Association of microbiome vs brain 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=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	9.234	4.644	1.988	0.061	-0.487	18.955	0.000
AgeAt1yrVisit	-0.013	0.012	-1.050	0.307	-0.039	0.013	0.052

Table 3: cvrt_vs_strange_yr1: Summed vs MAGE, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.679	3.263	1.740	0.098	-1.151	12.508	0.000
MAGE	-0.041	0.102	-0.402	0.693	-0.255	0.173	0.008

Table 4: cvrt_vs_strange_yr1: Summed vs PAGE, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.591	2.331	2.399	0.027	0.713	10.469	0.000
PAGE	-0.035	0.066	-0.529	0.603	-0.174	0.104	0.014

Table 5: cvrt_vs_strange_yr1: Summed vs MEDUY, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.937	3.799	1.036	0.313	-4.014	11.887	0.000
MEDUY	0.027	0.229	0.118	0.907	-0.452	0.506	0.001

Table 6: cvrt_vs_strange_yr1: Summed vs PEDUY, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	8.739	2.128	4.107	0.001	4.286	13.193	0.000
PEDUY	-0.282	0.135	-2.087	0.051	-0.566	0.001	0.179

Table 7: cvrt_vs_strange_yr1: Summed vs Income.code, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.556	0.703	6.479	0.000	3.078	6.033	0.00
Income.code.LOW	-0.056	1.268	-0.044	0.966	-2.719	2.608	0.00
Income.code.MID	-0.431	1.025	-0.420	0.679	-2.584	1.723	0.01

Table 8: cvrt_vs_strange_yr1: Summed vs OLDERSIBLINGS, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.125	0.726	5.682	0.000	2.606	5.644	0.00
OLDERSIBLINGS	0.413	0.923	0.448	0.659	-1.518	2.345	0.01

Table 9: cvrt_vs_strange_yr1: Summed vs SEX, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.394	1.358	3.236	0.004	1.552	7.236	0
SEX	-0.010	0.928	-0.010	0.992	-1.951	1.932	0

Table 10: cvrt_vs_strange_yr1: Summed vs GESTAGEBIRTH, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.017	16.777	0.418	0.680	-28.097	42.131	0.000
GESTAGEBIRTH	-0.010	0.061	-0.157	0.877	-0.137	0.118	0.001

Table 11: cvrt_vs_strange_yr1: Summed vs BW, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.213	3.771	-0.057	0.955	-8.105	7.679	0.00

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
BW	0.001	0.001	1.227	0.235	-0.001	0.004	0.07

Table 12: cvrt_vs_strange_yr1: Summed vs MaternalInfection, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.833	0.574	8.415	0.000	3.631	6.036	0.000
MaternalInfection	-1.056	0.877	-1.203	0.244	-2.892	0.781	0.067

Table 13: cvrt_vs_strange_yr1: Summed vs MPSYCH, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.75	0.486	9.774	0.000	3.733	5.767	0.000
MPSYCH	-1.55	0.996	-1.556	0.136	-3.635	0.535	0.108

Table 14: cvrt_vs_strange_yr1: Summed vs VITAMINDNEO, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.538	0.569	7.969	0.000	3.347	5.730	0.00
VITAMINDNEO	-0.413	0.923	-0.448	0.659	-2.345	1.518	0.01

Table 15: cvrt_vs_strange_yr1: Summed vs PrePregBMI, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.750	0.558	6.717	0.000	2.572	4.928	0.000
PrePregBMI.Obese	1.250	1.477	0.846	0.409	-1.866	4.366	0.030
PrePregBMI.Overweight	1.917	0.967	1.982	0.064	-0.123	3.957	0.168
PrePregBMI.Under	-0.750	2.013	-0.373	0.714	-4.997	3.497	0.006

Table 16: cvrt_vs_strange_yr1: Summed vs ANTIBIOTIC_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.091	0.630	6.499	0.000	2.768	5.413	0.000
ANTIBIOTIC_1yr	0.687	0.938	0.732	0.474	-1.285	2.658	0.027

Table 17: cvrt_vs_strange_yr1: Summed vs FEVER_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5	0.504	9.922	0.000	3.941	6.059	0.000
FEVER_1yr	-2	0.920	-2.174	0.043	-3.933	-0.067	0.199

Table 18: cvrt_vs_strange_yr1: Summed vs DAYCARE, df=14

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.000	0.744	6.722	0.000	3.405	6.595	0.000
DAYCARE	-0.571	1.125	-0.508	0.619	-2.983	1.841	0.017

Table 19: cvrt_vs_strange_yr1: Summed vs CURBRFEED_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.4	0.670	6.567	0	2.992	5.808	0
CURBRFEED_1yr	0.0	0.948	0.000	1	-1.991	1.991	0

Table 20: cvrt_vs_strange_yr1: Summed vs FORMULA_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.000	0.623	6.419	0.000	2.691	5.309	0.000
FORMULA_1yr	0.889	0.929	0.957	0.351	-1.063	2.841	0.046

Table 21: cvrt_vs_strange_yr1: Summed vs Milks_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.400	0.908	5.950	0.000	3.493	7.307	0.000
Milks_1yr	-1.333	1.048	-1.272	0.219	-3.535	0.868	0.079

Table 22: cvrt_vs_strange_yr1: Summed vs FrenchFries_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.778	0.678	5.572	0.000	2.353	5.202	0.000
FrenchFries_1yr	1.131	0.914	1.238	0.232	-0.789	3.052	0.075

Table 23: cvrt_vs_strange_yr1: Summed vs SweetFoods-Drinks_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.000	0.941	4.250	0.00	2.023	5.977	0.000
SweetFoodsDrinks_1yr	0.533	1.087	0.491	0.63	-1.750	2.817	0.013

Table 24: cvrt__vs_strange_yr1: Summed vs PeanutButter__1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.714	0.775	4.791	0.000	2.085	5.343	0.00
PeanutButter__1yr	1.055	0.962	1.097	0.287	-0.965	3.075	0.06

Table 25: cvrt__vs__strange__yr1: Summed vs FORMULA__6mo, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.636	0.617	7.52	0.000	3.346	5.927	0.000
FORMULA__6mo	-0.536	0.893	-0.60	0.555	-2.406	1.334	0.018

Table 26: cvrt__vs__strange__yr1: Summed vs WHSTOTHER, df=15

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.0	1.862	1.611	0.128	-0.969	6.969	0.000
WHSTOTHER.4 months	1.8	2.040	0.883	0.391	-2.547	6.147	0.096
WHSTOTHER.5 months	0.6	2.040	0.294	0.773	-3.747	4.947	0.011
WHSTOTHER.5.5 months	2.0	2.280	0.877	0.394	-2.860	6.860	0.056
WHSTOTHER.6 months	1.0	1.990	0.502	0.623	-3.243	5.243	0.036
WHSTOTHER.7 months	6.0	2.633	2.279	0.038	0.388	11.612	0.265

Table 27: cvrt__vs__strange__yr1: Summed vs VITAMIND__6mo, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.733	0.538	8.805	0.000	3.599	5.867	0.000
VITAMIND__6mo	-0.983	1.172	-0.839	0.413	-3.455	1.488	0.038

Table 28: cvrt__vs__strange__yr1: Summed vs Cereals__6mo, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.200	0.931	5.586	0.000	3.236	7.164	0.000
Cereals__6mo	-0.914	1.084	-0.843	0.411	-3.202	1.374	0.038

Table 29: cvrt__vs__strange__yr1: Summed vs NegativeLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.958	0.656	7.559	0.000	3.574	6.342	0.000
NegativeLifeEvents	-0.139	0.146	-0.954	0.353	-0.446	0.168	0.048

Table 30: cvrt_vs_strange_yr1: Summed vs PositiveLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.880	0.678	5.724	0.000	2.450	5.310	0.000
PositiveLifeEvents	0.111	0.084	1.310	0.208	-0.068	0.289	0.087

Table 31: cvrt_vs_strange_yr1: Summed vs TotalLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.928	0.943	4.164	0.001	1.938	5.918	0.000
TotalLifeEvents	0.067	0.091	0.737	0.471	-0.125	0.258	0.029

Table 32: cvrt_vs_strange_yr1: Summed vs STATE, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.083	1.855	2.201	0.043	0.15	8.015	0.000
STATE	0.006	0.059	0.108	0.915	-0.12	0.132	0.001

Table 33: cvrt_vs_strange_yr1: Summed vs TRAIT, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.248	1.802	3.467	0.003	2.446	10.050	0.000
TRAIT	-0.052	0.053	-0.990	0.336	-0.164	0.059	0.052

Table 34: cvrt_vs_strange_yr1: Summed vs Stranger, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	4.462	0.572	7.804	0.000	3.265	5.658	0.000
Stranger	-0.212	0.926	-0.228	0.822	-2.150	1.727	0.003

Table 35: cvrt_vs_strange_yr1: Average vs AgeAt1yrVisit, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.084	1.548	1.993	0.061	-0.156	6.323	0.000
AgeAt1yrVisit	-0.004	0.004	-1.054	0.305	-0.013	0.004	0.053

Table 36: cvrt_vs_strange_yr1: Average vs MAGE, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.895	1.087	1.742	0.098	-0.381	4.171	0.000
MAGE	-0.014	0.034	-0.404	0.691	-0.085	0.058	0.008

Table 37: cvrt_vs_strange_yr1: Average vs PAGE, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.866	0.777	2.403	0.027	0.241	3.492	0.000
PAGE	-0.012	0.022	-0.533	0.600	-0.058	0.035	0.014

Table 38: cvrt_vs_strange_yr1: Average vs MEDUY, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.312	1.266	1.036	0.313	-1.338	3.962	0.000
MEDUY	0.009	0.076	0.118	0.907	-0.151	0.169	0.001

Table 39: cvrt_vs_strange_yr1: Average vs PEDUY, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.911	0.709	4.104	0.001	1.427	4.396	0.000
PEDUY	-0.094	0.045	-2.084	0.051	-0.189	0.000	0.178

Table 40: cvrt_vs_strange_yr1: Average vs Income.code, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.518	0.234	6.476	0.000	1.025	2.010	0.00
Income.code.LOW	-0.018	0.422	-0.042	0.967	-0.905	0.870	0.00
Income.code.MID	-0.143	0.342	-0.418	0.681	-0.861	0.575	0.01

Table 41: cvrt_vs_strange_yr1: Average vs OLDERSIBLINGS, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.375	0.242	5.683	0.00	0.869	1.881	0.00
OLDERSIBLINGS	0.137	0.308	0.446	0.66	-0.506	0.781	0.01

Table 42: cvrt_vs_strange_yr1: Average vs SEX, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.463	0.453	3.233	0.004	0.516	2.410	0
SEX	-0.002	0.309	-0.007	0.995	-0.649	0.645	0

Table 43: cvrt_vs_strange_yr1: Average vs GESTAGEBIRTH, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.343	5.591	0.419	0.680	-9.360	14.046	0.000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
GESTAGEBIRTH	-0.003	0.020	-0.158	0.876	-0.046	0.039	0.001

Table 44: cvrt_vs_strange_yr1: Average vs BW, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.069	1.257	-0.055	0.957	-2.7	2.561	0.00
BW	0.000	0.000	1.225	0.236	0.0	0.001	0.07

Table 45: cvrt_vs_strange_yr1: Average vs MaternalInfection, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.611	0.191	8.415	0.000	1.210	2.011	0.000
MaternalInfection	-0.352	0.292	-1.204	0.244	-0.964	0.260	0.068

Table 46: cvrt_vs_strange_yr1: Average vs MPSYCH, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.583	0.162	9.775	0.000	1.244	1.922	0.000
MPSYCH	-0.517	0.332	-1.558	0.136	-1.212	0.178	0.108

Table 47: cvrt_vs_strange_yr1: Average vs VITAMINDNEO, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.512	0.190	7.968	0.00	1.115	1.910	0.00
VITAMINDNEO	-0.137	0.308	-0.446	0.66	-0.781	0.506	0.01

Table 48: cvrt_vs_strange_yr1: Average vs PrePregBMI, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.250	0.186	6.716	0.000	0.857	1.643	0.000
PrePregBMI.Obese	0.415	0.492	0.843	0.411	-0.624	1.454	0.030
PrePregBMI.Overweight	0.638	0.322	1.980	0.064	-0.042	1.318	0.167
PrePregBMI.Under	-0.250	0.671	-0.373	0.714	-1.666	1.166	0.006

Table 49: cvrt_vs_strange_yr1: Average vs ANTIBIOTIC_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.364	0.210	6.500	0.000	0.923	1.804	0.000
ANTIBIOTIC_1yr	0.229	0.313	0.731	0.474	-0.428	0.886	0.027

Table 50: cvrt__vs_strange_yr1: Average vs FEVER__1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.666	0.168	9.922	0.000	1.314	2.019	0.000
FEVER__1yr	-0.666	0.307	-2.173	0.043	-1.311	-0.022	0.199

Table 51: cvrt__vs_strange_yr1: Average vs DAYCARE, df=14

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.667	0.248	6.723	0.000	1.135	2.198	0.000
DAYCARE	-0.191	0.375	-0.510	0.618	-0.995	0.613	0.017

Table 52: cvrt__vs_strange_yr1: Average vs CURBRFEED__1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.467	0.223	6.570	0.000	0.998	1.936	0
CURBRFEED__1yr	-0.001	0.316	-0.003	0.998	-0.664	0.662	0

Table 53: cvrt__vs_strange_yr1: Average vs FORMULA__1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.333	0.208	6.418	0.00	0.896	1.769	0.000
FORMULA__1yr	0.297	0.310	0.960	0.35	-0.353	0.948	0.046

Table 54: cvrt__vs_strange_yr1: Average vs Milks__1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.800	0.302	5.951	0.000	1.165	2.435	0.000
Milks__1yr	-0.445	0.349	-1.273	0.219	-1.178	0.289	0.079

Table 55: cvrt__vs_strange_yr1: Average vs FrenchFries__1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.259	0.226	5.572	0.000	0.784	1.734	0.000
FrenchFries__1yr	0.377	0.305	1.239	0.231	-0.263	1.017	0.075

Table 56: cvrt__vs_strange_yr1: Average vs SweetFoods-Drinks__1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.334	0.314	4.252	0.000	0.675	1.993	0.000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
SweetFoodsDrinks_1yr	0.177	0.362	0.488	0.632	-0.584	0.938	0.012

Table 57: cvrt_vs_strange_yr1: Average vs PeanutButter_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.239	0.258	4.793	0.000	0.696	1.782	0.000
PeanutButter_1yr	0.351	0.321	1.094	0.288	-0.323	1.024	0.059

Table 58: cvrt_vs_strange_yr1: Average vs FORMULA_6mo, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.545	0.206	7.516	0.000	1.114	1.975	0.000
FORMULA_6mo	-0.178	0.298	-0.596	0.558	-0.801	0.446	0.017

Table 59: cvrt_vs_strange_yr1: Average vs WHSTOTHER, df=15

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.000	0.621	1.612	0.128	-0.323	2.323	0.000
WHSTOTHER.4 months	0.600	0.680	0.883	0.391	-0.849	2.049	0.096
WHSTOTHER.5 months	0.200	0.680	0.294	0.773	-1.249	1.649	0.011
WHSTOTHER.5.5 months	0.665	0.760	0.875	0.395	-0.955	2.285	0.056
WHSTOTHER.6 months	0.333	0.663	0.502	0.623	-1.081	1.747	0.036
WHSTOTHER.7 months	2.000	0.878	2.279	0.038	0.130	3.870	0.265

Table 60: cvrt_vs_strange_yr1: Average vs VITAMIND_6mo, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.577	0.179	8.804	0.000	1.199	1.955	0.000
VITAMIND_6mo	-0.327	0.390	-0.838	0.414	-1.151	0.497	0.038

Table 61: cvrt_vs_strange_yr1: Average vs Cereals_6mo, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.732	0.310	5.581	0.000	1.077	2.387	0.000
Cereals_6mo	-0.303	0.362	-0.839	0.413	-1.066	0.459	0.038

Table 62: cvrt__vs_strange_yr1: Average vs NegativeLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.652	0.219	7.558	0.000	1.191	2.114	0.000
NegativeLifeEvents	-0.046	0.049	-0.954	0.354	-0.149	0.056	0.048

Table 63: cvrt__vs_strange_yr1: Average vs PositiveLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.294	0.226	5.725	0.000	0.817	1.770	0.000
PositiveLifeEvents	0.037	0.028	1.306	0.209	-0.023	0.096	0.087

Table 64: cvrt__vs_strange_yr1: Average vs TotalLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.310	0.314	4.166	0.001	0.646	1.973	0.000
TotalLifeEvents	0.022	0.030	0.734	0.473	-0.042	0.086	0.029

Table 65: cvrt__vs_strange_yr1: Average vs STATE, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.360	0.618	2.20	0.043	0.049	2.670	0.000
STATE	0.002	0.020	0.11	0.914	-0.040	0.044	0.001

Table 66: cvrt__vs_strange_yr1: Average vs TRAIT, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.084	0.601	3.470	0.003	0.817	3.351	0.000
TRAIT	-0.017	0.018	-0.993	0.335	-0.055	0.020	0.052

Table 67: cvrt__vs_strange_yr1: Average vs Stranger, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.487	0.191	7.804	0.000	1.088	1.886	0.000
Stranger	-0.071	0.309	-0.229	0.821	-0.717	0.575	0.003

Table 68: cvrt__vs_strange_yr1: Max vs AgeAt1yrVisit, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.452	2.207	1.564	0.134	-1.167	8.070	0.000
AgeAt1yrVisit	-0.004	0.006	-0.769	0.451	-0.017	0.008	0.029

Table 69: cvrt_vs_strange_yr1: Max vs MAGE, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.46	1.535	0.951	0.354	-1.754	4.673	0.000
MAGE	0.01	0.048	0.199	0.845	-0.091	0.110	0.002

Table 70: cvrt_vs_strange_yr1: Max vs PAGE, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.612	1.101	1.464	0.159	-0.692	3.916	0.000
PAGE	0.004	0.031	0.139	0.891	-0.061	0.070	0.001

Table 71: cvrt_vs_strange_yr1: Max vs MEDUY, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.062	1.739	0.036	0.972	-3.577	3.701	0.000
MEDUY	0.103	0.105	0.985	0.337	-0.116	0.322	0.046

Table 72: cvrt_vs_strange_yr1: Max vs PEDUY, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.3	1.046	3.154	0.005	1.110	5.49	0.000
PEDUY	-0.1	0.067	-1.497	0.151	-0.239	0.04	0.101

Table 73: cvrt_vs_strange_yr1: Max vs Income.code, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.778	0.328	5.420	0.000	1.089	2.467	0.000
Income.code.LOW	-0.278	0.591	-0.470	0.644	-1.520	0.965	0.013
Income.code.MID	0.097	0.478	0.203	0.841	-0.907	1.102	0.002

Table 74: cvrt_vs_strange_yr1: Max vs OLDERSIBLINGS, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.750	0.342	5.113	0.000	1.034	2.466	0
OLDERSIBLINGS	0.019	0.435	0.044	0.965	-0.891	0.930	0

Table 75: cvrt_vs_strange_yr1: Max vs SEX, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.788	0.637	2.808	0.011	0.456	3.121	0
SEX	-0.019	0.435	-0.044	0.965	-0.930	0.891	0

Table 76: cvrt_vs_strange_yr1: Max vs GESTAGEBIRTH, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.258	7.873	0.160	0.875	-15.221	17.737	0
GESTAGEBIRTH	0.002	0.029	0.064	0.950	-0.058	0.062	0

Table 77: cvrt_vs_strange_yr1: Max vs BW, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.528	1.760	-0.30	0.767	-4.211	3.155	0.000
BW	0.001	0.001	1.31	0.206	0.000	0.002	0.079

Table 78: cvrt_vs_strange_yr1: Max vs MaternalInfection, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.083	0.256	8.145	0.00	1.548	2.619	0.000
MaternalInfection	-0.750	0.391	-1.920	0.07	-1.568	0.068	0.156

Table 79: cvrt_vs_strange_yr1: Max vs MPSYCH, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.938	0.228	8.516	0.00	1.461	2.414	0.000
MPSYCH	-0.738	0.466	-1.582	0.13	-1.713	0.238	0.111

Table 80: cvrt_vs_strange_yr1: Max vs VITAMINDNEO, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.692	0.267	6.332	0.000	1.133	2.252	0.000
VITAMINDNEO	0.183	0.433	0.422	0.678	-0.724	1.089	0.009

Table 81: cvrt_vs_strange_yr1: Max vs PrePregBMI, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.583	0.278	5.698	0.000	0.997	2.170	0.000
PrePregBMI.Obese	0.417	0.735	0.567	0.578	-1.134	1.968	0.015
PrePregBMI.Overweight	0.583	0.481	1.212	0.242	-0.432	1.599	0.071
PrePregBMI.Under	-0.583	1.002	-0.582	0.568	-2.697	1.530	0.016

Table 82: cvrt_vs_strange_yr1: Max vs ANTIBIOTIC_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.636	0.297	5.515	0.000	1.013	2.260	0.000
ANTIBIOTIC_1yr	0.253	0.442	0.571	0.575	-0.677	1.182	0.017

Table 83: cvrt__vs_strange_yr1: Max vs FEVER__1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.071	0.227	9.145	0.000	1.596	2.547	0.000
FEVER__1yr	-1.071	0.414	-2.591	0.018	-1.940	-0.203	0.261

Table 84: cvrt__vs_strange_yr1: Max vs DAYCARE, df=14

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.222	0.325	6.848	0.000	1.526	2.918	0.000
DAYCARE	-0.651	0.491	-1.326	0.206	-1.703	0.402	0.105

Table 85: cvrt__vs_strange_yr1: Max vs CURBRFEED__1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.6	0.310	5.161	0.000	0.949	2.251	0.000
CURBRFEED__1yr	0.3	0.438	0.684	0.503	-0.621	1.221	0.024

Table 86: cvrt__vs_strange_yr1: Max vs FORMULA__1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.636	0.297	5.515	0.000	1.013	2.260	0.000
FORMULA__1yr	0.253	0.442	0.571	0.575	-0.677	1.182	0.017

Table 87: cvrt__vs_strange_yr1: Max vs Milks_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.2	0.427	5.154	0.000	1.303	3.097	0.000
Milks__1yr	-0.6	0.493	-1.217	0.239	-1.636	0.436	0.072

Table 88: cvrt__vs_strange_yr1: Max vs FrenchFries__1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.444	0.316	4.565	0.000	0.780	2.109	0.000
FrenchFries__1yr	0.556	0.427	1.302	0.209	-0.341	1.452	0.082

Table 89: cvrt__vs_strange_yr1: Max vs SweetFoodsDrinks__1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.800	0.444	4.055	0.001	0.867	2.733	0.000
SweetFoodsDrinks__1yr	-0.067	0.513	-0.130	0.898	-1.144	1.010	0.001

Table 90: cvrt_vs_strange_yr1: Max vs PeanutButter_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.571	0.372	4.228	0.001	0.791	2.352	0.000
PeanutButter_1yr	0.275	0.461	0.596	0.559	-0.694	1.243	0.018

Table 91: cvrt_vs_strange_yr1: Max vs FORMULA_6mo, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.909	0.288	6.634	0.000	1.307	2.511	0.000
FORMULA_6mo	-0.309	0.417	-0.741	0.468	-1.182	0.564	0.027

Table 92: cvrt_vs_strange_yr1: Max vs WHSTOTHER, df=15

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.000	0.995	1.005	0.331	-1.121	3.121	0.000
WHSTOTHER.4 months	0.800	1.090	0.734	0.474	-1.524	3.124	0.076
WHSTOTHER.5 months	0.400	1.090	0.367	0.719	-1.924	2.724	0.019
WHSTOTHER.5.5 months	1.000	1.219	0.820	0.425	-1.598	3.598	0.057
WHSTOTHER.6 months	0.857	1.064	0.806	0.433	-1.411	3.125	0.107
WHSTOTHER.7 months	2.000	1.407	1.421	0.176	-1.000	5.000	0.119

Table 93: cvrt_vs_strange_yr1: Max vs VITAMIND_6mo, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.933	0.250	7.734	0.000	1.406	2.461	0.000
VITAMIND_6mo	-0.433	0.545	-0.795	0.437	-1.583	0.716	0.034

Table 94: cvrt_vs_strange_yr1: Max vs Cereals_6mo, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.000	0.439	4.559	0.00	1.074	2.926	0.00
Cereals_6mo	-0.214	0.511	-0.419	0.68	-1.292	0.864	0.01

Table 95: cvrt_vs_strange_yr1: Max vs NegativeLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.160	0.292	7.406	0.000	1.545	2.776	0.000
NegativeLifeEvents	-0.103	0.065	-1.582	0.132	-0.239	0.034	0.122

Table 96: cvrt_vs_strange_yr1: Max vs PositiveLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.562	0.317	4.935	0.000	0.894	2.230	0.000
PositiveLifeEvents	0.048	0.039	1.214	0.241	-0.035	0.131	0.076

Table 97: cvrt_vs_strange_yr1: Max vs TotalLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.727	0.443	3.894	0.001	0.791	2.662	0.000
TotalLifeEvents	0.013	0.043	0.302	0.766	-0.077	0.103	0.005

Table 98: cvrt_vs_strange_yr1: Max vs STATE, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.322	0.957	2.427	0.027	0.294	4.351	0.00
STATE	-0.018	0.031	-0.586	0.566	-0.083	0.047	0.02

Table 99: cvrt_vs_strange_yr1: Max vs TRAIT, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.624	0.837	3.134	0.006	0.857	4.391	0.000
TRAIT	-0.024	0.025	-0.968	0.347	-0.076	0.028	0.049

Table 100: cvrt_vs_strange_yr1: Max vs Stranger, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.692	0.267	6.332	0.000	1.133	2.252	0.000
Stranger	0.183	0.433	0.422	0.678	-0.724	1.089	0.009

Table 101: cvrt_vs_strange_yr1: Episode3.1 vs AgeAt1yrVisit, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.825	1.725	1.637	0.118	-0.787	6.436	0.000
AgeAt1yrVisit	-0.004	0.005	-0.841	0.411	-0.013	0.006	0.034

Table 102: cvrt_vs_strange_yr1: Episode3.1 vs MAGE, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.974	1.197	1.648	0.116	-0.532	4.48	0.000
MAGE	-0.019	0.038	-0.500	0.623	-0.097	0.06	0.012

Table 103: cvrt_vs_strange_yr1: Episode3.1 vs PAGE, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.831	0.857	2.136	0.046	0.037	3.625	0.000
PAGE	-0.013	0.024	-0.535	0.599	-0.064	0.038	0.014

Table 104: cvrt_vs_strange_yr1: Episode3.1 vs MEDUY, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.342	1.398	0.960	0.349	-1.583	4.268	0
MEDUY	0.002	0.084	0.028	0.978	-0.174	0.179	0

Table 105: cvrt_vs_strange_yr1: Episode3.1 vs PEDUY, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.721	0.809	3.363	0.003	1.027	4.415	0.000
PEDUY	-0.087	0.051	-1.687	0.108	-0.195	0.021	0.125

Table 106: cvrt_vs_strange_yr1: Episode3.1 vs Income.code, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.333	0.259	5.146	0.000	0.789	1.878	0.000
Income.code.LOW	0.167	0.467	0.357	0.725	-0.815	1.148	0.007
Income.code.MID	0.042	0.378	0.110	0.913	-0.752	0.835	0.001

Table 107: cvrt_vs_strange_yr1: Episode3.1 vs OLDERSIBLINGS, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.250	0.266	4.705	0.000	0.694	1.806	0.000
OLDERSIBLINGS	0.212	0.338	0.626	0.539	-0.495	0.918	0.019

Table 108: cvrt_vs_strange_yr1: Episode3.1 vs SEX, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.394	0.499	2.792	0.012	0.349	2.440	0
SEX	-0.010	0.341	-0.028	0.978	-0.724	0.704	0

Table 109: cvrt_vs_strange_yr1: Episode3.1 vs GESTAGEBIRTH, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.536	6.155	0.574	0.572	-9.347	16.418	0.000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
GESTAGEBIRTH	-0.008	0.022	-0.350	0.730	-0.055	0.039	0.006

Table 110: cvrt_vs_strange_yr1: Episode3.1 vs BW, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.173	1.395	-0.124	0.903	-3.093	2.748	0.000
BW	0.000	0.000	1.121	0.276	0.000	0.001	0.059

Table 111: cvrt_vs_strange_yr1: Episode3.1 vs MaternalInfection, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.500	0.215	6.971	0.000	1.050	1.95	0.000
MaternalInfection	-0.278	0.329	-0.845	0.409	-0.966	0.41	0.034

Table 112: cvrt_vs_strange_yr1: Episode3.1 vs MPSYCH, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.5	0.181	8.270	0.000	1.120	1.880	0.000
MPSYCH	-0.5	0.372	-1.345	0.194	-1.278	0.278	0.083

Table 113: cvrt_vs_strange_yr1: Episode3.1 vs VITAMINDNEO, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.538	0.202	7.606	0.000	1.115	1.962	0.000
VITAMINDNEO	-0.413	0.328	-1.262	0.222	-1.099	0.272	0.074

Table 114: cvrt_vs_strange_yr1: Episode3.1 vs PrePregBMI, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.250	0.222	5.622	0.000	0.781	1.719	0.000
PrePregBMI.Obese	0.250	0.588	0.425	0.676	-0.991	1.491	0.009
PrePregBMI.Overweight	0.417	0.385	1.082	0.294	-0.396	1.229	0.058
PrePregBMI.Under	-0.250	0.802	-0.312	0.759	-1.941	1.441	0.005

Table 115: cvrt_vs_strange_yr1: Episode3.1 vs ANTIBIOTIC_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.273	0.229	5.552	0.000	0.791	1.754	0.000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
ANTIBIOTIC_1yr	0.283	0.342	0.828	0.419	-0.435	1.001	0.035

Table 116: cvrt_vs_strange_yr1: Episode3.1 vs FEVER_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.571	0.193	8.124	0.000	1.165	1.978	0.000
FEVER_1yr	-0.571	0.353	-1.618	0.123	-1.313	0.171	0.121

Table 117: cvrt_vs_strange_yr1: Episode3.1 vs DAYCARE, df=14

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.556	0.281	5.539	0.000	0.953	2.158	0.000
DAYCARE	-0.127	0.425	-0.299	0.769	-1.038	0.784	0.006

Table 118: cvrt_vs_strange_yr1: Episode3.1 vs CURBRFEED_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.4	0.245	5.715	0	0.885	1.915	0
CURBRFEED_1yr	0.0	0.346	0.000	1	-0.728	0.728	0

Table 119: cvrt_vs_strange_yr1: Episode3.1 vs FORMULA_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.364	0.233	5.847	0.000	0.874	1.854	0.000
FORMULA_1yr	0.081	0.348	0.232	0.819	-0.650	0.811	0.003

Table 120: cvrt_vs_strange_yr1: Episode3.1 vs Milks_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.600	0.342	4.677	0.000	0.881	2.319	0.000
Milks_1yr	-0.267	0.395	-0.675	0.508	-1.097	0.563	0.023

Table 121: cvrt_vs_strange_yr1: Episode3.1 vs FrenchFries_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.222	0.252	4.851	0.000	0.693	1.752	0.000
FrenchFries_1yr	0.323	0.340	0.951	0.354	-0.390	1.037	0.045

Table 122: cvrt_vs_strange_yr1: Episode3.1 vs SweetFoods-Drinks_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.000	0.329	3.041	0.007	0.309	1.691	0.000
SweetFoodsDrinks_1yr	0.533	0.380	1.404	0.177	-0.264	1.331	0.094

Table 123: cvrt_vs_strange_yr1: Episode3.1 vs PeanutButter_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.000	0.268	3.726	0.002	0.436	1.564	0.000
PeanutButter_1yr	0.615	0.333	1.848	0.081	-0.084	1.315	0.152

Table 124: cvrt_vs_strange_yr1: Episode3.1 vs FORMULA_6mo, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.455	0.228	6.391	0.000	0.978	1.931	0.000
FORMULA_6mo	-0.155	0.330	-0.469	0.645	-0.845	0.536	0.011

Table 125: cvrt_vs_strange_yr1: Episode3.1 vs WHSTOTHER, df=15

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.000	0.719	1.391	0.185	-0.533	2.533	0.000
WHSTOTHER.4 months	0.400	0.788	0.508	0.619	-1.279	2.079	0.038
WHSTOTHER.5 months	0.400	0.788	0.508	0.619	-1.279	2.079	0.038
WHSTOTHER.5.5 months	0.500	0.881	0.568	0.579	-1.377	2.377	0.028
WHSTOTHER.6 months	0.143	0.769	0.186	0.855	-1.496	1.781	0.006
WHSTOTHER.7 months	2.000	1.017	1.967	0.068	-0.168	4.168	0.239

Table 126: cvrt_vs_strange_yr1: Episode3.1 vs VITAMIND_6mo, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.533	0.195	7.848	0.000	1.121	1.946	0.00
VITAMIND_6mo	-0.533	0.426	-1.253	0.227	-1.432	0.365	0.08

Table 127: cvrt_vs_strange_yr1: Episode3.1 vs Cereals_6mo, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.600	0.350	4.571	0.000	0.862	2.338	0.000
Cereals_6mo	-0.243	0.408	-0.596	0.559	-1.103	0.617	0.019

Table 128: cvrt_vs_strange_yr1: Episode3.1 vs NegativeLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.557	0.246	6.330	0.000	1.038	2.076	0.000
NegativeLifeEvents	-0.044	0.055	-0.802	0.434	-0.159	0.071	0.034

Table 129: cvrt_vs_strange_yr1: Episode3.1 vs PositiveLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.205	0.255	4.730	0.00	0.667	1.742	0.00
PositiveLifeEvents	0.037	0.032	1.166	0.26	-0.030	0.104	0.07

Table 130: cvrt_vs_strange_yr1: Episode3.1 vs TotalLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.212	0.352	3.445	0.003	0.470	1.954	0.000
TotalLifeEvents	0.023	0.034	0.691	0.499	-0.048	0.095	0.026

Table 131: cvrt_vs_strange_yr1: Episode3.1 vs STATE, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.241	0.703	1.764	0.097	-0.250	2.732	0.000
STATE	0.003	0.023	0.135	0.894	-0.045	0.051	0.001

Table 132: cvrt_vs_strange_yr1: Episode3.1 vs TRAIT, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.113	0.667	3.166	0.006	0.705	3.522	0.00
TRAIT	-0.021	0.020	-1.075	0.297	-0.062	0.020	0.06

Table 133: cvrt_vs_strange_yr1: Episode3.1 vs Stranger, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.462	0.208	7.012	0.000	1.025	1.898	0.000
Stranger	-0.212	0.338	-0.626	0.539	-0.918	0.495	0.019

Table 134: cvrt_vs_strange_yr1: Episode3.2 vs AgeAt1yrVisit, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.828	1.684	2.273	0.035	0.303	7.352	0.000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
AgeAt1yrVisit	-0.006	0.004	-1.431	0.169	-0.016	0.003	0.093

Table 135: cvrt_vs_strange_yr1: Episode3.2 vs MAGE, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.596	1.215	1.314	0.205	-0.947	4.140	0.000
MAGE	-0.005	0.038	-0.139	0.891	-0.085	0.074	0.001

Table 136: cvrt_vs_strange_yr1: Episode3.2 vs PAGE, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.075	0.858	2.419	0.026	0.279	3.871	0.000
PAGE	-0.019	0.024	-0.768	0.452	-0.070	0.032	0.029

Table 137: cvrt_vs_strange_yr1: Episode3.2 vs MEDUY, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.892	1.406	1.346	0.194	-1.050	4.834	0.000
MEDUY	-0.028	0.085	-0.332	0.743	-0.205	0.149	0.005

Table 138: cvrt_vs_strange_yr1: Episode3.2 vs PEDUY, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.640	0.828	3.189	0.005	0.907	4.374	0.0
PEDUY	-0.079	0.053	-1.491	0.152	-0.189	0.032	0.1

Table 139: cvrt_vs_strange_yr1: Episode3.2 vs Income.code, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.556	0.257	6.046	0.000	1.015	2.096	0.000
Income.code.LOW	-0.056	0.464	-0.120	0.906	-1.030	0.919	0.001
Income.code.MID	-0.306	0.375	-0.815	0.426	-1.093	0.482	0.037

Table 140: cvrt_vs_strange_yr1: Episode3.2 vs OLDERSIBLINGS, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.250	0.266	4.705	0.000	0.694	1.806	0.000
OLDERSIBLINGS	0.288	0.338	0.854	0.404	-0.418	0.995	0.035

Table 141: cvrt_vs_strange_yr1: Episode3.2 vs SEX, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.827	0.494	3.696	0.002	0.792	2.862	0.000
SEX	-0.288	0.338	-0.854	0.404	-0.995	0.418	0.035

Table 142: cvrt_vs_strange_yr1: Episode3.2 vs GESTAGEBIRTH, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.603	6.225	0.097	0.924	-12.427	13.633	0.000
GESTAGEBIRTH	0.003	0.023	0.133	0.896	-0.044	0.050	0.001

Table 143: cvrt_vs_strange_yr1: Episode3.2 vs BW, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.553	1.379	-0.401	0.693	-3.44	2.334	0.000
BW	0.001	0.000	1.447	0.164	0.00	0.001	0.095

Table 144: cvrt_vs_strange_yr1: Episode3.2 vs MaternalInfection, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.583	0.214	7.388	0.000	1.135	2.032	0.000
MaternalInfection	-0.361	0.327	-1.103	0.284	-1.046	0.324	0.057

Table 145: cvrt_vs_strange_yr1: Episode3.2 vs MPSYCH, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.5	0.188	7.958	0.000	1.105	1.895	0.000
MPSYCH	-0.3	0.386	-0.777	0.447	-1.108	0.508	0.029

Table 146: cvrt_vs_strange_yr1: Episode3.2 vs VITAMINDNEO, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.538	0.208	7.381	0.000	1.102	1.975	0.000
VITAMINDNEO	-0.288	0.338	-0.854	0.404	-0.995	0.418	0.035

Table 147: cvrt_vs_strange_yr1: Episode3.2 vs PrePregBMI, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.083	0.184	5.883	0.000	0.695	1.472	0.000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
PrePregBMI.Obese	0.917	0.487	1.882	0.077	-0.111	1.945	0.115
PrePregBMI.Overweight	0.917	0.319	2.874	0.011	0.244	1.590	0.271
PrePregBMI.Under	-0.083	0.664	-0.126	0.902	-1.484	1.317	0.000

Table 148: cvrt_vs_strange_yr1: Episode3.2 vs ANTIBI-OTIC_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.182	0.221	5.357	0.000	0.718	1.645	0.000
ANTIBIOTIC_1yr	0.485	0.329	1.474	0.158	-0.206	1.176	0.103

Table 149: cvrt_vs_strange_yr1: Episode3.2 vs FEVER_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.571	0.193	8.124	0.000	1.165	1.978	0.000
FEVER_1yr	-0.571	0.353	-1.618	0.123	-1.313	0.171	0.121

Table 150: cvrt_vs_strange_yr1: Episode3.2 vs DAYCARE, df=14

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.444	0.281	5.144	0.000	0.842	2.047	0.000
DAYCARE	0.127	0.425	0.299	0.769	-0.784	1.038	0.006

Table 151: cvrt_vs_strange_yr1: Episode3.2 vs CURBR-FEED_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.4	0.245	5.715	0	0.885	1.915	0
CURBRFEED_1yr	0.0	0.346	0.000	1	-0.728	0.728	0

Table 152: cvrt_vs_strange_yr1: Episode3.2 vs FORMULA_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.273	0.229	5.552	0.000	0.791	1.754	0.000
FORMULA_1yr	0.283	0.342	0.828	0.419	-0.435	1.001	0.035

Table 153: cvrt_vs_strange_yr1: Episode3.2 vs Milks_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.800	0.329	5.473	0.000	1.109	2.491	0.000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Milks__1yr	-0.533	0.380	-1.404	0.177	-1.331	0.264	0.094

Table 154: cvrt_vs_strange_yr1: Episode3.2 vs FrenchFries__1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.222	0.252	4.851	0.000	0.693	1.752	0.000
FrenchFries__1yr	0.323	0.340	0.951	0.354	-0.390	1.037	0.045

Table 155: cvrt_vs_strange_yr1: Episode3.2 vs SweetFoods-Drinks__1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.200	0.342	3.508	0.003	0.481	1.919	0.000
SweetFoodsDrinks__1yr	0.267	0.395	0.675	0.508	-0.563	1.097	0.023

Table 156: cvrt_vs_strange_yr1: Episode3.2 vs PeanutButter__1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.143	0.283	4.039	0.001	0.548	1.737	0.000
PeanutButter__1yr	0.396	0.351	1.127	0.274	-0.342	1.133	0.063

Table 157: cvrt_vs_strange_yr1: Episode3.2 vs FORMULA__6mo, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.636	0.220	7.427	0.000	1.175	2.098	0.000
FORMULA__6mo	-0.436	0.319	-1.367	0.188	-1.105	0.232	0.085

Table 158: cvrt_vs_strange_yr1: Episode3.2 vs WHSTOTHER, df=15

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.000	0.676	1.479	0.160	-0.441	2.441	0.000
WHSTOTHER.4 months	0.600	0.741	0.810	0.431	-0.979	2.179	0.084
WHSTOTHER.5 months	0.200	0.741	0.270	0.791	-1.379	1.779	0.009
WHSTOTHER.5.5 months	1.000	0.828	1.208	0.246	-0.765	2.765	0.110
WHSTOTHER.6 months	0.143	0.723	0.198	0.846	-1.398	1.683	0.006
WHSTOTHER.7 months	2.000	0.956	2.092	0.054	-0.038	4.038	0.233

Table 159: cvrt_vs_strange_yr1: Episode3.2 vs VITAMIND_6mo, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.533	0.203	7.562	0.00	1.106	1.961	0.000
VITAMIND_6mo	-0.283	0.442	-0.641	0.53	-1.216	0.649	0.022

Table 160: cvrt_vs_strange_yr1: Episode3.2 vs Cereals_6mo, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.800	0.343	5.244	0.000	1.076	2.524	0.000
Cereals_6mo	-0.443	0.400	-1.108	0.283	-1.286	0.401	0.064

Table 161: cvrt_vs_strange_yr1: Episode3.2 vs NegativeLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.581	0.249	6.347	0.000	1.055	2.106	0.000
NegativeLifeEvents	-0.034	0.055	-0.622	0.542	-0.151	0.082	0.021

Table 162: cvrt_vs_strange_yr1: Episode3.2 vs PositiveLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.052	0.226	4.657	0.00	0.576	1.529	0.000
PositiveLifeEvents	0.072	0.028	2.559	0.02	0.013	0.132	0.267

Table 163: cvrt_vs_strange_yr1: Episode3.2 vs TotalLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.893	0.319	2.800	0.012	0.22	1.566	0.000
TotalLifeEvents	0.065	0.031	2.116	0.049	0.00	0.130	0.199

Table 164: cvrt_vs_strange_yr1: Episode3.2 vs STATE, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.245	0.715	1.741	0.101	-0.271	2.761	0.000
STATE	0.005	0.023	0.207	0.839	-0.044	0.053	0.003

Table 165: cvrt_vs_strange_yr1: Episode3.2 vs TRAIT, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.013	0.68	2.961	0.009	0.579	3.447	0.000
TRAIT	-0.016	0.02	-0.822	0.422	-0.058	0.026	0.036

Table 166: cvrt_vs_strange_yr1: Episode3.2 vs Stranger, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.538	0.208	7.381	0.000	1.102	1.975	0.000
Stranger	-0.288	0.338	-0.854	0.404	-0.995	0.418	0.035

Table 167: cvrt_vs_strange_yr1: Episode3.3 vs AgeAt1yrVisit, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.582	2.053	1.258	0.224	-1.715	6.879	0.000
AgeAt1yrVisit	-0.003	0.005	-0.494	0.627	-0.014	0.009	0.012

Table 168: cvrt_vs_strange_yr1: Episode3.3 vs MAGE, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.108	1.412	1.493	0.152	-0.846	5.063	0.000
MAGE	-0.017	0.044	-0.384	0.705	-0.110	0.076	0.007

Table 169: cvrt_vs_strange_yr1: Episode3.3 vs PAGE, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.685	1.015	1.660	0.113	-0.439	3.810	0.000
PAGE	-0.003	0.029	-0.114	0.910	-0.064	0.057	0.001

Table 170: cvrt_vs_strange_yr1: Episode3.3 vs MEDUY, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.702	1.631	0.430	0.672	-2.712	4.116	0.000
MEDUY	0.053	0.098	0.537	0.598	-0.153	0.259	0.014

Table 171: cvrt_vs_strange_yr1: Episode3.3 vs PEDUY, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.378	0.929	3.636	0.002	1.434	5.322	0.000
PEDUY	-0.117	0.059	-1.981	0.062	-0.241	0.007	0.164

Table 172: cvrt_vs_strange_yr1: Episode3.3 vs Income.code, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.667	0.304	5.477	0.000	1.027	2.306	0.000
Income.code.LOW	-0.167	0.549	-0.304	0.765	-1.319	0.986	0.005
Income.code.MID	-0.167	0.444	-0.376	0.712	-1.099	0.765	0.008

Table 173: cvrt_vs_strange_yr1: Episode3.3 vs OLDERSIBLINGS, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.625	0.315	5.155	0.000	0.965	2.285	0.000
OLDERSIBLINGS	-0.087	0.401	-0.216	0.831	-0.925	0.752	0.002

Table 174: cvrt_vs_strange_yr1: Episode3.3 vs SEX, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.173	0.579	2.025	0.057	-0.039	2.385	0.000
SEX	0.288	0.396	0.729	0.475	-0.540	1.117	0.026

Table 175: cvrt_vs_strange_yr1: Episode3.3 vs GESTAGEBIRTH, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.878	7.255	0.397	0.696	-12.306	18.062	0.000
GESTAGEBIRTH	-0.005	0.026	-0.180	0.859	-0.060	0.051	0.002

Table 176: cvrt_vs_strange_yr1: Episode3.3 vs BW, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.513	1.676	0.306	0.763	-2.996	4.022	0.00
BW	0.000	0.001	0.636	0.533	-0.001	0.001	0.02

Table 177: cvrt_vs_strange_yr1: Episode3.3 vs MaternalInfection, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.750	0.250	7.000	0.000	1.227	2.273	0.000
MaternalInfection	-0.417	0.382	-1.091	0.289	-1.216	0.383	0.056

Table 178: cvrt_vs_strange_yr1: Episode3.3 vs MPSYCH, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.75	0.207	8.463	0.000	1.317	2.183	0.000
MPSYCH	-0.75	0.424	-1.770	0.093	-1.637	0.137	0.135

Table 179: cvrt_vs_strange_yr1: Episode3.3 vs VITAMINDNEO, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.462	0.244	5.985	0.000	0.95	1.973	0.000
VITAMINDNEO	0.288	0.396	0.729	0.475	-0.54	1.117	0.026

Table 180: cvrt_vs_strange_yr1: Episode3.3 vs PrePregBMI, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.417	0.256	5.524	0.000	0.876	1.958	0.000
PrePregBMI.Obese	0.083	0.679	0.123	0.904	-1.348	1.515	0.001
PrePregBMI.Overweight	0.583	0.444	1.313	0.207	-0.354	1.520	0.084
PrePregBMI.Under	-0.417	0.925	-0.451	0.658	-2.368	1.534	0.009

Table 181: cvrt_vs_strange_yr1: Episode3.3 vs ANTIBIOTIC_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.636	0.273	5.992	0.000	1.063	2.210	0.000
ANTIBIOTIC_1yr	-0.081	0.407	-0.198	0.845	-0.936	0.775	0.002

Table 182: cvrt_vs_strange_yr1: Episode3.3 vs FEVER_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.857	0.216	8.614	0.000	1.404	2.31	0.0
FEVER_1yr	-0.857	0.394	-2.177	0.043	-1.684	-0.03	0.2

Table 183: cvrt_vs_strange_yr1: Episode3.3 vs DAYCARE, df=14

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.000	0.305	6.559	0.000	1.346	2.654	0.000
DAYCARE	-0.571	0.461	-1.240	0.236	-1.560	0.417	0.093

Table 184: cvrt_vs_strange_yr1: Episode3.3 vs CURBR-FEED_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.6	0.287	5.58	0	0.998	2.202	0
CURBRFEED_1yr	0.0	0.406	0.00	1	-0.852	0.852	0

Table 185: cvrt_vs_strange_yr1: Episode3.3 vs FORMULA_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.364	0.260	5.235	0.000	0.816	1.911	0.000
FORMULA_1yr	0.525	0.388	1.353	0.193	-0.291	1.341	0.088

Table 186: cvrt_vs_strange_yr1: Episode3.3 vs Milks_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.000	0.391	5.120	0.000	1.179	2.821	0.000
Milks_1yr	-0.533	0.451	-1.182	0.252	-1.481	0.414	0.069

Table 187: cvrt_vs_strange_yr1: Episode3.3 vs FrenchFries_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.333	0.290	4.596	0.000	0.724	1.943	0.000
FrenchFries_1yr	0.485	0.391	1.239	0.231	-0.337	1.307	0.075

Table 188: cvrt_vs_strange_yr1: Episode3.3 vs SweetFoods-Drinks_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.800	0.402	4.479	0.000	0.956	2.644	0.000
SweetFoodsDrinks_1yr	-0.267	0.464	-0.575	0.573	-1.242	0.708	0.017

Table 189: cvrt_vs_strange_yr1: Episode3.3 vs PeanutButter_1yr, df=18

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.571	0.343	4.586	0.000	0.852	2.291	0.000
PeanutButter_1yr	0.044	0.425	0.103	0.919	-0.849	0.937	0.001

Table 190: cvrt__vs_strange_yr1: Episode3.3 vs FORMULA__6mo, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.545	0.269	5.744	0.00	0.982	2.109	0.000
FORMULA__6mo	0.055	0.390	0.140	0.89	-0.761	0.871	0.001

Table 191: cvrt_vs_strange_yr1: Episode3.3 vs WHSTOTHER, df=15

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.000	0.846	1.182	0.255	-0.803	2.803	0.000
WHSTOTHER.4 months	0.800	0.926	0.864	0.401	-1.175	2.775	0.104
WHSTOTHER.5 months	0.000	0.926	0.000	1.000	-1.975	1.975	0.000
WHSTOTHER.5.5 months	0.500	1.036	0.483	0.636	-1.708	2.708	0.019
WHSTOTHER.6 months	0.714	0.904	0.790	0.442	-1.213	2.641	0.102
WHSTOTHER.7 months	2.000	1.196	1.672	0.115	-0.549	4.549	0.163

Table 192: cvrt__vs_strange_yr1: Episode3.3 vs VITAMIND__6mo, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.667	0.237	7.030	0.000	1.166	2.167	0.000
VITAMIND__6mo	-0.167	0.517	-0.323	0.751	-1.257	0.924	0.006

Table 193: cvrt__vs_strange_yr1: Episode3.3 vs Cereals__6mo, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.800	0.409	4.399	0.000	0.937	2.663	0.000
Cereals__6mo	-0.229	0.477	-0.480	0.638	-1.234	0.777	0.013

Table 194: cvrt__vs_strange_yr1: Episode3.3 vs NegativeLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.820	0.284	6.404	0.000	1.221	2.420	0.000
NegativeLifeEvents	-0.061	0.063	-0.963	0.349	-0.194	0.072	0.049

Table 195: cvrt__vs_strange_yr1: Episode3.3 vs PositiveLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.622	0.308	5.263	0.000	0.972	2.273	0
PositiveLifeEvents	0.002	0.038	0.041	0.968	-0.080	0.083	0

Table 196: cvrt_vs_strange_yr1: Episode3.3 vs TotalLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.823	0.412	4.426	0.000	0.954	2.692	0.000
TotalLifeEvents	-0.021	0.040	-0.540	0.596	-0.105	0.062	0.016

Table 197: cvrt_vs_strange_yr1: Episode3.3 vs STATE, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.597	0.878	1.819	0.088	-0.264	3.457	0
STATE	-0.001	0.028	-0.048	0.962	-0.061	0.058	0

Table 198: cvrt_vs_strange_yr1: Episode3.3 vs TRAIT, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.121	0.794	2.672	0.016	0.446	3.796	0.000
TRAIT	-0.015	0.023	-0.639	0.531	-0.064	0.034	0.022

Table 199: cvrt_vs_strange_yr1: Episode3.3 vs Stranger, df=19

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.462	0.244	5.985	0.000	0.95	1.973	0.000
Stranger pdf 2	0.288	0.396	0.729	0.475	-0.54	1.117	0.026

Table 200: cvrt_vs_IBQr_yr1: IBQr_fear vs AgeAt1yrVisit, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.746	2.416	0.309	0.761	-4.352	5.844	0.000
AgeAt1yrVisit	0.006	0.006	0.943	0.359	-0.007	0.020	0.047

Table 201: cvrt_vs_IBQr_yr1: IBQr_fear vs MAGE, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.717	1.647	4.078	0.001	3.242	10.191	0.000
MAGE	-0.116	0.051	-2.268	0.037	-0.223	-0.008	0.222

Table 202: cvrt_vs_IBQr_yr1: IBQr_fear vs PAGE, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.601	1.323	1.967	0.066	-0.189	5.392	0.000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
PAGE	0.012	0.038	0.317	0.755	-0.069	0.093	0.006

Table 203: cvrt_vs_IBQr_yr1: IBQr_fear vs MEDUY, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	6.188	2.050	3.019	0.008	1.863	10.513	0.000
MEDUY	-0.190	0.122	-1.559	0.138	-0.446	0.067	0.119

Table 204: cvrt_vs_IBQr_yr1: IBQr_fear vs PEDUY, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	5.026	1.197	4.200	0.001	2.502	7.551	0.00
PEDUY	-0.128	0.075	-1.713	0.105	-0.286	0.030	0.14

Table 205: cvrt_vs_IBQr_yr1: IBQr_fear vs Income.code, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.679	0.374	7.167	0.000	1.887	3.472	0.000
Income.code.LOW	0.468	0.716	0.653	0.523	-1.050	1.985	0.025
Income.code.MID	0.618	0.529	1.169	0.259	-0.503	1.739	0.079

Table 206: cvrt_vs_IBQr_yr1: IBQr_fear vs OLDERSIBLINGS, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.238	0.399	8.120	0.000	2.397	4.079	0.000
OLDERSIBLINGS	-0.356	0.502	-0.709	0.488	-1.414	0.703	0.027

Table 207: cvrt_vs_IBQr_yr1: IBQr_fear vs SEX, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.436	0.724	3.366	0.004	0.909	3.962	0.000
SEX	0.422	0.499	0.847	0.409	-0.630	1.474	0.038

Table 208: cvrt_vs_IBQr_yr1: IBQr_fear vs GESTAGEBIRTH, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	13.748	8.451	1.627	0.122	-4.081	31.578	0.000
GESTAGEBIRTH	-0.039	0.031	-1.271	0.221	-0.104	0.026	0.082

Table 209: cvrt_vs_IBQr_yr1: IBQr_fear vs BW, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	7.683	1.728	4.447	0.000	4.038	11.327	0.000
BW	-0.001	0.001	-2.722	0.014	-0.003	0.000	0.292

Table 210: cvrt_vs_IBQr_yr1: IBQr_fear vs MaternalInfection, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.741	0.306	8.949	0.000	2.095	3.387	0.000
MaternalInfection	0.647	0.472	1.370	0.189	-0.349	1.642	0.094

Table 211: cvrt_vs_IBQr_yr1: IBQr_fear vs MPSYCH, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.049	0.276	11.057	0.000	2.467	3.631	0.000
MPSYCH	-0.170	0.601	-0.282	0.781	-1.437	1.098	0.004

Table 212: cvrt_vs_IBQr_yr1: IBQr_fear vs VITAMINDNEO, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.098	0.307	10.085	0.000	2.450	3.746	0.000
VITAMINDNEO	-0.229	0.506	-0.453	0.657	-1.297	0.839	0.011

Table 213: cvrt_vs_IBQr_yr1: IBQr_fear vs PrePregBMI, df=15

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.393	0.283	11.975	0.000	2.789	3.997	0.000
PrePregBMI.Obese	-0.929	0.722	-1.286	0.218	-2.469	0.611	0.068
PrePregBMI.Overweight	-1.180	0.507	-2.328	0.034	-2.261	-0.100	0.225
PrePregBMI.Under	0.535	0.982	0.545	0.594	-1.557	2.627	0.012

Table 214: cvrt_vs_IBQr_yr1: IBQr_fear vs ANTIBIOTIC_1yr, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.420	0.307	11.123	0.000	2.768	4.072	0.000
ANTIBIOTIC_1yr	-0.749	0.461	-1.625	0.124	-1.727	0.228	0.134

Table 215: cvrt_vs_IBQr_yr1: IBQr_fear vs FEVER_1yr, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.006	0.289	10.418	0.0	2.394	3.617	0.000
FEVER_1yr	0.293	0.547	0.534	0.6	-0.868	1.453	0.017

Table 216: cvrt_vs_IBQr_yr1: IBQr_fear vs DAYCARE, df=13

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.96	0.400	7.407	0.00	2.097	3.824	0.000
DAYCARE	0.19	0.585	0.325	0.75	-1.073	1.454	0.008

Table 217: cvrt_vs_IBQr_yr1: IBQr_fear vs CURBRFEED_1yr, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.086	0.371	8.317	0.000	2.299	3.873	0
CURBRFEED_1yr	0.002	0.498	0.004	0.997	-1.054	1.057	0

Table 218: cvrt_vs_IBQr_yr1: IBQr_fear vs FORMULA_1yr, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.052	0.332	9.204	0.000	2.349	3.755	0.000
FORMULA_1yr	0.078	0.497	0.157	0.877	-0.976	1.133	0.001

Table 219: cvrt_vs_IBQr_yr1: IBQr_fear vs Milks_1yr, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.166	0.469	6.754	0.000	2.172	4.16	0.000
Milks_1yr	-0.110	0.552	-0.199	0.845	-1.279	1.06	0.002

Table 220: cvrt_vs_IBQr_yr1: IBQr_fear vs FrenchFries_1yr, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.942	0.346	8.502	0.000	2.209	3.676	0.00
FrenchFries_1yr	0.289	0.489	0.591	0.563	-0.748	1.327	0.02

Table 221: cvrt_vs_IBQr_yr1: IBQr_fear vs SweetFoods-Drinks_1yr, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.513	0.452	7.768	0.000	2.555	4.472	0.000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
SweetFoodsDrinks_1yr	-0.591	0.532	-1.110	0.284	-1.719	0.538	0.068

Table 222: cvrt_vs_IBQr_yr1: IBQr_fear vs PeanutButter_1yr, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.166	0.428	7.401	0.000	2.259	4.073	0.000
PeanutButter_1yr	-0.119	0.524	-0.226	0.824	-1.229	0.992	0.003

Table 223: cvrt_vs_IBQr_yr1: IBQr_fear vs FORMULA_6mo, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.855	0.317	8.999	0.000	2.186	3.525	0.000
FORMULA_6mo	0.376	0.489	0.768	0.453	-0.656	1.407	0.032

Table 224: cvrt_vs_IBQr_yr1: IBQr_fear vs WHSTOTHER, df=13

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.714	1.166	2.329	0.037	0.196	5.232	0.000
WHSTOTHER.4 months	0.547	1.303	0.419	0.682	-2.269	3.362	0.035
WHSTOTHER.5 months	-0.087	1.303	-0.067	0.948	-2.902	2.728	0.001
WHSTOTHER.5.5 months	0.406	1.428	0.285	0.780	-2.678	3.490	0.011
WHSTOTHER.6 months	0.499	1.246	0.401	0.695	-2.193	3.191	0.041
WHSTOTHER.7 months	-0.464	1.648	-0.282	0.783	-4.025	3.097	0.008

Table 225: cvrt_vs_IBQr_yr1: IBQr_fear vs VITAMIND_6mo, df=15

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.923	0.307	9.517	0.000	2.269	3.578	0.000
VITAMIND_6mo	0.317	0.633	0.500	0.624	-1.033	1.666	0.015

Table 226: cvrt_vs_IBQr_yr1: IBQr_fear vs Cereals_6mo, df=15

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.948	0.499	5.906	0.000	1.884	4.012	0.000
Cereals_6mo	0.070	0.594	0.118	0.907	-1.196	1.337	0.001

Table 227: cvrt_vs_IBQr_yr1: IBQr_fear vs NegativeLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.942	0.338	8.696	0.000	2.228	3.655	0.000
NegativeLifeEvents	0.023	0.075	0.307	0.762	-0.135	0.182	0.005

Table 228: cvrt_vs_IBQr_yr1: IBQr_fear vs PositiveLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.315	0.344	9.639	0.000	2.589	4.041	0.000
PositiveLifeEvents	-0.052	0.043	-1.205	0.245	-0.142	0.039	0.075

Table 229: cvrt_vs_IBQr_yr1: IBQr_fear vs TotalLifeEvents, df=17

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.435	0.468	7.340	0.00	2.448	4.422	0.000
TotalLifeEvents	-0.047	0.045	-1.046	0.31	-0.142	0.048	0.057

Table 230: cvrt_vs_IBQr_yr1: IBQr_fear vs STATE, df=15

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.853	1.120	1.655	0.119	-0.534	4.241	0.000
STATE	0.036	0.035	1.026	0.321	-0.039	0.111	0.062

Table 231: cvrt_vs_IBQr_yr1: IBQr_fear vs TRAIT, df=16

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.748	0.940	1.860	0.081	-0.244	3.741	0.000
TRAIT	0.039	0.027	1.422	0.174	-0.019	0.096	0.106
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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	3.101	1.143	2.712	0.012	0.751	5.451	0.00
chao1	0.012	0.011	1.055	0.301	-0.011	0.035	0.04

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	3.217	1.195	2.692	0.012	0.761	5.673	0.000
observed_otus	0.018	0.020	0.904	0.374	-0.022	0.058	0.029

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	1.624	1.009	0.322	-1.700	4.977	0.000
PD_whole_tree	0.542	0.330	1.644	0.112	-0.136	1.220	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	4.338	1.634	2.655	0.013	0.980	7.697	0
shannon	-0.032	0.586	-0.055	0.956	-1.237	1.172	0

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	4.230	0.333	12.713	0.000	3.546	4.914	0.000
wunifrac.PC.1	2.143	1.152	1.861	0.074	-0.225	4.510	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	0.00	3.527	4.982	0.000
wunifrac.PC.2	0.622	2.557	0.243	0.81	-4.635	5.879	0.002

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	0.000	3.518	4.975	0.000
wunifrac.PC.3	0.489	2.884	0.17	0.867	-5.440	6.418	0.001

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	4.238	0.337	12.580	0.000	3.546	4.931	0.000
wunifrac.PC.4	-5.897	3.570	-1.652	0.111	-13.236	1.442	0.092

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

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.032	0.381	2.709	0.012	0.249	1.815	0.00
chao1	0.004	0.004	1.059	0.300	-0.004	0.012	0.04

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	1.070	0.398	2.687	0.012	0.251	1.888	0.00
observed_otus	0.006	0.007	0.910	0.371	-0.007	0.019	0.03

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	1.002	0.326	-0.570	1.654	0.000
PD_whole_tree	0.181	0.110	1.652	0.111	-0.044	0.407	0.092

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

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.443	0.544	2.65	0.014	0.323	2.562	0
shannon	-0.010	0.195	-0.05	0.961	-0.411	0.392	0

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	12.711	0.000	1.182	1.637	0.000
wunifrac.PC.1	0.714	0.384	1.860	0.074	-0.075	1.503	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	0.000	1.175	1.660	0.000
wunifrac.PC.2	0.204	0.852	0.239	0.813	-1.548	1.955	0.002

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	1.415	0.118	11.978	0.000	1.172	1.658	0.000
wunifrac.PC.3	0.160	0.961	0.166	0.869	-1.816	2.136	0.001

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	1.412	0.112	12.573	0.000	1.181	1.643	0.000
wunifrac.PC.4	-1.956	1.190	-1.643	0.112	-4.403	0.491	0.091

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

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.492	0.541	2.759	0.01	0.380	2.603	0.000
chao1	0.002	0.005	0.432	0.67	-0.009	0.013	0.007

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	1.529	0.563	2.717	0.012	0.372	2.686	0.000
observed_otus	0.003	0.009	0.344	0.734	-0.016	0.022	0.004

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	0.000
PD_whole_tree	0.142	0.159	0.892	0.381	-0.185	0.468	0.029

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

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	2.396	0.747	3.207	0.004	0.860	3.931	0.000
shannon	-0.250	0.268	-0.934	0.359	-0.801	0.300	0.031

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	1.705	0.154	11.064	0.000	1.388	2.022	0.00
wunifrac.PC.1	1.023	0.533	1.919	0.066	-0.073	2.120	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	0.000	1.384	2.056	0.000
wunifrac.PC.2	0.765	1.181	0.648	0.522	-1.661	3.192	0.015

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	1.717	0.165	10.432	0.000	1.379	2.055	0.000
wunifrac.PC.3	-0.380	1.339	-0.283	0.779	-3.133	2.374	0.003

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	1.709	0.159	10.777	0.00	1.383	2.036	0.000
wunifrac.PC.4	-2.375	1.681	-1.413	0.17	-5.831	1.080	0.069

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	1.098	0.428	2.569	0.016	0.220	1.977	0.000
chao1	0.003	0.004	0.635	0.531	-0.006	0.011	0.015

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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	1.264	0.447	2.824	0.009	0.344	2.183	0.000
observed_otus	0.002	0.007	0.219	0.829	-0.013	0.017	0.002

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	1.043	0.627	1.665	0.108	-0.245	2.331	0.00
PD_whole_tree	0.065	0.127	0.512	0.613	-0.196	0.327	0.01

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	3.597	0.001	0.901	3.302	0.000
shannon	-0.273	0.210	-1.305	0.203	-0.704	0.157	0.059

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	10.621	0.000	1.091	1.614	0.00
wunifrac.PC.1	0.523	0.441	1.186	0.246	-0.383	1.428	0.05

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	0.000	1.094	1.628	0.000
wunifrac.PC.2	0.594	0.938	0.634	0.532	-1.333	2.522	0.015

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	1.368	0.125	10.905	0.000	1.110	1.626	0.000
wunifrac.PC.3	-1.545	1.021	-1.513	0.142	-3.644	0.554	0.078

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	1.354	0.127	10.633	0.000	1.092	1.616	0.000
wunifrac.PC.4	-1.590	1.350	-1.178	0.249	-4.364	1.184	0.049

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	0.842	0.455	1.848	0.076	-0.094	1.778	0.000
chao1	0.006	0.004	1.353	0.188	-0.003	0.015	0.063

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	0.793	0.472	1.681	0.105	-0.177	1.764	0.000
observed_otus	0.011	0.008	1.407	0.171	-0.005	0.027	0.068

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	0.625	-1.018	1.662	0.0
PD_whole_tree	0.230	0.132	1.735	0.095	-0.042	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	0.000
shannon	0.203	0.233	0.871	0.392	-0.276	0.682	0.027

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	10.421	0.000	1.141	1.702	0.000
wunifrac.PC.1	0.753	0.472	1.594	0.123	-0.218	1.723	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	0.000	1.141	1.725	0.000
wunifrac.PC.2	0.602	1.026	0.586	0.563	-1.508	2.712	0.013

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	1.418	0.139	10.226	0.000	1.133	1.703	0.000
wunifrac.PC.3	1.469	1.128	1.302	0.204	-0.850	3.788	0.059

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	1.424	0.136	10.485	0.000	1.145	1.703	0.000
wunifrac.PC.4	-2.403	1.439	-1.670	0.107	-5.362	0.555	0.094

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	1.160	0.499	2.323	0.028	0.134	2.187	0.000
chao1	0.003	0.005	0.638	0.529	-0.007	0.013	0.015

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	1.160	0.519	2.233	0.034	0.092	2.228	0.000
observed_otus	0.005	0.008	0.613	0.545	-0.012	0.023	0.014

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	0.698	-1.157	1.704	0.000
PD_whole_tree	0.247	0.141	1.749	0.092	-0.043	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	0.064	-0.087	2.808	0.000
shannon	0.038	0.253	0.151	0.881	-0.481	0.557	0.001

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	10.071	0.000	1.159	1.754	0.0
wunifrac.PC.1	0.867	0.500	1.733	0.095	-0.161	1.896	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	0.000	1.148	1.773	0.00
wunifrac.PC.2	-0.574	1.098	-0.523	0.605	-2.832	1.683	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	0.000	1.147	1.773	0.000
wunifrac.PC.3	0.565	1.239	0.456	0.652	-1.983	3.112	0.008

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	1.460	0.149	9.830	0.000	1.155	1.766	0.000
wunifrac.PC.4	-1.903	1.575	-1.209	0.238	-5.140	1.333	0.051

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	2.412	0.662	3.645	0.001	1.046	3.778	0.000
chao1	0.008	0.007	1.220	0.234	-0.006	0.022	0.056

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	2.496	0.671	3.720	0.001	1.111	3.880	0.000
observed_otus	0.012	0.011	1.071	0.295	-0.011	0.035	0.044

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	2.266	0.033	0.198	4.230	0.000
PD_whole_tree	0.203	0.201	1.012	0.322	-0.211	0.617	0.039

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	1.817	0.082	-0.242	3.804	0.000
shannon	0.506	0.347	1.458	0.158	-0.210	1.222	0.078

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	3.177	0.197	16.101	0.000	2.769	3.584	0.000
wunifrac.PC.1	1.010	0.700	1.443	0.162	-0.435	2.455	0.077

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	3.182	0.187	16.983	0.000	2.795	3.569	0.000
wunifrac.PC.2	-2.949	1.331	-2.216	0.036	-5.695	-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	0.000	2.760	3.611	0.000
wunifrac.PC.3	-0.351	1.687	-0.208	0.837	-3.833	3.131	0.002

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	0.000	2.748	3.606	0.000
wunifrac.PC.4	0.345	2.248	0.153	0.879	-4.294	4.983	0.001

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

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	3.441	1.503	2.290	0.034	0.296	6.586	0.000
chao1	0.004	0.005	0.655	0.520	-0.008	0.015	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	3.147	1.598	1.969	0.064	-0.198	6.492	0.000
observed_otus	0.008	0.010	0.804	0.432	-0.012	0.028	0.031

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	-2.831	6.787	0.000
PD_whole_tree	0.239	0.224	1.065	0.3	-0.230	0.707	0.054

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	2.626	0.993	0.333	-2.888	8.105	0.000
shannon	0.411	0.600	0.685	0.502	-0.845	1.667	0.023

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	0.000	3.440	5.322	0.000
wunifrac.PC.1	-0.348	1.195	-0.291	0.774	-2.851	2.154	0.004

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	4.381	0.447	9.799	0.000	3.445	5.317	0.000
wunifrac.PC.2	-1.486	2.782	-0.534	0.599	-7.310	4.337	0.014

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	4.381	0.433	10.117	0.000	3.475	5.287	0.000
wunifrac.PC.3	-4.992	4.001	-1.248	0.227	-13.367	3.383	0.072

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	4.381	0.427	10.268	0.000	3.488	5.274	0.000
wunifrac.PC.4	-6.837	4.636	-1.475	0.157	-16.541	2.866	0.098

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

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	1.146	0.501	2.288	0.034	0.098	2.194	0.000
chao1	0.001	0.002	0.656	0.520	-0.003	0.005	0.021

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	1.048	0.533	1.968	0.064	-0.066	2.163	0.000
observed_otus	0.003	0.003	0.805	0.431	-0.004	0.009	0.031

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	0.659	0.766	0.860	0.4	-0.944	2.261	0.000
PD_whole_tree	0.080	0.075	1.066	0.3	-0.077	0.236	0.054

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	0.000
shannon	0.137	0.200	0.687	0.500	-0.281	0.556	0.023

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	0.000	1.146	1.774	0.000
wunifrac.PC.1	-0.115	0.398	-0.289	0.776	-0.949	0.719	0.004

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	0.0	1.148	1.772	0.000
wunifrac.PC.2	-0.495	0.927	-0.534	0.6	-2.436	1.446	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	1.460	0.144	10.117	0.000	1.158	1.762	0.000
wunifrac.PC.3	-1.666	1.333	-1.249	0.227	-4.457	1.125	0.072

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	1.460	0.142	10.265	0.000	1.162	1.758	0.000
wunifrac.PC.4	-2.275	1.545	-1.472	0.157	-5.510	0.959	0.098

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

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	0.841	0.678	1.241	0.230	-0.577	2.259	0.000
chao1	0.003	0.002	1.423	0.171	-0.002	0.009	0.092

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	0.669	0.716	0.935	0.362	-0.830	2.168	0.000
observed_otus	0.007	0.004	1.588	0.129	-0.002	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	-0.081	1.022	-0.079	0.938	-2.221	2.059	0.000
PD_whole_tree	0.183	0.100	1.836	0.082	-0.026	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	0.000	1.326	2.198	0.000
wunifrac.PC.1	-0.401	0.554	-0.724	0.478	-1.562	0.759	0.026

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	0.210	8.375	0.000	1.322	2.202	0.000
wunifrac.PC.2	-0.524	1.309	-0.400	0.693	-3.264	2.216	0.008

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	1.762	0.205	8.592	0.000	1.333	2.191	0.000
wunifrac.PC.3	-2.049	1.895	-1.081	0.293	-6.015	1.917	0.055

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	1.762	0.200	8.810	0.000	1.343	2.18	0.000
wunifrac.PC.4	-3.228	2.173	-1.485	0.154	-7.776	1.32	0.099

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	1.607	0.556	2.888	0.009	0.442	2.771	0.000
chao1	-0.001	0.002	-0.425	0.676	-0.005	0.003	0.009

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	1.503	0.597	2.517	0.021	0.253	2.752	0.000
observed_otus	-0.001	0.004	-0.212	0.834	-0.008	0.007	0.002

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	1.331	0.870	1.530	0.143	-0.490	3.152	0
PD_whole_tree	0.005	0.085	0.059	0.954	-0.172	0.182	0

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	1.698	0.975	1.741	0.098	-0.343	3.739	0.000
shannon	-0.073	0.223	-0.330	0.745	-0.540	0.393	0.005

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	0.000	1.036	1.726	0.000
wunifrac.PC.1	0.211	0.438	0.483	0.635	-0.705	1.128	0.012

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	8.478	0.000	1.040	1.722	0.000
wunifrac.PC.2	-0.821	1.014	-0.810	0.428	-2.943	1.300	0.032

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	0.000	1.035	1.727	0.000
wunifrac.PC.3	-0.403	1.528	-0.264	0.795	-3.602	2.795	0.003

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	1.381	0.161	8.557	0.000	1.043	1.719	0.000
wunifrac.PC.4	-1.776	1.754	-1.013	0.324	-5.446	1.894	0.049

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	1.068	0.557	1.917	0.070	-0.098	2.234	0.000
chao1	0.001	0.002	0.677	0.506	-0.003	0.006	0.022

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	0.962	0.592	1.623	0.121	-0.278	2.202	0.000
observed_otus	0.003	0.004	0.820	0.422	-0.005	0.010	0.033

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	0.832	0.280	0.783	-1.508	1.974	0.000
PD_whole_tree	0.119	0.081	1.464	0.159	-0.051	0.288	0.097

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	-1.133	2.965	0.000
shannon	0.119	0.224	0.531	0.602	-0.350	0.587	0.014

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	1.429	0.167	8.552	0.000	1.079	1.778	0.000
wunifrac.PC.1	0.052	0.444	0.118	0.908	-0.878	0.982	0.001

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	0.000	1.082	1.776	0.000
wunifrac.PC.2	-0.576	1.032	-0.558	0.583	-2.735	1.583	0.015

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	1.429	0.158	9.024	0.000	1.097	1.760	0.000
wunifrac.PC.3	-2.156	1.463	-1.474	0.157	-5.218	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	1.429	0.153	9.336	0.000	1.108	1.749	0.000
wunifrac.PC.4	-3.181	1.663	-1.913	0.071	-6.661	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	0.766	0.628	1.220	0.238	-0.549	2.081	0.000
chao1	0.003	0.002	1.342	0.195	-0.002	0.008	0.083

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	0.683	0.670	1.019	0.321	-0.719	2.085	0.000
observed_otus	0.006	0.004	1.380	0.184	-0.003	0.014	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	0.987	0.420	0.679	-1.651	2.479	0.000
PD_whole_tree	0.115	0.096	1.195	0.247	-0.086	0.316	0.067

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	-0.005	1.090	-0.005	0.996	-2.286	2.275	0.000
shannon	0.366	0.249	1.468	0.158	-0.156	0.887	0.097

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	8.380	0.000	1.179	1.964	0.00
wunifrac.PC.1	-0.612	0.499	-1.227	0.235	-1.656	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	8.067	0.000	1.164	1.979	0
wunifrac.PC.2	-0.089	1.212	-0.073	0.942	-2.626	2.448	0

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	1.571	0.185	8.484	0.000	1.184	1.959	0.000
wunifrac.PC.3	-2.433	1.711	-1.421	0.171	-6.015	1.150	0.092

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	1.571	0.191	8.239	0.000	1.172	1.971	0.00
wunifrac.PC.4	-1.880	2.072	-0.907	0.376	-6.218	2.457	0.04

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	3.621	0.788	4.596	0.000	1.959	5.283	0.000
chao1	-0.002	0.003	-0.810	0.429	-0.008	0.004	0.035

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	3.641	0.834	4.366	0.000	1.882	5.401	0.000
observed_otus	-0.004	0.005	-0.787	0.442	-0.015	0.007	0.033

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	3.177	1.228	2.588	0.019	0.587	5.767	0.000
PD_whole_tree	-0.016	0.120	-0.136	0.894	-0.269	0.236	0.001

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	2.67	1.379	1.936	0.070	-0.240	5.581	0.000
shannon	0.08	0.316	0.253	0.803	-0.586	0.746	0.004

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	3.011	0.244	12.349	0.000	2.497	3.525	0.000
wunifrac.PC.1	0.320	0.639	0.501	0.623	-1.028	1.669	0.014

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	3.027	0.243	12.474	0.000	2.515	3.539	0.000
wunifrac.PC.2	-1.088	1.512	-0.719	0.482	-4.278	2.103	0.028

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	3.001	0.241	12.429	0.000	2.491	3.510	0.000
wunifrac.PC.3	-1.756	2.163	-0.812	0.428	-6.320	2.807	0.035

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	3.054	0.229	13.333	0.000	2.571	3.538	0.000
wunifrac.PC.4	4.151	2.495	1.663	0.115	-1.114	9.415	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	2.5 %	97.5 %	R2
(Intercept)	0.9740112	0.3890177	2.5037710	0.212	1.736	0.000
chao1	0.0039606	0.0037541	1.0550143	-0.003	0.011	0.055
episodes2	0.0714286	0.1352703	0.5280432	-0.194	0.337	0.004
episodes3	0.1071429	0.1352703	0.7920648	-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	2.5 %	97.5 %	R2
(Intercept)	1.0127215	0.4058487	2.4953176	0.217	1.808	0.000
observed__otus	0.0058832	0.0065069	0.9041477	-0.007	0.019	0.041
episodes2	0.0714286	0.1352703	0.5280432	-0.194	0.337	0.004
episodes3	0.1071429	0.1352703	0.7920648	-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	2.5 %	97.5 %	R2
(Intercept)	0.4867037	0.5469789	0.8898034	-0.585	1.559	0.000
PD_whole_tree	0.1806947	0.1099387	1.6435955	-0.035	0.396	0.117
episodes2	0.0714286	0.1352703	0.5280432	-0.194	0.337	0.004
episodes3	0.1071429	0.1352703	0.7920648	-0.158	0.372	0.009

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

	Estimate	Std. Error	t value	2.5 %	97.5 %	R2
(Intercept)	1.3865860	0.5501706	2.5202839	0.308	2.465	0.000
shannon	-0.0108180	0.1953424	-0.0553796	-0.394	0.372	0.000
episodes2	0.0714286	0.1352703	0.5280432	-0.194	0.337	0.004
episodes3	0.1071429	0.1352703	0.7920648	-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	2.5 %	97.5 %	R2
(Intercept)	1.3505494	0.1356560	9.9556922	1.085	1.616	0.000
wunifrac.PC.1	0.7142536	0.3838906	1.8605654	-0.038	1.467	0.142
episodes2	0.0714286	0.1352703	0.5280432	-0.194	0.337	0.004
episodes3	0.1071429	0.1352703	0.7920648	-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	2.5 %	97.5 %	R2
(Intercept)	1.3586203	0.1415333	9.5992971	1.081	1.636	0.000
wunifrac.PC.2	0.2073472	0.8524837	0.2432271	-1.463	1.878	0.003
episodes2	0.0714286	0.1352703	0.5280432	-0.194	0.337	0.004
episodes3	0.1071429	0.1352703	0.7920648	-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	2.5 %	97.5 %	R2
(Intercept)	1.3559568	0.1416333	9.5737170	1.078	1.634	0.000
wunifrac.PC.3	0.1629746	0.9614696	0.1695057	-1.721	2.047	0.002
episodes2	0.0714286	0.1352703	0.5280432	-0.194	0.337	0.004
episodes3	0.1071429	0.1352703	0.7920648	-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	2.5 %	97.5 %	R2
(Intercept)	1.3531794	0.1367836	9.8928454	1.085	1.621	0.000
wunifrac.PC.4	-1.9656273	1.1901437	-1.6515881	-4.298	0.367	0.118
episodes2	0.0714286	0.1352703	0.5280432	-0.194	0.337	0.004
episodes3	0.1071429	0.1352703	0.7920648	-0.158	0.372	0.009

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

	Estimate	Std. Error	t value	2.5 %	97.5 %	R2
(Intercept)	1.0676301	0.5089944	2.097528	0.070	2.065	0.000
chao1	0.0011781	0.0017989	0.654902	-0.002	0.005	0.035
episodes2	0.0476190	0.1562505	0.304761	-0.259	0.354	0.002
episodes3	0.1904762	0.1562505	1.219044	-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	2.5 %	97.5 %	R2
(Intercept)	0.9697042	0.5402721	1.794844	-0.089	2.029	0.000
observed_otus	0.0025954	0.0032301	0.803511	-0.004	0.009	0.051
episodes2	0.0476190	0.1562505	0.304761	-0.259	0.354	0.002
episodes3	0.1904762	0.1562505	1.219044	-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	2.5 %	97.5 %	R2
(Intercept)	0.5799314	0.7711660	0.7520189	-0.932	2.091	0.000
PD_whole_tree	0.0795239	0.0746428	1.0653923	-0.067	0.226	0.085
episodes2	0.0476190	0.1562505	0.3047610	-0.259	0.354	0.002
episodes3	0.1904762	0.1562505	1.2190439	-0.116	0.497	0.028

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

	Estimate	Std. Error	t value	2.5 %	97.5 %	R2
(Intercept)	0.7902569	0.8800134	0.8980055	-0.935	2.515	0.000
shannon	0.1369971	0.2000863	0.6846899	-0.255	0.529	0.038
episodes2	0.0476190	0.1562505	0.3047610	-0.259	0.354	0.002
episodes3	0.1904762	0.1562505	1.2190439	-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	2.5 %	97.5 %	R2
(Intercept)	1.3809524	0.1748738	7.8968529	1.038	1.724	0.000
wunifrac.PC.1	-0.1161617	0.3984997	-0.2914975	-0.897	0.665	0.007
episodes2	0.0476190	0.1562505	0.3047610	-0.259	0.354	0.002
episodes3	0.1904762	0.1562505	1.2190439	-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	2.5 %	97.5 %	R2
(Intercept)	1.3809524	0.1742054	7.9271484	1.040	1.722	0.000
wunifrac.PC.2	-0.4954845	0.9273999	-0.5342727	-2.313	1.322	0.024
episodes2	0.0476190	0.1562505	0.3047610	-0.259	0.354	0.002
episodes3	0.1904762	0.1562505	1.2190439	-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	2.5 %	97.5 %	R2
(Intercept)	1.3809524	0.1702184	8.112825	1.047	1.715	0.000
wunifrac.PC.3	-1.6640483	1.3338193	-1.247581	-4.278	0.950	0.111
episodes2	0.0476190	0.1562505	0.304761	-0.259	0.354	0.002
episodes3	0.1904762	0.1562505	1.219044	-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	2.5 %	97.5 %	R2
(Intercept)	1.3809524	0.1684215	8.199385	1.051	1.711	0.000
wunifrac.PC.4	-2.2790695	1.5453973	-1.474747	-5.308	0.750	0.144
episodes2	0.0476190	0.1562505	0.304761	-0.259	0.354	0.002
episodes3	0.1904762	0.1562505	1.219044	-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	0.09	0.095	0.951	0.349	-0.104	0.284	0.00
L1.Cellular.Processes	0.00	0.000	-1.133	0.266	0.000	0.000	0.04

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	-0.02	0.083	-0.246	0.807	-0.189	0.149	0.000
L1.Environmental.Information.Processing	0.00	0.000	0.319	0.752	0.000	0.000	0.003

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	-0.026	0.113	-0.232	0.818	-0.257	0.205	0.000
L1.Genetic.Information.Processing	0.000	0.000	0.261	0.795	0.000	0.000	0.002

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	0.013	0.092	0.138	0.891	-0.174	0.2	0.000
L1.Human.Diseases	0.000	0.000	-0.169	0.867	0.000	0.0	0.001

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	0.038	0.1	0.378	0.708	-0.167	0.243	0.000
L1.Metabolism	0.000	0.0	-0.444	0.661	0.000	0.000	0.006

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	0.07	0.085	0.832	0.412	-0.102	0.243	0.000
L1.None	0.00	0.000	-1.052	0.301	0.000	0.000	0.034

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	0.148	0.108	1.366	0.182	-0.073	0.368	0.000
L1.Organismal.Systems	0.000	0.000	-1.547	0.132	0.000	0.000	0.072

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	0.042	0.091	0.462	0.648	-0.143	0.227	0.00
L1.Unclassified	0.000	0.000	-0.566	0.576	0.000	0.000	0.01

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	-0.004	0.046	-0.092	0.927	-0.097	0.089	0
L1.Cellular.Processes	0.000	0.000	0.110	0.913	0.000	0.000	0

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	0.017	0.039	0.443	0.661	-0.062	0.097	0.000
L1.Environmental.Information.Processing	0.000	0.000	-0.574	0.570	0.000	0.000	0.011

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	-0.011	0.053	-0.203	0.841	-0.12	0.098	0.000
L1.Genetic.Information.Processing	0.000	0.000	0.229	0.821	0.00	0.000	0.002

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	0.025	0.043	0.594	0.557	-0.062	0.113	0.000
L1.Human.Diseases	0.000	0.000	-0.725	0.474	0.000	0.000	0.017

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	0.019	0.047	0.399	0.693	-0.078	0.115	0.000
L1.Metabolism	0.000	0.000	-0.468	0.643	0.000	0.000	0.007

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	-0.011	0.04	-0.268	0.791	-0.094	0.072	0.000
L1.None	0.000	0.00	0.339	0.737	0.000	0.000	0.004

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	0.045	0.052	0.869	0.392	-0.061	0.152	0.00
L1.Organismal.Systems	0.000	0.000	-0.984	0.333	0.000	0.000	0.03

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	0.02	0.043	0.468	0.643	-0.067	0.107	0.00
L1.Unclassified	0.00	0.000	-0.573	0.571	0.000	0.000	0.01

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	-0.004	0.041	-0.097	0.923	-0.088	0.08	0
L1.Cellular.Processes	0.000	0.000	0.116	0.909	0.000	0.00	0

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	-0.033	0.034	-0.951	0.349	-0.103	0.037	0.000
L1.Environmental.Information.Processing	0.000	0.000	1.231	0.228	0.000	0.000	0.047

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	-0.074	0.046	-1.620	0.116	-0.167	0.019	0.000
L1.Genetic.Information.Processing	0.000	0.000	1.829	0.077	0.000	0.000	0.097

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	-0.052	0.037	-1.402	0.171	-0.128	0.024	0.000
L1.Human.Diseases	0.000	0.000	1.714	0.097	0.000	0.000	0.087

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	-0.064	0.04	-1.588	0.123	-0.147	0.018	0.000
L1.Metabolism	0.000	0.00	1.864	0.072	0.000	0.000	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	-0.035	0.036	-0.978	0.336	-0.108	0.038	0.000
L1.None	0.000	0.000	1.237	0.226	0.000	0.000	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	-0.07	0.045	-1.541	0.134	-0.162	0.023	0.000
L1.Organismal.Systems	0.00	0.000	1.745	0.091	0.000	0.000	0.089

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	-0.051	0.037	-1.385	0.176	-0.126	0.024	0.000
L1.Unclassified	0.000	0.000	1.698	0.100	0.000	0.000	0.085

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	-0.089	0.028	-3.186	0.003	-0.146	-0.032	0.000
L1.Cellular.Processes	0.000	0.000	3.796	0.001	0.000	0.000	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	-0.056	0.026	-2.158	0.039	-0.109	-0.003	0.000
L1.Environmental.Information.Processing	0.000	0.000	2.795	0.009	0.000	0.000	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	-0.086	0.036	-2.423	0.022	-0.159	-0.014	0.000
L1.Genetic.Information.Processing	0.000	0.000	2.736	0.010	0.000	0.000	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	-0.064	0.029	-2.245	0.032	-0.123	-0.006	0.000
L1.Human.Diseases	0.000	0.000	2.744	0.010	0.000	0.000	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	-0.072	0.032	-2.261	0.031	-0.137	-0.007	0.000
L1.Metabolism	0.000	0.000	2.654	0.013	0.000	0.000	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	-0.081	0.024	-3.394	0.002	-0.129	-0.032	0.000
L1.None	0.000	0.000	4.290	0.000	0.000	0.000	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	-0.077	0.036	-2.141	0.041	-0.15	-0.004	0.000
L1.Organismal.Systems	0.000	0.000	2.424	0.022	0.00	0.000	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	-0.069	0.028	-2.490	0.019	-0.126	-0.012	0.000
L1.Unclassified	0.000	0.000	3.052	0.005	0.000	0.000	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	0.036	0.101	0.356	0.724	-0.171	0.243	0.000
L2.Amino.Acid.Metabolism	0.000	0.000	-0.416	0.680	0.000	0.000	0.006

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	0.133	0.1	1.336	0.192	-0.07	0.337	0.000
L2.Biosynthesis.of.Other.Secondary.Metabolites	0.000	0.0	-1.552	0.131	0.00	0.000	0.072

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	0.064	0.079	0.811	0.424	-0.098	0.226	0.000
L2.Cancers	0.000	0.000	-1.069	0.294	0.000	0.000	0.036

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	0.042	0.094	0.442	0.662	-0.151	0.234	0.000
L2.Carbohydrate.Metabolism	0.000	0.000	-0.532	0.599	0.000	0.000	0.009

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	-0.040	0.056	-0.716	0.480	-0.155	0.075	0.000
L2.Cardiovascular.Diseases	0.003	0.002	1.624	0.115	-0.001	0.006	0.078

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)	0	0.052	0	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	-0.074	0.13	-0.573	0.571	-0.339	0.19	0.000
L2.Cell.Growth.and.Death	0.000	0.00	0.626	0.536	0.000	0.00	0.012

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	0.062	0.079	0.775	0.444	-0.101	0.224	0.000
L2.Cell.Motility	0.000	0.000	-1.021	0.315	0.000	0.000	0.033

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	0.053	0.084	0.635	0.530	-0.119	0.225	0.000
L2.Cellular.Processes.and.Signaling	0.000	0.000	-0.808	0.425	0.000	0.000	0.021

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	0.015	0.056	0.258	0.798	-0.1	0.129	0.000
L2.Circulatory.System	0.000	0.000	-0.700	0.489	0.0	0.000	0.016

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	0.149	0.085	1.755	0.089	-0.024	0.321	0.00
L2.Digestive.System	0.000	0.000	-2.153	0.039	0.000	0.000	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	0.138	0.111	1.248	0.222	-0.088	0.364	0.00
L2.Endocrine.System	0.000	0.000	-1.407	0.170	0.000	0.000	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	0.043	0.104	0.414	0.682	-0.169	0.255	0.000
L2.Energy.Metabolism	0.000	0.000	-0.480	0.635	0.000	0.000	0.007

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	0.033	0.103	0.317	0.753	-0.178	0.243	0.000
L2.Environmental.Adaptation	0.000	0.000	-0.369	0.715	0.000	0.000	0.004

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	0.003	0.104	0.031	0.975	-0.209	0.215	0
L2.Enzyme.Families	0.000	0.000	-0.036	0.971	0.000	0.000	0

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	0.039	0.067	0.584	0.564	-0.098	0.176	0.000
L2.Excretory.System	0.000	0.000	-0.921	0.364	0.000	0.000	0.027

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	0.022	0.107	0.209	0.836	-0.196	0.24	0.000
L2.Folding..Sorting.and.Degradation	0.000	0.000	-0.240	0.812	0.000	0.00	0.002

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	-0.013	0.102	-0.127	0.900	-0.222	0.196	0.000
L2.Genetic.Information.Processing	0.000	0.000	0.148	0.883	0.000	0.000	0.001

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	0.098	0.1	0.983	0.333	-0.105	0.301	0.000
L2.Glycan.Biosynthesis.and.Metabolism	0.000	0.0	-1.149	0.260	0.000	0.000	0.041

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	0.183	0.082	2.245	0.032	0.017	0.35	0.000
L2.Immune.System	0.000	0.000	-2.746	0.010	0.000	0.00	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	-0.074	0.117	-0.638	0.528	-0.313	0.164	0.000
L2.Immune.System.Diseases	0.000	0.000	0.714	0.481	0.000	0.000	0.016

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	0.002	0.087	0.018	0.986	-0.175	0.178	0
L2.Infectious.Diseases	0.000	0.000	-0.023	0.982	0.000	0.000	0

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	0.037	0.097	0.383	0.705	-0.16	0.234	0.000
L2.Lipid.Metabolism	0.000	0.000	-0.456	0.652	0.00	0.000	0.007

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	-0.026	0.082	-0.316	0.754	-0.194	0.142	0.000
L2.Membrane.Transport	0.000	0.000	0.410	0.685	0.000	0.000	0.005

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	-0.004	0.119	-0.030	0.976	-0.247	0.24	0
L2.Metabolic.Diseases	0.000	0.000	0.034	0.973	0.000	0.00	0

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	0.052	0.085	0.616	0.543	-0.122	0.226	0.000
L2.Metabolism	0.000	0.000	-0.778	0.443	0.000	0.000	0.019

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	0.05	0.101	0.502	0.619	-0.155	0.256	0.000
L2.Metabolism.of.Cofactors.and.Vitamins	0.00	0.000	-0.588	0.561	0.000	0.000	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	0.032	0.094	0.344	0.733	-0.159	0.223	0.000
L2.Metabolism.of.Other.Amino.Acids	0.000	0.000	-0.415	0.681	0.000	0.000	0.006

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	0.05	0.103	0.491	0.627	-0.16	0.26	0.00
L2.Metabolism.of.Terpenoids.and.Polyketides	0.00	0.000	-0.570	0.573	0.00	0.00	0.01

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	0.146	0.109	1.344	0.189	-0.076	0.369	0.000
L2.Nervous.System	0.000	0.000	-1.518	0.139	0.000	0.000	0.069

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	0.023	0.082	0.284	0.778	-0.145	0.192	0.000
L2.Neurodegenerative.Diseases	0.000	0.000	-0.368	0.715	0.000	0.000	0.004

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	-0.049	0.117	-0.418	0.679	-0.288	0.19	0.000
L2.Nucleotide.Metabolism	0.000	0.000	0.468	0.643	0.000	0.00	0.007

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	0.04	0.094	0.429	0.671	-0.151	0.231	0.000
L2.Poorly.Characterized	0.00	0.000	-0.518	0.608	0.000	0.000	0.009

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	-0.04	0.12	-0.334	0.741	-0.284	0.204	0.000
L2.Replication.and.Repair	0.00	0.00	0.372	0.713	0.000	0.000	0.004

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)	0	0.052	0	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	0.028	0.08	0.347	0.731	-0.136	0.191	0.000
L2.Signal.Transduction	0.000	0.00	-0.460	0.649	0.000	0.000	0.007

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	-0.097	0.128	-0.756	0.455	-0.358	0.164	0.000
L2.Signaling.Molecules.and.Interaction	0.000	0.000	0.828	0.414	0.000	0.000	0.022

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	0.029	0.088	0.326	0.746	-0.152	0.209	0.000
L2.Transcription	0.000	0.000	-0.406	0.688	0.000	0.000	0.005

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	-0.095	0.118	-0.800	0.43	-0.337	0.147	0.000
L2.Translation	0.000	0.000	0.891	0.38	0.000	0.000	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	0.245	0.089	2.743	0.010	0.063	0.428	0.000
L2.Transport.and.Catabolism	0.000	0.000	-3.188	0.003	0.000	0.000	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	0.008	0.083	0.093	0.927	-0.162	0.177	0
L2.Xenobiotics.Biodegradation.and.Metabolism	0.000	0.000	-0.120	0.906	0.000	0.000	0

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	0.014	0.048	0.283	0.779	-0.084	0.111	0.000
L2.Amino.Acid.Metabolism	0.000	0.000	-0.331	0.743	0.000	0.000	0.004

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	0.041	0.048	0.858	0.398	-0.057	0.139	0.000
L2.Biosynthesis.of.Other.Secondary.Metabolites	0.000	0.000	-0.996	0.327	0.000	0.000	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	-0.001	0.038	-0.031	0.975	-0.079	0.077	0
L2.Cancers	0.000	0.000	0.041	0.967	0.000	0.000	0

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	0.027	0.044	0.614	0.544	-0.063	0.117	0.000
L2.Carbohydrate.Metabolism	0.000	0.000	-0.740	0.465	0.000	0.000	0.017

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	0.001	0.028	0.045	0.964	-0.055	0.058	0
L2.Cardiovascular.Diseases	0.000	0.001	-0.102	0.920	-0.002	0.002	0

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)	0	0.024	0	1	-0.05	0.05	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	-0.05	0.061	-0.819	0.419	-0.174	0.074	0.000
L2.Cell.Growth.and.Death	0.00	0.000	0.895	0.378	0.000	0.000	0.025

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	-0.007	0.038	-0.183	0.856	-0.085	0.071	0.000
L2.Cell.Motility	0.000	0.000	0.241	0.811	0.000	0.000	0.002

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	0.025	0.04	0.619	0.541	-0.057	0.106	0.00
L2.Cellular.Processes.and.Signaling	0.000	0.00	-0.788	0.437	0.000	0.000	0.02

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	0.012	0.026	0.459	0.650	-0.041	0.065	0.000
L2.Circulatory.System	0.000	0.000	-1.243	0.224	0.000	0.000	0.047

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	0.065	0.04	1.604	0.119	-0.018	0.147	0.000
L2.Digestive.System	0.000	0.00	-1.967	0.058	0.000	0.000	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	0.082	0.051	1.615	0.117	-0.022	0.187	0.000
L2.Endocrine.System	0.000	0.000	-1.820	0.079	0.000	0.000	0.097

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	0.016	0.049	0.336	0.739	-0.084	0.117	0.000
L2.Energy.Metabolism	0.000	0.000	-0.390	0.700	0.000	0.000	0.005

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	-0.019	0.048	-0.395	0.696	-0.118	0.08	0.000
L2.Environmental.Adaptation	0.000	0.000	0.459	0.650	0.000	0.00	0.007

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	0.012	0.049	0.247	0.807	-0.088	0.112	0.000
L2.Enzyme.Families	0.000	0.000	-0.286	0.777	0.000	0.000	0.003

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	0.015	0.032	0.465	0.645	-0.05	0.08	0.000
L2.Excretory.System	0.000	0.000	-0.734	0.469	0.00	0.00	0.017

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	0.015	0.05	0.297	0.769	-0.088	0.117	0.000
L2.Folding..Sorting.and.Degradation	0.000	0.00	-0.341	0.735	0.000	0.000	0.004

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	0.006	0.048	0.128	0.899	-0.092	0.105	0.000
L2.Genetic.Information.Processing	0.000	0.000	-0.149	0.883	0.000	0.000	0.001

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	0.024	0.048	0.507	0.616	-0.073	0.122	0.000
L2.Glycan.Biosynthesis.and.Metabolism	0.000	0.000	-0.592	0.558	0.000	0.000	0.011

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	-0.004	0.043	-0.087	0.932	-0.092	0.084	0
L2.Immune.System	0.000	0.000	0.106	0.916	0.000	0.000	0

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	0.002	0.055	0.044	0.965	-0.111	0.116	0
L2.Immune.System.Diseases	0.000	0.000	-0.049	0.961	0.000	0.000	0

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	0.03	0.04	0.739	0.465	-0.052	0.112	0.000
L2.Infectious.Diseases	0.00	0.00	-0.932	0.359	0.000	0.000	0.027

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	0.027	0.045	0.601	0.552	-0.065	0.12	0.000
L2.Lipid.Metabolism	0.000	0.000	-0.716	0.480	0.000	0.00	0.016

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	0.015	0.039	0.400	0.692	-0.064	0.094	0.000
L2.Membrane.Transport	0.000	0.000	-0.519	0.607	0.000	0.000	0.009

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	-0.01	0.056	-0.171	0.865	-0.124	0.105	0.000
L2.Metabolic.Diseases	0.00	0.000	0.191	0.850	0.000	0.000	0.001

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	0.024	0.04	0.598	0.554	-0.058	0.106	0.000
L2.Metabolism	0.000	0.00	-0.756	0.455	0.000	0.000	0.018

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	0.003	0.048	0.054	0.957	-0.095	0.1	0
L2.Metabolism.of.Cofactors.and.Vitamins	0.000	0.000	-0.063	0.950	0.000	0.0	0

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	0.024	0.044	0.540	0.593	-0.066	0.113	0.000
L2.Metabolism.of.Other.Amino.Acids	0.000	0.000	-0.652	0.519	0.000	0.000	0.014

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	0.017	0.049	0.345	0.732	-0.082	0.116	0.000
L2.Metabolism.of.Terpenoids.and.Polyketides	0.000	0.000	-0.401	0.691	0.000	0.000	0.005

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	0.038	0.053	0.729	0.472	-0.069	0.146	0.000
L2.Nervous.System	0.000	0.000	-0.824	0.417	0.000	0.000	0.021

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	0.031	0.038	0.809	0.425	-0.047	0.109	0.000
L2.Neurodegenerative.Diseases	0.000	0.000	-1.049	0.302	0.000	0.000	0.034

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	-0.019	0.055	-0.349	0.730	-0.132	0.093	0.000
L2.Nucleotide.Metabolism	0.000	0.000	0.390	0.699	0.000	0.000	0.005

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	0.016	0.044	0.358	0.723	-0.074	0.106	0.000
L2.Poorly.Characterized	0.000	0.000	-0.433	0.668	0.000	0.000	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	-0.023	0.056	-0.410	0.684	-0.138	0.092	0.000
L2.Replication.and.Repair	0.000	0.000	0.457	0.651	0.000	0.000	0.007

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)	0	0.024	0	1	-0.05	0.05	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	0.029	0.037	0.779	0.442	-0.047	0.105	0.000
L2.Signal.Transduction	0.000	0.000	-1.032	0.310	0.000	0.000	0.033

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	-0.002	0.061	-0.040	0.968	-0.127	0.122	0
L2.Signaling.Molecules.and.Interaction	0.000	0.000	0.044	0.965	0.000	0.000	0

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	0.018	0.042	0.439	0.664	-0.067	0.103	0.00
L2.Transcription	0.000	0.000	-0.546	0.589	0.000	0.000	0.01

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	-0.04	0.056	-0.715	0.480	-0.154	0.074	0.00
L2.Translation	0.00	0.000	0.796	0.432	0.000	0.000	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	0.078	0.046	1.709	0.098	-0.015	0.172	0.000
L2.Transport.and.Catabolism	0.000	0.000	-1.987	0.056	0.000	0.000	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	0.029	0.039	0.759	0.454	-0.05	0.108	0.00
L2.Xenobiotics.Biodegradation.and.Metabolism	0.000	0.000	-0.981	0.335	0.00	0.000	0.03

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	-0.069	0.04	-1.71	0.098	-0.152	0.013	0.000
L2.Amino.Acid.Metabolism	0.000	0.00	2.00	0.055	0.000	0.000	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	-0.078	0.041	-1.911	0.066	-0.161	0.005	0.000
L2.Biosynthesis.of.Other.Secondary.Metabolites	0.000	0.000	2.219	0.034	0.000	0.000	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	-0.051	0.032	-1.582	0.124	-0.116	0.015	0.000
L2.Cancers	0.000	0.000	2.086	0.046	0.000	0.000	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	-0.053	0.038	-1.37	0.181	-0.131	0.026	0.000
L2.Carbohydrate.Metabolism	0.000	0.000	1.65	0.109	0.000	0.000	0.081

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	0.002	0.025	0.072	0.943	-0.049	0.053	0.000
L2.Cardiovascular.Diseases	0.000	0.001	-0.163	0.871	-0.002	0.001	0.001

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)	0	0.022	0	1	-0.045	0.045	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	-0.097	0.052	-1.873	0.071	-0.203	0.009	0.000
L2.Cell.Growth.and.Death	0.000	0.000	2.047	0.050	0.000	0.000	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	0.012	0.034	0.348	0.73	-0.058	0.082	0.000
L2.Cell.Motility	0.000	0.000	-0.459	0.65	0.000	0.000	0.007

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	-0.044	0.035	-1.267	0.215	-0.115	0.027	0.000
L2.Cellular.Processes.and.Signaling	0.000	0.000	1.612	0.117	0.000	0.000	0.077

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	-0.009	0.024	-0.365	0.717	-0.057	0.04	0.000
L2.Circulatory.System	0.000	0.000	0.990	0.330	0.000	0.00	0.031

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	-0.044	0.037	-1.183	0.246	-0.12	0.032	0.000
L2.Digestive.System	0.000	0.000	1.451	0.157	0.00	0.000	0.064

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	-0.071	0.046	-1.545	0.133	-0.166	0.023	0.000
L2.Endocrine.System	0.000	0.000	1.741	0.092	0.000	0.000	0.089

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	-0.064	0.042	-1.517	0.140	-0.15	0.022	0.000
L2.Energy.Metabolism	0.000	0.000	1.758	0.089	0.00	0.000	0.091

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	-0.03	0.043	-0.699	0.490	-0.119	0.058	0.000
L2.Environmental.Adaptation	0.00	0.000	0.813	0.423	0.000	0.000	0.021

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	-0.055	0.042	-1.291	0.206	-0.141	0.032	0.000
L2.Enzyme.Families	0.000	0.000	1.499	0.144	0.000	0.000	0.068

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	-0.033	0.027	-1.203	0.238	-0.089	0.023	0.000
L2.Excretory.System	0.000	0.000	1.898	0.067	0.000	0.000	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	-0.069	0.043	-1.618	0.116	-0.157	0.018	0.0
L2.Folding..Sorting.and.Degradation	0.000	0.000	1.860	0.073	0.000	0.000	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	-0.064	0.041	-1.559	0.129	-0.148	0.02	0.000
L2.Genetic.Information.Processing	0.000	0.000	1.819	0.079	0.000	0.00	0.096

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	-0.092	0.038	-2.395	0.023	-0.17	-0.014	0.000
L2.Glycan.Biosynthesis.and.Metabolism	0.000	0.000	2.799	0.009	0.00	0.000	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	-0.033	0.038	-0.854	0.400	-0.11	0.045	0.000
L2.Immune.System	0.000	0.000	1.045	0.304	0.00	0.000	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	-0.041	0.049	-0.827	0.415	-0.141	0.06	0.000
L2.Immune.System.Diseases	0.000	0.000	0.925	0.362	0.000	0.00	0.027

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	-0.044	0.035	-1.256	0.219	-0.116	0.028	0.000
L2.Infectious.Diseases	0.000	0.000	1.583	0.124	0.000	0.000	0.075

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	-0.055	0.039	-1.390	0.175	-0.135	0.026	0.000
L2.Lipid.Metabolism	0.000	0.000	1.655	0.108	0.000	0.000	0.081

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	-0.033	0.034	-0.969	0.341	-0.103	0.037	0.000
L2.Membrane.Transport	0.000	0.000	1.259	0.218	0.000	0.000	0.049

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	-0.093	0.047	-1.994	0.055	-0.189	0.002	0.000
L2.Metabolic.Diseases	0.000	0.000	2.223	0.034	0.000	0.000	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	-0.04	0.035	-1.130	0.268	-0.112	0.032	0.000
L2.Metabolism	0.00	0.000	1.428	0.164	0.000	0.000	0.062

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	-0.07	0.04	-1.753	0.090	-0.152	0.012	0.00
L2.Metabolism.of.Cofactors.and.Vitamins	0.00	0.00	2.052	0.049	0.000	0.000	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	-0.061	0.037	-1.633	0.113	-0.137	0.015	0.000
L2.Metabolism.of.Other.Amino.Acids	0.000	0.000	1.973	0.058	0.000	0.000	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	-0.065	0.042	-1.571	0.127	-0.15	0.02	0.000
L2.Metabolism.of.Terpenoids.and.Polyketides	0.000	0.000	1.825	0.078	0.00	0.00	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	-0.091	0.044	-2.065	0.048	-0.181	-0.001	0.000
L2.Nervous.System	0.000	0.000	2.334	0.027	0.000	0.000	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	-0.039	0.034	-1.154	0.257	-0.108	0.03	0.000
L2.Neurodegenerative.Diseases	0.000	0.000	1.498	0.145	0.000	0.00	0.068

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	-0.08	0.047	-1.710	0.098	-0.176	0.016	0.000
L2.Nucleotide.Metabolism	0.00	0.000	1.913	0.065	0.000	0.000	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	-0.058	0.038	-1.547	0.132	-0.135	0.019	0.000
L2.Poorly.Characterized	0.000	0.000	1.868	0.072	0.000	0.000	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	-0.083	0.048	-1.737	0.093	-0.181	0.015	0.000
L2.Replication.and.Repair	0.000	0.000	1.933	0.063	0.000	0.000	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)	0	0.022	0	1	-0.045	0.045	0
	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	-0.023	0.034	-0.688	0.497	-0.092	0.046	0.000
L2.Signal.Transduction	0.000	0.000	0.910	0.370	0.000	0.000	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	-0.084	0.052	-1.605	0.119	-0.19	0.023	0.000
L2.Signaling.Molecules.and.Interaction	0.000	0.000	1.757	0.089	0.00	0.000	0.091

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	-0.036	0.037	-0.994	0.328	-0.111	0.038	0.000
L2.Transcription	0.000	0.000	1.235	0.226	0.000	0.000	0.047

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	-0.085	0.048	-1.787	0.084	-0.183	0.012	0.000
L2.Translation	0.000	0.000	1.988	0.056	0.000	0.000	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	-0.07	0.041	-1.686	0.102	-0.154	0.015	0.00
L2.Transport.and.Catabolism	0.00	0.000	1.959	0.059	0.000	0.000	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	-0.035	0.034	-1.021	0.315	-0.105	0.035	0.000
L2.Xenobiotics.Biodegradation.and.Metabolism	0.000	0.000	1.319	0.197	0.000	0.000	0.053

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	-0.075	0.032	-2.344	0.026	-0.139	-0.01	0.000
L2.Amino.Acid.Metabolism	0.000	0.000	2.741	0.010	0.000	0.00	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	-0.058	0.034	-1.697	0.100	-0.128	0.012	0.000
L2.Biosynthesis.of.Other.Secondary.Metabolites	0.000	0.000	1.970	0.058	0.000	0.000	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	-0.072	0.022	-3.228	0.003	-0.118	-0.027	0.000
L2.Cancers	0.000	0.000	4.255	0.000	0.000	0.000	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	-0.064	0.03	-2.129	0.042	-0.125	-0.003	0.000
L2.Carbohydrate.Metabolism	0.000	0.00	2.564	0.016	0.000	0.000	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	-0.006	0.020	-0.289	0.775	-0.048	0.036	0.000
L2.Cardiovascular.Diseases	0.000	0.001	0.655	0.517	-0.001	0.002	0.014

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)	0	0.018	0	1	-0.037	0.037	0
	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	-0.088	0.042	-2.091	0.045	-0.174	-0.002	0.000
L2.Cell.Growth.and.Death	0.000	0.000	2.285	0.030	0.000	0.000	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	-0.069	0.023	-3.027	0.005	-0.116	-0.023	0.000
L2.Cell.Motility	0.000	0.000	3.990	0.000	0.000	0.000	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	-0.065	0.026	-2.514	0.018	-0.117	-0.012	0.000
L2.Cellular.Processes.and.Signaling	0.000	0.000	3.200	0.003	0.000	0.000	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	-0.013	0.019	-0.665	0.511	-0.051	0.026	0.000
L2.Circulatory.System	0.000	0.000	1.802	0.082	0.000	0.000	0.095

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	0.003	0.032	0.086	0.932	-0.062	0.068	0
L2.Digestive.System	0.000	0.000	-0.105	0.917	0.000	0.000	0

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	-0.036	0.039	-0.919	0.366	-0.116	0.044	0.000
L2.Endocrine.System	0.000	0.000	1.035	0.309	0.000	0.000	0.033

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	-0.08	0.032	-2.479	0.019	-0.146	-0.014	0.00
L2.Energy.Metabolism	0.00	0.000	2.872	0.007	0.000	0.000	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	-0.103	0.029	-3.593	0.001	-0.162	-0.045	0.00
L2.Environmental.Adaptation	0.000	0.000	4.177	0.000	0.000	0.000	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	-0.078	0.032	-2.400	0.023	-0.144	-0.012	0.0
L2.Enzyme.Families	0.000	0.000	2.786	0.009	0.000	0.000	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	-0.032	0.022	-1.475	0.151	-0.077	0.012	0.000
L2.Excretory.System	0.000	0.000	2.327	0.027	0.000	0.000	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	-0.078	0.034	-2.319	0.027	-0.147	-0.009	0.000
L2.Folding..Sorting.and.Degradation	0.000	0.000	2.665	0.012	0.000	0.000	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	-0.08	0.032	-2.538	0.017	-0.144	-0.016	0.00
L2.Genetic.Information.Processing	0.00	0.000	2.961	0.006	0.000	0.000	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	-0.05	0.034	-1.486	0.148	-0.12	0.019	0.000
L2.Glycan.Biosynthesis.and.Metabolism	0.00	0.000	1.736	0.093	0.00	0.000	0.089

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	-0.092	0.025	-3.738	0.001	-0.142	-0.042	0.000
L2.Immune.System	0.000	0.000	4.573	0.000	0.000	0.000	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	-0.077	0.038	-2.011	0.053	-0.155	0.001	0.00
L2.Immune.System.Diseases	0.000	0.000	2.249	0.032	0.000	0.000	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	-0.051	0.028	-1.814	0.080	-0.108	0.006	0.000
L2.Infectious.Diseases	0.000	0.000	2.286	0.029	0.000	0.000	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	-0.068	0.031	-2.237	0.033	-0.131	-0.006	0.000
L2.Lipid.Metabolism	0.000	0.000	2.664	0.012	0.000	0.000	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	-0.054	0.026	-2.096	0.045	-0.107	-0.001	0.000
L2.Membrane.Transport	0.000	0.000	2.725	0.011	0.000	0.000	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	-0.087	0.038	-2.288	0.029	-0.164	-0.009	0.000
L2.Metabolic.Diseases	0.000	0.000	2.550	0.016	0.000	0.000	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	-0.06	0.027	-2.254	0.032	-0.115	-0.006	0.000
L2.Metabolism	0.00	0.000	2.849	0.008	0.000	0.000	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	-0.076	0.032	-2.410	0.022	-0.14	-0.012	0.000
L2.Metabolism.of.Cofactors.and.Vitamins	0.000	0.000	2.822	0.008	0.00	0.000	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	-0.062	0.03	-2.089	0.045	-0.123	-0.001	0.000
L2.Metabolism.of.Other.Amino.Acids	0.000	0.00	2.525	0.017	0.000	0.000	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	-0.072	0.033	-2.200	0.036	-0.139	-0.005	0.000
L2.Metabolism.of.Terpenoids.and.Polyketides	0.000	0.000	2.556	0.016	0.000	0.000	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	-0.073	0.037	-1.997	0.055	-0.148	0.002	0.000
L2.Nervous.System	0.000	0.000	2.256	0.031	0.000	0.000	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	-0.057	0.026	-2.243	0.032	-0.11	-0.005	0.000
L2.Neurodegenerative.Diseases	0.000	0.000	2.910	0.007	0.00	0.000	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	-0.078	0.038	-2.073	0.047	-0.156	-0.001	0.000
L2.Nucleotide.Metabolism	0.000	0.000	2.319	0.027	0.000	0.000	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	-0.072	0.029	-2.486	0.019	-0.131	-0.013	0.000
L2.Poorly.Characterized	0.000	0.000	3.001	0.005	0.000	0.000	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	-0.091	0.038	-2.414	0.022	-0.168	-0.014	0.000
L2.Replication.and.Repair	0.000	0.000	2.687	0.012	0.000	0.000	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)	0	0.018	0	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	-0.06	0.024	-2.484	0.019	-0.109	-0.011	0.000
L2.Signal.Transduction	0.00	0.000	3.288	0.003	0.000	0.000	0.259

Table 551: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Signaling.Molecules.and.Interaction, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.062	0.044	-1.419	0.166	-0.151	0.027	0.000
L2.Signaling.Molecules.and.Interaction	0.000	0.000	1.553	0.131	0.000	0.000	0.072

Table 552: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Transcription, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.065	0.027	-2.402	0.023	-0.121	-0.01	0.000
L2.Transcription	0.000	0.000	2.986	0.006	0.000	0.00	0.223

Table 553: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Translation, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.082	0.039	-2.122	0.042	-0.161	-0.003	0.000
L2.Translation	0.000	0.000	2.362	0.025	0.000	0.000	0.153

Table 554: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Transport.and.Catabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.008	0.036	-0.231	0.819	-0.082	0.066	0.000
L2.Transport.and.Catabolism	0.000	0.000	0.268	0.790	0.000	0.000	0.002

Table 555: diversity_vs_picrust_L2_neo: wunifrac.PC.4 vs L2.Xenobiotics.Biodegradation.and.Metabolism, df=30

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
Intercept	-0.059	0.026	-2.300	0.029	-0.111	-0.007	0.000
L2.Xenobiotics.Biodegradation.and.Metabolism	0.000	0.000	2.971	0.006	0.000	0.000	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 %	9
Intercept	-0.013	0.052	-0.241	0.811	-0.119	
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	0.000	0.000	1.288	0.208	0.000	

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	-0.019	0.08	-0.239	0.813	-0.183	0.145	0.000
L3.ABC.transporters	0.000	0.00	0.316	0.754	0.000	0.000	0.003

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)	0	0.052	0	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	0.1	0.083	1.202	0.239	-0.07	0.27	0.000
L3.Adipocytokine.signaling.pathway	0.0	0.000	-1.516	0.140	0.00	0.00	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	-0.048	0.067	-0.714	0.481	-0.184	0.089	0.000
L3.African.trypanosomiasis	0.000	0.000	1.125	0.270	0.000	0.000	0.039

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	0.101	0.111	0.908	0.371	-0.126	0.328	0.000
L3.Alanine..aspartate.and.glutamate.metabolism	0.000	0.000	-1.026	0.313	0.000	0.000	0.033

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	-0.011	0.052	-0.214	0.832	-0.118	0.095	0.000
L3.Aldosterone.regulated.sodium.reabsorption	0.358	0.295	1.211	0.235	-0.246	0.961	0.045

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	-0.022	0.096	-0.225	0.823	-0.217	0.174	0.000
L3.Alzheimer.s.disease	0.000	0.000	0.269	0.790	0.000	0.000	0.002

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	0.042	0.078	0.534	0.597	-0.118	0.202	0.000
L3.Amino.acid.metabolism	0.000	0.000	-0.717	0.479	0.000	0.000	0.016

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	-0.013	0.114	-0.113	0.911	-0.246	0.221	0.000
L3.Amino.acid.related.enzymes	0.000	0.000	0.127	0.900	0.000	0.000	0.001

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	0.026	0.111	0.232	0.818	-0.201	0.252	0.000
L3.Amino.sugar.and.nucleotide.sugar.metabolism	0.000	0.000	-0.263	0.794	0.000	0.000	0.002

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	-0.145	0.118	-1.228	0.229	-0.385	0.096	0.000
L3.Aminoacyl.tRNA.biosynthesis	0.000	0.000	1.363	0.183	0.000	0.000	0.057

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	0.012	0.076	0.161	0.874	-0.143	0.167	0.000
L3.Aminobenzoate.degradation	0.000	0.000	-0.223	0.825	0.000	0.000	0.002

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	0.121	0.06	2.006	0.054	-0.002	0.244	0.000
L3.Amoebiasis	0.000	0.00	-3.093	0.004	0.000	0.000	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	0.02	0.062	0.329	0.744	-0.106	0.147	0.000
L3.Amyotrophic.lateral.sclerosis..ALS.	0.00	0.000	-0.611	0.545	0.000	0.000	0.012

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	0.172	0.08	2.142	0.040	0.008	0.336	0.000
L3.Antigen.processing.and.presentation	0.000	0.00	-2.655	0.013	0.000	0.000	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	-0.091	0.054	-1.666	0.106	-0.202	0.02	0.000
L3.Apoptosis	0.000	0.000	3.090	0.004	0.000	0.00	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	0.016	0.075	0.210	0.835	-0.137	0.169	0.000
L3.Arachidonic.acid.metabolism	0.000	0.000	-0.294	0.771	0.000	0.000	0.003

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	0.088	0.089	0.991	0.330	-0.093	0.269	0.000
L3.Arginine.and.proline.metabolism	0.000	0.000	-1.216	0.233	0.000	0.000	0.046

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)	0	0.052	0	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	0.025	0.066	0.388	0.701	-0.108	0.159	0.000
L3.Ascorbate.and.aldarate.metabolism	0.000	0.000	-0.645	0.524	0.000	0.000	0.013

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	0.01	0.058	0.169	0.867	-0.109	0.129	0.000
L3.Atrazine.degradation	0.00	0.000	-0.386	0.702	0.000	0.000	0.005

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	0.087	0.076	1.155	0.257	-0.067	0.242	0.000
L3.Bacterial.chemotaxis	0.000	0.000	-1.555	0.130	0.000	0.000	0.072

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	-0.007	0.056	-0.124	0.902	-0.121	0.107	0.000
L3.Bacterial.invasion.of.epithelial.cells	0.000	0.000	0.374	0.711	0.000	0.000	0.004

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	0.052	0.074	0.694	0.493	-0.1	0.203	0.000
L3.Bacterial.motility.proteins	0.000	0.000	-0.970	0.340	0.0	0.000	0.029

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	0.005	0.076	0.061	0.952	-0.151	0.161	0
L3.Bacterial.secretion.system	0.000	0.000	-0.084	0.934	0.000	0.000	0

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	-0.176	0.116	-1.524	0.138	-0.413	0.06	0.000
L3.Bacterial.toxins	0.000	0.000	1.692	0.101	0.000	0.00	0.085

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	0.016	0.056	0.289	0.775	-0.098	0.131	0.00
L3.Basal.transcription.factors	0.000	0.000	-0.789	0.437	0.000	0.000	0.02

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	-0.041	0.115	-0.359	0.722	-0.275	0.193	0.000
L3.Base.excision.repair	0.000	0.000	0.404	0.689	0.000	0.000	0.005

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	0.006	0.072	0.090	0.929	-0.14	0.153	0.000
L3.Benzoate.degradation	0.000	0.000	-0.133	0.895	0.00	0.000	0.001

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	0.014	0.055	0.260	0.796	-0.099	0.127	0.000
L3.Betalain.biosynthesis	0.000	0.000	-0.781	0.441	0.000	0.000	0.019

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	-0.009	0.059	-0.158	0.876	-0.129	0.110	0.000
L3.Bile.secretion	0.001	0.004	0.356	0.724	-0.006	0.009	0.004

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	0.019	0.062	0.314	0.755	-0.107	0.146
L3.Biosynthesis.and.biodegradation.of.secondary.metabolites	0.000	0.000	-0.592	0.558	0.000	0.000

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 %	0.
Intercept	-0.002	0.053	-0.029	0.977	-0.111	0.108	0.
L3.Biosynthesis.of.12. . . 14..and.16.membered.macrolides	0.049	0.302	0.163	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	0.033	0.075	0.442	0.662	-0.12	0.187	0.000
L3.Biosynthesis.of.ansamycins	0.000	0.000	-0.615	0.543	0.00	0.000	0.012

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	0.01	0.061	0.156	0.877	-0.115	0.134
L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides	0.00	0.000	-0.310	0.759	0.000	0.000

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)	0	0.052	0	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	0.014	0.056	0.260	0.796	-0.099	0.128	0.000
L3.Biosynthesis.of.type.II.polyketide.products	0.000	0.000	-0.758	0.455	0.000	0.000	0.018

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	0.009	0.071	0.120	0.905	-0.137	0.154	0.000
L3.Biosynthesis.of.unsaturated.fatty.acids	0.000	0.000	-0.178	0.860	0.000	0.000	0.001

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	0.225	0.106	2.120	0.042	0.008	0.441	0.000
L3.Biosynthesis.of.vancomycin.group.antibiotics	0.000	0.000	-2.382	0.024	0.000	0.000	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	0.121	0.089	1.349	0.187	-0.062	0.303	0.000
L3.Biotin.metabolism	0.000	0.000	-1.634	0.113	0.000	0.000	0.079

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	0.168	0.096	1.759	0.089	-0.027	0.364	0.00
L3.Bisphenol.degradation	0.000	0.000	-2.052	0.049	0.000	0.000	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	0.009	0.059	0.159	0.875	-0.111	0.13	0.000
L3.Bladder.cancer	0.000	0.000	-0.352	0.727	0.000	0.00	0.004

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	-0.017	0.084	-0.204	0.840	-0.189	0.155	0.000
L3.Butanoate.metabolism	0.000	0.000	0.261	0.796	0.000	0.000	0.002

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	0.185	0.131	1.416	0.167	-0.082	0.452	0.000
L3.Butirosin.and.neomycin.biosynthesis	0.000	0.000	-1.536	0.135	0.000	0.000	0.071

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	-0.04	0.101	-0.398	0.694	-0.246	0.166	0.000
L3.C5.Branched.dibasic.acid.metabolism	0.00	0.000	0.466	0.644	0.000	0.000	0.007

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)	0	0.052	0	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	0.055	-0.705	0.487	-0.152	0.074	0.000
L3.Caffeine.metabolism	0.048	0.028	1.693	0.101	-0.010	0.106	0.085

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	0.053	-1.305	0.202	-0.177	0.039	0.000
L3.Calcium.signaling.pathway	0.110	0.039	2.811	0.009	0.030	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	0	0.062	-0.007	0.994	-0.128	0.127	0
L3.Caprolactam.degradation	0	0.000	0.013	0.990	0.000	0.000	0

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	0.002	0.076	0.022	0.982	-0.153	0.156	0
L3.Carbohydrate.digestion.and.absorption	0.000	0.000	-0.031	0.975	0.000	0.000	0

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	0.067	0.086	0.778	0.442	-0.109	0.243	0.00
L3.Carbohydrate.metabolism	0.000	0.000	-0.974	0.338	0.000	0.000	0.03

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	0.049	0.094	0.521	0.606	-0.143	0.241	0.000
L3.Carbon.fixation.in.photosynthetic.organisms	0.000	0.000	-0.626	0.536	0.000	0.000	0.012

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	0.04	0.098	0.404	0.689	-0.161	0.24	0.000
L3.Carbon.fixation.pathways.in.prokaryotes	0.00	0.000	-0.478	0.636	0.000	0.00	0.007

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	0.015	0.056	0.258	0.798	-0.1	0.129	0.000
L3.Cardiac.muscle.contraction	0.000	0.000	-0.700	0.489	0.0	0.000	0.016

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	0.07	0.054	1.277	0.211	-0.042	0.181	0.000
L3.Carotenoid.biosynthesis	0.00	0.000	-2.617	0.014	0.000	0.000	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)	0	0.052	0	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	-0.04	0.129	-0.311	0.758	-0.304	0.223	0.000
L3.Cell.cycle. . . Caulobacter	0.00	0.000	0.341	0.735	0.000	0.000	0.004

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)	0	0.052	0	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	0.111	0.082	1.352	0.186	-0.057	0.28	0.000
L3.Cell.division	0.000	0.000	-1.707	0.098	0.000	0.00	0.086

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	0.02	0.087	0.226	0.823	-0.158	0.198	0.000
L3.Cell.motility.and.secretion	0.00	0.000	-0.283	0.779	0.000	0.000	0.003

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	0.108	0.08	1.350	0.187	-0.055	0.272	0.000
L3.Cellular.antigens	0.000	0.00	-1.733	0.093	0.000	0.000	0.088

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	-0.05	0.064	-0.781	0.441	-0.181	0.081	0.000
L3.Chagas.disease..American.trypanosomiasis.	0.00	0.000	1.300	0.204	0.000	0.000	0.052

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	0.036	0.101	0.357	0.723	-0.17	0.242	0.000
L3.Chaperones.and.folding.catalysts	0.000	0.000	-0.419	0.679	0.00	0.000	0.006

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	0.043	0.104	0.415	0.681	-0.169	0.255	0.000
L3.Chloroalkane.and.chloroalkene.degradation	0.000	0.000	-0.481	0.634	0.000	0.000	0.007

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 %	R2
Intercept	0.038	0.064	0.587	0.562	-0.094	0.17	0.00
L3.Chlorocyclohexane.and.chlorobenzene.degradation	0.000	0.000	-0.986	0.332	0.000	0.00	0.03

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)	0	0.052	0	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	-0.011	0.108	-0.100	0.921	-0.232	0.211	0
L3.Chromosome	0.000	0.000	0.114	0.910	0.000	0.000	0

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	0.011	0.057	0.189	0.851	-0.105	0.126	0.000
L3.Chronic.myeloid.leukemia	-0.043	0.086	-0.501	0.620	-0.218	0.132	0.008

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	-0.009	0.057	-0.165	0.870	-0.126	0.107	0.000
L3.Circadian.rhythm...plant	0.007	0.016	0.417	0.679	-0.026	0.039	0.006

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	0.045	0.081	0.556	0.583	-0.12	0.21	0.000
L3.Citrate.cycle..TCA.cycle.	0.000	0.000	-0.728	0.472	0.00	0.00	0.017

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)	0	0.052	0	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	-0.043	0.055	-0.770	0.447	-0.156	0.070	0.000
L3.Colorectal.cancer	0.004	0.002	1.801	0.082	0.000	0.008	0.095

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)	0	0.052	0	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	0.124	0.085	1.455	0.156	-0.05	0.297	0.000
L3.Cyanoamino.acid.metabolism	0.000	0.000	-1.801	0.082	0.00	0.000	0.095

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	-0.006	0.099	-0.065	0.949	-0.209	0.196	0
L3.Cysteine.and.methionine.metabolism	0.000	0.000	0.077	0.939	0.000	0.000	0

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	-0.001	0.053	-0.011	0.992	-0.11	0.109	0
L3.Cytochrome.P450	0.018	0.303	0.061	0.952	-0.60	0.636	0

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)	0	0.052	0	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)	0	0.052	0	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	0.046	0.112	0.410	0.685	-0.183	0.275	0.000
L3.Cytoskeleton.proteins	0.000	0.000	-0.464	0.646	0.000	0.000	0.007

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)	0	0.052	0	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	-0.152	0.105	-1.441	0.160	-0.367	0.063	0.00
L3.D.Alanine.metabolism	0.000	0.000	1.641	0.111	0.000	0.000	0.08

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	-0.025	0.057	-0.444	0.660	-0.142	0.091	0.000
L3.D.Arginine.and.D.ornithine.metabolism	0.000	0.000	1.039	0.307	0.000	0.000	0.034

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	-0.019	0.11	-0.173	0.864	-0.245	0.206	0.000
L3.D.Glutamine.and.D.glutamate.metabolism	0.000	0.00	0.197	0.845	0.000	0.000	0.001

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	-0.056	0.118	-0.477	0.637	-0.297	0.185	0.000
L3.DNA.repair.and.recombination.proteins	0.000	0.000	0.532	0.598	0.000	0.000	0.009

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	-0.05	0.127	-0.393	0.697	-0.31	0.21	0.000
L3.DNA.replication	0.00	0.000	0.431	0.670	0.00	0.00	0.006

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	-0.017	0.124	-0.141	0.889	-0.27	0.235	0.000
L3.DNA.replication.proteins	0.000	0.000	0.155	0.877	0.00	0.000	0.001

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)	0	0.052	0	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	-0.036	0.073	-0.497	0.623	-0.185	0.112	0.000
L3.Dioxin.degradation	0.000	0.000	0.715	0.480	0.000	0.000	0.016

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	0.001	0.068	0.013	0.990	-0.139	0.141	0
L3.Drug.metabolism...cytochrome.P450	0.000	0.000	-0.021	0.984	0.000	0.000	0

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	0.053	0.114	0.470	0.642	-0.179	0.286	0.000
L3.Drug.metabolism...other.enzymes	0.000	0.000	-0.529	0.600	0.000	0.000	0.009

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)	0	0.052	0	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	-0.019	0.067	-0.282	0.78	-0.155	0.117	0.000
L3.Electron.transfer.carriers	0.000	0.000	0.458	0.65	0.000	0.000	0.007

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)	0	0.052	0	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	-0.030	0.052	-0.577	0.568	-0.137	0.077	0.000
L3.Endocytosis	0.028	0.015	1.872	0.071	-0.003	0.059	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	0.1	0.085	1.171	0.251	-0.074	0.274	0.000
L3.Energy.metabolism	0.0	0.000	-1.461	0.155	0.000	0.000	0.064

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	0.061	0.094	0.646	0.523	-0.132	0.253	
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	0.000	0.000	-0.776	0.444	0.000	0.000	

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)	0	0.052	0	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	0.059	0.064	0.925	0.362	-0.071	0.189	0.00
L3.Ether.lipid.metabolism	0.000	0.000	-1.533	0.136	0.000	0.000	0.07

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	0.155	0.076	2.044	0.050	0	0.311	0.000
L3.Ethylbenzene.degradation	0.000	0.000	-2.619	0.014	0	0.000	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)	0	0.052	0	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	-0.012	0.108	-0.114	0.910	-0.233	0.208	0.000
L3.Fatty.acid.biosynthesis	0.000	0.000	0.131	0.897	0.000	0.000	0.001

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)	0	0.052	0	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	0.002	0.081	0.020	0.984	-0.163	0.166	0
L3.Fatty.acid.metabolism	0.000	0.000	-0.026	0.979	0.000	0.000	0

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)	0	0.052	0	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	-0.030	0.052	-0.577	0.568	-0.137	0.077	0.000
L3.Fc.gamma.R.mediated.phagocytosis	0.028	0.015	1.872	0.071	-0.003	0.059	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	0.018	0.066	0.274	0.786	-0.117	0.153	0.000
L3.Flagellar.assembly	0.000	0.000	-0.449	0.657	0.000	0.000	0.006

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	0.123	0.055	2.243	0.032	0.011	0.234	0.000
L3.Flavone.and.flavonol.biosynthesis	0.000	0.000	-3.716	0.001	0.000	0.000	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	0.005	0.054	0.097	0.923	-0.106	0.117	0.000
L3.Flavonoid.biosynthesis	0.000	0.000	-0.371	0.714	0.000	0.000	0.004

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	0.013	0.057	0.218	0.829	-0.105	0.13	0.000
L3.Fluorobenzoate.degradation	0.000	0.000	-0.539	0.594	0.000	0.00	0.009

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)	0	0.052	0	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	-0.021	0.11	-0.194	0.848	-0.245	0.203	0.000
L3.Folate.biosynthesis	0.000	0.00	0.221	0.827	0.000	0.000	0.002

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	0.06	0.09	0.667	0.510	-0.123	0.243	0.000
L3.Fructose.and.mannose.metabolism	0.00	0.00	-0.820	0.419	0.000	0.000	0.021

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	0.008	0.08	0.104	0.918	-0.156	0.173	0.000
L3.Function.unknown	0.000	0.00	-0.137	0.892	0.000	0.000	0.001

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)	0	0.052	0	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)	0	0.052	0	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	0.057	0.112	0.504	0.618	-0.173	0.286	0.00
L3.Galactose.metabolism	0.000	0.000	-0.570	0.573	0.000	0.000	0.01

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)	0	0.052	0	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	0.065	0.101	0.641	0.526	-0.141	0.27	0.000
L3.General.function.prediction.only	0.000	0.000	-0.750	0.459	0.000	0.00	0.018

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	0.022	0.065	0.346	0.732	-0.11	0.154	0.000
L3.Geraniol.degradation	0.000	0.000	-0.590	0.560	0.00	0.000	0.011

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	0.033	0.058	0.563	0.578	-0.086	0.151	0.000
L3.Germination	0.000	0.000	-1.209	0.236	0.000	0.000	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)	0	0.052	0	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	0.146	0.109	1.344	0.189	-0.076	0.369	0.000
L3.Glutamatergic.synapse	0.000	0.000	-1.518	0.139	0.000	0.000	0.069

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	0.014	0.083	0.173	0.863	-0.156	0.185	0.000
L3.Glutathione.metabolism	0.000	0.000	-0.224	0.825	0.000	0.000	0.002

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)	0	0.052	0	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	0.021	0.066	0.322	0.750	-0.114	0.156	0.000
L3.Glycan.biosynthesis.and.metabolism	0.000	0.000	-0.529	0.601	0.000	0.000	0.009

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	-0.017	0.092	-0.185	0.854	-0.204	0.17	0.000
L3.Glycerolipid.metabolism	0.000	0.000	0.226	0.822	0.000	0.00	0.002

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	0.029	0.092	0.309	0.76	-0.16	0.217	0.000
L3.Glycerophospholipid.metabolism	0.000	0.000	-0.376	0.71	0.00	0.000	0.005

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	0.039	0.098	0.397	0.694	-0.161	0.239	0.000
L3.Glycine..serine.and.threonine.metabolism	0.000	0.000	-0.471	0.641	0.000	0.000	0.007

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	-0.009	0.102	-0.090	0.929	-0.218	0.2	0
L3.Glycolysis. . . Gluconeogenesis	0.000	0.000	0.105	0.917	0.000	0.0	0

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 %	
Intercept	-0.014	0.053	-0.261	0.796	-0.122	0.094	0
L3.Glycosaminoglycan.biosynthesis. . . chondroitin.sulfate	0.055	0.049	1.138	0.264	-0.044	0.155	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	0.242	0.068	3.564	0.001	0.103	0.381	0.000
L3.Glycosaminoglycan.degradation	0.000	0.000	-4.459	0.000	0.000	0.000	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	0.209	0.069	3.039	0.005	0.068	0.349	0.000
L3.Glycosphingolipid.biosynthesis. . . ganglio.series	0.000	0.000	-3.893	0.001	0.000	0.000	0.328

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	0.208	0.079	2.630	0.013	0.047	0.37	0.00
L3.Glycosphingolipid.biosynthesis. . . globo.series	0.000	0.000	-3.212	0.003	0.000	0.00	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 %	97.5 %
Intercept	0.01	0.054	0.183	0.856	-0.1	0.119
L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series	0.00	0.000	-0.794	0.434	0.0	0.000

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)	0	0.052	0	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	0.001	0.098	0.010	0.992	-0.198	0.2	0
L3.Glycosyltransferases	0.000	0.000	-0.012	0.990	0.000	0.0	0

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	0.055	0.078	0.702	0.488	-0.105	0.215	0.000
L3.Glyoxylate.and.dicarboxylate.metabolism	0.000	0.000	-0.938	0.356	0.000	0.000	0.028

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	-0.030	0.052	-0.577	0.568	-0.137	0.077	0.000
L3.GnRH.signaling.pathway	0.028	0.015	1.872	0.071	-0.003	0.059	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)	0	0.052	0	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)	0	0.052	0	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)	0	0.052	0	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	0.142	0.109	1.296	0.205	-0.082	0.365	0.000
L3.Histidine.metabolism	0.000	0.000	-1.463	0.154	0.000	0.000	0.065

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	-0.062	0.123	-0.503	0.619	-0.314	0.19	0.00
L3.Homologous.recombination	0.000	0.000	0.555	0.583	0.000	0.00	0.01

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	0.055	0.092	0.600	0.553	-0.133	0.243	0.000
L3.Huntington.s.disease	0.000	0.000	-0.729	0.472	0.000	0.000	0.017

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	-0.008	0.055	-0.146	0.885	-0.119	0.103	0.000
L3.Hypertrophic.cardiomyopathy..HCM.	0.002	0.004	0.525	0.603	-0.006	0.010	0.009

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	-0.032	0.060	-0.531	0.599	-0.154	0.090	0.000
L3.Indole.alkaloid.biosynthesis	0.057	0.054	1.056	0.299	-0.053	0.166	0.035

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	-0.043	0.055	-0.770	0.447	-0.156	0.070	0.000
L3.Influenza.A	0.004	0.002	1.801	0.082	0.000	0.008	0.095

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	0.031	0.073	0.43	0.67	-0.117	0.18	0.000
L3.Inorganic.ion.transport.and.metabolism	0.000	0.000	-0.62	0.54	0.000	0.00	0.012

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	0.024	0.068	0.357	0.723	-0.115	0.164	0.00
L3.Inositol.phosphate.metabolism	0.000	0.000	-0.556	0.582	0.000	0.000	0.01

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	0.038	0.106	0.363	0.719	-0.178	0.255	0.000
L3.Insulin.signaling.pathway	0.000	0.000	-0.418	0.679	0.000	0.000	0.006

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	-0.097	0.09	-1.081	0.288	-0.28	0.086	0.000
L3.Ion.channels	0.000	0.00	1.317	0.198	0.00	0.000	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	-0.006	0.055	-0.107	0.916	-0.117	0.106	0.000
L3.Isoflavonoid.biosynthesis	0.003	0.008	0.391	0.699	-0.013	0.020	0.005

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	0.087	0.078	1.118	0.273	-0.072	0.245	0.000
L3.Isoquinoline.alkaloid.biosynthesis	0.000	0.000	-1.479	0.150	0.000	0.000	0.066

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)	0	0.052	0	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)	0	0.052	0	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	0.032	0.075	0.429	0.671	-0.121	0.186	0.000
L3.Limonene.and.pinene.degradation	0.000	0.000	-0.598	0.554	0.000	0.000	0.011

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	0.198	0.098	2.016	0.053	-0.003	0.399	0.000
L3.Linoleic.acid.metabolism	0.000	0.000	-2.318	0.027	0.000	0.000	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	0.025	0.103	0.245	0.808	-0.186	0.237	0.000
L3.Lipid.biosynthesis.proteins	0.000	0.000	-0.284	0.778	0.000	0.000	0.003

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	0.01	0.077	0.128	0.899	-0.147	0.166	0.000
L3.Lipid.metabolism	0.00	0.000	-0.176	0.861	0.000	0.000	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	0.13	0.086	1.516	0.140	-0.045	0.306	0.000
L3.Lipoic.acid.metabolism	0.00	0.000	-1.861	0.073	0.000	0.000	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	0.061	0.071	0.850	0.402	-0.085	0.207	0.000
L3.Lipopolysaccharide.biosynthesis	0.000	0.000	-1.223	0.231	0.000	0.000	0.046

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	0.058	0.076	0.772	0.446	-0.096	0.213	0.000
L3.Lipopolysaccharide.biosynthesis.proteins	0.000	0.000	-1.059	0.298	0.000	0.000	0.035

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)	0	0.052	0	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)	0	0.052	0	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	0.025	0.116	0.220	0.828	-0.211	0.262	0.000
L3.Lysine.biosynthesis	0.000	0.000	-0.246	0.807	0.000	0.000	0.002

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	0.036	0.072	0.500	0.621	-0.111	0.184	0.000
L3.Lysine.degradation	0.000	0.000	-0.723	0.475	0.000	0.000	0.017

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	0.273	0.063	4.324	0	0.144	0.401	0.000
L3.Lysosome	0.000	0.000	-5.383	0	0.000	0.000	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)	0	0.052	0	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	0.107	0.108	0.994	0.328	-0.113	0.328	0.00
L3.MAPK.signaling.pathway...yeast	0.000	0.000	-1.132	0.267	0.000	0.000	0.04

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)	0	0.052	0	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	-0.087	0.048	-1.834	0.077	-0.185	0.01	0.000
L3.Meiosis...yeast	0.000	0.000	4.026	0.000	0.000	0.00	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	0.014	0.055	0.260	0.797	-0.098	0.127	0.000
L3.Melanogenesis	0.000	0.000	-0.784	0.439	0.000	0.000	0.019

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	0.061	0.077	0.790	0.436	-0.096	0.218	0.000
L3.Membrane.and.intracellular.structural.molecules	0.000	0.000	-1.066	0.295	0.000	0.000	0.035

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	0.003	0.078	0.042	0.966	-0.155	0.162	0
L3.Metabolism.of.cofactors.and.vitamins	0.000	0.000	-0.058	0.954	0.000	0.000	0

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	-0.001	0.068	-0.010	0.992	-0.139	0.138	0
L3.Metabolism.of.xenobiotics.by.cytochrome.P450	0.000	0.000	0.017	0.987	0.000	0.000	0

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	0.045	0.107	0.425	0.674	-0.173	0.264	0.000
L3.Methane.metabolism	0.000	0.000	-0.488	0.629	0.000	0.000	0.008

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	-0.021	0.065	-0.326	0.747	-0.153	0.111	0.00
L3.Mineral.absorption	0.000	0.000	0.557	0.582	0.000	0.000	0.01

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	-0.019	0.125	-0.156	0.877	-0.274	0.235	0.000
L3.Mismatch.repair	0.000	0.000	0.172	0.864	0.000	0.000	0.001

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	0.123	0.062	1.969	0.058	-0.005	0.25	0.000
L3.N.Glycan.biosynthesis	0.000	0.000	-2.944	0.006	0.000	0.00	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	0.189	0.081	2.334	0.026	0.024	0.355	0.000
L3.NOD.like.receptor.signaling.pathway	0.000	0.000	-2.854	0.008	0.000	0.000	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	0.037	0.108	0.341	0.736	-0.183	0.256	0.000
L3.Naphthalene.degradation	0.000	0.000	-0.391	0.699	0.000	0.000	0.005

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)	0	0.052	0	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)	0	0.052	0	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	0.002	0.105	0.019	0.985	-0.212	0.216	0
L3.Nicotinate.and.nicotinamide.metabolism	0.000	0.000	-0.022	0.983	0.000	0.000	0

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	0.07	0.087	0.801	0.429	-0.108	0.248	0.000
L3.Nitrogen.metabolism	0.00	0.000	-0.995	0.328	0.000	0.000	0.031

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	-0.003	0.074	-0.040	0.969	-0.155	0.149	0
L3.Nitrotoluene.degradation	0.000	0.000	0.056	0.956	0.000	0.000	0

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	0.028	0.06	0.471	0.641	-0.094	0.15	0.000
L3.Non.homologous.end.joining	0.000	0.00	-0.959	0.345	0.000	0.00	0.029

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	0.011	0.057	0.189	0.851	-0.105	0.126	0.000
L3.Notch.signaling.pathway	-0.043	0.086	-0.501	0.620	-0.218	0.132	0.008

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	0.034	0.097	0.356	0.725	-0.163	0.232	0.000
L3.Novobiocin.biosynthesis	0.000	0.000	-0.423	0.675	0.000	0.000	0.006

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	-0.1	0.132	-0.755	0.456	-0.37	0.17	0.000
L3.Nucleotide.excision.repair	0.0	0.000	0.822	0.418	0.00	0.00	0.021

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	-0.022	0.069	-0.315	0.755	-0.164	0.12	0.000
L3.Nucleotide.metabolism	0.000	0.000	0.481	0.634	0.000	0.00	0.007

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)	0	0.052	0	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	-0.011	0.125	-0.089	0.930	-0.266	0.244	0
L3.One.carbon.pool.by.folate	0.000	0.000	0.098	0.923	0.000	0.000	0

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)	0	0.052	0	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	0.27	0.074	3.668	0.001	0.12	0.421	0.000
L3.Other.glycan.degradation	0.00	0.000	-4.414	0.000	0.00	0.000	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	0.039	0.083	0.476	0.637	-0.129	0.208	0.000
L3.Other.ion.coupled.transporters	0.000	0.000	-0.616	0.543	0.000	0.000	0.012

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	0.057	0.084	0.672	0.507	-0.116	0.229	0.000
L3.Other.transporters	0.000	0.000	-0.854	0.400	0.000	0.000	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)	0	0.052	0	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	0.036	0.096	0.374	0.711	-0.161	0.233	0.000
L3.Others	0.000	0.000	-0.446	0.659	0.000	0.000	0.006

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	0.037	0.106	0.349	0.730	-0.179	0.253	0.000
L3.Oxidative.phosphorylation	0.000	0.000	-0.402	0.691	0.000	0.000	0.005

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	0.097	0.111	0.873	0.390	-0.13	0.324	0.00
L3.PPAR.signaling.pathway	0.000	0.000	-0.987	0.332	0.00	0.000	0.03

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)	0	0.052	0	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)	0	0.052	0	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	0.011	0.109	0.105	0.917	-0.211	0.234	0
L3.Pantothenate.and.CoA.biosynthesis	0.000	0.000	-0.120	0.906	0.000	0.000	0

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	0.014	0.056	0.252	0.803	-0.101	0.129	0.000
L3.Parkinson.s.disease	0.000	0.000	-0.672	0.506	0.000	0.000	0.014

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	-0.025	0.053	-0.474	0.639	-0.133	0.083	0.000
L3.Pathogenic.Escherichia.coli.infection	0.018	0.011	1.603	0.119	-0.005	0.041	0.077

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	0.067	0.082	0.814	0.422	-0.101	0.235	0.000
L3.Pathways.in.cancer	0.000	0.000	-1.045	0.304	0.000	0.000	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	-0.07	0.083	-0.84	0.408	-0.241	0.1	0.000
L3.Penicillin.and.cephalosporin.biosynthesis	0.00	0.000	1.07	0.293	0.000	0.0	0.036

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	0.092	0.072	1.281	0.210	-0.055	0.24	0.000
L3.Pentose.and.glucuronate.interconversions	0.000	0.000	-1.780	0.085	0.000	0.00	0.093

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	0.052	0.097	0.533	0.598	-0.146	0.25	0.000
L3.Pentose.phosphate.pathway	0.000	0.000	-0.633	0.531	0.000	0.00	0.013

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	0.009	0.108	0.087	0.931	-0.212	0.231	0
L3.Peptidases	0.000	0.000	-0.099	0.922	0.000	0.000	0

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	-0.106	0.117	-0.909	0.370	-0.345	0.132	0.000
L3.Peptidoglycan.biosynthesis	0.000	0.000	1.015	0.318	0.000	0.000	0.032

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	0.115	0.099	1.170	0.251	-0.086	0.317	0.000
L3.Peroxisome	0.000	0.000	-1.368	0.182	0.000	0.000	0.057

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	0.025	0.06	0.413	0.682	-0.097	0.146	0.000
L3.Pertussis	0.000	0.00	-0.845	0.405	0.000	0.000	0.023

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)	0	0.052	0	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	0.042	0.068	0.622	0.539	-0.097	0.181	0.000
L3.Phenylalanine.metabolism	0.000	0.000	-0.959	0.345	0.000	0.000	0.029

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	-0.038	0.11	-0.345	0.733	-0.263	0.187	0.0
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis	0.000	0.00	0.392	0.698	0.000	0.000	0.0

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	0.179	0.071	2.520	0.017	0.034	0.324	0.000
L3.Phenylpropanoid.biosynthesis	0.000	0.000	-3.266	0.003	0.000	0.000	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	-0.005	0.116	-0.043	0.966	-0.241	0.231	0
L3.Phosphatidylinositol.signaling.system	0.000	0.000	0.049	0.961	0.000	0.000	0

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	-0.026	0.09	-0.286	0.777	-0.209	0.158	0.000
L3.Phosphonate.and.phosphinate.metabolism	0.000	0.00	0.353	0.727	0.000	0.000	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	-0.027	0.076	-0.355	0.725	-0.182	0.128	0.000
L3.Phosphotransferase.system..PTS.	0.000	0.000	0.489	0.628	0.000	0.000	0.008

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	-0.122	0.128	-0.953	0.348	-0.385	0.14	0.000
L3.Photosynthesis	0.000	0.000	1.041	0.306	0.000	0.00	0.034

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	-0.077	0.054	-1.437	0.161	-0.187	0.033	0.000
L3.Photosynthesis...antenna.proteins	0.007	0.002	2.876	0.007	0.002	0.012	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	-0.117	0.126	-0.926	0.362	-0.374	0.141	0.000
L3.Photosynthesis.proteins	0.000	0.000	1.016	0.318	0.000	0.000	0.032

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)	0	0.052	0	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)	0	0.052	0	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	0.033	0.103	0.317	0.753	-0.178	0.243	0.000
L3.Plant.pathogen.interaction	0.000	0.000	-0.369	0.715	0.000	0.000	0.004

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	-0.003	0.123	-0.024	0.981	-0.255	0.249	0
L3.Polycyclic.aromatic.hydrocarbon.degradation	0.000	0.000	0.026	0.979	0.000	0.000	0

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	0.14	0.107	1.305	0.202	-0.079	0.358	0.000
L3.Polyketide.sugar.unit.biosynthesis	0.00	0.000	-1.483	0.148	0.000	0.000	0.066

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	0.072	0.072	0.990	0.330	-0.076	0.219	0.000
L3.Pores.ion.channels	0.000	0.000	-1.399	0.172	0.000	0.000	0.059

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	0.086	0.084	1.025	0.313	-0.086	0.258	0.000
L3.Porphyrin.and.chlorophyll.metabolism	0.000	0.000	-1.292	0.206	0.000	0.000	0.051

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	0.065	0.121	0.535	0.596	-0.182	0.311	0.000
L3.Prenyltransferases	0.000	0.000	-0.594	0.557	0.000	0.000	0.011

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	0.111	0.102	1.092	0.284	-0.097	0.319	0.000
L3.Primary.bile.acid.biosynthesis	0.000	0.000	-1.264	0.216	0.000	0.000	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	-0.075	0.116	-0.648	0.522	-0.313	0.162	0.000
L3.Primary.immunodeficiency	0.000	0.000	0.725	0.474	0.000	0.000	0.017

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	0.007	0.063	0.105	0.917	-0.122	0.135	0.000
L3.Prion.diseases	0.000	0.000	-0.192	0.849	0.000	0.000	0.001

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	0.172	0.08	2.142	0.040	0.008	0.336	0.000
L3.Progesterone.mediated.oocyte.maturation	0.000	0.00	-2.655	0.013	0.000	0.000	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	0	0.09	0.001	0.999	-0.183	0.183	0
L3.Propanoate.metabolism	0	0.00	-0.001	0.999	0.000	0.000	0

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	0.176	0.077	2.287	0.029	0.019	0.334	0.00
L3.Prostate.cancer	0.000	0.000	-2.871	0.007	0.000	0.000	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	0.077	0.12	0.638	0.528	-0.169	0.322	0.000
L3.Proteasome	0.000	0.00	-0.708	0.484	0.000	0.000	0.016

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	0.192	0.058	3.304	0.002	0.073	0.31	0.000
L3.Protein.digestion.and.absorption	0.000	0.000	-4.600	0.000	0.000	0.00	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	-0.071	0.122	-0.583	0.564	-0.319	0.178	0.000
L3.Protein.export	0.000	0.000	0.646	0.523	0.000	0.000	0.013

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	0.021	0.093	0.225	0.823	-0.168	0.21	0.000
L3.Protein.folding.and.associated.processing	0.000	0.000	-0.274	0.786	0.000	0.00	0.002

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	-0.012	0.082	-0.152	0.880	-0.18	0.155	0.000
L3.Protein.kinases	0.000	0.000	0.199	0.844	0.00	0.000	0.001

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	0.284	0.075	3.777	0.001	0.13	0.437	0.000
L3.Protein.processing.in.endoplasmic.reticulum	0.000	0.000	-4.495	0.000	0.00	0.000	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	0.039	0.067	0.584	0.564	-0.098	0.176	0.000
L3.Proximal.tubule.bicarbonate.reclamation	0.000	0.000	-0.921	0.364	0.000	0.000	0.027

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	-0.05	0.114	-0.444	0.66	-0.283	0.182	0.000
L3.Purine.metabolism	0.00	0.000	0.500	0.62	0.000	0.000	0.008

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	-0.046	0.121	-0.379	0.707	-0.293	0.201	0.000
L3.Pyrimidine.metabolism	0.000	0.000	0.421	0.677	0.000	0.000	0.006

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	0.013	0.093	0.135	0.894	-0.178	0.203	0.000
L3.Pyruvate.metabolism	0.000	0.000	-0.163	0.872	0.000	0.000	0.001

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	0.016	0.065	0.248	0.806	-0.117	0.15	0.000
L3.RIG.I.like.receptor.signaling.pathway	0.000	0.000	-0.416	0.680	0.000	0.00	0.006

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	0.057	0.12	0.478	0.636	-0.187	0.301	0.000
L3.RNA.degradation	0.000	0.00	-0.532	0.598	0.000	0.000	0.009

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	-0.196	0.114	-1.715	0.097	-0.43	0.037	0.000
L3.RNA.polymerase	0.000	0.000	1.904	0.067	0.00	0.000	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	-0.054	0.1	-0.539	0.594	-0.258	0.15	0.000
L3.RNA.transport	0.000	0.0	0.632	0.532	0.000	0.00	0.013

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)	0	0.052	0	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	-0.039	0.065	-0.602	0.551	-0.172	0.094	0.000
L3.Renal.cell.carcinoma	0.000	0.000	0.996	0.327	0.000	0.000	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	-0.013	0.053	-0.252	0.803	-0.121	0.094	0.000
L3.Renin.angiotensin.system	0.001	0.001	1.205	0.238	0.000	0.002	0.045

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	-0.048	0.105	-0.461	0.648	-0.262	0.165	0.000
L3.Replication..recombination.and.repair.proteins	0.000	0.000	0.533	0.598	0.000	0.000	0.009

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	0.077	0.098	0.788	0.437	-0.123	0.277	0.000
L3.Restriction.enzyme	0.000	0.000	-0.931	0.359	0.000	0.000	0.027

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	-0.017	0.076	-0.223	0.825	-0.173	0.139	0.000
L3.Retinol.metabolism	0.000	0.000	0.307	0.761	0.000	0.000	0.003

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)	0	0.052	0	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	0.04	0.086	0.466	0.645	-0.135	0.215	0.000
L3.Riboflavin.metabolism	0.00	0.000	-0.588	0.561	0.000	0.000	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	-0.104	0.125	-0.831	0.412	-0.36	0.152	0.000
L3.Ribosome	0.000	0.000	0.914	0.368	0.00	0.000	0.026

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	-0.065	0.107	-0.605	0.550	-0.283	0.154	0.000
L3.Ribosome.Biogenesis	0.000	0.000	0.693	0.494	0.000	0.000	0.015

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	-0.144	0.109	-1.318	0.198	-0.368	0.079	0.000
L3.Ribosome.biogenesis.in.eukaryotes	0.000	0.000	1.488	0.147	0.000	0.000	0.067

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)	0	0.052	0	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	0.11	0.102	1.084	0.287	-0.097	0.318	0.000
L3.Secondary.bile.acid.biosynthesis	0.00	0.000	-1.256	0.219	0.000	0.000	0.048

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	-0.013	0.077	-0.170	0.866	-0.171	0.144	0.000
L3.Secretion.system	0.000	0.000	0.233	0.817	0.000	0.000	0.002

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	-0.007	0.099	-0.068	0.946	-0.209	0.195	0
L3.Selenocompound.metabolism	0.000	0.000	0.080	0.937	0.000	0.000	0

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)	0	0.052	0	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	-0.017	0.060	-0.284	0.778	-0.139	0.105	0.000
L3.Shigellosis	0.009	0.015	0.592	0.558	-0.022	0.040	0.011

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	0.005	0.095	0.049	0.962	-0.188	0.198	0
L3.Signal.transduction.mechanisms	0.000	0.000	-0.058	0.954	0.000	0.000	0

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	-0.043	0.055	-0.770	0.447	-0.156	0.070	0.000
L3.Small.cell.lung.cancer	0.004	0.002	1.801	0.082	0.000	0.008	0.095

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	0.289	0.067	4.304	0	0.152	0.426	0.000
L3.Sphingolipid.metabolism	0.000	0.000	-5.230	0	0.000	0.000	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)	0	0.052	0	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	0.035	0.074	0.478	0.636	-0.115	0.186	0.000
L3.Sporulation	0.000	0.000	-0.677	0.504	0.000	0.000	0.015

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	-0.104	0.057	-1.817	0.079	-0.221	0.013	0.000
L3.Staphylococcus.aureus.infection	0.000	0.000	3.055	0.005	0.000	0.000	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	0.105	0.097	1.087	0.286	-0.092	0.302	0.00
L3.Starch.and.sucrose.metabolism	0.000	0.000	-1.283	0.209	0.000	0.000	0.05

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	-0.048	0.055	-0.867	0.393	-0.161	0.065	0.00
L3.Steroid.biosynthesis	0.001	0.000	1.958	0.060	0.000	0.002	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	0.105	0.058	1.824	0.078	-0.013	0.223	0.000
L3.Steroid.hormone.biosynthesis	0.000	0.000	-3.036	0.005	0.000	0.000	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 %	0.
Intercept	-0.006	0.057	-0.101	0.920	-0.121	0.11	0.
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	0.000	0.000	0.272	0.787	0.000	0.00	0.

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	0.111	0.108	1.025	0.314	-0.11	0.331	0.000
L3.Streptomycin.biosynthesis	0.000	0.000	-1.167	0.253	0.00	0.000	0.042

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	0.01	0.058	0.181	0.858	-0.107	0.128	0.000
L3.Styrene.degradation	0.00	0.000	-0.437	0.665	0.000	0.000	0.006

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	0.071	0.096	0.744	0.463	-0.124	0.267	0.000
L3.Sulfur.metabolism	0.000	0.000	-0.886	0.383	0.000	0.000	0.025

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	0.007	0.08	0.085	0.933	-0.156	0.17	0
L3.Sulfur.relay.system	0.000	0.00	-0.113	0.910	0.000	0.00	0

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	-0.05	0.079	-0.624	0.537	-0.212	0.113	0.000
L3.Synthesis.and.degradation.of.ketone.bodies	0.00	0.000	0.827	0.415	0.000	0.000	0.022

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	0.015	0.056	0.273	0.787	-0.099	0.129	0.000
L3.Systemic.lupus.erythematosus	0.000	0.000	-0.774	0.445	0.000	0.000	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)	0	0.052	0	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	0.02	0.103	0.192	0.849	-0.191	0.23	0.000
L3.Taurine.and.hypotaurine.metabolism	0.00	0.000	-0.224	0.825	0.000	0.00	0.002

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	0.01	0.123	0.080	0.937	-0.241	0.26	0
L3.Terpenoid.backbone.biosynthesis	0.00	0.000	-0.088	0.930	0.000	0.00	0

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	-0.04	0.106	-0.382	0.705	-0.256	0.176	0.000
L3.Tetracycline.biosynthesis	0.00	0.000	0.440	0.663	0.000	0.000	0.006

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	-0.009	0.111	-0.079	0.937	-0.235	0.217	0
L3.Thiamine.metabolism	0.000	0.000	0.090	0.929	0.000	0.000	0

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)	0	0.052	0	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	-0.021	0.062	-0.342	0.735	-0.147	0.105	0.000
L3.Toluene.degradation	0.000	0.000	0.648	0.522	0.000	0.000	0.013

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	-0.043	0.055	-0.770	0.447	-0.156	0.070	0.000
L3.Toxoplasmosis	0.004	0.002	1.801	0.082	0.000	0.008	0.095

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	0.01	0.079	0.130	0.898	-0.15	0.171	0.000
L3.Transcription.factors	0.00	0.000	-0.175	0.862	0.00	0.000	0.001

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	0.214	0.114	1.871	0.071	-0.02	0.447	0.000
L3.Transcription.machinery	0.000	0.000	-2.074	0.047	0.00	0.000	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	0.011	0.06	0.191	0.850	-0.11	0.133	0.000
L3.Transcription.related.proteins	0.000	0.00	-0.405	0.688	0.00	0.000	0.005

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	-0.036	0.12	-0.301	0.765	-0.281	0.209	0.000
L3.Translation.factors	0.000	0.00	0.335	0.740	0.000	0.000	0.004

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	-0.037	0.108	-0.343	0.734	-0.257	0.183	0.000
L3.Translation.proteins	0.000	0.000	0.393	0.697	0.000	0.000	0.005

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	-0.037	0.086	-0.432	0.669	-0.212	0.138	0.00
L3.Transporters	0.000	0.000	0.546	0.589	0.000	0.000	0.01

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	0.07	0.084	0.830	0.413	-0.102	0.242	0
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis	0.00	0.000	-1.052	0.301	0.000	0.000	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	0.019	0.068	0.284	0.778	-0.119	0.158	0.000
L3.Tryptophan.metabolism	0.000	0.000	-0.449	0.656	0.000	0.000	0.006

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	-0.075	0.131	-0.574	0.570	-0.343	0.192	0.000
L3.Tuberculosis	0.000	0.000	0.627	0.536	0.000	0.000	0.013

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	0.027	0.078	0.342	0.735	-0.133	0.186	0.000
L3.Two.component.system	0.000	0.000	-0.462	0.648	0.000	0.000	0.007

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	-0.004	0.131	-0.032	0.975	-0.271	0.263	0
L3.Type.I.diabetes.mellitus	0.000	0.000	0.035	0.972	0.000	0.000	0

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	-0.003	0.107	-0.027	0.978	-0.222	0.216	0
L3.Type.II.diabetes.mellitus	0.000	0.000	0.031	0.975	0.000	0.000	0

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	0.035	0.087	0.4	0.692	-0.143	0.213	0.000
L3.Tyrosine.metabolism	0.000	0.000	-0.5	0.621	0.000	0.000	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	0.045	0.068	0.655	0.518	-0.095	0.185	0.
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis	0.000	0.000	-1.001	0.325	0.000	0.000	0.

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	0.006	0.064	0.096	0.924	-0.125	0.137	0.000
L3.Ubiquitin.system	0.000	0.000	-0.168	0.868	0.000	0.000	0.001

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)	0	0.052	0	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	-0.086	0.112	-0.769	0.448	-0.314	0.142	0.000
L3.Valine..leucine.and.isoleucine.biosynthesis	0.000	0.000	0.869	0.392	0.000	0.000	0.024

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	0.036	0.082	0.438	0.664	-0.131	0.202	0.00
L3.Valine..leucine.and.isoleucine.degradation	0.000	0.000	-0.572	0.572	0.000	0.000	0.01

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	0.059	-0.538	0.594	-0.154	0.089	0.000
L3.Various.types.of.N.glycan.biosynthesis	0.032	0.030	1.085	0.287	-0.028	0.092	0.037

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)	0	0.052	0	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	-0.018	0.054	-0.336	0.739	-0.128	0.092	0.000
L3.Vasopressin.regulated.water.reabsorption	0.072	0.062	1.165	0.253	-0.054	0.199	0.042

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	0.010	0.058	0.176	0.862	-0.108	0.129	0.000
L3.Vibrio.cholerae.infection	-0.014	0.034	-0.413	0.683	-0.084	0.056	0.005

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	0.037	0.083	0.451	0.655	-0.132	0.207	0.000
L3.Vibrio.cholerae.pathogenic.cycle	0.000	0.000	-0.581	0.565	0.000	0.000	0.011

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	-0.043	0.055	-0.770	0.447	-0.156	0.070	0.000
L3.Viral.myocarditis	0.004	0.002	1.801	0.082	0.000	0.008	0.095

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	0.083	0.09	0.924	0.363	-0.1	0.266	0.00
L3.Vitamin.B6.metabolism	0.000	0.00	-1.129	0.268	0.0	0.000	0.04

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	0.011	0.057	0.189	0.851	-0.105	0.126	0.000
L3.Wnt.signaling.pathway	-0.043	0.086	-0.501	0.620	-0.218	0.132	0.008

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	-0.047	0.078	-0.598	0.554	-0.207	0.113	0.00
L3.Xylene.degradation	0.000	0.000	0.802	0.429	0.000	0.000	0.02

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	0.125	0.132	0.948	0.351	-0.145	0.395	0.000
L3.Zeatin.biosynthesis	0.000	0.000	-1.030	0.311	0.000	0.000	0.033

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	0.012	0.058	0.205	0.839	-0.107	0.131	0.000
L3.alpha.Linolenic.acid.metabolism	0.000	0.000	-0.465	0.645	0.000	0.000	0.007

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	0.052	0.074	0.699	0.490	-0.099	0.203	0.00
L3.beta.Alanine.metabolism	0.000	0.000	-0.980	0.335	0.000	0.000	0.03

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	-0.045	0.094	-0.479	0.635	-0.236	0.146	0.000
L3.beta.Lactam.resistance	0.000	0.000	0.578	0.568	0.000	0.000	0.011

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)	0	0.052	0	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)	0	0.052	0	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	-0.043	0.055	-0.770	0.447	-0.156	0.070	0.000
L3.p53.signaling.pathway	0.004	0.002	1.801	0.082	0.000	0.008	0.095

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 %	9
Intercept	0.002	0.025	0.066	0.948	-0.05	
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	0.000	0.000	-0.353	0.727	0.00	

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	0.014	0.038	0.359	0.722	-0.064	0.091	0.000
L3.ABC.transporters	0.000	0.000	-0.475	0.638	0.000	0.000	0.007

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)	0	0.024	0	1	-0.05	0.05	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	0.065	0.038	1.712	0.097	-0.013	0.142	0.000
L3.Adipocytokine.signaling.pathway	0.000	0.000	-2.159	0.039	0.000	0.000	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	0.045	0.029	1.546	0.132	-0.015	0.105	0.000
L3.African.trypanosomiasis	0.000	0.000	-2.437	0.021	0.000	0.000	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	0.022	0.053	0.411	0.684	-0.087	0.131	0.000
L3.Alanine..aspartate.and.glutamate.metabolism	0.000	0.000	-0.464	0.646	0.000	0.000	0.007

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	0.002	0.025	0.065	0.949	-0.050	0.053	0.000
L3.Aldosterone.regulated.sodium.reabsorption	-0.052	0.142	-0.367	0.716	-0.343	0.238	0.004

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	0.014	0.045	0.302	0.765	-0.078	0.106	0.000
L3.Alzheimer.s.disease	0.000	0.000	-0.361	0.721	0.000	0.000	0.004

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	0.017	0.037	0.453	0.654	-0.059	0.092	0.000
L3.Amino.acid.metabolism	0.000	0.000	-0.608	0.548	0.000	0.000	0.012

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	-0.018	0.054	-0.332	0.742	-0.128	0.092	0.000
L3.Amino.acid.related.enzymes	0.000	0.000	0.374	0.711	0.000	0.000	0.004

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	0.013	0.052	0.241	0.811	-0.094	0.119	0.000
L3.Amino.sugar.and.nucleotide.sugar.metabolism	0.000	0.000	-0.274	0.786	0.000	0.000	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	-0.057	0.056	-1.022	0.315	-0.172	0.057	0.00
L3.Aminoacyl.tRNA.biosynthesis	0.000	0.000	1.134	0.266	0.000	0.000	0.04

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	0.042	0.034	1.219	0.232	-0.028	0.111	0.000
L3.Aminobenzoate.degradation	0.000	0.000	-1.693	0.101	0.000	0.000	0.085

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	0.019	0.032	0.588	0.561	-0.047	0.085	0.000
L3.Amoebiasis	0.000	0.000	-0.907	0.372	0.000	0.000	0.026

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	0.027	0.028	0.971	0.339	-0.03	0.084	0.000
L3.Amyotrophic.lateral.sclerosis..ALS.	0.000	0.000	-1.803	0.081	0.00	0.000	0.095

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	-0.004	0.042	-0.095	0.925	-0.09	0.082	0
L3.Antigen.processing.and.presentation	0.000	0.000	0.117	0.907	0.00	0.000	0

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	-0.008	0.029	-0.287	0.776	-0.068	0.051	0.000
L3.Apoptosis	0.000	0.000	0.532	0.599	0.000	0.000	0.009

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	0.025	0.035	0.718	0.478	-0.046	0.096	0.000
L3.Arachidonic.acid.metabolism	0.000	0.000	-1.009	0.321	0.000	0.000	0.032

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	0.024	0.042	0.553	0.584	-0.063	0.11	0.000
L3.Arginine.and.proline.metabolism	0.000	0.000	-0.679	0.502	0.000	0.00	0.015

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)	0	0.024	0	1	-0.05	0.05	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	0.021	0.03	0.697	0.491	-0.041	0.083	0.000
L3.Ascorbate.and.aldarate.metabolism	0.000	0.00	-1.157	0.256	0.000	0.000	0.041

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	0.019	0.026	0.703	0.488	-0.035	0.073	0.000
L3.Atrazine.degradation	0.000	0.000	-1.605	0.119	0.000	0.000	0.077

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	-0.01	0.037	-0.275	0.785	-0.086	0.065	0.000
L3.Bacterial.chemotaxis	0.00	0.000	0.371	0.713	0.000	0.000	0.004

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	0.004	0.026	0.164	0.871	-0.049	0.058	0.000
L3.Bacterial.invasion.of.epithelial.cells	0.000	0.000	-0.494	0.625	0.000	0.000	0.008

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	0.003	0.036	0.079	0.937	-0.07	0.075	0
L3.Bacterial.motility.proteins	0.000	0.000	-0.111	0.912	0.00	0.000	0

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	0.025	0.036	0.693	0.494	-0.048	0.097	0.000
L3.Bacterial.secretion.system	0.000	0.000	-0.956	0.347	0.000	0.000	0.029

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	-0.071	0.055	-1.280	0.210	-0.184	0.042	0.000
L3.Bacterial.toxins	0.000	0.000	1.421	0.166	0.000	0.000	0.061

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	-0.009	0.026	-0.352	0.727	-0.063	0.044	0.000
L3.Basal.transcription.factors	0.000	0.000	0.962	0.344	0.000	0.000	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	-0.018	0.054	-0.339	0.737	-0.129	0.092	0.000
L3.Base.excision.repair	0.000	0.000	0.381	0.706	0.000	0.000	0.005

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	0.013	0.034	0.388	0.701	-0.056	0.082	0.00
L3.Benzoate.degradation	0.000	0.000	-0.572	0.572	0.000	0.000	0.01

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	0.011	0.026	0.428	0.672	-0.041	0.063	0.000
L3.Betalain.biosynthesis	0.000	0.000	-1.285	0.209	0.000	0.000	0.051

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	0.008	0.027	0.299	0.767	-0.048	0.064	0.000
L3.Bile.secretion	-0.001	0.002	-0.674	0.505	-0.005	0.002	0.014

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	0.021	0.028	0.750	0.459	-0.037	0.079
L3.Biosynthesis.and.biodegradation.of.secondary.metabolites	0.000	0.000	-1.414	0.168	0.000	0.000

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	-0.001	0.025	-0.043	0.966	-0.053	0.050
L3.Biosynthesis.of.12...14..and.16.membered.macrolides	0.035	0.142	0.244	0.809	-0.256	0.326

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	0.013	0.036	0.372	0.713	-0.059	0.086	0.000
L3.Biosynthesis.of.ansamycins	0.000	0.000	-0.517	0.609	0.000	0.000	0.009

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	0.021	0.028	0.745	0.462	-0.036	0.077
L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides	0.000	0.000	-1.475	0.151	0.000	0.000

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)	0	0.024	0	1	-0.05	0.05	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	0.011	0.026	0.44	0.663	-0.041	0.064	0.00
L3.Biosynthesis.of.type.II.polyketide.products	0.000	0.000	-1.28	0.210	0.000	0.000	0.05

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	0.03	0.033	0.917	0.366	-0.037	0.097	0.000
L3.Biosynthesis.of.unsaturated.fatty.acids	0.00	0.000	-1.358	0.184	0.000	0.000	0.056

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	-0.01	0.054	-0.188	0.852	-0.121	0.101	0.000
L3.Biosynthesis.of.vancomycin.group.antibiotics	0.00	0.000	0.211	0.834	0.000	0.000	0.001

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	-0.007	0.044	-0.152	0.880	-0.096	0.083	0.000
L3.Biotin.metabolism	0.000	0.000	0.184	0.855	0.000	0.000	0.001

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	-0.004	0.048	-0.077	0.940	-0.102	0.095	0
L3.Bisphenol.degradation	0.000	0.000	0.089	0.929	0.000	0.000	0

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	0.02	0.027	0.761	0.452	-0.034	0.075	0.000
L3.Bladder.cancer	0.00	0.000	-1.681	0.103	0.000	0.000	0.084

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	0.021	0.039	0.528	0.601	-0.06	0.101	0.000
L3.Butanoate.metabolism	0.000	0.000	-0.676	0.504	0.00	0.000	0.015

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	0.046	0.063	0.731	0.471	-0.083	0.175	0.00
L3.Butirosin.and.neomycin.biosynthesis	0.000	0.000	-0.793	0.434	0.000	0.000	0.02

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	0.024	0.047	0.506	0.617	-0.073	0.121	0.000
L3.C5.Branched.dibasic.acid.metabolism	0.000	0.000	-0.593	0.558	0.000	0.000	0.011

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)	0	0.024	0	1	-0.05	0.05	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	-0.004	0.027	-0.133	0.895	-0.059	0.052	0.000
L3.Caffeine.metabolism	0.004	0.014	0.320	0.751	-0.024	0.033	0.003

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	0.021	0.027	0.788	0.437	-0.034	0.076	0.000
L3.Calcium.signaling.pathway	-0.034	0.020	-1.697	0.100	-0.074	0.007	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	0.022	0.028	0.778	0.442	-0.036	0.08	0.000
L3.Caprolactam.degradation	0.000	0.000	-1.447	0.158	0.000	0.00	0.063

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	0.032	0.035	0.917	0.366	-0.039	0.103	0.00
L3.Carbohydrate.digestion.and.absorption	0.000	0.000	-1.277	0.211	0.000	0.000	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	0.047	0.04	1.175	0.249	-0.035	0.128	0.000
L3.Carbohydrate.metabolism	0.000	0.00	-1.470	0.152	0.000	0.000	0.065

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	0.019	0.044	0.432	0.669	-0.072	0.11	0.000
L3.Carbon.fixation.in.photosynthetic.organisms	0.000	0.000	-0.519	0.608	0.000	0.00	0.009

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	0.016	0.046	0.345	0.732	-0.079	0.11	0.000
L3.Carbon.fixation.pathways.in.prokaryotes	0.000	0.000	-0.408	0.686	0.000	0.00	0.005

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	0.012	0.026	0.459	0.650	-0.041	0.065	0.000
L3.Cardiac.muscle.contraction	0.000	0.000	-1.243	0.224	0.000	0.000	0.047

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	0.001	0.028	0.032	0.975	-0.057	0.059	0
L3.Carotenoid.biosynthesis	0.000	0.000	-0.065	0.948	0.000	0.000	0

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)	0	0.024	0	1	-0.05	0.05	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	-0.05	0.06	-0.839	0.408	-0.173	0.072	0.000
L3.Cell.cycle. . . Caulobacter	0.00	0.00	0.919	0.365	0.000	0.000	0.027

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)	0	0.024	0	1	-0.05	0.05	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	0.029	0.04	0.735	0.468	-0.052	0.111	0.000
L3.Cell.division	0.000	0.00	-0.928	0.361	0.000	0.000	0.027

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	0	0.041	0.001	0.999	-0.084	0.084	0
L3.Cell.motility.and.secretion	0	0.000	-0.002	0.999	0.000	0.000	0

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	0.062	0.037	1.669	0.106	-0.014	0.137	0.000
L3.Cellular.antigens	0.000	0.000	-2.143	0.040	0.000	0.000	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	0.042	0.028	1.475	0.151	-0.016	0.1	0.000
L3.Chagas.disease..American.trypanosomiasis.	0.000	0.000	-2.454	0.020	0.000	0.0	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	0.026	0.047	0.552	0.585	-0.07	0.123	0.000
L3.Chaperones.and.folding.catalysts	0.000	0.000	-0.647	0.523	0.00	0.000	0.013

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	0.033	0.049	0.680	0.502	-0.066	0.132	0.00
L3.Chloroalkane.and.chloroalkene.degradation	0.000	0.000	-0.788	0.437	0.000	0.000	0.02

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 %	R2
Intercept	0.033	0.029	1.123	0.270	-0.027	0.092	0.000
L3.Chlorocyclohexane.and.chlorobenzene.degradation	0.000	0.000	-1.887	0.069	0.000	0.000	0.103

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)	0	0.024	0	1	-0.05	0.05	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	-0.004	0.051	-0.081	0.936	-0.109	0.1	0
L3.Chromosome	0.000	0.000	0.092	0.927	0.000	0.0	0

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	0.026	0.458	0.650	-0.041	0.065	0.000
L3.Chronic.myeloid.leukemia	-0.048	0.040	-1.212	0.235	-0.129	0.033	0.045

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	0.006	0.027	0.229	0.820	-0.049	0.061	0.000
L3.Circadian.rhythm. . . plant	-0.004	0.007	-0.580	0.566	-0.019	0.011	0.011

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	0.03	0.038	0.782	0.440	-0.048	0.107	0.000
L3.Citrate.cycle..TCA.cycle.	0.00	0.000	-1.025	0.314	0.000	0.000	0.033

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)	0	0.024	0	1	-0.05	0.05	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	-0.002	0.027	-0.061	0.952	-0.058	0.054	0.000
L3.Colorectal.cancer	0.000	0.001	0.142	0.888	-0.002	0.002	0.001

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)	0	0.024	0	1	-0.05	0.05	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	0.047	0.041	1.163	0.254	-0.036	0.131	0.000
L3.Cyanoamino.acid.metabolism	0.000	0.000	-1.439	0.160	0.000	0.000	0.063

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	0.001	0.047	0.015	0.988	-0.095	0.096	0
L3.Cysteine.and.methionine.metabolism	0.000	0.000	-0.018	0.986	0.000	0.000	0

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	-0.004	0.025	-0.168	0.868	-0.055	0.047	0.000
L3.Cytochrome.P450	0.133	0.141	0.948	0.351	-0.154	0.420	0.028

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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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	-0.074	0.051	-1.451	0.157	-0.178	0.03	0.00
L3.Cytoskeleton.proteins	0.000	0.000	1.641	0.111	0.000	0.00	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)	0	0.024	0	1	-0.05	0.05	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	-0.049	0.051	-0.958	0.346	-0.153	0.055	0.000
L3.D.Alanine.metabolism	0.000	0.000	1.090	0.284	0.000	0.000	0.037

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	-0.039	0.022	-1.780	0.085	-0.084	0.006	0.000
L3.D.Arginine.and.D.ornithine.metabolism	0.000	0.000	4.162	0.000	0.000	0.000	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	-0.019	0.052	-0.369	0.715	-0.125	0.087	0.000
L3.D.Glutamine.and.D.glutamate.metabolism	0.000	0.000	0.419	0.678	0.000	0.000	0.006

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	-0.021	0.056	-0.370	0.714	-0.134	0.093	0.000
L3.DNA.repair.and.recombination.proteins	0.000	0.000	0.413	0.682	0.000	0.000	0.005

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	-0.048	0.059	-0.811	0.424	-0.17	0.073	0.000
L3.DNA.replication	0.000	0.000	0.890	0.380	0.00	0.000	0.025

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	-0.016	0.058	-0.278	0.783	-0.135	0.103	0.000
L3.DNA.replication.proteins	0.000	0.000	0.307	0.761	0.000	0.000	0.003

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)	0	0.024	0	1	-0.05	0.05	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	0.016	0.034	0.470	0.642	-0.054	0.086	0.000
L3.Dioxin.degradation	0.000	0.000	-0.675	0.505	0.000	0.000	0.015

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	0.036	0.031	1.180	0.247	-0.026	0.099	0.000
L3.Drug.metabolism...cytochrome.P450	0.000	0.000	-1.846	0.075	0.000	0.000	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	-0.012	0.054	-0.216	0.830	-0.121	0.098	0.000
L3.Drug.metabolism...other.enzymes	0.000	0.000	0.244	0.809	0.000	0.000	0.002

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)	0	0.024	0	1	-0.05	0.05	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	0.023	0.031	0.756	0.455	-0.04	0.086	0.000
L3.Electron.transfer.carriers	0.000	0.000	-1.229	0.229	0.00	0.000	0.046

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)	0	0.024	0	1	-0.05	0.05	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	0.006	0.026	0.247	0.806	-0.046	0.059	0.00
L3.Endocytosis	-0.006	0.007	-0.802	0.429	-0.021	0.009	0.02

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	0.016	0.041	0.394	0.696	-0.068	0.101	0.000
L3.Energy.metabolism	0.000	0.000	-0.492	0.627	0.000	0.000	0.008

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	-0.007	0.045	-0.165	0.870	-0.099	0.084	
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	0.000	0.000	0.198	0.844	0.000	0.000	

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)	0	0.024	0	1	-0.05	0.05	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	-0.025	0.03	-0.825	0.416	-0.087	0.037	0.000
L3.Ether.lipid.metabolism	0.000	0.00	1.367	0.182	0.000	0.000	0.057

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	0.042	0.038	1.090	0.284	-0.037	0.121	0.000
L3.Ethylbenzene.degradation	0.000	0.000	-1.396	0.173	0.000	0.000	0.059

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)	0	0.024	0	1	-0.05	0.05	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	0.003	0.051	0.051	0.960	-0.101	0.107	0
L3.Fatty.acid.biosynthesis	0.000	0.000	-0.059	0.954	0.000	0.000	0

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)	0	0.024	0	1	-0.05	0.05	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	0.035	0.037	0.940	0.355	-0.041	0.111	0.000
L3.Fatty.acid.metabolism	0.000	0.000	-1.242	0.224	0.000	0.000	0.047

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)	0	0.024	0	1	-0.05	0.05	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	0.006	0.026	0.247	0.806	-0.046	0.059	0.00
L3.Fc.gamma.R.mediated.phagocytosis	-0.006	0.007	-0.802	0.429	-0.021	0.009	0.02

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	-0.004	0.031	-0.126	0.901	-0.068	0.06	0.000
L3.Flagellar.assembly	0.000	0.000	0.206	0.838	0.000	0.00	0.001

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	0.003	0.031	0.104	0.918	-0.06	0.067	0.000
L3.Flavone.and.flavonol.biosynthesis	0.000	0.000	-0.172	0.864	0.00	0.000	0.001

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	0.002	0.026	0.090	0.929	-0.05	0.055	0.000
L3.Flavonoid.biosynthesis	0.000	0.000	-0.343	0.734	0.00	0.000	0.004

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	0.017	0.026	0.672	0.507	-0.036	0.071	0.000
L3.Fluorobenzoate.degradation	0.000	0.000	-1.661	0.107	0.000	0.000	0.082

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)	0	0.024	0	1	-0.05	0.05	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	0.006	0.052	0.115	0.910	-0.1	0.112	0.000
L3.Folate.biosynthesis	0.000	0.000	-0.131	0.897	0.0	0.000	0.001

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	0.019	0.043	0.439	0.664	-0.068	0.105	0.000
L3.Fructose.and.mannose.metabolism	0.000	0.000	-0.539	0.594	0.000	0.000	0.009

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	0.023	0.038	0.622	0.539	-0.053	0.1	0.000
L3.Function.unknown	0.000	0.000	-0.823	0.417	0.000	0.0	0.021

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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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	0.035	0.053	0.661	0.513	-0.073	0.143	0.000
L3.Galactose.metabolism	0.000	0.000	-0.747	0.461	0.000	0.000	0.018

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)	0	0.024	0	1	-0.05	0.05	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	0.008	0.048	0.158	0.876	-0.09	0.105	0.000
L3.General.function.prediction.only	0.000	0.000	-0.184	0.855	0.00	0.000	0.001

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	0.029	0.029	0.993	0.329	-0.031	0.089	0.000
L3.Geraniol.degradation	0.000	0.000	-1.695	0.101	0.000	0.000	0.085

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	-0.009	0.028	-0.312	0.757	-0.066	0.048	0.000
L3.Germination	0.000	0.000	0.670	0.508	0.000	0.000	0.014

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)	0	0.024	0	1	-0.05	0.05	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	0.038	0.053	0.729	0.472	-0.069	0.146	0.000
L3.Glutamatergic.synapse	0.000	0.000	-0.824	0.417	0.000	0.000	0.021

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	0.03	0.039	0.769	0.448	-0.049	0.109	0.000
L3.Glutathione.metabolism	0.00	0.000	-0.991	0.329	0.000	0.000	0.031

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)	0	0.024	0	1	-0.05	0.05	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	0.02	0.031	0.650	0.521	-0.043	0.083	0.000
L3.Glycan.biosynthesis.and.metabolism	0.00	0.000	-1.066	0.295	0.000	0.000	0.035

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	0.008	0.043	0.188	0.852	-0.08	0.096	0.000
L3.Glycerolipid.metabolism	0.000	0.000	-0.229	0.820	0.00	0.000	0.002

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	0.015	0.044	0.339	0.737	-0.074	0.104	0.000
L3.Glycerophospholipid.metabolism	0.000	0.000	-0.412	0.684	0.000	0.000	0.005

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	0.022	0.046	0.485	0.631	-0.072	0.116	0.000
L3.Glycine..serine.and.threonine.metabolism	0.000	0.000	-0.575	0.570	0.000	0.000	0.011

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	0.018	0.048	0.381	0.706	-0.08	0.116	0.000
L3.Glycolysis…Gluconeogenesis	0.000	0.000	-0.444	0.660	0.00	0.000	0.006

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 %	R
Intercept	0	0.025	0.001	0.999	-0.052	0.052	
L3.Glycosaminoglycan.biosynthesis…chondroitin.sulfate	0	0.023	-0.006	0.995	-0.048	0.048	

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	0.037	0.04	0.918	0.366	-0.045	0.12	0.000
L3.Glycosaminoglycan.degradation	0.000	0.00	-1.148	0.260	0.000	0.00	0.041

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	0.056	0.038	1.484	0.148	-0.021	0.132	0.000
L3.Glycosphingolipid.biosynthesis. . . ganglio.series	0.000	0.000	-1.901	0.067	0.000	0.000	0.104

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	0.073	0.04	1.819	0.079	-0.009	0.155	0.000
L3.Glycosphingolipid.biosynthesis. . . globo.series	0.000	0.00	-2.221	0.034	0.000	0.000	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 %	97.5 %
Intercept	0.011	0.024	0.450	0.656	-0.038	0.06
L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series	0.000	0.000	-1.949	0.061	0.000	0.00

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)	0	0.024	0	1	-0.05	0.05	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	0.012	0.046	0.269	0.790	-0.081	0.106	0.000
L3.Glycosyltransferases	0.000	0.000	-0.320	0.751	0.000	0.000	0.003

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	0.021	0.037	0.569	0.574	-0.055	0.097	0.000
L3.Glyoxylate.and.dicarboxylate.metabolism	0.000	0.000	-0.759	0.453	0.000	0.000	0.018

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	0.006	0.026	0.247	0.806	-0.046	0.059	0.00
L3.GnRH.signaling.pathway	-0.006	0.007	-0.802	0.429	-0.021	0.009	0.02

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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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	-0.01	0.053	-0.179	0.859	-0.119	0.099	0.000
L3.Histidine.metabolism	0.00	0.000	0.202	0.841	0.000	0.000	0.001

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	-0.038	0.058	-0.650	0.520	-0.156	0.081	0.000
L3.Homologous.recombination	0.000	0.000	0.718	0.478	0.000	0.000	0.016

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	0.023	0.043	0.535	0.597	-0.065	0.112	0.000
L3.Huntington.s.disease	0.000	0.000	-0.650	0.521	0.000	0.000	0.013

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	0.004	0.026	0.142	0.888	-0.049	0.056	0.000
L3.Hypertrophic.cardiomyopathy..HCM.	-0.001	0.002	-0.512	0.613	-0.005	0.003	0.008

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	0.001	0.029	0.037	0.971	-0.058	0.060	0
L3.Indole.alkaloid.biosynthesis	-0.002	0.026	-0.073	0.942	-0.054	0.051	0

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	-0.002	0.027	-0.061	0.952	-0.058	0.054	0.000
L3.Influenza.A	0.000	0.001	0.142	0.888	-0.002	0.002	0.001

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	0.038	0.033	1.140	0.263	-0.03	0.105	0.00
L3.Inorganic.ion.transport.and.metabolism	0.000	0.000	-1.642	0.111	0.00	0.000	0.08

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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	0.029	0.031	0.936	0.357	-0.035	0.093	0.000
L3.Inositol.phosphate.metabolism	0.000	0.000	-1.456	0.156	0.000	0.000	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	0.045	0.049	0.909	0.370	-0.056	0.145	0.000
L3.Insulin.signaling.pathway	0.000	0.000	-1.047	0.304	0.000	0.000	0.034

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	0.017	0.043	0.398	0.694	-0.071	0.106	0.000
L3.Ion.channels	0.000	0.000	-0.484	0.632	0.000	0.000	0.008

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	0.003	0.026	0.119	0.906	-0.049	0.056	0.000
L3.Isoflavonoid.biosynthesis	-0.002	0.004	-0.436	0.666	-0.009	0.006	0.006

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	0.014	0.038	0.362	0.720	-0.063	0.091	0.000
L3.Isoquinoline.alkaloid.biosynthesis	0.000	0.000	-0.479	0.635	0.000	0.000	0.007

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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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	0.035	0.035	1.021	0.315	-0.035	0.106	0.000
L3.Limonene.and.pinene.degradation	0.000	0.000	-1.422	0.165	0.000	0.000	0.061

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	-0.027	0.05	-0.539	0.594	-0.129	0.075	0.000
L3.Linoleic.acid.metabolism	0.000	0.00	0.619	0.540	0.000	0.000	0.012

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	0.018	0.049	0.369	0.714	-0.081	0.117	0.000
L3.Lipid.biosynthesis.proteins	0.000	0.000	-0.429	0.671	0.000	0.000	0.006

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	0.018	0.036	0.516	0.610	-0.055	0.092	0.000
L3.Lipid.metabolism	0.000	0.000	-0.710	0.483	0.000	0.000	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	0.056	0.041	1.376	0.179	-0.027	0.14	0.000
L3.Lipoic.acid.metabolism	0.000	0.000	-1.689	0.102	0.000	0.00	0.084

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	0.006	0.034	0.176	0.862	-0.064	0.076	0.000
L3.Lipopolysaccharide.biosynthesis	0.000	0.000	-0.253	0.802	0.000	0.000	0.002

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	0.018	0.036	0.504	0.618	-0.055	0.092	0.000
L3.Lipopolysaccharide.biosynthesis.proteins	0.000	0.000	-0.691	0.495	0.000	0.000	0.015

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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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	-0.008	0.055	-0.144	0.886	-0.119	0.104	0.000
L3.Lysine.biosynthesis	0.000	0.000	0.162	0.872	0.000	0.000	0.001

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	0.022	0.034	0.658	0.516	-0.047	0.091	0.000
L3.Lysine.degradation	0.000	0.000	-0.952	0.349	0.000	0.000	0.028

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	0.052	0.04	1.291	0.207	-0.03	0.133	0.000
L3.Lysosome	0.000	0.00	-1.607	0.118	0.00	0.000	0.077

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)	0	0.024	0	1	-0.05	0.05	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	0.006	0.052	0.123	0.903	-0.1	0.112	0.000
L3.MAPK.signaling.pathway...yeast	0.000	0.000	-0.140	0.890	0.0	0.000	0.001

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)	0	0.024	0	1	-0.05	0.05	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	0.015	0.027	0.547	0.588	-0.041	0.071	0.000
L3.Meiosis...yeast	0.000	0.000	-1.201	0.239	0.000	0.000	0.044

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	0.011	0.026	0.426	0.673	-0.041	0.063	0.00
L3.Melanogenesis	0.000	0.000	-1.284	0.209	0.000	0.000	0.05

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	0.038	0.036	1.075	0.291	-0.035	0.111	0.000
L3.Membrane.and.intracellular.structural.molecules	0.000	0.000	-1.450	0.157	0.000	0.000	0.064

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	0.018	0.036	0.486	0.631	-0.057	0.092	0.000
L3.Metabolism.of.cofactors.and.vitamins	0.000	0.000	-0.660	0.514	0.000	0.000	0.014

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	0.036	0.03	1.180	0.247	-0.026	0.097	0.000
L3.Metabolism.of.xenobiotics.by.cytochrome.P450	0.000	0.00	-1.877	0.070	0.000	0.000	0.102

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	0.009	0.051	0.181	0.858	-0.094	0.113	0.000
L3.Methane.metabolism	0.000	0.000	-0.208	0.837	0.000	0.000	0.001

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	0.002	0.031	0.068	0.947	-0.06	0.065	0
L3.Mineral.absorption	0.000	0.000	-0.115	0.909	0.00	0.000	0

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	-0.045	0.058	-0.774	0.445	-0.164	0.074	0.000
L3.Mismatch.repair	0.000	0.000	0.853	0.400	0.000	0.000	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	-0.022	0.033	-0.685	0.499	-0.089	0.045	0.000
L3.N.Glycan.biosynthesis	0.000	0.000	1.024	0.314	0.000	0.000	0.033

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	-0.002	0.043	-0.058	0.954	-0.091	0.086	0
L3.NOD.like.receptor.signaling.pathway	0.000	0.000	0.071	0.944	0.000	0.000	0

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	0.055	0.05	1.112	0.275	-0.046	0.156	0.00
L3.Naphthalene.degradation	0.000	0.00	-1.275	0.212	0.000	0.000	0.05

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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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	0.028	0.049	0.574	0.570	-0.072	0.128	0.000
L3.Nicotinate.and.nicotinamide.metabolism	0.000	0.000	-0.664	0.511	0.000	0.000	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	0.03	0.041	0.731	0.470	-0.054	0.114	0.000
L3.Nitrogen.metabolism	0.00	0.000	-0.908	0.371	0.000	0.000	0.026

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	-0.004	0.035	-0.112	0.911	-0.075	0.068	0.000
L3.Nitrotoluene.degradation	0.000	0.000	0.159	0.875	0.000	0.000	0.001

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	0.008	0.028	0.297	0.768	-0.049	0.066	0.000
L3.Non.homologous.end.joining	0.000	0.000	-0.604	0.550	0.000	0.000	0.012

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	0.026	0.458	0.650	-0.041	0.065	0.000
L3.Notch.signaling.pathway	-0.048	0.040	-1.212	0.235	-0.129	0.033	0.045

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	-0.005	0.046	-0.114	0.910	-0.099	0.088	0.000
L3.Novobiocin.biosynthesis	0.000	0.000	0.136	0.892	0.000	0.000	0.001

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	-0.051	0.062	-0.816	0.421	-0.178	0.076	0.000
L3.Nucleotide.excision.repair	0.000	0.000	0.888	0.382	0.000	0.000	0.025

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	0.017	0.033	0.510	0.614	-0.05	0.083	0.000
L3.Nucleotide.metabolism	0.000	0.000	-0.777	0.443	0.00	0.000	0.019

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)	0	0.024	0	1	-0.05	0.05	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	-0.025	0.059	-0.425	0.674	-0.145	0.095	0.000
L3.One.carbon.pool.by.folate	0.000	0.000	0.469	0.642	0.000	0.000	0.007

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)	0	0.024	0	1	-0.05	0.05	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	0.059	0.043	1.383	0.177	-0.028	0.146	0.000
L3.Other.glycan.degradation	0.000	0.000	-1.665	0.106	0.000	0.000	0.082

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	0.026	0.039	0.668	0.509	-0.053	0.105	0.000
L3.Other.ion.coupled.transporters	0.000	0.000	-0.864	0.395	0.000	0.000	0.024

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	0.022	0.04	0.553	0.584	-0.059	0.104	0.000
L3.Other.transporters	0.000	0.00	-0.702	0.488	0.000	0.000	0.016

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)	0	0.024	0	1	-0.05	0.05	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	0.021	0.045	0.472	0.640	-0.071	0.114	0.00
L3.Others	0.000	0.000	-0.563	0.578	0.000	0.000	0.01

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	0.024	0.05	0.477	0.637	-0.078	0.125	0.00
L3.Oxidative.phosphorylation	0.000	0.00	-0.549	0.587	0.000	0.000	0.01

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	0.095	0.05	1.910	0.066	-0.007	0.196	0.000
L3.PPAR.signaling.pathway	0.000	0.00	-2.159	0.039	0.000	0.000	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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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	-0.008	0.051	-0.156	0.877	-0.113	0.097	0.000
L3.Pantothenate.and.CoA.biosynthesis	0.000	0.000	0.178	0.860	0.000	0.000	0.001

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	0.012	0.026	0.466	0.645	-0.041	0.065	0.000
L3.Parkinson.s.disease	0.000	0.000	-1.241	0.224	0.000	0.000	0.047

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	0.018	0.023	0.771	0.447	-0.030	0.066	0.00
L3.Pathogenic.Escherichia.coli.infection	-0.013	0.005	-2.609	0.014	-0.023	-0.003	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	-0.013	0.039	-0.339	0.737	-0.094	0.067	0.000
L3.Pathways.in.cancer	0.000	0.000	0.435	0.667	0.000	0.000	0.006

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	0.005	0.04	0.116	0.908	-0.077	0.086	0.000
L3.Penicillin.and.cephalosporin.biosynthesis	0.000	0.00	-0.148	0.884	0.000	0.000	0.001

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	0.032	0.035	0.915	0.368	-0.039	0.103	0.000
L3.Pentose.and.glucuronate.interconversions	0.000	0.000	-1.270	0.214	0.000	0.000	0.049

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	0.014	0.046	0.297	0.769	-0.08	0.107	0.000
L3.Pentose.phosphate.pathway	0.000	0.000	-0.353	0.727	0.00	0.000	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	0.001	0.051	0.021	0.983	-0.103	0.105	0
L3.Peptidases	0.000	0.000	-0.024	0.981	0.000	0.000	0

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	-0.02	0.056	-0.358	0.722	-0.134	0.094	0.000
L3.Peptidoglycan.biosynthesis	0.00	0.000	0.400	0.692	0.000	0.000	0.005

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	0.073	0.045	1.614	0.117	-0.019	0.166	0.000
L3.Peroxisome	0.000	0.000	-1.886	0.069	0.000	0.000	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	0.02	0.027	0.740	0.465	-0.036	0.076	0.000
L3.Pertussis	0.00	0.000	-1.513	0.141	0.000	0.000	0.069

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)	0	0.024	0	1	-0.05	0.05	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	0.024	0.032	0.737	0.467	-0.042	0.089	0.00
L3.Phenylalanine.metabolism	0.000	0.000	-1.137	0.265	0.000	0.000	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 %	R2
Intercept	0.002	0.052	0.032	0.974	-0.105	0.108	
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis	0.000	0.000	-0.037	0.971	0.000	0.000	

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	0.054	0.037	1.468	0.153	-0.021	0.129	0.000
L3.Phenylpropanoid.biosynthesis	0.000	0.000	-1.902	0.067	0.000	0.000	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	0.025	0.054	0.467	0.644	-0.086	0.136	0.000
L3.Phosphatidylinositol.signaling.system	0.000	0.000	-0.524	0.604	0.000	0.000	0.009

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	0.024	0.042	0.563	0.578	-0.062	0.11	0.000
L3.Phosphonate.and.phosphinate.metabolism	0.000	0.000	-0.694	0.493	0.000	0.00	0.015

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	0.005	0.036	0.137	0.892	-0.069	0.078	0.000
L3.Phosphotransferase.system..PTS.	0.000	0.000	-0.189	0.851	0.000	0.000	0.001

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	-0.073	0.06	-1.211	0.235	-0.195	0.05	0.000
L3.Photosynthesis	0.000	0.00	1.323	0.196	0.000	0.00	0.053

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	0.021	0.028	0.779	0.442	-0.035	0.078	0.000
L3.Photosynthesis. . . antenna.proteins	-0.002	0.001	-1.558	0.130	-0.004	0.001	0.073

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	-0.062	0.059	-1.044	0.305	-0.183	0.059	0.000
L3.Photosynthesis.proteins	0.000	0.000	1.145	0.261	0.000	0.000	0.041

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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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	-0.019	0.048	-0.395	0.696	-0.118	0.08	0.000
L3.Plant.pathogen.interaction	0.000	0.000	0.459	0.650	0.000	0.00	0.007

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	-0.053	0.057	-0.921	0.364	-0.169	0.064	0.000
L3.Polycyclic.aromatic.hydrocarbon.degradation	0.000	0.000	1.019	0.316	0.000	0.000	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	0.048	0.051	0.934	0.358	-0.057	0.153	0.000
L3.Polyketide.sugar.unit.biosynthesis	0.000	0.000	-1.061	0.297	0.000	0.000	0.035

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	0.03	0.034	0.886	0.383	-0.04	0.1	0.000
L3.Pores.ion.channels	0.00	0.000	-1.252	0.220	0.00	0.0	0.048

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	-0.026	0.04	-0.637	0.529	-0.108	0.057	0.00
L3.Porphyrin.and.chlorophyll.metabolism	0.000	0.00	0.803	0.429	0.000	0.000	0.02

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	-0.011	0.057	-0.199	0.843	-0.128	0.105	0.000
L3.Prenyltransferases	0.000	0.000	0.221	0.826	0.000	0.000	0.002

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	0.066	0.047	1.388	0.175	-0.031	0.162	0.000
L3.Primary.bile.acid.biosynthesis	0.000	0.000	-1.607	0.118	0.000	0.000	0.077

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	0.002	0.055	0.029	0.977	-0.111	0.115	0
L3.Primary.immunodeficiency	0.000	0.000	-0.033	0.974	0.000	0.000	0

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	0.025	0.028	0.883	0.384	-0.033	0.083	0.000
L3.Prion.diseases	0.000	0.000	-1.616	0.117	0.000	0.000	0.078

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	-0.004	0.042	-0.095	0.925	-0.09	0.082	0
L3.Progesterone.mediated.oocyte.maturation	0.000	0.000	0.117	0.907	0.00	0.000	0

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	0.02	0.042	0.483	0.632	-0.065	0.106	0.000
L3.Propanoate.metabolism	0.00	0.000	-0.597	0.555	0.000	0.000	0.011

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	0.007	0.041	0.179	0.859	-0.076	0.091	0.000
L3.Prostate.cancer	0.000	0.000	-0.224	0.824	0.000	0.000	0.002

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	0.039	0.057	0.683	0.500	-0.077	0.154	0.000
L3.Proteasome	0.000	0.000	-0.759	0.454	0.000	0.000	0.018

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	0.042	0.034	1.222	0.231	-0.028	0.111	0.000
L3.Protein.digestion.and.absorption	0.000	0.000	-1.701	0.099	0.000	0.000	0.085

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	-0.034	0.057	-0.593	0.558	-0.151	0.083	0.000
L3.Protein.export	0.000	0.000	0.656	0.517	0.000	0.000	0.014

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	0.023	0.043	0.539	0.594	-0.065	0.112	0.000
L3.Protein.folding.and.associated.processing	0.000	0.000	-0.655	0.518	0.000	0.000	0.014

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	0.036	0.038	0.961	0.344	-0.041	0.113	0.000
L3.Protein.kinases	0.000	0.000	-1.254	0.219	0.000	0.000	0.048

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	0.03	0.045	0.661	0.514	-0.063	0.123	0.00
L3.Protein.processing.in.endoplasmic.reticulum	0.00	0.000	-0.787	0.438	0.000	0.000	0.02

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	0.015	0.032	0.465	0.645	-0.05	0.08	0.000
L3.Proximal.tubule.bicarbonate.reclamation	0.000	0.000	-0.734	0.469	0.00	0.00	0.017

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	-0.012	0.054	-0.223	0.825	-0.122	0.098	0.000
L3.Purine.metabolism	0.000	0.000	0.251	0.803	0.000	0.000	0.002

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	-0.03	0.057	-0.524	0.604	-0.146	0.086	0.000
L3.Pyrimidine.metabolism	0.00	0.000	0.582	0.565	0.000	0.000	0.011

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	0.022	0.044	0.502	0.619	-0.067	0.111	0.000
L3.Pyruvate.metabolism	0.000	0.000	-0.607	0.548	0.000	0.000	0.012

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	-0.005	0.031	-0.147	0.884	-0.068	0.058	0.000
L3.RIG.I.like.receptor.signaling.pathway	0.000	0.000	0.247	0.806	0.000	0.000	0.002

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	0.005	0.057	0.095	0.925	-0.11	0.121	0
L3.RNA.degradation	0.000	0.000	-0.105	0.917	0.00	0.000	0

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	-0.064	0.056	-1.147	0.260	-0.177	0.05	0.00
L3.RNA.polymerase	0.000	0.000	1.274	0.212	0.000	0.00	0.05

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	0.008	0.047	0.159	0.875	-0.089	0.104	0.000
L3.RNA.transport	0.000	0.000	-0.186	0.854	0.000	0.000	0.001

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)	0	0.024	0	1	-0.05	0.05	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	-0.014	0.031	-0.442	0.661	-0.077	0.049	0.000
L3.Renal.cell.carcinoma	0.000	0.000	0.732	0.470	0.000	0.000	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	0.002	0.025	0.089	0.930	-0.049	0.054	0.000
L3.Renin.angiotensin.system	0.000	0.000	-0.424	0.675	-0.001	0.000	0.006

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	0.002	0.05	0.039	0.969	-0.099	0.103	0
L3.Replication..recombination.and.repair.proteins	0.000	0.00	-0.045	0.964	0.000	0.000	0

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	0.02	0.047	0.432	0.669	-0.075	0.115	0.000
L3.Restriction.enzyme	0.00	0.000	-0.510	0.614	0.000	0.000	0.008

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	0.047	0.034	1.386	0.176	-0.022	0.116	0.000
L3.Retinol.metabolism	0.000	0.000	-1.914	0.065	0.000	0.000	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)	0	0.024	0	1	-0.05	0.05	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	0.011	0.041	0.273	0.786	-0.072	0.094	0.000
L3.Riboflavin.metabolism	0.000	0.000	-0.346	0.732	0.000	0.000	0.004

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	-0.056	0.059	-0.945	0.352	-0.176	0.065	0.000
L3.Ribosome	0.000	0.000	1.039	0.307	0.000	0.000	0.034

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	-0.016	0.051	-0.310	0.759	-0.119	0.088	0.000
L3.Ribosome.Biogenesis	0.000	0.000	0.355	0.725	0.000	0.000	0.004

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	0.007	0.053	0.133	0.895	-0.102	0.116	0.000
L3.Ribosome.biogenesis.in.eukaryotes	0.000	0.000	-0.150	0.882	0.000	0.000	0.001

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)	0	0.024	0	1	-0.05	0.05	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	0.066	0.047	1.396	0.173	-0.03	0.162	0.000
L3.Secondary.bile.acid.biosynthesis	0.000	0.000	-1.618	0.116	0.00	0.000	0.078

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	0.023	0.036	0.630	0.534	-0.051	0.096	0.000
L3.Secretion.system	0.000	0.000	-0.861	0.396	0.000	0.000	0.023

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	0.011	0.047	0.243	0.810	-0.084	0.106	0.000
L3.Selenocompound.metabolism	0.000	0.000	-0.287	0.776	0.000	0.000	0.003

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)	0	0.024	0	1	-0.05	0.05	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	0.026	0.026	0.977	0.336	-0.028	0.08	0.000
L3.Shigellosis	-0.014	0.007	-2.039	0.050	-0.028	0.00	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	0.009	0.045	0.199	0.844	-0.082	0.1	0.000
L3.Signal.transduction.mechanisms	0.000	0.000	-0.239	0.813	0.000	0.0	0.002

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	-0.002	0.027	-0.061	0.952	-0.058	0.054	0.000
L3.Small.cell.lung.cancer	0.000	0.001	0.142	0.888	-0.002	0.002	0.001

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	0.067	0.041	1.638	0.112	-0.017	0.151	0.000
L3.Sphingolipid.metabolism	0.000	0.000	-1.990	0.056	0.000	0.000	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)	0	0.024	0	1	-0.05	0.05	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	-0.042	0.033	-1.273	0.213	-0.11	0.026	0.000
L3.Sporulation	0.000	0.000	1.803	0.081	0.00	0.000	0.095

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	-0.01	0.031	-0.329	0.745	-0.073	0.053	0.00
L3.Staphylococcus.aureus.infection	0.00	0.000	0.553	0.585	0.000	0.000	0.01

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	0.048	0.046	1.063	0.296	-0.045	0.142	0.000
L3.Starch.and.sucrose.metabolism	0.000	0.000	-1.254	0.219	0.000	0.000	0.048

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	-0.004	0.028	-0.143	0.887	-0.06	0.052	0.000
L3.Steroid.biosynthesis	0.000	0.000	0.323	0.749	0.00	0.001	0.003

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	0.039	0.029	1.363	0.183	-0.019	0.098	0.000
L3.Steroid.hormone.biosynthesis	0.000	0.000	-2.268	0.031	0.000	0.000	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	0.002	0.027	0.062	0.951	-0.053	0.056	0.
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	0.000	0.000	-0.167	0.869	0.000	0.000	0.

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	0.058	0.051	1.148	0.260	-0.045	0.161	0.000
L3.Streptomycin.biosynthesis	0.000	0.000	-1.306	0.201	0.000	0.000	0.052

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	0.018	0.026	0.673	0.506	-0.036	0.071	0.000
L3.Styrene.degradation	0.000	0.000	-1.625	0.115	0.000	0.000	0.079

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	0.033	0.045	0.728	0.472	-0.059	0.125	0.000
L3.Sulfur.metabolism	0.000	0.000	-0.867	0.393	0.000	0.000	0.024

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	0.018	0.037	0.481	0.634	-0.058	0.094	0.000
L3.Sulfur.relay.system	0.000	0.000	-0.641	0.527	0.000	0.000	0.013

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	-0.013	0.038	-0.337	0.738	-0.09	0.064	0.000
L3.Synthesis.and.degradation.of.ketone.bodies	0.000	0.000	0.447	0.658	0.00	0.000	0.006

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	0.011	0.026	0.429	0.671	-0.042	0.064	0.000
L3.Systemic.lupus.erythematosus	0.000	0.000	-1.218	0.233	0.000	0.000	0.046

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)	0	0.024	0	1	-0.05	0.05	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	0.021	0.048	0.428	0.672	-0.078	0.12	0.000
L3.Taurine.and.hypotaurine.metabolism	0.000	0.000	-0.498	0.622	0.000	0.00	0.008

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	-0.054	0.057	-0.946	0.352	-0.17	0.062	0.000
L3.Terpenoid.backbone.biosynthesis	0.000	0.000	1.048	0.303	0.00	0.000	0.034

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	-0.001	0.05	-0.025	0.980	-0.103	0.101	0
L3.Tetracycline.biosynthesis	0.000	0.00	0.029	0.977	0.000	0.000	0

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	0.002	0.052	0.040	0.969	-0.105	0.109	0
L3.Thiamine.metabolism	0.000	0.000	-0.045	0.964	0.000	0.000	0

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)	0	0.024	0	1	-0.05	0.05	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	0.018	0.029	0.624	0.538	-0.041	0.076	0.000
L3.Toluene.degradation	0.000	0.000	-1.181	0.247	0.000	0.000	0.043

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	-0.002	0.027	-0.061	0.952	-0.058	0.054	0.000
L3.Toxoplasmosis	0.000	0.001	0.142	0.888	-0.002	0.002	0.001

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	0.019	0.037	0.507	0.616	-0.056	0.094	0.000
L3.Transcription.factors	0.000	0.000	-0.683	0.500	0.000	0.000	0.015

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	0.007	0.058	0.128	0.899	-0.11	0.125	0.000
L3.Transcription.machinery	0.000	0.000	-0.141	0.889	0.00	0.000	0.001

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	0.02	0.027	0.756	0.455	-0.035	0.076	0.000
L3.Transcription.related.proteins	0.00	0.000	-1.603	0.119	0.000	0.000	0.077

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	-0.04	0.056	-0.712	0.482	-0.154	0.075	0.00
L3.Translation.factors	0.00	0.000	0.793	0.434	0.000	0.000	0.02

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	-0.018	0.051	-0.350	0.729	-0.122	0.086	0.000
L3.Translation.proteins	0.000	0.000	0.401	0.691	0.000	0.000	0.005

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	0.015	0.04	0.365	0.717	-0.068	0.097	0.000
L3.Transporters	0.000	0.00	-0.462	0.647	0.000	0.000	0.007

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	0.01	0.04	0.239	0.813	-0.073	0.092	0
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis	0.00	0.00	-0.303	0.764	0.000	0.000	0

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	0.024	0.031	0.763	0.452	-0.04	0.088	0.000
L3.Tryptophan.metabolism	0.000	0.000	-1.205	0.238	0.00	0.000	0.045

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	-0.023	0.062	-0.371	0.713	-0.15	0.104	0.000
L3.Tuberculosis	0.000	0.000	0.405	0.688	0.00	0.000	0.005

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	0.028	0.036	0.783	0.440	-0.046	0.102	0.000
L3.Two.component.system	0.000	0.000	-1.058	0.298	0.000	0.000	0.035

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	-0.02	0.061	-0.318	0.753	-0.145	0.106	0.000
L3.Type.I.diabetes.mellitus	0.00	0.000	0.347	0.731	0.000	0.000	0.004

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	-0.003	0.051	-0.061	0.951	-0.106	0.1	0
L3.Type.II.diabetes.mellitus	0.000	0.000	0.070	0.944	0.000	0.0	0

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	0.025	0.041	0.604	0.550	-0.059	0.108	0.000
L3.Tyrosine.metabolism	0.000	0.000	-0.756	0.456	0.000	0.000	0.018

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	0.027	0.032	0.856	0.399	-0.038	0.093	0.
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis	0.000	0.000	-1.308	0.201	0.000	0.000	0.

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	0.036	0.028	1.272	0.213	-0.022	0.093	0.000
L3.Ubiquitin.system	0.000	0.000	-2.221	0.034	0.000	0.000	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)	0	0.024	0	1	-0.05	0.05	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	0	0.053	0.008	0.994	-0.108	0.109	0
L3.Valine..leucine.and.isoleucine.biosynthesis	0	0.000	-0.009	0.993	0.000	0.000	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	0.022	0.038	0.585	0.563	-0.056	0.101	0.000
L3.Valine..leucine.and.isoleucine.degradation	0.000	0.000	-0.763	0.451	0.000	0.000	0.018

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	-0.027	0.027	-1.023	0.314	-0.082	0.027	0.000
L3.Various.types.of.N.glycan.biosynthesis	0.027	0.013	2.063	0.048	0.000	0.054	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)	0	0.024	0	1	-0.05	0.05	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	-0.005	0.026	-0.207	0.837	-0.058	0.047	0.000
L3.Vasopressin.regulated.water.reabsorption	0.021	0.030	0.717	0.479	-0.039	0.082	0.016

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	0.013	0.027	0.480	0.635	-0.042	0.068	0.000
L3.Vibrio.cholerae.infection	-0.018	0.016	-1.125	0.269	-0.050	0.015	0.039

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	0.034	0.039	0.875	0.388	-0.045	0.113	0.000
L3.Vibrio.cholerae.pathogenic.cycle	0.000	0.000	-1.128	0.268	0.000	0.000	0.039

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	-0.002	0.027	-0.061	0.952	-0.058	0.054	0.000
L3.Viral.myocarditis	0.000	0.001	0.142	0.888	-0.002	0.002	0.001

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	0.045	0.042	1.070	0.293	-0.041	0.131	0.000
L3.Vitamin.B6.metabolism	0.000	0.000	-1.308	0.201	0.000	0.000	0.052

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	0.026	0.458	0.650	-0.041	0.065	0.000
L3.Wnt.signaling.pathway	-0.048	0.040	-1.212	0.235	-0.129	0.033	0.045

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	0.015	0.037	0.417	0.680	-0.06	0.091	0.00
L3.Xylene.degradation	0.000	0.000	-0.558	0.581	0.00	0.000	0.01

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	-0.024	0.063	-0.386	0.702	-0.153	0.105	0.000
L3.Zeatin.biosynthesis	0.000	0.000	0.420	0.678	0.000	0.000	0.006

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	0.019	0.026	0.735	0.468	-0.035	0.073	0.000
L3.alpha.Linolenic.acid.metabolism	0.000	0.000	-1.671	0.105	0.000	0.000	0.083

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	0.024	0.035	0.683	0.500	-0.047	0.095	0.000
L3.beta.Alanine.metabolism	0.000	0.000	-0.958	0.346	0.000	0.000	0.029

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	-0.005	0.044	-0.109	0.914	-0.095	0.086	0.000
L3.beta.Lactam.resistance	0.000	0.000	0.131	0.896	0.000	0.000	0.001

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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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	-0.002	0.027	-0.061	0.952	-0.058	0.054	0.000
L3.p53.signaling.pathway	0.000	0.001	0.142	0.888	-0.002	0.002	0.001

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 %	9
Intercept	0.004	0.022	0.171	0.865	-0.042	
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	0.000	0.000	-0.914	0.368	0.000	

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	-0.033	0.033	-0.983	0.333	-0.1	0.035	0.000
L3.ABC.transporters	0.000	0.000	1.301	0.203	0.0	0.000	0.052

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)	0	0.022	0	1	-0.045	0.045	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	-0.047	0.035	-1.353	0.186	-0.119	0.024	0.000
L3.Adipocytokine.signaling.pathway	0.000	0.000	1.706	0.098	0.000	0.000	0.086

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	-0.018	0.028	-0.648	0.522	-0.076	0.04	0.000
L3.African.trypanosomiasis	0.000	0.000	1.021	0.316	0.000	0.00	0.033

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	-0.079	0.045	-1.759	0.089	-0.172	0.013	0.000
L3.Alanine..aspartate.and.glutamate.metabolism	0.000	0.000	1.986	0.056	0.000	0.000	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	0.004	0.022	0.168	0.867	-0.042	0.049	0.000
L3.Aldosterone.regulated.sodium.reabsorption	-0.120	0.126	-0.952	0.348	-0.379	0.138	0.028

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	-0.062	0.038	-1.622	0.115	-0.14	0.016	0.000
L3.Alzheimer.s.disease	0.000	0.000	1.941	0.062	0.00	0.000	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	-0.038	0.032	-1.187	0.245	-0.104	0.027	0.000
L3.Amino.acid.metabolism	0.000	0.000	1.593	0.122	0.000	0.000	0.076

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	-0.086	0.045	-1.894	0.068	-0.178	0.007	0.000
L3.Amino.acid.related.enzymes	0.000	0.000	2.134	0.041	0.000	0.000	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	-0.074	0.045	-1.662	0.107	-0.165	0.017	0.000
L3.Amino.sugar.and.nucleotide.sugar.metabolism	0.000	0.000	1.888	0.069	0.000	0.000	0.103

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	-0.085	0.048	-1.757	0.089	-0.184	0.014	0.000
L3.Aminoacyl.tRNA.biosynthesis	0.000	0.000	1.951	0.060	0.000	0.000	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	-0.028	0.031	-0.890	0.381	-0.092	0.036	0.000
L3.Aminobenzoate.degradation	0.000	0.000	1.235	0.226	0.000	0.000	0.047

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	-0.024	0.029	-0.839	0.408	-0.082	0.034	0.000
L3.Amoebiasis	0.000	0.000	1.294	0.206	0.000	0.000	0.051

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	-0.021	0.026	-0.808	0.425	-0.073	0.032	0.000
L3.Amyotrophic.lateral.sclerosis..ALS.	0.000	0.000	1.500	0.144	0.000	0.000	0.068

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	-0.031	0.037	-0.846	0.404	-0.107	0.044	0.000
L3.Antigen.processing.and.presentation	0.000	0.000	1.049	0.303	0.000	0.000	0.034

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	0.002	0.026	0.076	0.940	-0.052	0.056	0.000
L3.Apoptosis	0.000	0.000	-0.140	0.889	0.000	0.000	0.001

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	-0.016	0.032	-0.506	0.617	-0.08	0.048	0.000
L3.Arachidonic.acid.metabolism	0.000	0.000	0.711	0.483	0.00	0.000	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	-0.054	0.037	-1.488	0.147	-0.129	0.02	0.000
L3.Arginine.and.proline.metabolism	0.000	0.000	1.826	0.078	0.000	0.00	0.097

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)	0	0.022	0	1	-0.045	0.045	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	-0.024	0.027	-0.904	0.373	-0.079	0.031	0.000
L3.Ascorbate.and.aldarate.metabolism	0.000	0.000	1.501	0.144	0.000	0.000	0.068

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	-0.011	0.024	-0.459	0.650	-0.061	0.039	0.000
L3.Atrazine.degradation	0.000	0.000	1.049	0.303	0.000	0.000	0.034

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	0.025	0.033	0.754	0.456	-0.042	0.092	0.000
L3.Bacterial.chemotaxis	0.000	0.000	-1.016	0.318	0.000	0.000	0.032

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	0.001	0.024	0.054	0.957	-0.047	0.05	0.000
L3.Bacterial.invasion.of.epithelial.cells	0.000	0.000	-0.163	0.871	0.000	0.00	0.001

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	0.008	0.032	0.240	0.812	-0.057	0.073	0.000
L3.Bacterial.motility.proteins	0.000	0.000	-0.336	0.739	0.000	0.000	0.004

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	-0.036	0.031	-1.173	0.250	-0.1	0.027	0.000
L3.Bacterial.secretion.system	0.000	0.000	1.618	0.116	0.0	0.000	0.078

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	-0.061	0.05	-1.219	0.232	-0.163	0.041	0.000
L3.Bacterial.toxins	0.000	0.00	1.353	0.186	0.000	0.000	0.056

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	0.014	0.023	0.602	0.552	-0.033	0.061	0.00
L3.Basal.transcription.factors	0.000	0.000	-1.645	0.110	0.000	0.000	0.08

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	-0.083	0.046	-1.817	0.079	-0.176	0.01	0.000
L3.Base.excision.repair	0.000	0.000	2.045	0.050	0.000	0.00	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	-0.032	0.029	-1.118	0.273	-0.092	0.027	0.000
L3.Benzoate.degradation	0.000	0.000	1.649	0.110	0.000	0.000	0.081

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	-0.008	0.023	-0.352	0.727	-0.056	0.039	0.000
L3.Betalain.biosynthesis	0.000	0.000	1.057	0.299	0.000	0.000	0.035

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	0.003	0.025	0.118	0.907	-0.048	0.054	0.000
L3.Bile.secretion	0.000	0.002	-0.266	0.792	-0.004	0.003	0.002

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	-0.02	0.025	-0.806	0.426	-0.072	0.031
L3.Biosynthesis.and.biodegradation.of.secondary.metabolites	0.00	0.000	1.520	0.139	0.000	0.000

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	0.002	0.023	0.099	0.922	-0.044	0.048	0.
L3.Biosynthesis.of.12...14..and.16.membered.macrolides	-0.071	0.128	-0.557	0.582	-0.332	0.190	0.

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	-0.03	0.031	-0.954	0.348	-0.093	0.034	0.000
L3.Biosynthesis.of.ansamycins	0.00	0.000	1.328	0.194	0.000	0.000	0.054

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	-0.017	0.025	-0.685	0.498	-0.068	0.034
L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides	0.000	0.000	1.358	0.185	0.000	0.000

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)	0	0.022	0	1	-0.045	0.045	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	-0.008	0.023	-0.363	0.719	-0.056	0.039	0.000
L3.Biosynthesis.of.type.II.polyketide.products	0.000	0.000	1.056	0.300	0.000	0.000	0.035

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	-0.026	0.029	-0.879	0.386	-0.086	0.034	0.000
L3.Biosynthesis.of.unsaturated.fatty.acids	0.000	0.000	1.302	0.203	0.000	0.000	0.052

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	-0.068	0.047	-1.439	0.161	-0.164	0.028	0.000
L3.Biosynthesis.of.vancomycin.group.antibiotics	0.000	0.000	1.617	0.116	0.000	0.000	0.078

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	-0.089	0.034	-2.593	0.015	-0.159	-0.019	0.000
L3.Biotin.metabolism	0.000	0.000	3.141	0.004	0.000	0.000	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	-0.054	0.042	-1.284	0.209	-0.139	0.032	0.000
L3.Bisphenol.degradation	0.000	0.000	1.498	0.145	0.000	0.000	0.067

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	-0.012	0.025	-0.481	0.634	-0.062	0.038	0.000
L3.Bladder.cancer	0.000	0.000	1.062	0.297	0.000	0.000	0.035

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	-0.028	0.035	-0.797	0.432	-0.1	0.044	0.000
L3.Butanoate.metabolism	0.000	0.000	1.020	0.316	0.0	0.000	0.032

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	-0.097	0.054	-1.789	0.084	-0.208	0.014	0.000
L3.Butirosin.and.neomycin.biosynthesis	0.000	0.000	1.941	0.062	0.000	0.000	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	-0.062	0.041	-1.526	0.137	-0.145	0.021	0.000
L3.C5.Branched.dibasic.acid.metabolism	0.000	0.000	1.788	0.084	0.000	0.000	0.093

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)	0	0.022	0	1	-0.045	0.045	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	0.003	0.025	0.136	0.892	-0.047	0.053	0.000
L3.Caffeine.metabolism	-0.004	0.013	-0.328	0.745	-0.030	0.022	0.003

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	0.008	0.025	0.322	0.750	-0.043	0.059	0.000
L3.Calcium.signaling.pathway	-0.013	0.019	-0.693	0.494	-0.051	0.025	0.015

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	-0.019	0.026	-0.736	0.467	-0.071	0.034	0.000
L3.Caprolactam.degradation	0.000	0.000	1.368	0.181	0.000	0.000	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	-0.014	0.032	-0.442	0.661	-0.079	0.051	0.000
L3.Carbohydrate.digestion.and.absorption	0.000	0.000	0.616	0.543	0.000	0.000	0.012

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	-0.038	0.036	-1.053	0.301	-0.112	0.036	0.000
L3.Carbohydrate.metabolism	0.000	0.000	1.317	0.198	0.000	0.000	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	-0.063	0.038	-1.659	0.108	-0.14	0.014	0.000
L3.Carbon.fixation.in.photosynthetic.organisms	0.000	0.000	1.994	0.055	0.00	0.000	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	-0.052	0.04	-1.303	0.202	-0.134	0.03	0.000
L3.Carbon.fixation.pathways.in.prokaryotes	0.000	0.00	1.543	0.133	0.000	0.00	0.071

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	-0.009	0.024	-0.365	0.717	-0.057	0.04	0.000
L3.Cardiac.muscle.contraction	0.000	0.000	0.990	0.330	0.000	0.00	0.031

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	0.01	0.025	0.391	0.698	-0.042	0.062	0.00
L3.Carotenoid.biosynthesis	0.00	0.000	-0.802	0.429	0.000	0.000	0.02

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)	0	0.022	0	1	-0.045	0.045	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	-0.099	0.051	-1.948	0.061	-0.204	0.005	0.000
L3.Cell.cycle. . . Caulobacter	0.000	0.000	2.132	0.041	0.000	0.000	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)	0	0.022	0	1	-0.045	0.045	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	-0.038	0.036	-1.067	0.294	-0.11	0.035	0.000
L3.Cell.division	0.000	0.000	1.347	0.188	0.00	0.000	0.055

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	-0.07	0.033	-2.087	0.045	-0.138	-0.001	0.000
L3.Cell.motility.and.secretion	0.00	0.000	2.616	0.014	0.000	0.000	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	-0.045	0.034	-1.323	0.196	-0.114	0.024	0.000
L3.Cellular.antigens	0.000	0.000	1.699	0.100	0.000	0.000	0.085

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	-0.019	0.027	-0.693	0.494	-0.075	0.037	0.000
L3.Chagas.disease..American.trypanosomiasis.	0.000	0.000	1.153	0.258	0.000	0.000	0.041

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	-0.064	0.041	-1.565	0.128	-0.147	0.019	0.000
L3.Chaperones.and.folding.catalysts	0.000	0.000	1.834	0.077	0.000	0.000	0.098

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	-0.024	0.044	-0.559	0.581	-0.114	0.065	0.000
L3.Chloroalkane.and.chloroalkene.degradation	0.000	0.000	0.648	0.522	0.000	0.000	0.013

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 %	R
Intercept	-0.011	0.028	-0.416	0.68	-0.068	0.045	0.000
L3.Chlorocyclohexane.and.chlorobenzene.degradation	0.000	0.000	0.700	0.49	0.000	0.000	0.010

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)	0	0.022	0	1	-0.045	0.045	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	-0.069	0.044	-1.580	0.125	-0.158	0.02	0.000
L3.Chromosome	0.000	0.000	1.807	0.081	0.000	0.00	0.095

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	-0.008	0.024	-0.336	0.739	-0.057	0.041	0.000
L3.Chronic.myeloid.leukemia	0.032	0.036	0.888	0.381	-0.042	0.105	0.025

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	0.007	0.024	0.298	0.768	-0.042	0.056	0.000
L3.Circadian.rhythm...plant	-0.005	0.007	-0.753	0.457	-0.018	0.009	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	-0.037	0.033	-1.114	0.274	-0.105	0.031	0.000
L3.Citrate.cycle..TCA.cycle.	0.000	0.000	1.460	0.155	0.000	0.000	0.064

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)	0	0.022	0	1	-0.045	0.045	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	-0.001	0.025	-0.041	0.968	-0.051	0.049	0
L3.Colorectal.cancer	0.000	0.001	0.095	0.925	-0.002	0.002	0

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)	0	0.022	0	1	-0.045	0.045	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	-0.057	0.036	-1.60	0.120	-0.13	0.016	0.000
L3.Cyanoamino.acid.metabolism	0.000	0.000	1.98	0.057	0.00	0.000	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	-0.07	0.039	-1.767	0.087	-0.15	0.011	0.000
L3.Cysteine.and.methionine.metabolism	0.00	0.000	2.084	0.046	0.00	0.000	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	0.003	0.022	0.128	0.899	-0.043	0.049	0.000
L3.Cytochrome.P450	-0.092	0.127	-0.726	0.474	-0.352	0.167	0.017

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)	0	0.022	0	1	-0.045	0.045	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)	0	0.022	0	1	-0.045	0.045	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	-0.062	0.046	-1.343	0.189	-0.156	0.032	0.000
L3.Cytoskeleton.proteins	0.000	0.000	1.519	0.139	0.000	0.000	0.069

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)	0	0.022	0	1	-0.045	0.045	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	-0.068	0.044	-1.528	0.137	-0.159	0.023	0.000
L3.D.Alanine.metabolism	0.000	0.000	1.740	0.092	0.000	0.000	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	-0.033	0.02	-1.621	0.115	-0.074	0.009	0.000
L3.D.Arginine.and.D.ornithine.metabolism	0.000	0.00	3.790	0.001	0.000	0.000	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	-0.087	0.043	-2.010	0.053	-0.175	0.001	0.000
L3.D.Glutamine.and.D.glutamate.metabolism	0.000	0.000	2.287	0.029	0.000	0.000	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	-0.082	0.047	-1.730	0.094	-0.179	0.015	0.000
L3.DNA.repair.and.recombination.proteins	0.000	0.000	1.931	0.063	0.000	0.000	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	-0.095	0.051	-1.882	0.070	-0.199	0.008	0.000
L3.DNA.replication	0.000	0.000	2.066	0.048	0.000	0.000	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	-0.087	0.049	-1.761	0.088	-0.188	0.014	0.000
L3.DNA.replication.proteins	0.000	0.000	1.947	0.061	0.000	0.000	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)	0	0.022	0	1	-0.045	0.045	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	-0.026	0.03	-0.865	0.394	-0.088	0.036	0.000
L3.Dioxin.degradation	0.000	0.00	1.243	0.224	0.000	0.000	0.047

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	-0.017	0.029	-0.588	0.561	-0.075	0.042	0.000
L3.Drug.metabolism. . . cytochrome.P450	0.000	0.000	0.920	0.365	0.000	0.000	0.027

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	-0.079	0.046	-1.721	0.096	-0.172	0.015	0.000
L3.Drug.metabolism. . . other.enzymes	0.000	0.000	1.939	0.062	0.000	0.000	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)	0	0.022	0	1	-0.045	0.045	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	-0.014	0.028	-0.489	0.629	-0.071	0.044	0.00
L3.Electron.transfer.carriers	0.000	0.000	0.794	0.433	0.000	0.000	0.02

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)	0	0.022	0	1	-0.045	0.045	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	0.011	0.023	0.489	0.628	-0.035	0.057	0.000
L3.Endocytosis	-0.010	0.007	-1.587	0.123	-0.024	0.003	0.075

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	-0.042	0.036	-1.153	0.258	-0.115	0.032	0.000
L3.Energy.metabolism	0.000	0.000	1.437	0.161	0.000	0.000	0.062

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	-0.068	0.037	-1.818	0.079	-0.145	0.008
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	0.000	0.000	2.183	0.037	0.000	0.000

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)	0	0.022	0	1	-0.045	0.045	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	0.026	0.027	0.950	0.350	-0.029	0.081	0.000
L3.Ether.lipid.metabolism	0.000	0.000	-1.573	0.126	0.000	0.000	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	-0.031	0.035	-0.882	0.385	-0.102	0.041	0.00
L3.Ethylbenzene.degradation	0.000	0.000	1.130	0.268	0.000	0.000	0.04

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)	0	0.022	0	1	-0.045	0.045	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	-0.055	0.044	-1.251	0.221	-0.146	0.035	0.000
L3.Fatty.acid.biosynthesis	0.000	0.000	1.433	0.162	0.000	0.000	0.062

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)	0	0.022	0	1	-0.045	0.045	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	-0.032	0.033	-0.948	0.351	-0.1	0.036	0.000
L3.Fatty.acid.metabolism	0.000	0.000	1.252	0.220	0.0	0.000	0.048

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)	0	0.022	0	1	-0.045	0.045	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	0.011	0.023	0.489	0.628	-0.035	0.057	0.000
L3.Fc.gamma.R.mediated.phagocytosis	-0.010	0.007	-1.587	0.123	-0.024	0.003	0.075

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	0.017	0.028	0.605	0.550	-0.04	0.073	0.000
L3.Flagellar.assembly	0.000	0.000	-0.993	0.329	0.00	0.000	0.031

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	0.008	0.028	0.277	0.784	-0.049	0.065	0.000
L3.Flavone.and.flavonol.biosynthesis	0.000	0.000	-0.459	0.649	0.000	0.000	0.007

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	-0.004	0.023	-0.185	0.854	-0.051	0.043	0.000
L3.Flavonoid.biosynthesis	0.000	0.000	0.703	0.487	0.000	0.000	0.016

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	-0.013	0.024	-0.538	0.595	-0.061	0.036	0.000
L3.Fluorobenzoate.degradation	0.000	0.000	1.328	0.194	0.000	0.000	0.054

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)	0	0.022	0	1	-0.045	0.045	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	-0.081	0.043	-1.866	0.072	-0.17	0.008	0.000
L3.Folate.biosynthesis	0.000	0.000	2.127	0.042	0.00	0.000	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	-0.047	0.037	-1.261	0.217	-0.122	0.029	0.000
L3.Fructose.and.mannose.metabolism	0.000	0.000	1.549	0.132	0.000	0.000	0.072

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	-0.042	0.033	-1.291	0.207	-0.109	0.024	0.000
L3.Function.unknown	0.000	0.000	1.707	0.098	0.000	0.000	0.086

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)	0	0.022	0	1	-0.045	0.045	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)	0	0.022	0	1	-0.045	0.045	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	-0.066	0.046	-1.437	0.161	-0.16	0.028	0.000
L3.Galactose.metabolism	0.000	0.000	1.624	0.115	0.00	0.000	0.078

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)	0	0.022	0	1	-0.045	0.045	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	-0.067	0.041	-1.653	0.109	-0.15	0.016	0.000
L3.General.function.prediction.only	0.000	0.000	1.932	0.063	0.00	0.000	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	-0.025	0.026	-0.938	0.356	-0.079	0.029	0.000
L3.Geraniol.degradation	0.000	0.000	1.600	0.120	0.000	0.000	0.076

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	0.017	0.024	0.709	0.484	-0.032	0.067	0.00
L3.Germination	0.000	0.000	-1.522	0.139	0.000	0.000	0.07

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)	0	0.022	0	1	-0.045	0.045	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	-0.091	0.044	-2.065	0.048	-0.181	-0.001	0.000
L3.Glutamatergic.synapse	0.000	0.000	2.334	0.027	0.000	0.000	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	-0.041	0.034	-1.202	0.239	-0.11	0.029	0.000
L3.Glutathione.metabolism	0.000	0.000	1.550	0.132	0.00	0.000	0.072

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)	0	0.022	0	1	-0.045	0.045	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	-0.021	0.027	-0.756	0.455	-0.077	0.035	0.000
L3.Glycan.biosynthesis.and.metabolism	0.000	0.000	1.241	0.224	0.000	0.000	0.047

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	-0.036	0.038	-0.955	0.347	-0.114	0.041	0.000
L3.Glycerolipid.metabolism	0.000	0.000	1.167	0.253	0.000	0.000	0.042

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	-0.047	0.038	-1.247	0.222	-0.124	0.03	0.000
L3.Glycerophospholipid.metabolism	0.000	0.000	1.516	0.140	0.000	0.00	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	-0.067	0.039	-1.710	0.098	-0.147	0.013	0.000
L3.Glycine..serine.and.threonine.metabolism	0.000	0.000	2.025	0.052	0.000	0.000	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	-0.059	0.042	-1.415	0.167	-0.144	0.026	0.000
L3.Glycolysis. . . Gluconeogenesis	0.000	0.000	1.651	0.109	0.000	0.000	0.081

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	-0.004	0.023	-0.175	0.863	-0.050	0.042	0
L3.Glycosaminoglycan.biosynthesis. . . chondroitin.sulfate	0.016	0.021	0.761	0.453	-0.027	0.058	0

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	-0.064	0.034	-1.862	0.072	-0.133	0.006	0.000
L3.Glycosaminoglycan.degradation	0.000	0.000	2.329	0.027	0.000	0.000	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	-0.064	0.032	-1.978	0.057	-0.13	0.002	0.000
L3.Glycosphingolipid.biosynthesis. . . ganglio.series	0.000	0.000	2.534	0.017	0.00	0.000	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	-0.065	0.036	-1.797	0.082	-0.139	0.009	0.000
L3.Glycosphingolipid.biosynthesis. . . globo.series	0.000	0.000	2.195	0.036	0.000	0.000	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	-0.01	0.022	-0.466	0.645	-0.054	0.034
L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series	0.00	0.000	2.019	0.052	0.000	0.000

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)	0	0.022	0	1	-0.045	0.045	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	-0.069	0.039	-1.781	0.085	-0.147	0.01	0.000
L3.Glycosyltransferases	0.000	0.000	2.116	0.043	0.000	0.00	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	-0.043	0.032	-1.343	0.189	-0.108	0.022	0.000
L3.Glyoxylate.and.dicarboxylate.metabolism	0.000	0.000	1.793	0.083	0.000	0.000	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	0.011	0.023	0.489	0.628	-0.035	0.057	0.000
L3.GnRH.signaling.pathway	-0.010	0.007	-1.587	0.123	-0.024	0.003	0.075

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)	0	0.022	0	1	-0.045	0.045	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)	0	0.022	0	1	-0.045	0.045	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)	0	0.022	0	1	-0.045	0.045	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	-0.091	0.044	-2.055	0.049	-0.181	-0.001	0.000
L3.Histidine.metabolism	0.000	0.000	2.321	0.027	0.000	0.000	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	-0.09	0.049	-1.827	0.078	-0.191	0.011	0.000
L3.Homologous.recombination	0.00	0.000	2.018	0.053	0.000	0.000	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	-0.034	0.039	-0.877	0.387	-0.113	0.045	0.000
L3.Huntington.s.disease	0.000	0.000	1.066	0.295	0.000	0.000	0.035

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	0.004	0.023	0.159	0.875	-0.044	0.051	0.00
L3.Hypertrophic.cardiomyopathy..HCM.	-0.001	0.002	-0.573	0.571	-0.004	0.002	0.01

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	-0.007	0.026	-0.282	0.780	-0.060	0.045	0.00
L3.Indole.alkaloid.biosynthesis	0.013	0.023	0.561	0.579	-0.034	0.060	0.01

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	-0.001	0.025	-0.041	0.968	-0.051	0.049	0
L3.Influenza.A	0.000	0.001	0.095	0.925	-0.002	0.002	0

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	-0.03	0.03	-0.985	0.333	-0.091	0.032	0.000
L3.Inorganic.ion.transport.and.metabolism	0.00	0.00	1.418	0.166	0.000	0.000	0.061

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	-0.026	0.028	-0.915	0.367	-0.083	0.032	0.000
L3.Inositol.phosphate.metabolism	0.000	0.000	1.423	0.165	0.000	0.000	0.061

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	-0.048	0.044	-1.093	0.283	-0.138	0.042	0.000
L3.Insulin.signaling.pathway	0.000	0.000	1.259	0.218	0.000	0.000	0.049

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	-0.022	0.039	-0.573	0.571	-0.101	0.057	0.000
L3.Ion.channels	0.000	0.000	0.698	0.491	0.000	0.000	0.015

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	0.003	0.023	0.130	0.898	-0.044	0.050	0.000
L3.Isoflavonoid.biosynthesis	-0.002	0.003	-0.475	0.638	-0.009	0.005	0.007

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	-0.049	0.032	-1.520	0.139	-0.114	0.017	0.000
L3.Isoquinoline.alkaloid.biosynthesis	0.000	0.000	2.011	0.053	0.000	0.000	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)	0	0.022	0	1	-0.045	0.045	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)	0	0.022	0	1	-0.045	0.045	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	-0.025	0.031	-0.810	0.424	-0.09	0.039	0.000
L3.Limonene.and.pinene.degradation	0.000	0.000	1.129	0.268	0.00	0.000	0.039

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	-0.071	0.043	-1.653	0.109	-0.158	0.017	0.000
L3.Linoleic.acid.metabolism	0.000	0.000	1.900	0.067	0.000	0.000	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	-0.07	0.041	-1.689	0.102	-0.154	0.015	0.00
L3.Lipid.biosynthesis.proteins	0.00	0.000	1.961	0.059	0.000	0.000	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	-0.032	0.031	-1.014	0.319	-0.096	0.032	0.000
L3.Lipid.metabolism	0.000	0.000	1.396	0.173	0.000	0.000	0.059

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	-0.044	0.037	-1.196	0.241	-0.12	0.031	0.000
L3.Lipoic.acid.metabolism	0.000	0.000	1.468	0.153	0.00	0.000	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	-0.057	0.027	-2.108	0.043	-0.113	-0.002	0.000
L3.Lipopolysaccharide.biosynthesis	0.000	0.000	3.034	0.005	0.000	0.000	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	-0.06	0.029	-2.085	0.046	-0.119	-0.001	0.000
L3.Lipopolysaccharide.biosynthesis.proteins	0.00	0.000	2.858	0.008	0.000	0.000	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)	0	0.022	0	1	-0.045	0.045	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)	0	0.022	0	1	-0.045	0.045	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	-0.084	0.046	-1.820	0.079	-0.178	0.01	0.000
L3.Lysine.biosynthesis	0.000	0.000	2.043	0.050	0.000	0.00	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	-0.031	0.03	-1.058	0.298	-0.092	0.029	0.00
L3.Lysine.degradation	0.000	0.00	1.531	0.136	0.000	0.000	0.07

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	-0.049	0.036	-1.359	0.184	-0.122	0.024	0.000
L3.Lysosome	0.000	0.000	1.692	0.101	0.000	0.000	0.085

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)	0	0.022	0	1	-0.045	0.045	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	-0.11	0.041	-2.710	0.011	-0.193	-0.027	0.000
L3.MAPK.signaling.pathway. . . yeast	0.00	0.000	3.086	0.004	0.000	0.000	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)	0	0.022	0	1	-0.045	0.045	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	0.009	0.025	0.363	0.719	-0.042	0.06	0.00
L3.Meiosis. . . yeast	0.000	0.000	-0.797	0.432	0.000	0.00	0.02

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	-0.008	0.023	-0.350	0.729	-0.056	0.039	0.000
L3.Melanogenesis	0.000	0.000	1.055	0.300	0.000	0.000	0.035

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	-0.045	0.031	-1.418	0.166	-0.109	0.02	0.000
L3.Membrane.and.intracellular.structural.molecules	0.000	0.000	1.914	0.065	0.000	0.00	0.106

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	-0.031	0.032	-0.962	0.344	-0.096	0.035	0.000
L3.Metabolism.of.cofactors.and.vitamins	0.000	0.000	1.308	0.201	0.000	0.000	0.052

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	-0.018	0.028	-0.621	0.539	-0.075	0.04	0.000
L3.Metabolism.of.xenobiotics.by.cytochrome.P450	0.000	0.000	0.989	0.331	0.000	0.00	0.031

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	-0.06	0.044	-1.382	0.177	-0.15	0.029	0.000
L3.Methane.metabolism	0.00	0.000	1.585	0.123	0.00	0.000	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	0.029	0.026	1.117	0.273	-0.024	0.082	0.000
L3.Mineral.absorption	0.000	0.000	-1.908	0.066	0.000	0.000	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	-0.083	0.05	-1.653	0.109	-0.185	0.02	0.000
L3.Mismatch.repair	0.000	0.00	1.824	0.078	0.000	0.00	0.097

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	-0.047	0.027	-1.724	0.095	-0.102	0.009	0.000
L3.N.Glycan.biosynthesis	0.000	0.000	2.578	0.015	0.000	0.000	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	-0.035	0.038	-0.915	0.367	-0.112	0.043	0.000
L3.NOD.like.receptor.signaling.pathway	0.000	0.000	1.119	0.272	0.000	0.000	0.039

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	-0.042	0.045	-0.943	0.353	-0.134	0.049	0.000
L3.Naphthalene.degradation	0.000	0.000	1.080	0.289	0.000	0.000	0.036

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)	0	0.022	0	1	-0.045	0.045	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)	0	0.022	0	1	-0.045	0.045	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	-0.058	0.043	-1.355	0.186	-0.145	0.029	0.000
L3.Nicotinate.and.nicotinamide.metabolism	0.000	0.000	1.568	0.127	0.000	0.000	0.073

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	-0.049	0.036	-1.370	0.181	-0.123	0.024	0.000
L3.Nitrogen.metabolism	0.000	0.000	1.701	0.099	0.000	0.000	0.085

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	-0.015	0.031	-0.491	0.627	-0.079	0.048	0.000
L3.Nitrotoluene.degradation	0.000	0.000	0.696	0.492	0.000	0.000	0.015

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	0.002	0.026	0.080	0.937	-0.05	0.054	0.000
L3.Non.homologous.end.joining	0.000	0.000	-0.163	0.871	0.00	0.000	0.001

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	-0.008	0.024	-0.336	0.739	-0.057	0.041	0.000
L3.Notch.signaling.pathway	0.032	0.036	0.888	0.381	-0.042	0.105	0.025

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	-0.068	0.038	-1.761	0.089	-0.146	0.011	0.000
L3.Novobiocin.biosynthesis	0.000	0.000	2.096	0.045	0.000	0.000	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	-0.088	0.054	-1.635	0.113	-0.198	0.022	0.000
L3.Nucleotide.excision.repair	0.000	0.000	1.778	0.085	0.000	0.000	0.093

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	-0.027	0.029	-0.941	0.354	-0.085	0.031	0.000
L3.Nucleotide.metabolism	0.000	0.000	1.435	0.162	0.000	0.000	0.062

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)	0	0.022	0	1	-0.045	0.045	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	-0.102	0.049	-2.104	0.044	-0.202	-0.003	0.000
L3.One.carbon.pool.by.folate	0.000	0.000	2.320	0.027	0.000	0.000	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)	0	0.022	0	1	-0.045	0.045	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	-0.056	0.038	-1.472	0.151	-0.134	0.022	0.000
L3.Other.glycan.degradation	0.000	0.000	1.771	0.087	0.000	0.000	0.092

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	-0.046	0.034	-1.362	0.183	-0.114	0.023	0.000
L3.Other.ion.coupled.transporters	0.000	0.000	1.761	0.088	0.000	0.000	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	-0.043	0.035	-1.241	0.224	-0.114	0.028	0.000
L3.Other.transporters	0.000	0.000	1.577	0.125	0.000	0.000	0.074

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)	0	0.022	0	1	-0.045	0.045	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	-0.043	0.04	-1.079	0.289	-0.125	0.038	0.000
L3.Others	0.000	0.00	1.287	0.208	0.000	0.000	0.051

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	-0.058	0.043	-1.332	0.193	-0.146	0.031	0.000
L3.Oxidative.phosphorylation	0.000	0.000	1.535	0.135	0.000	0.000	0.071

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	-0.063	0.046	-1.376	0.179	-0.158	0.031	0.000
L3.PPAR.signaling.pathway	0.000	0.000	1.555	0.130	0.000	0.000	0.072

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)	0	0.022	0	1	-0.045	0.045	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)	0	0.022	0	1	-0.045	0.045	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	-0.076	0.043	-1.755	0.089	-0.165	0.012	0.000
L3.Pantothenate.and.CoA.biosynthesis	0.000	0.000	2.005	0.054	0.000	0.000	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	-0.009	0.024	-0.372	0.712	-0.057	0.04	0.000
L3.Parkinson.s.disease	0.000	0.000	0.992	0.329	0.000	0.00	0.031

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	0.003	0.023	0.118	0.907	-0.045	0.050	0.000
L3.Pathogenic.Escherichia.coli.infection	-0.002	0.005	-0.401	0.691	-0.012	0.008	0.005

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	-0.054	0.033	-1.637	0.112	-0.122	0.013	0.000
L3.Pathways.in.cancer	0.000	0.000	2.102	0.044	0.000	0.000	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	-0.042	0.035	-1.225	0.230	-0.113	0.028	0.000
L3.Penicillin.and.cephalosporin.biosynthesis	0.000	0.000	1.560	0.129	0.000	0.000	0.073

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	-0.031	0.031	-1.001	0.325	-0.095	0.032	0.000
L3.Pentose.and.glucuronate.interconversions	0.000	0.000	1.391	0.174	0.000	0.000	0.059

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	-0.059	0.039	-1.504	0.143	-0.139	0.021	0.000
L3.Pentose.phosphate.pathway	0.000	0.000	1.787	0.084	0.000	0.000	0.093

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	-0.062	0.044	-1.415	0.167	-0.152	0.028	0.000
L3.Peptidases	0.000	0.000	1.619	0.116	0.000	0.000	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	-0.067	0.048	-1.392	0.174	-0.166	0.032	0.000
L3.Peptidoglycan.biosynthesis	0.000	0.000	1.553	0.131	0.000	0.000	0.072

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	-0.062	0.041	-1.514	0.140	-0.146	0.022	0.000
L3.Peroxisome	0.000	0.000	1.770	0.087	0.000	0.000	0.092

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	-0.019	0.025	-0.775	0.445	-0.069	0.031	0.000
L3.Pertussis	0.000	0.000	1.584	0.124	0.000	0.000	0.075

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)	0	0.022	0	1	-0.045	0.045	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	-0.029	0.028	-1.038	0.307	-0.087	0.028	0.000
L3.Phenylalanine.metabolism	0.000	0.000	1.601	0.120	0.000	0.000	0.076

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	-0.089	0.043	-2.081	0.046	-0.177	-0.002	0.0
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis	0.000	0.000	2.367	0.025	0.000	0.000	0.1

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	-0.051	0.033	-1.563	0.128	-0.119	0.016	0.000
L3.Phenylpropanoid.biosynthesis	0.000	0.000	2.026	0.052	0.000	0.000	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	-0.053	0.048	-1.107	0.277	-0.151	0.045	0.000
L3.Phosphatidylinositol.signaling.system	0.000	0.000	1.243	0.223	0.000	0.000	0.047

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	-0.068	0.035	-1.948	0.061	-0.139	0.003	0.000
L3.Phosphonate.and.phosphinate.metabolism	0.000	0.000	2.402	0.023	0.000	0.000	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	-0.021	0.032	-0.656	0.517	-0.086	0.044	0.000
L3.Phosphotransferase.system..PTS.	0.000	0.000	0.905	0.373	0.000	0.000	0.026

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	-0.093	0.052	-1.782	0.085	-0.2	0.014	0.000
L3.Photosynthesis	0.000	0.000	1.947	0.061	0.0	0.000	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	0.011	0.025	0.421	0.676	-0.041	0.063	0.000
L3.Photosynthesis...antenna.proteins	-0.001	0.001	-0.843	0.406	-0.003	0.001	0.022

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	-0.089	0.051	-1.740	0.092	-0.194	0.015	0.000
L3.Photosynthesis.proteins	0.000	0.000	1.909	0.066	0.000	0.000	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)	0	0.022	0	1	-0.045	0.045	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)	0	0.022	0	1	-0.045	0.045	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	-0.03	0.043	-0.699	0.490	-0.119	0.058	0.000
L3.Plant.pathogen.interaction	0.00	0.000	0.813	0.422	0.000	0.000	0.021

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	-0.094	0.049	-1.929	0.063	-0.193	0.006	0.000
L3.Polycyclic.aromatic.hydrocarbon.degradation	0.000	0.000	2.133	0.041	0.000	0.000	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	-0.061	0.045	-1.347	0.188	-0.153	0.031	0.00
L3.Polyketide.sugar.unit.biosynthesis	0.000	0.000	1.531	0.136	0.000	0.000	0.07

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	-0.042	0.03	-1.412	0.168	-0.103	0.019	0.000
L3.Pores.ion.channels	0.000	0.00	1.995	0.055	0.000	0.000	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	-0.048	0.035	-1.373	0.180	-0.119	0.023	0.000
L3.Porphyrin.and.chlorophyll.metabolism	0.000	0.000	1.730	0.094	0.000	0.000	0.088

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	-0.1	0.047	-2.105	0.044	-0.196	-0.003	0.00
L3.Prenyltransferases	0.0	0.000	2.336	0.026	0.000	0.000	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	-0.086	0.04	-2.144	0.040	-0.169	-0.004	0.000
L3.Primary.bile.acid.biosynthesis	0.000	0.00	2.483	0.019	0.000	0.000	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	-0.04	0.049	-0.814	0.422	-0.14	0.06	0.000
L3.Primary.immunodeficiency	0.00	0.000	0.911	0.369	0.00	0.00	0.026

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	-0.011	0.026	-0.433	0.668	-0.065	0.042	0.00
L3.Prion.diseases	0.000	0.000	0.793	0.434	0.000	0.000	0.02

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	-0.031	0.037	-0.846	0.404	-0.107	0.044	0.000
L3.Progesterone.mediated.oocyte.maturation	0.000	0.000	1.049	0.303	0.000	0.000	0.034

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	-0.045	0.037	-1.226	0.23	-0.12	0.03	0.000
L3.Propanoate.metabolism	0.000	0.000	1.514	0.14	0.00	0.00	0.069

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	-0.039	0.036	-1.076	0.291	-0.112	0.035	0.000
L3.Prostate.cancer	0.000	0.000	1.351	0.187	0.000	0.000	0.056

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	-0.056	0.05	-1.124	0.270	-0.159	0.046	0.000
L3.Proteasome	0.000	0.00	1.248	0.222	0.000	0.000	0.048

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	-0.044	0.03	-1.479	0.150	-0.106	0.017	0.00
L3.Protein.digestion.and.absorption	0.000	0.00	2.059	0.048	0.000	0.000	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	-0.088	0.049	-1.812	0.080	-0.188	0.011	0.000
L3.Protein.export	0.000	0.000	2.007	0.054	0.000	0.000	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	-0.057	0.037	-1.526	0.138	-0.133	0.019	0.0
L3.Protein.folding.and.associated.processing	0.000	0.000	1.854	0.074	0.000	0.000	0.1

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	-0.025	0.034	-0.734	0.468	-0.095	0.045	0.000
L3.Protein.kinases	0.000	0.000	0.959	0.345	0.000	0.000	0.029

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	-0.045	0.04	-1.115	0.274	-0.126	0.037	0.000
L3.Protein.processing.in.endoplasmic.reticulum	0.000	0.00	1.327	0.195	0.000	0.000	0.054

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	-0.033	0.027	-1.203	0.238	-0.089	0.023	0.000
L3.Proximal.tubule.bicarbonate.reclamation	0.000	0.000	1.898	0.067	0.000	0.000	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	-0.078	0.046	-1.714	0.097	-0.171	0.015	0.000
L3.Purine.metabolism	0.000	0.000	1.932	0.063	0.000	0.000	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	-0.082	0.049	-1.693	0.101	-0.182	0.017	0.000
L3.Pyrimidine.metabolism	0.000	0.000	1.879	0.070	0.000	0.000	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	-0.053	0.038	-1.391	0.174	-0.13	0.025	0.000
L3.Pyruvate.metabolism	0.000	0.000	1.684	0.103	0.00	0.000	0.084

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	0.008	0.028	0.274	0.786	-0.049	0.064	0.000
L3.RIG.I.like.receptor.signaling.pathway	0.000	0.000	-0.461	0.648	0.000	0.000	0.007

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	-0.096	0.047	-2.050	0.049	-0.192	0	0.000
L3.RNA.degradation	0.000	0.000	2.281	0.030	0.000	0	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	-0.073	0.049	-1.495	0.145	-0.174	0.027	0.000
L3.RNA.polymerase	0.000	0.000	1.660	0.107	0.000	0.000	0.082

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	-0.025	0.042	-0.591	0.559	-0.112	0.062	0.000
L3.RNA.transport	0.000	0.000	0.693	0.494	0.000	0.000	0.015

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)	0	0.022	0	1	-0.045	0.045	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	-0.045	0.025	-1.828	0.078	-0.095	0.005	0.000
L3.Renal.cell.carcinoma	0.000	0.000	3.022	0.005	0.000	0.000	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	0.005	0.022	0.200	0.843	-0.041	0.05	0.000
L3.Renin.angiotensin.system	0.000	0.000	-0.958	0.346	-0.001	0.00	0.029

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	-0.054	0.043	-1.266	0.215	-0.142	0.033	0.000
L3.Replication..recombination.and.repair.proteins	0.000	0.000	1.463	0.154	0.000	0.000	0.065

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	-0.078	0.038	-2.032	0.051	-0.157	0	0.000
L3.Restriction.enzyme	0.000	0.000	2.398	0.023	0.000	0	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	-0.018	0.032	-0.557	0.581	-0.083	0.048	0.000
L3.Retinol.metabolism	0.000	0.000	0.770	0.447	0.000	0.000	0.019

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)	0	0.022	0	1	-0.045	0.045	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	-0.05	0.035	-1.432	0.162	-0.121	0.021	0.000
L3.Riboflavin.metabolism	0.00	0.000	1.810	0.080	0.000	0.000	0.096

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	-0.094	0.05	-1.854	0.074	-0.197	0.009	0.000
L3.Ribosome	0.000	0.00	2.038	0.050	0.000	0.000	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	-0.072	0.043	-1.671	0.105	-0.16	0.016	0.000
L3.Ribosome.Biogenesis	0.000	0.000	1.914	0.065	0.00	0.000	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	-0.071	0.046	-1.553	0.131	-0.165	0.022	0.00
L3.Ribosome.biogenesis.in.eukaryotes	0.000	0.000	1.753	0.090	0.000	0.000	0.09

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)	0	0.022	0	1	-0.045	0.045	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	-0.088	0.04	-2.194	0.036	-0.17	-0.006	0.000
L3.Secondary.bile.acid.biosynthesis	0.000	0.00	2.542	0.016	0.00	0.000	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	-0.031	0.032	-0.973	0.338	-0.096	0.034	0.000
L3.Secretion.system	0.000	0.000	1.331	0.193	0.000	0.000	0.054

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	-0.064	0.04	-1.604	0.119	-0.145	0.017	0.000
L3.Selenocompound.metabolism	0.000	0.00	1.894	0.068	0.000	0.000	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)	0	0.022	0	1	-0.045	0.045	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	-0.003	0.025	-0.098	0.922	-0.054	0.049	0.000
L3.Shigellosis	0.001	0.006	0.206	0.839	-0.012	0.015	0.001

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	-0.045	0.039	-1.158	0.256	-0.124	0.034	0.000
L3.Signal.transduction.mechanisms	0.000	0.000	1.395	0.173	0.000	0.000	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	-0.001	0.025	-0.041	0.968	-0.051	0.049	0
L3.Small.cell.lung.cancer	0.000	0.001	0.095	0.925	-0.002	0.002	0

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	-0.06	0.037	-1.636	0.112	-0.136	0.015	0.000
L3.Sphingolipid.metabolism	0.00	0.000	1.988	0.056	0.000	0.000	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)	0	0.022	0	1	-0.045	0.045	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	0.021	0.031	0.665	0.511	-0.043	0.084	0.000
L3.Sporulation	0.000	0.000	-0.941	0.354	0.000	0.000	0.028

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	0.006	0.028	0.215	0.831	-0.051	0.063	0.000
L3.Staphylococcus.aureus.infection	0.000	0.000	-0.361	0.721	0.000	0.000	0.004

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	-0.054	0.04	-1.329	0.194	-0.136	0.029	0.000
L3.Starch.and.sucrose.metabolism	0.000	0.00	1.568	0.127	0.000	0.000	0.073

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	0.003	0.025	0.110	0.913	-0.048	0.054	0.000
L3.Steroid.biosynthesis	0.000	0.000	-0.249	0.805	0.000	0.000	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	-0.046	0.024	-1.876	0.070	-0.095	0.004	0.000
L3.Steroid.hormone.biosynthesis	0.000	0.000	3.123	0.004	0.000	0.000	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	0.002	0.024	0.098	0.923	-0.047	0.051	0.
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	0.000	0.000	-0.264	0.794	0.000	0.000	0.

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	-0.07	0.044	-1.568	0.127	-0.161	0.021	0.000
L3.Streptomycin.biosynthesis	0.00	0.000	1.784	0.085	0.000	0.000	0.093

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	-0.011	0.024	-0.467	0.644	-0.06	0.038	0.000
L3.Styrene.degradation	0.000	0.000	1.127	0.269	0.00	0.000	0.039

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	-0.068	0.038	-1.777	0.086	-0.146	0.01	0.000
L3.Sulfur.metabolism	0.000	0.000	2.117	0.043	0.000	0.00	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	-0.028	0.033	-0.839	0.408	-0.096	0.04	0.000
L3.Sulfur.relay.system	0.000	0.000	1.117	0.273	0.000	0.00	0.039

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	-0.032	0.033	-0.958	0.346	-0.099	0.036	0.000
L3.Synthesis.and.degradation.of.ketone.bodies	0.000	0.000	1.270	0.214	0.000	0.000	0.049

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	-0.008	0.023	-0.345	0.732	-0.056	0.04	0.00
L3.Systemic.lupus.erythematosus	0.000	0.000	0.981	0.335	0.000	0.00	0.03

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)	0	0.022	0	1	-0.045	0.045	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	-0.081	0.04	-2.017	0.053	-0.163	0.001	0.000
L3.Taurine.and.hypotaurine.metabolism	0.000	0.00	2.346	0.026	0.000	0.000	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	-0.096	0.048	-1.990	0.056	-0.195	0.003	0.000
L3.Terpenoid.backbone.biosynthesis	0.000	0.000	2.203	0.035	0.000	0.000	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	-0.005	0.045	-0.107	0.916	-0.097	0.087	0
L3.Tetracycline.biosynthesis	0.000	0.000	0.123	0.903	0.000	0.000	0

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	-0.069	0.045	-1.533	0.136	-0.16	0.023	0.000
L3.Thiamine.metabolism	0.000	0.000	1.743	0.092	0.00	0.000	0.089

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)	0	0.022	0	1	-0.045	0.045	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	-0.003	0.026	-0.101	0.920	-0.056	0.051	0.000
L3.Toluene.degradation	0.000	0.000	0.191	0.849	0.000	0.000	0.001

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	-0.001	0.025	-0.041	0.968	-0.051	0.049	0
L3.Toxoplasmosis	0.000	0.001	0.095	0.925	-0.002	0.002	0

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	-0.026	0.033	-0.787	0.437	-0.093	0.041	0.000
L3.Transcription.factors	0.000	0.000	1.060	0.298	0.000	0.000	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	-0.078	0.049	-1.582	0.124	-0.179	0.023	0.00
L3.Transcription.machinery	0.000	0.000	1.753	0.090	0.000	0.000	0.09

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	-0.013	0.025	-0.541	0.592	-0.064	0.037	0.000
L3.Transcription.related.proteins	0.000	0.000	1.148	0.260	0.000	0.000	0.041

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	-0.095	0.047	-2.013	0.053	-0.191	0.001	0.000
L3.Translation.factors	0.000	0.000	2.240	0.033	0.000	0.000	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	-0.071	0.043	-1.629	0.114	-0.159	0.018	0.000
L3.Translation.proteins	0.000	0.000	1.865	0.072	0.000	0.000	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	-0.034	0.036	-0.965	0.342	-0.107	0.038	0.000
L3.Transporters	0.000	0.000	1.220	0.232	0.000	0.000	0.046

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	-0.053	0.034	-1.554	0.131	-0.123	0.017	0
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis	0.000	0.000	1.970	0.058	0.000	0.000	0

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	-0.024	0.028	-0.842	0.406	-0.081	0.034	0.000
L3.Tryptophan.metabolism	0.000	0.000	1.331	0.193	0.000	0.000	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	-0.094	0.053	-1.791	0.083	-0.202	0.013	0.00
L3.Tuberculosis	0.000	0.000	1.953	0.060	0.000	0.000	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	-0.021	0.033	-0.631	0.533	-0.088	0.046	0.000
L3.Two.component.system	0.000	0.000	0.854	0.400	0.000	0.000	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	-0.131	0.049	-2.678	0.012	-0.231	-0.031	0.000
L3.Type.I.diabetes.mellitus	0.000	0.000	2.927	0.006	0.000	0.000	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	-0.063	0.044	-1.458	0.155	-0.152	0.025	0.000
L3.Type.II.diabetes.mellitus	0.000	0.000	1.673	0.105	0.000	0.000	0.083

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	-0.044	0.036	-1.244	0.223	-0.117	0.029	0.000
L3.Tyrosine.metabolism	0.000	0.000	1.556	0.130	0.000	0.000	0.072

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 %	0.
Intercept	-0.037	0.028	-1.354	0.186	-0.094	0.019	0.
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis	0.000	0.000	2.069	0.047	0.000	0.000	0.

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	-0.024	0.026	-0.919	0.365	-0.077	0.029	0.000
L3.Ubiquitin.system	0.000	0.000	1.605	0.119	0.000	0.000	0.077

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)	0	0.022	0	1	-0.045	0.045	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	-0.07	0.046	-1.541	0.134	-0.164	0.023	0.000
L3.Valine..leucine.and.isoleucine.biosynthesis	0.00	0.000	1.742	0.092	0.000	0.000	0.089

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	-0.042	0.033	-1.276	0.212	-0.11	0.025	0.000
L3.Valine..leucine.and.isoleucine.degradation	0.000	0.000	1.665	0.106	0.00	0.000	0.082

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	-0.006	0.026	-0.232	0.818	-0.058	0.046	0.000
L3.Various.types.of.N.glycan.biosynthesis	0.006	0.013	0.468	0.643	-0.020	0.032	0.007

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)	0	0.022	0	1	-0.045	0.045	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	-0.001	0.023	-0.051	0.960	-0.049	0.046	0.000
L3.Vasopressin.regulated.water.reabsorption	0.005	0.027	0.176	0.861	-0.050	0.060	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	-0.007	0.024	-0.286	0.777	-0.057	0.043	0.000
L3.Vibrio.cholerae.infection	0.010	0.015	0.672	0.507	-0.020	0.039	0.014

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	-0.017	0.035	-0.494	0.625	-0.089	0.054	0.000
L3.Vibrio.cholerae.pathogenic.cycle	0.000	0.000	0.637	0.529	0.000	0.000	0.013

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	-0.001	0.025	-0.041	0.968	-0.051	0.049	0
L3.Viral.myocarditis	0.000	0.001	0.095	0.925	-0.002	0.002	0

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	-0.06	0.036	-1.650	0.109	-0.135	0.014	0.000
L3.Vitamin.B6.metabolism	0.00	0.000	2.017	0.053	0.000	0.000	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	-0.008	0.024	-0.336	0.739	-0.057	0.041	0.000
L3.Wnt.signaling.pathway	0.032	0.036	0.888	0.381	-0.042	0.105	0.025

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	-0.023	0.033	-0.706	0.485	-0.091	0.044	0.000
L3.Xylene.degradation	0.000	0.000	0.947	0.351	0.000	0.000	0.028

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	-0.129	0.051	-2.528	0.017	-0.233	-0.025	0.000
L3.Zeatin.biosynthesis	0.000	0.000	2.747	0.010	0.000	0.000	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	-0.014	0.024	-0.576	0.569	-0.063	0.035	0.000
L3.alpha.Linolenic.acid.metabolism	0.000	0.000	1.310	0.200	0.000	0.000	0.052

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	-0.034	0.031	-1.115	0.274	-0.097	0.028	0.000
L3.beta.Alanine.metabolism	0.000	0.000	1.564	0.128	0.000	0.000	0.073

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	-0.071	0.037	-1.933	0.063	-0.146	0.004	0.000
L3.beta.Lactam.resistance	0.000	0.000	2.332	0.027	0.000	0.000	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)	0	0.022	0	1	-0.045	0.045	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)	0	0.022	0	1	-0.045	0.045	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	-0.001	0.025	-0.041	0.968	-0.051	0.049	0
L3.p53.signaling.pathway	0.000	0.001	0.095	0.925	-0.002	0.002	0

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 %	9
Intercept	-0.005	0.018	-0.283	0.779	-0.042	
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	0.000	0.000	1.513	0.141	0.000	

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	-0.055	0.025	-2.207	0.035	-0.106	-0.004	0.000
L3.ABC.transporters	0.000	0.000	2.920	0.007	0.000	0.000	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)	0	0.018	0	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	0.02	0.03	0.664	0.512	-0.041	0.081	0.000
L3.Adipocytokine.signaling.pathway	0.00	0.00	-0.838	0.409	0.000	0.000	0.022

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	-0.019	0.023	-0.800	0.430	-0.066	0.029	0.000
L3.African.trypanosomiasis	0.000	0.000	1.261	0.217	0.000	0.000	0.049

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	-0.089	0.035	-2.527	0.017	-0.161	-0.017	0.000
L3.Alanine..aspartate.and.glutamate.metabolism	0.000	0.000	2.854	0.008	0.000	0.000	0.208

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	-0.005	0.018	-0.279	0.782	-0.042	0.032	0.000
L3.Aldosterone.regulated.sodium.reabsorption	0.161	0.102	1.579	0.125	-0.047	0.369	0.074

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	-0.063	0.031	-2.043	0.050	-0.125	0	0.000
L3.Alzheimer.s.disease	0.000	0.000	2.446	0.021	0.000	0	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	-0.048	0.025	-1.929	0.063	-0.099	0.003	0.000
L3.Amino.acid.metabolism	0.000	0.000	2.589	0.015	0.000	0.000	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	-0.085	0.036	-2.360	0.025	-0.159	-0.011	0.000
L3.Amino.acid.related.enzymes	0.000	0.000	2.659	0.012	0.000	0.000	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	-0.066	0.036	-1.809	0.081	-0.14	0.009	0.00
L3.Amino.sugar.and.nucleotide.sugar.metabolism	0.000	0.000	2.054	0.049	0.00	0.000	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	-0.078	0.039	-1.964	0.059	-0.158	0.003	0.000
L3.Aminoacyl.tRNA.biosynthesis	0.000	0.000	2.180	0.037	0.000	0.000	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	-0.04	0.025	-1.632	0.113	-0.09	0.01	0.000
L3.Aminobenzoate.degradation	0.00	0.000	2.266	0.031	0.00	0.00	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	0.007	0.024	0.290	0.774	-0.042	0.056	0.000
L3.Amoebiasis	0.000	0.000	-0.448	0.658	0.000	0.000	0.006

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	-0.027	0.02	-1.341	0.190	-0.067	0.014	0.000
L3.Amyotrophic.lateral.sclerosis..ALS.	0.000	0.00	2.489	0.019	0.000	0.000	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	-0.089	0.024	-3.754	0.001	-0.138	-0.041	0.000
L3.Antigen.processing.and.presentation	0.000	0.000	4.654	0.000	0.000	0.000	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	0.024	0.02	1.182	0.247	-0.018	0.066	0.000
L3.Apoptosis	0.000	0.00	-2.192	0.036	0.000	0.000	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	-0.041	0.024	-1.719	0.096	-0.09	0.008	0.000
L3.Arachidonic.acid.metabolism	0.000	0.000	2.415	0.022	0.00	0.000	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	-0.069	0.028	-2.467	0.020	-0.126	-0.012	0.000
L3.Arginine.and.proline.metabolism	0.000	0.000	3.028	0.005	0.000	0.000	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)	0	0.018	0	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	-0.032	0.021	-1.531	0.136	-0.075	0.011	0.000
L3.Ascorbate.and.aldarate.metabolism	0.000	0.000	2.543	0.016	0.000	0.000	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	-0.02	0.019	-1.068	0.294	-0.058	0.018	0.000
L3.Atrazine.degradation	0.00	0.000	2.440	0.021	0.000	0.000	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	-0.048	0.025	-1.937	0.062	-0.099	0.003	0.00
L3.Bacterial.chemotaxis	0.000	0.000	2.609	0.014	0.000	0.000	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	-0.011	0.019	-0.599	0.554	-0.049	0.027	0.000
L3.Bacterial.invasion.of.epithelial.cells	0.000	0.000	1.807	0.081	0.000	0.000	0.095

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	-0.063	0.021	-2.985	0.006	-0.106	-0.02	0.000
L3.Bacterial.motility.proteins	0.000	0.000	4.170	0.000	0.000	0.00	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	-0.043	0.025	-1.755	0.089	-0.093	0.007	0.000
L3.Bacterial.secretion.system	0.000	0.000	2.421	0.022	0.000	0.000	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	-0.062	0.041	-1.538	0.135	-0.145	0.02	0.000
L3.Bacterial.toxins	0.000	0.000	1.708	0.098	0.000	0.00	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	-0.002	0.02	-0.125	0.901	-0.043	0.038	0.000
L3.Basal.transcription.factors	0.000	0.00	0.341	0.735	0.000	0.000	0.004

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	-0.085	0.036	-2.360	0.025	-0.159	-0.012	0.000
L3.Base.excision.repair	0.000	0.000	2.656	0.013	0.000	0.000	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	-0.044	0.022	-1.962	0.059	-0.089	0.002	0.000
L3.Benzoate.degradation	0.000	0.000	2.896	0.007	0.000	0.000	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	-0.011	0.019	-0.577	0.568	-0.049	0.027	0.000
L3.Betalain.biosynthesis	0.000	0.000	1.730	0.094	0.000	0.000	0.088

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	-0.017	0.019	-0.897	0.377	-0.057	0.022	0.000
L3.Bile.secretion	0.003	0.001	2.021	0.052	0.000	0.005	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	-0.022	0.02	-1.086	0.286	-0.064	0.019
L3.Biosynthesis.and.biodegradation.of.secondary.metabolites	0.000	0.00	2.047	0.050	0.000	0.000

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	-0.002	0.019	-0.124	0.902	-0.040	0.036	0.
L3.Biosynthesis.of.12. . . 14..and.16.membered.macrolides	0.074	0.105	0.703	0.488	-0.141	0.289	0.

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	-0.051	0.023	-2.184	0.037	-0.098	-0.003	0.00
L3.Biosynthesis.of.ansamycins	0.000	0.000	3.040	0.005	0.000	0.000	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	-0.019	0.02	-0.939	0.355	-0.06	0.022
L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides	0.000	0.00	1.861	0.073	0.00	0.000

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)	0	0.018	0	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	-0.011	0.019	-0.595	0.556	-0.049	0.027	0.000
L3.Biosynthesis.of.type.II.polyketide.products	0.000	0.000	1.731	0.094	0.000	0.000	0.088

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	-0.038	0.023	-1.673	0.105	-0.085	0.008	0.000
L3.Biosynthesis.of.unsaturated.fatty.acids	0.000	0.000	2.478	0.019	0.000	0.000	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	-0.014	0.04	-0.357	0.724	-0.097	0.068	0.000
L3.Biosynthesis.of.vancomycin.group.antibiotics	0.000	0.00	0.401	0.691	0.000	0.000	0.005

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	-0.063	0.03	-2.119	0.042	-0.123	-0.002	0.000
L3.Biotin.metabolism	0.000	0.00	2.567	0.016	0.000	0.000	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	-0.086	0.031	-2.779	0.009	-0.149	-0.023	0.000
L3.Bisphenol.degradation	0.000	0.000	3.242	0.003	0.000	0.000	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	-0.024	0.018	-1.306	0.201	-0.061	0.013	0.000
L3.Bladder.cancer	0.000	0.000	2.886	0.007	0.000	0.000	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	-0.068	0.025	-2.728	0.011	-0.119	-0.017	0.000
L3.Butanoate.metabolism	0.000	0.000	3.491	0.002	0.000	0.000	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	-0.049	0.047	-1.056	0.299	-0.144	0.046	0.000
L3.Butirosin.and.neomycin.biosynthesis	0.000	0.000	1.146	0.261	0.000	0.000	0.041

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	-0.05	0.034	-1.474	0.151	-0.119	0.019	0.000
L3.C5.Branched.dibasic.acid.metabolism	0.00	0.000	1.728	0.094	0.000	0.000	0.088

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)	0	0.018	0	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	0.004	0.02	0.188	0.852	-0.037	0.045	0.000
L3.Caffeine.metabolism	-0.005	0.01	-0.452	0.655	-0.026	0.016	0.007

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	-0.004	0.021	-0.190	0.851	-0.046	0.038	0.000
L3.Calcium.signaling.pathway	0.006	0.015	0.409	0.685	-0.025	0.038	0.005

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	-0.027	0.02	-1.332	0.193	-0.067	0.014	0.000
L3.Caprolactam.degradation	0.000	0.00	2.476	0.019	0.000	0.000	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	-0.019	0.026	-0.74	0.465	-0.073	0.034	0.000
L3.Carbohydrate.digestion.and.absorption	0.000	0.000	1.03	0.311	0.000	0.000	0.033

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	-0.028	0.03	-0.939	0.355	-0.089	0.033	0.000
L3.Carbohydrate.metabolism	0.000	0.00	1.174	0.249	0.000	0.000	0.043

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	-0.064	0.03	-2.127	0.042	-0.126	-0.003	0.000
L3.Carbon.fixation.in.photosynthetic.organisms	0.000	0.00	2.558	0.016	0.000	0.000	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	-0.081	0.03	-2.730	0.010	-0.142	-0.02	0.000
L3.Carbon.fixation.pathways.in.prokaryotes	0.000	0.00	3.231	0.003	0.000	0.00	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	-0.013	0.019	-0.665	0.511	-0.051	0.026	0.000
L3.Cardiac.muscle.contraction	0.000	0.000	1.802	0.082	0.000	0.000	0.095

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	0.004	0.021	0.208	0.837	-0.039	0.047	0.000
L3.Carotenoid.biosynthesis	0.000	0.000	-0.425	0.674	0.000	0.000	0.006

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)	0	0.018	0	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	-0.095	0.041	-2.318	0.027	-0.179	-0.011	0.000
L3.Cell.cycle. . . Caulobacter	0.000	0.000	2.538	0.017	0.000	0.000	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)	0	0.018	0	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	-0.068	0.026	-2.641	0.013	-0.121	-0.015	0.000
L3.Cell.division	0.000	0.000	3.334	0.002	0.000	0.000	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	-0.063	0.027	-2.339	0.026	-0.118	-0.008	0.000
L3.Cell.motility.and.secretion	0.000	0.000	2.932	0.006	0.000	0.000	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	-0.013	0.029	-0.453	0.654	-0.073	0.046	0.000
L3.Cellular.antigens	0.000	0.000	0.582	0.565	0.000	0.000	0.011

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	-0.015	0.023	-0.676	0.504	-0.061	0.031	0.000
L3.Chagas.disease..American.trypanosomiasis.	0.000	0.000	1.124	0.270	0.000	0.000	0.039

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	-0.071	0.032	-2.208	0.035	-0.136	-0.005	0.000
L3.Chaperones.and.folding.catalysts	0.000	0.000	2.587	0.015	0.000	0.000	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	-0.076	0.033	-2.335	0.026	-0.143	-0.01	0.000
L3.Chloroalkane.and.chloroalkene.degradation	0.000	0.000	2.708	0.011	0.000	0.00	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 %	R2
Intercept	-0.036	0.02	-1.818	0.079	-0.077	0.005	0.000
L3.Chlorocyclohexane.and.chlorobenzene.degradation	0.000	0.00	3.054	0.005	0.000	0.000	0.231

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)	0	0.018	0	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	-0.09	0.033	-2.728	0.011	-0.158	-0.023	0.000
L3.Chromosome	0.00	0.000	3.120	0.004	0.000	0.000	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	-0.016	0.018	-0.856	0.399	-0.053	0.022	0.000
L3.Chronic.myeloid.leukemia	0.063	0.028	2.266	0.031	0.006	0.120	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	-0.012	0.019	-0.643	0.525	-0.052	0.027	0.000
L3.Circadian.rhythm...plant	0.009	0.005	1.628	0.114	-0.002	0.019	0.079

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	-0.053	0.026	-2.075	0.047	-0.105	-0.001	0.000
L3.Citrate.cycle..TCA.cycle.	0.000	0.000	2.718	0.011	0.000	0.000	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)	0	0.018	0	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	0.002	0.020	0.116	0.909	-0.039	0.044	0.000
L3.Colorectal.cancer	0.000	0.001	-0.271	0.788	-0.002	0.001	0.002

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)	0	0.018	0	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	-0.054	0.029	-1.869	0.071	-0.113	0.005	0.000
L3.Cyanoamino.acid.metabolism	0.000	0.000	2.313	0.028	0.000	0.000	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	-0.074	0.031	-2.377	0.024	-0.137	-0.01	0.000
L3.Cysteine.and.methionine.metabolism	0.000	0.000	2.802	0.009	0.000	0.00	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	0.00	0.019	-0.017	0.987	-0.039	0.038	0
L3.Cytochrome.P450	0.01	0.106	0.096	0.924	-0.206	0.227	0

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)	0	0.018	0	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)	0	0.018	0	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	-0.115	0.031	-3.664	0.001	-0.18	-0.051	0.000
L3.Cytoskeleton.proteins	0.000	0.000	4.145	0.000	0.00	0.000	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)	0	0.018	0	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	-0.055	0.037	-1.506	0.143	-0.131	0.02	0.000
L3.D.Alanine.metabolism	0.000	0.000	1.715	0.097	0.000	0.00	0.087

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	-0.005	0.02	-0.268	0.791	-0.047	0.036	0.000
L3.D.Arginine.and.D.ornithine.metabolism	0.000	0.00	0.626	0.536	0.000	0.000	0.012

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	-0.078	0.035	-2.206	0.035	-0.149	-0.006	0.000
L3.D.Glutamine.and.D.glutamate.metabolism	0.000	0.000	2.509	0.018	0.000	0.000	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	-0.086	0.038	-2.271	0.030	-0.162	-0.009	0.000
L3.DNA.repair.and.recombination.proteins	0.000	0.000	2.536	0.017	0.000	0.000	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	-0.089	0.041	-2.155	0.039	-0.173	-0.005	0.000
L3.DNA.replication	0.000	0.000	2.365	0.025	0.000	0.000	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	-0.095	0.039	-2.455	0.020	-0.175	-0.016	0.000
L3.DNA.replication.proteins	0.000	0.000	2.714	0.011	0.000	0.000	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)	0	0.018	0	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	-0.033	0.024	-1.378	0.178	-0.083	0.016	0.000
L3.Dioxin.degradation	0.000	0.000	1.980	0.057	0.000	0.000	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	-0.027	0.023	-1.207	0.237	-0.074	0.019	0.000
L3.Drug.metabolism. . . cytochrome.P450	0.000	0.000	1.889	0.069	0.000	0.000	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	-0.077	0.037	-2.085	0.046	-0.152	-0.002	0.000
L3.Drug.metabolism. . . other.enzymes	0.000	0.000	2.349	0.026	0.000	0.000	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)	0	0.018	0	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	-0.03	0.022	-1.39	0.175	-0.074	0.014	0.000
L3.Electron.transfer.carriers	0.00	0.000	2.26	0.031	0.000	0.000	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)	0	0.018	0	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	0.004	0.019	0.211	0.835	-0.035	0.043	0.000
L3.Endocytosis	-0.004	0.006	-0.683	0.500	-0.015	0.008	0.015

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	-0.072	0.026	-2.766	0.010	-0.126	-0.019	0.000
L3.Energy.metabolism	0.000	0.000	3.449	0.002	0.000	0.000	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	-0.078	0.029	-2.742	0.010	-0.137	-0.02
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	0.000	0.000	3.292	0.003	0.000	0.00

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)	0	0.018	0	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	-0.008	0.023	-0.328	0.745	-0.055	0.039	0.000
L3.Ether.lipid.metabolism	0.000	0.000	0.544	0.590	0.000	0.000	0.009

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	-0.075	0.024	-3.143	0.004	-0.123	-0.026	0.000
L3.Ethylbenzene.degradation	0.000	0.000	4.026	0.000	0.000	0.000	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)	0	0.018	0	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	-0.069	0.035	-1.980	0.057	-0.141	0.002	0.000
L3.Fatty.acid.biosynthesis	0.000	0.000	2.268	0.031	0.000	0.000	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)	0	0.018	0	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	-0.052	0.025	-2.068	0.047	-0.104	-0.001	0.000
L3.Fatty.acid.metabolism	0.000	0.000	2.731	0.010	0.000	0.000	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)	0	0.018	0	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	0.004	0.019	0.211	0.835	-0.035	0.043	0.000
L3.Fc.gamma.R.mediated.phagocytosis	-0.004	0.006	-0.683	0.500	-0.015	0.008	0.015

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	-0.039	0.02	-1.955	0.060	-0.08	0.002	0.000
L3.Flagellar.assembly	0.000	0.00	3.207	0.003	0.00	0.000	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	-0.006	0.023	-0.282	0.780	-0.054	0.041	0.000
L3.Flavone.and.flavonol.biosynthesis	0.000	0.000	0.467	0.644	0.000	0.000	0.007

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	-0.008	0.018	-0.430	0.670	-0.045	0.03	0.000
L3.Flavonoid.biosynthesis	0.000	0.000	1.634	0.113	0.000	0.00	0.079

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	-0.017	0.019	-0.914	0.368	-0.055	0.021	0.000
L3.Fluorobenzoate.degradation	0.000	0.000	2.258	0.031	0.000	0.000	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)	0	0.018	0	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	-0.065	0.036	-1.796	0.083	-0.138	0.009	0.000
L3.Folate.biosynthesis	0.000	0.000	2.047	0.049	0.000	0.000	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	-0.062	0.029	-2.158	0.039	-0.12	-0.003	0.000
L3.Fructose.and.mannose.metabolism	0.000	0.000	2.651	0.013	0.00	0.000	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	-0.051	0.025	-2.007	0.054	-0.103	0.001	0.000
L3.Function.unknown	0.000	0.000	2.654	0.013	0.000	0.000	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)	0	0.018	0	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)	0	0.018	0	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	-0.045	0.039	-1.170	0.251	-0.124	0.034	0.000
L3.Galactose.metabolism	0.000	0.000	1.322	0.196	0.000	0.000	0.053

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)	0	0.018	0	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	-0.083	0.031	-2.702	0.011	-0.146	-0.02	0.000
L3.General.function.prediction.only	0.000	0.000	3.158	0.004	0.000	0.00	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	-0.03	0.021	-1.433	0.162	-0.072	0.013	0.000
L3.Geraniol.degradation	0.00	0.000	2.447	0.020	0.000	0.000	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	-0.001	0.021	-0.049	0.961	-0.044	0.042	0
L3.Germination	0.000	0.000	0.105	0.917	0.000	0.000	0

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)	0	0.018	0	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	-0.073	0.037	-1.997	0.055	-0.148	0.002	0.000
L3.Glutamatergic.synapse	0.000	0.000	2.256	0.031	0.000	0.000	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	-0.044	0.027	-1.627	0.114	-0.1	0.011	0.000
L3.Glutathione.metabolism	0.000	0.000	2.097	0.045	0.0	0.000	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)	0	0.018	0	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	-0.043	0.019	-2.215	0.035	-0.083	-0.003	0.000
L3.Glycan.biosynthesis.and.metabolism	0.000	0.000	3.635	0.001	0.000	0.000	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	-0.071	0.028	-2.533	0.017	-0.128	-0.014	0.000
L3.Glycerolipid.metabolism	0.000	0.000	3.095	0.004	0.000	0.000	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	-0.077	0.028	-2.815	0.009	-0.134	-0.021	0.000
L3.Glycerophospholipid.metabolism	0.000	0.000	3.422	0.002	0.000	0.000	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	-0.061	0.032	-1.911	0.066	-0.126	0.004	0.000
L3.Glycine..serine.and.threonine.metabolism	0.000	0.000	2.264	0.031	0.000	0.000	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	-0.068	0.033	-2.062	0.048	-0.135	-0.001	0.000
L3.Glycolysis. . . Gluconeogenesis	0.000	0.000	2.405	0.023	0.000	0.000	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	0.006	0.018	0.301	0.766	-0.032	0.043	0
L3.Glycosaminoglycan.biosynthesis. . . chondroitin.sulfate	-0.022	0.017	-1.311	0.200	-0.057	0.012	0

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	-0.004	0.031	-0.122	0.904	-0.066	0.059	0.000
L3.Glycosaminoglycan.degradation	0.000	0.000	0.152	0.880	0.000	0.000	0.001

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	0.025	0.029	0.847	0.404	-0.035	0.084	0.000
L3.Glycosphingolipid.biosynthesis. . . ganglio.series	0.000	0.000	-1.084	0.287	0.000	0.000	0.037

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	0.004	0.032	0.133	0.895	-0.061	0.07	0.000
L3.Glycosphingolipid.biosynthesis. . . globo.series	0.000	0.000	-0.162	0.872	0.000	0.00	0.001

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 %	97.5 %
Intercept	-0.002	0.019	-0.109	0.914	-0.041	0.037
L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series	0.000	0.000	0.471	0.641	0.000	0.000

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)	0	0.018	0	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	-0.048	0.033	-1.485	0.148	-0.115	0.018	0.000
L3.Glycosyltransferases	0.000	0.000	1.764	0.088	0.000	0.000	0.091

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	-0.058	0.024	-2.405	0.023	-0.107	-0.009	0.00
L3.Glyoxylate.and.dicarboxylate.metabolism	0.000	0.000	3.213	0.003	0.000	0.000	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	0.004	0.019	0.211	0.835	-0.035	0.043	0.000
L3.GnRH.signaling.pathway	-0.004	0.006	-0.683	0.500	-0.015	0.008	0.015

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)	0	0.018	0	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)	0	0.018	0	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)	0	0.018	0	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	-0.09	0.035	-2.567	0.015	-0.162	-0.018	0.000
L3.Histidine.metabolism	0.00	0.000	2.899	0.007	0.000	0.000	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	-0.088	0.04	-2.235	0.033	-0.169	-0.008	0.000
L3.Homologous.recombination	0.000	0.00	2.468	0.020	0.000	0.000	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	-0.068	0.029	-2.362	0.025	-0.127	-0.009	0.00
L3.Huntington.s.disease	0.000	0.000	2.870	0.007	0.000	0.000	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	-0.011	0.018	-0.619	0.540	-0.047	0.025	0.000
L3.Hypertrophic.cardiomyopathy..HCM.	0.003	0.001	2.229	0.033	0.000	0.005	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	-0.010	0.021	-0.469	0.642	-0.053	0.033	0.000
L3.Indole.alkaloid.biosynthesis	0.018	0.019	0.933	0.358	-0.021	0.056	0.027

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	0.002	0.020	0.116	0.909	-0.039	0.044	0.000
L3.Influenza.A	0.000	0.001	-0.271	0.788	-0.002	0.001	0.002

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	-0.036	0.024	-1.532	0.136	-0.085	0.012	0.000
L3.Inorganic.ion.transport.and.metabolism	0.000	0.000	2.206	0.035	0.000	0.000	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	-0.029	0.023	-1.291	0.207	-0.075	0.017	0.000
L3.Inositol.phosphate.metabolism	0.000	0.000	2.008	0.054	0.000	0.000	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	-0.046	0.036	-1.266	0.215	-0.119	0.028	0.000
L3.Insulin.signaling.pathway	0.000	0.000	1.458	0.155	0.000	0.000	0.064

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	-0.018	0.032	-0.568	0.574	-0.084	0.047	0.000
L3.Ion.channels	0.000	0.000	0.692	0.494	0.000	0.000	0.015

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	-0.010	0.018	-0.576	0.569	-0.047	0.026	0.000
L3.Isoflavonoid.biosynthesis	0.006	0.003	2.112	0.043	0.000	0.011	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	-0.053	0.025	-2.130	0.041	-0.105	-0.002	0.000
L3.Isoquinoline.alkaloid.biosynthesis	0.000	0.000	2.818	0.008	0.000	0.000	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)	0	0.018	0	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)	0	0.018	0	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	-0.055	0.022	-2.458	0.020	-0.101	-0.009	0.000
L3.Limonene.and.pinene.degradation	0.000	0.000	3.424	0.002	0.000	0.000	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	-0.079	0.034	-2.354	0.025	-0.147	-0.01	0.000
L3.Linoleic.acid.metabolism	0.000	0.000	2.706	0.011	0.000	0.00	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	-0.065	0.034	-1.945	0.061	-0.134	0.003	0.000
L3.Lipid.biosynthesis.proteins	0.000	0.000	2.259	0.031	0.000	0.000	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	-0.048	0.024	-1.987	0.056	-0.097	0.001	0.000
L3.Lipid.metabolism	0.000	0.000	2.735	0.010	0.000	0.000	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	-0.022	0.031	-0.691	0.495	-0.086	0.042	0.000
L3.Lipoic.acid.metabolism	0.000	0.000	0.848	0.403	0.000	0.000	0.023

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	-0.04	0.023	-1.707	0.098	-0.088	0.008	0.000
L3.Lipopolysaccharide.biosynthesis	0.00	0.000	2.456	0.020	0.000	0.000	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	-0.042	0.025	-1.710	0.098	-0.093	0.008	0.000
L3.Lipopolysaccharide.biosynthesis.proteins	0.000	0.000	2.344	0.026	0.000	0.000	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)	0	0.018	0	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)	0	0.018	0	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	-0.091	0.036	-2.510	0.018	-0.164	-0.017	0.000
L3.Lysine.biosynthesis	0.000	0.000	2.817	0.008	0.000	0.000	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	-0.049	0.022	-2.197	0.036	-0.094	-0.003	0.000
L3.Lysine.degradation	0.000	0.000	3.178	0.003	0.000	0.000	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	0.02	0.031	0.646	0.523	-0.043	0.082	0.00
L3.Lysosome	0.00	0.000	-0.804	0.428	0.000	0.000	0.02

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)	0	0.018	0	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	-0.063	0.036	-1.739	0.092	-0.137	0.011	0.000
L3.MAPK.signaling.pathway...yeast	0.000	0.000	1.979	0.057	0.000	0.000	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)	0	0.018	0	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	0.007	0.021	0.331	0.743	-0.035	0.049	0.000
L3.Meiosis...yeast	0.000	0.000	-0.726	0.473	0.000	0.000	0.017

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	-0.011	0.019	-0.573	0.571	-0.049	0.027	0.000
L3.Melanogenesis	0.000	0.000	1.727	0.094	0.000	0.000	0.088

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	-0.044	0.025	-1.752	0.090	-0.096	0.007	0.000
L3.Membrane.and.intracellular.structural.molecules	0.000	0.000	2.364	0.025	0.000	0.000	0.153

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	-0.051	0.024	-2.139	0.041	-0.101	-0.002	0.000
L3.Metabolism.of.cofactors.and.vitamins	0.000	0.000	2.909	0.007	0.000	0.000	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	-0.026	0.023	-1.147	0.261	-0.072	0.02	0.000
L3.Metabolism.of.xenobiotics.by.cytochrome.P450	0.000	0.000	1.824	0.078	0.000	0.00	0.097

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	-0.08	0.034	-2.372	0.024	-0.149	-0.011	0.000
L3.Methane.metabolism	0.00	0.000	2.721	0.011	0.000	0.000	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	-0.004	0.023	-0.184	0.856	-0.051	0.042	0.000
L3.Mineral.absorption	0.000	0.000	0.314	0.756	0.000	0.000	0.003

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	-0.096	0.039	-2.458	0.020	-0.176	-0.016	0.000
L3.Mismatch.repair	0.000	0.000	2.711	0.011	0.000	0.000	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	0.007	0.025	0.266	0.792	-0.044	0.057	0.000
L3.N.Glycan.biosynthesis	0.000	0.000	-0.398	0.694	0.000	0.000	0.005

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	-0.088	0.025	-3.497	0.001	-0.14	-0.037	0.000
L3.NOD.like.receptor.signaling.pathway	0.000	0.000	4.274	0.000	0.00	0.000	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	-0.075	0.034	-2.178	0.037	-0.145	-0.005	0.000
L3.Naphthalene.degradation	0.000	0.000	2.496	0.018	0.000	0.000	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)	0	0.018	0	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)	0	0.018	0	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	-0.078	0.033	-2.399	0.023	-0.145	-0.012	0.000
L3.Nicotinate.and.nicotinamide.metabolism	0.000	0.000	2.776	0.009	0.000	0.000	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	-0.059	0.028	-2.096	0.045	-0.116	-0.002	0.000
L3.Nitrogen.metabolism	0.000	0.000	2.604	0.014	0.000	0.000	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	-0.065	0.02	-3.297	0.003	-0.106	-0.025	0.000
L3.Nitrotoluene.degradation	0.000	0.00	4.671	0.000	0.000	0.000	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	-0.015	0.02	-0.736	0.467	-0.057	0.027	0.000
L3.Non.homologous.end.joining	0.000	0.00	1.498	0.145	0.000	0.000	0.067

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	-0.016	0.018	-0.856	0.399	-0.053	0.022	0.000
L3.Notch.signaling.pathway	0.063	0.028	2.266	0.031	0.006	0.120	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	-0.083	0.029	-2.888	0.007	-0.142	-0.024	0.000
L3.Novobiocin.biosynthesis	0.000	0.000	3.438	0.002	0.000	0.000	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	-0.093	0.043	-2.167	0.038	-0.181	-0.005	0.000
L3.Nucleotide.excision.repair	0.000	0.000	2.357	0.025	0.000	0.000	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	-0.035	0.022	-1.546	0.133	-0.081	0.011	0.000
L3.Nucleotide.metabolism	0.000	0.000	2.358	0.025	0.000	0.000	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)	0	0.018	0	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	-0.071	0.041	-1.727	0.095	-0.156	0.013	0.000
L3.One.carbon.pool.by.folate	0.000	0.000	1.904	0.066	0.000	0.000	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)	0	0.018	0	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	0.028	0.033	0.873	0.390	-0.038	0.095	0.000
L3.Other.glycan.degradation	0.000	0.000	-1.050	0.302	0.000	0.000	0.034

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	-0.061	0.025	-2.395	0.023	-0.112	-0.009	0.000
L3.Other.ion.coupled.transporters	0.000	0.000	3.096	0.004	0.000	0.000	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	-0.069	0.025	-2.741	0.010	-0.121	-0.018	0.000
L3.Other.transporters	0.000	0.000	3.482	0.002	0.000	0.000	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)	0	0.018	0	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	-0.069	0.03	-2.260	0.031	-0.131	-0.007	0.00
L3.Others	0.000	0.00	2.695	0.011	0.000	0.000	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	-0.087	0.032	-2.701	0.011	-0.153	-0.021	0.000
L3.Oxidative.phosphorylation	0.000	0.000	3.113	0.004	0.000	0.000	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	-0.024	0.039	-0.603	0.551	-0.104	0.057	0.000
L3.PPAR.signaling.pathway	0.000	0.000	0.681	0.501	0.000	0.000	0.015

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)	0	0.018	0	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)	0	0.018	0	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	-0.075	0.035	-2.151	0.04	-0.146	-0.004	0.000
L3.Pantothenate.and.CoA.biosynthesis	0.000	0.000	2.458	0.02	0.000	0.000	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	-0.013	0.019	-0.675	0.505	-0.051	0.026	0.000
L3.Parkinson.s.disease	0.000	0.000	1.798	0.082	0.000	0.000	0.094

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	-0.005	0.019	-0.284	0.778	-0.044	0.033	0.000
L3.Pathogenic.Escherichia.coli.infection	0.004	0.004	0.963	0.343	-0.004	0.012	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	-0.08	0.023	-3.558	0.001	-0.126	-0.034	0.000
L3.Pathways.in.cancer	0.00	0.000	4.569	0.000	0.000	0.000	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	0.009	0.03	0.295	0.77	-0.052	0.069	0.000
L3.Penicillin.and.cephalosporin.biosynthesis	0.000	0.00	-0.375	0.71	0.000	0.000	0.005

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	-0.043	0.024	-1.760	0.089	-0.092	0.007	0.000
L3.Pentose.and.glucuronate.interconversions	0.000	0.000	2.445	0.021	0.000	0.000	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	-0.072	0.03	-2.370	0.024	-0.134	-0.01	0.000
L3.Pentose.phosphate.pathway	0.000	0.00	2.815	0.009	0.000	0.00	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	-0.084	0.034	-2.513	0.018	-0.153	-0.016	0.000
L3.Peptidases	0.000	0.000	2.875	0.007	0.000	0.000	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	-0.065	0.039	-1.660	0.107	-0.146	0.015	0.0
L3.Peptidoglycan.biosynthesis	0.000	0.000	1.853	0.074	0.000	0.000	0.1

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	-0.034	0.035	-0.965	0.342	-0.105	0.038	0.000
L3.Peroxisome	0.000	0.000	1.127	0.268	0.000	0.000	0.039

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	-0.022	0.02	-1.104	0.278	-0.062	0.018	0.000
L3.Pertussis	0.000	0.00	2.258	0.031	0.000	0.000	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)	0	0.018	0	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	-0.041	0.021	-1.920	0.064	-0.084	0.003	0.000
L3.Phenylalanine.metabolism	0.000	0.000	2.962	0.006	0.000	0.000	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	-0.064	0.036	-1.751	0.090	-0.138	0.011	0.0
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis	0.000	0.000	1.992	0.056	0.000	0.000	0.1

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	-0.032	0.028	-1.145	0.261	-0.089	0.025	0.000
L3.Phenylpropanoid.biosynthesis	0.000	0.000	1.483	0.148	0.000	0.000	0.066

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	-0.058	0.039	-1.486	0.148	-0.137	0.022	0.000
L3.Phosphatidylinositol.signaling.system	0.000	0.000	1.669	0.105	0.000	0.000	0.082

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	-0.056	0.029	-1.926	0.064	-0.115	0.003	0.000
L3.Phosphonate.and.phosphinate.metabolism	0.000	0.000	2.375	0.024	0.000	0.000	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	-0.051	0.023	-2.173	0.038	-0.099	-0.003	0.000
L3.Phosphotransferase.system..PTS.	0.000	0.000	2.997	0.005	0.000	0.000	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	-0.082	0.043	-1.918	0.065	-0.169	0.005	0.000
L3.Photosynthesis	0.000	0.000	2.096	0.045	0.000	0.000	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	-0.006	0.021	-0.291	0.773	-0.049	0.037	0.000
L3.Photosynthesis. . . antenna.proteins	0.001	0.001	0.582	0.565	-0.001	0.002	0.011

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	-0.085	0.042	-2.057	0.048	-0.17	-0.001	0.000
L3.Photosynthesis.proteins	0.000	0.000	2.256	0.032	0.00	0.000	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)	0	0.018	0	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)	0	0.018	0	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	-0.103	0.029	-3.593	0.001	-0.162	-0.045	0.00
L3.Plant.pathogen.interaction	0.000	0.000	4.177	0.000	0.000	0.000	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	-0.076	0.04	-1.884	0.069	-0.159	0.006	0.000
L3.Polycyclic.aromatic.hydrocarbon.degradation	0.000	0.00	2.083	0.046	0.000	0.000	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	0.015	0.039	0.394	0.696	-0.064	0.094	0.000
L3.Polyketide.sugar.unit.biosynthesis	0.000	0.000	-0.448	0.657	0.000	0.000	0.006

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	-0.039	0.024	-1.60	0.120	-0.088	0.011	0.000
L3.Pores.ion.channels	0.000	0.000	2.26	0.031	0.000	0.000	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	-0.071	0.026	-2.759	0.010	-0.123	-0.018	0.000
L3.Porphyrin.and.chlorophyll.metabolism	0.000	0.000	3.479	0.002	0.000	0.000	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	-0.09	0.038	-2.343	0.026	-0.169	-0.012	0.000
L3.Prenyltransferases	0.00	0.000	2.600	0.014	0.000	0.000	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	-0.023	0.036	-0.634	0.531	-0.097	0.051	0.000
L3.Primary.bile.acid.biosynthesis	0.000	0.000	0.734	0.468	0.000	0.000	0.017

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	-0.076	0.038	-1.984	0.057	-0.154	0.002	0.000
L3.Primary.immunodeficiency	0.000	0.000	2.219	0.034	0.000	0.000	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	-0.038	0.018	-2.097	0.045	-0.075	-0.001	0.000
L3.Prion.diseases	0.000	0.000	3.835	0.001	0.000	0.000	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	-0.089	0.024	-3.754	0.001	-0.138	-0.041	0.000
L3.Progesterone.mediated.oocyte.maturation	0.000	0.000	4.654	0.000	0.000	0.000	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	-0.063	0.028	-2.251	0.032	-0.12	-0.006	0.0
L3.Propanoate.metabolism	0.000	0.000	2.781	0.009	0.00	0.000	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	-0.076	0.025	-3.052	0.005	-0.127	-0.025	0.000
L3.Prostate.cancer	0.000	0.000	3.832	0.001	0.000	0.000	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	-0.108	0.036	-2.983	0.006	-0.183	-0.034	0.000
L3.Proteasome	0.000	0.000	3.312	0.002	0.000	0.000	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	0.029	0.025	1.130	0.268	-0.023	0.081	0.000
L3.Protein.digestion.and.absorption	0.000	0.000	-1.572	0.126	0.000	0.000	0.074

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	-0.073	0.04	-1.817	0.079	-0.156	0.009	0.000
L3.Protein.export	0.000	0.00	2.012	0.053	0.000	0.000	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	-0.06	0.03	-2.037	0.051	-0.121	0	0.000
L3.Protein.folding.and.associated.processing	0.00	0.00	2.476	0.019	0.000	0	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	-0.045	0.027	-1.706	0.098	-0.1	0.009	0.000
L3.Protein.kinases	0.000	0.000	2.227	0.034	0.0	0.000	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	-0.053	0.032	-1.645	0.111	-0.118	0.013	0.00
L3.Protein.processing.in.endoplasmic.reticulum	0.000	0.000	1.957	0.060	0.000	0.000	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	-0.032	0.022	-1.475	0.151	-0.077	0.012	0.000
L3.Proximal.tubule.bicarbonate.reclamation	0.000	0.000	2.327	0.027	0.000	0.000	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	-0.077	0.037	-2.082	0.046	-0.152	-0.001	0.000
L3.Purine.metabolism	0.000	0.000	2.347	0.026	0.000	0.000	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	-0.08	0.039	-2.046	0.050	-0.161	0	0.000
L3.Pyrimidine.metabolism	0.00	0.000	2.271	0.031	0.000	0	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	-0.058	0.03	-1.919	0.065	-0.119	0.004	0.000
L3.Pyruvate.metabolism	0.000	0.00	2.323	0.027	0.000	0.000	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	-0.023	0.022	-1.077	0.290	-0.068	0.021	0.000
L3.RIG.I.like.receptor.signaling.pathway	0.000	0.000	1.808	0.081	0.000	0.000	0.095

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	-0.086	0.038	-2.235	0.033	-0.164	-0.007	0.000
L3.RNA.degradation	0.000	0.000	2.487	0.019	0.000	0.000	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	-0.063	0.041	-1.547	0.132	-0.145	0.02	0.000
L3.RNA.polymerase	0.000	0.000	1.718	0.096	0.000	0.00	0.087

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	-0.063	0.033	-1.915	0.065	-0.129	0.004	0.00
L3.RNA.transport	0.000	0.000	2.246	0.032	0.000	0.000	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)	0	0.018	0	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	-0.036	0.021	-1.742	0.092	-0.078	0.006	0.000
L3.Renal.cell.carcinoma	0.000	0.000	2.881	0.007	0.000	0.000	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	-0.007	0.018	-0.364	0.718	-0.043	0.030	0.000
L3.Renin.angiotensin.system	0.000	0.000	1.743	0.092	0.000	0.001	0.089

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	-0.099	0.03	-3.249	0.003	-0.161	-0.037	0.000
L3.Replication..recombination.and.repair.proteins	0.000	0.00	3.755	0.001	0.000	0.000	0.313

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	-0.042	0.034	-1.240	0.225	-0.11	0.027	0.000
L3.Restriction.enzyme	0.000	0.000	1.463	0.154	0.00	0.000	0.065

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	-0.022	0.026	-0.834	0.411	-0.075	0.032	0.000
L3.Retinol.metabolism	0.000	0.000	1.152	0.258	0.000	0.000	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)	0	0.018	0	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	-0.068	0.026	-2.642	0.013	-0.121	-0.015	0.000
L3.Riboflavin.metabolism	0.000	0.000	3.338	0.002	0.000	0.000	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	-0.08	0.042	-1.932	0.063	-0.165	0.005	0.000
L3.Ribosome	0.00	0.000	2.123	0.042	0.000	0.000	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	-0.079	0.034	-2.307	0.028	-0.148	-0.009	0.000
L3.Ribosome.Biogenesis	0.000	0.000	2.643	0.013	0.000	0.000	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	-0.07	0.037	-1.894	0.068	-0.146	0.005	0.000
L3.Ribosome.biogenesis.in.eukaryotes	0.00	0.000	2.139	0.041	0.000	0.000	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)	0	0.018	0	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	-0.021	0.036	-0.580	0.566	-0.095	0.053	0.000
L3.Secondary.bile.acid.biosynthesis	0.000	0.000	0.672	0.507	0.000	0.000	0.014

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	-0.047	0.024	-1.916	0.065	-0.097	0.003	0.000
L3.Secretion.system	0.000	0.000	2.622	0.014	0.000	0.000	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	-0.067	0.032	-2.138	0.041	-0.132	-0.003	0.000
L3.Selenocompound.metabolism	0.000	0.000	2.525	0.017	0.000	0.000	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)	0	0.018	0	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	-0.026	0.019	-1.374	0.180	-0.064	0.012	0.00
L3.Shigellosis	0.014	0.005	2.867	0.008	0.004	0.023	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	-0.077	0.029	-2.681	0.012	-0.135	-0.018	0.000
L3.Signal.transduction.mechanisms	0.000	0.000	3.229	0.003	0.000	0.000	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	0.002	0.020	0.116	0.909	-0.039	0.044	0.000
L3.Small.cell.lung.cancer	0.000	0.001	-0.271	0.788	-0.002	0.001	0.002

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	0.006	0.032	0.186	0.853	-0.06	0.072	0.000
L3.Sphingolipid.metabolism	0.000	0.000	-0.226	0.822	0.00	0.000	0.002

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)	0	0.018	0	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	-0.054	0.022	-2.452	0.020	-0.099	-0.009	0.00
L3.Sporulation	0.000	0.000	3.474	0.002	0.000	0.000	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	0.022	0.022	1.005	0.323	-0.023	0.067	0.000
L3.Staphylococcus.aureus.infection	0.000	0.000	-1.690	0.101	0.000	0.000	0.084

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	-0.058	0.032	-1.801	0.082	-0.125	0.008	0.000
L3.Starch.and.sucrose.metabolism	0.000	0.000	2.125	0.042	0.000	0.000	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	0	0.021	0.003	0.998	-0.042	0.042	0
L3.Steroid.biosynthesis	0	0.000	-0.006	0.995	0.000	0.000	0

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	-0.012	0.023	-0.545	0.590	-0.059	0.034	0.000
L3.Steroid.hormone.biosynthesis	0.000	0.000	0.906	0.372	0.000	0.000	0.026

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	-0.008	0.019	-0.419	0.678	-0.048	0.032	0.
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	0.000	0.000	1.132	0.267	0.000	0.000	0.

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	-0.019	0.038	-0.483	0.633	-0.097	0.06	0.00
L3.Streptomycin.biosynthesis	0.000	0.000	0.549	0.587	0.000	0.00	0.01

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	-0.018	0.019	-0.960	0.345	-0.056	0.02	0.000
L3.Styrene.degradation	0.000	0.000	2.319	0.027	0.000	0.00	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	-0.06	0.031	-1.913	0.065	-0.124	0.004	0.000
L3.Sulfur.metabolism	0.00	0.000	2.278	0.030	0.000	0.000	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	-0.06	0.024	-2.487	0.019	-0.108	-0.011	0.000
L3.Sulfur.relay.system	0.00	0.000	3.310	0.002	0.000	0.000	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	-0.058	0.024	-2.372	0.024	-0.108	-0.008	0.000
L3.Synthesis.and.degradation.of.ketone.bodies	0.000	0.000	3.143	0.004	0.000	0.000	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	-0.012	0.019	-0.627	0.535	-0.05	0.027	0.000
L3.Systemic.lupus.erythematosus	0.000	0.000	1.782	0.085	0.00	0.000	0.093

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)	0	0.018	0	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	-0.05	0.035	-1.457	0.155	-0.121	0.02	0.000
L3.Taurine.and.hypotaurine.metabolism	0.00	0.000	1.695	0.100	0.000	0.00	0.085

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	-0.094	0.039	-2.440	0.021	-0.173	-0.015	0.000
L3.Terpenoid.backbone.biosynthesis	0.000	0.000	2.702	0.011	0.000	0.000	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	-0.074	0.034	-2.206	0.035	-0.143	-0.006	0.000
L3.Tetracycline.biosynthesis	0.000	0.000	2.541	0.016	0.000	0.000	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	-0.086	0.034	-2.496	0.018	-0.156	-0.016	0.000
L3.Thiamine.metabolism	0.000	0.000	2.837	0.008	0.000	0.000	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)	0	0.018	0	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	-0.027	0.02	-1.348	0.188	-0.067	0.014	0.000
L3.Toluene.degradation	0.000	0.00	2.554	0.016	0.000	0.000	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	0.002	0.020	0.116	0.909	-0.039	0.044	0.000
L3.Toxoplasmosis	0.000	0.001	-0.271	0.788	-0.002	0.001	0.002

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	-0.053	0.024	-2.177	0.037	-0.103	-0.003	0.000
L3.Transcription.factors	0.000	0.000	2.931	0.006	0.000	0.000	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	-0.093	0.038	-2.416	0.022	-0.171	-0.014	0.000
L3.Transcription.machinery	0.000	0.000	2.678	0.012	0.000	0.000	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	-0.024	0.019	-1.292	0.206	-0.062	0.014	0.000
L3.Transcription.related.proteins	0.000	0.000	2.738	0.010	0.000	0.000	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	-0.088	0.038	-2.313	0.028	-0.166	-0.01	0.000
L3.Translation.factors	0.000	0.000	2.573	0.015	0.000	0.00	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	-0.084	0.034	-2.515	0.018	-0.153	-0.016	0.000
L3.Translation.proteins	0.000	0.000	2.879	0.007	0.000	0.000	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	-0.056	0.027	-2.051	0.049	-0.111	0	0.000
L3.Transporters	0.000	0.000	2.594	0.015	0.000	0	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	-0.077	0.024	-3.168	0.004	-0.126	-0.027	0
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis	0.000	0.000	4.016	0.000	0.000	0.000	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	-0.036	0.021	-1.662	0.107	-0.08	0.008	0.000
L3.Tryptophan.metabolism	0.000	0.000	2.626	0.013	0.00	0.000	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	-0.076	0.044	-1.746	0.091	-0.165	0.013	0.000
L3.Tuberculosis	0.000	0.000	1.905	0.066	0.000	0.000	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	-0.058	0.023	-2.475	0.019	-0.106	-0.01	0.000
L3.Two.component.system	0.000	0.000	3.346	0.002	0.000	0.00	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	-0.068	0.044	-1.547	0.132	-0.157	0.022	0.000
L3.Type.I.diabetes.mellitus	0.000	0.000	1.691	0.101	0.000	0.000	0.084

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	-0.089	0.033	-2.729	0.011	-0.156	-0.022	0.00
L3.Type.II.diabetes.mellitus	0.000	0.000	3.132	0.004	0.000	0.000	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	-0.061	0.027	-2.236	0.033	-0.117	-0.005	0.000
L3.Tyrosine.metabolism	0.000	0.000	2.796	0.009	0.000	0.000	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	-0.032	0.023	-1.415	0.168	-0.078	0.014	0.
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis	0.000	0.000	2.162	0.039	0.000	0.000	0.

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	-0.014	0.022	-0.627	0.536	-0.059	0.031	0.000
L3.Ubiquitin.system	0.000	0.000	1.094	0.283	0.000	0.000	0.037

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)	0	0.018	0	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	-0.055	0.038	-1.452	0.157	-0.133	0.022	0.00
L3.Valine..leucine.and.isoleucine.biosynthesis	0.000	0.000	1.641	0.111	0.000	0.000	0.08

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	-0.053	0.026	-2.052	0.049	-0.106	0	0.000
L3.Valine..leucine.and.isoleucine.degradation	0.000	0.000	2.676	0.012	0.000	0	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	0.009	0.021	0.429	0.671	-0.034	0.052	0.000
L3.Various.types.of.N.glycan.biosynthesis	-0.009	0.010	-0.865	0.394	-0.030	0.012	0.024

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)	0	0.018	0	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	0.003	0.019	0.174	0.863	-0.036	0.042	0.000
L3.Vasopressin.regulated.water.reabsorption	-0.013	0.022	-0.604	0.550	-0.059	0.032	0.012

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	-0.020	0.019	-1.066	0.295	-0.058	0.018	0.000
L3.Vibrio.cholerae.infection	0.028	0.011	2.502	0.018	0.005	0.050	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	-0.068	0.025	-2.748	0.010	-0.118	-0.017	0.000
L3.Vibrio.cholerae.pathogenic.cycle	0.000	0.000	3.539	0.001	0.000	0.000	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	0.002	0.020	0.116	0.909	-0.039	0.044	0.000
L3.Viral.myocarditis	0.000	0.001	-0.271	0.788	-0.002	0.001	0.002

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	-0.051	0.03	-1.700	0.099	-0.112	0.01	0.000
L3.Vitamin.B6.metabolism	0.000	0.00	2.077	0.046	0.000	0.00	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	-0.016	0.018	-0.856	0.399	-0.053	0.022	0.000
L3.Wnt.signaling.pathway	0.063	0.028	2.266	0.031	0.006	0.120	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	-0.044	0.025	-1.737	0.093	-0.096	0.008	0.000
L3.Xylene.degradation	0.000	0.000	2.328	0.027	0.000	0.000	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	-0.061	0.046	-1.334	0.192	-0.154	0.032	0.000
L3.Zeatin.biosynthesis	0.000	0.000	1.450	0.157	0.000	0.000	0.064

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	-0.02	0.019	-1.094	0.283	-0.059	0.018	0.000
L3.alpha.Linolenic.acid.metabolism	0.00	0.000	2.487	0.019	0.000	0.000	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	-0.052	0.023	-2.266	0.031	-0.098	-0.005	0.000
L3.beta.Alanine.metabolism	0.000	0.000	3.178	0.003	0.000	0.000	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	0.004	0.033	0.112	0.912	-0.064	0.071	0.000
L3.beta.Lactam.resistance	0.000	0.000	-0.135	0.894	0.000	0.000	0.001

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)	0	0.018	0	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)	0	0.018	0	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	0.002	0.020	0.116	0.909	-0.039	0.044	0.000
L3.p53.signaling.pathway	0.000	0.001	-0.271	0.788	-0.002	0.001	0.002

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	0.072	0.16	0.447	0.660	-0.263	0.406	0.000
L1.Cellular.Processes	0.000	0.00	-0.529	0.603	0.000	0.000	0.014

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	0.139	0.161	0.863	0.399	-0.198	0.476	0.000
L1.Environmental.Information.Processing	0.000	0.000	-1.012	0.324	0.000	0.000	0.049

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	0.09	0.189	0.478	0.638	-0.305	0.486	0.000
L1.Genetic.Information.Processing	0.00	0.000	-0.537	0.598	0.000	0.000	0.014

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	0.044	0.193	0.228	0.822	-0.359	0.447	0.000
L1.Human.Diseases	0.000	0.000	-0.255	0.802	0.000	0.000	0.003

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	0.064	0.195	0.328	0.746	-0.344	0.472	0.000
L1.Metabolism	0.000	0.000	-0.366	0.719	0.000	0.000	0.007

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	0.15	0.164	0.912	0.373	-0.194	0.494	0.000
L1.None	0.00	0.000	-1.060	0.303	0.000	0.000	0.053

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	-0.067	0.197	-0.342	0.736	-0.48	0.346	0.000
L1.Organismal.Systems	0.000	0.000	0.379	0.709	0.00	0.000	0.007

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	0.074	0.193	0.382	0.707	-0.331	0.479	0.000
L1.Unclassified	0.000	0.000	-0.426	0.675	0.000	0.000	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	0.075	0.066	1.135	0.271	-0.063	0.213	0.000
L1.Cellular.Processes	0.000	0.000	-1.343	0.195	0.000	0.000	0.083

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	0.1	0.065	1.538	0.141	-0.036	0.237	0.00
L1.Environmental.Information.Processing	0.0	0.000	-1.802	0.087	0.000	0.000	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	0.082	0.079	1.046	0.309	-0.082	0.247	0.000
L1.Genetic.Information.Processing	0.000	0.000	-1.173	0.255	0.000	0.000	0.064

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	0.063	0.081	0.783	0.443	-0.106	0.233	0.000
L1.Human.Diseases	0.000	0.000	-0.875	0.393	0.000	0.000	0.037

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	0.075	0.081	0.921	0.368	-0.095	0.245	0.00
L1.Metabolism	0.000	0.000	-1.026	0.318	0.000	0.000	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	0.092	0.068	1.356	0.191	-0.05	0.235	0.00
L1.None	0.000	0.000	-1.576	0.132	0.00	0.000	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	0.037	0.084	0.441	0.664	-0.139	0.213	0.000
L1.Organismal.Systems	0.000	0.000	-0.489	0.630	0.000	0.000	0.012

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	0.081	0.08	1.003	0.329	-0.088	0.249	0.000
L1.Unclassified	0.000	0.00	-1.119	0.277	0.000	0.000	0.059

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	0.025	0.046	0.546	0.591	-0.071	0.121	0.00
L1.Cellular.Processes	0.000	0.000	-0.646	0.526	0.000	0.000	0.02

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	0.021	0.047	0.442	0.664	-0.078	0.12	0.000
L1.Environmental.Information.Processing	0.000	0.000	-0.518	0.611	0.000	0.00	0.013

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	0.028	0.054	0.520	0.609	-0.085	0.142	0.000
L1.Genetic.Information.Processing	0.000	0.000	-0.584	0.566	0.000	0.000	0.017

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	0.035	0.055	0.636	0.533	-0.08	0.15	0.000
L1.Human.Diseases	0.000	0.000	-0.711	0.486	0.00	0.00	0.025

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	0.029	0.056	0.513	0.614	-0.088	0.146	0.000
L1.Metabolism	0.000	0.000	-0.571	0.574	0.000	0.000	0.016

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	0.018	0.048	0.374	0.713	-0.083	0.12	0.000
L1.None	0.000	0.000	-0.435	0.669	0.000	0.00	0.009

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	0.037	0.056	0.649	0.524	-0.081	0.154	0.000
L1.Organismal.Systems	0.000	0.000	-0.721	0.480	0.000	0.000	0.025

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	0.031	0.055	0.558	0.583	-0.085	0.147	0.000
L1.Unclassified	0.000	0.000	-0.623	0.541	0.000	0.000	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	-0.002	0.039	-0.056	0.956	-0.085	0.08	0
L1.Cellular.Processes	0.000	0.000	0.066	0.948	0.000	0.00	0

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	-0.015	0.04	-0.381	0.708	-0.1	0.069	0.00
L1.Environmental.Information.Processing	0.000	0.00	0.446	0.660	0.0	0.000	0.01

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	0.001	0.047	0.014	0.989	-0.097	0.098	0
L1.Genetic.Information.Processing	0.000	0.000	-0.016	0.987	0.000	0.000	0

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	-0.003	0.047	-0.066	0.948	-0.102	0.096	0
L1.Human.Diseases	0.000	0.000	0.073	0.942	0.000	0.000	0

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	-0.004	0.048	-0.094	0.926	-0.105	0.096	0.000
L1.Metabolism	0.000	0.000	0.105	0.918	0.000	0.000	0.001

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	-0.009	0.041	-0.208	0.837	-0.095	0.078	0.000
L1.None	0.000	0.000	0.242	0.811	0.000	0.000	0.003

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	0.019	0.048	0.391	0.700	-0.082	0.12	0.000
L1.Organismal.Systems	0.000	0.000	-0.434	0.669	0.000	0.00	0.009

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	-0.008	0.048	-0.172	0.865	-0.108	0.091	0.000
L1.Unclassified	0.000	0.000	0.192	0.850	0.000	0.000	0.002

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	0.083	0.192	0.432	0.670	-0.319	0.484	0.000
L2.Amino.Acid.Metabolism	0.000	0.000	-0.483	0.634	0.000	0.000	0.012

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	0.012	0.192	0.064	0.949	-0.39	0.415	0
L2.Biosynthesis.of.Other.Secondary.Metabolites	0.000	0.000	-0.072	0.943	0.00	0.000	0

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	0.034	0.182	0.187	0.854	-0.347	0.415	0.000
L2.Cancers	0.000	0.000	-0.212	0.834	0.000	0.000	0.002

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	0.05	0.191	0.261	0.797	-0.35	0.45	0.000
L2.Carbohydrate.Metabolism	0.00	0.000	-0.292	0.773	0.00	0.00	0.004

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	-0.006	0.088	-0.072	0.943	-0.191	0.178	0.000
L2.Cardiovascular.Diseases	0.000	0.000	0.330	0.745	0.000	0.000	0.005

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)	0	0.084	0	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	0.08	0.19	0.420	0.679	-0.318	0.478	0.000
L2.Cell.Growth.and.Death	0.00	0.00	-0.471	0.643	0.000	0.000	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	0.083	0.143	0.581	0.568	-0.216	0.382	0.000
L2.Cell.Motility	0.000	0.000	-0.724	0.478	0.000	0.000	0.026

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	0.052	0.196	0.265	0.794	-0.359	0.463	0.000
L2.Cellular.Processes.and.Signaling	0.000	0.000	-0.295	0.771	0.000	0.000	0.004

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	-0.007	0.089	-0.075	0.941	-0.192	0.179	0.000
L2.Circulatory.System	0.000	0.000	0.312	0.759	0.000	0.000	0.005

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	-0.312	0.177	-1.761	0.094	-0.684	0.059	0.000
L2.Digestive.System	0.000	0.000	1.965	0.064	0.000	0.000	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	-0.099	0.199	-0.499	0.623	-0.515	0.317	0.000
L2.Endocrine.System	0.000	0.000	0.553	0.587	0.000	0.000	0.015

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	0.074	0.191	0.388	0.703	-0.326	0.474	0.000
L2.Energy.Metabolism	0.000	0.000	-0.434	0.669	0.000	0.000	0.009

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	0.072	0.173	0.416	0.682	-0.289	0.433	0.000
L2.Environmental.Adaptation	0.000	0.000	-0.479	0.637	0.000	0.000	0.011

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	0.08	0.191	0.419	0.680	-0.319	0.479	0.000
L2.Enzyme.Families	0.00	0.000	-0.469	0.645	0.000	0.000	0.011

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	-0.261	0.14	-1.859	0.079	-0.554	0.033	0.000
L2.Excretory.System	0.000	0.00	2.222	0.039	0.000	0.000	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	0.049	0.199	0.245	0.809	-0.367	0.465	0.000
L2.Folding..Sorting.and.Degradation	0.000	0.000	-0.272	0.789	0.000	0.000	0.004

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	0.116	0.189	0.613	0.547	-0.28	0.511	0.000
L2.Genetic.Information.Processing	0.000	0.000	-0.686	0.501	0.00	0.000	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	-0.121	0.221	-0.548	0.590	-0.584	0.342	0.000
L2.Glycan.Biosynthesis.and.Metabolism	0.000	0.000	0.594	0.559	0.000	0.000	0.017

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	0.007	0.195	0.038	0.970	-0.401	0.416	0
L2.Immune.System	0.000	0.000	-0.042	0.967	0.000	0.000	0

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	0.036	0.188	0.190	0.851	-0.358	0.43	0.000
L2.Immune.System.Diseases	0.000	0.000	-0.214	0.833	0.000	0.00	0.002

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	0.048	0.195	0.245	0.809	-0.36	0.456	0.000
L2.Infectious.Diseases	0.000	0.000	-0.273	0.788	0.00	0.000	0.004

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	0.038	0.192	0.199	0.845	-0.364	0.44	0.000
L2.Lipid.Metabolism	0.000	0.000	-0.222	0.826	0.000	0.00	0.002

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	0.143	0.158	0.903	0.378	-0.188	0.474	0.000
L2.Membrane.Transport	0.000	0.000	-1.064	0.301	0.000	0.000	0.054

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	-0.012	0.199	-0.059	0.954	-0.428	0.405	0
L2.Metabolic.Diseases	0.000	0.000	0.065	0.949	0.000	0.000	0

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	0.071	0.194	0.368	0.717	-0.335	0.477	0.000
L2.Metabolism	0.000	0.000	-0.410	0.686	0.000	0.000	0.008

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	0.093	0.197	0.473	0.641	-0.319	0.506	0.000
L2.Metabolism.of.Cofactors.and.Vitamins	0.000	0.000	-0.526	0.605	0.000	0.000	0.014

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	0.054	0.197	0.272	0.789	-0.359	0.466	0.000
L2.Metabolism.of.Other.Amino.Acids	0.000	0.000	-0.302	0.766	0.000	0.000	0.005

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	0.068	0.201	0.337	0.740	-0.353	0.489	0.000
L2.Metabolism.of.Terpenoids.and.Polyketides	0.000	0.000	-0.373	0.714	0.000	0.000	0.007

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	-0.089	0.192	-0.461	0.650	-0.492	0.314	0.000
L2.Nervous.System	0.000	0.000	0.515	0.613	0.000	0.000	0.013

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	0.075	0.171	0.439	0.666	-0.283	0.433	0.000
L2.Neurodegenerative.Diseases	0.000	0.000	-0.507	0.618	0.000	0.000	0.013

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	0.094	0.195	0.481	0.636	-0.315	0.502	0.000
L2.Nucleotide.Metabolism	0.000	0.000	-0.535	0.599	0.000	0.000	0.014

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	0.07	0.192	0.366	0.718	-0.332	0.472	0.000
L2.Poorly.Characterized	0.00	0.000	-0.410	0.687	0.000	0.000	0.008

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	0.081	0.192	0.420	0.679	-0.322	0.483	0.000
L2.Replication.and.Repair	0.000	0.000	-0.469	0.644	0.000	0.000	0.011

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)	0	0.084	0	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	0.101	0.174	0.580	0.569	-0.264	0.466	0.000
L2.Signal.Transduction	0.000	0.000	-0.665	0.514	0.000	0.000	0.022

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	-0.113	0.226	-0.498	0.624	-0.586	0.361	0.000
L2.Signaling.Molecules.and.Interaction	0.000	0.000	0.538	0.597	0.000	0.000	0.014

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	0.115	0.177	0.650	0.523	-0.256	0.487	0.000
L2.Transcription	0.000	0.000	-0.741	0.468	0.000	0.000	0.027

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	0.104	0.185	0.562	0.581	-0.283	0.491	0.00
L2.Translation	0.000	0.000	-0.633	0.534	0.000	0.000	0.02

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	-0.268	0.199	-1.344	0.195	-0.685	0.149	0.000
L2.Transport.and.Catabolism	0.000	0.000	1.474	0.157	0.000	0.000	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	0.107	0.185	0.578	0.570	-0.28	0.493	0.000
L2.Xenobiotics.Biodegradation.and.Metabolism	0.000	0.000	-0.651	0.523	0.00	0.000	0.021

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	0.079	0.08	0.984	0.337	-0.089	0.246	0.000
L2.Amino.Acid.Metabolism	0.000	0.00	-1.100	0.285	0.000	0.000	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	0.057	0.081	0.709	0.487	-0.112	0.227	0.000
L2.Biosynthesis.of.Other.Secondary.Metabolites	0.000	0.000	-0.793	0.437	0.000	0.000	0.031

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	0.042	0.077	0.542	0.594	-0.12	0.203	0.000
L2.Cancers	0.000	0.000	-0.615	0.546	0.00	0.000	0.019

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	0.077	0.079	0.968	0.345	-0.089	0.243	0.000
L2.Carbohydrate.Metabolism	0.000	0.000	-1.084	0.292	0.000	0.000	0.056

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	0	0.038	0.004	0.997	-0.079	0.079	0
L2.Cardiovascular.Diseases	0	0.000	-0.017	0.987	0.000	0.000	0

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)	0	0.036	0	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	0.075	0.08	0.940	0.359	-0.092	0.241	0.000
L2.Cell.Growth.and.Death	0.000	0.00	-1.053	0.306	0.000	0.000	0.052

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	0.075	0.058	1.301	0.209	-0.046	0.197	0.000
L2.Cell.Motility	0.000	0.000	-1.620	0.122	0.000	0.000	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	0.08	0.082	0.975	0.342	-0.091	0.25	0.000
L2.Cellular.Processes.and.Signaling	0.00	0.000	-1.085	0.291	0.000	0.00	0.056

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	0	0.038	0.009	0.993	-0.079	0.08	0
L2.Circulatory.System	0	0.000	-0.038	0.970	0.000	0.00	0

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	-0.136	0.076	-1.798	0.088	-0.294	0.022	0.000
L2.Digestive.System	0.000	0.000	2.006	0.059	0.000	0.000	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	0.008	0.086	0.094	0.926	-0.171	0.187	0.000
L2.Endocrine.System	0.000	0.000	-0.104	0.918	0.000	0.000	0.001

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	0.08	0.079	1.008	0.326	-0.086	0.246	0.00
L2.Energy.Metabolism	0.00	0.000	-1.128	0.273	0.000	0.000	0.06

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	0.087	0.071	1.234	0.232	-0.061	0.235	0.000
L2.Environmental.Adaptation	0.000	0.000	-1.422	0.171	0.000	0.000	0.092

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	0.084	0.079	1.060	0.302	-0.082	0.25	0.000
L2.Enzyme.Families	0.000	0.000	-1.187	0.250	0.000	0.00	0.066

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	-0.004	0.067	-0.062	0.951	-0.145	0.137	0
L2.Excretory.System	0.000	0.000	0.075	0.941	0.000	0.000	0

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	0.07	0.083	0.845	0.408	-0.104	0.245	0.000
L2.Folding..Sorting.and.Degradation	0.00	0.000	-0.938	0.360	0.000	0.000	0.042

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	0.086	0.079	1.100	0.285	-0.078	0.251	0.000
L2.Genetic.Information.Processing	0.000	0.000	-1.233	0.233	0.000	0.000	0.071

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	-0.013	0.095	-0.136	0.894	-0.212	0.187	0.000
L2.Glycan.Biosynthesis.and.Metabolism	0.000	0.000	0.147	0.885	0.000	0.000	0.001

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	0.043	0.083	0.516	0.612	-0.13	0.216	0.000
L2.Immune.System	0.000	0.000	-0.575	0.572	0.00	0.000	0.016

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	0.045	0.08	0.560	0.582	-0.122	0.212	0.000
L2.Immune.System.Diseases	0.000	0.00	-0.629	0.537	0.000	0.000	0.019

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	0.086	0.081	1.070	0.298	-0.082	0.255	0.000
L2.Infectious.Diseases	0.000	0.000	-1.192	0.248	0.000	0.000	0.066

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	0.071	0.08	0.880	0.390	-0.097	0.239	0.000
L2.Lipid.Metabolism	0.000	0.00	-0.984	0.337	0.000	0.000	0.046

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	0.101	0.064	1.580	0.131	-0.033	0.235	0.000
L2.Membrane.Transport	0.000	0.000	-1.862	0.078	0.000	0.000	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	0.068	0.083	0.810	0.428	-0.107	0.242	0.000
L2.Metabolic.Diseases	0.000	0.000	-0.898	0.380	0.000	0.000	0.039

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	0.073	0.081	0.902	0.378	-0.097	0.243	0.000
L2.Metabolism	0.000	0.000	-1.006	0.327	0.000	0.000	0.048

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	0.077	0.083	0.932	0.363	-0.096	0.25	0.000
L2.Metabolism.of.Cofactors.and.Vitamins	0.000	0.000	-1.035	0.314	0.000	0.00	0.051

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	0.074	0.082	0.898	0.380	-0.098	0.246	0.000
L2.Metabolism.of.Other.Amino.Acids	0.000	0.000	-0.998	0.331	0.000	0.000	0.047

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	0.07	0.084	0.823	0.421	-0.107	0.246	0.00
L2.Metabolism.of.Terpenoids.and.Polyketides	0.00	0.000	-0.910	0.374	0.000	0.000	0.04

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	0.068	0.081	0.841	0.411	-0.101	0.238	0.000
L2.Nervous.System	0.000	0.000	-0.939	0.359	0.000	0.000	0.042

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	0.009	0.074	0.124	0.903	-0.145	0.163	0.000
L2.Neurodegenerative.Diseases	0.000	0.000	-0.143	0.888	0.000	0.000	0.001

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	0.08	0.082	0.983	0.338	-0.09	0.251	0.000
L2.Nucleotide.Metabolism	0.00	0.000	-1.094	0.288	0.00	0.000	0.056

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	0.081	0.08	1.02	0.321	-0.086	0.248	0.000
L2.Poorly.Characterized	0.000	0.00	-1.14	0.268	0.000	0.000	0.061

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	0.079	0.08	0.990	0.334	-0.088	0.247	0.000
L2.Replication.and.Repair	0.000	0.00	-1.106	0.282	0.000	0.000	0.058

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)	0	0.036	0	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	0.087	0.072	1.204	0.243	-0.064	0.237	0.000
L2.Signal.Transduction	0.000	0.000	-1.381	0.183	0.000	0.000	0.087

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	0.026	0.097	0.265	0.794	-0.178	0.229	0.000
L2.Signaling.Molecules.and.Interaction	0.000	0.000	-0.286	0.778	0.000	0.000	0.004

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	0.094	0.073	1.292	0.212	-0.058	0.247	0.000
L2.Transcription	0.000	0.000	-1.472	0.157	0.000	0.000	0.098

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	0.082	0.077	1.065	0.300	-0.079	0.243	0.000
L2.Translation	0.000	0.000	-1.200	0.245	0.000	0.000	0.067

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	-0.093	0.087	-1.069	0.299	-0.274	0.089	0.000
L2.Transport.and.Catabolism	0.000	0.000	1.172	0.256	0.000	0.000	0.064

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	0.081	0.077	1.056	0.304	-0.08	0.243	0.000
L2.Xenobiotics.Biodegradation.and.Metabolism	0.000	0.000	-1.190	0.249	0.00	0.000	0.066

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	0.026	0.055	0.472	0.642	-0.089	0.141	0.000
L2.Amino.Acid.Metabolism	0.000	0.000	-0.527	0.604	0.000	0.000	0.014

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	0.035	0.055	0.638	0.531	-0.079	0.149	0.000
L2.Biosynthesis.of.Other.Secondary.Metabolites	0.000	0.000	-0.714	0.484	0.000	0.000	0.025

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	0.045	0.051	0.875	0.393	-0.062	0.152	0.000
L2.Cancers	0.000	0.000	-0.993	0.333	0.000	0.000	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	0.028	0.055	0.510	0.616	-0.087	0.142	0.000
L2.Carbohydrate.Metabolism	0.000	0.000	-0.571	0.574	0.000	0.000	0.016

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	0.005	0.025	0.215	0.832	-0.047	0.057	0.000
L2.Cardiovascular.Diseases	0.000	0.000	-0.981	0.339	0.000	0.000	0.046

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)	0	0.024	0	1	-0.05	0.05	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	0.029	0.055	0.540	0.595	-0.085	0.144	0.000
L2.Cell.Growth.and.Death	0.000	0.000	-0.605	0.552	0.000	0.000	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	0.022	0.041	0.523	0.607	-0.065	0.108	0.000
L2.Cell.Motility	0.000	0.000	-0.651	0.523	0.000	0.000	0.021

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	0.03	0.056	0.541	0.595	-0.087	0.148	0.000
L2.Cellular.Processes.and.Signaling	0.00	0.000	-0.602	0.555	0.000	0.000	0.018

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	0.006	0.025	0.245	0.809	-0.046	0.058	0.00
L2.Circulatory.System	0.000	0.000	-1.025	0.318	0.000	0.000	0.05

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	0.008	0.056	0.139	0.891	-0.109	0.125	0.000
L2.Digestive.System	0.000	0.000	-0.156	0.878	0.000	0.000	0.001

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	0.039	0.057	0.681	0.504	-0.08	0.158	0.000
L2.Endocrine.System	0.000	0.000	-0.755	0.460	0.00	0.000	0.028

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	0.028	0.055	0.511	0.616	-0.087	0.143	0.000
L2.Energy.Metabolism	0.000	0.000	-0.571	0.574	0.000	0.000	0.016

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	0.029	0.049	0.583	0.567	-0.075	0.132	0.000
L2.Environmental.Adaptation	0.000	0.000	-0.672	0.510	0.000	0.000	0.022

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	0.027	0.055	0.501	0.622	-0.087	0.142	0.000
L2.Enzyme.Families	0.000	0.000	-0.561	0.581	0.000	0.000	0.015

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	0.046	0.043	1.060	0.302	-0.045	0.137	0.000
L2.Excretory.System	0.000	0.000	-1.267	0.220	0.000	0.000	0.074

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	0.031	0.057	0.552	0.588	-0.087	0.15	0.000
L2.Folding..Sorting.and.Degradation	0.000	0.000	-0.612	0.548	0.000	0.00	0.018

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	0.027	0.055	0.504	0.620	-0.087	0.142	0.000
L2.Genetic.Information.Processing	0.000	0.000	-0.564	0.579	0.000	0.000	0.016

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	0.034	0.064	0.530	0.602	-0.1	0.167	0.000
L2.Glycan.Biosynthesis.and.Metabolism	0.000	0.000	-0.574	0.572	0.0	0.000	0.016

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	0.026	0.056	0.464	0.648	-0.091	0.143	0.000
L2.Immune.System	0.000	0.000	-0.518	0.611	0.000	0.000	0.013

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	0.023	0.054	0.436	0.668	-0.089	0.136	0.000
L2.Immune.System.Diseases	0.000	0.000	-0.490	0.630	0.000	0.000	0.012

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	0.028	0.056	0.497	0.625	-0.089	0.145	0.000
L2.Infectious.Diseases	0.000	0.000	-0.554	0.586	0.000	0.000	0.015

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	0.038	0.055	0.690	0.499	-0.077	0.152	0.000
L2.Lipid.Metabolism	0.000	0.000	-0.772	0.450	0.000	0.000	0.029

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	0.02	0.047	0.420	0.679	-0.078	0.117	0.000
L2.Membrane.Transport	0.00	0.000	-0.495	0.626	0.000	0.000	0.012

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	0.036	0.057	0.629	0.537	-0.083	0.154	0.000
L2.Metabolic.Diseases	0.000	0.000	-0.698	0.493	0.000	0.000	0.024

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	0.036	0.055	0.660	0.517	-0.079	0.152	0.000
L2.Metabolism	0.000	0.000	-0.736	0.471	0.000	0.000	0.026

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	0.024	0.057	0.423	0.677	-0.095	0.143	0.000
L2.Metabolism.of.Cofactors.and.Vitamins	0.000	0.000	-0.469	0.644	0.000	0.000	0.011

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	0.034	0.056	0.603	0.554	-0.084	0.152	0.000
L2.Metabolism.of.Other.Amino.Acids	0.000	0.000	-0.670	0.511	0.000	0.000	0.022

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	0.026	0.058	0.453	0.656	-0.095	0.147	0.000
L2.Metabolism.of.Terpenoids.and.Polyketides	0.000	0.000	-0.501	0.622	0.000	0.000	0.012

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	0.031	0.055	0.553	0.587	-0.085	0.146	0.000
L2.Nervous.System	0.000	0.000	-0.617	0.544	0.000	0.000	0.019

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	0.039	0.049	0.805	0.431	-0.062	0.141	0.000
L2.Neurodegenerative.Diseases	0.000	0.000	-0.930	0.364	0.000	0.000	0.041

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	0.027	0.056	0.473	0.642	-0.091	0.144	0.000
L2.Nucleotide.Metabolism	0.000	0.000	-0.526	0.605	0.000	0.000	0.014

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	0.03	0.055	0.547	0.591	-0.085	0.145	0.000
L2.Poorly.Characterized	0.00	0.000	-0.611	0.548	0.000	0.000	0.018

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	0.028	0.055	0.511	0.615	-0.087	0.144	0.000
L2.Replication.and.Repair	0.000	0.000	-0.571	0.575	0.000	0.000	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)	0	0.024	0	1	-0.05	0.05	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	0.031	0.05	0.623	0.541	-0.074	0.136	0.000
L2.Signal.Transduction	0.000	0.00	-0.715	0.484	0.000	0.000	0.025

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	0.013	0.066	0.202	0.842	-0.124	0.15	0.000
L2.Signaling.Molecules.and.Interaction	0.000	0.000	-0.218	0.830	0.000	0.00	0.002

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	0.022	0.051	0.421	0.678	-0.086	0.129	0.000
L2.Transcription	0.000	0.000	-0.480	0.637	0.000	0.000	0.011

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	0.03	0.053	0.572	0.574	-0.081	0.142	0.00
L2.Translation	0.00	0.000	-0.644	0.527	0.000	0.000	0.02

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	0.018	0.06	0.301	0.767	-0.108	0.145	0.000
L2.Transport.and.Catabolism	0.000	0.00	-0.330	0.745	0.000	0.000	0.005

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	0.031	0.053	0.575	0.572	-0.081	0.142	0.000
L2.Xenobiotics.Biodegradation.and.Metabolism	0.000	0.000	-0.649	0.524	0.000	0.000	0.021

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	0	0.047	0.009	0.993	-0.098	0.099	0
L2.Amino.Acid.Metabolism	0	0.000	-0.010	0.992	0.000	0.000	0

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	-0.017	0.047	-0.353	0.728	-0.115	0.082	0.000
L2.Biosynthesis.of.Other.Secondary.Metabolites	0.000	0.000	0.395	0.697	0.000	0.000	0.008

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	-0.007	0.045	-0.167	0.869	-0.101	0.086	0.000
L2.Cancers	0.000	0.000	0.189	0.852	0.000	0.000	0.002

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	-0.008	0.047	-0.161	0.874	-0.106	0.091	0.000
L2.Carbohydrate.Metabolism	0.000	0.000	0.180	0.859	0.000	0.000	0.002

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	0.004	0.021	0.206	0.839	-0.04	0.049	0.000
L2.Cardiovascular.Diseases	0.000	0.000	-0.938	0.360	0.00	0.000	0.042

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)	0	0.021	0	1	-0.043	0.043	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	-0.002	0.047	-0.050	0.961	-0.1	0.096	0
L2.Cell.Growth.and.Death	0.000	0.000	0.056	0.956	0.0	0.000	0

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	-0.003	0.035	-0.078	0.939	-0.077	0.071	0
L2.Cell.Motility	0.000	0.000	0.097	0.924	0.000	0.000	0

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	-0.01	0.048	-0.212	0.834	-0.111	0.09	0.000
L2.Cellular.Processes.and.Signaling	0.00	0.000	0.236	0.816	0.000	0.00	0.003

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	0.005	0.021	0.221	0.828	-0.04	0.049	0.000
L2.Circulatory.System	0.000	0.000	-0.922	0.368	0.00	0.000	0.041

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	-0.022	0.047	-0.474	0.641	-0.121	0.077	0.000
L2.Digestive.System	0.000	0.000	0.529	0.603	0.000	0.000	0.014

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	0.023	0.049	0.462	0.649	-0.079	0.125	0.000
L2.Endocrine.System	0.000	0.000	-0.512	0.615	0.000	0.000	0.013

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	-0.005	0.047	-0.114	0.91	-0.104	0.093	0.000
L2.Energy.Metabolism	0.000	0.000	0.128	0.90	0.000	0.000	0.001

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	0.007	0.042	0.171	0.866	-0.082	0.096	0.000
L2.Environmental.Adaptation	0.000	0.000	-0.197	0.846	0.000	0.000	0.002

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	-0.004	0.047	-0.08	0.937	-0.102	0.095	0
L2.Enzyme.Families	0.000	0.000	0.09	0.930	0.000	0.000	0

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	0.049	0.036	1.357	0.191	-0.027	0.125	0.000
L2.Excretory.System	0.000	0.000	-1.622	0.121	0.000	0.000	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	0.001	0.049	0.020	0.984	-0.101	0.103	0
L2.Folding..Sorting.and.Degradation	0.000	0.000	-0.022	0.982	0.000	0.000	0

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	0	0.047	0.007	0.995	-0.098	0.098	0
L2.Genetic.Information.Processing	0	0.000	-0.007	0.994	0.000	0.000	0

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	-0.011	0.055	-0.203	0.841	-0.125	0.103	0.000
L2.Glycan.Biosynthesis.and.Metabolism	0.000	0.000	0.220	0.828	0.000	0.000	0.002

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	0.016	0.048	0.326	0.748	-0.084	0.115	0.000
L2.Immune.System	0.000	0.000	-0.364	0.720	0.000	0.000	0.007

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	-0.029	0.046	-0.635	0.533	-0.124	0.066	0.000
L2.Immune.System.Diseases	0.000	0.000	0.714	0.484	0.000	0.000	0.025

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	0.001	0.048	0.019	0.985	-0.099	0.101	0
L2.Infectious.Diseases	0.000	0.000	-0.021	0.983	0.000	0.000	0

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	-0.001	0.047	-0.024	0.981	-0.1	0.097	0
L2.Lipid.Metabolism	0.000	0.000	0.027	0.979	0.0	0.000	0

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	-0.016	0.04	-0.401	0.693	-0.099	0.067	0.000
L2.Membrane.Transport	0.000	0.00	0.473	0.642	0.000	0.000	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	-0.001	0.049	-0.026	0.979	-0.103	0.101	0
L2.Metabolic.Diseases	0.000	0.000	0.029	0.977	0.000	0.000	0

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	-0.01	0.048	-0.204	0.841	-0.109	0.09	0.000
L2.Metabolism	0.00	0.000	0.227	0.823	0.000	0.00	0.003

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	-0.006	0.049	-0.133	0.896	-0.108	0.095	0.000
L2.Metabolism.of.Cofactors.and.Vitamins	0.000	0.000	0.147	0.884	0.000	0.000	0.001

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	-0.009	0.048	-0.184	0.856	-0.11	0.092	0.000
L2.Metabolism.of.Other.Amino.Acids	0.000	0.000	0.204	0.841	0.00	0.000	0.002

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	0	0.049	0.002	0.998	-0.103	0.104	0
L2.Metabolism.of.Terpenoids.and.Polyketides	0	0.000	-0.003	0.998	0.000	0.000	0

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	0.022	0.047	0.464	0.648	-0.077	0.12	0.000
L2.Nervous.System	0.000	0.000	-0.518	0.610	0.000	0.00	0.013

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	-0.001	0.042	-0.032	0.975	-0.09	0.087	0
L2.Neurodegenerative.Diseases	0.000	0.000	0.037	0.971	0.00	0.000	0

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	-0.004	0.048	-0.075	0.941	-0.104	0.097	0
L2.Nucleotide.Metabolism	0.000	0.000	0.084	0.934	0.000	0.000	0

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	-0.01	0.047	-0.216	0.832	-0.109	0.088	0.000
L2.Poorly.Characterized	0.00	0.000	0.241	0.812	0.000	0.000	0.003

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	0.002	0.047	0.050	0.960	-0.097	0.101	0
L2.Replication.and.Repair	0.000	0.000	-0.056	0.956	0.000	0.000	0

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)	0	0.021	0	1	-0.043	0.043	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	-0.009	0.043	-0.215	0.832	-0.099	0.081	0.000
L2.Signal.Transduction	0.000	0.000	0.247	0.808	0.000	0.000	0.003

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	0.002	0.056	0.034	0.973	-0.115	0.119	0
L2.Signaling.Molecules.and.Interaction	0.000	0.000	-0.037	0.971	0.000	0.000	0

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	-0.002	0.044	-0.055	0.957	-0.095	0.09	0
L2.Transcription	0.000	0.000	0.063	0.951	0.000	0.00	0

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	0	0.046	-0.003	0.997	-0.096	0.096	0
L2.Translation	0	0.000	0.004	0.997	0.000	0.000	0

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	0.011	0.051	0.218	0.830	-0.096	0.119	0.000
L2.Transport.and.Catabolism	0.000	0.000	-0.239	0.814	0.000	0.000	0.003

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	0.003	0.046	0.065	0.949	-0.093	0.099	0
L2.Xenobiotics.Biodegradation.and.Metabolism	0.000	0.000	-0.073	0.943	0.000	0.000	0

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 %	9
Intercept	0.01	0.099	0.099	0.922	-0.198	
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	0.00	0.000	-0.199	0.844	0.000	

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	0.154	0.154	1.002	0.329	-0.168	0.477	0.000
L3.ABC.transporters	0.000	0.000	-1.190	0.249	0.000	0.000	0.066

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)	0	0.084	0	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	-0.235	0.184	-1.275	0.218	-0.62	0.151	0.000
L3.Adipocytokine.signaling.pathway	0.000	0.000	1.424	0.171	0.00	0.000	0.092

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	0.129	0.109	1.191	0.248	-0.098	0.356	0.000
L3.African.trypanosomiasis	0.000	0.000	-1.760	0.094	0.000	0.000	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	-0.002	0.201	-0.012	0.990	-0.423	0.418	0
L3.Alanine..aspartate.and.glutamate.metabolism	0.000	0.000	0.014	0.989	0.000	0.000	0

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)	0	0.084	0	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	0.052	0.169	0.307	0.762	-0.303	0.407	0.000
L3.Alzheimer.s.disease	0.000	0.000	-0.356	0.725	0.000	0.000	0.006

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	0.143	0.172	0.834	0.415	-0.217	0.503	0.000
L3.Amino.acid.metabolism	0.000	0.000	-0.957	0.351	0.000	0.000	0.044

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	0.092	0.19	0.481	0.636	-0.307	0.49	0.000
L3.Amino.acid.related.enzymes	0.000	0.00	-0.539	0.596	0.000	0.00	0.014

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	-0.007	0.196	-0.038	0.970	-0.418	0.403	0
L3.Amino.sugar.and.nucleotide.sugar.metabolism	0.000	0.000	0.042	0.967	0.000	0.000	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	0.109	0.177	0.613	0.547	-0.262	0.479	0.000
L3.Aminoacyl.tRNA.biosynthesis	0.000	0.000	-0.700	0.492	0.000	0.000	0.024

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	0.017	0.2	0.087	0.931	-0.4	0.435	0
L3.Aminobenzoate.degradation	0.000	0.0	-0.097	0.924	0.0	0.000	0

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	0.004	0.131	0.03	0.976	-0.271	0.279	0
L3.Amoebiasis	0.000	0.000	-0.04	0.969	0.000	0.000	0

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	0.071	0.144	0.495	0.626	-0.23	0.372	0.000
L3.Amyotrophic.lateral.sclerosis..ALS.	0.000	0.000	-0.616	0.546	0.00	0.000	0.019

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	0.034	0.188	0.181	0.858	-0.359	0.428	0.000
L3.Antigen.processing.and.presentation	0.000	0.000	-0.204	0.841	0.000	0.000	0.002

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	-0.02	0.097	-0.210	0.836	-0.222	0.182	0.00
L3.Apoptosis	0.00	0.000	0.459	0.651	0.000	0.000	0.01

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	-0.051	0.214	-0.237	0.816	-0.499	0.398	0.000
L3.Arachidonic.acid.metabolism	0.000	0.000	0.258	0.799	0.000	0.000	0.003

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	0.079	0.192	0.412	0.685	-0.322	0.48	0.000
L3.Arginine.and.proline.metabolism	0.000	0.000	-0.461	0.650	0.000	0.00	0.011

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)	0	0.084	0	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	0.092	0.174	0.528	0.604	-0.273	0.457	0.000
L3.Ascorbate.and.aldarate.metabolism	0.000	0.000	-0.606	0.552	0.000	0.000	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	0.152	0.12	1.274	0.218	-0.098	0.403	0.000
L3.Atrazine.degradation	0.000	0.00	-1.717	0.102	0.000	0.000	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	0.13	0.141	0.923	0.368	-0.165	0.424	0.000
L3.Bacterial.chemotaxis	0.00	0.000	-1.145	0.266	0.000	0.000	0.062

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	0.118	0.104	1.133	0.271	-0.100	0.336	0.000
L3.Bacterial.invasion.of.epithelial.cells	0.000	0.000	-1.764	0.094	-0.001	0.000	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	0.075	0.137	0.549	0.590	-0.211	0.361	0.000
L3.Bacterial.motility.proteins	0.000	0.000	-0.702	0.491	0.000	0.000	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	0.077	0.194	0.396	0.696	-0.33	0.484	0.00
L3.Bacterial.secretion.system	0.000	0.000	-0.442	0.664	0.00	0.000	0.01

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	0.025	0.196	0.130	0.898	-0.386	0.436	0.000
L3.Bacterial.toxins	0.000	0.000	-0.144	0.887	0.000	0.000	0.001

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	-0.03	0.095	-0.320	0.753	-0.228	0.168	0.000
L3.Basal.transcription.factors	0.00	0.000	0.731	0.474	0.000	0.000	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	0.094	0.185	0.508	0.617	-0.293	0.48	0.000
L3.Base.excision.repair	0.000	0.000	-0.573	0.573	0.000	0.00	0.016

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	0.128	0.174	0.735	0.471	-0.237	0.493	0.000
L3.Benzoate.degradation	0.000	0.000	-0.841	0.411	0.000	0.000	0.034

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	0.002	0.092	0.025	0.981	-0.191	0.195	0
L3.Betalain.biosynthesis	0.000	0.005	-0.070	0.945	-0.011	0.010	0

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	0.031	0.082	0.371	0.715	-0.142	0.203	0.000
L3.Bile.secretion	-0.642	0.377	-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	0.034	0.192	0.177	0.862	-0.367	0.435
L3.Biosynthesis.and.biodegradation.of.secondary.metabolites	0.000	0.000	-0.198	0.845	0.000	0.000

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)	0	0.084	0	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	0.081	0.173	0.469	0.644	-0.281	0.444	0.000
L3.Biosynthesis.of.ansamycins	0.000	0.000	-0.540	0.596	0.000	0.000	0.014

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	-0.067	0.224	-0.299	0.768	-0.536	0.402
L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides	0.000	0.000	0.324	0.749	0.000	0.000

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)	0	0.084	0	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	0.006	0.093	0.067	0.947	-0.189	0.201	0.000
L3.Biosynthesis.of.type.II.polyketide.products	-0.001	0.005	-0.177	0.861	-0.011	0.009	0.002

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	0.118	0.175	0.673	0.509	-0.248	0.484	0.000
L3.Biosynthesis.of.unsaturated.fatty.acids	0.000	0.000	-0.769	0.451	0.000	0.000	0.029

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	0.028	0.216	0.129	0.899	-0.424	0.48	0.000
L3.Biosynthesis.of.vancomycin.group.antibiotics	0.000	0.000	-0.141	0.889	0.000	0.00	0.001

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	0.072	0.189	0.381	0.708	-0.324	0.468	0.000
L3.Biotin.metabolism	0.000	0.000	-0.427	0.674	0.000	0.000	0.009

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	0.023	0.184	0.126	0.901	-0.362	0.408	0.000
L3.Bisphenol.degradation	0.000	0.000	-0.143	0.888	0.000	0.000	0.001

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	0.049	0.107	0.453	0.656	-0.176	0.273	0.000
L3.Bladder.cancer	0.000	0.000	-0.742	0.467	-0.001	0.001	0.027

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	0.101	0.185	0.547	0.590	-0.285	0.487	0.000
L3.Butanoate.metabolism	0.000	0.000	-0.617	0.544	0.000	0.000	0.019

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	-0.017	0.176	-0.096	0.924	-0.385	0.351	0.000
L3.Butirosin.and.neomycin.biosynthesis	0.000	0.000	0.110	0.913	0.000	0.000	0.001

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	0.124	0.17	0.726	0.477	-0.233	0.48	0.000
L3.C5.Branched.dibasic.acid.metabolism	0.000	0.00	-0.837	0.413	0.000	0.00	0.034

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)	0	0.084	0	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	0.035	0.093	0.379	0.709	-0.159	0.229	0.00
L3.Caffeine.metabolism	0.000	0.000	-0.914	0.372	-0.001	0.000	0.04

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	0.012	0.091	0.128	0.900	-0.179	0.202	0.000
L3.Calcium.signaling.pathway	-0.003	0.007	-0.383	0.706	-0.018	0.013	0.007

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	0.198	0.143	1.389	0.181	-0.1	0.497	0.000
L3.Caprolactam.degradation	0.000	0.000	-1.682	0.109	0.0	0.000	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	0.083	0.153	0.54	0.596	-0.238	0.403	0.000
L3.Carbohydrate.digestion.and.absorption	0.000	0.000	-0.65	0.523	0.000	0.000	0.021

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	0.019	0.184	0.103	0.919	-0.367	0.405	0.000
L3.Carbohydrate.metabolism	0.000	0.000	-0.117	0.908	0.000	0.000	0.001

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	0.038	0.194	0.196	0.847	-0.369	0.445	0.000
L3.Carbon.fixation.in.photosynthetic.organisms	0.000	0.000	-0.219	0.829	0.000	0.000	0.002

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	0.025	0.204	0.121	0.905	-0.402	0.452	0.000
L3.Carbon.fixation.pathways.in.prokaryotes	0.000	0.000	-0.133	0.895	0.000	0.000	0.001

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	-0.007	0.089	-0.075	0.941	-0.192	0.179	0.000
L3.Cardiac.muscle.contraction	0.000	0.000	0.312	0.759	0.000	0.000	0.005

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	0.269	0.086	3.122	0.006	0.089	0.449	0.000
L3.Carotenoid.biosynthesis	0.000	0.000	-4.402	0.000	0.000	0.000	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)	0	0.084	0	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	0.082	0.191	0.428	0.674	-0.319	0.482	0.000
L3.Cell.cycle. . . Caulobacter	0.000	0.000	-0.478	0.638	0.000	0.000	0.011

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)	0	0.084	0	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	0.06	0.188	0.318	0.754	-0.333	0.453	0.000
L3.Cell.division	0.00	0.000	-0.357	0.725	0.000	0.000	0.006

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	0.042	0.204	0.207	0.838	-0.385	0.47	0.000
L3.Cell.motility.and.secretion	0.000	0.000	-0.228	0.822	0.000	0.00	0.003

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	-0.332	0.159	-2.083	0.051	-0.665	0.002	0.000
L3.Cellular.antigens	0.000	0.000	2.368	0.029	0.000	0.000	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	0.119	0.106	1.125	0.275	-0.102	0.34	0.00
L3.Chagas.disease..American.trypanosomiasis.	0.000	0.000	-1.729	0.100	0.000	0.00	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	0.013	0.203	0.066	0.948	-0.411	0.438	0
L3.Chaperones.and.folding.catalysts	0.000	0.000	-0.073	0.943	0.000	0.000	0

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	0.162	0.163	0.993	0.333	-0.179	0.503	0.000
L3.Chloroalkane.and.chloroalkene.degradation	0.000	0.000	-1.156	0.262	0.000	0.000	0.063

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 %	R
Intercept	0.207	0.119	1.743	0.098	-0.042	0.456	0.00
L3.Chlorocyclohexane.and.chlorobenzene.degradation	0.000	0.000	-2.276	0.035	0.000	0.000	0.20

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)	0	0.084	0	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	0.073	0.19	0.383	0.706	-0.324	0.47	0.000
L3.Chromosome	0.000	0.00	-0.430	0.672	0.000	0.00	0.009

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)	0	0.084	0	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	0.036	0.093	0.384	0.705	-0.159	0.23	0.000
L3.Circadian.rhythm...plant	0.000	0.000	-0.921	0.369	-0.001	0.00	0.041

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	-0.034	0.208	-0.163	0.872	-0.469	0.401	0.000
L3.Citrate.cycle..TCA.cycle.	0.000	0.000	0.179	0.860	0.000	0.000	0.002

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	0.020	0.086	0.230	0.820	-0.16	0.200	0.000
L3.Clavulanic.acid.biosynthesis	-0.208	0.197	-1.056	0.304	-0.62	0.204	0.053

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	-0.006	0.088	-0.072	0.943	-0.191	0.178	0.000
L3.Colorectal.cancer	0.000	0.000	0.330	0.745	0.000	0.000	0.005

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)	0	0.084	0	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	0.022	0.175	0.126	0.901	-0.345	0.389	0.000
L3.Cyanoamino.acid.metabolism	0.000	0.000	-0.145	0.887	0.000	0.000	0.001

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	0.095	0.191	0.499	0.624	-0.304	0.494	0.000
L3.Cysteine.and.methionine.metabolism	0.000	0.000	-0.558	0.583	0.000	0.000	0.015

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)	0	0.084	0	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)	0	0.084	0	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)	0	0.084	0	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	0.077	0.171	0.453	0.656	-0.28	0.435	0.000
L3.Cytoskeleton.proteins	0.000	0.000	-0.524	0.607	0.00	0.000	0.014

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)	0	0.084	0	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	0.127	0.185	0.687	0.500	-0.26	0.515	0.000
L3.D.Alanine.metabolism	0.000	0.000	-0.773	0.449	0.00	0.000	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	0.17	0.118	1.440	0.166	-0.077	0.417	0.000
L3.D.Arginine.and.D.ornithine.metabolism	0.00	0.000	-1.937	0.068	0.000	0.000	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	0.029	0.202	0.142	0.889	-0.393	0.451	0.000
L3.D.Glutamine.and.D.glutamate.metabolism	0.000	0.000	-0.157	0.877	0.000	0.000	0.001

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	0.093	0.192	0.487	0.632	-0.308	0.495	0.000
L3.DNA.repair.and.recombination.proteins	0.000	0.000	-0.544	0.593	0.000	0.000	0.015

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	0.075	0.199	0.378	0.71	-0.34	0.491	0.000
L3.DNA.replication	0.000	0.000	-0.419	0.68	0.00	0.000	0.009

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	0.061	0.197	0.311	0.759	-0.35	0.472	0.000
L3.DNA.replication.proteins	0.000	0.000	-0.346	0.733	0.00	0.000	0.006

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)	0	0.084	0	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	0.102	0.143	0.715	0.483	-0.196	0.4	0.000
L3.Dioxin.degradation	0.000	0.000	-0.888	0.386	0.000	0.0	0.038

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	-0.011	0.165	-0.070	0.945	-0.356	0.333	0
L3.Drug.metabolism...cytochrome.P450	0.000	0.000	0.082	0.936	0.000	0.000	0

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	0.052	0.204	0.257	0.80	-0.375	0.48	0.000
L3.Drug.metabolism...other.enzymes	0.000	0.000	-0.283	0.78	0.000	0.00	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)	0	0.084	0	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	0.177	0.124	1.428	0.170	-0.083	0.437	0.000
L3.Electron.transfer.carriers	0.000	0.000	-1.857	0.079	0.000	0.000	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)	0	0.084	0	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	0.018	0.089	0.198	0.845	-0.169	0.204	0.000
L3.Endocytosis	-0.124	0.183	-0.677	0.507	-0.506	0.259	0.022

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	0.041	0.201	0.207	0.839	-0.379	0.462	0.000
L3.Energy.metabolism	0.000	0.000	-0.229	0.822	0.000	0.000	0.003

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	0.113	0.174	0.648	0.525	-0.252	0.477
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	0.000	0.000	-0.743	0.467	0.000	0.000

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)	0	0.084	0	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	0.113	0.119	0.948	0.355	-0.136	0.362	0.00
L3.Ether.lipid.metabolism	0.000	0.000	-1.318	0.203	0.000	0.000	0.08

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	-0.072	0.189	-0.382	0.707	-0.469	0.324	0.000
L3.Ethylbenzene.degradation	0.000	0.000	0.428	0.673	0.000	0.000	0.009

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)	0	0.084	0	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	0.06	0.192	0.311	0.759	-0.342	0.461	0.000
L3.Fatty.acid.biosynthesis	0.00	0.000	-0.348	0.732	0.000	0.000	0.006

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	0.035	0.093	0.377	0.711	-0.159	0.229	0.00
L3.Fatty.acid.elongation.in.mitochondria	0.000	0.000	-0.910	0.374	-0.001	0.000	0.04

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	0.117	0.19	0.613	0.547	-0.282	0.515	0.000
L3.Fatty.acid.metabolism	0.000	0.00	-0.685	0.501	0.000	0.000	0.023

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)	0	0.084	0	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	0.018	0.089	0.198	0.845	-0.169	0.204	0.000
L3.Fc.gamma.R.mediated.phagocytosis	-0.124	0.183	-0.677	0.507	-0.506	0.259	0.022

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	0.037	0.129	0.284	0.779	-0.233	0.307	0.000
L3.Flagellar.assembly	0.000	0.000	-0.381	0.707	0.000	0.000	0.007

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	0.078	0.161	0.483	0.635	-0.26	0.415	0.000
L3.Flavone.and.flavonol.biosynthesis	0.000	0.000	-0.569	0.576	0.00	0.000	0.016

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	0.092	0.117	0.781	0.445	-0.154	0.337	0.000
L3.Flavonoid.biosynthesis	0.000	0.000	-1.111	0.280	0.000	0.000	0.058

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	0.117	0.112	1.045	0.309	-0.117	0.352	0.000
L3.Fluorobenzoate.degradation	0.000	0.000	-1.521	0.145	-0.001	0.000	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)	0	0.084	0	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	0.047	0.211	0.225	0.824	-0.393	0.488	0.000
L3.Folate.biosynthesis	0.000	0.000	-0.247	0.808	0.000	0.000	0.003

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	0.046	0.184	0.251	0.805	-0.339	0.431	0.000
L3.Fructose.and.mannose.metabolism	0.000	0.000	-0.284	0.780	0.000	0.000	0.004

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	0.072	0.186	0.386	0.704	-0.318	0.461	0.000
L3.Function.unknown	0.000	0.000	-0.435	0.668	0.000	0.000	0.009

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	0.023	0.096	0.239	0.814	-0.178	0.224	0.000
L3.G.protein.coupled.receptors	-0.017	0.033	-0.525	0.606	-0.086	0.052	0.014

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)	0	0.084	0	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	-0.005	0.191	-0.026	0.980	-0.404	0.394	0
L3.Galactose.metabolism	0.000	0.000	0.029	0.977	0.000	0.000	0

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)	0	0.084	0	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	0.069	0.194	0.358	0.724	-0.336	0.474	0.000
L3.General.function.prediction.only	0.000	0.000	-0.399	0.694	0.000	0.000	0.008

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	-0.338	0.198	-1.708	0.104	-0.752	0.076	0.000
L3.Geraniol.degradation	0.000	0.000	1.864	0.078	0.000	0.000	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	0.115	0.13	0.879	0.390	-0.158	0.387	0.000
L3.Germination	0.000	0.00	-1.144	0.267	0.000	0.000	0.061

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)	0	0.084	0	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	-0.089	0.192	-0.461	0.650	-0.492	0.314	0.000
L3.Glutamatergic.synapse	0.000	0.000	0.515	0.613	0.000	0.000	0.013

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	0.004	0.232	0.018	0.986	-0.482	0.49	0
L3.Glutathione.metabolism	0.000	0.000	-0.019	0.985	0.000	0.00	0

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)	0	0.084	0	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	-0.097	0.176	-0.552	0.588	-0.467	0.272	0.000
L3.Glycan.biosynthesis.and.metabolism	0.000	0.000	0.630	0.536	0.000	0.000	0.019

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	0.107	0.165	0.648	0.525	-0.238	0.452	0.000
L3.Glycerolipid.metabolism	0.000	0.000	-0.756	0.459	0.000	0.000	0.028

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	0.087	0.177	0.489	0.630	-0.284	0.457	0.000
L3.Glycerophospholipid.metabolism	0.000	0.000	-0.559	0.583	0.000	0.000	0.015

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	0.104	0.2	0.519	0.610	-0.314	0.521	0.000
L3.Glycine..serine.and.threonine.metabolism	0.000	0.0	-0.574	0.573	0.000	0.000	0.016

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	0.075	0.187	0.401	0.693	-0.317	0.467	0.00
L3.Glycolysis...Gluconeogenesis	0.000	0.000	-0.451	0.657	0.000	0.000	0.01

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	0.005	0.088	0.058	0.954	-0.180	0.190	0
L3.Glycosaminoglycan.biosynthesis...chondroitin.sulfate	-0.004	0.015	-0.258	0.799	-0.035	0.028	0

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	-0.391	0.133	-2.941	0.008	-0.669	-0.113	0.000
L3.Glycosaminoglycan.degradation	0.000	0.000	3.420	0.003	0.000	0.000	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	-0.367	0.116	-3.166	0.005	-0.61	-0.124	0.000
L3.Glycosphingolipid.biosynthesis...ganglio.series	0.000	0.000	3.819	0.001	0.00	0.000	0.422

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	-0.331	0.172	-1.924	0.069	-0.691	0.029	0.000
L3.Glycosphingolipid.biosynthesis. . . globo.series	0.000	0.000	2.155	0.044	0.000	0.000	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	-0.056	0.084	-0.668	0.512	-0.233	0.120
L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series	0.000	0.000	1.899	0.073	0.000	0.001

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)	0	0.084	0	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	0.049	0.215	0.226	0.824	-0.401	0.499	0.000
L3.Glycosyltransferases	0.000	0.000	-0.246	0.808	0.000	0.000	0.003

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	0.074	0.19	0.391	0.700	-0.323	0.472	0.00
L3.Glyoxylate.and.dicarboxylate.metabolism	0.000	0.00	-0.439	0.666	0.000	0.000	0.01

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	0.018	0.089	0.198	0.845	-0.169	0.204	0.000
L3.GnRH.signaling.pathway	-0.124	0.183	-0.677	0.507	-0.506	0.259	0.022

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)	0	0.084	0	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)	0	0.084	0	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)	0	0.084	0	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	0.033	0.196	0.168	0.868	-0.377	0.443	0.000
L3.Histidine.metabolism	0.000	0.000	-0.187	0.853	0.000	0.000	0.002

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	0.07	0.195	0.362	0.722	-0.337	0.478	0.000
L3.Homologous.recombination	0.00	0.000	-0.403	0.692	0.000	0.000	0.008

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	0.058	0.177	0.326	0.748	-0.314	0.429	0.000
L3.Huntington.s.disease	0.000	0.000	-0.373	0.713	0.000	0.000	0.007

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	0.004	0.088	0.048	0.962	-0.180	0.189	0.000
L3.Hypertrophic.cardiomyopathy..HCM.	-0.013	0.058	-0.220	0.828	-0.134	0.108	0.002

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)	0	0.084	0	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	-0.006	0.088	-0.072	0.943	-0.191	0.178	0.000
L3.Influenza.A	0.000	0.000	0.330	0.745	0.000	0.000	0.005

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	-0.043	0.193	-0.224	0.825	-0.447	0.361	0.000
L3.Inorganic.ion.transport.and.metabolism	0.000	0.000	0.251	0.805	0.000	0.000	0.003

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	0.023	0.198	0.116	0.909	-0.392	0.438	0.000
L3.Inositol.phosphate.metabolism	0.000	0.000	-0.128	0.899	0.000	0.000	0.001

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	-0.013	0.174	-0.075	0.941	-0.377	0.351	0
L3.Insulin.signaling.pathway	0.000	0.000	0.086	0.932	0.000	0.000	0

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	0.088	0.205	0.428	0.674	-0.341	0.516	0.000
L3.Ion.channels	0.000	0.000	-0.471	0.643	0.000	0.000	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	-0.005	0.090	-0.059	0.953	-0.194	0.183	0.000
L3.Isoflavonoid.biosynthesis	0.037	0.185	0.202	0.842	-0.349	0.424	0.002

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	0.005	0.225	0.024	0.981	-0.465	0.476	0
L3.Isoquinoline.alkaloid.biosynthesis	0.000	0.000	-0.026	0.979	0.000	0.000	0

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)	0	0.084	0	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)	0	0.084	0	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	0.166	0.187	0.885	0.387	-0.226	0.558	0.000
L3.Limonene.and.pinene.degradation	0.000	0.000	-0.990	0.335	0.000	0.000	0.047

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	-0.008	0.183	-0.043	0.966	-0.392	0.376	0
L3.Linoleic.acid.metabolism	0.000	0.000	0.049	0.961	0.000	0.000	0

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	0.029	0.198	0.148	0.884	-0.386	0.445	0.000
L3.Lipid.biosynthesis.proteins	0.000	0.000	-0.164	0.871	0.000	0.000	0.001

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	0.085	0.169	0.504	0.620	-0.269	0.439	0.000
L3.Lipid.metabolism	0.000	0.000	-0.584	0.566	0.000	0.000	0.017

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	-0.258	0.171	-1.508	0.148	-0.616	0.1	0.000
L3.Lipoic.acid.metabolism	0.000	0.000	1.708	0.104	0.000	0.0	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	-0.142	0.199	-0.715	0.483	-0.559	0.274	0.00
L3.Lipopolysaccharide.biosynthesis	0.000	0.000	0.791	0.439	0.000	0.000	0.03

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	-0.145	0.213	-0.679	0.505	-0.591	0.301	0.000
L3.Lipopolysaccharide.biosynthesis.proteins	0.000	0.000	0.741	0.468	0.000	0.000	0.027

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)	0	0.084	0	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)	0	0.084	0	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	0.107	0.181	0.593	0.56	-0.272	0.486	0.000
L3.Lysine.biosynthesis	0.000	0.000	-0.672	0.51	0.000	0.000	0.022

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	0.166	0.196	0.849	0.406	-0.243	0.576	0.000
L3.Lysine.degradation	0.000	0.000	-0.941	0.358	0.000	0.000	0.042

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	-0.356	0.16	-2.223	0.039	-0.691	-0.021	0.00
L3.Lysosome	0.000	0.00	2.513	0.021	0.000	0.000	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)	0	0.084	0	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	-0.073	0.206	-0.355	0.726	-0.505	0.358	0.000
L3.MAPK.signaling.pathway…yeast	0.000	0.000	0.391	0.700	0.000	0.000	0.008

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)	0	0.084	0	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	0.012	0.096	0.122	0.904	-0.19	0.213	0.000
L3.Meiosis…yeast	0.000	0.000	-0.271	0.789	0.00	0.000	0.004

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	0.002	0.092	0.025	0.981	-0.191	0.195	0
L3.Melanogenesis	0.000	0.005	-0.070	0.945	-0.011	0.010	0

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	-0.249	0.209	-1.195	0.247	-0.686	0.187	0.000
L3.Membrane.and.intracellular.structural.molecules	0.000	0.000	1.302	0.209	0.000	0.000	0.078

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	0.137	0.165	0.828	0.418	-0.209	0.483	0.000
L3.Metabolism.of.cofactors.and.vitamins	0.000	0.000	-0.962	0.348	0.000	0.000	0.044

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	-0.014	0.163	-0.088	0.931	-0.356	0.327	0.000
L3.Metabolism.of.xenobiotics.by.cytochrome.P450	0.000	0.000	0.104	0.918	0.000	0.000	0.001

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	0.109	0.181	0.603	0.553	-0.27	0.488	0.000
L3.Methane.metabolism	0.000	0.000	-0.684	0.502	0.00	0.000	0.023

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	-0.014	0.123	-0.114	0.911	-0.272	0.244	0.000
L3.Mineral.absorption	0.000	0.000	0.159	0.875	0.000	0.000	0.001

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	0.083	0.191	0.435	0.668	-0.317	0.483	0.000
L3.Mismatch.repair	0.000	0.000	-0.487	0.632	0.000	0.000	0.012

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	0.105	0.194	0.543	0.593	-0.3	0.511	0.000
L3.N.Glycan.biosynthesis	0.000	0.000	-0.605	0.552	0.0	0.000	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	-0.061	0.196	-0.313	0.758	-0.472	0.349	0.000
L3.NOD.like.receptor.signaling.pathway	0.000	0.000	0.348	0.732	0.000	0.000	0.006

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	0.016	0.193	0.082	0.936	-0.389	0.42	0
L3.Naphthalene.degradation	0.000	0.000	-0.092	0.928	0.000	0.00	0

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)	0	0.084	0	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)	0	0.084	0	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	0.073	0.192	0.378	0.709	-0.33	0.475	0.000
L3.Nicotinate.and.nicotinamide.metabolism	0.000	0.000	-0.423	0.677	0.00	0.000	0.009

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	0.075	0.206	0.365	0.719	-0.356	0.506	0.000
L3.Nitrogen.metabolism	0.000	0.000	-0.402	0.692	0.000	0.000	0.008

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	0.156	0.136	1.152	0.264	-0.128	0.441	0.000
L3.Nitrotoluene.degradation	0.000	0.000	-1.443	0.165	0.000	0.000	0.094

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	0.058	0.125	0.465	0.647	-0.203	0.319	0.00
L3.Non.homologous.end.joining	0.000	0.000	-0.638	0.531	0.000	0.000	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)	0	0.084	0	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	0.09	0.192	0.470	0.644	-0.311	0.492	0.000
L3.Novobiocin.biosynthesis	0.00	0.000	-0.525	0.606	0.000	0.000	0.014

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	0.088	0.186	0.475	0.640	-0.3	0.476	0.000
L3.Nucleotide.excision.repair	0.000	0.000	-0.536	0.598	0.0	0.000	0.014

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	0.151	0.147	1.030	0.316	-0.156	0.459	0.000
L3.Nucleotide.metabolism	0.000	0.000	-1.248	0.227	0.000	0.000	0.072

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)	0	0.084	0	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	0.04	0.203	0.194	0.848	-0.386	0.465	0.000
L3.One.carbon.pool.by.folate	0.00	0.000	-0.215	0.832	0.000	0.000	0.002

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)	0	0.084	0	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	-0.273	0.196	-1.390	0.181	-0.684	0.138	0.000
L3.Other.glycan.degradation	0.000	0.000	1.527	0.143	0.000	0.000	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	0.039	0.206	0.188	0.853	-0.393	0.47	0.000
L3.Other.ion.coupled.transporters	0.000	0.000	-0.207	0.838	0.000	0.00	0.002

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	0.035	0.194	0.182	0.858	-0.371	0.441	0.000
L3.Other.transporters	0.000	0.000	-0.203	0.841	0.000	0.000	0.002

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)	0	0.084	0	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	0.083	0.191	0.433	0.670	-0.317	0.482	0.000
L3.Others	0.000	0.000	-0.485	0.633	0.000	0.000	0.012

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	0.058	0.191	0.305	0.764	-0.341	0.458	0.000
L3.Oxidative.phosphorylation	0.000	0.000	-0.341	0.737	0.000	0.000	0.006

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	-0.122	0.205	-0.595	0.559	-0.552	0.308	0.000
L3.PPAR.signaling.pathway	0.000	0.000	0.654	0.521	0.000	0.000	0.021

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)	0	0.084	0	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)	0	0.084	0	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	0.087	0.184	0.472	0.642	-0.298	0.471	0.000
L3.Pantothenate.and.CoA.biosynthesis	0.000	0.000	-0.533	0.600	0.000	0.000	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	-0.007	0.088	-0.074	0.942	-0.192	0.179	0.000
L3.Parkinson.s.disease	0.000	0.000	0.316	0.756	0.000	0.000	0.005

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)	0	0.084	0	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	0.051	0.183	0.282	0.781	-0.331	0.434	0.000
L3.Pathways.in.cancer	0.000	0.000	-0.319	0.753	0.000	0.000	0.005

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	-0.208	0.176	-1.185	0.250	-0.576	0.159	0.000
L3.Penicillin.and.cephalosporin.biosynthesis	0.000	0.000	1.342	0.195	0.000	0.000	0.083

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	0.019	0.195	0.099	0.922	-0.389	0.428	0.000
L3.Pentose.and.glucuronate.interconversions	0.000	0.000	-0.111	0.913	0.000	0.000	0.001

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	0.082	0.185	0.440	0.665	-0.306	0.47	0.000
L3.Pentose.phosphate.pathway	0.000	0.000	-0.496	0.626	0.000	0.00	0.012

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	0.068	0.195	0.351	0.729	-0.34	0.476	0.000
L3.Peptidases	0.000	0.000	-0.391	0.700	0.00	0.000	0.008

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	0.11	0.186	0.593	0.560	-0.279	0.499	0.000
L3.Peptidoglycan.biosynthesis	0.00	0.000	-0.668	0.512	0.000	0.000	0.022

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	-0.073	0.211	-0.345	0.734	-0.513	0.368	0.000
L3.Peroxisome	0.000	0.000	0.378	0.710	0.000	0.000	0.007

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	-0.279	0.186	-1.501	0.150	-0.669	0.11	0.000
L3.Pertussis	0.000	0.000	1.665	0.112	0.000	0.00	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)	0	0.084	0	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	-0.021	0.2	-0.106	0.917	-0.439	0.397	0.000
L3.Phenylalanine.metabolism	0.000	0.0	0.118	0.908	0.000	0.000	0.001

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	0.092	0.182	0.504	0.620	-0.289	0.473	0.0
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis	0.000	0.000	-0.571	0.575	0.000	0.000	0.0

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	0.027	0.16	0.170	0.866	-0.308	0.363	0.000
L3.Phenylpropanoid.biosynthesis	0.000	0.00	-0.202	0.842	0.000	0.000	0.002

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	0.011	0.207	0.053	0.958	-0.423	0.445	0
L3.Phosphatidylinositol.signaling.system	0.000	0.000	-0.058	0.954	0.000	0.000	0

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	-0.071	0.187	-0.376	0.711	-0.462	0.321	0.000
L3.Phosphonate.and.phosphinate.metabolism	0.000	0.000	0.424	0.677	0.000	0.000	0.009

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	0.12	0.133	0.907	0.376	-0.157	0.398	0.000
L3.Phosphotransferase.system..PTS.	0.00	0.000	-1.166	0.258	0.000	0.000	0.064

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	0.1	0.166	0.605	0.552	-0.247	0.448	0.000
L3.Photosynthesis	0.0	0.000	-0.705	0.490	0.000	0.000	0.024

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	0.012	0.091	0.133	0.895	-0.179	0.203	0.000
L3.Photosynthesis...antenna.proteins	0.000	0.000	-0.398	0.695	-0.001	0.001	0.008

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	0.101	0.166	0.608	0.550	-0.246	0.448	0.000
L3.Photosynthesis.proteins	0.000	0.000	-0.708	0.487	0.000	0.000	0.024

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)	0	0.084	0	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)	0	0.084	0	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	0.071	0.172	0.413	0.684	-0.29	0.432	0.000
L3.Plant.pathogen.interaction	0.000	0.000	-0.476	0.639	0.00	0.000	0.011

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	0.06	0.186	0.324	0.749	-0.329	0.45	0.000
L3.Polycyclic.aromatic.hydrocarbon.degradation	0.00	0.000	-0.365	0.719	0.000	0.00	0.007

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	-0.013	0.206	-0.062	0.951	-0.445	0.419	0
L3.Polyketide.sugar.unit.biosynthesis	0.000	0.000	0.068	0.946	0.000	0.000	0

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	-0.315	0.217	-1.455	0.162	-0.769	0.138	0.00
L3.Pores.ion.channels	0.000	0.000	1.569	0.133	0.000	0.000	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	0.183	0.175	1.047	0.308	-0.183	0.548	0.000
L3.Porphyrin.and.chlorophyll.metabolism	0.000	0.000	-1.191	0.248	0.000	0.000	0.066

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	0.03	0.204	0.147	0.884	-0.397	0.457	0.000
L3.Prenyltransferases	0.00	0.000	-0.163	0.872	0.000	0.000	0.001

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	-0.16	0.166	-0.968	0.345	-0.507	0.186	0.000
L3.Primary.bile.acid.biosynthesis	0.00	0.000	1.121	0.276	0.000	0.000	0.059

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	0.034	0.188	0.179	0.860	-0.359	0.426	0.000
L3.Primary.immunodeficiency	0.000	0.000	-0.202	0.842	0.000	0.000	0.002

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	0.174	0.124	1.404	0.177	-0.085	0.432	0.000
L3.Prion.diseases	0.000	0.000	-1.833	0.083	0.000	0.000	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	0.034	0.188	0.181	0.858	-0.359	0.428	0.000
L3.Progesterone.mediated.oocyte.maturation	0.000	0.000	-0.204	0.841	0.000	0.000	0.002

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	0.139	0.188	0.738	0.469	-0.254	0.532	0.000
L3.Propanoate.metabolism	0.000	0.000	-0.827	0.418	0.000	0.000	0.033

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	-0.001	0.191	-0.007	0.994	-0.401	0.399	0
L3.Prostate.cancer	0.000	0.000	0.008	0.993	0.000	0.000	0

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	0.05	0.185	0.271	0.790	-0.338	0.438	0.000
L3.Proteasome	0.00	0.000	-0.306	0.763	0.000	0.000	0.005

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	-0.346	0.132	-2.623	0.017	-0.623	-0.07	0.000
L3.Protein.digestion.and.absorption	0.000	0.000	3.098	0.006	0.000	0.00	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	0.081	0.194	0.419	0.680	-0.325	0.487	0.000
L3.Protein.export	0.000	0.000	-0.467	0.646	0.000	0.000	0.011

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	0.132	0.194	0.677	0.506	-0.275	0.538	0.000
L3.Protein.folding.and.associated.processing	0.000	0.000	-0.753	0.461	0.000	0.000	0.028

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	0.124	0.167	0.744	0.466	-0.225	0.473	0.000
L3.Protein.kinases	0.000	0.000	-0.863	0.399	0.000	0.000	0.036

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	-0.212	0.213	-0.998	0.331	-0.657	0.233	0.000
L3.Protein.processing.in.endoplasmic.reticulum	0.000	0.000	1.086	0.291	0.000	0.000	0.056

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	-0.261	0.14	-1.859	0.079	-0.554	0.033	0.000
L3.Proximal.tubule.bicarbonate.reclamation	0.000	0.00	2.222	0.039	0.000	0.000	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	0.1	0.194	0.513	0.614	-0.307	0.507	0.000
L3.Purine.metabolism	0.0	0.000	-0.571	0.575	0.000	0.000	0.016

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	0.086	0.196	0.441	0.664	-0.323	0.495	0.000
L3.Pyrimidine.metabolism	0.000	0.000	-0.490	0.630	0.000	0.000	0.012

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	0.065	0.19	0.344	0.735	-0.333	0.464	0.000
L3.Pyruvate.metabolism	0.000	0.00	-0.385	0.704	0.000	0.000	0.007

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	0.143	0.1	1.439	0.167	-0.065	0.351	0.000
L3.RIG.I.like.receptor.signaling.pathway	0.000	0.0	-2.254	0.036	0.000	0.000	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	0.067	0.201	0.335	0.741	-0.354	0.489	0.000
L3.RNA.degradation	0.000	0.000	-0.370	0.715	0.000	0.000	0.007

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	0.148	0.189	0.783	0.443	-0.248	0.544	0.000
L3.RNA.polymerase	0.000	0.000	-0.875	0.393	0.000	0.000	0.037

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	0.115	0.165	0.695	0.496	-0.231	0.461	0.000
L3.RNA.transport	0.000	0.000	-0.809	0.428	0.000	0.000	0.032

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)	0	0.084	0	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	0.123	0.142	0.865	0.398	-0.174	0.419	0.000
L3.Renal.cell.carcinoma	0.000	0.000	-1.072	0.297	0.000	0.000	0.054

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	0.014	0.089	0.152	0.881	-0.174	0.201	0.000
L3.Renin.angiotensin.system	-0.019	0.036	-0.522	0.608	-0.095	0.057	0.013

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	0.142	0.175	0.810	0.428	-0.225	0.509	0.000
L3.Replication..recombination.and.repair.proteins	0.000	0.000	-0.924	0.367	0.000	0.000	0.041

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	-0.223	0.197	-1.132	0.272	-0.634	0.189	0.000
L3.Restriction.enzyme	0.000	0.000	1.248	0.227	0.000	0.000	0.072

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	-0.134	0.166	-0.811	0.427	-0.481	0.213	0.000
L3.Retinol.metabolism	0.000	0.000	0.942	0.358	0.000	0.000	0.042

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)	0	0.084	0	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	0.033	0.206	0.160	0.875	-0.399	0.465	0.000
L3.Riboflavin.metabolism	0.000	0.000	-0.176	0.862	0.000	0.000	0.002

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	0.097	0.189	0.510	0.616	-0.3	0.493	0.000
L3.Ribosome	0.000	0.000	-0.572	0.574	0.0	0.000	0.016

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	0.111	0.183	0.607	0.551	-0.272	0.494	0.000
L3.Ribosome.Biogenesis	0.000	0.000	-0.686	0.501	0.000	0.000	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	0.094	0.183	0.510	0.616	-0.29	0.477	0.000
L3.Ribosome.biogenesis.in.eukaryotes	0.000	0.000	-0.577	0.571	0.00	0.000	0.016

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)	0	0.084	0	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	-0.176	0.166	-1.061	0.302	-0.524	0.172	0.00
L3.Secondary.bile.acid.biosynthesis	0.000	0.000	1.225	0.236	0.000	0.000	0.07

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	0.09	0.17	0.531	0.602	-0.266	0.447	0.000
L3.Secretion.system	0.00	0.00	-0.613	0.547	0.000	0.000	0.018

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	0.109	0.188	0.581	0.568	-0.284	0.502	0.000
L3.Selenocompound.metabolism	0.000	0.000	-0.652	0.522	0.000	0.000	0.021

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)	0	0.084	0	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	-0.019	0.093	-0.207	0.838	-0.213	0.175	0.000
L3.Shigellosis	0.010	0.018	0.543	0.593	-0.029	0.049	0.015

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	0.156	0.17	0.915	0.372	-0.2	0.511	0.000
L3.Signal.transduction.mechanisms	0.000	0.00	-1.052	0.306	0.0	0.000	0.052

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	-0.006	0.088	-0.072	0.943	-0.191	0.178	0.000
L3.Small.cell.lung.cancer	0.000	0.000	0.330	0.745	0.000	0.000	0.005

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	-0.199	0.192	-1.035	0.314	-0.601	0.203	0.000
L3.Sphingolipid.metabolism	0.000	0.000	1.149	0.265	0.000	0.000	0.062

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)	0	0.084	0	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	0.13	0.138	0.938	0.360	-0.159	0.419	0.000
L3.Sporulation	0.00	0.000	-1.176	0.254	0.000	0.000	0.065

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	0.149	0.119	1.250	0.227	-0.1	0.397	0.000
L3.Staphylococcus.aureus.infection	0.000	0.000	-1.696	0.106	0.0	0.000	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	0.032	0.178	0.182	0.858	-0.341	0.405	0.000
L3.Starch.and.sucrose.metabolism	0.000	0.000	-0.208	0.838	0.000	0.000	0.002

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	0.037	0.093	0.392	0.699	-0.158	0.231	0.000
L3.Steroid.biosynthesis	0.000	0.000	-0.925	0.367	0.000	0.000	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	-0.27	0.113	-2.399	0.027	-0.506	-0.034	0.000
L3.Steroid.hormone.biosynthesis	0.00	0.000	3.077	0.006	0.000	0.000	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	0.049	0.103	0.474	0.641	-0.167	0.266	0.
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	0.000	0.000	-0.827	0.418	-0.001	0.000	0.

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	-0.03	0.202	-0.147	0.885	-0.453	0.394	0.000
L3.Streptomycin.biosynthesis	0.00	0.000	0.163	0.873	0.000	0.000	0.001

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	0.148	0.13	1.132	0.272	-0.125	0.421	0.000
L3.Styrene.degradation	0.000	0.00	-1.454	0.162	0.000	0.000	0.096

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	0.019	0.2	0.095	0.925	-0.4	0.438	0.000
L3.Sulfur.metabolism	0.000	0.0	-0.106	0.917	0.0	0.000	0.001

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	0.107	0.171	0.624	0.540	-0.251	0.465	0.000
L3.Sulfur.relay.system	0.000	0.000	-0.720	0.481	0.000	0.000	0.025

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	0.129	0.156	0.828	0.418	-0.197	0.455	0.000
L3.Synthesis.and.degradation.of.ketone.bodies	0.000	0.000	-0.984	0.338	0.000	0.000	0.046

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	0.047	0.096	0.483	0.634	-0.155	0.248	0.000
L3.Systemic.lupus.erythematosus	0.000	0.000	-0.992	0.334	-0.001	0.000	0.047

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)	0	0.084	0	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	-0.059	0.216	-0.275	0.786	-0.511	0.392	0.000
L3.Taurine.and.hypotaurine.metabolism	0.000	0.000	0.300	0.767	0.000	0.000	0.004

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	0.101	0.196	0.517	0.611	-0.309	0.512	0.000
L3.Terpenoid.backbone.biosynthesis	0.000	0.000	-0.574	0.573	0.000	0.000	0.016

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	0.106	0.17	0.625	0.539	-0.25	0.463	0.000
L3.Tetracycline.biosynthesis	0.000	0.00	-0.722	0.479	0.00	0.000	0.025

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	0.091	0.189	0.480	0.636	-0.305	0.487	0.000
L3.Thiamine.metabolism	0.000	0.000	-0.539	0.596	0.000	0.000	0.014

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)	0	0.084	0	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	0.006	0.149	0.042	0.967	-0.305	0.317	0
L3.Toluene.degradation	0.000	0.000	-0.052	0.959	0.000	0.000	0

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	-0.006	0.088	-0.072	0.943	-0.191	0.178	0.000
L3.Toxoplasmosis	0.000	0.000	0.330	0.745	0.000	0.000	0.005

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	0.141	0.161	0.873	0.393	-0.197	0.479	0.00
L3.Transcription.factors	0.000	0.000	-1.023	0.319	0.000	0.000	0.05

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	0.026	0.199	0.129	0.899	-0.392	0.443	0.000
L3.Transcription.machinery	0.000	0.000	-0.143	0.888	0.000	0.000	0.001

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	0.031	0.108	0.283	0.781	-0.196	0.257	0.000
L3.Transcription.related.proteins	0.000	0.000	-0.463	0.648	0.000	0.000	0.011

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	0.094	0.195	0.485	0.634	-0.313	0.502	0.000
L3.Translation.factors	0.000	0.000	-0.539	0.596	0.000	0.000	0.014

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	0.111	0.189	0.586	0.565	-0.285	0.506	0.000
L3.Translation.proteins	0.000	0.000	-0.657	0.519	0.000	0.000	0.021

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	0.142	0.156	0.910	0.374	-0.185	0.47	0.000
L3.Transporters	0.000	0.000	-1.077	0.295	0.000	0.00	0.055

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	0.041	0.2	0.203	0.841	-0.379	0.46	0
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis	0.000	0.0	-0.225	0.825	0.000	0.00	0

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	0.21	0.176	1.195	0.247	-0.158	0.578	0.000
L3.Tryptophan.metabolism	0.00	0.000	-1.353	0.192	0.000	0.000	0.084

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	0.044	0.188	0.235	0.817	-0.35	0.439	0.000
L3.Tuberculosis	0.000	0.000	-0.264	0.794	0.00	0.000	0.003

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	0.106	0.171	0.622	0.541	-0.251	0.463	0.000
L3.Two.component.system	0.000	0.000	-0.718	0.481	0.000	0.000	0.025

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	-0.085	0.198	-0.429	0.673	-0.499	0.329	0.000
L3.Type.I.diabetes.mellitus	0.000	0.000	0.476	0.640	0.000	0.000	0.011

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	0.07	0.194	0.358	0.724	-0.337	0.476	0.000
L3.Type.II.diabetes.mellitus	0.00	0.000	-0.400	0.694	0.000	0.000	0.008

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	0.085	0.19	0.445	0.661	-0.314	0.483	0.000
L3.Tyrosine.metabolism	0.000	0.00	-0.499	0.624	0.000	0.000	0.012

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 %	0.
Intercept	-0.162	0.224	-0.721	0.480	-0.631	0.308	0.
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis	0.000	0.000	0.779	0.446	0.000	0.000	0.

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	-0.356	0.125	-2.859	0.010	-0.617	-0.095	0.000
L3.Ubiquitin.system	0.000	0.000	3.409	0.003	0.000	0.000	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)	0	0.084	0	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	0.108	0.175	0.619	0.543	-0.258	0.475	0.000
L3.Valine..leucine.and.isoleucine.biosynthesis	0.000	0.000	-0.708	0.487	0.000	0.000	0.024

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	0.119	0.222	0.536	0.598	-0.346	0.584	0.000
L3.Valine..leucine.and.isoleucine.degradation	0.000	0.000	-0.581	0.568	0.000	0.000	0.017

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	0.022	0.095	0.227	0.823	-0.178	0.221	0.000
L3.Various.types.of.N.glycan.biosynthesis	-0.002	0.003	-0.516	0.612	-0.009	0.005	0.013

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)	0	0.084	0	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	-0.025	0.090	-0.282	0.781	-0.213	0.162	0.000
L3.Vasopressin.regulated.water.reabsorption	0.106	0.124	0.858	0.401	-0.153	0.365	0.036

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	0.021	0.089	0.234	0.818	-0.165	0.207	0.00
L3.Vibrio.cholerae.infection	-0.044	0.055	-0.787	0.441	-0.160	0.072	0.03

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	-0.003	0.189	-0.014	0.989	-0.399	0.393	0
L3.Vibrio.cholerae.pathogenic.cycle	0.000	0.000	0.016	0.987	0.000	0.000	0

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	-0.006	0.088	-0.072	0.943	-0.191	0.178	0.000
L3.Viral.myocarditis	0.000	0.000	0.330	0.745	0.000	0.000	0.005

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	-0.005	0.202	-0.027	0.979	-0.428	0.418	0
L3.Vitamin.B6.metabolism	0.000	0.000	0.030	0.977	0.000	0.000	0

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)	0	0.084	0	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	0.092	0.139	0.662	0.516	-0.199	0.383	0.000
L3.Xylene.degradation	0.000	0.000	-0.835	0.414	0.000	0.000	0.034

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	-0.034	0.212	-0.161	0.874	-0.478	0.41	0.000
L3.Zeatin.biosynthesis	0.000	0.000	0.176	0.862	0.000	0.00	0.002

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	-0.032	0.123	-0.262	0.796	-0.29	0.225	0.000
L3.alpha.Linolenic.acid.metabolism	0.000	0.000	0.367	0.718	0.00	0.000	0.007

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	0.079	0.192	0.411	0.686	-0.323	0.48	0.00
L3.beta.Alanine.metabolism	0.000	0.000	-0.459	0.651	0.000	0.00	0.01

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	0.021	0.159	0.134	0.895	-0.312	0.354	0.000
L3.beta.Lactam.resistance	0.000	0.000	-0.159	0.875	0.000	0.000	0.001

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)	0	0.084	0	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)	0	0.084	0	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	-0.006	0.088	-0.072	0.943	-0.191	0.178	0.000
L3.p53.signaling.pathway	0.000	0.000	0.330	0.745	0.000	0.000	0.005

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 %	9
Intercept	0	0.042	0.007	0.994	-0.089	
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	0	0.000	-0.014	0.989	0.000	

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	0.103	0.062	1.647	0.116	-0.028	0.233	0.000
L3.ABC.transporters	0.000	0.000	-1.957	0.065	0.000	0.000	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)	0	0.036	0	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	-0.09	0.079	-1.128	0.273	-0.256	0.077	0.000
L3.Adipocytokine.signaling.pathway	0.00	0.000	1.260	0.223	0.000	0.000	0.074

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	0.077	0.043	1.819	0.085	-0.012	0.167	0.000
L3.African.trypanosomiasis	0.000	0.000	-2.690	0.015	0.000	0.000	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	0.06	0.085	0.708	0.487	-0.117	0.237	0.00
L3.Alanine..aspartate.and.glutamate.metabolism	0.00	0.000	-0.784	0.443	0.000	0.000	0.03

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)	0	0.036	0	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	0.054	0.071	0.759	0.457	-0.095	0.203	0.000
L3.Alzheimer.s.disease	0.000	0.000	-0.881	0.389	0.000	0.000	0.037

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	0.098	0.071	1.390	0.181	-0.05	0.246	0.000
L3.Amino.acid.metabolism	0.000	0.000	-1.594	0.127	0.00	0.000	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	0.079	0.079	0.991	0.334	-0.088	0.245	0.000
L3.Amino.acid.related.enzymes	0.000	0.000	-1.110	0.281	0.000	0.000	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	0.074	0.082	0.904	0.377	-0.097	0.245	0.000
L3.Amino.sugar.and.nucleotide.sugar.metabolism	0.000	0.000	-1.007	0.327	0.000	0.000	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	0.084	0.073	1.143	0.267	-0.07	0.237	0.000
L3.Aminoacyl.tRNA.biosynthesis	0.000	0.000	-1.304	0.208	0.00	0.000	0.078

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	0.055	0.084	0.652	0.522	-0.121	0.231	0.000
L3.Aminobenzoate.degradation	0.000	0.000	-0.723	0.478	0.000	0.000	0.025

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	0.062	0.053	1.169	0.257	-0.049	0.172	0.000
L3.Amoebiasis	0.000	0.000	-1.551	0.137	0.000	0.000	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	-0.017	0.062	-0.273	0.787	-0.147	0.113	0.000
L3.Amyotrophic.lateral.sclerosis..ALS.	0.000	0.000	0.340	0.738	0.000	0.000	0.006

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	0.048	0.08	0.601	0.555	-0.119	0.214	0.000
L3.Antigen.processing.and.presentation	0.000	0.00	-0.676	0.507	0.000	0.000	0.022

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	0.008	0.041	0.183	0.857	-0.079	0.094	0.000
L3.Apoptosis	0.000	0.000	-0.399	0.695	0.000	0.000	0.008

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	-0.099	0.088	-1.116	0.278	-0.283	0.086	0.000
L3.Arachidonic.acid.metabolism	0.000	0.000	1.219	0.238	0.000	0.000	0.069

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	0.075	0.08	0.935	0.362	-0.093	0.242	0.000
L3.Arginine.and.proline.metabolism	0.000	0.00	-1.045	0.309	0.000	0.000	0.052

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)	0	0.036	0	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	0.067	0.073	0.921	0.369	-0.086	0.22	0.000
L3.Ascorbate.and.aldarate.metabolism	0.000	0.000	-1.056	0.304	0.000	0.00	0.053

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	0.084	0.048	1.738	0.098	-0.017	0.185	0.000
L3.Atrazine.degradation	0.000	0.000	-2.343	0.030	0.000	0.000	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	0.078	0.058	1.351	0.192	-0.043	0.2	0.000
L3.Bacterial.chemotaxis	0.000	0.000	-1.678	0.110	0.000	0.0	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	0.086	0.037	2.329	0.031	0.009	0.163	0.000
L3.Bacterial.invasion.of.epithelial.cells	0.000	0.000	-3.627	0.002	0.000	0.000	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	0.07	0.055	1.263	0.222	-0.046	0.186	0.000
L3.Bacterial.motility.proteins	0.00	0.000	-1.615	0.123	0.000	0.000	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	0.074	0.081	0.905	0.377	-0.097	0.244	0.000
L3.Bacterial.secretion.system	0.000	0.000	-1.008	0.326	0.000	0.000	0.048

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	0.087	0.081	1.079	0.294	-0.082	0.257	0.000
L3.Bacterial.toxins	0.000	0.000	-1.201	0.244	0.000	0.000	0.067

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	0.001	0.041	0.030	0.976	-0.085	0.087	0
L3.Basal.transcription.factors	0.000	0.000	-0.069	0.946	0.000	0.000	0

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	0.084	0.077	1.092	0.289	-0.077	0.244	0.000
L3.Base.excision.repair	0.000	0.000	-1.232	0.233	0.000	0.000	0.071

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	0.087	0.072	1.204	0.243	-0.064	0.239	0.000
L3.Benzoate.degradation	0.000	0.000	-1.377	0.184	0.000	0.000	0.087

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	0.017	0.038	0.461	0.650	-0.062	0.096	0.000
L3.Betalain.biosynthesis	-0.003	0.002	-1.300	0.209	-0.007	0.002	0.078

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	-0.007	0.037	-0.176	0.862	-0.084	0.071	0.000
L3.Bile.secretion	0.137	0.170	0.806	0.430	-0.219	0.494	0.031

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	0.1	0.078	1.285	0.214	-0.063	0.263
L3.Biosynthesis.and.biodegradation.of.secondary.metabolites	0.0	0.000	-1.438	0.167	0.000	0.000

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)	0	0.036	0	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	0.097	0.07	1.378	0.184	-0.05	0.243	0.000
L3.Biosynthesis.of.ansamycins	0.000	0.00	-1.584	0.130	0.00	0.000	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	-0.036	0.096	-0.381	0.707	-0.237	0.164
L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides	0.000	0.000	0.413	0.684	0.000	0.000

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)	0	0.036	0	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	0.022	0.037	0.599	0.556	-0.056	0.101	0.000
L3.Biosynthesis.of.type.II.polyketide.products	-0.003	0.002	-1.587	0.129	-0.007	0.001	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	0.105	0.071	1.490	0.153	-0.043	0.253	0.000
L3.Biosynthesis.of.unsaturated.fatty.acids	0.000	0.000	-1.705	0.105	0.000	0.000	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	0.047	0.092	0.512	0.615	-0.145	0.239	0.000
L3.Biosynthesis.of.vancomycin.group.antibiotics	0.000	0.000	-0.558	0.583	0.000	0.000	0.015

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	0.072	0.079	0.917	0.371	-0.093	0.238	0.00
L3.Biotin.metabolism	0.000	0.000	-1.029	0.316	0.000	0.000	0.05

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	0.068	0.077	0.892	0.383	-0.092	0.229	0.000
L3.Bisphenol.degradation	0.000	0.000	-1.010	0.325	0.000	0.000	0.049

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	0.079	0.036	2.210	0.040	0.004	0.154	0.000
L3.Bladder.cancer	0.000	0.000	-3.625	0.002	-0.001	0.000	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	0.081	0.077	1.060	0.303	-0.079	0.242	0.000
L3.Butanoate.metabolism	0.000	0.000	-1.195	0.247	0.000	0.000	0.067

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	0.053	0.074	0.721	0.480	-0.101	0.208	0.000
L3.Butirosin.and.neomycin.biosynthesis	0.000	0.000	-0.827	0.418	0.000	0.000	0.033

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	0.091	0.07	1.295	0.211	-0.056	0.238	0.0
L3.C5.Branched.dibasic.acid.metabolism	0.000	0.00	-1.492	0.152	0.000	0.000	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)	0	0.036	0	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	-0.003	0.04	-0.086	0.933	-0.088	0.081	0.000
L3.Caffeine.metabolism	0.000	0.00	0.207	0.838	0.000	0.000	0.002

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	0.002	0.039	0.04	0.969	-0.080	0.083	0.000
L3.Calcium.signaling.pathway	0.000	0.003	-0.12	0.906	-0.007	0.006	0.001

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	0.112	0.058	1.939	0.067	-0.009	0.232	0.000
L3.Caprolactam.degradation	0.000	0.000	-2.347	0.030	0.000	0.000	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	-0.027	0.066	-0.408	0.688	-0.164	0.111	0.000
L3.Carbohydrate.digestion.and.absorption	0.000	0.000	0.491	0.629	0.000	0.000	0.012

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	0.056	0.078	0.728	0.475	-0.106	0.219	0.000
L3.Carbohydrate.metabolism	0.000	0.000	-0.824	0.420	0.000	0.000	0.033

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	0.072	0.081	0.889	0.385	-0.098	0.242	0.000
L3.Carbon.fixation.in.photosynthetic.organisms	0.000	0.000	-0.992	0.334	0.000	0.000	0.047

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	0.053	0.086	0.617	0.545	-0.127	0.234	0.000
L3.Carbon.fixation.pathways.in.prokaryotes	0.000	0.000	-0.681	0.504	0.000	0.000	0.023

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	0	0.038	0.009	0.993	-0.079	0.08	0
L3.Cardiac.muscle.contraction	0	0.000	-0.038	0.970	0.000	0.00	0

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	-0.047	0.05	-0.932	0.363	-0.151	0.058	0.000
L3.Carotenoid.biosynthesis	0.000	0.00	1.314	0.205	0.000	0.000	0.079

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)	0	0.036	0	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	0.075	0.08	0.941	0.359	-0.092	0.243	0.000
L3.Cell.cycle. . . Caulobacter	0.000	0.00	-1.053	0.306	0.000	0.000	0.052

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)	0	0.036	0	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	0.084	0.078	1.086	0.291	-0.078	0.247	0.000
L3.Cell.division	0.000	0.000	-1.222	0.237	0.000	0.000	0.069

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	0.062	0.086	0.717	0.482	-0.118	0.242	0.00
L3.Cell.motility.and.secretion	0.000	0.000	-0.791	0.439	0.000	0.000	0.03

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	-0.143	0.068	-2.106	0.049	-0.285	-0.001	0.000
L3.Cellular.antigens	0.000	0.000	2.395	0.027	0.000	0.000	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	0.075	0.041	1.828	0.083	-0.011	0.16	0.000
L3.Chagas.disease..American.trypanosomiasis.	0.000	0.000	-2.810	0.011	0.000	0.00	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	0.063	0.085	0.735	0.471	-0.116	0.241	0.000
L3.Chaperones.and.folding.catalysts	0.000	0.000	-0.812	0.427	0.000	0.000	0.032

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	0.078	0.069	1.129	0.273	-0.066	0.222	0.000
L3.Chloroalkane.and.chloroalkene.degradation	0.000	0.000	-1.314	0.204	0.000	0.000	0.079

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 %	R2
Intercept	0.064	0.054	1.189	0.249	-0.049	0.177	0.000
L3.Chlorocyclohexane.and.chlorobenzene.degradation	0.000	0.000	-1.553	0.137	0.000	0.000	0.108

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)	0	0.036	0	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	0.082	0.079	1.044	0.310	-0.083	0.247	0.000
L3.Chromosome	0.000	0.000	-1.170	0.256	0.000	0.000	0.064

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)	0	0.036	0	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	-0.003	0.041	-0.084	0.934	-0.088	0.081	0.000
L3.Circadian.rhythm...plant	0.000	0.000	0.202	0.842	0.000	0.000	0.002

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	0.02	0.089	0.222	0.827	-0.166	0.205	0.000
L3.Citrate.cycle..TCA.cycle.	0.00	0.000	-0.244	0.810	0.000	0.000	0.003

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	0.017	0.033	0.498	0.625	-0.053	0.087	0.000
L3.Clavulanic.acid.biosynthesis	-0.175	0.077	-2.280	0.034	-0.335	-0.014	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	0	0.038	0.004	0.997	-0.079	0.079	0
L3.Colorectal.cancer	0	0.000	-0.017	0.987	0.000	0.000	0

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)	0	0.036	0	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	0.041	0.074	0.557	0.584	-0.114	0.197	0.00
L3.Cyanoamino.acid.metabolism	0.000	0.000	-0.640	0.530	0.000	0.000	0.02

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	0.091	0.079	1.158	0.261	-0.074	0.256	0.000
L3.Cysteine.and.methionine.metabolism	0.000	0.000	-1.296	0.210	0.000	0.000	0.077

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)	0	0.036	0	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)	0	0.036	0	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)	0	0.036	0	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	0.086	0.07	1.237	0.231	-0.06	0.233	0.000
L3.Cytoskeleton.proteins	0.000	0.00	-1.430	0.169	0.00	0.000	0.093

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)	0	0.036	0	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	0.087	0.077	1.132	0.272	-0.074	0.249	0.000
L3.D.Alanine.metabolism	0.000	0.000	-1.273	0.218	0.000	0.000	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	0.04	0.054	0.750	0.462	-0.072	0.153	0.000
L3.D.Arginine.and.D.ornithine.metabolism	0.00	0.000	-1.009	0.326	0.000	0.000	0.048

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	0.078	0.084	0.926	0.366	-0.098	0.253	0.00
L3.D.Glutamine.and.D.glutamate.metabolism	0.000	0.000	-1.024	0.319	0.000	0.000	0.05

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	0.08	0.08	1.001	0.329	-0.087	0.248	0.000
L3.DNA.repair.and.recombination.proteins	0.00	0.00	-1.119	0.277	0.000	0.000	0.059

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	0.071	0.083	0.852	0.405	-0.103	0.245	0.000
L3.DNA.replication	0.000	0.000	-0.945	0.357	0.000	0.000	0.043

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	0.076	0.082	0.933	0.363	-0.095	0.248	0.000
L3.DNA.replication.proteins	0.000	0.000	-1.037	0.313	0.000	0.000	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)	0	0.036	0	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	0.087	0.057	1.519	0.145	-0.033	0.206	0.000
L3.Dioxin.degradation	0.000	0.000	-1.886	0.075	0.000	0.000	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	0.001	0.07	0.015	0.989	-0.146	0.148	0
L3.Drug.metabolism…cytochrome.P450	0.000	0.00	-0.017	0.987	0.000	0.000	0

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	0.052	0.086	0.606	0.552	-0.129	0.233	0.000
L3.Drug.metabolism…other.enzymes	0.000	0.000	-0.668	0.512	0.000	0.000	0.022

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)	0	0.036	0	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	0.066	0.054	1.223	0.236	-0.047	0.18	0.000
L3.Electron.transfer.carriers	0.000	0.000	-1.590	0.128	0.000	0.00	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)	0	0.036	0	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	0.012	0.037	0.315	0.756	-0.067	0.090	0.000
L3.Endocytosis	-0.083	0.077	-1.077	0.295	-0.243	0.078	0.055

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	0.053	0.085	0.625	0.539	-0.125	0.231	0.000
L3.Energy.metabolism	0.000	0.000	-0.692	0.497	0.000	0.000	0.023

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	0.096	0.071	1.346	0.194	-0.053	0.245
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	0.000	0.000	-1.542	0.140	0.000	0.000

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)	0	0.036	0	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	0.014	0.053	0.272	0.788	-0.096	0.125	0.000
L3.Ether.lipid.metabolism	0.000	0.000	-0.378	0.709	0.000	0.000	0.007

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	-0.015	0.081	-0.186	0.855	-0.185	0.155	0.000
L3.Ethylbenzene.degradation	0.000	0.000	0.208	0.837	0.000	0.000	0.002

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)	0	0.036	0	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	0.073	0.08	0.917	0.370	-0.094	0.241	0.00
L3.Fatty.acid.biosynthesis	0.000	0.00	-1.026	0.318	0.000	0.000	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	-0.003	0.04	-0.086	0.932	-0.088	0.081	0.000
L3.Fatty.acid.elongation.in.mitochondria	0.000	0.00	0.208	0.837	0.000	0.000	0.002

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	0.078	0.08	0.976	0.341	-0.089	0.245	0.000
L3.Fatty.acid.metabolism	0.000	0.00	-1.092	0.289	0.000	0.000	0.056

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)	0	0.036	0	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	0.012	0.037	0.315	0.756	-0.067	0.090	0.000
L3.Fc.gamma.R.mediated.phagocytosis	-0.083	0.077	-1.077	0.295	-0.243	0.078	0.055

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	0.061	0.052	1.176	0.254	-0.048	0.17	0.00
L3.Flagellar.assembly	0.000	0.000	-1.576	0.132	0.000	0.00	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	-0.035	0.069	-0.503	0.621	-0.179	0.11	0.000
L3.Flavone.and.flavonol.biosynthesis	0.000	0.000	0.593	0.560	0.000	0.00	0.017

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	0.028	0.051	0.543	0.593	-0.079	0.134	0.000
L3.Flavonoid.biosynthesis	0.000	0.000	-0.773	0.449	0.000	0.000	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	0.078	0.044	1.784	0.090	-0.013	0.169	0.000
L3.Fluorobenzoate.degradation	0.000	0.000	-2.597	0.018	0.000	0.000	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)	0	0.036	0	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	0.065	0.089	0.732	0.473	-0.121	0.25	0.000
L3.Folate.biosynthesis	0.000	0.000	-0.802	0.432	0.000	0.00	0.031

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	0.078	0.076	1.023	0.319	-0.081	0.237	0.000
L3.Fructose.and.mannose.metabolism	0.000	0.000	-1.158	0.261	0.000	0.000	0.063

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	0.089	0.077	1.159	0.261	-0.071	0.249	0.000
L3.Function.unknown	0.000	0.000	-1.306	0.207	0.000	0.000	0.079

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	0.023	0.040	0.575	0.572	-0.060	0.106	0.000
L3.G.protein.coupled.receptors	-0.017	0.014	-1.262	0.222	-0.046	0.011	0.074

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)	0	0.036	0	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	0.066	0.08	0.823	0.421	-0.101	0.233	0.000
L3.Galactose.metabolism	0.000	0.00	-0.922	0.368	0.000	0.000	0.041

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)	0	0.036	0	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	0.078	0.081	0.967	0.346	-0.091	0.247	0.000
L3.General.function.prediction.only	0.000	0.000	-1.079	0.294	0.000	0.000	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	-0.064	0.091	-0.703	0.490	-0.253	0.126	0.000
L3.Geraniol.degradation	0.000	0.000	0.768	0.452	0.000	0.000	0.029

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	0.093	0.05	1.849	0.080	-0.012	0.199	0.000
L3.Germination	0.000	0.00	-2.406	0.026	0.000	0.000	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)	0	0.036	0	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	0.068	0.081	0.841	0.411	-0.101	0.238	0.000
L3.Glutamatergic.synapse	0.000	0.000	-0.939	0.359	0.000	0.000	0.042

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	0.024	0.099	0.240	0.813	-0.184	0.231	0.000
L3.Glutathione.metabolism	0.000	0.000	-0.258	0.799	0.000	0.000	0.003

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)	0	0.036	0	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	-0.031	0.076	-0.406	0.689	-0.189	0.128	0.000
L3.Glycan.biosynthesis.and.metabolism	0.000	0.000	0.464	0.648	0.000	0.000	0.011

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	0.087	0.068	1.293	0.212	-0.054	0.229	0.000
L3.Glycerolipid.metabolism	0.000	0.000	-1.509	0.148	0.000	0.000	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	0.088	0.073	1.210	0.241	-0.064	0.24	0.000
L3.Glycerophospholipid.metabolism	0.000	0.000	-1.383	0.183	0.000	0.00	0.087

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	0.073	0.084	0.867	0.397	-0.103	0.249	0.000
L3.Glycine..serine.and.threonine.metabolism	0.000	0.000	-0.959	0.349	0.000	0.000	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	0.084	0.078	1.078	0.295	-0.079	0.246	0.000
L3.Glycolysis. . . Gluconeogenesis	0.000	0.000	-1.212	0.240	0.000	0.000	0.068

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	0.002	0.038	0.043	0.966	-0.078	0.081	0
L3.Glycosaminoglycan.biosynthesis. . . chondroitin.sulfate	-0.001	0.006	-0.190	0.852	-0.015	0.012	0

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	-0.112	0.066	-1.700	0.105	-0.25	0.026	0.000
L3.Glycosaminoglycan.degradation	0.000	0.000	1.977	0.063	0.00	0.000	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	-0.099	0.06	-1.658	0.114	-0.225	0.026	0.000
L3.Glycosphingolipid.biosynthesis. . . ganglio.series	0.000	0.00	2.000	0.060	0.000	0.000	0.167

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	-0.039	0.081	-0.477	0.639	-0.209	0.131	0.000
L3.Glycosphingolipid.biosynthesis. . . globo.series	0.000	0.000	0.534	0.600	0.000	0.000	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 %	97.5 %
Intercept	-0.001	0.039	-0.015	0.988	-0.083	0.082
L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series	0.000	0.000	0.043	0.966	0.000	0.000

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)	0	0.036	0	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	0.068	0.09	0.750	0.462	-0.121	0.257	0.000
L3.Glycosyltransferases	0.000	0.00	-0.819	0.423	0.000	0.000	0.032

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	0.084	0.079	1.068	0.299	-0.081	0.249	0.000
L3.Glyoxylate.and.dicarboxylate.metabolism	0.000	0.000	-1.197	0.246	0.000	0.000	0.067

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	0.012	0.037	0.315	0.756	-0.067	0.090	0.000
L3.GnRH.signaling.pathway	-0.083	0.077	-1.077	0.295	-0.243	0.078	0.055

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)	0	0.036	0	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)	0	0.036	0	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)	0	0.036	0	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	0.056	0.083	0.680	0.505	-0.117	0.229	0.000
L3.Histidine.metabolism	0.000	0.000	-0.757	0.458	0.000	0.000	0.028

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	0.073	0.081	0.897	0.381	-0.097	0.244	0.000
L3.Homologous.recombination	0.000	0.000	-0.999	0.330	0.000	0.000	0.048

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	-0.059	0.075	-0.795	0.437	-0.215	0.097	0.00
L3.Huntington.s.disease	0.000	0.000	0.908	0.375	0.000	0.000	0.04

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	0.001	0.038	0.030	0.977	-0.078	0.080	0.000
L3.Hypertrophic.cardiomyopathy..HCM.	-0.003	0.025	-0.136	0.894	-0.055	0.048	0.001

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)	0	0.036	0	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	0	0.038	0.004	0.997	-0.079	0.079	0
L3.Influenza.A	0	0.000	-0.017	0.987	0.000	0.000	0

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	0.058	0.081	0.718	0.482	-0.112	0.228	0.000
L3.Inorganic.ion.transport.and.metabolism	0.000	0.000	-0.802	0.432	0.000	0.000	0.031

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	0.037	0.084	0.438	0.666	-0.139	0.213	0.000
L3.Inositol.phosphate.metabolism	0.000	0.000	-0.487	0.632	0.000	0.000	0.012

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	0.058	0.073	0.794	0.437	-0.094	0.21	0.00
L3.Insulin.signaling.pathway	0.000	0.000	-0.915	0.372	0.000	0.00	0.04

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	0.049	0.087	0.567	0.578	-0.133	0.232	0.000
L3.Ion.channels	0.000	0.000	-0.624	0.540	0.000	0.000	0.019

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	0.001	0.039	0.022	0.983	-0.080	0.082	0
L3.Isoflavonoid.biosynthesis	-0.006	0.079	-0.074	0.942	-0.171	0.160	0

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	0.039	0.096	0.411	0.686	-0.161	0.239	0.00
L3.Isoquinoline.alkaloid.biosynthesis	0.000	0.000	-0.445	0.661	0.000	0.000	0.01

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)	0	0.036	0	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)	0	0.036	0	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	0.06	0.081	0.740	0.468	-0.109	0.229	0.000
L3.Limonene.and.pinene.degradation	0.00	0.000	-0.828	0.418	0.000	0.000	0.033

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	0.069	0.076	0.902	0.378	-0.091	0.228	0.00
L3.Linoleic.acid.metabolism	0.000	0.000	-1.022	0.320	0.000	0.000	0.05

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	0.055	0.084	0.657	0.519	-0.12	0.23	0.000
L3.Lipid.biosynthesis.proteins	0.000	0.000	-0.729	0.475	0.00	0.00	0.026

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	0.101	0.068	1.483	0.155	-0.041	0.243	0.000
L3.Lipid.metabolism	0.000	0.000	-1.719	0.102	0.000	0.000	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	-0.126	0.071	-1.763	0.094	-0.275	0.024	0.000
L3.Lipoic.acid.metabolism	0.000	0.000	1.997	0.060	0.000	0.000	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	-0.124	0.081	-1.544	0.139	-0.293	0.044	0.000
L3.Lipopolysaccharide.biosynthesis	0.000	0.000	1.707	0.104	0.000	0.000	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	-0.09	0.09	-1.004	0.328	-0.278	0.098	0.000
L3.Lipopolysaccharide.biosynthesis.proteins	0.00	0.00	1.095	0.287	0.000	0.000	0.057

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)	0	0.036	0	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)	0	0.036	0	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	0.086	0.075	1.146	0.266	-0.071	0.243	0.000
L3.Lysine.biosynthesis	0.000	0.000	-1.298	0.210	0.000	0.000	0.078

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	0.081	0.083	0.969	0.345	-0.093	0.254	0.000
L3.Lysine.degradation	0.000	0.000	-1.074	0.296	0.000	0.000	0.055

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	-0.122	0.072	-1.686	0.108	-0.273	0.029	0.000
L3.Lysosome	0.000	0.000	1.906	0.072	0.000	0.000	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)	0	0.036	0	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	0.014	0.088	0.160	0.874	-0.171	0.199	0.000
L3.MAPK.signaling.pathway…yeast	0.000	0.000	-0.176	0.862	0.000	0.000	0.002

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)	0	0.036	0	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	0.01	0.041	0.241	0.812	-0.076	0.096	0.000
L3.Meiosis...yeast	0.00	0.000	-0.536	0.598	0.000	0.000	0.014

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	0.017	0.038	0.461	0.650	-0.062	0.096	0.000
L3.Melanogenesis	-0.003	0.002	-1.300	0.209	-0.007	0.002	0.078

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	-0.011	0.093	-0.123	0.904	-0.206	0.183	0.000
L3.Membrane.and.intracellular.structural.molecules	0.000	0.000	0.134	0.895	0.000	0.000	0.001

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	0.097	0.068	1.432	0.168	-0.045	0.238	0.000
L3.Metabolism.of.cofactors.and.vitamins	0.000	0.000	-1.664	0.113	0.000	0.000	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	0	0.07	0.006	0.996	-0.146	0.146	0
L3.Metabolism.of.xenobiotics.by.cytochrome.P450	0	0.00	-0.007	0.995	0.000	0.000	0

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	0.092	0.075	1.236	0.232	-0.064	0.248	0.000
L3.Methane.metabolism	0.000	0.000	-1.400	0.178	0.000	0.000	0.089

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	0.043	0.051	0.853	0.404	-0.063	0.15	0.000
L3.Mineral.absorption	0.000	0.000	-1.195	0.247	0.000	0.00	0.067

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	0.081	0.079	1.016	0.322	-0.086	0.247	0.000
L3.Mismatch.repair	0.000	0.000	-1.137	0.270	0.000	0.000	0.061

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	-0.001	0.084	-0.011	0.991	-0.176	0.174	0
L3.N.Glycan.biosynthesis	0.000	0.000	0.012	0.990	0.000	0.000	0

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	0.043	0.083	0.514	0.613	-0.132	0.218	0.000
L3.NOD.like.receptor.signaling.pathway	0.000	0.000	-0.572	0.574	0.000	0.000	0.016

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	0.036	0.082	0.440	0.665	-0.136	0.208	0.000
L3.Naphthalene.degradation	0.000	0.000	-0.491	0.629	0.000	0.000	0.012

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)	0	0.036	0	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)	0	0.036	0	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	0.071	0.081	0.875	0.392	-0.098	0.239	0.000
L3.Nicotinate.and.nicotinamide.metabolism	0.000	0.000	-0.978	0.340	0.000	0.000	0.046

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	0.065	0.087	0.744	0.466	-0.117	0.247	0.000
L3.Nitrogen.metabolism	0.000	0.000	-0.819	0.423	0.000	0.000	0.032

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	0.098	0.054	1.801	0.088	-0.016	0.212	0.000
L3.Nitrotoluene.degradation	0.000	0.000	-2.256	0.036	0.000	0.000	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	0.052	0.051	1.015	0.323	-0.055	0.159	0.000
L3.Non.homologous.end.joining	0.000	0.000	-1.394	0.179	0.000	0.000	0.089

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)	0	0.036	0	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	0.083	0.08	1.041	0.311	-0.084	0.25	0.000
L3.Novobiocin.biosynthesis	0.000	0.00	-1.163	0.259	0.000	0.00	0.063

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	0.083	0.077	1.085	0.292	-0.078	0.244	0.00
L3.Nucleotide.excision.repair	0.000	0.000	-1.223	0.236	0.000	0.000	0.07

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	0.111	0.058	1.924	0.069	-0.01	0.231	0.000
L3.Nucleotide.metabolism	0.000	0.000	-2.331	0.031	0.00	0.000	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)	0	0.036	0	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	0.059	0.086	0.694	0.496	-0.12	0.239	0.000
L3.One.carbon.pool.by.folate	0.000	0.000	-0.766	0.453	0.00	0.000	0.028

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)	0	0.036	0	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	-0.074	0.087	-0.851	0.405	-0.256	0.108	0.000
L3.Other.glycan.degradation	0.000	0.000	0.935	0.362	0.000	0.000	0.042

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	0.064	0.087	0.739	0.469	-0.117	0.246	0.000
L3.Other.ion.coupled.transporters	0.000	0.000	-0.814	0.426	0.000	0.000	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	0.068	0.081	0.839	0.412	-0.102	0.238	0.000
L3.Other.transporters	0.000	0.000	-0.936	0.361	0.000	0.000	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)	0	0.036	0	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	0.072	0.08	0.895	0.382	-0.096	0.239	0.000
L3.Others	0.000	0.00	-1.002	0.329	0.000	0.000	0.048

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	0.074	0.08	0.928	0.365	-0.093	0.24	0.000
L3.Oxidative.phosphorylation	0.000	0.00	-1.039	0.312	0.000	0.00	0.051

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	0.001	0.089	0.008	0.993	-0.185	0.187	0
L3.PPAR.signaling.pathway	0.000	0.000	-0.009	0.993	0.000	0.000	0

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)	0	0.036	0	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)	0	0.036	0	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	0.09	0.076	1.195	0.247	-0.068	0.249	0.000
L3.Pantothenate.and.CoA.biosynthesis	0.00	0.000	-1.351	0.193	0.000	0.000	0.084

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	0	0.038	0.008	0.994	-0.079	0.08	0
L3.Parkinson.s.disease	0	0.000	-0.033	0.974	0.000	0.00	0

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)	0	0.036	0	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	0.048	0.077	0.627	0.538	-0.113	0.21	0.000
L3.Pathways.in.cancer	0.000	0.000	-0.711	0.486	0.000	0.00	0.025

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	0.079	0.076	1.045	0.309	-0.08	0.238	0.000
L3.Penicillin.and.cephalosporin.biosynthesis	0.000	0.000	-1.183	0.251	0.00	0.000	0.065

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	0.058	0.082	0.706	0.489	-0.114	0.23	0.00
L3.Pentose.and.glucuronate.interconversions	0.000	0.000	-0.787	0.441	0.000	0.00	0.03

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	0.082	0.077	1.066	0.300	-0.079	0.243	0.000
L3.Pentose.phosphate.pathway	0.000	0.000	-1.202	0.244	0.000	0.000	0.067

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	0.08	0.081	0.982	0.339	-0.09	0.249	0.000
L3.Peptidases	0.00	0.000	-1.093	0.288	0.00	0.000	0.056

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	0.087	0.077	1.127	0.274	-0.074	0.248	0.000
L3.Peptidoglycan.biosynthesis	0.000	0.000	-1.269	0.220	0.000	0.000	0.075

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	-0.027	0.09	-0.296	0.771	-0.215	0.162	0.000
L3.Peroxisome	0.000	0.00	0.324	0.749	0.000	0.000	0.005

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	-0.084	0.082	-1.022	0.320	-0.257	0.088	0.00
L3.Pertussis	0.000	0.000	1.134	0.271	0.000	0.000	0.06

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)	0	0.036	0	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	0.046	0.085	0.544	0.593	-0.131	0.223	0.000
L3.Phenylalanine.metabolism	0.000	0.000	-0.604	0.553	0.000	0.000	0.018

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	0.092	0.075	1.227	0.235	-0.065	0.248	0.0
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis	0.000	0.000	-1.390	0.181	0.000	0.000	0.0

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	0.028	0.068	0.404	0.691	-0.115	0.17	0.000
L3.Phenylpropanoid.biosynthesis	0.000	0.000	-0.479	0.637	0.000	0.00	0.011

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	0.03	0.088	0.346	0.734	-0.154	0.215	0.000
L3.Phosphatidylinositol.signaling.system	0.00	0.000	-0.380	0.708	0.000	0.000	0.007

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	0.076	0.078	0.973	0.343	-0.087	0.239	0.000
L3.Phosphonate.and.phosphinate.metabolism	0.000	0.000	-1.095	0.287	0.000	0.000	0.057

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	0.09	0.052	1.711	0.103	-0.02	0.199	0.000
L3.Phosphotransferase.system..PTS.	0.00	0.000	-2.200	0.040	0.00	0.000	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	0.094	0.067	1.401	0.177	-0.047	0.235	0.000
L3.Photosynthesis	0.000	0.000	-1.633	0.119	0.000	0.000	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	0.001	0.039	0.036	0.972	-0.08	0.083	0.000
L3.Photosynthesis...antenna.proteins	0.000	0.000	-0.107	0.916	0.00	0.000	0.001

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	0.094	0.067	1.397	0.178	-0.047	0.235	0.000
L3.Photosynthesis.proteins	0.000	0.000	-1.628	0.120	0.000	0.000	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)	0	0.036	0	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)	0	0.036	0	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	0.087	0.07	1.235	0.232	-0.06	0.235	0.000
L3.Plant.pathogen.interaction	0.000	0.00	-1.424	0.171	0.00	0.000	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	0.073	0.078	0.935	0.362	-0.09	0.235	0.000
L3.Polycyclic.aromatic.hydrocarbon.degradation	0.000	0.000	-1.054	0.305	0.00	0.000	0.053

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	0.064	0.087	0.732	0.473	-0.118	0.245	0.000
L3.Polyketide.sugar.unit.biosynthesis	0.000	0.000	-0.805	0.431	0.000	0.000	0.031

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	-0.089	0.096	-0.928	0.365	-0.29	0.112	0.000
L3.Pores.ion.channels	0.000	0.000	1.000	0.330	0.00	0.000	0.048

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	0.089	0.074	1.213	0.240	-0.065	0.244	0.000
L3.Porphyrin.and.chlorophyll.metabolism	0.000	0.000	-1.380	0.184	0.000	0.000	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	0.047	0.086	0.542	0.594	-0.134	0.228	0.000
L3.Prenyltransferases	0.000	0.000	-0.598	0.557	0.000	0.000	0.018

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	0.071	0.071	1.006	0.327	-0.077	0.219	0.000
L3.Primary.bile.acid.biosynthesis	0.000	0.000	-1.165	0.258	0.000	0.000	0.064

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	0.044	0.079	0.559	0.583	-0.122	0.211	0.000
L3.Primary.immunodeficiency	0.000	0.000	-0.629	0.537	0.000	0.000	0.019

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	0.017	0.057	0.290	0.775	-0.103	0.136	0.000
L3.Prion.diseases	0.000	0.000	-0.378	0.709	0.000	0.000	0.007

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	0.048	0.08	0.601	0.555	-0.119	0.214	0.000
L3.Progesterone.mediated.oocyte.maturation	0.000	0.00	-0.676	0.507	0.000	0.000	0.022

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	0.086	0.079	1.100	0.285	-0.078	0.251	0.000
L3.Propanoate.metabolism	0.000	0.000	-1.232	0.233	0.000	0.000	0.071

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	0.032	0.081	0.397	0.696	-0.138	0.202	0.00
L3.Prostate.cancer	0.000	0.000	-0.445	0.661	0.000	0.000	0.01

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	0.057	0.078	0.731	0.474	-0.106	0.22	0.000
L3.Proteasome	0.000	0.000	-0.825	0.420	0.000	0.00	0.033

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	-0.128	0.06	-2.132	0.046	-0.253	-0.002	0.000
L3.Protein.digestion.and.absorption	0.000	0.00	2.518	0.021	0.000	0.000	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	0.073	0.081	0.904	0.377	-0.097	0.243	0.000
L3.Protein.export	0.000	0.000	-1.007	0.326	0.000	0.000	0.048

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	0.073	0.082	0.886	0.387	-0.099	0.245	0.000
L3.Protein.folding.and.associated.processing	0.000	0.000	-0.985	0.337	0.000	0.000	0.046

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	0.097	0.068	1.431	0.169	-0.045	0.239	0.000
L3.Protein.kinases	0.000	0.000	-1.660	0.113	0.000	0.000	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	-0.047	0.093	-0.507	0.618	-0.242	0.147	0.000
L3.Protein.processing.in.endoplasmic.reticulum	0.000	0.000	0.552	0.588	0.000	0.000	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	-0.004	0.067	-0.062	0.951	-0.145	0.137	0
L3.Proximal.tubule.bicarbonate.reclamation	0.000	0.000	0.075	0.941	0.000	0.000	0

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	0.083	0.081	1.026	0.318	-0.087	0.253	0.000
L3.Purine.metabolism	0.000	0.000	-1.143	0.267	0.000	0.000	0.061

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	0.076	0.082	0.927	0.365	-0.095	0.247	0.000
L3.Pyrimidine.metabolism	0.000	0.000	-1.032	0.315	0.000	0.000	0.051

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	0.086	0.079	1.093	0.288	-0.079	0.25	0.00
L3.Pyruvate.metabolism	0.000	0.000	-1.225	0.236	0.000	0.00	0.07

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	-0.022	0.047	-0.463	0.649	-0.121	0.077	0.000
L3.RIG.I.like.receptor.signaling.pathway	0.000	0.000	0.726	0.477	0.000	0.000	0.026

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	0.061	0.085	0.722	0.479	-0.116	0.239	0.000
L3.RNA.degradation	0.000	0.000	-0.798	0.435	0.000	0.000	0.031

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	0.094	0.079	1.196	0.246	-0.071	0.259	0.000
L3.RNA.polymerase	0.000	0.000	-1.337	0.197	0.000	0.000	0.082

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	0.097	0.067	1.448	0.164	-0.043	0.237	0.000
L3.RNA.transport	0.000	0.000	-1.687	0.108	0.000	0.000	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)	0	0.036	0	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	0.042	0.061	0.690	0.498	-0.086	0.17	0.000
L3.Renal.cell.carcinoma	0.000	0.000	-0.856	0.403	0.000	0.00	0.035

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	0.005	0.038	0.125	0.901	-0.075	0.085	0.000
L3.Renin.angiotensin.system	-0.007	0.016	-0.432	0.671	-0.039	0.026	0.009

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	0.096	0.072	1.335	0.198	-0.055	0.248	0.000
L3.Replication..recombination.and.repair.proteins	0.000	0.000	-1.523	0.144	0.000	0.000	0.104

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	0.002	0.087	0.027	0.979	-0.181	0.185	0
L3.Restriction.enzyme	0.000	0.000	-0.030	0.977	0.000	0.000	0

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	-0.033	0.072	-0.457	0.653	-0.184	0.118	0.000
L3.Retinol.metabolism	0.000	0.000	0.531	0.602	0.000	0.000	0.014

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)	0	0.036	0	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	0.083	0.086	0.971	0.344	-0.096	0.263	0.000
L3.Riboflavin.metabolism	0.000	0.000	-1.069	0.299	0.000	0.000	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	0.077	0.079	0.965	0.346	-0.089	0.242	0.000
L3.Ribosome	0.000	0.000	-1.082	0.293	0.000	0.000	0.055

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	0.088	0.076	1.157	0.261	-0.071	0.246	0.000
L3.Ribosome.Biogenesis	0.000	0.000	-1.308	0.207	0.000	0.000	0.079

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	0.078	0.076	1.022	0.320	-0.082	0.238	0.000
L3.Ribosome.biogenesis.in.eukaryotes	0.000	0.000	-1.155	0.262	0.000	0.000	0.063

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)	0	0.036	0	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	0.067	0.072	0.942	0.358	-0.082	0.217	0.000
L3.Secondary.bile.acid.biosynthesis	0.000	0.000	-1.088	0.290	0.000	0.000	0.056

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	0.09	0.07	1.298	0.21	-0.055	0.236	0.000
L3.Secretion.system	0.00	0.00	-1.500	0.15	0.000	0.000	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	0.094	0.077	1.213	0.240	-0.068	0.256	0.000
L3.Selenocompound.metabolism	0.000	0.000	-1.362	0.189	0.000	0.000	0.085

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)	0	0.036	0	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	0.011	0.039	0.291	0.774	-0.071	0.094	0.000
L3.Shigellosis	-0.006	0.008	-0.766	0.453	-0.022	0.010	0.028

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	0.095	0.07	1.354	0.192	-0.052	0.243	0.000
L3.Signal.transduction.mechanisms	0.000	0.00	-1.557	0.136	0.000	0.000	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	0	0.038	0.004	0.997	-0.079	0.079	0
L3.Small.cell.lung.cancer	0	0.000	-0.017	0.987	0.000	0.000	0

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	-0.036	0.084	-0.430	0.672	-0.213	0.14	0.000
L3.Sphingolipid.metabolism	0.000	0.000	0.477	0.639	0.000	0.00	0.011

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)	0	0.036	0	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	0.094	0.055	1.710	0.104	-0.021	0.209	0.000
L3.Sporulation	0.000	0.000	-2.143	0.045	0.000	0.000	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	0.038	0.053	0.716	0.483	-0.073	0.149	0.000
L3.Staphylococcus.aureus.infection	0.000	0.000	-0.972	0.343	0.000	0.000	0.045

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	0.069	0.074	0.933	0.362	-0.086	0.224	0.000
L3.Starch.and.sucrose.metabolism	0.000	0.000	-1.066	0.300	0.000	0.000	0.054

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	-0.004	0.041	-0.087	0.931	-0.089	0.082	0.000
L3.Steroid.biosynthesis	0.000	0.000	0.206	0.839	0.000	0.000	0.002

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	-0.078	0.054	-1.448	0.164	-0.192	0.035	0.000
L3.Steroid.hormone.biosynthesis	0.000	0.000	1.856	0.079	0.000	0.000	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	0.03	0.043	0.695	0.495	-0.061	0.121	0.
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	0.00	0.000	-1.212	0.240	0.000	0.000	0.

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	0.058	0.085	0.677	0.507	-0.121	0.236	0.000
L3.Streptomycin.biosynthesis	0.000	0.000	-0.748	0.464	0.000	0.000	0.027

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	0.097	0.051	1.899	0.073	-0.01	0.205	0.000
L3.Styrene.degradation	0.000	0.000	-2.439	0.025	0.00	0.000	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	0.061	0.084	0.721	0.480	-0.116	0.237	0.000
L3.Sulfur.metabolism	0.000	0.000	-0.798	0.435	0.000	0.000	0.031

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	0.106	0.069	1.554	0.137	-0.037	0.25	0.000
L3.Sulfur.relay.system	0.000	0.000	-1.792	0.089	0.000	0.00	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	0.076	0.065	1.168	0.257	-0.06	0.212	0.000
L3.Synthesis.and.degradation.of.ketone.bodies	0.000	0.000	-1.388	0.181	0.00	0.000	0.088

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	-0.001	0.042	-0.027	0.979	-0.089	0.087	0
L3.Systemic.lupus.erythematosus	0.000	0.000	0.056	0.956	0.000	0.000	0

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)	0	0.036	0	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	0.057	0.091	0.622	0.541	-0.134	0.248	0.000
L3.Taurine.and.hypotaurine.metabolism	0.000	0.000	-0.678	0.506	0.000	0.000	0.022

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	0.071	0.083	0.859	0.401	-0.102	0.244	0.000
L3.Terpenoid.backbone.biosynthesis	0.000	0.000	-0.955	0.352	0.000	0.000	0.044

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	0.092	0.07	1.327	0.200	-0.053	0.238	0.000
L3.Tetracycline.biosynthesis	0.000	0.00	-1.532	0.142	0.000	0.000	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	0.086	0.078	1.100	0.285	-0.078	0.25	0.000
L3.Thiamine.metabolism	0.000	0.000	-1.234	0.232	0.000	0.00	0.071

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)	0	0.036	0	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	0.014	0.063	0.218	0.830	-0.119	0.147	0.000
L3.Toluene.degradation	0.000	0.000	-0.267	0.792	0.000	0.000	0.004

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	0	0.038	0.004	0.997	-0.079	0.079	0
L3.Toxoplasmosis	0	0.000	-0.017	0.987	0.000	0.000	0

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	0.101	0.065	1.540	0.140	-0.036	0.238	0.00
L3.Transcription.factors	0.000	0.000	-1.804	0.087	0.000	0.000	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	0.061	0.084	0.726	0.476	-0.115	0.236	0.000
L3.Transcription.machinery	0.000	0.000	-0.805	0.431	0.000	0.000	0.031

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	0.052	0.042	1.231	0.233	-0.036	0.14	0.000
L3.Transcription.related.proteins	0.000	0.000	-2.018	0.058	0.000	0.00	0.169

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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	0.075	0.082	0.917	0.371	-0.096	0.246	0.00
L3.Translation.factors	0.000	0.000	-1.021	0.320	0.000	0.000	0.05

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	0.082	0.079	1.046	0.309	-0.083	0.247	0.000
L3.Translation.proteins	0.000	0.000	-1.172	0.256	0.000	0.000	0.064

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	0.1	0.063	1.571	0.133	-0.033	0.232	0.000
L3.Transporters	0.0	0.000	-1.860	0.078	0.000	0.000	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	0.059	0.084	0.704	0.490	-0.117	0.236	0
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis	0.000	0.000	-0.779	0.445	0.000	0.000	0

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	0.08	0.076	1.055	0.305	-0.079	0.239	0.000
L3.Tryptophan.metabolism	0.00	0.000	-1.194	0.247	0.000	0.000	0.067

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	0.067	0.079	0.853	0.404	-0.098	0.232	0.000
L3.Tuberculosis	0.000	0.000	-0.959	0.350	0.000	0.000	0.044

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	0.088	0.07	1.262	0.222	-0.058	0.235	0.000
L3.Two.component.system	0.000	0.00	-1.456	0.162	0.000	0.000	0.096

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	0.051	0.084	0.607	0.551	-0.125	0.227	0.000
L3.Type.I.diabetes.mellitus	0.000	0.000	-0.674	0.509	0.000	0.000	0.022

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	0.082	0.081	1.017	0.322	-0.087	0.251	0.00
L3.Type.II.diabetes.mellitus	0.000	0.000	-1.134	0.271	0.000	0.000	0.06

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	0.071	0.08	0.887	0.386	-0.096	0.238	0.000
L3.Tyrosine.metabolism	0.000	0.00	-0.993	0.333	0.000	0.000	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	-0.106	0.094	-1.124	0.275	-0.302	0.091	0.
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis	0.000	0.000	1.214	0.239	0.000	0.000	0.

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	-0.083	0.064	-1.303	0.208	-0.216	0.05	0.000
L3.Ubiquitin.system	0.000	0.000	1.554	0.137	0.000	0.00	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)	0	0.036	0	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	0.093	0.072	1.292	0.212	-0.058	0.243	0.000
L3.Valine..leucine.and.isoleucine.biosynthesis	0.000	0.000	-1.479	0.156	0.000	0.000	0.099

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	0.024	0.096	0.250	0.805	-0.176	0.224	0.000
L3.Valine..leucine.and.isoleucine.degradation	0.000	0.000	-0.271	0.789	0.000	0.000	0.004

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	-0.013	0.040	-0.331	0.744	-0.098	0.071	0.000
L3.Various.types.of.N.glycan.biosynthesis	0.001	0.001	0.752	0.461	-0.002	0.004	0.027

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)	0	0.036	0	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	0.000	0.039	0.004	0.997	-0.082	0.082	0
L3.Vasopressin.regulated.water.reabsorption	-0.001	0.054	-0.013	0.989	-0.114	0.112	0

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	0.017	0.036	0.476	0.640	-0.059	0.093	0.000
L3.Vibrio.cholerae.infection	-0.036	0.023	-1.603	0.125	-0.084	0.011	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	0.091	0.077	1.171	0.256	-0.071	0.253	0.00
L3.Vibrio.cholerae.pathogenic.cycle	0.000	0.000	-1.315	0.204	0.000	0.000	0.08

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	0	0.038	0.004	0.997	-0.079	0.079	0
L3.Viral.myocarditis	0	0.000	-0.017	0.987	0.000	0.000	0

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	0.032	0.086	0.372	0.714	-0.148	0.212	0.000
L3.Vitamin.B6.metabolism	0.000	0.000	-0.411	0.686	0.000	0.000	0.008

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)	0	0.036	0	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	0.08	0.056	1.439	0.167	-0.037	0.197	0.000
L3.Xylene.degradation	0.00	0.000	-1.815	0.085	0.000	0.000	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	0.017	0.091	0.189	0.852	-0.173	0.207	0.000
L3.Zeatin.biosynthesis	0.000	0.000	-0.207	0.838	0.000	0.000	0.002

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	0.075	0.047	1.592	0.128	-0.024	0.173	0.000
L3.alpha.Linolenic.acid.metabolism	0.000	0.000	-2.226	0.038	0.000	0.000	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	0.099	0.078	1.258	0.224	-0.066	0.263	0.00
L3.beta.Alanine.metabolism	0.000	0.000	-1.406	0.176	0.000	0.000	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	0.1	0.062	1.614	0.123	-0.03	0.231	0.000
L3.beta.Lactam.resistance	0.0	0.000	-1.921	0.070	0.00	0.000	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)	0	0.036	0	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)	0	0.036	0	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	0	0.038	0.004	0.997	-0.079	0.079	0
L3.p53.signaling.pathway	0	0.000	-0.017	0.987	0.000	0.000	0

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 %	9
Intercept	0.027	0.026	1.043	0.310	-0.027	
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	0.000	0.000	-2.100	0.049	0.000	

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	0.018	0.046	0.389	0.702	-0.078	0.113	0.000
L3.ABC.transporters	0.000	0.000	-0.462	0.650	0.000	0.000	0.011

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)	0	0.024	0	1	-0.05	0.05	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	0.034	0.055	0.609	0.550	-0.082	0.149	0.000
L3.Adipocytokine.signaling.pathway	0.000	0.000	-0.681	0.504	0.000	0.000	0.023

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	0.03	0.032	0.94	0.359	-0.037	0.097	0.000
L3.African.trypanosomiasis	0.00	0.000	-1.39	0.181	0.000	0.000	0.088

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	0.028	0.057	0.493	0.627	-0.092	0.148	0.000
L3.Alanine..aspartate.and.glutamate.metabolism	0.000	0.000	-0.546	0.591	0.000	0.000	0.015

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)	0	0.024	0	1	-0.05	0.05	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	0.027	0.048	0.553	0.586	-0.075	0.128	0.00
L3.Alzheimer.s.disease	0.000	0.000	-0.642	0.528	0.000	0.000	0.02

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	0.008	0.051	0.165	0.870	-0.098	0.114	0.000
L3.Amino.acid.metabolism	0.000	0.000	-0.190	0.851	0.000	0.000	0.002

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	0.027	0.055	0.491	0.629	-0.088	0.142	0.000
L3.Amino.acid.related.enzymes	0.000	0.000	-0.549	0.589	0.000	0.000	0.015

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	0.02	0.056	0.347	0.732	-0.098	0.137	0.000
L3.Amino.sugar.and.nucleotide.sugar.metabolism	0.00	0.000	-0.386	0.703	0.000	0.000	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	0.03	0.051	0.595	0.559	-0.076	0.137	0.000
L3.Aminoacyl.tRNA.biosynthesis	0.00	0.000	-0.678	0.506	0.000	0.000	0.022

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	0.024	0.057	0.427	0.674	-0.095	0.144	0.000
L3.Aminobenzoate.degradation	0.000	0.000	-0.474	0.641	0.000	0.000	0.011

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	0.031	0.037	0.848	0.407	-0.046	0.108	0.000
L3.Amoebiasis	0.000	0.000	-1.125	0.275	0.000	0.000	0.059

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	0.029	0.041	0.703	0.491	-0.057	0.115	0.000
L3.Amyotrophic.lateral.sclerosis..ALS.	0.000	0.000	-0.873	0.393	0.000	0.000	0.037

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	0.028	0.054	0.527	0.605	-0.084	0.141	0.000
L3.Antigen.processing.and.presentation	0.000	0.000	-0.592	0.561	0.000	0.000	0.017

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	0.015	0.027	0.576	0.572	-0.041	0.072	0.000
L3.Apoptosis	0.000	0.000	-1.256	0.224	0.000	0.000	0.073

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	0.02	0.062	0.324	0.749	-0.109	0.149	0.000
L3.Arachidonic.acid.metabolism	0.00	0.000	-0.354	0.727	0.000	0.000	0.006

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	0.021	0.055	0.383	0.706	-0.094	0.137	0.000
L3.Arginine.and.proline.metabolism	0.000	0.000	-0.428	0.673	0.000	0.000	0.009

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)	0	0.024	0	1	-0.05	0.05	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	0.023	0.05	0.463	0.648	-0.082	0.129	0.000
L3.Ascorbate.and.aldarate.metabolism	0.000	0.00	-0.532	0.601	0.000	0.000	0.014

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	0.002	0.037	0.042	0.967	-0.076	0.079	0
L3.Atrazine.degradation	0.000	0.000	-0.056	0.956	0.000	0.000	0

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	0.016	0.042	0.376	0.711	-0.072	0.103	0.000
L3.Bacterial.chemotaxis	0.000	0.000	-0.467	0.646	0.000	0.000	0.011

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	0.012	0.032	0.362	0.721	-0.056	0.079	0.000
L3.Bacterial.invasion.of.epithelial.cells	0.000	0.000	-0.564	0.579	0.000	0.000	0.016

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	0.022	0.039	0.565	0.579	-0.06	0.104	0.000
L3.Bacterial.motility.proteins	0.000	0.000	-0.723	0.479	0.00	0.000	0.025

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	0.04	0.055	0.716	0.483	-0.076	0.155	0.000
L3.Bacterial.secretion.system	0.00	0.000	-0.798	0.435	0.000	0.000	0.031

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	0.014	0.056	0.243	0.811	-0.104	0.132	0.000
L3.Bacterial.toxins	0.000	0.000	-0.270	0.790	0.000	0.000	0.004

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	0.011	0.027	0.388	0.702	-0.046	0.067	0.000
L3.Basal.transcription.factors	0.000	0.000	-0.888	0.386	0.000	0.000	0.038

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	0.024	0.053	0.449	0.659	-0.088	0.135	0.000
L3.Base.excision.repair	0.000	0.000	-0.506	0.618	0.000	0.000	0.013

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	0.021	0.051	0.42	0.679	-0.085	0.128	0.000
L3.Benzoate.degradation	0.000	0.000	-0.48	0.636	0.000	0.000	0.011

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	-0.007	0.026	-0.265	0.794	-0.062	0.048	0.000
L3.Betalain.biosynthesis	0.001	0.001	0.748	0.464	-0.002	0.004	0.027

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	-0.004	0.025	-0.173	0.864	-0.057	0.048	0.000
L3.Bile.secretion	0.091	0.115	0.795	0.437	-0.149	0.331	0.031

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	0.022	0.055	0.399	0.694	-0.093	0.137
L3.Biosynthesis.and.biodegradation.of.secondary.metabolites	0.000	0.000	-0.446	0.660	0.000	0.000

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)	0	0.024	0	1	-0.05	0.05	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	0.015	0.05	0.294	0.772	-0.09	0.12	0.000
L3.Biosynthesis.of.ansamycins	0.000	0.00	-0.338	0.739	0.00	0.00	0.006

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	-0.018	0.065	-0.275	0.786	-0.153	0.117
L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides	0.000	0.000	0.298	0.769	0.000	0.000

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)	0	0.024	0	1	-0.05	0.05	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	-0.007	0.026	-0.265	0.794	-0.062	0.048	0.000
L3.Biosynthesis.of.type.II.polyketide.products	0.001	0.001	0.701	0.491	-0.002	0.004	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	0.029	0.051	0.579	0.569	-0.076	0.135	0.000
L3.Biosynthesis.of.unsaturated.fatty.acids	0.000	0.000	-0.663	0.515	0.000	0.000	0.021

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	0.021	0.062	0.334	0.742	-0.109	0.15	0.000
L3.Biosynthesis.of.vancomycin.group.antibiotics	0.000	0.000	-0.365	0.719	0.000	0.00	0.007

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	0.021	0.054	0.377	0.710	-0.093	0.134	0.000
L3.Biotin.metabolism	0.000	0.000	-0.423	0.677	0.000	0.000	0.009

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	0.022	0.053	0.420	0.679	-0.088	0.132	0.000
L3.Bisphenol.degradation	0.000	0.000	-0.476	0.640	0.000	0.000	0.011

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	0.003	0.031	0.099	0.922	-0.062	0.069	0.000
L3.Bladder.cancer	0.000	0.000	-0.163	0.872	0.000	0.000	0.001

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	0.035	0.053	0.659	0.518	-0.076	0.146	0.000
L3.Butanoate.metabolism	0.000	0.000	-0.743	0.467	0.000	0.000	0.027

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	0.037	0.05	0.752	0.461	-0.067	0.141	0.000
L3.Butirosin.and.neomycin.biosynthesis	0.000	0.00	-0.863	0.399	0.000	0.000	0.036

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	0.026	0.049	0.535	0.599	-0.077	0.13	0.000
L3.C5.Branched.dibasic.acid.metabolism	0.000	0.000	-0.617	0.545	0.000	0.00	0.019

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)	0	0.024	0	1	-0.05	0.05	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	-0.002	0.027	-0.070	0.945	-0.059	0.055	0.000
L3.Caffeine.metabolism	0.000	0.000	0.169	0.868	0.000	0.000	0.001

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	0.005	0.026	0.193	0.849	-0.050	0.060	0.000
L3.Calcium.signaling.pathway	-0.001	0.002	-0.580	0.569	-0.006	0.003	0.017

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	0.036	0.043	0.832	0.416	-0.054	0.126	0.000
L3.Caprolactam.degradation	0.000	0.000	-1.007	0.327	0.000	0.000	0.048

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	0.043	0.043	0.997	0.331	-0.047	0.133	0.000
L3.Carbohydrate.digestion.and.absorption	0.000	0.000	-1.201	0.245	0.000	0.000	0.067

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	0.049	0.052	0.956	0.351	-0.059	0.157	0.000
L3.Carbohydrate.metabolism	0.000	0.000	-1.081	0.293	0.000	0.000	0.055

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	0.024	0.056	0.427	0.674	-0.093	0.14	0.000
L3.Carbon.fixation.in.photosynthetic.organisms	0.000	0.000	-0.476	0.640	0.000	0.00	0.011

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	0.041	0.058	0.703	0.491	-0.08	0.162	0.000
L3.Carbon.fixation.pathways.in.prokaryotes	0.000	0.000	-0.776	0.448	0.00	0.000	0.029

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	0.006	0.025	0.245	0.809	-0.046	0.058	0.00
L3.Cardiac.muscle.contraction	0.000	0.000	-1.025	0.318	0.000	0.000	0.05

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	-0.006	0.035	-0.182	0.857	-0.08	0.067	0.000
L3.Carotenoid.biosynthesis	0.000	0.000	0.257	0.800	0.00	0.000	0.003

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)	0	0.024	0	1	-0.05	0.05	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	0.027	0.055	0.485	0.633	-0.088	0.142	0.000
L3.Cell.cycle. . . Caulobacter	0.000	0.000	-0.543	0.594	0.000	0.000	0.015

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)	0	0.024	0	1	-0.05	0.05	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	0.02	0.054	0.362	0.721	-0.093	0.133	0.000
L3.Cell.division	0.00	0.000	-0.407	0.688	0.000	0.000	0.008

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	0.041	0.058	0.702	0.491	-0.081	0.162	0.000
L3.Cell.motility.and.secretion	0.000	0.000	-0.775	0.448	0.000	0.000	0.029

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	-0.006	0.052	-0.106	0.917	-0.115	0.104	0.000
L3.Cellular.antigens	0.000	0.000	0.120	0.905	0.000	0.000	0.001

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	0.032	0.031	1.061	0.302	-0.032	0.097	0.000
L3.Chagas.disease..American.trypanosomiasis.	0.000	0.000	-1.631	0.119	0.000	0.000	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	0.031	0.058	0.530	0.602	-0.09	0.152	0.000
L3.Chaperones.and.folding.catalysts	0.000	0.000	-0.586	0.565	0.00	0.000	0.017

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	0.021	0.048	0.433	0.67	-0.08	0.122	0.000
L3.Chloroalkane.and.chloroalkene.degradation	0.000	0.000	-0.504	0.62	0.00	0.000	0.013

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 %	R2
Intercept	0.005	0.039	0.124	0.903	-0.076	0.086	0.000
L3.Chlorocyclohexane.and.chlorobenzene.degradation	0.000	0.000	-0.162	0.873	0.000	0.000	0.001

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)	0	0.024	0	1	-0.05	0.05	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	0.028	0.054	0.520	0.609	-0.086	0.142	0.000
L3.Chromosome	0.000	0.000	-0.583	0.566	0.000	0.000	0.017

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)	0	0.024	0	1	-0.05	0.05	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	-0.002	0.027	-0.070	0.945	-0.059	0.055	0.000
L3.Circadian.rhythm...plant	0.000	0.000	0.168	0.868	0.000	0.000	0.001

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	0.056	0.058	0.968	0.345	-0.065	0.178	0.000
L3.Citrate.cycle..TCA.cycle.	0.000	0.000	-1.064	0.301	0.000	0.000	0.054

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	0.002	0.025	0.070	0.945	-0.051	0.055	0.000
L3.Clavulanic.acid.biosynthesis	-0.019	0.058	-0.319	0.753	-0.140	0.103	0.005

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	0.005	0.025	0.214	0.832	-0.047	0.057	0.000
L3.Colorectal.cancer	0.000	0.000	-0.979	0.340	0.000	0.000	0.046

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)	0	0.024	0	1	-0.05	0.05	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	0.041	0.049	0.829	0.417	-0.062	0.144	0.000
L3.Cyanoamino.acid.metabolism	0.000	0.000	-0.952	0.353	0.000	0.000	0.043

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	0.029	0.055	0.525	0.605	-0.086	0.144	0.000
L3.Cysteine.and.methionine.metabolism	0.000	0.000	-0.588	0.563	0.000	0.000	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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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	0.023	0.049	0.460	0.651	-0.08	0.125	0.000
L3.Cytoskeleton.proteins	0.000	0.000	-0.532	0.601	0.00	0.000	0.014

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)	0	0.024	0	1	-0.05	0.05	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	0.025	0.054	0.471	0.643	-0.087	0.138	0.000
L3.D.Alanine.metabolism	0.000	0.000	-0.530	0.602	0.000	0.000	0.014

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	-0.001	0.037	-0.032	0.975	-0.079	0.077	0
L3.D.Arginine.and.D.ornithine.metabolism	0.000	0.000	0.043	0.966	0.000	0.000	0

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	0.037	0.057	0.642	0.528	-0.083	0.157	0.000
L3.D.Glutamine.and.D.glutamate.metabolism	0.000	0.000	-0.710	0.486	0.000	0.000	0.025

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	0.029	0.055	0.527	0.604	-0.086	0.145	0.000
L3.DNA.repair.and.recombination.proteins	0.000	0.000	-0.589	0.563	0.000	0.000	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	0.027	0.057	0.475	0.640	-0.092	0.146	0.000
L3.DNA.replication	0.000	0.000	-0.527	0.605	0.000	0.000	0.014

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	0.025	0.056	0.436	0.668	-0.093	0.143	0.000
L3.DNA.replication.proteins	0.000	0.000	-0.485	0.633	0.000	0.000	0.012

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)	0	0.024	0	1	-0.05	0.05	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	0.024	0.041	0.581	0.568	-0.062	0.11	0.000
L3.Dioxin.degradation	0.000	0.000	-0.721	0.480	0.000	0.00	0.025

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	0.055	0.045	1.222	0.237	-0.039	0.149	0.000
L3.Drug.metabolism...cytochrome.P450	0.000	0.000	-1.435	0.168	0.000	0.000	0.093

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	0.013	0.059	0.216	0.831	-0.11	0.136	0.000
L3.Drug.metabolism...other.enzymes	0.000	0.000	-0.238	0.815	0.00	0.000	0.003

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)	0	0.024	0	1	-0.05	0.05	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	0.019	0.038	0.497	0.625	-0.061	0.1	0.00
L3.Electron.transfer.carriers	0.000	0.000	-0.646	0.526	0.000	0.0	0.02

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)	0	0.024	0	1	-0.05	0.05	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	0.008	0.025	0.317	0.755	-0.045	0.061	0.000
L3.Endocytosis	-0.056	0.052	-1.081	0.293	-0.164	0.052	0.055

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	0.029	0.057	0.507	0.618	-0.091	0.149	0.000
L3.Energy.metabolism	0.000	0.000	-0.561	0.581	0.000	0.000	0.016

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	0.018	0.051	0.358	0.724	-0.088	0.124	
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	0.000	0.000	-0.410	0.686	0.000	0.000	

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)	0	0.024	0	1	-0.05	0.05	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	0.001	0.036	0.033	0.974	-0.074	0.076	0
L3.Ether.lipid.metabolism	0.000	0.000	-0.045	0.964	0.000	0.000	0

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	0.015	0.055	0.279	0.783	-0.099	0.13	0.000
L3.Ethylbenzene.degradation	0.000	0.000	-0.313	0.758	0.000	0.00	0.005

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)	0	0.024	0	1	-0.05	0.05	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	0.041	0.054	0.753	0.461	-0.073	0.155	0.000
L3.Fatty.acid.biosynthesis	0.000	0.000	-0.842	0.410	0.000	0.000	0.034

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	-0.002	0.027	-0.070	0.945	-0.059	0.055	0.000
L3.Fatty.acid.elongation.in.mitochondria	0.000	0.000	0.169	0.868	0.000	0.000	0.001

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	0.027	0.055	0.495	0.626	-0.088	0.142	0.000
L3.Fatty.acid.metabolism	0.000	0.000	-0.554	0.586	0.000	0.000	0.015

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)	0	0.024	0	1	-0.05	0.05	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	0.008	0.025	0.317	0.755	-0.045	0.061	0.000
L3.Fc.gamma.R.mediated.phagocytosis	-0.056	0.052	-1.081	0.293	-0.164	0.052	0.055

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	0.021	0.037	0.573	0.573	-0.056	0.098	0.000
L3.Flagellar.assembly	0.000	0.000	-0.768	0.452	0.000	0.000	0.029

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	-0.002	0.047	-0.046	0.963	-0.1	0.096	0
L3.Flavone.and.flavonol.biosynthesis	0.000	0.000	0.055	0.957	0.0	0.000	0

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	0.015	0.035	0.437	0.667	-0.057	0.087	0.000
L3.Flavonoid.biosynthesis	0.000	0.000	-0.622	0.541	0.000	0.000	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	-0.006	0.034	-0.164	0.872	-0.077	0.066	0.000
L3.Fluorobenzoate.degradation	0.000	0.000	0.238	0.814	0.000	0.000	0.003

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)	0	0.024	0	1	-0.05	0.05	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	0.026	0.06	0.426	0.675	-0.101	0.152	0.000
L3.Folate.biosynthesis	0.000	0.00	-0.466	0.646	0.000	0.000	0.011

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	0.016	0.053	0.295	0.771	-0.095	0.126	0.000
L3.Fructose.and.mannose.metabolism	0.000	0.000	-0.334	0.742	0.000	0.000	0.006

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	0.038	0.053	0.719	0.481	-0.073	0.149	0.000
L3.Function.unknown	0.000	0.000	-0.810	0.428	0.000	0.000	0.032

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	0.002	0.028	0.074	0.942	-0.056	0.060	0.000
L3.G.protein.coupled.receptors	-0.002	0.010	-0.162	0.873	-0.021	0.018	0.001

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)	0	0.024	0	1	-0.05	0.05	0
	NA	NA	NA	NA	NA	NA	0

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	0.037	0.054	0.679	0.506	-0.077	0.15	0.000
L3.Galactose.metabolism	0.000	0.000	-0.761	0.456	0.000	0.00	0.028

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)	0	0.024	0	1	-0.05	0.05	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	0.027	0.056	0.484	0.634	-0.089	0.143	0.000
L3.General.function.prediction.only	0.000	0.000	-0.540	0.595	0.000	0.000	0.014

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	0.019	0.062	0.313	0.758	-0.11	0.149	0.000
L3.Geraniol.degradation	0.000	0.000	-0.341	0.737	0.00	0.000	0.006

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	0.011	0.039	0.285	0.778	-0.07	0.092	0.000
L3.Germination	0.000	0.000	-0.371	0.714	0.00	0.000	0.007

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)	0	0.024	0	1	-0.05	0.05	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	0.031	0.055	0.553	0.587	-0.085	0.146	0.000
L3.Glutamatergic.synapse	0.000	0.000	-0.617	0.544	0.000	0.000	0.019

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	0.037	0.066	0.564	0.579	-0.101	0.176	0.000
L3.Glutathione.metabolism	0.000	0.000	-0.608	0.551	0.000	0.000	0.018

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)	0	0.024	0	1	-0.05	0.05	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	0.074	0.048	1.560	0.135	-0.025	0.174	0.000
L3.Glycan.biosynthesis.and.metabolism	0.000	0.000	-1.782	0.091	0.000	0.000	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	0.034	0.047	0.713	0.484	-0.065	0.133	0.000
L3.Glycerolipid.metabolism	0.000	0.000	-0.832	0.416	0.000	0.000	0.033

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	0.028	0.051	0.559	0.583	-0.078	0.135	0.00
L3.Glycerophospholipid.metabolism	0.000	0.000	-0.638	0.531	0.000	0.000	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	0.019	0.058	0.335	0.741	-0.102	0.14	0.000
L3.Glycine..serine.and.threonine.metabolism	0.000	0.000	-0.371	0.715	0.000	0.00	0.007

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	0.024	0.054	0.455	0.654	-0.088	0.137	0.000
L3.Glycolysis...Gluconeogenesis	0.000	0.000	-0.511	0.615	0.000	0.000	0.013

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	0.006	0.025	0.227	0.823	-0.046	0.058	0
L3.Glycosaminoglycan.biosynthesis...chondroitin.sulfate	-0.004	0.004	-1.002	0.329	-0.013	0.005	0

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	-0.004	0.049	-0.079	0.938	-0.106	0.098	0
L3.Glycosaminoglycan.degradation	0.000	0.000	0.092	0.928	0.000	0.000	0

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	-0.008	0.044	-0.187	0.854	-0.101	0.084	0.000
L3.Glycosphingolipid.biosynthesis...ganglio.series	0.000	0.000	0.226	0.824	0.000	0.000	0.003

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	0.027	0.055	0.497	0.625	-0.087	0.142	0.000
L3.Glycosphingolipid.biosynthesis...globo.series	0.000	0.000	-0.557	0.584	0.000	0.000	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	-0.006	0.026	-0.226	0.824	-0.061	0.049
L3.Glycosphingolipid.biosynthesis...lacto.and.neolacto.series	0.000	0.000	0.642	0.528	0.000	0.000

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)	0	0.024	0	1	-0.05	0.05	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	0.033	0.061	0.543	0.594	-0.095	0.162	0.000
L3.Glycosyltransferases	0.000	0.000	-0.592	0.561	0.000	0.000	0.017

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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	0.025	0.055	0.463	0.649	-0.089	0.14	0.000
L3.Glyoxylate.and.dicarboxylate.metabolism	0.000	0.000	-0.518	0.610	0.000	0.00	0.013

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	0.008	0.025	0.317	0.755	-0.045	0.061	0.000
L3.GnRH.signaling.pathway	-0.056	0.052	-1.081	0.293	-0.164	0.052	0.055

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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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	0.031	0.056	0.546	0.591	-0.087	0.148	0.000
L3.Histidine.metabolism	0.000	0.000	-0.608	0.550	0.000	0.000	0.018

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	0.031	0.056	0.550	0.589	-0.086	0.147	0.000
L3.Homologous.recombination	0.000	0.000	-0.612	0.548	0.000	0.000	0.018

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	0.04	0.05	0.804	0.432	-0.065	0.145	0.00
L3.Huntington.s.disease	0.00	0.00	-0.918	0.370	0.000	0.000	0.04

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	0.005	0.025	0.222	0.827	-0.046	0.057	0.000
L3.Hypertrophic.cardiomyopathy..HCM.	-0.016	0.016	-1.017	0.322	-0.050	0.017	0.049

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)	0	0.024	0	1	-0.05	0.05	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	0.005	0.025	0.214	0.832	-0.047	0.057	0.000
L3.Influenza.A	0.000	0.000	-0.979	0.340	0.000	0.000	0.046

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	0.044	0.055	0.801	0.433	-0.07	0.158	0.000
L3.Inorganic.ion.transport.and.metabolism	0.000	0.000	-0.895	0.382	0.00	0.000	0.039

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	0.023	0.057	0.409	0.687	-0.096	0.142	0.00
L3.Inositol.phosphate.metabolism	0.000	0.000	-0.454	0.655	0.000	0.000	0.01

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	0.04	0.049	0.810	0.428	-0.063	0.142	0.000
L3.Insulin.signaling.pathway	0.00	0.000	-0.933	0.363	0.000	0.000	0.042

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	0.025	0.059	0.431	0.671	-0.098	0.149	0.000
L3.Ion.channels	0.000	0.000	-0.474	0.641	0.000	0.000	0.011

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	0.01	0.025	0.407	0.689	-0.042	0.062	0.000
L3.Isoflavonoid.biosynthesis	-0.07	0.051	-1.389	0.181	-0.177	0.036	0.088

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	0.009	0.065	0.133	0.896	-0.127	0.144	0.000
L3.Isoquinoline.alkaloid.biosynthesis	0.000	0.000	-0.144	0.887	0.000	0.000	0.001

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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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	0.022	0.055	0.396	0.697	-0.093	0.137	0.00
L3.Limonene.and.pinene.degradation	0.000	0.000	-0.443	0.663	0.000	0.000	0.01

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	0.031	0.052	0.595	0.559	-0.078	0.14	0.000
L3.Linoleic.acid.metabolism	0.000	0.000	-0.674	0.508	0.000	0.00	0.022

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	0.042	0.056	0.756	0.459	-0.075	0.16	0.000
L3.Lipid.biosynthesis.proteins	0.000	0.000	-0.839	0.412	0.000	0.00	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	0.035	0.048	0.720	0.481	-0.066	0.136	0.000
L3.Lipid.metabolism	0.000	0.000	-0.834	0.415	0.000	0.000	0.034

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	0.017	0.053	0.317	0.755	-0.094	0.127	0.000
L3.Lipoic.acid.metabolism	0.000	0.000	-0.359	0.724	0.000	0.000	0.006

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	0.034	0.058	0.592	0.561	-0.086	0.155	0.000
L3.Lipopolysaccharide.biosynthesis	0.000	0.000	-0.654	0.521	0.000	0.000	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	0.035	0.062	0.574	0.572	-0.094	0.164	0.000
L3.Lipopolysaccharide.biosynthesis.proteins	0.000	0.000	-0.626	0.538	0.000	0.000	0.019

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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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	0.022	0.052	0.414	0.683	-0.088	0.131	0.000
L3.Lysine.biosynthesis	0.000	0.000	-0.470	0.644	0.000	0.000	0.011

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	0.028	0.057	0.492	0.629	-0.092	0.148	0.000
L3.Lysine.degradation	0.000	0.000	-0.545	0.592	0.000	0.000	0.015

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	0.003	0.053	0.048	0.962	-0.109	0.114	0
L3.Lysosome	0.000	0.000	-0.054	0.957	0.000	0.000	0

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)	0	0.024	0	1	-0.05	0.05	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	-0.002	0.06	-0.036	0.972	-0.127	0.123	0
L3.MAPK.signaling.pathway...yeast	0.000	0.00	0.039	0.969	0.000	0.000	0

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)	0	0.024	0	1	-0.05	0.05	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	0.03	0.023	1.300	0.209	-0.018	0.079	0.000
L3.Meiosis...yeast	0.00	0.000	-2.891	0.009	0.000	0.000	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	-0.007	0.026	-0.265	0.794	-0.062	0.048	0.000
L3.Melanogenesis	0.001	0.001	0.748	0.464	-0.002	0.004	0.027

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	0.039	0.062	0.632	0.535	-0.09	0.169	0.000
L3.Membrane.and.intracellular.structural.molecules	0.000	0.000	-0.689	0.499	0.00	0.000	0.023

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	0.032	0.048	0.664	0.515	-0.069	0.132	0.000
L3.Metabolism.of.cofactors.and.vitamins	0.000	0.000	-0.771	0.450	0.000	0.000	0.029

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	0.055	0.045	1.230	0.234	-0.038	0.148	0.000
L3.Metabolism.of.xenobiotics.by.cytochrome.P450	0.000	0.000	-1.448	0.164	0.000	0.000	0.095

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	0.019	0.053	0.357	0.725	-0.091	0.129	0.000
L3.Methane.metabolism	0.000	0.000	-0.404	0.691	0.000	0.000	0.008

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	-0.005	0.035	-0.137	0.893	-0.079	0.069	0.000
L3.Mineral.absorption	0.000	0.000	0.191	0.850	0.000	0.000	0.002

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	0.028	0.055	0.504	0.620	-0.087	0.142	0.000
L3.Mismatch.repair	0.000	0.000	-0.564	0.579	0.000	0.000	0.016

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	-0.023	0.056	-0.419	0.680	-0.141	0.094	0.000
L3.N.Glycan.biosynthesis	0.000	0.000	0.467	0.646	0.000	0.000	0.011

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	0.025	0.056	0.452	0.657	-0.092	0.143	0.000
L3.NOD.like.receptor.signaling.pathway	0.000	0.000	-0.502	0.621	0.000	0.000	0.012

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	0.026	0.055	0.474	0.641	-0.089	0.142	0.000
L3.Naphthalene.degradation	0.000	0.000	-0.530	0.602	0.000	0.000	0.014

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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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	0.032	0.055	0.588	0.564	-0.083	0.147	0.000
L3.Nicotinate.and.nicotinamide.metabolism	0.000	0.000	-0.657	0.519	0.000	0.000	0.021

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	0.029	0.059	0.499	0.624	-0.094	0.153	0.000
L3.Nitrogen.metabolism	0.000	0.000	-0.549	0.590	0.000	0.000	0.015

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	0.017	0.041	0.409	0.687	-0.069	0.102	0.000
L3.Nitrotoluene.degradation	0.000	0.000	-0.512	0.614	0.000	0.000	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	0.016	0.036	0.458	0.652	-0.059	0.091	0.000
L3.Non.homologous.end.joining	0.000	0.000	-0.629	0.537	0.000	0.000	0.019

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)	0	0.024	0	1	-0.05	0.05	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	0.028	0.055	0.507	0.618	-0.087	0.143	0.000
L3.Novobiocin.biosynthesis	0.000	0.000	-0.567	0.577	0.000	0.000	0.016

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	0.033	0.053	0.619	0.543	-0.078	0.144	0.000
L3.Nucleotide.excision.repair	0.000	0.000	-0.698	0.494	0.000	0.000	0.024

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	0.031	0.043	0.717	0.482	-0.059	0.121	0.000
L3.Nucleotide.metabolism	0.000	0.000	-0.869	0.396	0.000	0.000	0.036

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)	0	0.024	0	1	-0.05	0.05	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	0.026	0.058	0.454	0.655	-0.095	0.148	0.000
L3.One.carbon.pool.by.folate	0.000	0.000	-0.501	0.622	0.000	0.000	0.012

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)	0	0.024	0	1	-0.05	0.05	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	0.024	0.06	0.402	0.692	-0.101	0.149	0.00
L3.Other.glycan.degradation	0.000	0.00	-0.442	0.663	0.000	0.000	0.01

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	0.033	0.059	0.564	0.579	-0.09	0.156	0.000
L3.Other.ion.coupled.transporters	0.000	0.000	-0.621	0.542	0.00	0.000	0.019

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	0.035	0.055	0.631	0.535	-0.081	0.15	0.000
L3.Other.transporters	0.000	0.000	-0.705	0.490	0.000	0.00	0.024

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)	0	0.024	0	1	-0.05	0.05	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	0.04	0.054	0.740	0.468	-0.073	0.154	0.000
L3.Others	0.00	0.000	-0.828	0.418	0.000	0.000	0.033

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	0.032	0.054	0.596	0.558	-0.082	0.146	0.000
L3.Oxidative.phosphorylation	0.000	0.000	-0.668	0.512	0.000	0.000	0.022

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	0.031	0.059	0.520	0.609	-0.093	0.155	0.000
L3.PPAR.signaling.pathway	0.000	0.000	-0.572	0.574	0.000	0.000	0.016

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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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	0.023	0.053	0.434	0.669	-0.088	0.134	0.000
L3.Pantothenate.and.CoA.biosynthesis	0.000	0.000	-0.491	0.629	0.000	0.000	0.012

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	0.006	0.025	0.238	0.814	-0.046	0.058	0.000
L3.Parkinson.s.disease	0.000	0.000	-1.016	0.322	0.000	0.000	0.049

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)	0	0.024	0	1	-0.05	0.05	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	0.038	0.052	0.740	0.468	-0.07	0.147	0.000
L3.Pathways.in.cancer	0.000	0.000	-0.839	0.412	0.00	0.000	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	0.023	0.053	0.437	0.667	-0.087	0.133	0.000
L3.Penicillin.and.cephalosporin.biosynthesis	0.000	0.000	-0.495	0.626	0.000	0.000	0.012

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	0.022	0.056	0.390	0.701	-0.095	0.139	0.000
L3.Pentose.and.glucuronate.interconversions	0.000	0.000	-0.435	0.669	0.000	0.000	0.009

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	0.02	0.053	0.382	0.707	-0.091	0.132	0.000
L3.Pentose.phosphate.pathway	0.00	0.000	-0.431	0.672	0.000	0.000	0.009

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	0.029	0.056	0.518	0.61	-0.088	0.146	0.000
L3.Peptidases	0.000	0.000	-0.578	0.57	0.000	0.000	0.016

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	0.028	0.054	0.517	0.611	-0.084	0.14	0.000
L3.Peptidoglycan.biosynthesis	0.000	0.000	-0.582	0.567	0.000	0.00	0.017

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	0.031	0.06	0.522	0.608	-0.095	0.158	0.000
L3.Peroxisome	0.000	0.00	-0.571	0.574	0.000	0.000	0.016

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	-0.031	0.057	-0.55	0.589	-0.15	0.088	0.000
L3.Pertussis	0.000	0.000	0.61	0.549	0.00	0.000	0.018

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)	0	0.024	0	1	-0.05	0.05	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	0.043	0.056	0.765	0.454	-0.075	0.161	0.000
L3.Phenylalanine.metabolism	0.000	0.000	-0.848	0.407	0.000	0.000	0.035

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	0.027	0.052	0.511	0.615	-0.083	0.136	0.0
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis	0.000	0.000	-0.579	0.570	0.000	0.000	0.0

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	0.04	0.045	0.898	0.381	-0.054	0.134	0.000
L3.Phenylpropanoid.biosynthesis	0.00	0.000	-1.064	0.300	0.000	0.000	0.054

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	0.043	0.059	0.725	0.477	-0.08	0.165	0.000
L3.Phosphatidylinositol.signaling.system	0.000	0.000	-0.797	0.435	0.00	0.000	0.031

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	0.052	0.052	0.991	0.334	-0.058	0.162	0.000
L3.Phosphonate.and.phosphinate.metabolism	0.000	0.000	-1.114	0.279	0.000	0.000	0.058

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	0.007	0.039	0.178	0.861	-0.076	0.09	0.000
L3.Phosphotransferase.system..PTS.	0.000	0.000	-0.228	0.822	0.000	0.00	0.003

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	0.021	0.048	0.446	0.660	-0.079	0.122	0.000
L3.Photosynthesis	0.000	0.000	-0.520	0.609	0.000	0.000	0.013

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	0.005	0.026	0.197	0.846	-0.05	0.06	0.000
L3.Photosynthesis. . . antenna.proteins	0.000	0.000	-0.587	0.564	0.00	0.00	0.017

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	0.022	0.048	0.456	0.654	-0.079	0.122	0.000
L3.Photosynthesis.proteins	0.000	0.000	-0.531	0.602	0.000	0.000	0.014

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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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	0.029	0.049	0.584	0.566	-0.074	0.132	0.000
L3.Plant.pathogen.interaction	0.000	0.000	-0.673	0.509	0.000	0.000	0.022

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	0.028	0.053	0.517	0.611	-0.084	0.139	0.000
L3.Polycyclic.aromatic.hydrocarbon.degradation	0.000	0.000	-0.582	0.567	0.000	0.000	0.017

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	0.026	0.059	0.445	0.661	-0.097	0.15	0.000
L3.Polyketide.sugar.unit.biosynthesis	0.000	0.000	-0.490	0.630	0.000	0.00	0.012

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	0.032	0.066	0.481	0.636	-0.106	0.169	0.000
L3.Pores.ion.channels	0.000	0.000	-0.518	0.610	0.000	0.000	0.013

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	0.012	0.052	0.237	0.815	-0.096	0.121	0.000
L3.Porphyrin.and.chlorophyll.metabolism	0.000	0.000	-0.270	0.790	0.000	0.000	0.004

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	0.033	0.058	0.565	0.579	-0.089	0.155	0.000
L3.Prenyltransferases	0.000	0.000	-0.623	0.541	0.000	0.000	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	0.027	0.049	0.562	0.581	-0.075	0.129	0.000
L3.Primary.bile.acid.biosynthesis	0.000	0.000	-0.651	0.523	0.000	0.000	0.021

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	0.023	0.054	0.434	0.669	-0.089	0.136	0.000
L3.Primary.immunodeficiency	0.000	0.000	-0.488	0.631	0.000	0.000	0.012

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	0.015	0.038	0.395	0.698	-0.065	0.095	0.000
L3.Prion.diseases	0.000	0.000	-0.515	0.612	0.000	0.000	0.013

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	0.028	0.054	0.527	0.605	-0.084	0.141	0.000
L3.Progesterone.mediated.oocyte.maturation	0.000	0.000	-0.592	0.561	0.000	0.000	0.017

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	0.03	0.055	0.542	0.594	-0.085	0.144	0.000
L3.Propanoate.metabolism	0.00	0.000	-0.607	0.551	0.000	0.000	0.018

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	0.044	0.054	0.816	0.424	-0.069	0.157	0.00
L3.Prostate.cancer	0.000	0.000	-0.915	0.372	0.000	0.000	0.04

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	0.034	0.053	0.653	0.522	-0.076	0.145	0.000
L3.Proteasome	0.000	0.000	-0.738	0.470	0.000	0.000	0.026

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	-0.015	0.046	-0.316	0.756	-0.112	0.083	0.000
L3.Protein.digestion.and.absorption	0.000	0.000	0.373	0.713	0.000	0.000	0.007

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	0.034	0.055	0.619	0.543	-0.082	0.15	0.000
L3.Protein.export	0.000	0.000	-0.690	0.498	0.000	0.00	0.023

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	0.027	0.056	0.478	0.638	-0.091	0.145	0.000
L3.Protein.folding.and.associated.processing	0.000	0.000	-0.532	0.601	0.000	0.000	0.014

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	0.02	0.049	0.401	0.693	-0.082	0.121	0.000
L3.Protein.kinases	0.00	0.000	-0.466	0.647	0.000	0.000	0.011

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	0.012	0.063	0.194	0.848	-0.12	0.144	0.000
L3.Protein.processing.in.endoplasmic.reticulum	0.000	0.000	-0.211	0.835	0.00	0.000	0.002

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	0.046	0.043	1.060	0.302	-0.045	0.137	0.000
L3.Proximal.tubule.bicarbonate.reclamation	0.000	0.000	-1.267	0.220	0.000	0.000	0.074

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	0.026	0.056	0.470	0.643	-0.091	0.144	0.000
L3.Purine.metabolism	0.000	0.000	-0.524	0.606	0.000	0.000	0.014

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	0.027	0.056	0.474	0.641	-0.091	0.144	0.000
L3.Pyrimidine.metabolism	0.000	0.000	-0.527	0.604	0.000	0.000	0.014

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	0.025	0.055	0.463	0.649	-0.089	0.14	0.000
L3.Pyruvate.metabolism	0.000	0.000	-0.519	0.610	0.000	0.00	0.013

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	-0.008	0.032	-0.262	0.796	-0.076	0.059	0.000
L3.RIG.I.like.receptor.signaling.pathway	0.000	0.000	0.410	0.686	0.000	0.000	0.008

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	0.028	0.058	0.484	0.634	-0.093	0.149	0.000
L3.RNA.degradation	0.000	0.000	-0.536	0.598	0.000	0.000	0.014

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	0.022	0.055	0.391	0.700	-0.094	0.137	0.000
L3.RNA.polymerase	0.000	0.000	-0.437	0.667	0.000	0.000	0.009

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	0.02	0.048	0.426	0.675	-0.08	0.121	0.000
L3.RNA.transport	0.00	0.000	-0.496	0.625	0.00	0.000	0.012

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)	0	0.024	0	1	-0.05	0.05	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	0.052	0.039	1.332	0.198	-0.03	0.135	0.00
L3.Renal.cell.carcinoma	0.000	0.000	-1.651	0.115	0.00	0.000	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	0.008	0.025	0.317	0.755	-0.045	0.061	0.000
L3.Renin.angiotensin.system	-0.011	0.010	-1.092	0.289	-0.033	0.010	0.056

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	0.022	0.051	0.424	0.676	-0.086	0.129	0.000
L3.Replication..recombination.and.repair.proteins	0.000	0.000	-0.484	0.634	0.000	0.000	0.012

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	0.025	0.059	0.420	0.679	-0.098	0.147	0.000
L3.Restriction.enzyme	0.000	0.000	-0.464	0.648	0.000	0.000	0.011

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	0.071	0.045	1.568	0.133	-0.024	0.165	0.000
L3.Retinol.metabolism	0.000	0.000	-1.821	0.084	0.000	0.000	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)	0	0.024	0	1	-0.05	0.05	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	0.021	0.059	0.360	0.723	-0.103	0.145	0.000
L3.Riboflavin.metabolism	0.000	0.000	-0.396	0.697	0.000	0.000	0.008

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	0.031	0.054	0.567	0.577	-0.083	0.145	0.00
L3.Ribosome	0.000	0.000	-0.636	0.533	0.000	0.000	0.02

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	0.03	0.053	0.576	0.571	-0.08	0.141	0.000
L3.Ribosome.Biogenesis	0.00	0.000	-0.651	0.523	0.00	0.000	0.021

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	0.041	0.052	0.794	0.437	-0.068	0.151	0.000
L3.Ribosome.biogenesis.in.eukaryotes	0.000	0.000	-0.898	0.380	0.000	0.000	0.039

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)	0	0.024	0	1	-0.05	0.05	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	0.029	0.049	0.595	0.559	-0.074	0.132	0.000
L3.Secondary.bile.acid.biosynthesis	0.000	0.000	-0.687	0.500	0.000	0.000	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	0.036	0.049	0.739	0.469	-0.066	0.138	0.000
L3.Secretion.system	0.000	0.000	-0.854	0.404	0.000	0.000	0.035

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	0.022	0.054	0.400	0.694	-0.092	0.136	0.00
L3.Selenocompound.metabolism	0.000	0.000	-0.449	0.658	0.000	0.000	0.01

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)	0	0.024	0	1	-0.05	0.05	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	-0.012	0.026	-0.450	0.658	-0.066	0.043	0.000
L3.Shigellosis	0.006	0.005	1.182	0.252	-0.005	0.017	0.065

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	0.02	0.05	0.394	0.698	-0.085	0.125	0.00
L3.Signal.transduction.mechanisms	0.00	0.00	-0.452	0.656	0.000	0.000	0.01

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	0.005	0.025	0.214	0.832	-0.047	0.057	0.000
L3.Small.cell.lung.cancer	0.000	0.000	-0.979	0.340	0.000	0.000	0.046

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	0.04	0.056	0.704	0.490	-0.078	0.157	0.00
L3.Sphingolipid.metabolism	0.00	0.000	-0.782	0.444	0.000	0.000	0.03

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)	0	0.024	0	1	-0.05	0.05	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	0.013	0.041	0.314	0.757	-0.073	0.099	0.000
L3.Sporulation	0.000	0.000	-0.394	0.698	0.000	0.000	0.008

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	0.014	0.036	0.372	0.714	-0.063	0.09	0.000
L3.Staphylococcus.aureus.infection	0.000	0.000	-0.505	0.619	0.000	0.00	0.013

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	0.034	0.051	0.664	0.515	-0.072	0.14	0.000
L3.Starch.and.sucrose.metabolism	0.000	0.000	-0.759	0.457	0.000	0.00	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	-0.002	0.027	-0.062	0.951	-0.059	0.056	0.000
L3.Steroid.biosynthesis	0.000	0.000	0.146	0.885	0.000	0.000	0.001

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	0	0.04	0.005	0.996	-0.083	0.083	0
L3.Steroid.hormone.biosynthesis	0	0.00	-0.006	0.995	0.000	0.000	0

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	0.004	0.03	0.132	0.897	-0.059	0.067	0.
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	0.000	0.00	-0.230	0.821	0.000	0.000	0.

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	0.032	0.058	0.549	0.589	-0.089	0.152	0.000
L3.Streptomycin.biosynthesis	0.000	0.000	-0.607	0.551	0.000	0.000	0.018

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	0.002	0.04	0.044	0.965	-0.081	0.085	0
L3.Styrene.degradation	0.000	0.00	-0.056	0.956	0.000	0.000	0

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	0.032	0.057	0.564	0.579	-0.087	0.152	0.000
L3.Sulfur.metabolism	0.000	0.000	-0.625	0.539	0.000	0.000	0.019

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	0.03	0.049	0.605	0.552	-0.073	0.133	0.000
L3.Sulfur.relay.system	0.00	0.000	-0.698	0.494	0.000	0.000	0.024

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	0.003	0.046	0.066	0.948	-0.093	0.099	0
L3.Synthesis.and.degradation.of.ketone.bodies	0.000	0.000	-0.078	0.939	0.000	0.000	0

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	0.001	0.028	0.037	0.971	-0.058	0.061	0
L3.Systemic.lupus.erythematosus	0.000	0.000	-0.077	0.940	0.000	0.000	0

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)	0	0.024	0	1	-0.05	0.05	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	0.027	0.062	0.439	0.666	-0.102	0.157	0.000
L3.Taurine.and.hypotaurine.metabolism	0.000	0.000	-0.478	0.638	0.000	0.000	0.011

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	0.023	0.057	0.406	0.689	-0.096	0.142	0.00
L3.Terpenoid.backbone.biosynthesis	0.000	0.000	-0.451	0.657	0.000	0.000	0.01

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	0.028	0.049	0.570	0.575	-0.075	0.131	0.000
L3.Tetracycline.biosynthesis	0.000	0.000	-0.658	0.518	0.000	0.000	0.021

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	0.022	0.055	0.403	0.691	-0.092	0.136	0.00
L3.Thiamine.metabolism	0.000	0.000	-0.452	0.656	0.000	0.000	0.01

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)	0	0.024	0	1	-0.05	0.05	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	0.059	0.039	1.486	0.154	-0.024	0.141	0.000
L3.Toluene.degradation	0.000	0.000	-1.825	0.084	0.000	0.000	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	0.005	0.025	0.214	0.832	-0.047	0.057	0.000
L3.Toxoplasmosis	0.000	0.000	-0.979	0.340	0.000	0.000	0.046

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	0.018	0.047	0.377	0.710	-0.081	0.117	0.00
L3.Transcription.factors	0.000	0.000	-0.442	0.663	0.000	0.000	0.01

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	0.028	0.057	0.483	0.635	-0.092	0.147	0.000
L3.Transcription.machinery	0.000	0.000	-0.535	0.599	0.000	0.000	0.014

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	0.045	0.026	1.705	0.105	-0.01	0.1	0.000
L3.Transcription.related.proteins	0.000	0.000	-2.795	0.012	0.00	0.0	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	0.03	0.056	0.531	0.601	-0.087	0.147	0.000
L3.Translation.factors	0.00	0.000	-0.591	0.561	0.000	0.000	0.017

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	0.031	0.054	0.575	0.572	-0.083	0.145	0.00
L3.Translation.proteins	0.000	0.000	-0.644	0.527	0.000	0.000	0.02

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	0.018	0.046	0.385	0.704	-0.079	0.114	0.00
L3.Transporters	0.000	0.000	-0.456	0.654	0.000	0.000	0.01

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	0.027	0.057	0.467	0.646	-0.093	0.147	0
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis	0.000	0.000	-0.517	0.611	0.000	0.000	0

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	0.026	0.053	0.490	0.630	-0.084	0.136	0.000
L3.Tryptophan.metabolism	0.000	0.000	-0.555	0.585	0.000	0.000	0.015

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	0.033	0.054	0.624	0.540	-0.079	0.146	0.000
L3.Tuberculosis	0.000	0.000	-0.701	0.492	0.000	0.000	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	0.031	0.049	0.628	0.537	-0.072	0.134	0.000
L3.Two.component.system	0.000	0.000	-0.725	0.477	0.000	0.000	0.026

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	0.041	0.056	0.721	0.480	-0.077	0.158	0.000
L3.Type.I.diabetes.mellitus	0.000	0.000	-0.800	0.433	0.000	0.000	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	0.028	0.056	0.506	0.619	-0.088	0.145	0.000
L3.Type.II.diabetes.mellitus	0.000	0.000	-0.564	0.579	0.000	0.000	0.016

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	0.027	0.055	0.491	0.629	-0.088	0.141	0.000
L3.Tyrosine.metabolism	0.000	0.000	-0.550	0.589	0.000	0.000	0.015

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	0.029	0.065	0.451	0.657	-0.107	0.166	0.
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis	0.000	0.000	-0.487	0.632	0.000	0.000	0.

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	-0.022	0.045	-0.481	0.636	-0.116	0.073	0.000
L3.Ubiquitin.system	0.000	0.000	0.573	0.573	0.000	0.000	0.016

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)	0	0.024	0	1	-0.05	0.05	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	0.025	0.051	0.491	0.629	-0.081	0.131	0.000
L3.Valine..leucine.and.isoleucine.biosynthesis	0.000	0.000	-0.561	0.581	0.000	0.000	0.016

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	0.02	0.064	0.308	0.761	-0.115	0.154	0.000
L3.Valine..leucine.and.isoleucine.degradation	0.00	0.000	-0.334	0.742	0.000	0.000	0.006

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	0.014	0.027	0.522	0.608	-0.042	0.070	0.000
L3.Various.types.of.N.glycan.biosynthesis	-0.001	0.001	-1.185	0.250	-0.003	0.001	0.066

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)	0	0.024	0	1	-0.05	0.05	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	0.005	0.026	0.182	0.857	-0.050	0.059	0.000
L3.Vasopressin.regulated.water.reabsorption	-0.020	0.036	-0.554	0.586	-0.095	0.055	0.015

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	0.001	0.026	0.023	0.982	-0.054	0.055	0
L3.Vibrio.cholerae.infection	-0.001	0.016	-0.079	0.938	-0.035	0.033	0

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	0.013	0.054	0.247	0.808	-0.1	0.127	0.000
L3.Vibrio.cholerae.pathogenic.cycle	0.000	0.000	-0.277	0.785	0.0	0.000	0.004

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	0.005	0.025	0.214	0.832	-0.047	0.057	0.000
L3.Viral.myocarditis	0.000	0.000	-0.979	0.340	0.000	0.000	0.046

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	0.037	0.057	0.637	0.531	-0.084	0.157	0.000
L3.Vitamin.B6.metabolism	0.000	0.000	-0.705	0.489	0.000	0.000	0.024

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)	0	0.024	0	1	-0.05	0.05	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	0.02	0.04	0.485	0.634	-0.065	0.104	0.000
L3.Xylene.degradation	0.00	0.00	-0.611	0.548	0.000	0.000	0.018

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	0.028	0.061	0.456	0.653	-0.099	0.155	0.000
L3.Zeatin.biosynthesis	0.000	0.000	-0.499	0.623	0.000	0.000	0.012

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	0.012	0.035	0.344	0.735	-0.062	0.086	0.000
L3.alpha.Linolenic.acid.metabolism	0.000	0.000	-0.481	0.636	0.000	0.000	0.011

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	0.018	0.055	0.328	0.747	-0.098	0.134	0.000
L3.beta.Alanine.metabolism	0.000	0.000	-0.367	0.718	0.000	0.000	0.007

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	0.001	0.046	0.027	0.979	-0.095	0.097	0
L3.beta.Lactam.resistance	0.000	0.000	-0.032	0.974	0.000	0.000	0

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)	0	0.024	0	1	-0.05	0.05	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)	0	0.024	0	1	-0.05	0.05	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	0.005	0.025	0.214	0.832	-0.047	0.057	0.000
L3.p53.signaling.pathway	0.000	0.000	-0.979	0.340	0.000	0.000	0.046

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 %	9
Intercept	-0.003	0.024	-0.121	0.905	-0.054	
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	0.000	0.000	0.244	0.810	0.000	

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	-0.018	0.039	-0.464	0.648	-0.099	0.063	0.000
L3.ABC.transporters	0.000	0.000	0.551	0.588	0.000	0.000	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)	0	0.021	0	1	-0.043	0.043	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	0.027	0.047	0.583	0.567	-0.071	0.125	0.000
L3.Adipocytokine.signaling.pathway	0.000	0.000	-0.652	0.523	0.000	0.000	0.021

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	-0.034	0.026	-1.298	0.21	-0.089	0.021	0.000
L3.African.trypanosomiasis	0.000	0.000	1.919	0.07	0.000	0.000	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	0.008	0.049	0.161	0.874	-0.095	0.111	0.000
L3.Alanine..aspartate.and.glutamate.metabolism	0.000	0.000	-0.179	0.860	0.000	0.000	0.002

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)	0	0.021	0	1	-0.043	0.043	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	0.018	0.041	0.426	0.675	-0.069	0.104	0.000
L3.Alzheimer.s.disease	0.000	0.000	-0.494	0.627	0.000	0.000	0.012

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	-0.021	0.043	-0.501	0.622	-0.111	0.068	0.000
L3.Amino.acid.metabolism	0.000	0.000	0.574	0.573	0.000	0.000	0.016

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	0.001	0.047	0.028	0.978	-0.097	0.1	0
L3.Amino.acid.related.enzymes	0.000	0.000	-0.031	0.976	0.000	0.0	0

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	-0.013	0.048	-0.276	0.785	-0.113	0.087	0.000
L3.Amino.sugar.and.nucleotide.sugar.metabolism	0.000	0.000	0.307	0.762	0.000	0.000	0.005

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	-0.003	0.044	-0.073	0.943	-0.095	0.089	0
L3.Aminoacyl.tRNA.biosynthesis	0.000	0.000	0.083	0.935	0.000	0.000	0

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	0.013	0.049	0.267	0.793	-0.089	0.115	0.000
L3.Aminobenzoate.degradation	0.000	0.000	-0.296	0.771	0.000	0.000	0.004

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	-0.046	0.029	-1.571	0.133	-0.106	0.015	0.000
L3.Amoebiasis	0.000	0.000	2.084	0.051	0.000	0.000	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	-0.044	0.033	-1.309	0.206	-0.113	0.026	0.000
L3.Amyotrophic.lateral.sclerosis..ALS.	0.000	0.000	1.627	0.120	0.000	0.000	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	0.008	0.046	0.169	0.868	-0.089	0.104	0.000
L3.Antigen.processing.and.presentation	0.000	0.000	-0.190	0.851	0.000	0.000	0.002

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	0.017	0.022	0.767	0.452	-0.029	0.063	0.000
L3.Apoptosis	0.000	0.000	-1.674	0.111	0.000	0.000	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	0.04	0.052	0.772	0.449	-0.068	0.148	0.000
L3.Arachidonic.acid.metabolism	0.00	0.000	-0.843	0.409	0.000	0.000	0.034

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	0.005	0.047	0.113	0.911	-0.093	0.104	0.000
L3.Arginine.and.proline.metabolism	0.000	0.000	-0.127	0.900	0.000	0.000	0.001

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)	0	0.021	0	1	-0.043	0.043	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	-0.056	0.04	-1.384	0.182	-0.141	0.029	0.000
L3.Ascorbate.and.aldarate.metabolism	0.000	0.00	1.588	0.129	0.000	0.000	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	-0.015	0.031	-0.489	0.630	-0.08	0.05	0.000
L3.Atrazine.degradation	0.000	0.000	0.660	0.517	0.00	0.00	0.021

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	-0.008	0.036	-0.227	0.823	-0.082	0.066	0.000
L3.Bacterial.chemotaxis	0.000	0.000	0.282	0.781	0.000	0.000	0.004

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	-0.031	0.025	-1.228	0.234	-0.084	0.022	0.000
L3.Bacterial.invasion.of.epithelial.cells	0.000	0.000	1.912	0.071	0.000	0.000	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	-0.003	0.034	-0.102	0.920	-0.074	0.067	0.000
L3.Bacterial.motility.proteins	0.000	0.000	0.130	0.898	0.000	0.000	0.001

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	0.009	0.048	0.186	0.855	-0.091	0.109	0.000
L3.Bacterial.secretion.system	0.000	0.000	-0.207	0.838	0.000	0.000	0.002

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	-0.011	0.048	-0.233	0.818	-0.112	0.089	0.000
L3.Bacterial.toxins	0.000	0.000	0.260	0.798	0.000	0.000	0.003

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	0.008	0.023	0.336	0.740	-0.041	0.056	0.000
L3.Basal.transcription.factors	0.000	0.000	-0.769	0.451	0.000	0.000	0.029

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	-0.008	0.046	-0.184	0.856	-0.104	0.087	0.000
L3.Base.excision.repair	0.000	0.000	0.207	0.838	0.000	0.000	0.002

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	0.032	0.043	0.746	0.465	-0.058	0.121	0.000
L3.Benzoate.degradation	0.000	0.000	-0.853	0.404	0.000	0.000	0.035

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	-0.013	0.021	-0.595	0.559	-0.057	0.032	0.000
L3.Betalain.biosynthesis	0.002	0.001	1.677	0.110	0.000	0.004	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	-0.002	0.022	-0.071	0.944	-0.047	0.044	0.000
L3.Bile.secretion	0.032	0.099	0.324	0.750	-0.175	0.239	0.005

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	0.003	0.047	0.066	0.948	-0.095	0.101
L3.Biosynthesis.and.biodegradation.of.secondary.metabolites	0.000	0.000	-0.074	0.942	0.000	0.000

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)	0	0.021	0	1	-0.043	0.043	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	-0.013	0.043	-0.296	0.771	-0.102	0.077	0.000
L3.Biosynthesis.of.ansamycins	0.000	0.000	0.340	0.738	0.000	0.000	0.006

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	-0.032	0.054	-0.580	0.569	-0.145	0.082
L3.Biosynthesis.of.siderophore.group.nonribosomal.peptides	0.000	0.000	0.628	0.538	0.000	0.000

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)	0	0.021	0	1	-0.043	0.043	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	-0.013	0.021	-0.597	0.558	-0.058	0.032	0.000
L3.Biosynthesis.of.type.II.polyketide.products	0.002	0.001	1.582	0.130	-0.001	0.004	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	-0.015	0.043	-0.337	0.740	-0.105	0.076	0.000
L3.Biosynthesis.of.unsaturated.fatty.acids	0.000	0.000	0.385	0.704	0.000	0.000	0.007

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	-0.014	0.053	-0.273	0.788	-0.125	0.096	0.000
L3.Biosynthesis.of.vancomycin.group.antibiotics	0.000	0.000	0.297	0.769	0.000	0.000	0.004

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	-0.039	0.045	-0.866	0.397	-0.134	0.056	0.000
L3.Biotin.metabolism	0.000	0.000	0.972	0.343	0.000	0.000	0.045

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	-0.007	0.045	-0.153	0.880	-0.101	0.087	0.000
L3.Bisphenol.degradation	0.000	0.000	0.173	0.865	0.000	0.000	0.001

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	-0.029	0.024	-1.175	0.255	-0.08	0.022	0.000
L3.Bladder.cancer	0.000	0.000	1.927	0.069	0.00	0.000	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	0.024	0.045	0.535	0.599	-0.07	0.119	0.000
L3.Butanoate.metabolism	0.000	0.000	-0.604	0.553	0.00	0.000	0.018

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	-0.003	0.043	-0.068	0.947	-0.093	0.087	0
L3.Butirosin.and.neomycin.biosynthesis	0.000	0.000	0.078	0.939	0.000	0.000	0

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	-0.014	0.042	-0.328	0.747	-0.102	0.075	0.000
L3.C5.Branched.dibasic.acid.metabolism	0.000	0.000	0.378	0.710	0.000	0.000	0.007

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)	0	0.021	0	1	-0.043	0.043	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	0.002	0.023	0.072	0.943	-0.047	0.05	0.000
L3.Caffeine.metabolism	0.000	0.000	-0.175	0.863	0.000	0.00	0.002

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	0.007	0.022	0.331	0.745	-0.038	0.053	0.000
L3.Calcium.signaling.pathway	-0.002	0.002	-0.992	0.334	-0.005	0.002	0.047

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	-0.053	0.034	-1.541	0.140	-0.125	0.019	0.000
L3.Caprolactam.degradation	0.000	0.000	1.866	0.078	0.000	0.000	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	-0.053	0.035	-1.505	0.149	-0.126	0.021	0.000
L3.Carbohydrate.digestion.and.absorption	0.000	0.000	1.813	0.086	0.000	0.000	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	-0.021	0.045	-0.458	0.652	-0.114	0.073	0.000
L3.Carbohydrate.metabolism	0.000	0.000	0.518	0.610	0.000	0.000	0.013

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	-0.002	0.048	-0.043	0.966	-0.102	0.098	0
L3.Carbon.fixation.in.photosynthetic.organisms	0.000	0.000	0.048	0.962	0.000	0.000	0

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	0.011	0.05	0.230	0.821	-0.093	0.116	0.000
L3.Carbon.fixation.pathways.in.prokaryotes	0.000	0.00	-0.254	0.802	0.000	0.000	0.003

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	0.005	0.021	0.221	0.828	-0.04	0.049	0.000
L3.Cardiac.muscle.contraction	0.000	0.000	-0.922	0.368	0.00	0.000	0.041

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	-0.017	0.029	-0.566	0.578	-0.078	0.045	0.000
L3.Carotenoid.biosynthesis	0.000	0.000	0.798	0.435	0.000	0.000	0.031

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)	0	0.021	0	1	-0.043	0.043	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	-0.002	0.047	-0.051	0.959	-0.101	0.096	0
L3.Cell.cycle. . . Caulobacter	0.000	0.000	0.058	0.955	0.000	0.000	0

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)	0	0.021	0	1	-0.043	0.043	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	-0.026	0.046	-0.559	0.583	-0.121	0.07	0.000
L3.Cell.division	0.000	0.000	0.628	0.537	0.000	0.00	0.019

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	-0.034	0.049	-0.694	0.496	-0.137	0.069	0.000
L3.Cell.motility.and.secretion	0.000	0.000	0.766	0.453	0.000	0.000	0.028

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	0.044	0.043	1.016	0.323	-0.046	0.133	0.000
L3.Cellular.antigens	0.000	0.000	-1.155	0.262	0.000	0.000	0.063

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	-0.031	0.026	-1.202	0.244	-0.084	0.023	0.000
L3.Chagas.disease..American.trypanosomiasis.	0.000	0.000	1.848	0.080	0.000	0.000	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	0.005	0.05	0.105	0.917	-0.099	0.109	0.000
L3.Chaperones.and.folding.catalysts	0.000	0.00	-0.116	0.909	0.000	0.000	0.001

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	-0.02	0.041	-0.488	0.631	-0.106	0.066	0.000
L3.Chloroalkane.and.chloroalkene.degradation	0.00	0.000	0.568	0.576	0.000	0.000	0.016

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 %	R2
Intercept	-0.041	0.03	-1.344	0.195	-0.105	0.023	0.000
L3.Chlorocyclohexane.and.chlorobenzene.degradation	0.000	0.00	1.756	0.095	0.000	0.000	0.134

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)	0	0.021	0	1	-0.043	0.043	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	0.002	0.047	0.035	0.973	-0.096	0.099	0
L3.Chromosome	0.000	0.000	-0.039	0.969	0.000	0.000	0

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)	0	0.021	0	1	-0.043	0.043	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	0.002	0.023	0.074	0.942	-0.047	0.05	0.000
L3.Circadian.rhythm...plant	0.000	0.000	-0.177	0.861	0.000	0.00	0.002

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	0.005	0.051	0.102	0.920	-0.101	0.112	0.000
L3.Citrate.cycle..TCA.cycle.	0.000	0.000	-0.112	0.912	0.000	0.000	0.001

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	0.003	0.021	0.140	0.890	-0.042	0.048	0.00
L3.Clavulanic.acid.biosynthesis	-0.031	0.049	-0.642	0.529	-0.134	0.071	0.02

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	0.004	0.021	0.205	0.84	-0.04	0.049	0.000
L3.Colorectal.cancer	0.000	0.000	-0.937	0.36	0.00	0.000	0.042

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)	0	0.021	0	1	-0.043	0.043	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	-0.025	0.042	-0.592	0.561	-0.114	0.064	0.000
L3.Cyanoamino.acid.metabolism	0.000	0.000	0.680	0.505	0.000	0.000	0.023

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	-0.005	0.047	-0.115	0.910	-0.104	0.093	0.000
L3.Cysteine.and.methionine.metabolism	0.000	0.000	0.129	0.899	0.000	0.000	0.001

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)	0	0.021	0	1	-0.043	0.043	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)	0	0.021	0	1	-0.043	0.043	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)	0	0.021	0	1	-0.043	0.043	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	0.011	0.042	0.269	0.791	-0.077	0.099	0.000
L3.Cytoskeleton.proteins	0.000	0.000	-0.311	0.759	0.000	0.000	0.005

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)	0	0.021	0	1	-0.043	0.043	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	0.019	0.046	0.418	0.681	-0.077	0.115	0.000
L3.D.Alanine.metabolism	0.000	0.000	-0.470	0.644	0.000	0.000	0.011

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	-0.052	0.027	-1.912	0.071	-0.109	0.005	0.000
L3.D.Arginine.and.D.ornithine.metabolism	0.000	0.000	2.571	0.019	0.000	0.000	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	0.011	0.049	0.222	0.827	-0.092	0.114	0.000
L3.D.Glutamine.and.D.glutamate.metabolism	0.000	0.000	-0.246	0.809	0.000	0.000	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	0.001	0.047	0.031	0.976	-0.098	0.101	0
L3.DNA.repair.and.recombination.proteins	0.000	0.000	-0.034	0.973	0.000	0.000	0

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	0.004	0.049	0.082	0.935	-0.098	0.106	0
L3.DNA.replication	0.000	0.000	-0.091	0.928	0.000	0.000	0

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	0.01	0.048	0.210	0.836	-0.091	0.111	0.000
L3.DNA.replication.proteins	0.00	0.000	-0.234	0.818	0.000	0.000	0.003

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)	0	0.021	0	1	-0.043	0.043	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	0.003	0.036	0.078	0.939	-0.072	0.077	0
L3.Dioxin.degradation	0.000	0.000	-0.097	0.924	0.000	0.000	0

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	0.014	0.04	0.348	0.732	-0.07	0.098	0.000
L3.Drug.metabolism…cytochrome.P450	0.000	0.00	-0.408	0.688	0.00	0.000	0.008

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	0.016	0.05	0.311	0.759	-0.089	0.12	0.000
L3.Drug.metabolism…other.enzymes	0.000	0.00	-0.343	0.736	0.000	0.00	0.006

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)	0	0.021	0	1	-0.043	0.043	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	-0.033	0.032	-1.054	0.305	-0.099	0.033	0.000
L3.Electron.transfer.carriers	0.000	0.000	1.370	0.187	0.000	0.000	0.086

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)	0	0.021	0	1	-0.043	0.043	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	0.004	0.022	0.182	0.857	-0.042	0.050	0.000
L3.Endocytosis	-0.028	0.045	-0.622	0.541	-0.122	0.066	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	0.012	0.049	0.254	0.803	-0.09	0.115	0.000
L3.Energy.metabolism	0.000	0.000	-0.281	0.782	0.00	0.000	0.004

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	-0.011	0.043	-0.261	0.797	-0.102	0.079
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	0.000	0.000	0.300	0.768	0.000	0.000

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)	0	0.021	0	1	-0.043	0.043	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	-0.049	0.026	-1.884	0.075	-0.104	0.005	0.000
L3.Ether.lipid.metabolism	0.000	0.000	2.616	0.017	0.000	0.000	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	0.054	0.044	1.209	0.241	-0.039	0.147	0.000
L3.Ethylbenzene.degradation	0.000	0.000	-1.357	0.191	0.000	0.000	0.084

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)	0	0.021	0	1	-0.043	0.043	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	0.011	0.047	0.230	0.82	-0.088	0.109	0.000
L3.Fatty.acid.biosynthesis	0.000	0.000	-0.258	0.80	0.000	0.000	0.003

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	0.002	0.023	0.072	0.943	-0.047	0.05	0.000
L3.Fatty.acid.elongation.in.mitochondria	0.000	0.000	-0.174	0.864	0.000	0.00	0.002

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	0.019	0.047	0.398	0.695	-0.08	0.117	0.00
L3.Fatty.acid.metabolism	0.000	0.000	-0.445	0.661	0.00	0.000	0.01

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)	0	0.021	0	1	-0.043	0.043	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	0.004	0.022	0.182	0.857	-0.042	0.050	0.000
L3.Fc.gamma.R.mediated.phagocytosis	-0.028	0.045	-0.622	0.541	-0.122	0.066	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	-0.003	0.032	-0.092	0.927	-0.069	0.063	0.000
L3.Flagellar.assembly	0.000	0.000	0.124	0.903	0.000	0.000	0.001

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	-0.004	0.04	-0.105	0.918	-0.087	0.079	0.000
L3.Flavone.and.flavonol.biosynthesis	0.000	0.00	0.124	0.903	0.000	0.000	0.001

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	-0.01	0.03	-0.324	0.75	-0.071	0.052	0.000
L3.Flavonoid.biosynthesis	0.00	0.00	0.461	0.65	0.000	0.000	0.011

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	-0.028	0.027	-1.027	0.317	-0.086	0.029	0.000
L3.Fluorobenzoate.degradation	0.000	0.000	1.495	0.151	0.000	0.000	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)	0	0.021	0	1	-0.043	0.043	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	-0.016	0.051	-0.305	0.764	-0.123	0.092	0.000
L3.Folate.biosynthesis	0.000	0.000	0.334	0.742	0.000	0.000	0.006

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	-0.02	0.045	-0.436	0.668	-0.113	0.074	0.000
L3.Fructose.and.mannose.metabolism	0.00	0.000	0.493	0.627	0.000	0.000	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	-0.021	0.045	-0.463	0.649	-0.116	0.074	0.000
L3.Function.unknown	0.000	0.000	0.522	0.608	0.000	0.000	0.013

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	-0.007	0.023	-0.317	0.754	-0.056	0.042	0.000
L3.G.protein.coupled.receptors	0.006	0.008	0.697	0.494	-0.011	0.022	0.024

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)	0	0.021	0	1	-0.043	0.043	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	-0.016	0.047	-0.337	0.74	-0.113	0.082	0.000
L3.Galactose.metabolism	0.000	0.000	0.378	0.71	0.000	0.000	0.007

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)	0	0.021	0	1	-0.043	0.043	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	-0.006	0.048	-0.127	0.900	-0.106	0.094	0.000
L3.General.function.prediction.only	0.000	0.000	0.142	0.889	0.000	0.000	0.001

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	-0.027	0.052	-0.517	0.611	-0.136	0.082	0.000
L3.Geraniol.degradation	0.000	0.000	0.565	0.579	0.000	0.000	0.016

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	-0.013	0.033	-0.389	0.701	-0.081	0.056	0.000
L3.Germination	0.000	0.000	0.507	0.618	0.000	0.000	0.013

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)	0	0.021	0	1	-0.043	0.043	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	0.022	0.047	0.464	0.648	-0.077	0.12	0.000
L3.Glutamatergic.synapse	0.000	0.000	-0.518	0.610	0.000	0.00	0.013

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	0.029	0.056	0.512	0.615	-0.089	0.147	0.000
L3.Glutathione.metabolism	0.000	0.000	-0.551	0.588	0.000	0.000	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)	0	0.021	0	1	-0.043	0.043	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	-0.011	0.044	-0.263	0.796	-0.103	0.08	0.000
L3.Glycan.biosynthesis.and.metabolism	0.000	0.000	0.300	0.767	0.000	0.00	0.004

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	-0.016	0.041	-0.386	0.704	-0.101	0.07	0.00
L3.Glycerolipid.metabolism	0.000	0.000	0.450	0.658	0.000	0.00	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	-0.005	0.044	-0.111	0.913	-0.096	0.086	0.000
L3.Glycerophospholipid.metabolism	0.000	0.000	0.127	0.901	0.000	0.000	0.001

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	-0.003	0.049	-0.061	0.952	-0.106	0.1	0
L3.Glycine..serine.and.threonine.metabolism	0.000	0.000	0.068	0.947	0.000	0.0	0

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	0.001	0.046	0.027	0.979	-0.095	0.098	0
L3.Glycolysis...Gluconeogenesis	0.000	0.000	-0.031	0.976	0.000	0.000	0

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	0.002	0.022	0.071	0.944	-0.044	0.047	0
L3.Glycosaminoglycan.biosynthesis...chondroitin.sulfate	-0.001	0.004	-0.315	0.757	-0.009	0.007	0

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	0.014	0.041	0.351	0.730	-0.072	0.101	0.000
L3.Glycosaminoglycan.degradation	0.000	0.000	-0.408	0.688	0.000	0.000	0.008

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	0.015	0.038	0.402	0.692	-0.063	0.094	0.000
L3.Glycosphingolipid.biosynthesis...ganglio.series	0.000	0.000	-0.485	0.633	0.000	0.000	0.012

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	-0.009	0.047	-0.184	0.856	-0.107	0.09	0.000
L3.Glycosphingolipid.biosynthesis...globo.series	0.000	0.000	0.206	0.839	0.000	0.00	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	-0.01	0.022	-0.454	0.655	-0.055	0.035
L3.Glycosphingolipid.biosynthesis...lacto.and.neolacto.series	0.00	0.000	1.292	0.212	0.000	0.000

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)	0	0.021	0	1	-0.043	0.043	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	-0.02	0.052	-0.386	0.704	-0.13	0.09	0.000
L3.Glycosyltransferases	0.00	0.000	0.421	0.679	0.00	0.00	0.009

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	-0.01	0.047	-0.210	0.836	-0.108	0.088	0.000
L3.Glyoxylate.and.dicarboxylate.metabolism	0.00	0.000	0.236	0.816	0.000	0.000	0.003

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	0.004	0.022	0.182	0.857	-0.042	0.050	0.000
L3.GnRH.signaling.pathway	-0.028	0.045	-0.622	0.541	-0.122	0.066	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)	0	0.021	0	1	-0.043	0.043	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)	0	0.021	0	1	-0.043	0.043	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)	0	0.021	0	1	-0.043	0.043	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	0.004	0.048	0.074	0.942	-0.097	0.104	0
L3.Histidine.metabolism	0.000	0.000	-0.082	0.935	0.000	0.000	0

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	0.007	0.048	0.138	0.891	-0.094	0.107	0.000
L3.Homologous.recombination	0.000	0.000	-0.154	0.879	0.000	0.000	0.001

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	-0.002	0.044	-0.045	0.964	-0.093	0.089	0
L3.Huntington.s.disease	0.000	0.000	0.052	0.959	0.000	0.000	0

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	0.002	0.022	0.078	0.938	-0.043	0.047	0.000
L3.Hypertrophic.cardiomyopathy..HCM.	-0.005	0.014	-0.359	0.724	-0.035	0.024	0.006

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)	0	0.021	0	1	-0.043	0.043	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	0.004	0.021	0.205	0.84	-0.04	0.049	0.000
L3.Influenza.A	0.000	0.000	-0.937	0.36	0.00	0.000	0.042

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	-0.036	0.046	-0.766	0.453	-0.133	0.062	0.000
L3.Inorganic.ion.transport.and.metabolism	0.000	0.000	0.855	0.403	0.000	0.000	0.035

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	0.002	0.049	0.049	0.961	-0.099	0.104	0
L3.Inositol.phosphate.metabolism	0.000	0.000	-0.055	0.957	0.000	0.000	0

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	0.004	0.043	0.101	0.920	-0.085	0.093	0.000
L3.Insulin.signaling.pathway	0.000	0.000	-0.117	0.908	0.000	0.000	0.001

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	-0.065	0.048	-1.366	0.188	-0.165	0.035	0.000
L3.Ion.channels	0.000	0.000	1.505	0.149	0.000	0.000	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	0.006	0.021	0.300	0.767	-0.039	0.051	0.00
L3.Isoflavonoid.biosynthesis	-0.045	0.044	-1.026	0.318	-0.137	0.047	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	0.015	0.055	0.274	0.787	-0.1	0.13	0.000
L3.Isoquinoline.alkaloid.biosynthesis	0.000	0.000	-0.297	0.770	0.0	0.00	0.004

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)	0	0.021	0	1	-0.043	0.043	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)	0	0.021	0	1	-0.043	0.043	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	0.015	0.047	0.314	0.757	-0.083	0.113	0.000
L3.Limonene.and.pinene.degradation	0.000	0.000	-0.351	0.729	0.000	0.000	0.006

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	-0.015	0.045	-0.333	0.743	-0.108	0.079	0.000
L3.Linoleic.acid.metabolism	0.000	0.000	0.377	0.710	0.000	0.000	0.007

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	0.01	0.049	0.205	0.839	-0.092	0.112	0.000
L3.Lipid.biosynthesis.proteins	0.00	0.000	-0.228	0.822	0.000	0.000	0.003

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	-0.008	0.042	-0.186	0.854	-0.095	0.08	0.000
L3.Lipid.metabolism	0.000	0.000	0.216	0.831	0.000	0.00	0.002

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	-0.006	0.045	-0.128	0.899	-0.1	0.088	0.000
L3.Lipoic.acid.metabolism	0.000	0.000	0.145	0.886	0.0	0.000	0.001

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	-0.034	0.049	-0.689	0.499	-0.136	0.069	0.000
L3.Lipopolysaccharide.biosynthesis	0.000	0.000	0.761	0.456	0.000	0.000	0.028

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	-0.029	0.052	-0.552	0.587	-0.139	0.081	0.000
L3.Lipopolysaccharide.biosynthesis.proteins	0.000	0.000	0.602	0.554	0.000	0.000	0.018

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)	0	0.021	0	1	-0.043	0.043	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)	0	0.021	0	1	-0.043	0.043	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	-0.003	0.045	-0.056	0.956	-0.096	0.091	0
L3.Lysine.biosynthesis	0.000	0.000	0.064	0.950	0.000	0.000	0

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	0.008	0.049	0.156	0.878	-0.095	0.11	0.000
L3.Lysine.degradation	0.000	0.000	-0.172	0.865	0.000	0.00	0.001

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	0.01	0.045	0.217	0.831	-0.085	0.104	0.000
L3.Lysosome	0.00	0.000	-0.245	0.809	0.000	0.000	0.003

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)	0	0.021	0	1	-0.043	0.043	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	-0.003	0.051	-0.068	0.946	-0.109	0.103	0
L3.MAPK.signaling.pathway...yeast	0.000	0.000	0.075	0.941	0.000	0.000	0

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)	0	0.021	0	1	-0.043	0.043	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	-0.01	0.023	-0.437	0.667	-0.058	0.038	0.000
L3.Meiosis...yeast	0.00	0.000	0.971	0.344	0.000	0.000	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	-0.013	0.021	-0.595	0.559	-0.057	0.032	0.000
L3.Melanogenesis	0.002	0.001	1.677	0.110	0.000	0.004	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	-0.014	0.053	-0.264	0.795	-0.125	0.097	0.000
L3.Membrane.and.intracellular.structural.molecules	0.000	0.000	0.287	0.777	0.000	0.000	0.004

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	-0.044	0.04	-1.107	0.282	-0.127	0.039	0.000
L3.Metabolism.of.cofactors.and.vitamins	0.000	0.00	1.286	0.214	0.000	0.000	0.076

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	0.015	0.04	0.366	0.718	-0.069	0.098	0.000
L3.Metabolism.of.xenobiotics.by.cytochrome.P450	0.000	0.00	-0.431	0.671	0.000	0.000	0.009

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	-0.006	0.045	-0.138	0.891	-0.1	0.088	0.000
L3.Methane.metabolism	0.000	0.000	0.157	0.877	0.0	0.000	0.001

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	-0.05	0.026	-1.952	0.066	-0.103	0.004	0.000
L3.Mineral.absorption	0.00	0.000	2.734	0.013	0.000	0.000	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	0.001	0.047	0.030	0.977	-0.097	0.1	0
L3.Mismatch.repair	0.000	0.000	-0.033	0.974	0.000	0.0	0

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	-0.07	0.044	-1.566	0.134	-0.163	0.023	0.000
L3.N.Glycan.biosynthesis	0.00	0.000	1.744	0.097	0.000	0.000	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	0.022	0.048	0.466	0.646	-0.078	0.123	0.000
L3.NOD.like.receptor.signaling.pathway	0.000	0.000	-0.519	0.610	0.000	0.000	0.013

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	0.027	0.047	0.566	0.578	-0.072	0.125	0.00
L3.Naphthalene.degradation	0.000	0.000	-0.632	0.535	0.000	0.000	0.02

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)	0	0.021	0	1	-0.043	0.043	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)	0	0.021	0	1	-0.043	0.043	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	-0.004	0.047	-0.077	0.939	-0.103	0.095	0
L3.Nicotinate.and.nicotinamide.metabolism	0.000	0.000	0.086	0.932	0.000	0.000	0

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	-0.018	0.05	-0.347	0.732	-0.123	0.088	0.000
L3.Nitrogen.metabolism	0.000	0.00	0.382	0.707	0.000	0.000	0.007

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	-0.017	0.035	-0.482	0.635	-0.089	0.056	0.000
L3.Nitrotoluene.degradation	0.000	0.000	0.604	0.553	0.000	0.000	0.018

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	-0.06	0.024	-2.443	0.025	-0.111	-0.009	0.00
L3.Non.homologous.end.joining	0.00	0.000	3.354	0.003	0.000	0.000	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)	0	0.021	0	1	-0.043	0.043	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	0.005	0.047	0.096	0.925	-0.094	0.104	0.000
L3.Novobiocin.biosynthesis	0.000	0.000	-0.107	0.916	0.000	0.000	0.001

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	-0.005	0.046	-0.104	0.919	-0.1	0.091	0.000
L3.Nucleotide.excision.repair	0.000	0.000	0.117	0.908	0.0	0.000	0.001

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	-0.037	0.036	-1.031	0.316	-0.112	0.038	0.000
L3.Nucleotide.metabolism	0.000	0.000	1.249	0.227	0.000	0.000	0.072

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)	0	0.021	0	1	-0.043	0.043	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	0.011	0.05	0.230	0.820	-0.093	0.116	0.000
L3.One.carbon.pool.by.folate	0.000	0.00	-0.254	0.802	0.000	0.000	0.003

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)	0	0.021	0	1	-0.043	0.043	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	0.003	0.051	0.054	0.957	-0.104	0.109	0
L3.Other.glycan.degradation	0.000	0.000	-0.060	0.953	0.000	0.000	0

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	-0.009	0.05	-0.179	0.860	-0.115	0.097	0.000
L3.Other.ion.coupled.transporters	0.000	0.00	0.197	0.846	0.000	0.000	0.002

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	-0.005	0.048	-0.114	0.91	-0.105	0.094	0.000
L3.Other.transporters	0.000	0.000	0.128	0.90	0.000	0.000	0.001

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)	0	0.021	0	1	-0.043	0.043	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	-0.013	0.047	-0.283	0.781	-0.111	0.085	0.000
L3.Others	0.000	0.000	0.316	0.755	0.000	0.000	0.005

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	-0.004	0.047	-0.078	0.939	-0.102	0.094	0
L3.Oxidative.phosphorylation	0.000	0.000	0.087	0.932	0.000	0.000	0

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	0.039	0.05	0.772	0.449	-0.066	0.143	0.000
L3.PPAR.signaling.pathway	0.000	0.00	-0.849	0.406	0.000	0.000	0.035

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)	0	0.021	0	1	-0.043	0.043	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)	0	0.021	0	1	-0.043	0.043	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	-0.003	0.045	-0.071	0.944	-0.098	0.092	0
L3.Pantothenate.and.CoA.biosynthesis	0.000	0.000	0.080	0.937	0.000	0.000	0

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	0.005	0.021	0.217	0.830	-0.04	0.049	0.000
L3.Parkinson.s.disease	0.000	0.000	-0.925	0.367	0.00	0.000	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)	0	0.021	0	1	-0.043	0.043	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	-0.003	0.045	-0.077	0.939	-0.097	0.09	0
L3.Pathways.in.cancer	0.000	0.000	0.088	0.931	0.000	0.00	0

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	-0.033	0.044	-0.743	0.467	-0.125	0.06	0.000
L3.Penicillin.and.cephalosporin.biosynthesis	0.000	0.000	0.841	0.411	0.000	0.00	0.034

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	-0.006	0.048	-0.126	0.901	-0.106	0.094	0.000
L3.Pentose.and.glucuronate.interconversions	0.000	0.000	0.140	0.890	0.000	0.000	0.001

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	-0.01	0.046	-0.219	0.829	-0.105	0.085	0.000
L3.Pentose.phosphate.pathway	0.00	0.000	0.247	0.808	0.000	0.000	0.003

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	-0.003	0.048	-0.061	0.952	-0.103	0.097	0
L3.Peptidases	0.000	0.000	0.068	0.946	0.000	0.000	0

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	-0.001	0.046	-0.026	0.980	-0.097	0.095	0
L3.Peptidoglycan.biosynthesis	0.000	0.000	0.029	0.977	0.000	0.000	0

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	0.009	0.052	0.180	0.859	-0.099	0.118	0.000
L3.Peroxisome	0.000	0.000	-0.198	0.845	0.000	0.000	0.002

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	-0.014	0.049	-0.278	0.784	-0.115	0.088	0.000
L3.Pertussis	0.000	0.000	0.308	0.761	0.000	0.000	0.005

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)	0	0.021	0	1	-0.043	0.043	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	0.011	0.049	0.228	0.822	-0.091	0.113	0.000
L3.Phenylalanine.metabolism	0.000	0.000	-0.253	0.803	0.000	0.000	0.003

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	-0.011	0.045	-0.246	0.808	-0.105	0.083	0.0
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis	0.000	0.000	0.279	0.783	0.000	0.000	0.0

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	-0.032	0.038	-0.837	0.413	-0.112	0.048	0.000
L3.Phenylpropanoid.biosynthesis	0.000	0.000	0.993	0.333	0.000	0.000	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	-0.001	0.051	-0.024	0.981	-0.107	0.105	0
L3.Phosphatidylinositol.signaling.system	0.000	0.000	0.026	0.979	0.000	0.000	0

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	0.009	0.046	0.191	0.850	-0.087	0.105	0.000
L3.Phosphonate.and.phosphinate.metabolism	0.000	0.000	-0.215	0.832	0.000	0.000	0.002

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	-0.031	0.032	-0.947	0.356	-0.098	0.037	0.000
L3.Phosphotransferase.system..PTS.	0.000	0.000	1.217	0.238	0.000	0.000	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	-0.013	0.041	-0.307	0.762	-0.098	0.073	0.000
L3.Photosynthesis	0.000	0.000	0.358	0.724	0.000	0.000	0.006

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	0.007	0.022	0.327	0.747	-0.039	0.053	0.000
L3.Photosynthesis. . . antenna.proteins	0.000	0.000	-0.976	0.341	0.000	0.000	0.045

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	-0.012	0.041	-0.304	0.765	-0.098	0.073	0.000
L3.Photosynthesis.proteins	0.000	0.000	0.354	0.727	0.000	0.000	0.006

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)	0	0.021	0	1	-0.043	0.043	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)	0	0.021	0	1	-0.043	0.043	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	0.007	0.042	0.171	0.866	-0.082	0.096	0.000
L3.Plant.pathogen.interaction	0.000	0.000	-0.197	0.846	0.000	0.000	0.002

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	0.004	0.046	0.098	0.923	-0.091	0.1	0.000
L3.Polycyclic.aromatic.hydrocarbon.degradation	0.000	0.000	-0.110	0.913	0.000	0.0	0.001

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	-0.019	0.05	-0.385	0.705	-0.125	0.086	0.000
L3.Polyketide.sugar.unit.biosynthesis	0.000	0.00	0.424	0.677	0.000	0.000	0.009

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	0.005	0.056	0.085	0.933	-0.113	0.123	0
L3.Pores.ion.channels	0.000	0.000	-0.092	0.928	0.000	0.000	0

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	-0.013	0.044	-0.289	0.776	-0.105	0.08	0.000
L3.Porphyrin.and.chlorophyll.metabolism	0.000	0.000	0.329	0.746	0.000	0.00	0.005

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	0	0.05	-0.007	0.995	-0.105	0.104	0
L3.Prenyltransferases	0	0.00	0.008	0.994	0.000	0.000	0

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	-0.02	0.042	-0.475	0.641	-0.107	0.067	0.000
L3.Primary.bile.acid.biosynthesis	0.00	0.000	0.550	0.589	0.000	0.000	0.015

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	-0.029	0.045	-0.635	0.533	-0.124	0.066	0.000
L3.Primary.immunodeficiency	0.000	0.000	0.715	0.483	0.000	0.000	0.025

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	-0.026	0.032	-0.814	0.426	-0.093	0.041	0.000
L3.Prion.diseases	0.000	0.000	1.062	0.301	0.000	0.000	0.053

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	0.008	0.046	0.169	0.868	-0.089	0.104	0.000
L3.Progesterone.mediated.oocyte.maturation	0.000	0.000	-0.190	0.851	0.000	0.000	0.002

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	0.003	0.047	0.069	0.946	-0.095	0.101	0
L3.Propanoate.metabolism	0.000	0.000	-0.077	0.939	0.000	0.000	0

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	-0.005	0.047	-0.110	0.913	-0.103	0.093	0.000
L3.Prostate.cancer	0.000	0.000	0.124	0.903	0.000	0.000	0.001

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	0.002	0.045	0.041	0.968	-0.093	0.097	0
L3.Proteasome	0.000	0.000	-0.046	0.964	0.000	0.000	0

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	0.019	0.039	0.471	0.643	-0.064	0.101	0.000
L3.Protein.digestion.and.absorption	0.000	0.000	-0.557	0.584	0.000	0.000	0.015

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	-0.004	0.048	-0.091	0.928	-0.104	0.096	0.000
L3.Protein.export	0.000	0.000	0.102	0.920	0.000	0.000	0.001

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	-0.02	0.048	-0.413	0.684	-0.12	0.081	0.00
L3.Protein.folding.and.associated.processing	0.00	0.000	0.459	0.651	0.00	0.000	0.01

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	-0.007	0.042	-0.169	0.868	-0.094	0.08	0.000
L3.Protein.kinases	0.000	0.000	0.196	0.847	0.000	0.00	0.002

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	0.03	0.053	0.569	0.576	-0.081	0.141	0.000
L3.Protein.processing.in.endoplasmic.reticulum	0.00	0.000	-0.619	0.543	0.000	0.000	0.019

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	0.049	0.036	1.357	0.191	-0.027	0.125	0.000
L3.Proximal.tubule.bicarbonate.reclamation	0.000	0.000	-1.623	0.121	0.000	0.000	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	-0.01	0.048	-0.203	0.841	-0.11	0.091	0.000
L3.Purine.metabolism	0.00	0.000	0.226	0.824	0.00	0.000	0.003

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	0.004	0.048	0.080	0.937	-0.097	0.105	0
L3.Pyrimidine.metabolism	0.000	0.000	-0.089	0.930	0.000	0.000	0

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	0.009	0.047	0.191	0.851	-0.089	0.107	0.000
L3.Pyruvate.metabolism	0.000	0.000	-0.214	0.833	0.000	0.000	0.002

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	0.003	0.027	0.117	0.908	-0.054	0.061	0.000
L3.RIG.I.like.receptor.signaling.pathway	0.000	0.000	-0.183	0.857	0.000	0.000	0.002

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	-0.001	0.049	-0.023	0.982	-0.105	0.102	0
L3.RNA.degradation	0.000	0.000	0.025	0.980	0.000	0.000	0

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	0.002	0.047	0.037	0.971	-0.097	0.101	0
L3.RNA.polymerase	0.000	0.000	-0.041	0.967	0.000	0.000	0

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	-0.004	0.041	-0.103	0.919	-0.09	0.082	0.000
L3.RNA.transport	0.000	0.000	0.120	0.905	0.00	0.000	0.001

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)	0	0.021	0	1	-0.043	0.043	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	-0.055	0.032	-1.714	0.103	-0.122	0.012	0.000
L3.Renal.cell.carcinoma	0.000	0.000	2.125	0.047	0.000	0.000	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	0.003	0.022	0.153	0.880	-0.042	0.049	0.000
L3.Renin.angiotensin.system	-0.005	0.009	-0.528	0.603	-0.023	0.014	0.014

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	0.008	0.044	0.183	0.857	-0.084	0.1	0.000
L3.Replication..recombination.and.repair.proteins	0.000	0.000	-0.209	0.837	0.000	0.0	0.002

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	0.039	0.049	0.786	0.441	-0.064	0.141	0.000
L3.Restriction.enzyme	0.000	0.000	-0.867	0.397	0.000	0.000	0.036

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	0.009	0.041	0.216	0.831	-0.078	0.096	0.000
L3.Retinol.metabolism	0.000	0.000	-0.251	0.805	0.000	0.000	0.003

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)	0	0.021	0	1	-0.043	0.043	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	-0.001	0.051	-0.020	0.984	-0.107	0.105	0
L3.Riboflavin.metabolism	0.000	0.000	0.022	0.983	0.000	0.000	0

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	0.003	0.047	0.066	0.948	-0.095	0.101	0
L3.Ribosome	0.000	0.000	-0.074	0.942	0.000	0.000	0

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	-0.002	0.045	-0.044	0.965	-0.097	0.093	0
L3.Ribosome.Biogenesis	0.000	0.000	0.050	0.960	0.000	0.000	0

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	0	0.045	0.007	0.995	-0.094	0.095	0
L3.Ribosome.biogenesis.in.eukaryotes	0	0.000	-0.007	0.994	0.000	0.000	0

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)	0	0.021	0	1	-0.043	0.043	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	-0.015	0.042	-0.362	0.721	-0.103	0.073	0.000
L3.Secondary.bile.acid.biosynthesis	0.000	0.000	0.418	0.681	0.000	0.000	0.009

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	-0.005	0.042	-0.112	0.912	-0.093	0.083	0.000
L3.Secretion.system	0.000	0.000	0.130	0.898	0.000	0.000	0.001

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	-0.015	0.046	-0.317	0.755	-0.112	0.082	0.000
L3.Selenocompound.metabolism	0.000	0.000	0.356	0.726	0.000	0.000	0.006

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)	0	0.021	0	1	-0.043	0.043	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	-0.005	0.023	-0.230	0.820	-0.053	0.042	0.000
L3.Shigellosis	0.003	0.005	0.605	0.552	-0.007	0.012	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	-0.004	0.043	-0.105	0.918	-0.094	0.085	0.000
L3.Signal.transduction.mechanisms	0.000	0.000	0.120	0.905	0.000	0.000	0.001

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	0.004	0.021	0.205	0.84	-0.04	0.049	0.000
L3.Small.cell.lung.cancer	0.000	0.000	-0.937	0.36	0.00	0.000	0.042

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	-0.009	0.049	-0.189	0.852	-0.111	0.092	0.000
L3.Sphingolipid.metabolism	0.000	0.000	0.210	0.836	0.000	0.000	0.002

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)	0	0.021	0	1	-0.043	0.043	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	-0.003	0.035	-0.086	0.932	-0.076	0.07	0.000
L3.Sporulation	0.000	0.000	0.108	0.915	0.000	0.00	0.001

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	0.019	0.031	0.611	0.548	-0.045	0.083	0.000
L3.Staphylococcus.aureus.infection	0.000	0.000	-0.830	0.417	0.000	0.000	0.033

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	-0.019	0.043	-0.446	0.661	-0.11	0.071	0.000
L3.Starch.and.sucrose.metabolism	0.000	0.000	0.509	0.616	0.00	0.000	0.013

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	0.002	0.023	0.089	0.930	-0.047	0.051	0.000
L3.Steroid.biosynthesis	0.000	0.000	-0.209	0.836	0.000	0.000	0.002

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	-0.002	0.034	-0.069	0.946	-0.073	0.068	0
L3.Steroid.hormone.biosynthesis	0.000	0.000	0.088	0.931	0.000	0.000	0

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	-0.012	0.025	-0.458	0.652	-0.065	0.041	0.
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	0.000	0.000	0.799	0.434	0.000	0.000	0.

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	-0.015	0.049	-0.308	0.762	-0.119	0.088	0.000
L3.Streptomycin.biosynthesis	0.000	0.000	0.340	0.738	0.000	0.000	0.006

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	-0.018	0.033	-0.544	0.593	-0.088	0.051	0.000
L3.Styrene.degradation	0.000	0.000	0.699	0.493	0.000	0.000	0.024

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	-0.007	0.049	-0.134	0.895	-0.109	0.096	0.000
L3.Sulfur.metabolism	0.000	0.000	0.149	0.883	0.000	0.000	0.001

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	-0.004	0.042	-0.099	0.922	-0.093	0.085	0.000
L3.Sulfur.relay.system	0.000	0.000	0.114	0.910	0.000	0.000	0.001

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	0.06	0.036	1.692	0.107	-0.014	0.134	0.000
L3.Synthesis.and.degradation.of.ketone.bodies	0.00	0.000	-2.010	0.059	0.000	0.000	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	0.002	0.024	0.076	0.940	-0.049	0.052	0.000
L3.Systemic.lupus.erythematosus	0.000	0.000	-0.156	0.878	0.000	0.000	0.001

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)	0	0.021	0	1	-0.043	0.043	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	0.021	0.053	0.400	0.694	-0.089	0.131	0.000
L3.Taurine.and.hypotaurine.metabolism	0.000	0.000	-0.436	0.668	0.000	0.000	0.009

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	0.009	0.048	0.195	0.847	-0.092	0.111	0.000
L3.Terpenoid.backbone.biosynthesis	0.000	0.000	-0.217	0.831	0.000	0.000	0.002

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	0.008	0.042	0.202	0.842	-0.08	0.097	0.000
L3.Tetracycline.biosynthesis	0.000	0.000	-0.233	0.818	0.00	0.000	0.003

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	0.001	0.047	0.015	0.989	-0.097	0.098	0
L3.Thiamine.metabolism	0.000	0.000	-0.016	0.987	0.000	0.000	0

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)	0	0.021	0	1	-0.043	0.043	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	-0.008	0.036	-0.217	0.831	-0.084	0.068	0.000
L3.Toluene.degradation	0.000	0.000	0.266	0.793	0.000	0.000	0.004

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	0.004	0.021	0.205	0.84	-0.04	0.049	0.000
L3.Toxoplasmosis	0.000	0.000	-0.937	0.36	0.00	0.000	0.042

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	-0.01	0.04	-0.246	0.809	-0.095	0.075	0.000
L3.Transcription.factors	0.00	0.00	0.287	0.777	0.000	0.000	0.004

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	0.016	0.049	0.337	0.739	-0.085	0.118	0.000
L3.Transcription.machinery	0.000	0.000	-0.374	0.712	0.000	0.000	0.007

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	-0.023	0.025	-0.901	0.379	-0.076	0.03	0.000
L3.Transcription.related.proteins	0.000	0.000	1.477	0.156	0.000	0.00	0.098

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	0	0.048	0.010	0.992	-0.1	0.101	0
L3.Translation.factors	0	0.000	-0.011	0.992	0.0	0.000	0

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	0.001	0.047	0.030	0.977	-0.096	0.099	0
L3.Translation.proteins	0.000	0.000	-0.033	0.974	0.000	0.000	0

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	-0.015	0.039	-0.391	0.700	-0.097	0.067	0.000
L3.Transporters	0.000	0.000	0.463	0.649	0.000	0.000	0.011

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	0.016	0.049	0.329	0.746	-0.086	0.119	0
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis	0.000	0.000	-0.364	0.720	0.000	0.000	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	-0.016	0.045	-0.354	0.727	-0.11	0.078	0.000
L3.Tryptophan.metabolism	0.000	0.000	0.401	0.693	0.00	0.000	0.008

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	0.015	0.046	0.327	0.747	-0.081	0.111	0.000
L3.Tuberculosis	0.000	0.000	-0.367	0.718	0.000	0.000	0.007

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	-0.01	0.042	-0.225	0.824	-0.098	0.079	0.000
L3.Two.component.system	0.00	0.000	0.260	0.798	0.000	0.000	0.003

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	0.012	0.049	0.245	0.809	-0.09	0.114	0.000
L3.Type.I.diabetes.mellitus	0.000	0.000	-0.272	0.788	0.00	0.000	0.004

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	-0.016	0.048	-0.332	0.744	-0.115	0.084	0.000
L3.Type.II.diabetes.mellitus	0.000	0.000	0.370	0.715	0.000	0.000	0.007

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	0.006	0.047	0.125	0.901	-0.092	0.104	0.000
L3.Tyrosine.metabolism	0.000	0.000	-0.141	0.890	0.000	0.000	0.001

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	-0.042	0.055	-0.768	0.452	-0.157	0.073	0.
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis	0.000	0.000	0.829	0.417	0.000	0.000	0.

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	0.029	0.038	0.760	0.457	-0.051	0.108	0.000
L3.Ubiquitin.system	0.000	0.000	-0.906	0.376	0.000	0.000	0.039

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)	0	0.021	0	1	-0.043	0.043	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	0	0.043	0.001	1	-0.091	0.091	0
L3.Valine..leucine.and.isoleucine.biosynthesis	0	0.000	-0.001	1	0.000	0.000	0

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	0.02	0.055	0.369	0.717	-0.094	0.135	0.000
L3.Valine..leucine.and.isoleucine.degradation	0.00	0.000	-0.399	0.694	0.000	0.000	0.008

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	0.001	0.024	0.046	0.964	-0.048	0.050	0.000
L3.Various.types.of.N.glycan.biosynthesis	0.000	0.001	-0.104	0.918	-0.002	0.002	0.001

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)	0	0.021	0	1	-0.043	0.043	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	0.002	0.022	0.068	0.946	-0.045	0.048	0.000
L3.Vasopressin.regulated.water.reabsorption	-0.006	0.031	-0.207	0.838	-0.071	0.058	0.002

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	-0.010	0.021	-0.489	0.631	-0.053	0.033	0.000
L3.Vibrio.cholerae.infection	0.021	0.013	1.645	0.116	-0.006	0.048	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	0.017	0.046	0.358	0.724	-0.08	0.113	0.000
L3.Vibrio.cholerae.pathogenic.cycle	0.000	0.000	-0.402	0.692	0.00	0.000	0.008

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	0.004	0.021	0.205	0.84	-0.04	0.049	0.000
L3.Viral.myocarditis	0.000	0.000	-0.937	0.36	0.00	0.000	0.042

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	0.015	0.049	0.304	0.764	-0.088	0.118	0.000
L3.Vitamin.B6.metabolism	0.000	0.000	-0.336	0.740	0.000	0.000	0.006

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)	0	0.021	0	1	-0.043	0.043	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	0.005	0.035	0.143	0.888	-0.067	0.077	0.000
L3.Xylene.degradation	0.000	0.000	-0.181	0.859	0.000	0.000	0.002

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	0.009	0.052	0.181	0.858	-0.099	0.118	0.000
L3.Zeatin.biosynthesis	0.000	0.000	-0.198	0.845	0.000	0.000	0.002

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	-0.035	0.028	-1.263	0.222	-0.094	0.023	0.000
L3.alpha.Linolenic.acid.metabolism	0.000	0.000	1.766	0.093	0.000	0.000	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	-0.02	0.047	-0.433	0.670	-0.119	0.078	0.000
L3.beta.Alanine.metabolism	0.00	0.000	0.484	0.634	0.000	0.000	0.012

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	-0.037	0.038	-0.979	0.340	-0.116	0.042	0.000
L3.beta.Lactam.resistance	0.000	0.000	1.165	0.258	0.000	0.000	0.064

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)	0	0.021	0	1	-0.043	0.043	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)	0	0.021	0	1	-0.043	0.043	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	0.004	0.021	0.205	0.84	-0.04	0.049	0.000
L3.p53.signaling.pathway	0.000	0.000	-0.937	0.36	0.00	0.000	0.042

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	4.130	0.951	4.343	0.000	2.124	6.136	0.000
chao1	0.001	0.005	0.292	0.774	-0.009	0.011	0.005

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	3.956	0.988	4.005	0.001	1.872	6.040	0.000
observed_otus	0.004	0.009	0.479	0.638	-0.014	0.022	0.013

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	0.000
PD_whole_tree	0.136	0.232	0.586	0.566	-0.353	0.625	0.019

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	4.090	0.001	1.710	5.355	0.000
shannon	0.537	0.466	1.152	0.265	-0.447	1.521	0.069

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	1.376	0.317	4.342	0.000	0.707	2.045	0.000
chao1	0.000	0.002	0.293	0.773	-0.003	0.004	0.005

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	1.318	0.329	4.004	0.001	0.624	2.012	0.000
observed_otus	0.001	0.003	0.480	0.637	-0.005	0.007	0.013

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	1.214	0.443	2.737	0.014	0.278	2.149	0.000
PD_whole_tree	0.045	0.077	0.586	0.566	-0.118	0.208	0.019

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	4.088	0.001	0.569	1.784	0.000
shannon	0.179	0.155	1.154	0.264	-0.148	0.507	0.069

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	1.328	0.416	3.191	0.005	0.450	2.206	0.000
chao1	0.002	0.002	1.142	0.269	-0.002	0.007	0.068

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	1.252	0.430	2.912	0.010	0.345	2.158	0.000

	Estimate	Std. Error	t value	Pr(>|t|)	2.5 %	97.5 %	R2
observed_otus	0.005	0.004	1.294	0.213	-0.003	0.013	0.085

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	0.559	1.448	0.166	-0.370	1.989	0.00
PD_whole_tree	0.173	0.097	1.780	0.093	-0.032	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	3.020	0.008	0.328	1.850	0.000
shannon	0.416	0.195	2.137	0.047	0.005	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	1.558	0.348	4.479	0.000	0.824	2.292	0.000
chao1	-0.001	0.002	-0.635	0.534	-0.005	0.003	0.022

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	1.503	0.365	4.114	0.001	0.732	2.274	0.00
observed_otus	-0.001	0.003	-0.422	0.678	-0.008	0.005	0.01

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	1.53	0.494	3.094	0.007	0.487	2.573	0.000
PD_whole_tree	-0.03	0.086	-0.351	0.730	-0.212	0.152	0.007

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	1.402	0.331	4.235	0.001	0.703	2.100	0.000
shannon	-0.021	0.179	-0.120	0.906	-0.398	0.356	0.001

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	1.434	0.357	4.016	0.001	0.681	2.188	0.000
chao1	0.000	0.002	0.128	0.900	-0.004	0.004	0.001

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	1.367	0.372	3.680	0.002	0.583	2.151	0.000
observed_otus	0.001	0.003	0.329	0.746	-0.006	0.008	0.006

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	1.123	0.495	2.268	0.037	0.078	2.169	0.000
PD_whole_tree	0.066	0.086	0.758	0.459	-0.117	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	0.001	0.558	1.951	0.000
shannon	0.141	0.178	0.79	0.440	-0.235	0.517	0.034

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	1.137	0.373	3.046	0.007	0.350	1.925	0.000
chao1	0.002	0.002	1.211	0.242	-0.002	0.006	0.075

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	1.086	0.387	2.806	0.012	0.269	1.902	0.000
observed_otus	0.004	0.003	1.305	0.209	-0.003	0.011	0.086

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	0.530	1.863	0.080	-0.131	2.107	0.000
PD_whole_tree	0.101	0.092	1.088	0.292	-0.094	0.296	0.062

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	2.787	0.013	0.213	1.540	0.000
shannon	0.418	0.170	2.461	0.025	0.060	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	3.438	0.483	7.115	0.000	2.414	4.462	0.000
chao1	-0.003	0.002	-1.068	0.301	-0.008	0.003	0.063

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	3.453	0.503	6.860	0.000	2.386	4.520	0.00
observed_otus	-0.005	0.004	-1.045	0.311	-0.014	0.005	0.06

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	3.354	0.698	4.809	0.000	1.875	4.833	0.000
PD_whole_tree	-0.066	0.121	-0.551	0.589	-0.322	0.189	0.018

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	3.137	0.467	6.722	0.000	2.148	4.126	0.000
shannon	-0.090	0.250	-0.361	0.723	-0.621	0.440	0.008

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