

# Association of microbiome vs strange situation in GIMA dataset

*Kai Xia*

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

Table 1: Correlation matrix of Mask task and strange situation

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

## Association analysis for covariates vs strange situation using linear model

Table 2: cvrt\_vs\_strange\_yr1: Summed vs AgeAt1yrVisit, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	8.189	3.490	2.346	0.026	1.040	15.338	0.000
AgeAt1yrVisit	-0.010	0.009	-1.129	0.269	-0.028	0.008	0.042

Table 3: cvrt\_vs\_strange\_yr1: Summed vs MAGE, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	5.255	2.12	2.479	0.019	0.913	9.597	0.000
MAGE	-0.033	0.07	-0.472	0.640	-0.176	0.110	0.008

Table 4: cvrt\_vs\_strange\_yr1: Summed vs PAGE, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	5.088	1.631	3.120	0.004	1.747	8.428	0.000
PAGE	-0.025	0.049	-0.514	0.611	-0.126	0.075	0.009

Table 5: cvrt\_vs\_strange\_yr1: Summed vs MEDUY, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.687	2.612	1.412	0.169	-1.663	9.038	0.000
MEDUY	0.036	0.162	0.224	0.825	-0.295	0.367	0.002

Table 6: cvrt\_vs\_strange\_yr1: Summed vs PEDUY, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	8.675	1.764	4.917	0.000	5.062	12.289	0.000
PEDUY	-0.284	0.112	-2.537	0.017	-0.514	-0.055	0.182

Table 7: cvrt\_vs\_strange\_yr1: Summed vs Income.code, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	4.333	0.542	7.990	0.000	3.221	5.446	0.000
Income.code.LOW	0.095	0.893	0.107	0.916	-1.738	1.928	0.000
Income.code.MID	-0.242	0.784	-0.309	0.760	-1.851	1.367	0.004

Table 8: cvrt\_vs\_strange\_yr1: Summed vs OLDERSIBLINGS, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	4.286	0.495	8.667	0.000	3.273	5.299	0
OLDERSIBLINGS	-0.036	0.677	-0.053	0.958	-1.423	1.351	0

Table 9: cvrt\_vs\_strange\_yr1: Summed vs SEX, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	4.4	1.013	4.343	0.00	2.325	6.475	0.000
SEX	-0.1	0.716	-0.140	0.89	-1.567	1.367	0.001

Table 10: cvrt\_vs\_strange\_yr1: Summed vs GESTAGEBIRTH, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	8.150	12.217	0.667	0.510	-16.875	33.175	0.000
GESTAGEBIRTH	-0.014	0.044	-0.318	0.753	-0.105	0.077	0.003

Table 11: cvrt\_vs\_strange\_yr1: Summed vs BW, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	0.023	3.065	0.008	0.994	-6.256	6.302	0.000

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
BW	0.001	0.001	1.392	0.175	-0.001	0.003	0.063

Table 12: cvrt\_vs\_strange\_yr1: Summed vs MaternalInfection, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	4.579	0.413	11.083	0.000	3.733	5.425	0.000
MaternalInfection	-0.852	0.682	-1.248	0.222	-2.249	0.546	0.051

Table 13: cvrt\_vs\_strange\_yr1: Summed vs MPSYCH, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	4.409	0.391	11.275	0.000	3.608	5.210	0.000
MPSYCH	-0.534	0.757	-0.705	0.486	-2.085	1.017	0.017

Table 14: cvrt\_vs\_strange\_yr1: Summed vs VITAMINDNEO, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	4.421	0.422	10.482	0.00	3.557	5.285	0.000
VITAMINDNEO	-0.421	0.697	-0.605	0.55	-1.848	1.006	0.012

Table 15: cvrt\_vs\_strange\_yr1: Summed vs PrePregBMI, df=26

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.857	0.378	10.211	0.000	3.081	4.634	0.000
PrePregBMI.Obese	1.143	1.281	0.892	0.380	-1.490	3.776	0.023
PrePregBMI.Overweight	1.810	0.801	2.258	0.033	0.162	3.457	0.149
PrePregBMI.Under	-0.857	1.772	-0.484	0.633	-4.499	2.785	0.007

Table 16: cvrt\_vs\_strange\_yr1: Summed vs ANTIBIOTIC\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.937	0.461	8.546	0.000	2.992	4.883	0.000
ANTIBIOTIC_1yr.1	0.755	0.688	1.097	0.282	-0.657	2.167	0.041
ANTIBIOTIC_1yr.NA	0.063	1.900	0.033	0.974	-3.835	3.960	0.000

Table 17: cvrt\_vs\_strange\_yr1: Summed vs FORMULA\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.941	0.446	8.842	0.000	3.027	4.856	0.000

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
FORMULA_1yr.1	0.809	0.693	1.167	0.253	-0.613	2.231	0.046
FORMULA_1yr.NA	0.059	1.891	0.031	0.975	-3.821	3.939	0.000

Table 18: cvrt\_vs\_strange\_yr1: Summed vs FORMULA\_6mo, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	4.438	0.460	9.643	0.000	3.495	5.380	0.00
FORMULA_6mo	-0.366	0.674	-0.543	0.591	-1.746	1.014	0.01

Table 19: cvrt\_vs\_strange\_yr1: Summed vs FEVER\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	4.714	0.378	12.460	0.000	3.938	5.491	0.000
FEVER_1yr.1	-1.589	0.720	-2.206	0.036	-3.067	-0.111	0.145
FEVER_1yr.NA	-0.714	1.775	-0.403	0.690	-4.355	2.927	0.005

Table 20: cvrt\_vs\_strange\_yr1: Summed vs DAYCARE, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	4.562	0.453	10.067	0.000	3.633	5.492	0.000
DAYCARE.1	-0.229	0.755	-0.303	0.764	-1.779	1.321	0.003
DAYCARE.NA	-1.363	0.929	-1.467	0.154	-3.268	0.543	0.075

Table 21: cvrt\_vs\_strange\_yr1: Summed vs CURBRFEED\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	4.357	0.503	8.663	0.000	3.325	5.389	0.000
CURBRFEED_1yr.1	-0.157	0.699	-0.225	0.824	-1.592	1.278	0.002
CURBRFEED_1yr.NA	-0.357	1.948	-0.183	0.856	-4.354	3.640	0.001

Table 22: cvrt\_vs\_strange\_yr1: Summed vs Milks\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	5.000	0.694	7.208	0.000	3.577	6.423	0.000
Milks_1yr.1	-0.955	0.796	-1.198	0.241	-2.589	0.680	0.051
Milks_1yr.NA	-1.000	1.962	-0.510	0.614	-5.026	3.026	0.009

Table 23: cvrt\_vs\_strange\_yr1: Summed vs FrenchFries\_1yr,  
df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.727	0.552	6.754	0.000	2.595	4.860	0.000
FrenchFries_1yr.1	0.884	0.701	1.262	0.218	-0.553	2.321	0.055
FrenchFries_1yr.NA	0.273	1.912	0.143	0.888	-3.650	4.195	0.001

Table 24: cvrt\_vs\_strange\_yr1: Summed vs SweetFoods-  
Drinks\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	4.0	0.625	6.404	0.000	2.718	5.282	0.00
SweetFoodsDrinks_1yr.1	0.4	0.752	0.532	0.599	-1.143	1.943	0.01
SweetFoodsDrinks_1yr.NA	0.0	1.975	0.000	1.000	-4.053	4.053	0.00

Table 25: cvrt\_vs\_strange\_yr1: Summed vs PeanutButter\_1yr,  
df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.600	0.574	6.277	0.000	2.423	4.777	0.000
PeanutButter_1yr.1	1.032	0.709	1.456	0.157	-0.422	2.485	0.072
PeanutButter_1yr.NA	0.400	1.902	0.210	0.835	-3.503	4.303	0.002

Table 26: cvrt\_vs\_strange\_yr1: Summed vs WHSTOTHER, df=22

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.500	1.227	2.853	0.009	0.956	6.044	0.000
WHSTOTHER.3.5 months	-0.500	2.125	-0.235	0.816	-4.906	3.906	0.002
WHSTOTHER.4 months	1.071	1.391	0.770	0.449	-1.813	3.956	0.047
WHSTOTHER.4.5 months	-0.500	2.125	-0.235	0.816	-4.906	3.906	0.002
WHSTOTHER.5 months	0.500	1.391	0.359	0.723	-2.385	3.385	0.010
WHSTOTHER.5.5 months	1.500	1.735	0.865	0.397	-2.098	5.098	0.032
WHSTOTHER.6 months	0.500	1.356	0.369	0.716	-2.313	3.313	0.012
WHSTOTHER.7 months	5.500	2.125	2.589	0.017	1.094	9.906	0.224

Table 27: cvrt\_vs\_strange\_yr1: Summed vs VITAMIND\_6mo,  
df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	4.737	0.404	11.737	0.000	3.909	5.565	0.000
VITAMIND_6mo.1	-1.112	0.741	-1.500	0.145	-2.633	0.409	0.069
VITAMIND_6mo.NA	-1.737	1.093	-1.589	0.124	-3.979	0.506	0.077

Table 28: cvrt\_vs\_strange\_yr1: Summed vs Cereals\_6mo, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	4.714	0.705	6.686	0.000	3.268	6.161	0.000
Cereals_6mo.1	-0.556	0.825	-0.675	0.506	-2.249	1.136	0.021
Cereals_6mo.NA	-0.714	1.169	-0.611	0.546	-3.113	1.685	0.017

Table 29: cvrt\_vs\_strange\_yr1: Summed vs STATE, df=15

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.000	2.072	1.448	0.168	-1.417	7.417	0.000
STATE.22	0.667	2.393	0.279	0.784	-4.434	5.767	0.006
STATE.23	1.500	2.538	0.591	0.563	-3.910	6.910	0.021
STATE.24	2.000	2.393	0.836	0.416	-3.100	7.100	0.055
STATE.26	0.000	2.538	0.000	1.000	-5.410	5.410	0.000
STATE.27	0.000	2.931	0.000	1.000	-6.247	6.247	0.000
STATE.29	0.500	2.538	0.197	0.846	-4.910	5.910	0.002
STATE.33	2.000	2.931	0.682	0.505	-4.247	8.247	0.020
STATE.35	2.000	2.538	0.788	0.443	-3.410	7.410	0.038
STATE.38	0.000	2.931	0.000	1.000	-6.247	6.247	0.000
STATE.39	3.000	2.538	1.182	0.256	-2.410	8.410	0.085
STATE.40	0.000	2.538	0.000	1.000	-5.410	5.410	0.000
STATE.41	1.000	2.393	0.418	0.682	-4.100	6.100	0.014
STATE.73	4.000	2.931	1.365	0.192	-2.247	10.247	0.078
STATE.NA	1.750	2.317	0.755	0.462	-3.188	6.688	0.054

Table 30: cvrt\_vs\_strange\_yr1: Summed vs TRAIT, df=13

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.000	1.651	1.818	0.092	-0.566	6.566	0.000
TRAIT.22	0.000	2.334	0.000	1.000	-5.043	5.043	0.000
TRAIT.24	0.000	2.022	0.000	1.000	-4.367	4.367	0.000
TRAIT.25	0.000	2.334	0.000	1.000	-5.043	5.043	0.000
TRAIT.26	4.500	2.022	2.226	0.044	0.133	8.867	0.211
TRAIT.27	0.667	1.906	0.350	0.732	-3.451	4.784	0.007
TRAIT.28	3.000	2.022	1.484	0.162	-1.367	7.367	0.094
TRAIT.29	0.000	2.334	0.000	1.000	-5.043	5.043	0.000
TRAIT.30	4.000	2.022	1.979	0.069	-0.367	8.367	0.167
TRAIT.32	0.000	2.334	0.000	1.000	-5.043	5.043	0.000
TRAIT.33	0.500	2.022	0.247	0.809	-3.867	4.867	0.003
TRAIT.36	0.000	2.334	0.000	1.000	-5.043	5.043	0.000
TRAIT.39	1.500	1.845	0.813	0.431	-2.487	5.487	0.043
TRAIT.48	0.000	2.334	0.000	1.000	-5.043	5.043	0.000
TRAIT.49	1.000	2.334	0.428	0.675	-4.043	6.043	0.005
TRAIT.52	0.000	2.334	0.000	1.000	-5.043	5.043	0.000
TRAIT.NA	1.250	1.845	0.677	0.510	-2.737	5.237	0.030

Table 31: cvrt\_vs\_strange\_yr1: Summed vs NegativeLifeEvents,  
df=19

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	4.250	0.966	4.400	0.000	2.228	6.272	0.000
NegativeLifeEvents.1	0.083	1.247	0.067	0.947	-2.527	2.693	0.000
NegativeLifeEvents.14	-1.250	2.160	-0.579	0.570	-5.771	3.271	0.011
NegativeLifeEvents.2	0.417	1.247	0.334	0.742	-2.193	3.027	0.006
NegativeLifeEvents.26	2.750	2.160	1.273	0.218	-1.771	7.271	0.056
NegativeLifeEvents.3	0.250	1.673	0.149	0.883	-3.252	3.752	0.001
NegativeLifeEvents.4	-1.250	1.673	-0.747	0.464	-4.752	2.252	0.022
NegativeLifeEvents.5	1.750	1.673	1.046	0.309	-1.752	5.252	0.043
NegativeLifeEvents.6	-1.250	2.160	-0.579	0.570	-5.771	3.271	0.011
NegativeLifeEvents.7	-1.250	2.160	-0.579	0.570	-5.771	3.271	0.011
NegativeLifeEvents.NA	-0.750	1.366	-0.549	0.589	-3.609	2.109	0.015

Table 32: cvrt\_vs\_strange\_yr1: Summed vs PositiveLifeEvents,  
df=19

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.500	0.647	5.408	0.000	2.145	4.855	0.000
PositiveLifeEvents.11	-0.500	1.712	-0.292	0.773	-4.084	3.084	0.002
PositiveLifeEvents.12	-0.500	1.712	-0.292	0.773	-4.084	3.084	0.002
PositiveLifeEvents.25	3.500	1.712	2.044	0.055	-0.084	7.084	0.090
PositiveLifeEvents.3	2.167	0.915	2.367	0.029	0.251	4.082	0.172
PositiveLifeEvents.5	0.167	1.121	0.149	0.883	-2.180	2.513	0.001
PositiveLifeEvents.6	-0.250	1.023	-0.244	0.810	-2.392	1.892	0.002
PositiveLifeEvents.7	-0.500	1.712	-0.292	0.773	-4.084	3.084	0.002
PositiveLifeEvents.8	2.500	1.712	1.460	0.161	-1.084	6.084	0.046
PositiveLifeEvents.9	3.000	1.294	2.318	0.032	0.291	5.709	0.128
PositiveLifeEvents.NA	0.000	1.023	0.000	1.000	-2.142	2.142	0.000

Table 33: cvrt\_vs\_strange\_yr1: Summed vs TotalLifeEvents,  
df=14

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.50	1.363	2.568	0.022	0.577	6.423	0.000
TotalLifeEvents.10	2.50	1.927	1.297	0.216	-1.634	6.634	0.071
TotalLifeEvents.11	0.50	2.360	0.212	0.835	-4.563	5.563	0.001
TotalLifeEvents.12	-0.50	2.360	-0.212	0.835	-5.563	4.563	0.001
TotalLifeEvents.13	-0.50	2.360	-0.212	0.835	-5.563	4.563	0.001
TotalLifeEvents.14	-0.50	2.360	-0.212	0.835	-5.563	4.563	0.001
TotalLifeEvents.15	-0.50	2.360	-0.212	0.835	-5.563	4.563	0.001
TotalLifeEvents.2	0.50	1.927	0.259	0.799	-3.634	4.634	0.003
TotalLifeEvents.27	3.50	2.360	1.483	0.160	-1.563	8.563	0.072
TotalLifeEvents.29	3.50	2.360	1.483	0.160	-1.563	8.563	0.072
TotalLifeEvents.4	-0.50	2.360	-0.212	0.835	-5.563	4.563	0.001
TotalLifeEvents.5	2.00	1.927	1.038	0.317	-2.134	6.134	0.045
TotalLifeEvents.6	1.00	1.927	0.519	0.612	-3.134	5.134	0.011
TotalLifeEvents.7	-0.25	1.669	-0.150	0.883	-3.830	3.330	0.001
TotalLifeEvents.8	1.75	1.669	1.049	0.312	-1.830	5.330	0.064

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
TotalLifeEvents.NA	0.00	1.669	0.000	1.000	-3.580	3.580	0.000

Table 34: cvrt\_vs\_strange\_yr1: Summed vs Stranger, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	4.400	0.476	9.235	0.000	3.424	5.376	0.000
Stranger	-0.267	0.674	-0.396	0.695	-1.647	1.113	0.005

Table 35: cvrt\_vs\_strange\_yr1: Average vs AgeAt1yrVisit, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	2.734	1.163	2.351	0.026	0.352	5.116	0.000
AgeAt1yrVisit	-0.003	0.003	-1.134	0.267	-0.009	0.003	0.042

Table 36: cvrt\_vs\_strange\_yr1: Average vs MAGE, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.750	0.706	2.478	0.020	0.304	3.197	0.000
MAGE	-0.011	0.023	-0.471	0.641	-0.059	0.037	0.008

Table 37: cvrt\_vs\_strange\_yr1: Average vs PAGE, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.696	0.543	3.122	0.004	0.583	2.809	0.000
PAGE	-0.008	0.016	-0.517	0.609	-0.042	0.025	0.009

Table 38: cvrt\_vs\_strange\_yr1: Average vs MEDUY, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.228	0.870	1.411	0.169	-0.555	3.011	0.000
MEDUY	0.012	0.054	0.224	0.824	-0.098	0.122	0.002

Table 39: cvrt\_vs\_strange\_yr1: Average vs PEDUY, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	2.889	0.588	4.914	0.000	1.685	4.094	0.000
PEDUY	-0.095	0.037	-2.534	0.017	-0.171	-0.018	0.181



Table 40: cvrt\_vs\_strange\_yr1: Average vs Income.code, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.444	0.181	7.991	0.000	1.073	1.815	0.000
Income.code.LOW	0.032	0.298	0.106	0.916	-0.579	0.642	0.000
Income.code.MID	-0.081	0.261	-0.312	0.758	-0.618	0.455	0.004

Table 41: cvrt\_vs\_strange\_yr1: Average vs OLDERSIBLINGS, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.428	0.165	8.665	0.000	1.090	1.765	0
OLDERSIBLINGS	-0.012	0.226	-0.051	0.959	-0.474	0.451	0

Table 42: cvrt\_vs\_strange\_yr1: Average vs SEX, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.465	0.338	4.339	0.000	0.773	2.157	0.000
SEX	-0.032	0.239	-0.136	0.893	-0.522	0.457	0.001

Table 43: cvrt\_vs\_strange\_yr1: Average vs GESTAGEBIRTH, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	2.715	4.071	0.667	0.510	-5.624	11.055	0.000
GESTAGEBIRTH	-0.005	0.015	-0.318	0.753	-0.035	0.026	0.003

Table 44: cvrt\_vs\_strange\_yr1: Average vs BW, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	0.007	1.021	0.007	0.994	-2.085	2.100	0.000
BW	0.000	0.000	1.393	0.175	0.000	0.001	0.063

Table 45: cvrt\_vs\_strange\_yr1: Average vs MaternalInfection, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.526	0.138	11.082	0.000	1.244	1.808	0.000
MaternalInfection	-0.284	0.227	-1.249	0.222	-0.750	0.182	0.051

Table 46: cvrt\_vs\_strange\_yr1: Average vs MPSYCH, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.469	0.130	11.274	0.000	1.202	1.736	0.000

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
MPSYCH	-0.178	0.252	-0.705	0.487	-0.695	0.339	0.017

Table 47: cvrt\_vs\_strange\_yr1: Average vs VITAMINDNEO, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.473	0.141	10.482	0.00	1.185	1.761	0.000
VITAMINDNEO	-0.140	0.232	-0.605	0.55	-0.616	0.335	0.012

Table 48: cvrt\_vs\_strange\_yr1: Average vs PrePregBMI, df=26

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.285	0.126	10.210	0.000	1.026	1.544	0.000
PrePregBMI.Obese	0.380	0.427	0.890	0.382	-0.498	1.257	0.023
PrePregBMI.Overweight	0.603	0.267	2.258	0.033	0.054	1.152	0.149
PrePregBMI.Under	-0.285	0.590	-0.483	0.633	-1.499	0.928	0.007

Table 49: cvrt\_vs\_strange\_yr1: Average vs ANTIBIOTIC\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.312	0.154	8.545	0.000	0.997	1.627	0.000
ANTIBIOTIC_1yr.1	0.252	0.229	1.099	0.282	-0.219	0.722	0.041
ANTIBIOTIC_1yr.NA	0.018	0.633	0.029	0.977	-1.281	1.317	0.000

Table 50: cvrt\_vs\_strange\_yr1: Average vs FORMULA\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.313	0.149	8.841	0.000	1.008	1.618	0.000
FORMULA_1yr.1	0.270	0.231	1.171	0.252	-0.203	0.744	0.046
FORMULA_1yr.NA	0.017	0.630	0.027	0.979	-1.276	1.310	0.000

Table 51: cvrt\_vs\_strange\_yr1: Average vs FORMULA\_6mo, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.478	0.153	9.638	0.000	1.164	1.792	0.00
FORMULA_6mo	-0.121	0.224	-0.539	0.594	-0.581	0.339	0.01

Table 52: cvrt\_vs\_strange\_yr1: Average vs FEVER\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.571	0.126	12.461	0.000	1.312	1.830	0.000
FEVER_1yr.1	-0.530	0.240	-2.207	0.036	-1.022	-0.037	0.145
FEVER_1yr.NA	-0.241	0.591	-0.407	0.687	-1.454	0.972	0.005

Table 53: cvrt\_vs\_strange\_yr1: Average vs DAYCARE, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.520	0.151	10.064	0.000	1.210	1.830	0.000
DAYCARE.1	-0.076	0.252	-0.300	0.766	-0.592	0.441	0.003
DAYCARE.NA	-0.454	0.310	-1.467	0.154	-1.089	0.181	0.075

Table 54: cvrt\_vs\_strange\_yr1: Average vs CURBRFEED\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.452	0.168	8.665	0.000	1.108	1.796	0.000
CURBRFEED_1yr.1	-0.053	0.233	-0.227	0.822	-0.531	0.425	0.002
CURBRFEED_1yr.NA	-0.122	0.649	-0.188	0.852	-1.454	1.210	0.001

Table 55: cvrt\_vs\_strange\_yr1: Average vs Milks\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.667	0.231	7.213	0.000	1.193	2.141	0.000
Milks_1yr.1	-0.319	0.265	-1.204	0.239	-0.864	0.225	0.052
Milks_1yr.NA	-0.337	0.654	-0.516	0.610	-1.678	1.004	0.010

Table 56: cvrt\_vs\_strange\_yr1: Average vs FrenchFries\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.242	0.184	6.753	0.000	0.864	1.619	0.000
FrenchFries_1yr.1	0.295	0.233	1.263	0.217	-0.184	0.774	0.055
FrenchFries_1yr.NA	0.088	0.637	0.138	0.891	-1.219	1.395	0.001

Table 57: cvrt\_vs\_strange\_yr1: Average vs SweetFoodsDrinks\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.333	0.208	6.406	0.000	0.906	1.760	0.00
SweetFoodsDrinks_1yr.1	0.133	0.251	0.529	0.601	-0.382	0.647	0.01
SweetFoodsDrinks_1yr.NA	-0.003	0.658	-0.005	0.996	-1.354	1.347	0.00

Table 58: cvrt\_vs\_strange\_yr1: Average vs PeanutButter\_1yr,  
df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.200	0.191	6.278	0.000	0.808	1.592	0.000
PeanutButter_1yr.1	0.343	0.236	1.453	0.158	-0.141	0.828	0.072
PeanutButter_1yr.NA	0.130	0.634	0.205	0.839	-1.171	1.431	0.001

Table 59: cvrt\_vs\_strange\_yr1: Average vs WHSTOTHER, df=22

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.165	0.409	2.850	0.009	0.317	2.013	0.000
WHSTOTHER.3.5 months	-0.165	0.708	-0.233	0.818	-1.633	1.303	0.002
WHSTOTHER.4 months	0.358	0.463	0.772	0.448	-0.603	1.319	0.047
WHSTOTHER.4.5 months	-0.165	0.708	-0.233	0.818	-1.633	1.303	0.002
WHSTOTHER.5 months	0.168	0.463	0.362	0.721	-0.793	1.129	0.010
WHSTOTHER.5.5 months	0.500	0.578	0.865	0.396	-0.699	1.699	0.032
WHSTOTHER.6 months	0.168	0.452	0.372	0.713	-0.769	1.106	0.012
WHSTOTHER.7 months	1.835	0.708	2.592	0.017	0.367	3.303	0.225

Table 60: cvrt\_vs\_strange\_yr1: Average vs VITAMIND\_6mo,  
df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.578	0.134	11.736	0.000	1.302	1.854	0.000
VITAMIND_6mo.1	-0.371	0.247	-1.501	0.145	-0.878	0.136	0.069
VITAMIND_6mo.NA	-0.578	0.364	-1.588	0.124	-1.326	0.169	0.077

Table 61: cvrt\_vs\_strange\_yr1: Average vs Cereals\_6mo, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.570	0.235	6.681	0.000	1.088	2.052	0.000
Cereals_6mo.1	-0.184	0.275	-0.670	0.508	-0.748	0.380	0.020
Cereals_6mo.NA	-0.237	0.390	-0.609	0.547	-1.037	0.562	0.017

Table 62: cvrt\_vs\_strange\_yr1: Average vs STATE, df=15

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.000	0.691	1.448	0.168	-0.472	2.472	0.000
STATE.22	0.220	0.797	0.276	0.786	-1.480	1.920	0.006
STATE.23	0.500	0.846	0.591	0.563	-1.303	2.303	0.021
STATE.24	0.667	0.797	0.836	0.416	-1.033	2.366	0.055
STATE.26	0.000	0.846	0.000	1.000	-1.803	1.803	0.000
STATE.27	0.000	0.977	0.000	1.000	-2.082	2.082	0.000
STATE.29	0.165	0.846	0.195	0.848	-1.638	1.968	0.002
STATE.33	0.670	0.977	0.686	0.503	-1.412	2.752	0.020
STATE.35	0.665	0.846	0.786	0.444	-1.138	2.468	0.038

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
STATE.38	0.000	0.977	0.000	1.000	-2.082	2.082	0.000
STATE.39	1.000	0.846	1.182	0.256	-0.803	2.803	0.085
STATE.40	0.000	0.846	0.000	1.000	-1.803	1.803	0.000
STATE.41	0.333	0.797	0.418	0.682	-1.366	2.033	0.014
STATE.73	1.330	0.977	1.362	0.193	-0.752	3.412	0.078
STATE.NA	0.583	0.772	0.754	0.462	-1.063	2.228	0.053

Table 63: cvrt\_vs\_strange\_yr1: Average vs TRAIT, df=13

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.000	0.549	1.821	0.092	-0.186	2.186	0.000
TRAIT.22	0.000	0.776	0.000	1.000	-1.677	1.677	0.000
TRAIT.24	0.000	0.672	0.000	1.000	-1.453	1.453	0.000
TRAIT.25	0.000	0.776	0.000	1.000	-1.677	1.677	0.000
TRAIT.26	1.500	0.672	2.231	0.044	0.047	2.953	0.211
TRAIT.27	0.220	0.634	0.347	0.734	-1.150	1.590	0.007
TRAIT.28	1.000	0.672	1.487	0.161	-0.453	2.453	0.094
TRAIT.29	0.000	0.776	0.000	1.000	-1.677	1.677	0.000
TRAIT.30	1.335	0.672	1.985	0.069	-0.118	2.788	0.167
TRAIT.32	0.000	0.776	0.000	1.000	-1.677	1.677	0.000
TRAIT.33	0.165	0.672	0.245	0.810	-1.288	1.618	0.003
TRAIT.36	0.000	0.776	0.000	1.000	-1.677	1.677	0.000
TRAIT.39	0.500	0.614	0.815	0.430	-0.826	1.826	0.044
TRAIT.48	0.000	0.776	0.000	1.000	-1.677	1.677	0.000
TRAIT.49	0.330	0.776	0.425	0.678	-1.347	2.007	0.005
TRAIT.52	0.000	0.776	0.000	1.000	-1.677	1.677	0.000
TRAIT.NA	0.415	0.614	0.676	0.511	-0.911	1.741	0.030

Table 64: cvrt\_vs\_strange\_yr1: Average vs NegativeLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.418	0.322	4.403	0.000	0.744	2.091	0.000
NegativeLifeEvents.1	0.026	0.416	0.062	0.951	-0.844	0.896	0.000
NegativeLifeEvents.14	-0.417	0.720	-0.580	0.569	-1.924	1.089	0.012
NegativeLifeEvents.2	0.138	0.416	0.331	0.744	-0.732	1.007	0.006
NegativeLifeEvents.26	0.912	0.720	1.268	0.220	-0.594	2.419	0.055
NegativeLifeEvents.3	0.083	0.558	0.148	0.884	-1.085	1.250	0.001
NegativeLifeEvents.4	-0.418	0.558	-0.749	0.463	-1.585	0.750	0.022
NegativeLifeEvents.5	0.582	0.558	1.045	0.309	-0.585	1.750	0.043
NegativeLifeEvents.6	-0.417	0.720	-0.580	0.569	-1.924	1.089	0.012
NegativeLifeEvents.7	-0.417	0.720	-0.580	0.569	-1.924	1.089	0.012
NegativeLifeEvents.NA	-0.252	0.455	-0.555	0.586	-1.205	0.700	0.015

Table 65: cvrt\_vs\_strange\_yr1: Average vs PositiveLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.167	0.216	5.406	0.000	0.715	1.618	0.000
PositiveLifeEvents.11	-0.167	0.571	-0.292	0.774	-1.362	1.028	0.002
PositiveLifeEvents.12	-0.167	0.571	-0.292	0.774	-1.362	1.028	0.002
PositiveLifeEvents.25	1.163	0.571	2.037	0.056	-0.032	2.358	0.090
PositiveLifeEvents.3	0.722	0.305	2.365	0.029	0.083	1.360	0.172
PositiveLifeEvents.5	0.057	0.374	0.152	0.881	-0.726	0.839	0.001
PositiveLifeEvents.6	-0.084	0.341	-0.247	0.808	-0.798	0.630	0.002
PositiveLifeEvents.7	-0.167	0.571	-0.292	0.774	-1.362	1.028	0.002
PositiveLifeEvents.8	0.833	0.571	1.459	0.161	-0.362	2.028	0.046
PositiveLifeEvents.9	0.998	0.432	2.313	0.032	0.095	1.902	0.128
PositiveLifeEvents.NA	-0.002	0.341	-0.005	0.996	-0.716	0.713	0.000

Table 66: cvrt\_vs\_strange\_yr1: Average vs TotalLifeEvents, df=14

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.165	0.454	2.565	0.022	0.191	2.139	0.000
TotalLifeEvents.10	0.835	0.642	1.300	0.215	-0.542	2.212	0.071
TotalLifeEvents.11	0.165	0.787	0.210	0.837	-1.522	1.852	0.001
TotalLifeEvents.12	-0.165	0.787	-0.210	0.837	-1.852	1.522	0.001
TotalLifeEvents.13	-0.165	0.787	-0.210	0.837	-1.852	1.522	0.001
TotalLifeEvents.14	-0.165	0.787	-0.210	0.837	-1.852	1.522	0.001
TotalLifeEvents.15	-0.165	0.787	-0.210	0.837	-1.852	1.522	0.001
TotalLifeEvents.2	0.170	0.642	0.265	0.795	-1.207	1.547	0.003
TotalLifeEvents.27	1.165	0.787	1.481	0.161	-0.522	2.852	0.071
TotalLifeEvents.29	1.165	0.787	1.481	0.161	-0.522	2.852	0.071
TotalLifeEvents.4	-0.165	0.787	-0.210	0.837	-1.852	1.522	0.001
TotalLifeEvents.5	0.670	0.642	1.043	0.314	-0.707	2.047	0.046
TotalLifeEvents.6	0.335	0.642	0.522	0.610	-1.042	1.712	0.011
TotalLifeEvents.7	-0.082	0.556	-0.148	0.884	-1.275	1.110	0.001
TotalLifeEvents.8	0.585	0.556	1.052	0.311	-0.608	1.778	0.065
TotalLifeEvents.NA	0.000	0.556	0.000	1.000	-1.193	1.193	0.000

Table 67: cvrt\_vs\_strange\_yr1: Average vs Stranger, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.466	0.159	9.234	0.000	1.141	1.791	0.000
Stranger	-0.089	0.225	-0.395	0.696	-0.549	0.371	0.005

Table 68: cvrt\_vs\_strange\_yr1: Max vs AgeAt1yrVisit, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.242	1.680	1.929	0.064	-0.200	6.683	0.000
AgeAt1yrVisit	-0.004	0.004	-0.902	0.375	-0.013	0.005	0.027

Table 69: cvrt\_vs\_strange\_yr1: Max vs MAGE, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.776	1.016	1.748	0.091	-0.306	3.858	0
MAGE	-0.001	0.033	-0.043	0.966	-0.070	0.067	0

Table 70: cvrt\_vs\_strange\_yr1: Max vs PAGE, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.699	0.782	2.172	0.038	0.097	3.302	0
PAGE	0.001	0.024	0.044	0.965	-0.047	0.049	0

Table 71: cvrt\_vs\_strange\_yr1: Max vs MEDUY, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	0.354	1.221	0.29	0.774	-2.146	2.854	0.000
MEDUY	0.086	0.075	1.14	0.264	-0.069	0.241	0.043

Table 72: cvrt\_vs\_strange\_yr1: Max vs PEDUY, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.343	0.882	3.791	0.001	1.536	5.149	0.000
PEDUY	-0.104	0.056	-1.853	0.074	-0.219	0.011	0.106

Table 73: cvrt\_vs\_strange\_yr1: Max vs Income.code, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.667	0.256	6.502	0.000	1.141	2.193	0.000
Income.code.LOW	-0.095	0.422	-0.226	0.823	-0.962	0.771	0.002
Income.code.MID	0.242	0.371	0.654	0.519	-0.518	1.003	0.018

Table 74: cvrt\_vs\_strange\_yr1: Max vs OLDERSIBLINGS, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.857	0.234	7.937	0.000	1.378	2.336	0.000
OLDERSIBLINGS	-0.232	0.320	-0.725	0.475	-0.888	0.424	0.018

Table 75: cvrt\_vs\_strange\_yr1: Max vs SEX, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.80	0.484	3.720	0.001	0.809	2.791	0.000
SEX	-0.05	0.342	-0.146	0.885	-0.751	0.651	0.001

Table 76: cvrt\_vs\_strange\_yr1: Max vs GESTAGEBIRTH, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.246	5.838	0.556	0.583	-8.713	15.205	0.000
GESTAGEBIRTH	-0.005	0.021	-0.259	0.797	-0.049	0.038	0.002

Table 77: cvrt\_vs\_strange\_yr1: Max vs BW, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	-0.151	1.471	-0.103	0.919	-3.164	2.862	0.000
BW	0.001	0.000	1.289	0.208	0.000	0.001	0.054

Table 78: cvrt\_vs\_strange\_yr1: Max vs MaternalInfection, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.947	0.191	10.173	0.000	1.555	2.339	0.000
MaternalInfection	-0.584	0.316	-1.847	0.075	-1.231	0.064	0.105

Table 79: cvrt\_vs\_strange\_yr1: Max vs MPSYCH, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.818	0.186	9.784	0.000	1.438	2.199	0.000
MPSYCH	-0.318	0.360	-0.884	0.384	-1.055	0.419	0.026

Table 80: cvrt\_vs\_strange\_yr1: Max vs VITAMINDNEO, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.684	0.202	8.331	0.000	1.27	2.098	0.000
VITAMINDNEO	0.134	0.334	0.401	0.691	-0.55	0.818	0.006

Table 81: cvrt\_vs\_strange\_yr1: Max vs PrePregBMI, df=26

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.619	0.190	8.505	0.000	1.228	2.010	0.000
PrePregBMI.Obese	0.381	0.646	0.590	0.560	-0.946	1.708	0.011
PrePregBMI.Overweight	0.548	0.404	1.356	0.187	-0.282	1.378	0.060
PrePregBMI.Under	-0.619	0.893	-0.693	0.494	-2.454	1.216	0.015

Table 82: cvrt\_vs\_strange\_yr1: Max vs ANTIBIOTIC\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.625	0.223	7.294	0.000	1.168	2.082	0.000
ANTIBIOTIC_1yr.1	0.221	0.333	0.665	0.512	-0.462	0.904	0.015



	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
ANTIBIOTIC_1yr.NA	0.375	0.919	0.408	0.686	-1.510	2.260	0.006

Table 83: cvrt\_vs\_strange\_yr1: Max vs FORMULA\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.647	0.217	7.602	0.000	1.202	2.092	0.000
FORMULA_1yr.1	0.186	0.337	0.553	0.585	-0.505	0.877	0.011
FORMULA_1yr.NA	0.353	0.919	0.384	0.704	-1.533	2.239	0.005

Table 84: cvrt\_vs\_strange\_yr1: Max vs FORMULA\_6mo, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.875	0.217	8.624	0.000	1.430	2.320	0.00
FORMULA_6mo	-0.304	0.318	-0.954	0.348	-0.956	0.348	0.03

Table 85: cvrt\_vs\_strange\_yr1: Max vs FEVER\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.952	0.177	11.011	0.000	1.589	2.316	0.000
FEVER_1yr.1	-0.827	0.338	-2.451	0.021	-1.520	-0.135	0.173
FEVER_1yr.NA	0.048	0.832	0.057	0.955	-1.659	1.754	0.000

Table 86: cvrt\_vs\_strange\_yr1: Max vs DAYCARE, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	2.000	0.21	9.531	0.000	1.569	2.431	0.000
DAYCARE.1	-0.444	0.35	-1.271	0.215	-1.162	0.273	0.051
DAYCARE.NA	-0.800	0.43	-1.860	0.074	-1.682	0.082	0.110

Table 87: cvrt\_vs\_strange\_yr1: Max vs CURBRFEED\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.643	0.239	6.870	0.000	1.152	2.134	0.000
CURBRFEED_1yr.1	0.157	0.332	0.473	0.640	-0.525	0.839	0.008
CURBRFEED_1yr.NA	0.357	0.926	0.386	0.703	-1.543	2.257	0.005

Table 88: cvrt\_vs\_strange\_yr1: Max vs Milks\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	2.000	0.334	5.987	0.000	1.315	2.685	0.000
Milks_1yr.1	-0.364	0.384	-0.948	0.351	-1.151	0.423	0.033

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Milks_1yr.NA	0.000	0.945	0.000	1.000	-1.939	1.939	0.000

Table 89: cvrt\_vs\_strange\_yr1: Max vs FrenchFries\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.455	0.263	5.536	0.000	0.915	1.994	0.000
FrenchFries_1yr.1	0.434	0.334	1.302	0.204	-0.250	1.119	0.057
FrenchFries_1yr.NA	0.545	0.910	0.599	0.554	-1.322	2.413	0.012

Table 90: cvrt\_vs\_strange\_yr1: Max vs SweetFoodsDrinks\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.778	0.299	5.941	0.000	1.164	2.392	0.000
SweetFoodsDrinks_1yr.1	-0.078	0.360	-0.216	0.831	-0.817	0.661	0.002
SweetFoodsDrinks_1yr.NA	0.222	0.946	0.235	0.816	-1.719	2.164	0.002

Table 91: cvrt\_vs\_strange\_yr1: Max vs PeanutButter\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.500	0.279	5.375	0.000	0.927	2.073	0.000
PeanutButter_1yr.1	0.342	0.345	0.992	0.330	-0.365	1.050	0.034
PeanutButter_1yr.NA	0.500	0.926	0.540	0.593	-1.399	2.399	0.010

Table 92: cvrt\_vs\_strange\_yr1: Max vs WHSTOTHER, df=22

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.500	0.651	2.305	0.031	0.151	2.849	0.000
WHSTOTHER.3.5 months	-0.500	1.127	-0.444	0.662	-2.837	1.837	0.008
WHSTOTHER.4 months	0.357	0.738	0.484	0.633	-1.173	1.887	0.024
WHSTOTHER.4.5 months	-0.500	1.127	-0.444	0.662	-2.837	1.837	0.008
WHSTOTHER.5 months	0.071	0.738	0.097	0.924	-1.459	1.601	0.001
WHSTOTHER.5.5 months	0.500	0.920	0.543	0.592	-1.408	2.408	0.016
WHSTOTHER.6 months	0.278	0.719	0.386	0.703	-1.214	1.770	0.017
WHSTOTHER.7 months	1.500	1.127	1.331	0.197	-0.837	3.837	0.075

Table 93: cvrt\_vs\_strange\_yr1: Max vs VITAMIND\_6mo, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.947	0.192	10.133	0.000	1.553	2.342	0.000
VITAMIND_6mo.1	-0.447	0.353	-1.267	0.216	-1.172	0.277	0.049
VITAMIND_6mo.NA	-0.947	0.520	-1.820	0.080	-2.015	0.120	0.101

Table 94: cvrt\_vs\_strange\_yr1: Max vs Cereals\_6mo, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.857	0.338	5.501	0.000	1.164	2.550	0.000
Cereals_6mo.1	-0.120	0.395	-0.305	0.763	-0.931	0.690	0.004
Cereals_6mo.NA	-0.357	0.560	-0.638	0.529	-1.506	0.792	0.019

Table 95: cvrt\_vs\_strange\_yr1: Max vs STATE, df=15

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.000	0.940	1.064	0.304	-1.003	3.003	0.000
STATE.22	0.667	1.085	0.614	0.548	-1.646	2.980	0.025
STATE.23	1.000	1.151	0.869	0.399	-1.453	3.453	0.038
STATE.24	1.333	1.085	1.229	0.238	-0.980	3.646	0.099
STATE.26	0.000	1.151	0.000	1.000	-2.453	2.453	0.000
STATE.27	0.000	1.329	0.000	1.000	-2.833	2.833	0.000
STATE.29	0.500	1.151	0.434	0.670	-1.953	2.953	0.010
STATE.33	2.000	1.329	1.505	0.153	-0.833	4.833	0.080
STATE.35	1.000	1.151	0.869	0.399	-1.453	3.453	0.038
STATE.38	0.000	1.329	0.000	1.000	-2.833	2.833	0.000
STATE.39	1.000	1.151	0.869	0.399	-1.453	3.453	0.038
STATE.40	0.000	1.151	0.000	1.000	-2.453	2.453	0.000
STATE.41	0.667	1.085	0.614	0.548	-1.646	2.980	0.025
STATE.73	2.000	1.329	1.505	0.153	-0.833	4.833	0.080
STATE.NA	0.750	1.051	0.714	0.486	-1.490	2.990	0.040

Table 96: cvrt\_vs\_strange\_yr1: Max vs TRAIT, df=13

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.000	0.716	1.396	0.186	-0.547	2.547	0.000
TRAIT.22	0.000	1.013	0.000	1.000	-2.188	2.188	0.000
TRAIT.24	0.000	0.877	0.000	1.000	-1.895	1.895	0.000
TRAIT.25	0.000	1.013	0.000	1.000	-2.188	2.188	0.000
TRAIT.26	2.000	0.877	2.280	0.040	0.105	3.895	0.170
TRAIT.27	0.667	0.827	0.806	0.435	-1.120	2.453	0.027
TRAIT.28	2.000	0.877	2.280	0.040	0.105	3.895	0.170
TRAIT.29	0.000	1.013	0.000	1.000	-2.188	2.188	0.000
TRAIT.30	2.000	0.877	2.280	0.040	0.105	3.895	0.170
TRAIT.32	0.000	1.013	0.000	1.000	-2.188	2.188	0.000
TRAIT.33	0.500	0.877	0.570	0.578	-1.395	2.395	0.011
TRAIT.36	0.000	1.013	0.000	1.000	-2.188	2.188	0.000
TRAIT.39	0.750	0.801	0.937	0.366	-0.980	2.480	0.045
TRAIT.48	0.000	1.013	0.000	1.000	-2.188	2.188	0.000
TRAIT.49	1.000	1.013	0.987	0.341	-1.188	3.188	0.022
TRAIT.52	0.000	1.013	0.000	1.000	-2.188	2.188	0.000
TRAIT.NA	0.750	0.801	0.937	0.366	-0.980	2.480	0.045

Table 97: cvrt\_vs\_strange\_yr1: Max vs NegativeLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	2.000	0.464	4.314	0.000	1.030	2.970	0.000
NegativeLifeEvents.1	-0.333	0.598	-0.557	0.584	-1.586	0.919	0.017
NegativeLifeEvents.14	-1.000	1.037	-0.965	0.347	-3.170	1.170	0.030
NegativeLifeEvents.2	0.000	0.598	0.000	1.000	-1.253	1.253	0.000
NegativeLifeEvents.26	1.000	1.037	0.965	0.347	-1.170	3.170	0.030
NegativeLifeEvents.3	0.000	0.803	0.000	1.000	-1.681	1.681	0.000
NegativeLifeEvents.4	-1.000	0.803	-1.245	0.228	-2.681	0.681	0.058
NegativeLifeEvents.5	0.000	0.803	0.000	1.000	-1.681	1.681	0.000
NegativeLifeEvents.6	-1.000	1.037	-0.965	0.347	-3.170	1.170	0.030
NegativeLifeEvents.7	-1.000	1.037	-0.965	0.347	-3.170	1.170	0.030
NegativeLifeEvents.NA	-0.500	0.656	-0.763	0.455	-1.872	0.872	0.027

Table 98: cvrt\_vs\_strange\_yr1: Max vs PositiveLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.333	0.319	4.183	0.001	0.666	2.001	0.000
PositiveLifeEvents.11	-0.333	0.843	-0.395	0.697	-2.099	1.432	0.003
PositiveLifeEvents.12	-0.333	0.843	-0.395	0.697	-2.099	1.432	0.003
PositiveLifeEvents.25	1.667	0.843	1.976	0.063	-0.099	3.432	0.086
PositiveLifeEvents.3	1.000	0.451	2.218	0.039	0.056	1.944	0.154
PositiveLifeEvents.5	0.333	0.552	0.604	0.553	-0.822	1.489	0.010
PositiveLifeEvents.6	-0.083	0.504	-0.165	0.870	-1.138	0.972	0.001
PositiveLifeEvents.7	-0.333	0.843	-0.395	0.697	-2.099	1.432	0.003
PositiveLifeEvents.8	1.667	0.843	1.976	0.063	-0.099	3.432	0.086
PositiveLifeEvents.9	1.167	0.638	1.830	0.083	-0.168	2.501	0.082
PositiveLifeEvents.NA	0.167	0.504	0.331	0.745	-0.888	1.222	0.003

Table 99: cvrt\_vs\_strange\_yr1: Max vs TotalLifeEvents, df=14

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.50	0.620	2.421	0.030	0.171	2.829	0.000
TotalLifeEvents.10	0.50	0.876	0.571	0.577	-1.379	2.379	0.014
TotalLifeEvents.11	0.50	1.073	0.466	0.648	-1.802	2.802	0.007
TotalLifeEvents.12	-0.50	1.073	-0.466	0.648	-2.802	1.802	0.007
TotalLifeEvents.13	-0.50	1.073	-0.466	0.648	-2.802	1.802	0.007
TotalLifeEvents.14	-0.50	1.073	-0.466	0.648	-2.802	1.802	0.007
TotalLifeEvents.15	-0.50	1.073	-0.466	0.648	-2.802	1.802	0.007
TotalLifeEvents.2	0.00	0.876	0.000	1.000	-1.879	1.879	0.000
TotalLifeEvents.27	1.50	1.073	1.398	0.184	-0.802	3.802	0.063
TotalLifeEvents.29	1.50	1.073	1.398	0.184	-0.802	3.802	0.063
TotalLifeEvents.4	-0.50	1.073	-0.466	0.648	-2.802	1.802	0.007
TotalLifeEvents.5	1.50	0.876	1.712	0.109	-0.379	3.379	0.123
TotalLifeEvents.6	0.50	0.876	0.571	0.577	-1.379	2.379	0.014
TotalLifeEvents.7	-0.25	0.759	-0.329	0.747	-1.878	1.378	0.006
TotalLifeEvents.8	0.50	0.759	0.659	0.521	-1.128	2.128	0.025
TotalLifeEvents.NA	0.00	0.759	0.000	1.000	-1.628	1.628	0.000

Table 100: cvrt\_vs\_strange\_yr1: Max vs Stranger, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.733	0.228	7.597	0	1.266	2.201	0
Stranger	0.000	0.323	0.000	1	-0.661	0.661	0

Table 101: cvrt\_vs\_strange\_yr1: Episode3.1 vs AgeAt1yrVisit, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	2.970	1.277	2.327	0.027	0.355	5.585	0.000
AgeAt1yrVisit	-0.004	0.003	-1.262	0.217	-0.011	0.003	0.052

Table 102: cvrt\_vs\_strange\_yr1: Episode3.1 vs MAGE, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.496	0.782	1.912	0.066	-0.107	3.098	0.000
MAGE	-0.004	0.026	-0.167	0.869	-0.057	0.048	0.001

Table 103: cvrt\_vs\_strange\_yr1: Episode3.1 vs PAGE, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.500	0.602	2.492	0.019	0.267	2.733	0.000
PAGE	-0.004	0.018	-0.227	0.822	-0.041	0.033	0.002

Table 104: cvrt\_vs\_strange\_yr1: Episode3.1 vs MEDUY, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	0.677	0.952	0.711	0.483	-1.274	2.628	0.000
MEDUY	0.043	0.059	0.730	0.471	-0.078	0.164	0.018

Table 105: cvrt\_vs\_strange\_yr1: Episode3.1 vs PEDUY, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	2.451	0.689	3.559	0.001	1.04	3.862	0.000
PEDUY	-0.070	0.044	-1.599	0.121	-0.16	0.020	0.081

Table 106: cvrt\_vs\_strange\_yr1: Episode3.1 vs Income.code, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.250	0.196	6.388	0.000	0.849	1.651	0.000
Income.code.LOW	0.036	0.322	0.111	0.913	-0.626	0.697	0.000

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Income.code.MID	0.295	0.283	1.044	0.306	-0.285	0.876	0.044

Table 107: cvrt\_vs\_strange\_yr1: Episode3.1 vs OLDERSIBLINGS, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.357	0.182	7.463	0.000	0.985	1.730	0
OLDERSIBLINGS	0.018	0.249	0.072	0.943	-0.492	0.528	0

Table 108: cvrt\_vs\_strange\_yr1: Episode3.1 vs SEX, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.30	0.372	3.49	0.002	0.537	2.063	0.000
SEX	0.05	0.263	0.19	0.851	-0.490	0.590	0.001

Table 109: cvrt\_vs\_strange\_yr1: Episode3.1 vs GESTAGEBIRTH, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	4.980	4.449	1.119	0.272	-4.133	14.093	0.000
GESTAGEBIRTH	-0.013	0.016	-0.813	0.423	-0.046	0.020	0.022

Table 110: cvrt\_vs\_strange\_yr1: Episode3.1 vs BW, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	0.6	1.157	0.519	0.608	-1.769	2.970	0.000
BW	0.0	0.000	0.666	0.511	0.000	0.001	0.015

Table 111: cvrt\_vs\_strange\_yr1: Episode3.1 vs MaternalInfection, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.421	0.155	9.157	0.000	1.103	1.739	0.000
MaternalInfection	-0.148	0.256	-0.579	0.567	-0.673	0.377	0.011

Table 112: cvrt\_vs\_strange\_yr1: Episode3.1 vs MPSYCH, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.5	0.137	10.978	0.000	1.220	1.780	0.00
MPSYCH	-0.5	0.265	-1.890	0.069	-1.042	0.042	0.11

Table 113: cvrt\_vs\_strange\_yr1: Episode3.1 vs VITAMINDNEO,  
df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.421	0.155	9.157	0.000	1.103	1.739	0.000
VITAMINDNEO	-0.148	0.256	-0.579	0.567	-0.673	0.377	0.011

Table 114: cvrt\_vs\_strange\_yr1: Episode3.1 vs PrePregBMI,  
df=26

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.286	0.149	8.630	0.000	0.979	1.592	0.000
PrePregBMI.Obese	0.214	0.505	0.424	0.675	-0.824	1.253	0.006
PrePregBMI.Overweight	0.381	0.316	1.205	0.239	-0.269	1.031	0.048
PrePregBMI.Under	-0.286	0.699	-0.409	0.686	-1.722	1.151	0.005

Table 115: cvrt\_vs\_strange\_yr1: Episode3.1 vs ANTIBI-  
OTIC\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.375	0.172	7.980	0.000	1.021	1.729	0.00
ANTIBIOTIC_1yr.1	0.010	0.257	0.037	0.970	-0.518	0.538	0.00
ANTIBIOTIC_1yr.NA	-0.375	0.710	-0.528	0.602	-1.833	1.083	0.01

Table 116: cvrt\_vs\_strange\_yr1: Episode3.1 vs FORMULA\_1yr,  
df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.412	0.167	8.459	0.000	1.069	1.754	0.000
FORMULA_1yr.1	-0.078	0.259	-0.302	0.765	-0.611	0.454	0.003
FORMULA_1yr.NA	-0.412	0.708	-0.582	0.566	-1.865	1.041	0.012

Table 117: cvrt\_vs\_strange\_yr1: Episode3.1 vs FORMULA\_6mo,  
df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.500	0.166	9.032	0.00	1.160	1.840	0.000
FORMULA_6mo	-0.286	0.243	-1.175	0.25	-0.784	0.212	0.045

Table 118: cvrt\_vs\_strange\_yr1: Episode3.1 vs FEVER\_1yr,  
df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.476	0.146	10.100	0.000	1.176	1.776	0.000
FEVER_1yr.1	-0.351	0.278	-1.262	0.218	-0.922	0.220	0.052

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
FEVER_1yr.NA	-0.476	0.686	-0.695	0.493	-1.883	0.930	0.016

Table 119: cvrt\_vs\_strange\_yr1: Episode3.1 vs DAYCARE, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.500	0.167	9.000	0.000	1.158	1.842	0.000
DAYCARE.1	-0.167	0.278	-0.600	0.554	-0.737	0.403	0.012
DAYCARE.NA	-0.500	0.342	-1.464	0.155	-1.201	0.201	0.074

Table 120: cvrt\_vs\_strange\_yr1: Episode3.1 vs CURBRFEED\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.357	0.184	7.371	0.000	0.979	1.735	0.000
CURBRFEED_1yr.1	0.043	0.256	0.167	0.868	-0.482	0.568	0.001
CURBRFEED_1yr.NA	-0.357	0.713	-0.501	0.621	-1.820	1.106	0.009

Table 121: cvrt\_vs\_strange\_yr1: Episode3.1 vs Milks\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.429	0.260	5.488	0.000	0.894	1.963	0.000
Milks_1yr.1	-0.065	0.299	-0.217	0.830	-0.678	0.548	0.002
Milks_1yr.NA	-0.429	0.736	-0.582	0.565	-1.939	1.082	0.013

Table 122: cvrt\_vs\_strange\_yr1: Episode3.1 vs FrenchFries\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.273	0.206	6.173	0.000	0.850	1.696	0.000
FrenchFries_1yr.1	0.172	0.262	0.656	0.517	-0.365	0.709	0.015
FrenchFries_1yr.NA	-0.273	0.714	-0.382	0.706	-1.738	1.193	0.005

Table 123: cvrt\_vs\_strange\_yr1: Episode3.1 vs SweetFoodsDrinks\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.222	0.227	5.388	0.000	0.757	1.688	0.000
SweetFoodsDrinks_1yr.1	0.228	0.273	0.834	0.412	-0.333	0.788	0.025
SweetFoodsDrinks_1yr.NA	-0.222	0.717	-0.310	0.759	-1.694	1.250	0.003



Table 124: cvrt\_vs\_strange\_yr1: Episode3.1 vs PeanutButter\_1yr,  
df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.100	0.208	5.299	0.000	0.674	1.526	0.000
PeanutButter_1yr.1	0.426	0.256	1.662	0.108	-0.100	0.953	0.092
PeanutButter_1yr.NA	-0.100	0.689	-0.145	0.886	-1.513	1.313	0.001

Table 125: cvrt\_vs\_strange\_yr1: Episode3.1 vs WHSTOTHER,  
df=22

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.500	0.453	3.311	0.003	0.560	2.440	0.000
WHSTOTHER.3.5 months	-0.500	0.785	-0.637	0.531	-2.127	1.127	0.015
WHSTOTHER.4 months	0.071	0.514	0.139	0.891	-0.994	1.137	0.002
WHSTOTHER.4.5 months	-0.500	0.785	-0.637	0.531	-2.127	1.127	0.015
WHSTOTHER.5 months	-0.214	0.514	-0.417	0.681	-1.280	0.851	0.016
WHSTOTHER.5.5 months	0.000	0.641	0.000	1.000	-1.329	1.329	0.000
WHSTOTHER.6 months	-0.389	0.501	-0.776	0.446	-1.428	0.650	0.060
WHSTOTHER.7 months	1.500	0.785	1.911	0.069	-0.127	3.127	0.138

Table 126: cvrt\_vs\_strange\_yr1: Episode3.1 vs VITAMIND\_6mo,  
df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.474	0.154	9.542	0.000	1.157	1.791	0.000
VITAMIND_6mo.1	-0.224	0.284	-0.788	0.437	-0.806	0.358	0.021
VITAMIND_6mo.NA	-0.474	0.418	-1.133	0.267	-1.332	0.384	0.043

Table 127: cvrt\_vs\_strange\_yr1: Episode3.1 vs Cereals\_6mo,  
df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.571	0.253	6.202	0.000	1.052	2.091	0.000
Cereals_6mo.1	-0.203	0.296	-0.685	0.499	-0.811	0.405	0.020
Cereals_6mo.NA	-0.571	0.420	-1.360	0.185	-1.434	0.291	0.078

Table 128: cvrt\_vs\_strange\_yr1: Episode3.1 vs STATE, df=15

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.000	0.756	1.322	0.206	-0.612	2.612	0.000
STATE.22	0.333	0.873	0.382	0.708	-1.528	2.195	0.012
STATE.23	0.000	0.926	0.000	1.000	-1.975	1.975	0.000
STATE.24	1.000	0.873	1.145	0.270	-0.862	2.862	0.112
STATE.26	0.000	0.926	0.000	1.000	-1.975	1.975	0.000
STATE.27	0.000	1.070	0.000	1.000	-2.280	2.280	0.000
STATE.29	0.000	0.926	0.000	1.000	-1.975	1.975	0.000

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
STATE.33	0.000	1.070	0.000	1.000	-2.280	2.280	0.000
STATE.35	0.500	0.926	0.540	0.597	-1.475	2.475	0.019
STATE.38	0.000	1.070	0.000	1.000	-2.280	2.280	0.000
STATE.39	1.000	0.926	1.079	0.297	-0.975	2.975	0.077
STATE.40	0.000	0.926	0.000	1.000	-1.975	1.975	0.000
STATE.41	0.333	0.873	0.382	0.708	-1.528	2.195	0.012
STATE.73	0.000	1.070	0.000	1.000	-2.280	2.280	0.000
STATE.NA	0.750	0.846	0.887	0.389	-1.053	2.553	0.081

Table 129: cvrt\_vs\_strange\_yr1: Episode3.1 vs TRAIT, df=13

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.000	0.630	1.586	0.137	-0.362	2.362	0.000
TRAIT.22	0.000	0.892	0.000	1.000	-1.926	1.926	0.000
TRAIT.24	0.000	0.772	0.000	1.000	-1.668	1.668	0.000
TRAIT.25	0.000	0.892	0.000	1.000	-1.926	1.926	0.000
TRAIT.26	2.000	0.772	2.590	0.022	0.332	3.668	0.331
TRAIT.27	0.333	0.728	0.458	0.655	-1.239	1.906	0.013
TRAIT.28	0.500	0.772	0.648	0.529	-1.168	2.168	0.021
TRAIT.29	0.000	0.892	0.000	1.000	-1.926	1.926	0.000
TRAIT.30	1.000	0.772	1.295	0.218	-0.668	2.668	0.083
TRAIT.32	0.000	0.892	0.000	1.000	-1.926	1.926	0.000
TRAIT.33	0.500	0.772	0.648	0.529	-1.168	2.168	0.021
TRAIT.36	0.000	0.892	0.000	1.000	-1.926	1.926	0.000
TRAIT.39	0.250	0.705	0.355	0.729	-1.273	1.773	0.010
TRAIT.48	0.000	0.892	0.000	1.000	-1.926	1.926	0.000
TRAIT.49	0.000	0.892	0.000	1.000	-1.926	1.926	0.000
TRAIT.52	0.000	0.892	0.000	1.000	-1.926	1.926	0.000
TRAIT.NA	0.250	0.705	0.355	0.729	-1.273	1.773	0.010

Table 130: cvrt\_vs\_strange\_yr1: Episode3.1 vs NegativeLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.500	0.378	3.973	0.001	0.710	2.290	0.000
NegativeLifeEvents.1	0.000	0.487	0.000	1.000	-1.020	1.020	0.000
NegativeLifeEvents.14	-0.500	0.844	-0.592	0.561	-2.267	1.267	0.013
NegativeLifeEvents.2	-0.167	0.487	-0.342	0.736	-1.187	0.854	0.007
NegativeLifeEvents.26	-0.500	0.844	-0.592	0.561	-2.267	1.267	0.013
NegativeLifeEvents.3	-0.500	0.654	-0.765	0.454	-1.869	0.869	0.025
NegativeLifeEvents.4	-0.500	0.654	-0.765	0.454	-1.869	0.869	0.025
NegativeLifeEvents.5	0.500	0.654	0.765	0.454	-0.869	1.869	0.025
NegativeLifeEvents.6	-0.500	0.844	-0.592	0.561	-2.267	1.267	0.013
NegativeLifeEvents.7	-0.500	0.844	-0.592	0.561	-2.267	1.267	0.013
NegativeLifeEvents.NA	0.000	0.534	0.000	1.000	-1.118	1.118	0.000

Table 131: cvrt\_vs\_strange\_yr1: Episode3.1 vs PositiveLifeEvents,  
df=19

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.00	0.252	3.965	0.001	0.472	1.528	0.000
PositiveLifeEvents.11	0.00	0.667	0.000	1.000	-1.396	1.396	0.000
PositiveLifeEvents.12	0.00	0.667	0.000	1.000	-1.396	1.396	0.000
PositiveLifeEvents.25	1.00	0.667	1.499	0.150	-0.396	2.396	0.048
PositiveLifeEvents.3	0.50	0.357	1.402	0.177	-0.246	1.246	0.060
PositiveLifeEvents.5	0.00	0.437	0.000	1.000	-0.914	0.914	0.000
PositiveLifeEvents.6	0.25	0.399	0.627	0.538	-0.585	1.085	0.011
PositiveLifeEvents.7	0.00	0.667	0.000	1.000	-1.396	1.396	0.000
PositiveLifeEvents.8	2.00	0.667	2.998	0.007	0.604	3.396	0.193
PositiveLifeEvents.9	1.00	0.504	1.983	0.062	-0.056	2.056	0.093
PositiveLifeEvents.NA	0.50	0.399	1.254	0.225	-0.335	1.335	0.043

Table 132: cvrt\_vs\_strange\_yr1: Episode3.1 vs TotalLifeEvents,  
df=14

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.00	0.543	1.842	0.087	-0.164	2.164	0.000
TotalLifeEvents.10	1.00	0.768	1.303	0.214	-0.646	2.646	0.075
TotalLifeEvents.11	0.00	0.940	0.000	1.000	-2.016	2.016	0.000
TotalLifeEvents.12	0.00	0.940	0.000	1.000	-2.016	2.016	0.000
TotalLifeEvents.13	0.00	0.940	0.000	1.000	-2.016	2.016	0.000
TotalLifeEvents.14	0.00	0.940	0.000	1.000	-2.016	2.016	0.000
TotalLifeEvents.15	0.00	0.940	0.000	1.000	-2.016	2.016	0.000
TotalLifeEvents.2	0.00	0.768	0.000	1.000	-1.646	1.646	0.000
TotalLifeEvents.27	1.00	0.940	1.064	0.305	-1.016	3.016	0.039
TotalLifeEvents.29	0.00	0.940	0.000	1.000	-2.016	2.016	0.000
TotalLifeEvents.4	0.00	0.940	0.000	1.000	-2.016	2.016	0.000
TotalLifeEvents.5	0.50	0.768	0.651	0.525	-1.146	2.146	0.019
TotalLifeEvents.6	0.00	0.768	0.000	1.000	-1.646	1.646	0.000
TotalLifeEvents.7	0.25	0.665	0.376	0.713	-1.176	1.676	0.009
TotalLifeEvents.8	1.00	0.665	1.504	0.155	-0.426	2.426	0.139
TotalLifeEvents.NA	0.50	0.665	0.752	0.464	-0.926	1.926	0.035

Table 133: cvrt\_vs\_strange\_yr1: Episode3.1 vs Stranger, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.533	0.17	9.021	0.000	1.185	1.881	0.000
Stranger	-0.333	0.24	-1.387	0.176	-0.826	0.159	0.062

Table 134: cvrt\_vs\_strange\_yr1: Episode3.2 vs AgeAt1yrVisit,  
df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	2.864	1.394	2.055	0.049	0.009	5.718	0.000
AgeAt1yrVisit	-0.004	0.004	-1.055	0.300	-0.011	0.004	0.037

Table 135: cvrt\_vs\_strange\_yr1: Episode3.2 vs MAGE, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.830	0.843	2.170	0.039	0.102	3.557	0.000
MAGE	-0.014	0.028	-0.516	0.610	-0.071	0.043	0.009

Table 136: cvrt\_vs\_strange\_yr1: Episode3.2 vs PAGE, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.983	0.643	3.086	0.005	0.667	3.299	0.000
PAGE	-0.018	0.019	-0.928	0.362	-0.058	0.022	0.029

Table 137: cvrt\_vs\_strange\_yr1: Episode3.2 vs MEDUY, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.939	1.036	1.871	0.072	-0.183	4.061	0.000
MEDUY	-0.034	0.064	-0.524	0.604	-0.165	0.098	0.009

Table 138: cvrt\_vs\_strange\_yr1: Episode3.2 vs PEDUY, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	2.80	0.731	3.828	0.001	1.302	4.298	0.000
PEDUY	-0.09	0.046	-1.943	0.062	-0.185	0.005	0.115

Table 139: cvrt\_vs\_strange\_yr1: Episode3.2 vs Income.code, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.500	0.210	7.127	0.000	1.068	1.932	0.000
Income.code.LOW	0.071	0.347	0.206	0.838	-0.640	0.783	0.002
Income.code.MID	-0.318	0.304	-1.046	0.305	-0.943	0.306	0.044

Table 140: cvrt\_vs\_strange\_yr1: Episode3.2 vs OLDERSIBLINGS, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.357	0.197	6.903	0.000	0.954	1.760	0.000
OLDERSIBLINGS	0.080	0.269	0.298	0.768	-0.471	0.632	0.003

Table 141: cvrt\_vs\_strange\_yr1: Episode3.2 vs SEX, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.8	0.396	4.551	0.000	0.990	2.610	0.000

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
SEX	-0.3	0.280	-1.073	0.293	-0.873	0.273	0.038

Table 142: cvrt\_vs\_strange\_yr1: Episode3.2 vs GESTAGEBIRTH, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	0.638	4.871	0.131	0.897	-9.340	10.616	0.000
GESTAGEBIRTH	0.003	0.018	0.156	0.877	-0.033	0.039	0.001

Table 143: cvrt\_vs\_strange\_yr1: Episode3.2 vs BW, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	-0.725	1.196	-0.607	0.549	-3.175	1.724	0.000
BW	0.001	0.000	1.788	0.085	0.000	0.001	0.099

Table 144: cvrt\_vs\_strange\_yr1: Episode3.2 vs MaternalInfection, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.526	0.164	9.286	0.000	1.190	1.863	0.000
MaternalInfection	-0.344	0.271	-1.269	0.215	-0.901	0.212	0.053

Table 145: cvrt\_vs\_strange\_yr1: Episode3.2 vs MPSYCH, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.364	0.157	8.712	0.000	1.043	1.684	0.000
MPSYCH	0.136	0.303	0.450	0.656	-0.485	0.757	0.007

Table 146: cvrt\_vs\_strange\_yr1: Episode3.2 vs VITAMINDNEO, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.526	0.164	9.286	0.000	1.190	1.863	0.000
VITAMINDNEO	-0.344	0.271	-1.269	0.215	-0.901	0.212	0.053

Table 147: cvrt\_vs\_strange\_yr1: Episode3.2 vs PrePregBMI, df=26

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.19	0.143	8.298	0.000	0.896	1.485	0.000
PrePregBMI.Obese	0.81	0.487	1.664	0.108	-0.191	1.810	0.072
PrePregBMI.Overweight	0.81	0.304	2.660	0.013	0.184	1.435	0.186

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
PrePregBMI.Under	-0.19	0.673	-0.283	0.779	-1.574	1.193	0.002

Table 148: cvrt\_vs\_strange\_yr1: Episode3.2 vs ANTIBI-  
OTIC\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.125	0.170	6.609	0.000	0.776	1.474	0.000
ANTIBIOTIC_1yr.1	0.567	0.254	2.231	0.034	0.046	1.089	0.143
ANTIBIOTIC_1yr.NA	0.875	0.702	1.247	0.223	-0.565	2.315	0.045

Table 149: cvrt\_vs\_strange\_yr1: Episode3.2 vs FORMULA\_1yr,  
df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.235	0.174	7.079	0.000	0.877	1.593	0.000
FORMULA_1yr.1	0.348	0.271	1.283	0.210	-0.209	0.905	0.053
FORMULA_1yr.NA	0.765	0.740	1.033	0.311	-0.754	2.284	0.034

Table 150: cvrt\_vs\_strange\_yr1: Episode3.2 vs FORMULA\_6mo,  
df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.500	0.182	8.237	0.000	1.127	1.873	0.000
FORMULA_6mo	-0.214	0.267	-0.804	0.428	-0.760	0.332	0.022

Table 151: cvrt\_vs\_strange\_yr1: Episode3.2 vs FEVER\_1yr,  
df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.524	0.153	9.973	0.000	1.210	1.837	0.000
FEVER_1yr.1	-0.524	0.291	-1.801	0.083	-1.121	0.073	0.100
FEVER_1yr.NA	0.476	0.717	0.664	0.512	-0.994	1.947	0.014

Table 152: cvrt\_vs\_strange\_yr1: Episode3.2 vs DAYCARE, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.375	0.185	7.436	0.000	0.996	1.754	0.000
DAYCARE.1	0.181	0.308	0.586	0.563	-0.452	0.813	0.013
DAYCARE.NA	-0.175	0.379	-0.462	0.648	-0.953	0.603	0.008

Table 153: cvrt\_vs\_strange\_yr1: Episode3.2 vs CURBRFEED\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.429	0.198	7.229	0.000	1.023	1.834	0.000
CURBRFEED_1yr.1	-0.095	0.275	-0.347	0.732	-0.659	0.469	0.004
CURBRFEED_1yr.NA	0.571	0.765	0.747	0.462	-0.999	2.142	0.019

Table 154: cvrt\_vs\_strange\_yr1: Episode3.2 vs Milks\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.714	0.270	6.346	0.000	1.160	2.269	0.000
Milks_1yr.1	-0.442	0.310	-1.424	0.166	-1.078	0.195	0.071
Milks_1yr.NA	0.286	0.764	0.374	0.711	-1.282	1.853	0.005

Table 155: cvrt\_vs\_strange\_yr1: Episode3.2 vs FrenchFries\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.182	0.218	5.417	0.000	0.734	1.629	0.000
FrenchFries_1yr.1	0.318	0.277	1.149	0.261	-0.250	0.886	0.044
FrenchFries_1yr.NA	0.818	0.756	1.083	0.289	-0.733	2.369	0.039

Table 156: cvrt\_vs\_strange\_yr1: Episode3.2 vs SweetFoodsDrinks\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.222	0.244	5.002	0.000	0.721	1.724	0.000
SweetFoodsDrinks_1yr.1	0.228	0.294	0.774	0.446	-0.376	0.831	0.021
SweetFoodsDrinks_1yr.NA	0.778	0.773	1.007	0.323	-0.808	2.363	0.035

Table 157: cvrt\_vs\_strange\_yr1: Episode3.2 vs PeanutButter\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.100	0.225	4.895	0.000	0.639	1.561	0.000
PeanutButter_1yr.1	0.426	0.278	1.535	0.136	-0.143	0.996	0.076
PeanutButter_1yr.NA	0.900	0.745	1.207	0.238	-0.629	2.429	0.047

Table 158: cvrt\_vs\_strange\_yr1: Episode3.2 vs WHSTOTHER, df=22

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.000	0.500	2.001	0.058	-0.036	2.036	0.000
WHSTOTHER.3.5 months	0.000	0.865	0.000	1.000	-1.795	1.795	0.000

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
WHSTOTHER.4 months	0.429	0.567	0.756	0.457	-0.746	1.603	0.044
WHSTOTHER.4.5 months	0.000	0.865	0.000	1.000	-1.795	1.795	0.000
WHSTOTHER.5 months	0.429	0.567	0.756	0.457	-0.746	1.603	0.044
WHSTOTHER.5.5 months	1.000	0.707	1.415	0.171	-0.465	2.465	0.083
WHSTOTHER.6 months	0.222	0.552	0.402	0.691	-0.923	1.368	0.014
WHSTOTHER.7 months	2.000	0.865	2.311	0.031	0.205	3.795	0.172

Table 159: cvrt\_vs\_strange\_yr1: Episode3.2 vs VITAMIND\_6mo, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.579	0.162	9.731	0.000	1.246	1.912	0.000
VITAMIND_6mo.1	-0.454	0.298	-1.523	0.139	-1.066	0.158	0.073
VITAMIND_6mo.NA	-0.579	0.439	-1.318	0.199	-1.481	0.323	0.054

Table 160: cvrt\_vs\_strange\_yr1: Episode3.2 vs Cereals\_6mo, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.571	0.280	5.612	0.000	0.997	2.146	0.000
Cereals_6mo.1	-0.256	0.328	-0.780	0.442	-0.928	0.416	0.028
Cereals_6mo.NA	-0.071	0.464	-0.154	0.879	-1.024	0.881	0.001

Table 161: cvrt\_vs\_strange\_yr1: Episode3.2 vs STATE, df=15

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.000	0.796	1.257	0.228	-0.696	2.696	0.000
STATE.22	0.333	0.919	0.363	0.722	-1.625	2.292	0.011
STATE.23	0.500	0.975	0.513	0.615	-1.577	2.577	0.017
STATE.24	0.333	0.919	0.363	0.722	-1.625	2.292	0.011
STATE.26	0.000	0.975	0.000	1.000	-2.077	2.077	0.000
STATE.27	0.000	1.125	0.000	1.000	-2.399	2.399	0.000
STATE.29	0.000	0.975	0.000	1.000	-2.077	2.077	0.000
STATE.33	0.000	1.125	0.000	1.000	-2.399	2.399	0.000
STATE.35	1.000	0.975	1.026	0.321	-1.077	3.077	0.066
STATE.38	0.000	1.125	0.000	1.000	-2.399	2.399	0.000
STATE.39	1.000	0.975	1.026	0.321	-1.077	3.077	0.066
STATE.40	0.000	0.975	0.000	1.000	-2.077	2.077	0.000
STATE.41	0.333	0.919	0.363	0.722	-1.625	2.292	0.011
STATE.73	2.000	1.125	1.777	0.096	-0.399	4.399	0.137
STATE.NA	0.500	0.890	0.562	0.582	-1.396	2.396	0.031

Table 162: cvrt\_vs\_strange\_yr1: Episode3.2 vs TRAIT, df=13

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.000	0.851	1.175	0.261	-0.839	2.839	0.000



	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
TRAIT.22	0.000	1.204	0.000	1.000	-2.600	2.600	0.000
TRAIT.24	0.000	1.042	0.000	1.000	-2.252	2.252	0.000
TRAIT.25	0.000	1.204	0.000	1.000	-2.600	2.600	0.000
TRAIT.26	1.500	1.042	1.439	0.174	-0.752	3.752	0.137
TRAIT.27	0.333	0.983	0.339	0.740	-1.790	2.456	0.010
TRAIT.28	0.500	1.042	0.480	0.639	-1.752	2.752	0.015
TRAIT.29	0.000	1.204	0.000	1.000	-2.600	2.600	0.000
TRAIT.30	1.000	1.042	0.959	0.355	-1.252	3.252	0.061
TRAIT.32	0.000	1.204	0.000	1.000	-2.600	2.600	0.000
TRAIT.33	0.000	1.042	0.000	1.000	-2.252	2.252	0.000
TRAIT.36	0.000	1.204	0.000	1.000	-2.600	2.600	0.000
TRAIT.39	0.750	0.952	0.788	0.445	-1.306	2.806	0.064
TRAIT.48	0.000	1.204	0.000	1.000	-2.600	2.600	0.000
TRAIT.49	0.000	1.204	0.000	1.000	-2.600	2.600	0.000
TRAIT.52	0.000	1.204	0.000	1.000	-2.600	2.600	0.000
TRAIT.NA	0.500	0.952	0.525	0.608	-1.556	2.556	0.028

Table 163: cvrt\_vs\_strange\_yr1: Episode3.2 vs NegativeLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.250	0.361	3.460	0.003	0.494	2.006	0.000
NegativeLifeEvents.1	0.083	0.466	0.179	0.860	-0.893	1.059	0.002
NegativeLifeEvents.14	-0.250	0.808	-0.310	0.760	-1.941	1.441	0.003
NegativeLifeEvents.2	0.417	0.466	0.893	0.383	-0.559	1.393	0.040
NegativeLifeEvents.26	1.750	0.808	2.167	0.043	0.059	3.441	0.143
NegativeLifeEvents.3	0.250	0.626	0.400	0.694	-1.060	1.560	0.006
NegativeLifeEvents.4	-0.250	0.626	-0.400	0.694	-1.560	1.060	0.006
NegativeLifeEvents.5	0.750	0.626	1.199	0.245	-0.560	2.060	0.051
NegativeLifeEvents.6	-0.250	0.808	-0.310	0.760	-1.941	1.441	0.003
NegativeLifeEvents.7	-0.250	0.808	-0.310	0.760	-1.941	1.441	0.003
NegativeLifeEvents.NA	-0.250	0.511	-0.489	0.630	-1.319	0.819	0.010

Table 164: cvrt\_vs\_strange\_yr1: Episode3.2 vs PositiveLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.167	0.233	5.016	0.000	0.680	1.653	0.000
PositiveLifeEvents.11	-0.167	0.615	-0.271	0.789	-1.455	1.121	0.001
PositiveLifeEvents.12	-0.167	0.615	-0.271	0.789	-1.455	1.121	0.001
PositiveLifeEvents.25	1.833	0.615	2.979	0.008	0.545	3.121	0.170
PositiveLifeEvents.3	0.667	0.329	2.027	0.057	-0.022	1.355	0.112
PositiveLifeEvents.5	-0.167	0.403	-0.414	0.684	-1.010	0.676	0.004
PositiveLifeEvents.6	-0.167	0.368	-0.453	0.656	-0.936	0.603	0.005
PositiveLifeEvents.7	-0.167	0.615	-0.271	0.789	-1.455	1.121	0.001
PositiveLifeEvents.8	0.833	0.615	1.354	0.192	-0.455	2.121	0.035
PositiveLifeEvents.9	1.333	0.465	2.866	0.010	0.360	2.307	0.173
PositiveLifeEvents.NA	-0.167	0.368	-0.453	0.656	-0.936	0.603	0.005

Table 165: cvrt\_vs\_strange\_yr1: Episode3.2 vs TotalLifeEvents, df=14

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.00	0.453	2.207	0.045	0.028	1.972	0.000
TotalLifeEvents.10	1.00	0.641	1.560	0.141	-0.375	2.375	0.074
TotalLifeEvents.11	1.00	0.785	1.274	0.223	-0.683	2.683	0.038
TotalLifeEvents.12	0.00	0.785	0.000	1.000	-1.683	1.683	0.000
TotalLifeEvents.13	0.00	0.785	0.000	1.000	-1.683	1.683	0.000
TotalLifeEvents.14	0.00	0.785	0.000	1.000	-1.683	1.683	0.000
TotalLifeEvents.15	0.00	0.785	0.000	1.000	-1.683	1.683	0.000
TotalLifeEvents.2	0.50	0.641	0.780	0.448	-0.875	1.875	0.018
TotalLifeEvents.27	2.00	0.785	2.548	0.023	0.317	3.683	0.152
TotalLifeEvents.29	2.00	0.785	2.548	0.023	0.317	3.683	0.152
TotalLifeEvents.4	0.00	0.785	0.000	1.000	-1.683	1.683	0.000
TotalLifeEvents.5	0.00	0.641	0.000	1.000	-1.375	1.375	0.000
TotalLifeEvents.6	0.50	0.641	0.780	0.448	-0.875	1.875	0.018
TotalLifeEvents.7	0.00	0.555	0.000	1.000	-1.190	1.190	0.000
TotalLifeEvents.8	0.75	0.555	1.351	0.198	-0.440	1.940	0.077
TotalLifeEvents.NA	0.00	0.555	0.000	1.000	-1.190	1.190	0.000

Table 166: cvrt\_vs\_strange\_yr1: Episode3.2 vs Stranger, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.467	0.189	7.744	0.000	1.079	1.855	0.000
Stranger	-0.133	0.268	-0.498	0.623	-0.682	0.415	0.008

Table 167: cvrt\_vs\_strange\_yr1: Episode3.3 vs AgeAt1yrVisit, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	2.354	1.601	1.470	0.153	-0.926	5.634	0.00
AgeAt1yrVisit	-0.002	0.004	-0.536	0.596	-0.011	0.006	0.01

Table 168: cvrt\_vs\_strange\_yr1: Episode3.3 vs MAGE, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.930	0.956	2.018	0.053	-0.029	3.889	0.000
MAGE	-0.014	0.031	-0.455	0.652	-0.079	0.050	0.007

Table 169: cvrt\_vs\_strange\_yr1: Episode3.3 vs PAGE, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.604	0.739	2.172	0.038	0.091	3.117	0.000
PAGE	-0.003	0.022	-0.144	0.886	-0.049	0.042	0.001

Table 170: cvrt\_vs\_strange\_yr1: Episode3.3 vs MEDUY, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.072	1.176	0.911	0.370	-1.338	3.481	0.000
MEDUY	0.027	0.073	0.367	0.716	-0.122	0.176	0.005

Table 171: cvrt\_vs\_strange\_yr1: Episode3.3 vs PEDUY, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.424	0.801	4.273	0.000	1.783	5.066	0.00
PEDUY	-0.124	0.051	-2.438	0.021	-0.228	-0.020	0.17

Table 172: cvrt\_vs\_strange\_yr1: Episode3.3 vs Income.code, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.583	0.243	6.508	0.000	1.084	2.083	0.000
Income.code.LOW	-0.012	0.401	-0.030	0.977	-0.834	0.810	0.000
Income.code.MID	-0.220	0.352	-0.625	0.538	-0.942	0.502	0.016

Table 173: cvrt\_vs\_strange\_yr1: Episode3.3 vs OLDERSIBLINGS, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.571	0.222	7.07	0.000	1.116	2.027	0.000
OLDERSIBLINGS	-0.134	0.304	-0.44	0.663	-0.757	0.490	0.007

Table 174: cvrt\_vs\_strange\_yr1: Episode3.3 vs SEX, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.30	0.455	2.855	0.008	0.367	2.233	0.000
SEX	0.15	0.322	0.466	0.645	-0.510	0.810	0.007

Table 175: cvrt\_vs\_strange\_yr1: Episode3.3 vs GESTAGEBIRTH, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	2.532	5.516	0.459	0.650	-8.768	13.831	0.000
GESTAGEBIRTH	-0.004	0.020	-0.187	0.853	-0.045	0.037	0.001

Table 176: cvrt\_vs\_strange\_yr1: Episode3.3 vs BW, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	0.148	1.406	0.105	0.917	-2.732	3.029	0.000

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
BW	0.000	0.000	0.967	0.342	0.000	0.001	0.031

Table 177: cvrt\_vs\_strange\_yr1: Episode3.3 vs MaternalInfection, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.632	0.187	8.725	0.000	1.249	2.015	0.000
MaternalInfection	-0.359	0.309	-1.162	0.255	-0.991	0.274	0.044

Table 178: cvrt\_vs\_strange\_yr1: Episode3.3 vs MPSYCH, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.545	0.177	8.724	0.000	1.183	1.908	0.000
MPSYCH	-0.170	0.343	-0.497	0.623	-0.873	0.532	0.008

Table 179: cvrt\_vs\_strange\_yr1: Episode3.3 vs VITAMINDNEO, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.474	0.191	7.704	0.000	1.082	1.865	0.000
VITAMINDNEO	0.072	0.316	0.227	0.822	-0.575	0.719	0.002

Table 180: cvrt\_vs\_strange\_yr1: Episode3.3 vs PrePregBMI, df=26

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.381	0.179	7.724	0.000	1.013	1.748	0.000
PrePregBMI.Obese	0.119	0.606	0.196	0.846	-1.127	1.365	0.001
PrePregBMI.Overweight	0.619	0.379	1.632	0.115	-0.161	1.399	0.086
PrePregBMI.Under	-0.381	0.839	-0.454	0.653	-2.105	1.343	0.007

Table 181: cvrt\_vs\_strange\_yr1: Episode3.3 vs ANTIBIOTIC\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.437	0.210	6.852	0.000	1.007	1.868	0.000
ANTIBIOTIC_1yr.1	0.178	0.313	0.568	0.575	-0.465	0.821	0.011
ANTIBIOTIC_1yr.NA	-0.437	0.865	-0.506	0.617	-2.212	1.337	0.009

Table 182: cvrt\_vs\_strange\_yr1: Episode3.3 vs FORMULA\_1yr,  
df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.294	0.194	6.686	0.000	0.897	1.691	0.000
FORMULA_1yr.1	0.539	0.301	1.792	0.084	-0.078	1.157	0.101
FORMULA_1yr.NA	-0.294	0.821	-0.358	0.723	-1.979	1.391	0.004

Table 183: cvrt\_vs\_strange\_yr1: Episode3.3 vs FORMULA\_6mo,  
df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.437	0.208	6.914	0.000	1.012	1.863	0.000
FORMULA_6mo	0.134	0.304	0.440	0.663	-0.490	0.757	0.007

Table 184: cvrt\_vs\_strange\_yr1: Episode3.3 vs FEVER\_1yr,  
df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.714	0.169	10.115	0.000	1.367	2.062	0.000
FEVER_1yr.1	-0.714	0.323	-2.214	0.035	-1.376	-0.052	0.143
FEVER_1yr.NA	-0.714	0.795	-0.899	0.377	-2.345	0.917	0.024

Table 185: cvrt\_vs\_strange\_yr1: Episode3.3 vs DAYCARE, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.687	0.202	8.346	0.000	1.273	2.102	0.000
DAYCARE.1	-0.243	0.337	-0.721	0.477	-0.934	0.448	0.017
DAYCARE.NA	-0.688	0.414	-1.659	0.109	-1.538	0.163	0.092

Table 186: cvrt\_vs\_strange\_yr1: Episode3.3 vs CURBR-  
FEED\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.571	0.225	6.979	0.000	1.109	2.033	0.000
CURBRFEED_1yr.1	-0.105	0.313	-0.335	0.740	-0.747	0.538	0.004
CURBRFEED_1yr.NA	-0.571	0.872	-0.655	0.518	-2.361	1.218	0.015

Table 187: cvrt\_vs\_strange\_yr1: Episode3.3 vs Milks\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.857	0.310	5.989	0.000	1.221	2.493	0.000
Milks_1yr.1	-0.448	0.356	-1.258	0.219	-1.179	0.282	0.055
Milks_1yr.NA	-0.857	0.877	-0.977	0.337	-2.657	0.943	0.033

Table 188: cvrt\_vs\_strange\_yr1: Episode3.3 vs FrenchFries\_1yr,  
df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.273	0.247	5.144	0.000	0.765	1.780	0.000
FrenchFries_1yr.1	0.394	0.314	1.254	0.220	-0.250	1.038	0.054
FrenchFries_1yr.NA	-0.273	0.857	-0.318	0.753	-2.031	1.486	0.003

Table 189: cvrt\_vs\_strange\_yr1: Episode3.3 vs SweetFoods-  
Drinks\_1yr, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.556	0.281	5.531	0.000	0.978	2.133	0.000
SweetFoodsDrinks_1yr.1	-0.056	0.339	-0.164	0.871	-0.750	0.639	0.001
SweetFoodsDrinks_1yr.NA	-0.556	0.889	-0.625	0.537	-2.380	1.269	0.014

Table 190: cvrt\_vs\_strange\_yr1: Episode3.3 vs PeanutButter\_1yr,  
df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.400	0.265	5.273	0.000	0.855	1.945	0.000
PeanutButter_1yr.1	0.179	0.328	0.546	0.590	-0.494	0.852	0.011
PeanutButter_1yr.NA	-0.400	0.881	-0.454	0.653	-2.207	1.407	0.007

Table 191: cvrt\_vs\_strange\_yr1: Episode3.3 vs WHSTOTHER,  
df=22

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.000	0.596	1.677	0.108	-0.237	2.237	0.000
WHSTOTHER.3.5 months	0.000	1.033	0.000	1.000	-2.142	2.142	0.000
WHSTOTHER.4 months	0.571	0.676	0.845	0.407	-0.831	1.974	0.059
WHSTOTHER.4.5 months	0.000	1.033	0.000	1.000	-2.142	2.142	0.000
WHSTOTHER.5 months	0.286	0.676	0.423	0.677	-1.116	1.688	0.015
WHSTOTHER.5.5 months	0.500	0.843	0.593	0.559	-1.249	2.249	0.016
WHSTOTHER.6 months	0.667	0.659	1.011	0.323	-0.700	2.034	0.094
WHSTOTHER.7 months	2.000	1.033	1.937	0.066	-0.142	4.142	0.129

Table 192: cvrt\_vs\_strange\_yr1: Episode3.3 vs VITAMIND\_6mo,  
df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.684	0.185	9.091	0.000	1.304	2.064	0.000
VITAMIND_6mo.1	-0.434	0.340	-1.276	0.213	-1.133	0.264	0.052
VITAMIND_6mo.NA	-0.684	0.502	-1.364	0.184	-1.714	0.345	0.059

Table 193: cvrt\_vs\_strange\_yr1: Episode3.3 vs Cereals\_6mo, df=27

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.571	0.321	4.898	0.000	0.913	2.230	0.000
Cereals_6mo.1	-0.098	0.375	-0.260	0.796	-0.868	0.672	0.003
Cereals_6mo.NA	-0.071	0.532	-0.134	0.894	-1.163	1.020	0.001

Table 194: cvrt\_vs\_strange\_yr1: Episode3.3 vs STATE, df=15

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.000	0.869	1.150	0.268	-0.853	2.853	0.000
STATE.22	0.000	1.004	0.000	1.000	-2.139	2.139	0.000
STATE.23	1.000	1.065	0.939	0.362	-1.269	3.269	0.051
STATE.24	0.667	1.004	0.664	0.517	-1.473	2.806	0.033
STATE.26	0.000	1.065	0.000	1.000	-2.269	2.269	0.000
STATE.27	0.000	1.229	0.000	1.000	-2.620	2.620	0.000
STATE.29	0.500	1.065	0.470	0.645	-1.769	2.769	0.013
STATE.33	2.000	1.229	1.627	0.125	-0.620	4.620	0.105
STATE.35	0.500	1.065	0.470	0.645	-1.769	2.769	0.013
STATE.38	0.000	1.229	0.000	1.000	-2.620	2.620	0.000
STATE.39	1.000	1.065	0.939	0.362	-1.269	3.269	0.051
STATE.40	0.000	1.065	0.000	1.000	-2.269	2.269	0.000
STATE.41	0.333	1.004	0.332	0.744	-1.806	2.473	0.008
STATE.73	2.000	1.229	1.627	0.125	-0.620	4.620	0.105
STATE.NA	0.500	0.972	0.514	0.614	-1.571	2.571	0.024

Table 195: cvrt\_vs\_strange\_yr1: Episode3.3 vs TRAIT, df=13

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.0	0.679	1.472	0.165	-0.468	2.468	0.000
TRAIT.22	0.0	0.961	0.000	1.000	-2.076	2.076	0.000
TRAIT.24	0.0	0.832	0.000	1.000	-1.798	1.798	0.000
TRAIT.25	0.0	0.961	0.000	1.000	-2.076	2.076	0.000
TRAIT.26	1.0	0.832	1.202	0.251	-0.798	2.798	0.057
TRAIT.27	0.0	0.784	0.000	1.000	-1.695	1.695	0.000
TRAIT.28	2.0	0.832	2.404	0.032	0.202	3.798	0.227
TRAIT.29	0.0	0.961	0.000	1.000	-2.076	2.076	0.000
TRAIT.30	2.0	0.832	2.404	0.032	0.202	3.798	0.227
TRAIT.32	0.0	0.961	0.000	1.000	-2.076	2.076	0.000
TRAIT.33	0.0	0.832	0.000	1.000	-1.798	1.798	0.000
TRAIT.36	0.0	0.961	0.000	1.000	-2.076	2.076	0.000
TRAIT.39	0.5	0.760	0.658	0.522	-1.141	2.141	0.026
TRAIT.48	0.0	0.961	0.000	1.000	-2.076	2.076	0.000
TRAIT.49	1.0	0.961	1.041	0.317	-1.076	3.076	0.029
TRAIT.52	0.0	0.961	0.000	1.000	-2.076	2.076	0.000
TRAIT.NA	0.5	0.760	0.658	0.522	-1.141	2.141	0.026

Table 196: cvrt\_vs\_strange\_yr1: Episode3.3 vs NegativeLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.500	0.427	3.516	0.002	0.607	2.393	0.000
NegativeLifeEvents.1	0.000	0.551	0.000	1.000	-1.153	1.153	0.000
NegativeLifeEvents.14	-0.500	0.954	-0.524	0.606	-2.497	1.497	0.009
NegativeLifeEvents.2	0.167	0.551	0.303	0.765	-0.986	1.319	0.005
NegativeLifeEvents.26	1.500	0.954	1.572	0.132	-0.497	3.497	0.082
NegativeLifeEvents.3	0.500	0.739	0.677	0.507	-1.047	2.047	0.018
NegativeLifeEvents.4	-0.500	0.739	-0.677	0.507	-2.047	1.047	0.018
NegativeLifeEvents.5	0.500	0.739	0.677	0.507	-1.047	2.047	0.018
NegativeLifeEvents.6	-0.500	0.954	-0.524	0.606	-2.497	1.497	0.009
NegativeLifeEvents.7	-0.500	0.954	-0.524	0.606	-2.497	1.497	0.009
NegativeLifeEvents.NA	-0.500	0.603	-0.829	0.418	-1.763	0.763	0.033

Table 197: cvrt\_vs\_strange\_yr1: Episode3.3 vs PositiveLifeEvents, df=19

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.333	0.315	4.229	0.000	0.673	1.993	0.000
PositiveLifeEvents.11	-0.333	0.834	-0.400	0.694	-2.079	1.413	0.004
PositiveLifeEvents.12	-0.333	0.834	-0.400	0.694	-2.079	1.413	0.004
PositiveLifeEvents.25	0.667	0.834	0.799	0.434	-1.079	2.413	0.017
PositiveLifeEvents.3	1.000	0.446	2.243	0.037	0.067	1.933	0.193
PositiveLifeEvents.5	0.333	0.546	0.610	0.549	-0.810	1.476	0.012
PositiveLifeEvents.6	-0.333	0.499	-0.669	0.512	-1.377	0.710	0.015
PositiveLifeEvents.7	-0.333	0.834	-0.400	0.694	-2.079	1.413	0.004
PositiveLifeEvents.8	-0.333	0.834	-0.400	0.694	-2.079	1.413	0.004
PositiveLifeEvents.9	0.667	0.631	1.057	0.304	-0.653	1.987	0.033
PositiveLifeEvents.NA	-0.333	0.499	-0.669	0.512	-1.377	0.710	0.015

Table 198: cvrt\_vs\_strange\_yr1: Episode3.3 vs TotalLifeEvents, df=14

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.5	0.535	2.806	0.014	0.354	2.646	0.000
TotalLifeEvents.10	0.5	0.756	0.661	0.519	-1.121	2.121	0.017
TotalLifeEvents.11	-0.5	0.926	-0.540	0.598	-2.486	1.486	0.009
TotalLifeEvents.12	-0.5	0.926	-0.540	0.598	-2.486	1.486	0.009
TotalLifeEvents.13	-0.5	0.926	-0.540	0.598	-2.486	1.486	0.009
TotalLifeEvents.14	-0.5	0.926	-0.540	0.598	-2.486	1.486	0.009
TotalLifeEvents.15	-0.5	0.926	-0.540	0.598	-2.486	1.486	0.009
TotalLifeEvents.2	0.0	0.756	0.000	1.000	-1.621	1.621	0.000
TotalLifeEvents.27	0.5	0.926	0.540	0.598	-1.486	2.486	0.009
TotalLifeEvents.29	1.5	0.926	1.620	0.127	-0.486	3.486	0.080
TotalLifeEvents.4	-0.5	0.926	-0.540	0.598	-2.486	1.486	0.009
TotalLifeEvents.5	1.5	0.756	1.984	0.067	-0.121	3.121	0.154
TotalLifeEvents.6	0.5	0.756	0.661	0.519	-1.121	2.121	0.017
TotalLifeEvents.7	-0.5	0.655	-0.764	0.458	-1.904	0.904	0.032
TotalLifeEvents.8	0.0	0.655	0.000	1.000	-1.404	1.404	0.000



	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
TotalLifeEvents.NA	-0.5	0.655	-0.764	0.458	-1.904	0.904	0.032

Table 199: cvrt\_vs\_strange\_yr1: Episode3.3 vs Stranger, df=28

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.4	0.214	6.548	0.000	0.962	1.838	0.000
Stranger	0.2	0.302	0.661	0.514	-0.419	0.819	0.015

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Table 200: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs AgeAt1yrVisit, df=25

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.116	1.905	0.586	0.563	-2.806	5.039	0.000
AgeAt1yrVisit	0.005	0.005	1.092	0.285	-0.005	0.015	0.044

Table 201: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs MAGE, df=25

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	6.378	1.075	5.931	0.000	4.163	8.593	0.000
MAGE	-0.105	0.035	-3.006	0.006	-0.176	-0.033	0.258

Table 202: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs PAGE, df=25

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.511	0.992	3.540	0.002	1.469	5.554	0.000
PAGE	-0.010	0.030	-0.334	0.741	-0.072	0.052	0.004

Table 203: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs MEDUY, df=25

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	6.198	1.29	4.807	0.000	3.542	8.854	0.000
MEDUY	-0.189	0.08	-2.359	0.026	-0.353	-0.024	0.176

Table 204: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs PEDUY, df=25

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	4.575	1.067	4.288	0.000	2.378	6.772	0.000
PEDUY	-0.088	0.066	-1.323	0.198	-0.224	0.049	0.063

Table 205: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs Income.code, df=24

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	2.841	0.300	9.463	0.000	2.222	3.461	0.000
Income.code.LOW	0.760	0.481	1.578	0.128	-0.234	1.754	0.100
Income.code.MID	0.444	0.448	0.992	0.331	-0.480	1.368	0.039

Table 206: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs OLDERSIBLINGS, df=25

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.40	0.305	11.153	0.000	2.772	4.028	0.000
OLDERSIBLINGS	-0.36	0.396	-0.910	0.372	-1.176	0.455	0.031

Table 207: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs SEX, df=25

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.243	0.595	5.449	0.000	2.017	4.468	0
SEX	-0.044	0.433	-0.101	0.921	-0.935	0.848	0

Table 208: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs GESTAGEBIRTH, df=25

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	9.134	7.307	1.250	0.223	-5.915	24.183	0.000
GESTAGEBIRTH	-0.022	0.027	-0.814	0.423	-0.076	0.033	0.025

Table 209: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs BW, df=25

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	7.144	1.632	4.376	0.000	3.782	10.506	0.000
BW	-0.001	0.000	-2.439	0.022	-0.002	0.000	0.186

Table 210: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs MaternalInfection, df=25

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.077	0.247	12.475	0.000	2.569	3.585	0.00
MaternalInfection	0.296	0.405	0.730	0.472	-0.539	1.131	0.02

Table 211: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs MPSYCH, df=25

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.148	0.229	13.730	0.000	2.676	3.621	0.000

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
MPSYCH	0.146	0.450	0.325	0.748	-0.781	1.074	0.004

Table 212: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs VITAMINDNEO, df=25

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.296	0.239	13.777	0.000	2.803	3.788	0.000
VITAMINDNEO	-0.329	0.414	-0.793	0.435	-1.182	0.525	0.024

Table 213: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs PrePregBMI, df=23

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.479	0.205	16.935	0.000	3.054	3.904	0.000
PrePregBMI.Obese	-1.015	0.666	-1.525	0.141	-2.392	0.362	0.065
PrePregBMI.Overweight	-1.266	0.450	-2.812	0.010	-2.197	-0.335	0.221
PrePregBMI.Under	0.449	0.919	0.489	0.629	-1.451	2.350	0.007

Table 214: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs ANTIBIOTIC\_1yr, df=24

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.428	0.262	13.092	0.000	2.888	3.969	0.000
ANTIBIOTIC_1yr.1	-0.399	0.385	-1.036	0.311	-1.195	0.396	0.037
ANTIBIOTIC_1yr.NA	-1.741	1.014	-1.716	0.099	-3.834	0.352	0.101

Table 215: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs FORMULA\_1yr, df=24

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.192	0.267	11.946	0.000	2.640	3.743	0.000
FORMULA_1yr.1	0.113	0.393	0.288	0.776	-0.698	0.925	0.003
FORMULA_1yr.NA	-1.504	1.035	-1.454	0.159	-3.640	0.632	0.077

Table 216: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs FORMULA\_6mo, df=25

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.009	0.270	11.151	0.000	2.453	3.565	0.000
FORMULA_6mo	0.368	0.389	0.945	0.354	-0.433	1.169	0.033

Table 217: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs FEVER\_1yr, df=24

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.222	0.230	14.036	0.000	2.749	3.696	0.000
FEVER_1yr.1	0.080	0.442	0.181	0.858	-0.833	0.993	0.001
FEVER_1yr.NA	-1.535	1.027	-1.495	0.148	-3.654	0.584	0.080

Table 218: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs DAYCARE, df=24

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.349	0.276	12.150	0.000	2.780	3.918	0.000
DAYCARE.1	-0.280	0.441	-0.635	0.532	-1.189	0.630	0.016
DAYCARE.NA	-0.470	0.585	-0.803	0.430	-1.676	0.737	0.026

Table 219: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs CURBRFEED\_1yr, df=24

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.275	0.289	11.335	0.000	2.679	3.872	0.000
CURBRFEED_1yr.1	-0.058	0.394	-0.148	0.884	-0.871	0.754	0.001
CURBRFEED_1yr.NA	-1.588	1.042	-1.524	0.141	-3.738	0.562	0.085

Table 220: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs Milks\_1yr, df=24

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.222	0.378	8.513	0.000	2.441	4.003	0.00
Milks_1yr.1	0.030	0.443	0.068	0.946	-0.884	0.944	0.00
Milks_1yr.NA	-1.534	1.070	-1.433	0.165	-3.744	0.675	0.08

Table 221: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs FrenchFries\_1yr, df=24

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.166	0.288	10.982	0.000	2.571	3.761	0.000
FrenchFries_1yr.1	0.145	0.393	0.370	0.715	-0.666	0.956	0.005
FrenchFries_1yr.NA	-1.478	1.039	-1.422	0.168	-3.623	0.667	0.075

Table 222: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs SweetFoods-Drinks\_1yr, df=24

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.536	0.347	10.200	0.000	2.821	4.252	0.000
SweetFoodsDrinks_1yr.1	-0.422	0.417	-1.014	0.321	-1.282	0.438	0.036
SweetFoodsDrinks_1yr.NA	-1.849	1.040	-1.777	0.088	-3.996	0.298	0.112

Table 223: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs PeanutButter\_1yr,  
df=24

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.201	0.334	9.594	0.000	2.512	3.890	0.000
PeanutButter_1yr.1	0.066	0.413	0.159	0.875	-0.786	0.917	0.001
PeanutButter_1yr.NA	-1.513	1.055	-1.434	0.164	-3.691	0.664	0.078

Table 224: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs WHSTOTHER,  
df=19

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.187	0.802	3.974	0.001	1.509	4.866	0.000
WHSTOTHER.3.5 months	-0.473	1.389	-0.341	0.737	-3.381	2.434	0.006
WHSTOTHER.4 months	0.073	0.982	0.075	0.941	-1.983	2.129	0.001
WHSTOTHER.4.5 months	0.250	1.389	0.180	0.859	-2.658	3.158	0.002
WHSTOTHER.5 months	-0.210	0.926	-0.227	0.823	-2.148	1.729	0.006
WHSTOTHER.5.5 months	-0.067	1.134	-0.059	0.954	-2.441	2.307	0.000
WHSTOTHER.6 months	0.223	0.879	0.254	0.803	-1.616	2.062	0.009
WHSTOTHER.7 months	-0.937	1.389	-0.675	0.508	-3.845	1.970	0.024

Table 225: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs VITAMIND\_6mo,  
df=24

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.040	0.258	11.784	0.000	2.508	3.573	0.000
VITAMIND_6mo.1	0.365	0.468	0.780	0.443	-0.601	1.330	0.024
VITAMIND_6mo.NA	0.346	0.577	0.600	0.554	-0.844	1.537	0.014

Table 226: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs Cereals\_6mo, df=24

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.168	0.382	8.294	0.000	2.380	3.957	0.000
Cereals_6mo.1	-0.153	0.463	-0.330	0.744	-1.108	0.802	0.006
Cereals_6mo.NA	0.555	0.592	0.938	0.357	-0.666	1.777	0.045

Table 227: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs STATE, df=12

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	2.042	0.439	4.653	0.001	1.086	2.998	0.000
STATE.23	0.179	0.694	0.259	0.800	-1.332	1.691	0.001
STATE.24	0.921	0.621	1.484	0.164	-0.431	2.273	0.034
STATE.26	0.976	0.694	1.407	0.185	-0.535	2.488	0.026
STATE.27	2.583	0.878	2.944	0.012	0.671	4.495	0.096
STATE.29	2.208	0.694	3.183	0.008	0.697	3.720	0.135
STATE.33	2.708	0.878	3.086	0.009	0.796	4.620	0.106
STATE.35	1.016	0.694	1.465	0.169	-0.495	2.528	0.029

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
STATE.36	2.030	0.878	2.313	0.039	0.118	3.942	0.059
STATE.38	-0.042	0.878	-0.047	0.963	-1.954	1.870	0.000
STATE.39	0.677	0.694	0.976	0.348	-0.835	2.189	0.013
STATE.40	0.972	0.694	1.401	0.187	-0.540	2.483	0.026
STATE.41	1.565	0.694	2.256	0.043	0.054	3.077	0.068
STATE.73	3.030	0.878	3.452	0.005	1.118	4.942	0.132
STATE.NA	1.321	0.694	1.904	0.081	-0.190	2.833	0.048

Table 228: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs TRAIT, df=10

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	1.250	1.198	1.043	0.321	-1.419	3.919	0.000
TRAIT.22	1.036	1.694	0.611	0.555	-2.739	4.811	0.007
TRAIT.24	1.500	1.694	0.885	0.397	-2.275	5.275	0.015
TRAIT.25	3.000	1.694	1.771	0.107	-0.775	6.775	0.061
TRAIT.26	1.915	1.467	1.305	0.221	-1.354	5.184	0.048
TRAIT.27	1.917	1.383	1.386	0.196	-1.166	4.999	0.069
TRAIT.28	1.250	1.467	0.852	0.414	-2.019	4.519	0.020
TRAIT.29	2.188	1.694	1.291	0.226	-1.588	5.963	0.033
TRAIT.30	2.440	1.383	1.764	0.108	-0.642	5.523	0.112
TRAIT.32	1.938	1.694	1.144	0.279	-1.838	5.713	0.026
TRAIT.33	0.750	1.694	0.443	0.667	-3.025	4.525	0.004
TRAIT.36	2.500	1.694	1.476	0.171	-1.275	6.275	0.042
TRAIT.39	1.929	1.339	1.440	0.180	-1.056	4.913	0.089
TRAIT.48	2.679	1.694	1.581	0.145	-1.096	6.454	0.049
TRAIT.49	3.000	1.694	1.771	0.107	-0.775	6.775	0.061
TRAIT.52	1.464	1.694	0.864	0.408	-2.311	5.239	0.015
TRAIT.NA	2.555	1.467	1.741	0.112	-0.714	5.824	0.085

Table 229: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs NegativeLifeEvents, df=25

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	2.963	0.225	13.168	0.000	2.499	3.426	0.000
NegativeLifeEvents	0.063	0.035	1.774	0.088	-0.010	0.136	0.108

Table 230: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs PositiveLifeEvents, df=25

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.508	0.273	12.848	0.000	2.946	4.071	0.000
PositiveLifeEvents	-0.060	0.037	-1.626	0.116	-0.135	0.016	0.092

Table 231: cvrt\_vs\_IBQr\_yr1: IBQr\_fear vs TotalLifeEvents,  
df=25

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	3.151	0.337	9.346	0.000	2.456	3.845	0.000
TotalLifeEvents	0.004	0.030	0.130	0.897	-0.059	0.067	0.001

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## Association analysis for diversity vs strange situation or questionnaire 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

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 questionnaire using linear mixed effect model

Table 344: diversity\_vs\_strange\_combine\_neo: strange\_response  
VS chao1, df=52

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

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

Table 345: diversity\_vs\_strange\_combine\_neo: strange\_response  
VS observed\_otus, df=52

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

Table 346: diversity\_vs\_strange\_combine\_neo: strange\_response  
VS PD\_whole\_tree, df=52

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

Table 347: diversity\_vs\_strange\_combine\_neo: strange\_response  
VS shannon, df=52

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

Table 348: diversity\_vs\_strange\_combine\_neo: strange\_response  
VS wunifrac.PC.1, df=52

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

Table 349: diversity\_vs\_strange\_combine\_neo: strange\_response  
VS wunifrac.PC.2, df=52

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

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

Table 350: diversity\_vs\_strange\_combine\_neo: strange\_response  
VS wunifrac.PC.3, df=52

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

Table 351: diversity\_vs\_strange\_combine\_neo: strange\_response  
VS wunifrac.PC.4, df=52

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

Table 352: diversity\_vs\_strange\_combine\_yr1: strange\_response  
VS chao1, df=38

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

Table 353: diversity\_vs\_strange\_combine\_yr1: strange\_response  
VS observed\_otus, df=38

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

Table 354: diversity\_vs\_strange\_combine\_yr1: strange\_response  
VS PD\_whole\_tree, df=38

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

Table 355: diversity\_vs\_strange\_combine\_yr1: strange\_response  
VS shannon, df=38

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

Table 356: diversity\_vs\_strange\_combine\_yr1: strange\_response  
VS wunifrac.PC.1, df=38

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

Table 357: diversity\_vs\_strange\_combine\_yr1: strange\_response  
VS wunifrac.PC.2, df=38

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

Table 358: diversity\_vs\_strange\_combine\_yr1: strange\_response  
VS wunifrac.PC.3, df=38

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

Table 359: diversity\_vs\_strange\_combine\_yr1: strange\_response  
VS wunifrac.PC.4, df=38

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

## Association analysis for diversity vs picrust using linear model

Table 360: diversity\_vs\_picrust\_L1\_neo: wunifrac.PC.1 vs  
L1.Cellular.Processes, df=30

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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



	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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



	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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



	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
NA	NA	NA	NA	NA	NA	0

Table 509: diversity\_vs\_picrust\_L2\_neo: wunifrac.PC.3 vs L2.Signal.Transduction, df=30

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	-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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
	NA	NA	NA	NA	NA	NA	0

Table 521: diversity\_vs\_picrust\_L2\_neo: wunifrac.PC.4 vs L2.Cell.Growth.and.Death, df=30

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
Intercept	-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



	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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 %	97.5 %
Intercept	-0.013	0.052	-0.241	0.811	-0.119	0.085
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	0.000	0.000	1.288	0.208	0.000	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 %
Intercept	-0.002	0.053	-0.029	0.977	-0.111	0.108
L3.Biosynthesis.of.12...14..and.16.membered.macrolides	0.049	0.302	0.163	0.872	-0.568	0.667

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	0
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	0.000	0.000	-0.776	0.444	0.000	0.000	0

Table 653: diversity\_vs\_picrust\_L3\_neo: wunifrac.PC.1 vs  
L3.ErbB.signaling.pathway, df=31

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
(Intercept)	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 %	R2
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 %	R2
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 %	R2
Intercept	-0.038	0.11	-0.345	0.733	-0.263	0.187	0.000
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis	0.000	0.00	0.392	0.698	0.000	0.000	0.000

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.Potosynthesis, 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.Potosynthesis	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.Potosynthesis... 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.Potosynthesis... 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.Potosynthesis.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.Potosynthesis.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 %	
Intercept	-0.006	0.057	-0.101	0.920	-0.121	0.11	0.0
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	0.000	0.000	0.272	0.787	0.000	0.00	0.0

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 %	97.5 %	R2
Intercept	0.002	0.025	0.066	0.948	-0.05	0.05	0.000
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	0.000	0.000	-0.353	0.727	0.00	0.00	0.000

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 %	R2
Intercept	-0.007	0.045	-0.165	0.870	-0.099	0.084	0.000
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	0.000	0.000	0.198	0.844	0.000	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 %	R2
Intercept	0	0.025	0.001	0.999	-0.052	0.052	0.000
L3.Glycosaminoglycan.biosynthesis...chondroitin.sulfate	0	0.023	-0.006	0.995	-0.048	0.048	0.000

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	0.066
L3.Glycosphingolipid.biosynthesis. . . lacto.and.neolacto.series	0.000	0.000	-1.949	0.061	0.000	0.000

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

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.potential, 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	0
L3.Phenylalanine.tyrosine.and.tryptophan.biosynthesis	0.000	0.000	-0.037	0.971	0.000	0.000	0



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.Potosynthesis.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.Potosynthesis.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	0.000
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	0.000	0.000	-0.167	0.869	0.000	0.000	0.000

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 %	R2
Intercept	0.01	0.04	0.239	0.813	-0.073	0.092	0.000
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis	0.00	0.00	-0.303	0.764	0.000	0.000	0.000

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 %	R2
Intercept	0.027	0.032	0.856	0.399	-0.038	0.093	0.000
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis	0.000	0.000	-1.308	0.201	0.000	0.000	0.000

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 %	97.5 %	R2
Intercept	0.004	0.022	0.171	0.865	-0.042	0.050	0.000
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	0.000	0.000	-0.914	0.368	-0.000	0.000	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 %	R2
Intercept	-0.02	0.025	-0.806	0.426	-0.072	0.031	0.000
L3.Biosynthesis.and.biodegradation.of.secondary.metabolites	0.00	0.000	1.520	0.139	0.000	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 %	R2
Intercept	0.002	0.023	0.099	0.922	-0.044	0.048	0.000
L3.Biosynthesis.of.12...14..and.16.membered.macrolides	-0.071	0.128	-0.557	0.582	-0.332	0.190	0.000



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 %	R2
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 %	R2
Intercept	-0.089	0.043	-2.081	0.046	-0.177	-0.002	0.000
L3.Phenylalanine.tyrosine.and.tryptophan.biosynthesis	0.000	0.000	2.367	0.025	0.000	0.000	0.117

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.Phytosynthesis, 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.Phytosynthesis	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.Phytosynthesis...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.Phytosynthesis...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.Phytosynthesis.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.Phytosynthesis.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 %	R2
Intercept	0.002	0.024	0.098	0.923	-0.047	0.051	0.000
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	0.000	0.000	-0.264	0.794	0.000	0.000	0.000

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 %	R2
Intercept	-0.053	0.034	-1.554	0.131	-0.123	0.017	0.000
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis	0.000	0.000	1.970	0.058	0.000	0.000	0.046

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	0.000
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 %	
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 %	97.5 %
Intercept	-0.005	0.018	-0.283	0.779	-0.042	0.032
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	0.000	0.000	1.513	0.141	0.000	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
L3.Biosynthesis.of.12...14..and.16.membered.macrolides	0.074	0.105	0.703	0.488	-0.141	0.289

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	0.23

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 %	R2
Intercept	0.006	0.018	0.301	0.766	-0.032	0.043	0.000
L3.Glycosaminoglycan.biosynthesis...chondroitin.sulfate	-0.022	0.017	-1.311	0.200	-0.057	0.012	0.000

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 %	R2
Intercept	-0.002	0.019	-0.109	0.914	-0.041	0.037	0.000
L3.Glycosphingolipid.biosynthesis...lacto.and.neolacto.series	0.000	0.000	0.471	0.641	0.000	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 %	R2
Intercept	-0.064	0.036	-1.751	0.090	-0.138	0.011	0.000
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis	0.000	0.000	1.992	0.056	0.000	0.000	0.138

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.Potosynthesis, 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.Potosynthesis	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.Potosynthesis...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.Potosynthesis...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.Potosynthesis.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.Potosynthesis.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 %	R2
Intercept	-0.008	0.019	-0.419	0.678	-0.048	0.032	0.000
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	0.000	0.000	1.132	0.267	0.000	0.000	0.000

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 %	97.5 %	R2
Intercept	0.01	0.099	0.099	0.922	-0.198	0.218	0
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	0.00	0.000	-0.199	0.844	0.000	0.000	0

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 %	R2
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 %	R2
Intercept	0.207	0.119	1.743	0.098	-0.042	0.456	0.000
L3.Chlorocyclohexane.and.chlorobenzene.degradation	0.000	0.000	-2.276	0.035	0.000	0.000	0.200

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 %	R2
Intercept	0.092	0.182	0.504	0.620	-0.289	0.473	0.000
L3.Phenylalanine.tyrosine.and.tryptophan.biosynthesis	0.000	0.000	-0.571	0.575	0.000	0.000	0.000

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.Potosynthesis, 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.Potosynthesis	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.Potosynthesis...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.Potosynthesis...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.Potosynthesis.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.Potosynthesis.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 %	R2
Intercept	0.049	0.103	0.474	0.641	-0.167	0.266	0.000
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	0.000	0.000	-0.827	0.418	-0.001	0.000	0.000

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 %	
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 %	97.5 %
Intercept	0	0.042	0.007	0.994	-0.089	0.089
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	0	0.000	-0.014	0.989	0.000	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	0.103

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	0
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	0.000	0.000	-1.542	0.140	0.000	0.000	0

Table 2489: diversity\_vs\_picrust\_L3\_yr1: wunifrac.PC.2 vs  
L3.ErbB.signaling.pathway, df=20

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
(Intercept)	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 %	R2
Intercept	0.002	0.038	0.043	0.966	-0.078	0.081	0.000
L3.Glycosaminoglycan.biosynthesis...chondroitin.sulfate	-0.001	0.006	-0.190	0.852	-0.015	0.012	0.000

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 %	R2
Intercept	-0.001	0.039	-0.015	0.988	-0.083	0.082	0.000
L3.Glycosphingolipid.biosynthesis...lacto.and.neolacto.series	0.000	0.000	0.043	0.966	0.000	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 %	R2
Intercept	0.092	0.075	1.227	0.235	-0.065	0.248	0.000
L3.Phenylalanine..tyrosine.and.tryptophan.biosynthesis	0.000	0.000	-1.390	0.181	0.000	0.000	0.000

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.Potosynthesis, 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.Potosynthesis	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.Potosynthesis...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.Potosynthesis...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.Potosynthesis.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.Potosynthesis.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 %	R2
Intercept	0.03	0.043	0.695	0.495	-0.061	0.121	0.000
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	0.00	0.000	-1.212	0.240	0.000	0.000	0.000

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

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	0.000
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis	0.000	0.000	1.214	0.239	0.000	0.000	0.000

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 %	97.5 %	R2
Intercept	0.027	0.026	1.043	0.310	-0.027	0.080	0.000
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	0.000	0.000	-2.100	0.049	0.000	0.000	0.011

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	0.000

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 %	R2
Intercept	0.018	0.051	0.358	0.724	-0.088	0.124	0.000
L3.Epithelial.cell.signaling.in.Helicobacter.pylori.infection	0.000	0.000	-0.410	0.686	0.000	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 %	R2
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

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.potential, 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 %	R2
Intercept	0.027	0.052	0.511	0.615	-0.083	0.136	0.000
L3.Phenylalanine.tyrosine.and.tryptophan.biosynthesis	0.000	0.000	-0.579	0.570	0.000	0.000	0.000

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.Potosynthesis.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.Potosynthesis.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 %	R2
Intercept	0.027	0.057	0.467	0.646	-0.093	0.147	0.00
L3.Tropane..piperidine.and.pyridine.alkaloid.biosynthesis	0.000	0.000	-0.517	0.611	0.000	0.000	0.00

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 %	R2
Intercept	0.029	0.065	0.451	0.657	-0.107	0.166	0.000
L3.Ubiquinone.and.other.terpenoid.quinone.biosynthesis	0.000	0.000	-0.487	0.632	0.000	0.000	0.000

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 %	97.5 %	R2
Intercept	-0.003	0.024	-0.121	0.905	-0.054	0.048	0.000
L3.1.1.1.Trichloro.2.2.bis.4.chlorophenyl.ethane..DDT..degradation	0.000	0.000	0.244	0.810	0.000	0.000	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 %	R2
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 %	R2
Intercept	-0.011	0.045	-0.246	0.808	-0.105	0.083	0.000
L3.Phenylalanine.tyrosine.and.tryptophan.biosynthesis	0.000	0.000	0.279	0.783	0.000	0.000	0.000

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.Phytosynthesis, 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.Phytosynthesis	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.Phytosynthesis...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.Phytosynthesis...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.Phytosynthesis.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.Phytosynthesis.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 %	R2
Intercept	-0.012	0.025	-0.458	0.652	-0.065	0.041	0.000
L3.Stilbenoid..diarylheptanoid.and.gingerol.biosynthesis	0.000	0.000	0.799	0.434	0.000	0.000	0.000

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 %	R2
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

	Estimate	Std. Error	t value	Pr(> t )	2.5 %	97.5 %	R2
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
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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## Microbiome alpha diversity difference (yr1 vs neo) vs SS, IBQ-R using linear mixed effect model

Table 3404: div\_diff\_vs\_strange\_combine\_yr1: strange\_response VS chao1, df=34

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	1.2889403	0.3296680	3.9098130	0.0000924	0.643	1.935	0.000
chao1	0.0004615	0.0015830	0.2915561	0.7706260	-0.003	0.004	0.009
episodes2	0.1052632	0.1569171	0.6708204	0.5023350	-0.202	0.413	0.010
episodes3	0.1578947	0.1569171	1.0062306	0.3143047	-0.150	0.465	0.023

Table 3405: div\_diff\_vs\_strange\_combine\_yr1: strange\_response VS observed\_otus, df=34

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	1.2309272	0.3414731	3.6047559	0.0003124	0.562	1.900	0.000
observed_otus	0.0013612	0.0028428	0.4788158	0.6320697	-0.004	0.007	0.024
episodes2	0.1052632	0.1569171	0.6708204	0.5023350	-0.202	0.413	0.010
episodes3	0.1578947	0.1569171	1.0062306	0.3143047	-0.150	0.465	0.023



Table 3406: div\_diff\_vs\_strange\_combine\_yr1: strange\_response  
VS PD\_whole\_tree, df=34

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	1.1261240	0.4526513	2.4878402	0.0128521	0.239	2.013	0.000
PD_whole_tree	0.0453133	0.0773163	0.5860772	0.5578236	-0.106	0.197	0.036
episodes2	0.1052632	0.1569171	0.6708204	0.5023350	-0.202	0.413	0.010
episodes3	0.1578947	0.1569171	1.0062306	0.3143047	-0.150	0.465	0.022

Table 3407: div\_diff\_vs\_strange\_combine\_yr1: strange\_response  
VS shannon, df=34

	Estimate	Std. Error	t value	Pval	2.5 %	97.5 %	R2
(Intercept)	1.0898094	0.3018315	3.6106547	0.0003054	0.498	1.681	0.000
shannon	0.1790150	0.1554182	1.1518281	0.2493917	-0.126	0.484	0.120
episodes2	0.1052632	0.1569170	0.6708204	0.5023350	-0.202	0.413	0.009
episodes3	0.1578947	0.1569170	1.0062306	0.3143047	-0.150	0.465	0.021