repair	1.95e-08	1.67e-07	0.117	0.908	-3.3e-07	3.68e-07	0.00068

Table 3239: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Nucleotide.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.71e-02	3.60e-02	-1.03	0.316	-1.12e-01	3.82e-02	0.0000
L3.Nucleotide.metabolism	1.34e-06	1.07e-06	1.25	0.227	-9.04e-07	3.58e-06	0.0723

Table 3240: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Olfactory.transduction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3241: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.One.carbon.pool.by.folate, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.15e-02	4.98e-02	0.230	0.820	-9.27e-02	1.16e-01	0.00000
L3.One.carbon.pool.by.folate	-2.92e-08	1.15e-07	-0.254	0.802	-2.69e-07	2.11e-07	0.00322

Table 3242: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Oocyte.meiosis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3243: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Other.glycan.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.77e-03	5.09e-02	0.0543	0.957	-1.04e-01	1.09e-01	0.000000
L3.Other.glycan.degradation	-9.78e-09	1.64e-07	-0.0597	0.953	-3.53e-07	3.33e-07	0.000178

Table 3244: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Other.ion.coupled.transporters, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.04e-03	5.05e-02	-0.179	0.860	-1.15e-01	9.66e-02	0.00000
L3.Other.ion.coupled.transporters	1.02e-08	5.18e-08	0.197	0.846	-9.83e-08	1.19e-07	0.00194

Table 3245: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Other.transporters, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.43e-03	4.75e-02	-0.114	0.91	-1.05e-01	9.40e-02	0.000000
L3.Other.transporters	3.08e-08	2.41e-07	0.128	0.90	-4.75e-07	5.36e-07	0.000814

Table 3246: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Other.types.of.O.glycan.biosynthesis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3247: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Others, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.32e-02	4.69e-02	-0.283	0.781	-1.11e-01	8.49e-02	0.00000
L3.Others	2.16e-08	6.82e-08	0.316	0.755	-1.21e-07	1.64e-07	0.00498

Table 3248: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Oxidative.phosphorylation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.64e-03	4.69e-02	-0.0777	0.939	-1.02e-01	9.44e-02	0.000000
L3.Oxidative.phosphorylation	4.88e-09	5.61e-08	0.0871	0.932	-1.12e-07	1.22e-07	0.000379

Table 3249: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.PPAR.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.85e-02	4.99e-02	0.772	0.449	-6.59e-02	1.43e-01	0.0000
L3.PPAR.signaling.pathway	-5.42e-07	6.39e-07	-0.849	0.406	-1.88e-06	7.94e-07	0.0348

Table 3250: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Pancreatic.cancer, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3251: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Pancreatic.secretion, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3252: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Pantothenate.and.CoA.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.21e-03	4.53e-02	-0.0709	0.944	-9.80e-02	9.16e-02	0.000000
L3.Pantothenate.and.CoA.biosynthesis	7.82e-09	9.77e-08	0.0801	0.937	-1.97e-07	2.12e-07	0.000321

Table 3253: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Parkinson.s.disease, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.61e-03	2.12e-02	0.217	0.830	-3.99e-02	4.91e-02	0.000
L3.Parkinson.s.disease	-3.82e-06	4.13e-06	-0.925	0.367	-1.25e-05	4.82e-06	0.041

Table 3254: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Pathogenic.Escherichia.coli.infection, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3255: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Pathways.in.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.46e-03	4.48e-02	-0.0773	0.939	-9.73e-02	9.03e-02	0.000000
L3.Pathways.in.cancer	1.15e-07	1.31e-06	0.0876	0.931	-2.62e-06	2.85e-06	0.000383

Table 3256: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Penicillin.and.cephalosporin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.28e-02	4.42e-02	-0.743	0.467	-1.25e-01	5.97e-02	0.0000
L3.Penicillin.and.cephalosporin.biosynthesis	1.85e-06	2.20e-06	0.841	0.411	-2.75e-06	6.45e-06	0.0342

Table 3257: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Pentose.and.glucuronate.interconversions, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.02e-03	4.78e-02	-0.126	0.901	-1.06e-01	9.40e-02	0.000000
L3.Pentose.and.glucuronate.interconversions	1.40e-08	9.96e-08	0.140	0.890	-1.94e-07	2.22e-07	0.000984

Table 3258: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Pentose.phosphate.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.98e-03	4.56e-02	-0.219	0.829	-1.05e-01	8.55e-02	0.00000
L3.Pentose.phosphate.pathway	1.68e-08	6.79e-08	0.247	0.808	-1.25e-07	1.59e-07	0.00304

Table 3259: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Peptidases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.94e-03	4.79e-02	-0.0613	0.952	-1.03e-01	9.73e-02	0.000000
L3.Peptidases	2.46e-09	3.60e-08	0.0683	0.946	-7.28e-08	7.77e-08	0.000233

Table 3260: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Peptidoglycan.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.17e-03	4.60e-02	-0.0255	0.980	-9.74e-02	9.51e-02	0.00e+00
L3.Peptidoglycan.biosynthesis	2.32e-09	8.06e-08	0.0287	0.977	-1.66e-07	1.71e-07	4.13e-05

Table 3261: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Peroxisome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.33e-03	5.17e-02	0.180	0.859	-9.89e-02	1.18e-01	0.00000
L3.Peroxisome	-8.09e-08	4.09e-07	-0.198	0.845	-9.38e-07	7.76e-07	0.00195

Table 3262: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Pertussis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.35e-02	4.86e-02	-0.278	0.784	-1.15e-01	8.83e-02	0.00000
L3.Pertussis	7.36e-07	2.39e-06	0.308	0.761	-4.26e-06	5.73e-06	0.00472

Table 3263: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Phagosome, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3264: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Phenylalanine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.11e-02	4.88e-02	0.228	0.822	-9.11e-02	1.13e-01	0.00000
L3.Phenylalanine.metabolism	-9.21e-08	3.65e-07	-0.253	0.803	-8.56e-07	6.71e-07	0.00318

Table 3265: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-1.10e-02	4.49e-02	-0.246	0.808	-1.05e-01	8.29e-02
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis	2.01e-08	7.23e-08	0.279	0.783	-1.31e-07	1.71e-07

Table 3266: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Phenylpropanoid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.21e-02	3.83e-02	-0.837	0.413	-1.12e-01	4.81e-02	0.000
L3.Phenylpropanoid.biosynthesis	2.15e-07	2.16e-07	0.993	0.333	-2.38e-07	6.67e-07	0.047

Table 3267: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Phosphatidylinositol.signaling.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.2e-03	5.07e-02	-0.0237	0.981	-1.07e-01	1.05e-01	0.00e+00
L3.Phosphatidylinositol.signaling.system	2.1e-08	8.05e-07	0.0261	0.979	-1.66e-06	1.70e-06	3.41e-05

Table 3268: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Phosphonate.and.phosphinate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.80e-03	4.60e-02	0.191	0.850	-8.75e-02	1.05e-01	0.00000
L3.Phosphonate.and.phosphinate.metabolism	-2.02e-07	9.39e-07	-0.215	0.832	-2.17e-06	1.76e-06	0.00231

Table 3269: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Phosphotransferase.system..PTS., df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.06e-02	3.24e-02	-0.947	0.356	-9.84e-02	3.71e-02	0.000
L3.Phosphotransferase.system..PTS.	1.23e-07	1.01e-07	1.217	0.238	-8.87e-08	3.35e-07	0.069

Table 3270: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Photosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.26e-02	4.10e-02	-0.307	0.762	-9.85e-02	7.32e-02	0.00000
L3.Photosynthesis	4.68e-08	1.31e-07	0.358	0.724	-2.27e-07	3.20e-07	0.00638

Table 3271: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Photosynthesis. . . antenna.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.007149	0.021865	0.327	0.747	-0.038616	0.052913	0.0000
L3.Photosynthesis. . . antenna.proteins	-0.000102	0.000105	-0.976	0.341	-0.000321	0.000117	0.0455

Table 3272: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Photosynthesis.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.25e-02	4.1e-02	-0.304	0.765	-9.83e-02	7.34e-02	0.00000
L3.Photosynthesis.proteins	4.59e-08	1.3e-07	0.354	0.727	-2.26e-07	3.17e-07	0.00622

Table 3273: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Phototransduction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3274: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Phototransduction...fly, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3275: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Plant.pathogen.interaction, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.25e-03	4.24e-02	0.171	0.866	-8.16e-02	9.61e-02	0.00000
L3.Plant.pathogen.interaction	-7.33e-08	3.72e-07	-0.197	0.846	-8.52e-07	7.06e-07	0.00193

Table 3276: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Polycyclic.aromatic.hydrocarbon.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.47e-03	4.57e-02	0.0977	0.923	-9.13e-02	1.00e-01	0.000
L3.Polycyclic.aromatic.hydrocarbon.degradation	-6.41e-08	5.82e-07	-0.1101	0.913	-1.28e-06	1.15e-06	0.000

Table 3277: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Polyketide.sugar.unit.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.94e-02	5.03e-02	-0.385	0.705	-1.25e-01	8.59e-02	0.00000
L3.Polyketide.sugar.unit.biosynthesis	1.33e-07	3.14e-07	0.424	0.677	-5.24e-07	7.90e-07	0.00889

Table 3278: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Pores.ion.channels, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.80e-03	5.64e-02	0.0851	0.933	-1.13e-01	1.23e-01	0.000000
L3.Pores.ion.channels	-2.03e-08	2.21e-07	-0.0918	0.928	-4.83e-07	4.43e-07	0.000421

Table 3279: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Porphyrin.and.chlorophyll.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.28e-02	4.42e-02	-0.289	0.776	-1.05e-01	7.97e-02	0.00000
L3.Porphyrin.and.chlorophyll.metabolism	1.92e-08	5.85e-08	0.329	0.746	-1.03e-07	1.42e-07	0.00537

Table 3280: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Prenyltransferases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.41e-04	5.00e-02	-0.00682	0.995	-1.05e-01	1.04e-01	0.00e+00
L3.Prenyltransferases	1.76e-09	2.35e-07	0.00752	0.994	-4.89e-07	4.93e-07	2.83e-06

Table 3281: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Primary.bile.acid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.97e-02	4.15e-02	-0.475	0.641	-0.106656	6.72e-02	0.0000
L3.Primary.bile.acid.biosynthesis	7.12e-07	1.30e-06	0.550	0.589	-0.000002	3.42e-06	0.0149

Table 3282: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Primary.immunodeficiency, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.88e-02	4.54e-02	-0.635	0.533	-1.24e-01	6.61e-02	0.0000
L3.Primary.immunodeficiency	9.32e-07	1.30e-06	0.715	0.483	-1.80e-06	3.66e-06	0.0249

Table 3283: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Prion.diseases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.6e-02	3.19e-02	-0.814	0.426	-9.27e-02	4.08e-02	0.0000
L3.Prion.diseases	6.7e-06	6.31e-06	1.062	0.301	-6.50e-06	1.99e-05	0.0534

Table 3284: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Progesterone.mediated.oocyte.maturation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.77e-03	4.60e-02	0.169	0.868	-8.86e-02	1.04e-01	0.0000
L3.Progesterone.mediated.oocyte.maturation	-2.96e-07	1.56e-06	-0.190	0.851	-3.56e-06	2.97e-06	0.0018

Table 3285: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Propanoate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.21e-03	4.68e-02	0.0687	0.946	-9.48e-02	1.01e-01	0.000000
L3.Propanoate.metabolism	-1.04e-08	1.36e-07	-0.0769	0.939	-2.94e-07	2.73e-07	0.000296

Table 3286: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Prostate.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-5.16e-03	4.68e-02	-0.110	0.913	-1.03e-01	9.27e-02	0.000000
L3.Prostate.cancer	1.83e-07	1.48e-06	0.124	0.903	-2.92e-06	3.28e-06	0.000763

Table 3287: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Proteasome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.86e-03	4.54e-02	0.0409	0.968	-9.33e-02	9.70e-02	0.000000
L3.Proteasome	-6.86e-08	1.49e-06	-0.0462	0.964	-3.18e-06	3.04e-06	0.000107

Table 3288: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Protein.digestion.and.absorption, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.85e-02	3.94e-02	0.471	0.643	-6.38e-02	1.01e-01	0.0000
L3.Protein.digestion.and.absorption	-1.06e-06	1.91e-06	-0.557	0.584	-5.05e-06	2.93e-06	0.0153

Table 3289: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Protein.export, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.36e-03	4.77e-02	-0.0913	0.928	-1.04e-01	9.56e-02	0.000000
L3.Protein.export	1.16e-08	1.14e-07	0.1018	0.920	-2.26e-07	2.50e-07	0.000518

Table 3290: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Protein.folding.and.associated.processing, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.98e-02	4.80e-02	-0.413	0.684	-1.20e-01	8.07e-02	0.0000
L3.Protein.folding.and.associated.processing	4.87e-08	1.06e-07	0.459	0.651	-1.73e-07	2.71e-07	0.0104

Table 3291: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Protein.kinases, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.03e-03	4.16e-02	-0.169	0.868	-9.41e-02	8.00e-02	0.00000
L3.Protein.kinases	3.58e-08	1.83e-07	0.196	0.847	-3.46e-07	4.18e-07	0.00192

Table 3292: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Protein.processing.in.endoplasmic.reticulum, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.02e-02	5.31e-02	0.569	0.576	-8.10e-02	1.41e-01	0.0000
L3.Protein.processing.in.endoplasmic.reticulum	-7.19e-07	1.16e-06	-0.619	0.543	-3.15e-06	1.71e-06	0.0188

Table 3293: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Proximal.tubule.bicarbonate.reclamation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.90e-02	3.61e-02	1.36	0.191	-2.66e-02	1.25e-01	0.000
L3.Proximal.tubule.bicarbonate.reclamation	-3.52e-06	2.17e-06	-1.62	0.121	-8.05e-06	1.02e-06	0.116

Table 3294: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Purine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.73e-03	4.79e-02	-0.203	0.841	-1.10e-01	9.06e-02	0.00000
L3.Purine.metabolism	7.03e-09	3.11e-08	0.226	0.824	-5.81e-08	7.21e-08	0.00255

Table 3295: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Pyrimidine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.87e-03	4.82e-02	0.0804	0.937	-9.69e-02	1.05e-01	0e+00
L3.Pyrimidine.metabolism	-3.38e-09	3.78e-08	-0.0894	0.930	-8.25e-08	7.57e-08	4e-04

Table 3296: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Pyruvate.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.92e-03	4.67e-02	0.191	0.851	-8.88e-02	1.07e-01	0.00000
L3.Pyruvate.metabolism	-1.33e-08	6.20e-08	-0.214	0.833	-1.43e-07	1.16e-07	0.00229

Table 3297: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.RIG.I.like.receptor.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.20e-03	2.74e-02	0.117	0.908	-5.41e-02	0.060552	0.00000
L3.RIG.I.like.receptor.signaling.pathway	-2.39e-06	1.31e-05	-0.183	0.857	-2.98e-05	0.000025	0.00167

Table 3298: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.RNA.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.13e-03	4.94e-02	-0.0228	0.982	-1.05e-01	1.02e-01	0.00e+00
L3.RNA.degradation	3.71e-09	1.47e-07	0.0252	0.980	-3.04e-07	3.12e-07	3.18e-05

Table 3299: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.RNA.polymerase, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.75e-03	4.72e-02	0.0370	0.971	-9.71e-02	1.01e-01	0.00e+00
L3.RNA.polymerase	-1.85e-08	4.47e-07	-0.0414	0.967	-9.54e-07	9.17e-07	8.56e-05

Table 3300: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.RNA.transport, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.25e-03	4.11e-02	-0.103	0.919	-9.03e-02	8.18e-02	0.000000
L3.RNA.transport	4.87e-08	4.04e-07	0.120	0.905	-7.98e-07	8.95e-07	0.000724

Table 3301: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Regulation.of.actin.cytoskeleton, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3302: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Renal.cell.carcinoma, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.055074	3.21e-02	-1.71	0.1027	-1.22e-01	1.22e-02	0.000
L3.Renal.cell.carcinoma	0.000015	7.07e-06	2.12	0.0469	2.26e-07	2.98e-05	0.184

Table 3303: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Renin.angiotensin.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00336	0.02190	0.153	0.880	-0.0425	0.0492	0.0000
L3.Renin.angiotensin.system	-0.00470	0.00891	-0.528	0.603	-0.0233	0.0139	0.0138

Table 3304: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Replication..recombination.and.repair.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.01e-03	4.38e-02	0.183	0.857	-8.37e-02	9.97e-02	0.00
L3.Replication..recombination.and.repair.proteins	-1.67e-08	8.01e-08	-0.209	0.837	-1.84e-07	1.51e-07	0.00

Table 3305: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Restriction.enzyme, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.86e-02	4.91e-02	0.786	0.441	-6.42e-02	1.41e-01	0.0000
L3.Restriction.enzyme	-3.34e-07	3.85e-07	-0.867	0.397	-1.14e-06	4.72e-07	0.0362

Table 3306: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Retinol.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.96e-03	4.15e-02	0.216	0.831	-7.78e-02	9.57e-02	0.00000
L3.Retinol.metabolism	-6.06e-07	2.41e-06	-0.251	0.805	-5.66e-06	4.45e-06	0.00314

Table 3307: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Rheumatoid.arthritis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3308: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Riboflavin.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.01e-03	5.06e-02	-0.0201	0.984	-1.07e-01	1.05e-01	0.00e+00
L3.Riboflavin.metabolism	6.83e-09	3.09e-07	0.0221	0.983	-6.41e-07	6.54e-07	2.44e-05

Table 3309: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Ribosome, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.08e-03	4.68e-02	0.0658	0.948	-9.48e-02	1.01e-01	0.000000
L3.Ribosome	-2.15e-09	2.92e-08	-0.0737	0.942	-6.33e-08	5.90e-08	0.000272

Table 3310: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Ribosome.Biogenesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.02e-03	4.53e-02	-0.0445	0.965	-9.69e-02	9.29e-02	0.000000
L3.Ribosome.Biogenesis	2.35e-09	4.68e-08	0.0502	0.960	-9.56e-08	1.00e-07	0.000126

Table 3311: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Ribosome.biogenesis.in.eukaryotes, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.00e-04	4.53e-02	0.00661	0.995	-9.45e-02	9.51e-02	0.0e+00
L3.Ribosome.biogenesis.in.eukaryotes	-1.03e-08	1.38e-06	-0.00748	0.994	-2.90e-06	2.88e-06	2.8e-06

Table 3312: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Salivary.secretion, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3313: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Secondary.bile.acid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.52e-02	4.21e-02	-0.362	0.721	-1.03e-01	7.28e-02	0.00000
L3.Secondary.bile.acid.biosynthesis	5.65e-07	1.35e-06	0.418	0.681	-2.26e-06	3.39e-06	0.00865

Table 3314: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Secretion.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.73e-03	4.21e-02	-0.112	0.912	-9.29e-02	8.34e-02	0.000000
L3.Secretion.system	7.22e-09	5.56e-08	0.130	0.898	-1.09e-07	1.24e-07	0.000843

Table 3315: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Selenocompound.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.47e-02	4.63e-02	-0.317	0.755	-1.12e-01	8.23e-02	0.0000
L3.Selenocompound.metabolism	6.27e-08	1.76e-07	0.356	0.726	-3.06e-07	4.31e-07	0.0063

Table 3316: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Sesquiterpenoid.biosynthesis, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3317: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Shigellosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.00521	0.02261	-0.230	0.820	-0.05254	0.0421	0.000
L3.Shigellosis	0.00273	0.00452	0.605	0.552	-0.00672	0.0122	0.018

Table 3318: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Signal.transduction.mechanisms, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.48e-03	4.28e-02	-0.105	0.918	-9.40e-02	8.51e-02	0.000000
L3.Signal.transduction.mechanisms	1.52e-08	1.26e-07	0.120	0.905	-2.49e-07	2.80e-07	0.000724

Table 3319: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Small.cell.lung.cancer, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.34e-03	2.12e-02	0.205	0.84	-3.99e-02	0.048620	0.0000
L3.Small.cell.lung.cancer	-1.54e-05	1.65e-05	-0.937	0.36	-4.99e-05	0.000019	0.0421

Table 3320: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Sphingolipid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.18e-03	4.86e-02	-0.189	0.852	-1.11e-01	9.25e-02	0.0000
L3.Sphingolipid.metabolism	4.53e-08	2.16e-07	0.210	0.836	-4.07e-07	4.97e-07	0.0022

Table 3321: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Spliceosome, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3322: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Sporulation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.01e-03	3.50e-02	-0.086	0.932	-7.63e-02	7.03e-02	0.000000
L3.Sporulation	6.21e-09	5.76e-08	0.108	0.915	-1.14e-07	1.27e-07	0.000581

Table 3323: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Staphylococcus.aureus.infection, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.87e-02	3.07e-02	0.611	0.548	-4.54e-02	8.29e-02	0.0000
L3.Staphylococcus.aureus.infection	-5.52e-06	6.65e-06	-0.830	0.417	-1.94e-05	8.40e-06	0.0333

Table 3324: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Starch.and.sucrose.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.93e-02	4.34e-02	-0.446	0.661	-1.10e-01	7.15e-02	0.0000
L3.Starch.and.sucrose.metabolism	2.56e-08	5.03e-08	0.509	0.616	-7.97e-08	1.31e-07	0.0128

Table 3325: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Steroid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.07e-03	2.33e-02	0.0888	0.930	-4.67e-02	5.08e-02	0.00000
L3.Steroid.biosynthesis	-7.32e-06	3.49e-05	-0.2095	0.836	-8.04e-05	6.58e-05	0.00219

Table 3326: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Steroid.hormone.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.31e-03	3.37e-02	-0.0686	0.946	-7.29e-02	6.83e-02	0.000000
L3.Steroid.hormone.biosynthesis	1.47e-07	1.67e-06	0.0879	0.931	-3.35e-06	3.64e-06	0.000386

Table 3327: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-1.16e-02	2.53e-02	-0.458	0.652	-6.47e-02	0.041446
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	3.95e-05	4.95e-05	0.799	0.434	-6.41e-05	0.000143

Table 3328: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Streptomycin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.52e-02	4.94e-02	-0.308	0.762	-1.19e-01	8.82e-02	0.00000
L3.Streptomycin.biosynthesis	6.84e-08	2.01e-07	0.340	0.738	-3.52e-07	4.89e-07	0.00575

Table 3329: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Styrene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.81e-02	3.32e-02	-0.544	0.593	-8.76e-02	5.15e-02	0.0000
L3.Styrene.degradation	1.48e-06	2.12e-06	0.699	0.493	-2.95e-06	5.91e-06	0.0238

Table 3330: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Sulfur.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-6.57e-03	4.90e-02	-0.134	0.895	-1.09e-01	9.60e-02	0.0000
L3.Sulfur.metabolism	3.49e-08	2.35e-07	0.149	0.883	-4.57e-07	5.27e-07	0.0011

Table 3331: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Sulfur.relay.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-4.20e-03	4.24e-02	-0.099	0.922	-9.30e-02	8.46e-02	0.000000
L3.Sulfur.relay.system	2.57e-08	2.25e-07	0.114	0.910	-4.45e-07	4.96e-07	0.000651

Table 3332: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Synthesis.and.degradation.of.ketone.bodies, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.01e-02	3.55e-02	1.69	0.1069	-1.42e-02	1.34e-01	0.000
L3.Synthesis.and.degradation.of.ketone.bodies	-3.93e-06	1.96e-06	-2.01	0.0588	-8.03e-06	1.62e-07	0.168

Table 3333: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Systemic.lupus.erythematosus, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.84e-03	0.024161	0.076	0.940	-0.048733	0.052405	0.00000
L3.Systemic.lupus.erythematosus	-1.63e-05	0.000105	-0.156	0.878	-0.000235	0.000202	0.00122

Table 3334: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.TGF.beta.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3335: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Taurine.and.hypotaurine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.10e-02	5.26e-02	0.400	0.694	-8.91e-02	1.31e-01	0.00000
L3.Taurine.and.hypotaurine.metabolism	-3.06e-07	7.02e-07	-0.436	0.668	-1.77e-06	1.16e-06	0.00942

Table 3336: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Terpenoid.backbone.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.44e-03	4.84e-02	0.195	0.847	-9.18e-02	1.11e-01	0.00000
L3.Terpenoid.backbone.biosynthesis	-2.67e-08	1.23e-07	-0.217	0.831	-2.85e-07	2.31e-07	0.00234

Table 3337: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Tetracycline.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.5e-03	4.22e-02	0.202	0.842	-7.97e-02	9.67e-02	0.0000
L3.Tetracycline.biosynthesis	-9.4e-08	4.04e-07	-0.233	0.818	-9.39e-07	7.51e-07	0.0027

Table 3338: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Thiamine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.79e-04	4.66e-02	0.0146	0.989	-9.69e-02	9.83e-02	0.00e+00
L3.Thiamine.metabolism	-2.12e-09	1.30e-07	-0.0163	0.987	-2.74e-07	2.69e-07	1.33e-05

Table 3339: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Tight.junction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3340: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Toluene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-7.87e-03	3.63e-02	-0.217	0.831	-8.39e-02	6.82e-02	0.00000
L3.Toluene.degradation	1.07e-07	4.04e-07	0.266	0.793	-7.38e-07	9.53e-07	0.00352

Table 3341: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Toxoplasmosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.34e-03	2.12e-02	0.205	0.84	-3.99e-02	0.048620	0.0000
L3.Toxoplasmosis	-1.54e-05	1.65e-05	-0.937	0.36	-4.99e-05	0.000019	0.0421

Table 3342: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Transcription.factors, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.94e-03	4.05e-02	-0.246	0.809	-9.47e-02	7.48e-02	0.00000
L3.Transcription.factors	9.28e-09	3.23e-08	0.287	0.777	-5.83e-08	7.68e-08	0.00412

Table 3343: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Transcription.machinery, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.64e-02	4.87e-02	0.337	0.739	-8.54e-02	1.18e-01	0.00000
L3.Transcription.machinery	-2.41e-08	6.45e-08	-0.374	0.712	-1.59e-07	1.11e-07	0.00695

Table 3344: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Transcription.related.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.27e-02	2.52e-02	-0.901	0.379	-7.56e-02	3.01e-02	0.0000
L3.Transcription.related.proteins	1.09e-05	7.35e-06	1.477	0.156	-4.53e-06	2.62e-05	0.0984

Table 3345: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Translation.factors, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.62e-04	4.80e-02	0.00962	0.992	-1.00e-01	1.01e-01	0.00e+00
L3.Translation.factors	-1.41e-09	1.31e-07	-0.01071	0.992	-2.76e-07	2.73e-07	5.74e-06

Table 3346: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Translation.proteins, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.39e-03	4.67e-02	0.0297	0.977	-9.64e-02	9.92e-02	0.00e+00
L3.Translation.proteins	-2.53e-09	7.59e-08	-0.0333	0.974	-1.61e-07	1.56e-07	5.54e-05

Table 3347: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Transporters, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.53e-02	3.92e-02	-0.391	0.700	-9.74e-02	6.68e-02	0.0000
L3.Transporters	3.48e-09	7.52e-09	0.463	0.649	-1.23e-08	1.92e-08	0.0106

Table 3348: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	1.61e-02	4.89e-02	0.329	0.746	-8.63e-02	1.19e-0
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis	-2.12e-07	5.83e-07	-0.364	0.720	-1.43e-06	1.01e-0(

Table 3349: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Tryptophan.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.59e-02	4.48e-02	-0.354	0.727	-1.10e-01	7.80e-02	0.00000
L3.Tryptophan.metabolism	2.14e-07	5.35e-07	0.401	0.693	-9.05e-07	1.33e-06	0.00796

Table 3350: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Tuberculosis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.5e-02	4.61e-02	0.327	0.747	-8.14e-02	1.11e-01	0.0000
L3.Tuberculosis	-1.6e-07	4.35e-07	-0.367	0.718	-1.07e-06	7.51e-07	0.0067

Table 3351: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.Two.component.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-9.51e-03	4.22e-02	-0.225	0.824	-9.79e-02	7.89e-02	0.00000
L3.Two.component.system	1.01e-08	3.89e-08	0.260	0.798	-7.13e-08	9.15e-08	0.00336

Table 3352: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Type.I.diabetes.mellitus, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.19e-02	4.86e-02	0.245	0.809	-8.98e-02	1.14e-01	0.00000
L3.Type.I.diabetes.mellitus	-3.56e-07	1.31e-06	-0.272	0.788	-3.09e-06	2.38e-06	0.00369

Table 3353: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Type.II.diabetes.mellitus, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-1.58e-02	4.75e-02	-0.332	0.744	-1.15e-01	8.37e-02	0.00000
L3.Type.II.diabetes.mellitus	5.46e-07	1.47e-06	0.370	0.715	-2.54e-06	3.63e-06	0.00681

Table 3354: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Tyrosine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.88e-03	4.69e-02	0.125	0.901	-9.22e-02	1.04e-01	0.000000
L3.Tyrosine.metabolism	-2.92e-08	2.08e-07	-0.141	0.890	-4.64e-07	4.06e-07	0.000987

Table 3355: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %
Intercept	-4.21e-02	5.48e-02	-0.768	0.452	-1.57e-01	7.27e-02
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis	4.15e-07	5.00e-07	0.829	0.417	-6.32e-07	1.46e-06

Table 3356: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Ubiquitin.system, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.88e-02	3.79e-02	0.760	0.457	-0.050578	1.08e-01	0.0000
L3.Ubiquitin.system	-5.13e-06	5.66e-06	-0.906	0.376	-0.000017	6.71e-06	0.0394

Table 3357: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.VEGF.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3358: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Valine..leucine.and.isoleucine.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.33e-05	4.35e-02	0.000536	1	-9.09e-02	9.10e-02	0.00e+
L3.Valine..leucine.and.isoleucine.biosynthesis	-4.76e-11	7.75e-08	-0.000614	1	-1.62e-07	1.62e-07	1.88e-(

Table 3359: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Valine..leucine.and.isoleucine.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.01e-02	5.46e-02	0.369	0.717	-9.42e-02	1.35e-01	0.00000
L3.Valine..leucine.and.isoleucine.degradation	-1.53e-07	3.82e-07	-0.399	0.694	-9.52e-07	6.47e-07	0.00791

Table 3360: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Various.types.of.N.glycan.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.001076	0.023505	0.0458	0.964	-0.04812	0.05027	0.000000
L3.Various.types.of.N.glycan.biosynthesis	-0.000084	0.000807	-0.1040	0.918	-0.00177	0.00161	0.000541

Table 3361: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Vascular.smooth.muscle.contraction, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3362: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Vasopressin.regulated.water.reabsorption, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.00152	0.0223	0.068	0.946	-0.0452	0.0483	0.00000
L3.Vasopressin.regulated.water.reabsorption	-0.00638	0.0309	-0.207	0.838	-0.0710	0.0582	0.00213

Table 3363: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Vibrio.cholerae.infection, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.0101	0.0207	-0.489	0.631	-0.05340	0.0332	0.000
L3.Vibrio.cholerae.infection	0.0212	0.0129	1.645	0.116	-0.00578	0.0482	0.119

Table 3364: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Vibrio.cholerae.pathogenic.cycle, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.65e-02	4.61e-02	0.358	0.724	-8.00e-02	1.13e-01	0.00000
L3.Vibrio.cholerae.pathogenic.cycle	-3.91e-07	9.72e-07	-0.402	0.692	-2.43e-06	1.64e-06	0.00802

Table 3365: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Viral.myocarditis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.34e-03	2.12e-02	0.205	0.84	-3.99e-02	0.048620	0.0000
L3.Viral.myocarditis	-1.54e-05	1.65e-05	-0.937	0.36	-4.99e-05	0.000019	0.0421

Table 3366: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Vitamin.B6.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.50e-02	4.93e-02	0.304	0.764	-8.82e-02	1.18e-01	0.00000
L3.Vitamin.B6.metabolism	-1.14e-07	3.40e-07	-0.336	0.740	-8.27e-07	5.98e-07	0.00562

Table 3367: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Wnt.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3368: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Xylene.degradation, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.95e-03	3.46e-02	0.143	0.888	-6.75e-02	7.74e-02	0.00000
L3.Xylene.degradation	-1.62e-07	8.99e-07	-0.181	0.859	-2.04e-06	1.72e-06	0.00163

Table 3369: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs
L3.Zeatin.biosynthesis, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.40e-03	5.19e-02	0.181	0.858	-9.92e-02	1.18e-01	0.00000
L3.Zeatin.biosynthesis	-2.69e-07	1.35e-06	-0.198	0.845	-3.10e-06	2.57e-06	0.00196

Table 3370: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.alpha.Linolenic.acid.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.54e-02	2.8e-02	-1.26	0.2219	-9.39e-02	2.32e-02	0.000
L3.alpha.Linolenic.acid.metabolism	2.83e-05	1.6e-05	1.77	0.0935	-5.23e-06	6.17e-05	0.135

Table 3371: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.beta.Alanine.metabolism, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-2.03e-02	4.69e-02	-0.433	0.670	-1.19e-01	7.79e-02	0.0000
L3.beta.Alanine.metabolism	1.76e-07	3.64e-07	0.484	0.634	-5.85e-07	9.37e-07	0.0116

Table 3372: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.beta.Lactam.resistance, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-3.69e-02	3.76e-02	-0.979	0.340	-1.16e-01	4.19e-02	0.0000
L3.beta.Lactam.resistance	1.82e-06	1.56e-06	1.165	0.258	-1.45e-06	5.09e-06	0.0636

Table 3373: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.mRNA.surveillance.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3374: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.mTOR.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
(Intercept)	6.67e-14	0.0206	3.24e-12	1	-0.0429	0.0429	0
	NA	NA	NA	NA	NA	NA	0

Table 3375: diversity_vs_picrust_L3_yr1: wunifrac.PC.4 vs L3.p53.signaling.pathway, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.34e-03	2.12e-02	0.205	0.84	-3.99e-02	0.048620	0.0000
L3.p53.signaling.pathway	-1.54e-05	1.65e-05	-0.937	0.36	-4.99e-05	0.000019	0.0421

Microbiome alpha diversity difference (yr1 vs neo) vs SS, IBQ-R

Table 3376: div_diff_vs_strange_yr1: Summed vs chao1, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.12998	0.95093	4.343	0.000442	2.12370	6.1363	0.0000
chao1	0.00138	0.00475	0.292	0.774154	-0.00864	0.0114	0.0047

Table 3377: div_diff_vs_strange_yr1: Summed vs observed_otus, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.95594	0.98771	4.005	0.000917	1.8721	6.0398	0.0000
observed_otus	0.00408	0.00853	0.479	0.638170	-0.0139	0.0221	0.0126

Table 3378: div_diff_vs_strange_yr1: Summed vs PD_whole_tree, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.642	1.330	2.737	0.014	0.834	6.449	0.0000
PD_whole_tree	0.136	0.232	0.586	0.566	-0.353	0.625	0.0187

Table 3379: div_diff_vs_strange_yr1: Summed vs shannon, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.533	0.864	4.09	0.000763	1.710	5.35	0.0000
shannon	0.537	0.466	1.15	0.265334	-0.447	1.52	0.0686

Table 3380: div_diff_vs_strange_yr1: Average vs chao1, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.375954	0.31692	4.342	0.000443	0.70732	2.0446	0.00000
chao1	0.000464	0.00158	0.293	0.773134	-0.00288	0.0038	0.00474

Table 3381: div_diff_vs_strange_yr1: Average vs observed_otus, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.31800	0.32917	4.00	0.000919	0.62351	2.01250	0.0000
observed_otus	0.00136	0.00284	0.48	0.637398	-0.00463	0.00736	0.0126

Table 3382: div_diff_vs_strange_yr1: Average vs PD_whole_tree, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.2137	0.4434	2.737	0.014	0.278	2.149	0.0000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
PD__whole_tree	0.0453	0.0773	0.586	0.566	-0.118	0.208	0.0187

Table 3383: div_diff_vs_strange_yr1: Average vs shannon, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.177	0.288	4.09	0.000766	0.569	1.784	0.0000
shannon	0.179	0.155	1.15	0.264373	-0.148	0.507	0.0689

Table 3384: div_diff_vs_strange_yr1: Max vs chao1, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.32804	0.41620	3.19	0.00535	0.44994	2.20614	0.0000
chao1	0.00237	0.00208	1.14	0.26925	-0.00201	0.00676	0.0676

Table 3385: div_diff_vs_strange_yr1: Max vs observed_otus, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.2516	0.42978	2.91	0.00971	0.34484	2.1584	0.0000
observed_otus	0.0048	0.00371	1.29	0.21280	-0.00303	0.0126	0.0852

Table 3386: div_diff_vs_strange_yr1: Max vs PD__whole_tree, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.810	0.5590	1.45	0.166	-0.3697	1.989	0.00
PD__whole_tree	0.173	0.0974	1.78	0.093	-0.0322	0.379	0.15

Table 3387: div_diff_vs_strange_yr1: Max vs shannon, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.089	0.361	3.02	0.00772	0.32818	1.850	0.000
shannon	0.416	0.195	2.14	0.04741	0.00532	0.827	0.202

Table 3388: div_diff_vs_strange_yr1: Episode3.1 vs chao1, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.5583	0.34793	4.479	0.00033	0.82425	2.29240	0.0000
chao1	-0.0011	0.00174	-0.635	0.53412	-0.00477	0.00256	0.0219

Table 3389: div_diff_vs_strange_yr1: Episode3.1 vs observed_otus, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.50288	0.36528	4.114	0.000724	0.73221	2.27354	0.0000
observed_otus	-0.00133	0.00315	-0.422	0.678292	-0.00799	0.00532	0.0098

Table 3390: div_diff_vs_strange_yr1: Episode3.1 vs PD_whole_tree, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.5300	0.4945	3.094	0.00658	0.487	2.573	0.00000
PD_whole_tree	-0.0302	0.0862	-0.351	0.73022	-0.212	0.152	0.00678

Table 3391: div_diff_vs_strange_yr1: Episode3.1 vs shannon, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.4018	0.331	4.23	0.000558	0.703	2.100	0e+00
shannon	-0.0215	0.179	-0.12	0.905850	-0.398	0.356	8e-04

Table 3392: div_diff_vs_strange_yr1: Episode3.2 vs chao1, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.434312	0.35715	4.016	0.000896	0.68079	2.18783	0.000000
chao1	0.000229	0.00178	0.128	0.899510	-0.00353	0.00399	0.000912

Table 3393: div_diff_vs_strange_yr1: Episode3.2 vs observed_otus, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.36717	0.37153	3.680	0.00186	0.58331	2.15103	0.00000
observed_otus	0.00105	0.00321	0.329	0.74639	-0.00571	0.00782	0.00597

Table 3394: div_diff_vs_strange_yr1: Episode3.2 vs PD_whole_tree, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.1234	0.4954	2.268	0.0367	0.0782	2.169	0.000
PD_whole_tree	0.0655	0.0864	0.758	0.4585	-0.1167	0.248	0.031

Table 3395: div_diff_vs_strange_yr1: Episode3.2 vs shannon, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.254	0.330	3.80	0.00143	0.558	1.951	0.0000
shannon	0.141	0.178	0.79	0.44020	-0.235	0.517	0.0335

Table 3396: div_diff_vs_strange_yr1: Episode3.3 vs chao1, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.13734	0.37340	3.05	0.0073	0.34953	1.92516	0.0000
chao1	0.00226	0.00186	1.21	0.2424	-0.00168	0.00619	0.0754

Table 3397: div_diff_vs_strange_yr1: Episode3.3 vs observed_otus, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.08589	0.38702	2.81	0.0122	0.26934	1.9024	0.0000
observed_otus	0.00436	0.00334	1.30	0.2094	-0.00269	0.0114	0.0864

Table 3398: div_diff_vs_strange_yr1: Episode3.3 vs PD_whole_tree, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.988	0.5305	1.86	0.0799	-0.1310	2.107	0.0000
PD_whole_tree	0.101	0.0925	1.09	0.2916	-0.0945	0.296	0.0617

Table 3399: div_diff_vs_strange_yr1: Episode3.3 vs shannon, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.876	0.314	2.79	0.0126	0.2130	1.540	0.000
shannon	0.418	0.170	2.46	0.0248	0.0596	0.776	0.252

Table 3400: div_diff_vs_strange_yr1: IBQr_fear vs chao1, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.43806	0.48320	7.12	2.45e-06	2.41372	4.46240	0.0000
chao1	-0.00255	0.00239	-1.07	3.01e-01	-0.00762	0.00251	0.0629

Table 3401: div_diff_vs_strange_yr1: IBQr_fear vs observed_otus, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.45297	0.50338	6.86	3.84e-06	2.3859	4.52008	0.0000
observed_otus	-0.00451	0.00431	-1.05	3.11e-01	-0.0137	0.00464	0.0604

Table 3402: div_diff_vs_strange_yr1: IBQr_fear vs PD_whole_tree, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.3542	0.698	4.809	0.000193	1.875	4.833	0.0000
PD_whole_tree	-0.0665	0.121	-0.551	0.589319	-0.322	0.189	0.0175

Table 3403: div_diff_vs_strange_yr1: IBQr_fear vs shannon, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.1371	0.467	6.722	4.90e-06	2.148	4.13	0.0000
shannon	-0.0903	0.250	-0.361	7.23e-01	-0.621	0.44	0.0076
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Microbiome alpha diversity difference (yr1 vs neo) vs SS, IBQ-R using linear mixed effect model

Table 3404: div_diff_vs_strange_combine_yr1: strange_response VS chao1, df=34

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	1.2889403	0.3296680	3.9098130	0.0000924	0.643	1.935	0.000
chao1	0.0004615	0.0015830	0.2915561	0.7706260	-0.003	0.004	0.009
episodes2	0.1052632	0.1569171	0.6708204	0.5023350	-0.202	0.413	0.010
episodes3	0.1578947	0.1569171	1.0062306	0.3143047	-0.150	0.465	0.023

Table 3405: div_diff_vs_strange_combine_yr1: strange_response VS observed_otus, df=34

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	1.2309272	0.3414731	3.6047559	0.0003124	0.562	1.900	0.000
observed_otus	0.0013612	0.0028428	0.4788158	0.6320697	-0.004	0.007	0.024
episodes2	0.1052632	0.1569171	0.6708204	0.5023350	-0.202	0.413	0.010
episodes3	0.1578947	0.1569171	1.0062306	0.3143047	-0.150	0.465	0.023

Table 3406: div_diff_vs_strange_combine_yr1: strange_response VS PD_whole_tree, df=34

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	1.1261240	0.4526513	2.4878402	0.0128521	0.239	2.013	0.000
PD_whole_tree	0.0453133	0.0773163	0.5860772	0.5578236	-0.106	0.197	0.036
episodes2	0.1052632	0.1569171	0.6708204	0.5023350	-0.202	0.413	0.010
episodes3	0.1578947	0.1569171	1.0062306	0.3143047	-0.150	0.465	0.022

Table 3407: div_diff_vs_strange_combine_yr1: strange_response VS shannon, df=34

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	1.0898094	0.3018315	3.6106547	0.0003054	0.498	1.681	0.000
shannon	0.1790150	0.1554182	1.1518281	0.2493917	-0.126	0.484	0.120
episodes2	0.1052632	0.1569170	0.6708204	0.5023350	-0.202	0.413	0.009
episodes3	0.1578947	0.1569170	1.0062306	0.3143047	-0.150	0.465	0.021