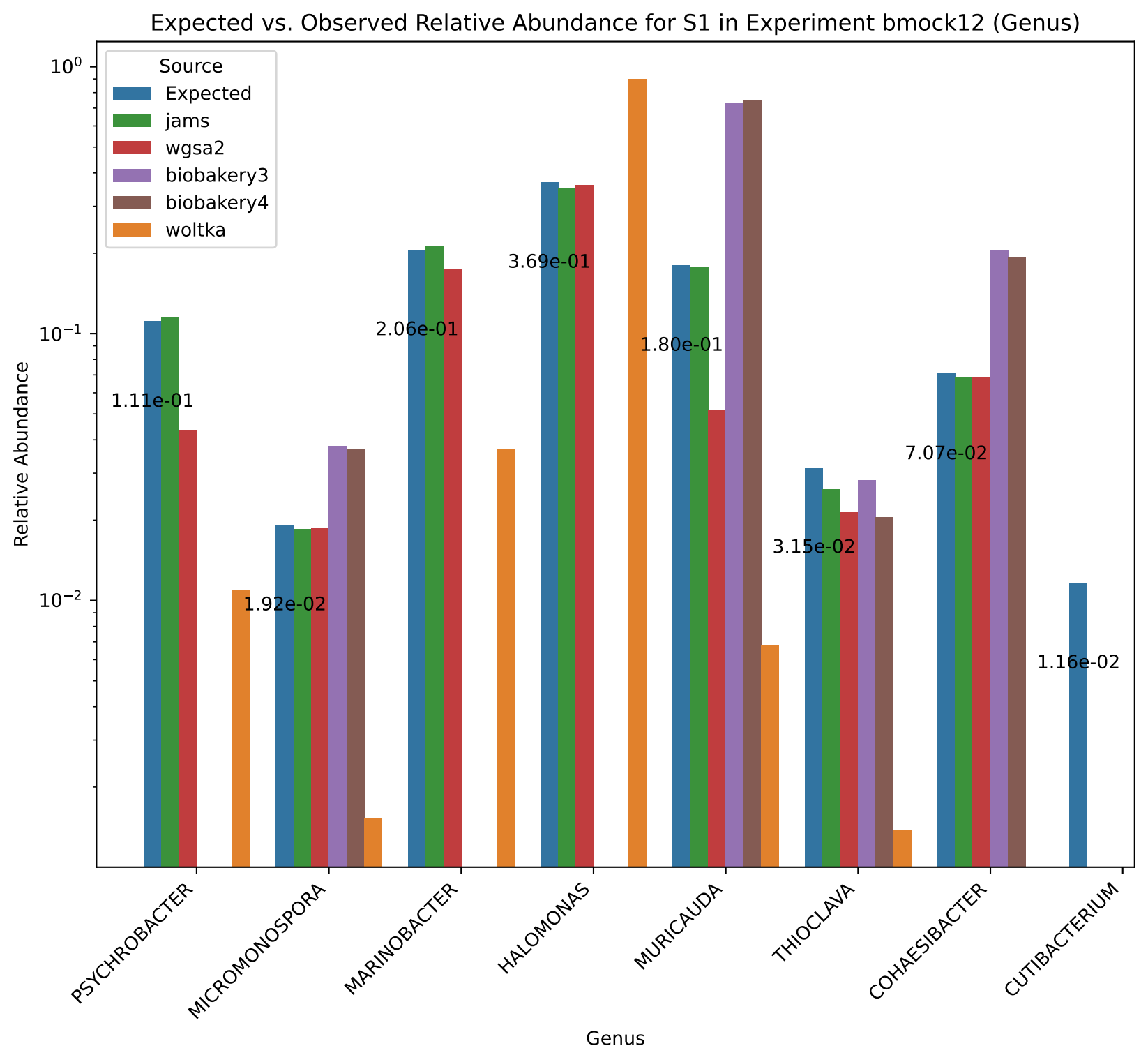
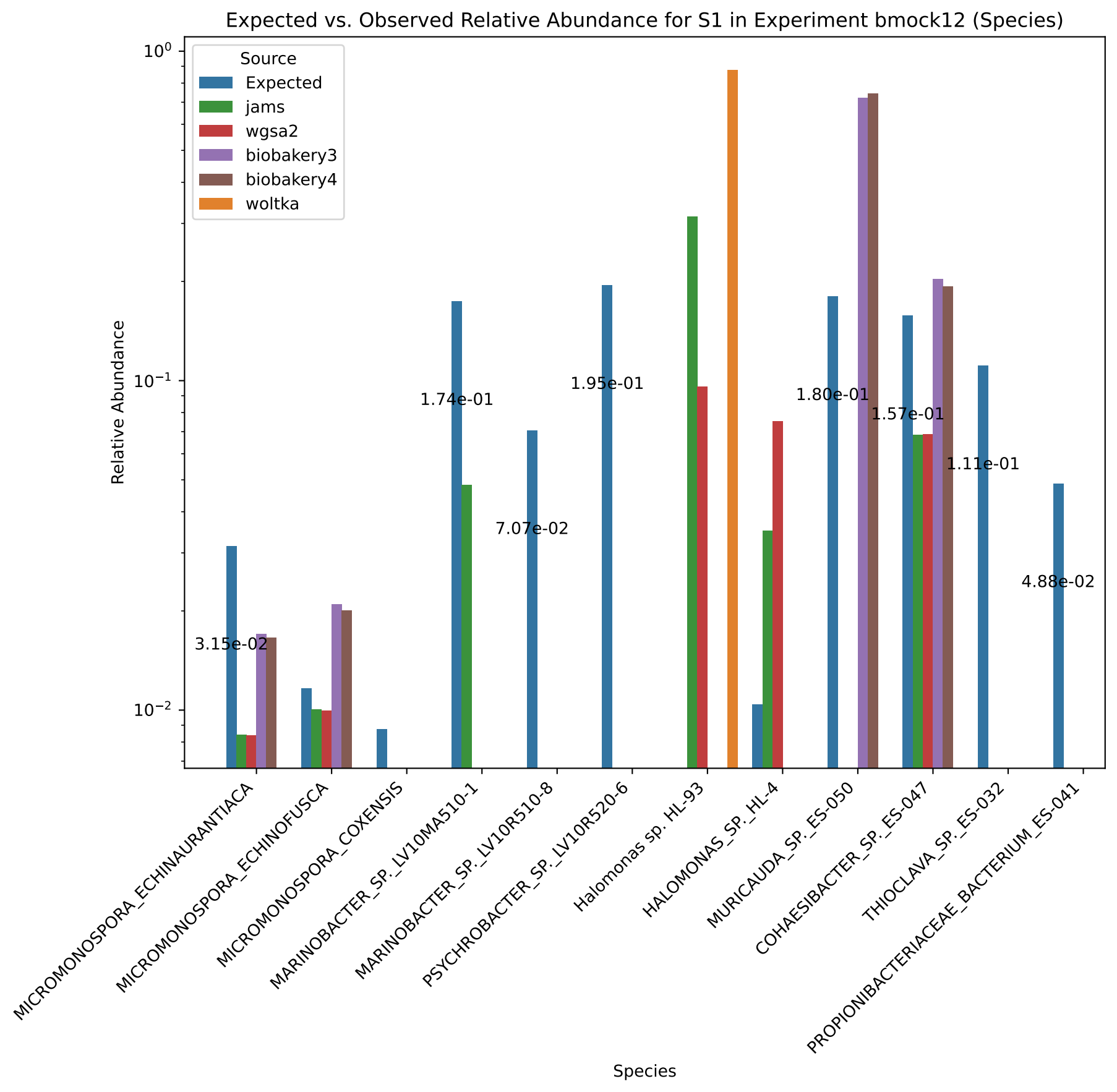
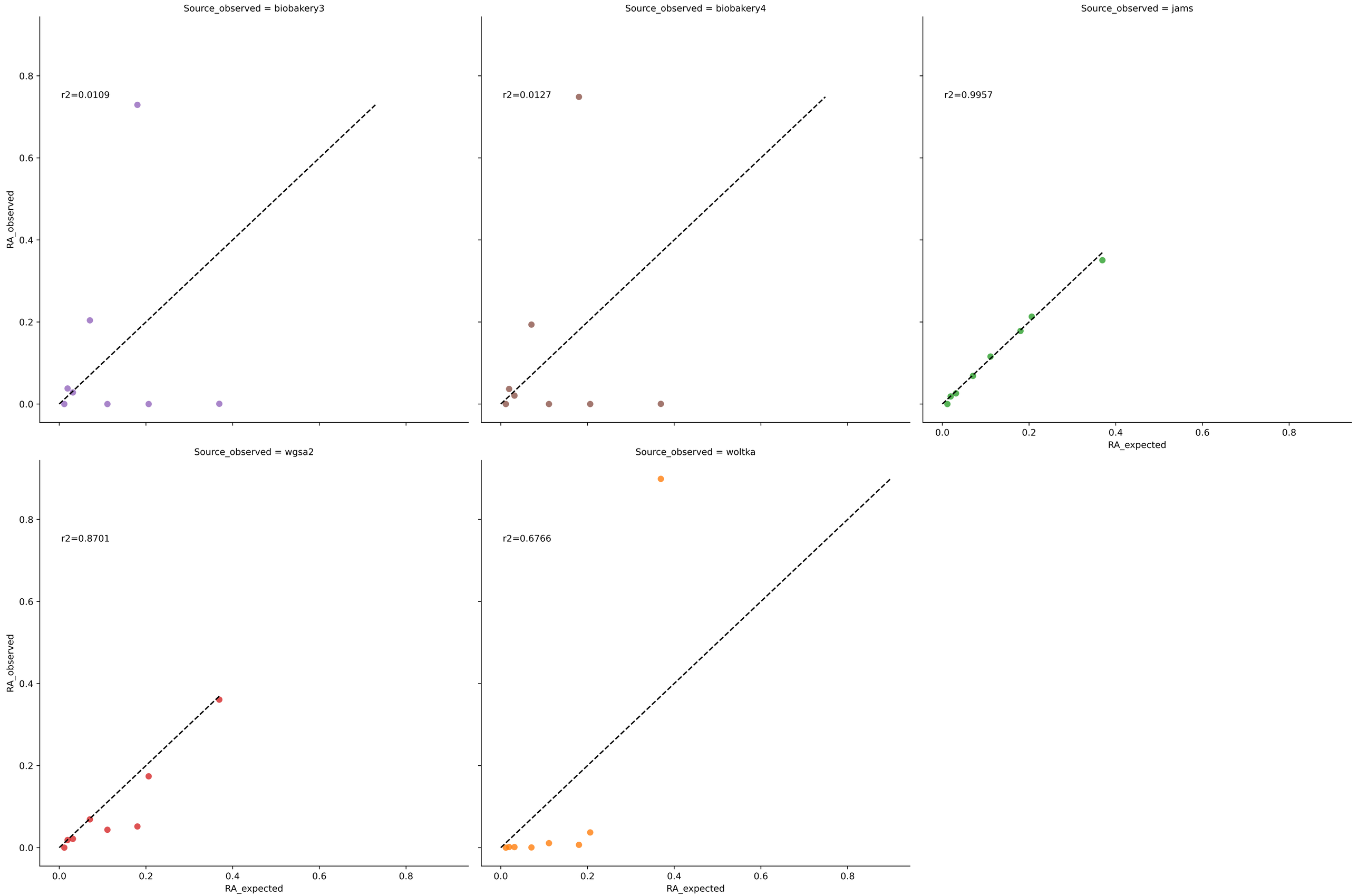
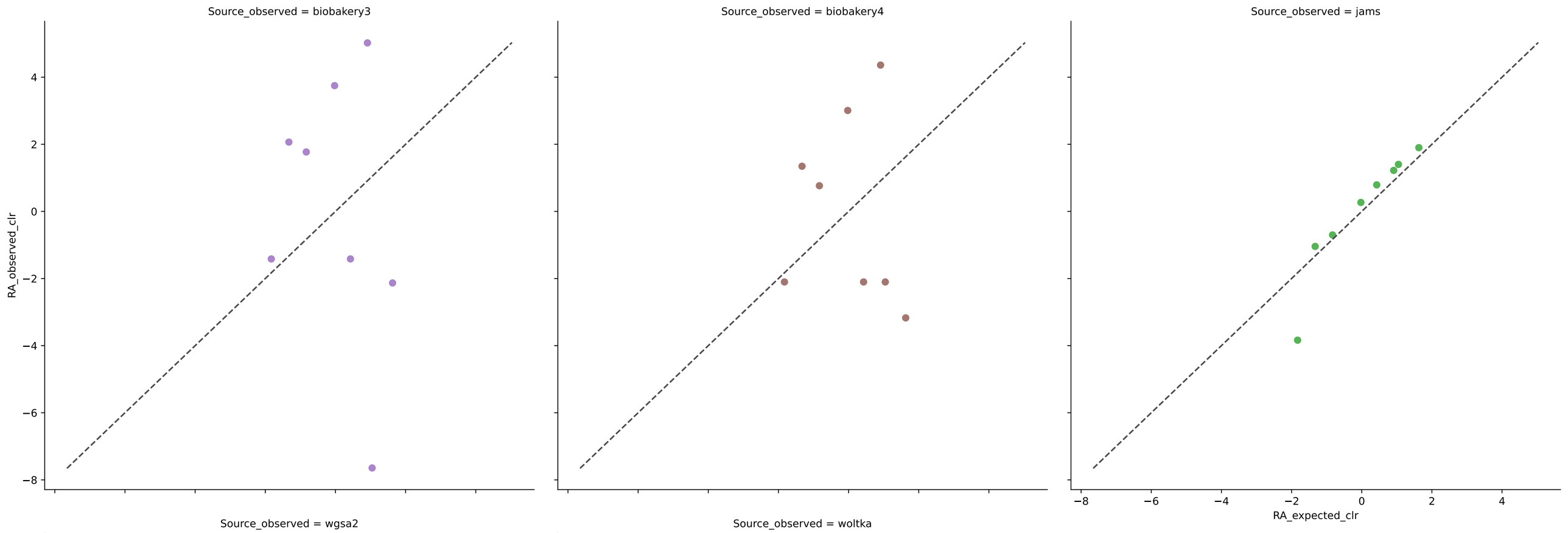

Expected vs. Observed Relative Abundance for S1 in Experiment bmock12 (Genus)
Source
Expected
jams
wgsa2
biobakery3
biobakery4
woltka
Relative Abundance
10^{0}
10^{-1}
10^{-2}
1.11e-01
1.92e-02
2.06e-01
3.69e-01
1.80e-01
3.15e-02
7.07e-02
1.16e-02
PSYCHROBACTER
MICROMONOSPORA
MARINOBACTER
HALOMONAS
MURICAUDA
THIOCLAVA
COHAESIBACTER
CUTIBACTERIUM
Genus


Expected vs. Observed Relative Abundance for S1 in Experiment bmock12 (Species)
Source
Expected
jams
wgsa2
biobakery3
biobakery4
woltka
Relative Abundance
10^{0}
10^{-1}
10^{-2}
3.15e-02
1.74e-01
7.07e-02
1.95e-01
1.80e-01
1.57e-01
1.11e-01
4.88e-02
MICROMONOSPORA_ECHINAURANTIACA
MICROMONOSPORA_ECHINOFUSCA
MICROMONOSPORA_COXENSIS
MARINOBACTER_SP._LV10MA510-1
MARINOBACTER_SP._LV10R510-8
PSYCHROBACTER_SP._LV10R520-6
Halomonas sp. HL-93
HALOMONAS_SP._HL-4
MURICAUDA_SP._ES-050
COHAESIBACTER_SP._ES-047
THIOCLAVA_SP._ES-032
PROPIONIBACTERIACEAE_BACTERIUM_ES-041
Species

Bivariate Linear Regression for Sample S1 in Experiment bmock12 (Genus)

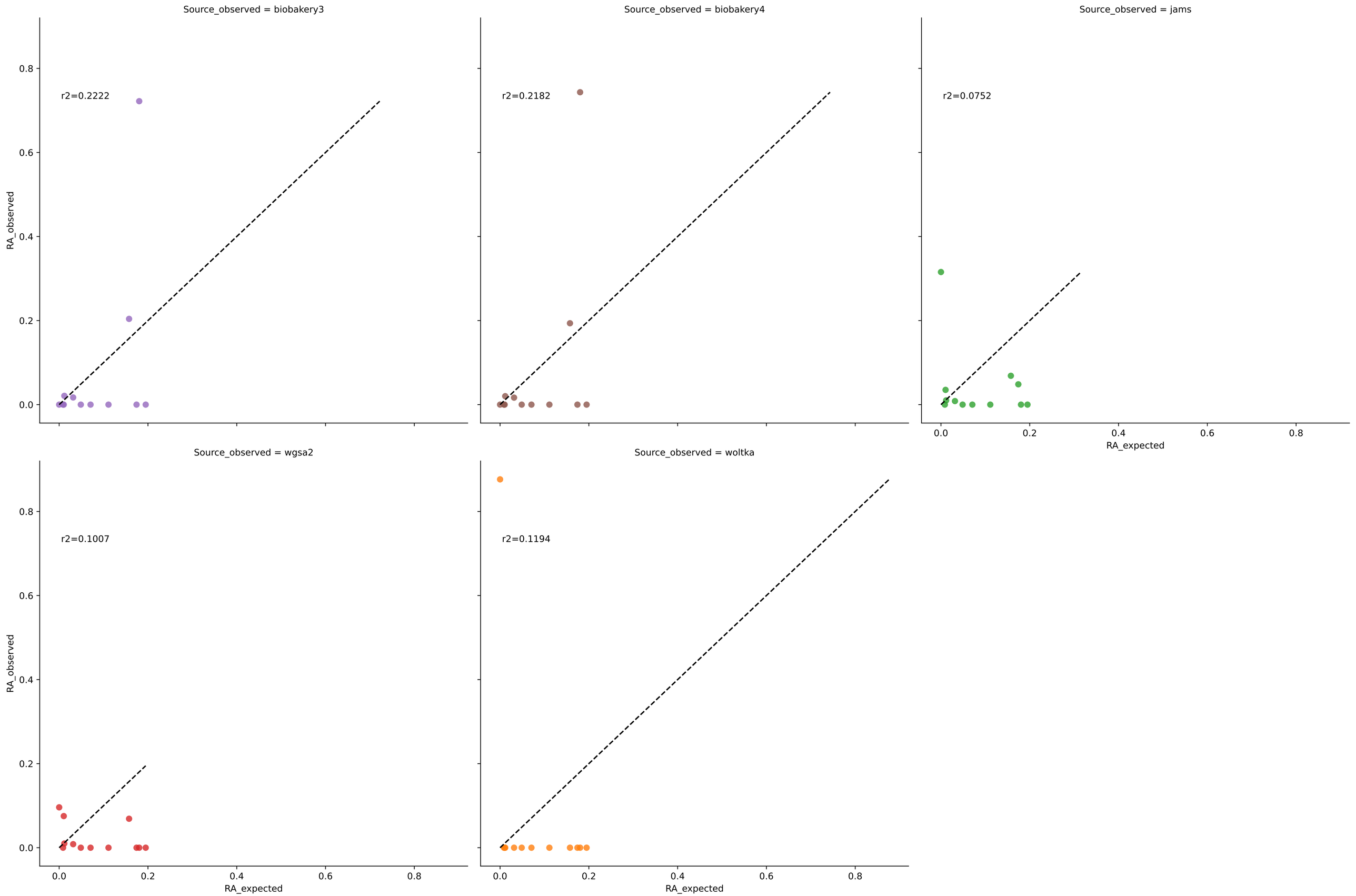


Bivariate Linear Regression for Sample S1 in Experiment bmock12 (Genus)

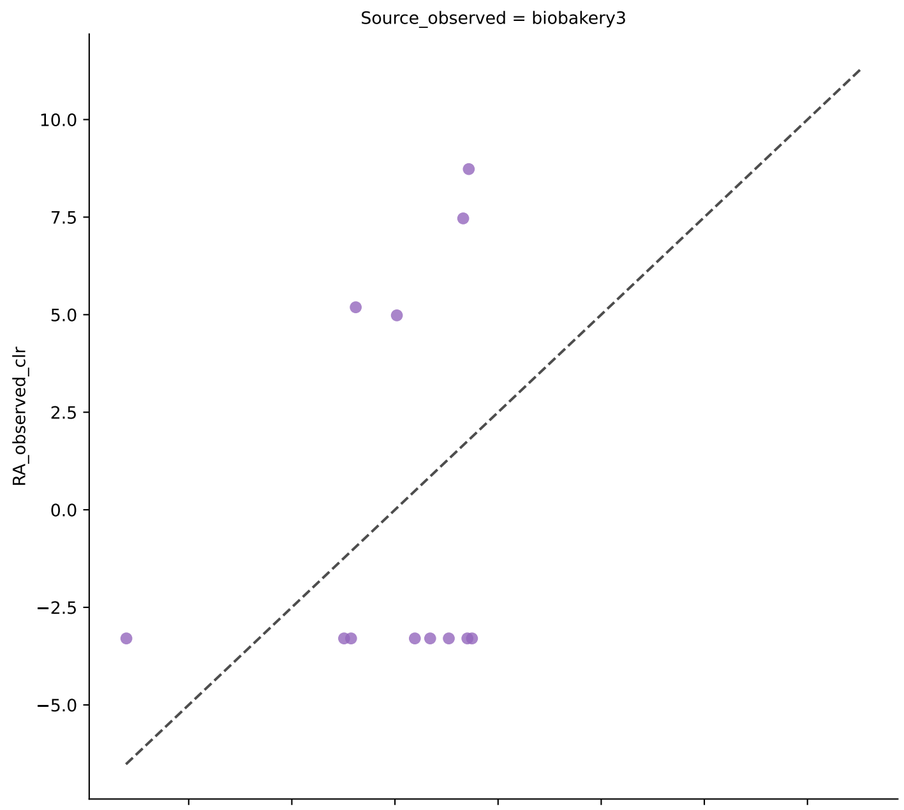


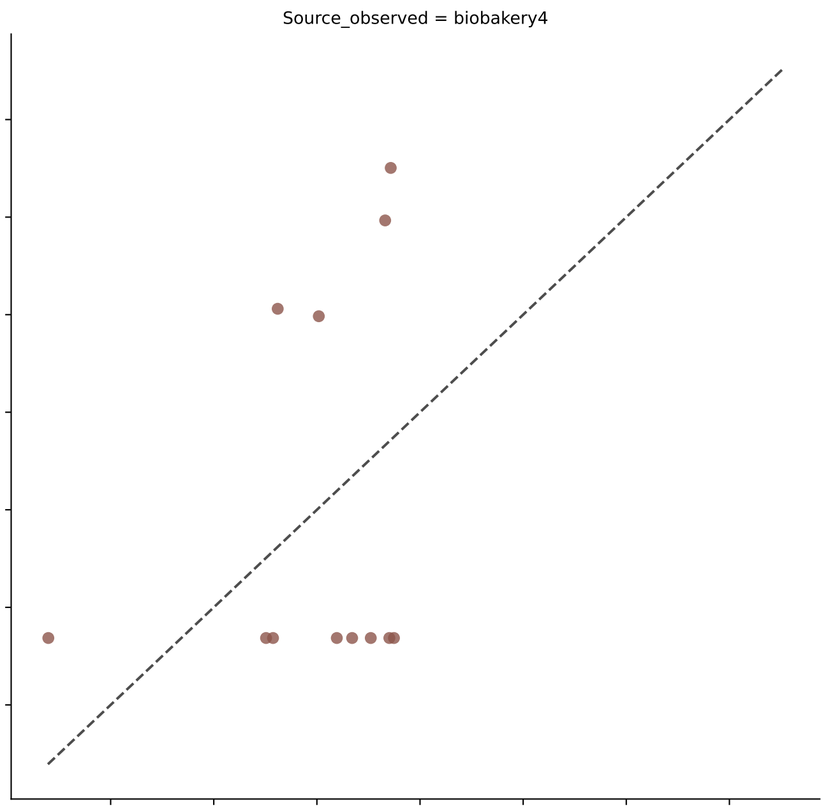
	R^2	MAE	AD	1-BC	RMSE
biobakery3	0.0109	0.1752	11.9441	0.2991	0.2526
biobakery4	0.0127	0.1772	8.3803	0.2912	0.2573
jams	0.9957	0.0065	2.1554	0.9736	0.0086
wgsa2	0.8701	0.0326	5.5177	0.8499	0.0530
woltka	0.6766	0.1378	4.3798	0.4368	0.2108

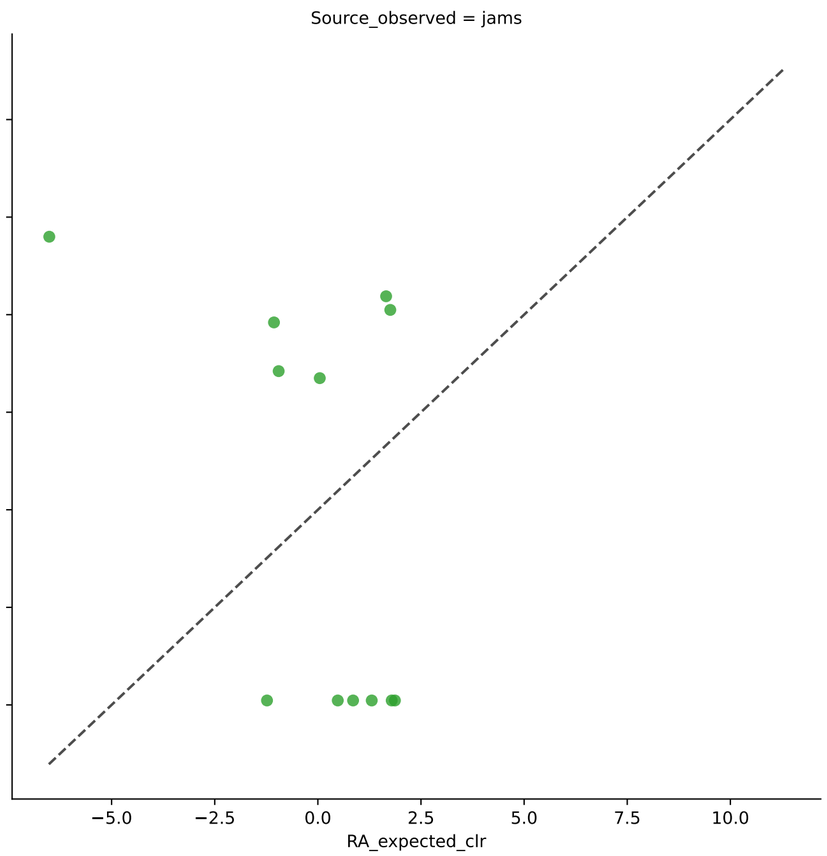
Bivariate Linear Regression for Sample S1 in Experiment bmock12 (Species)

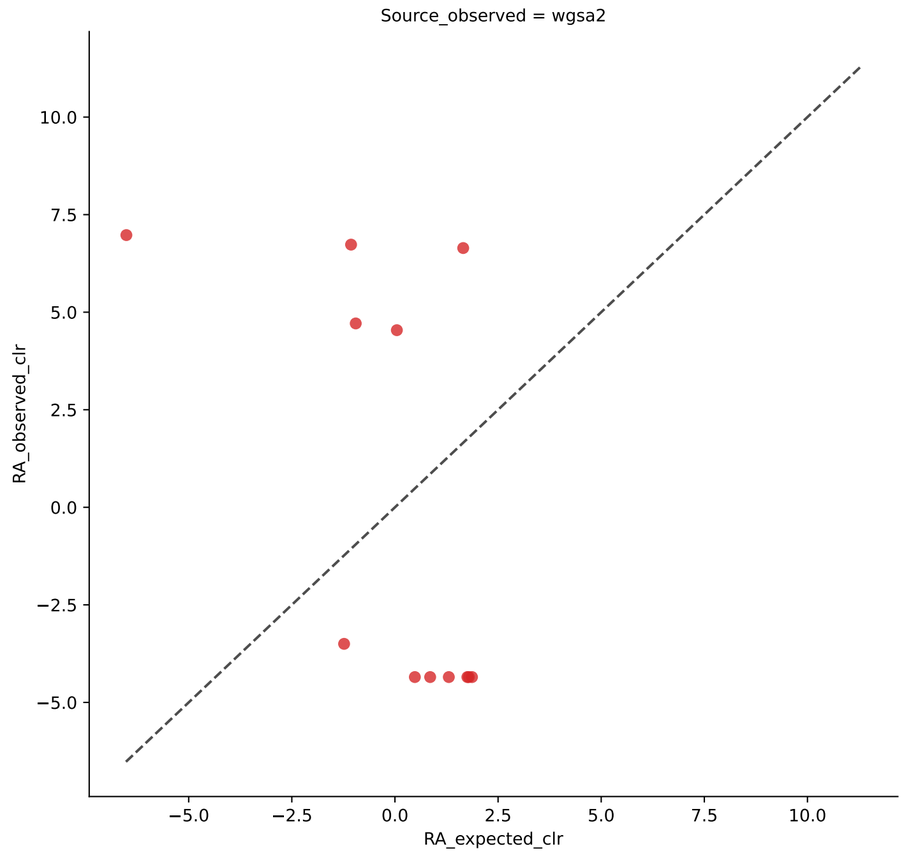


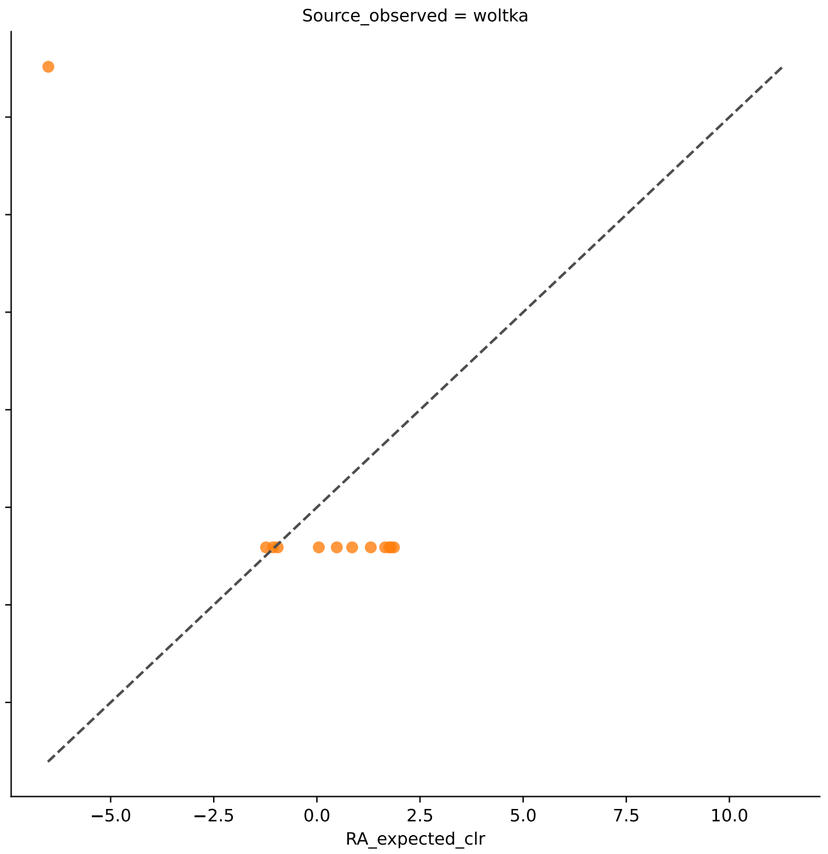
Bivariate Linear Regression for Sample S1 in Experiment bmock12 (Species)



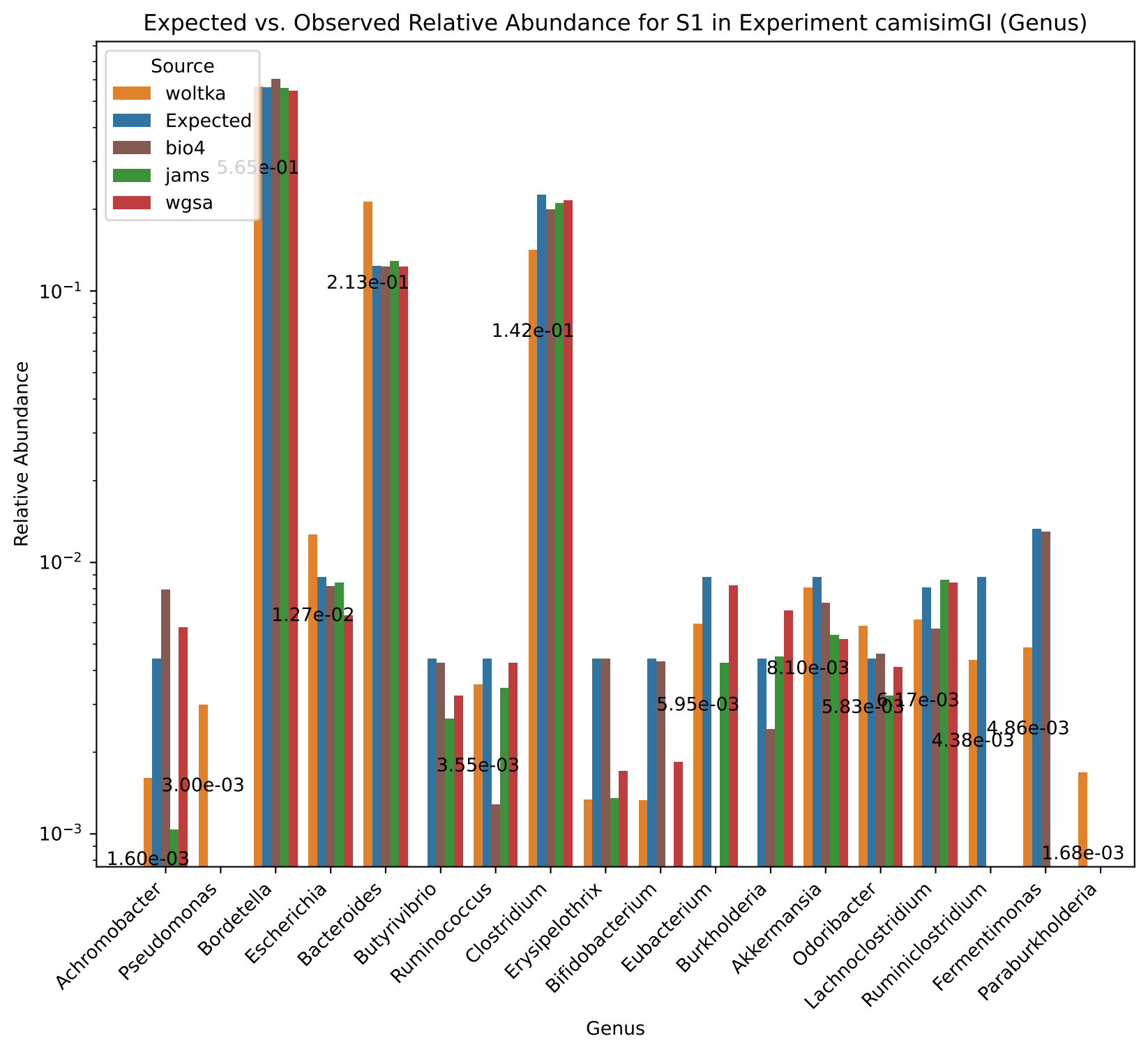


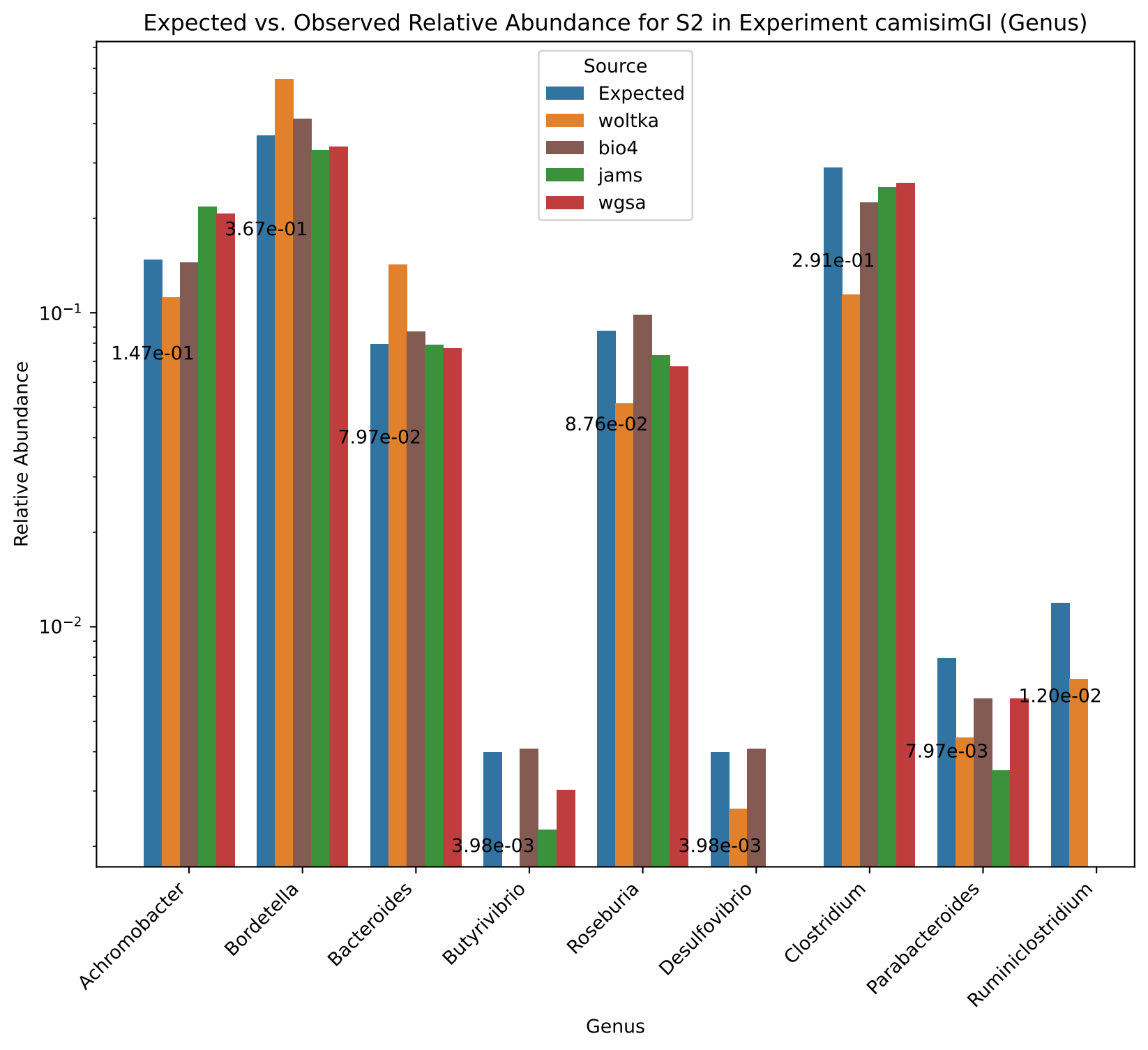


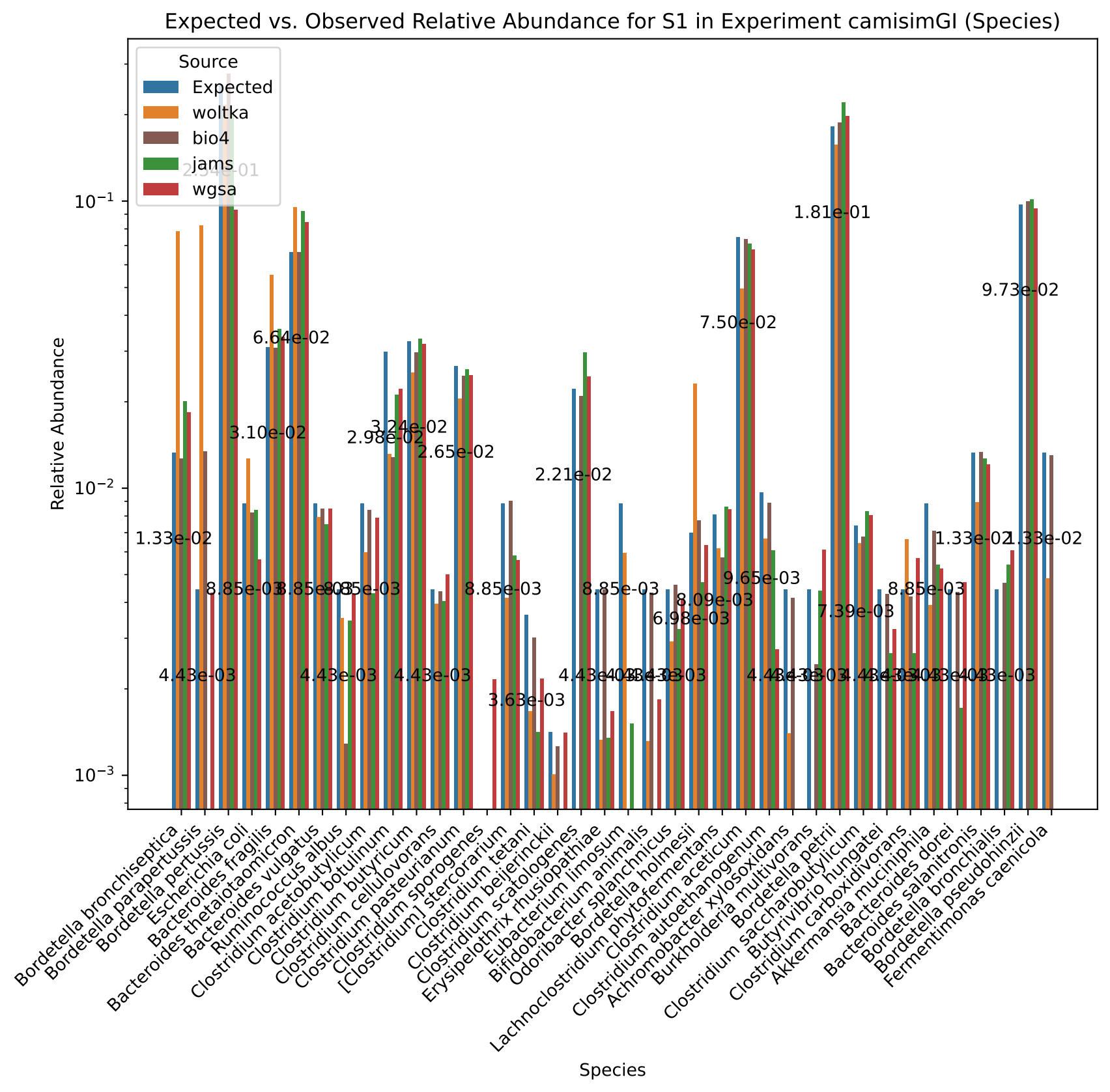


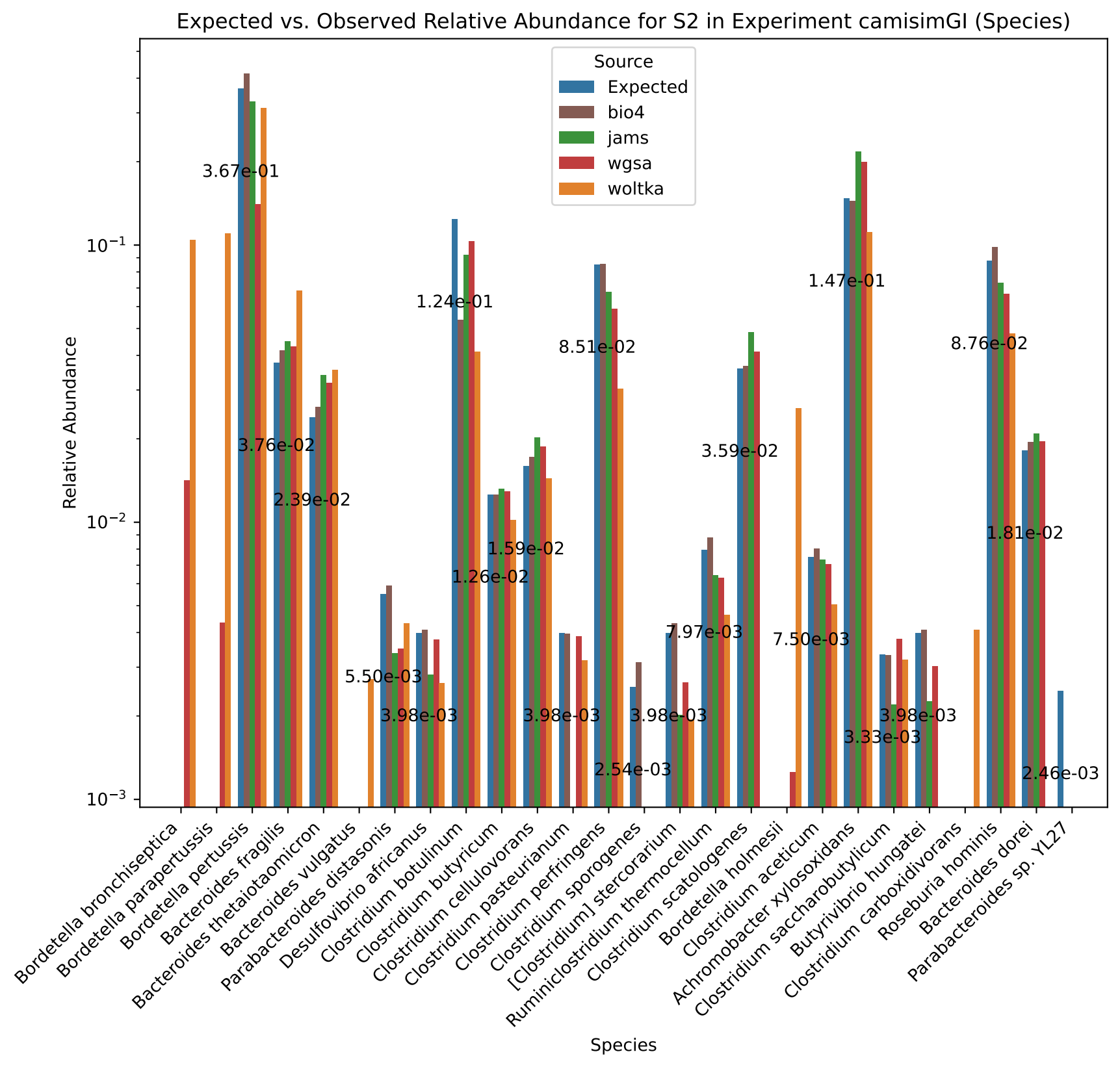


	R^2	MAE	AD	1-BC	RMSE
biobakery3	0.2222	0.1026	16.3856	0.3732	0.1789
biobakery4	0.2182	0.1035	16.3433	0.3709	0.1841
jams	0.0752	0.0995	21.8589	0.1963	0.1338
wgsa2	0.1007	0.0886	22.8257	0.1553	0.1090
woltka	0.1194	0.1564	18.9883	0.0000	0.2761

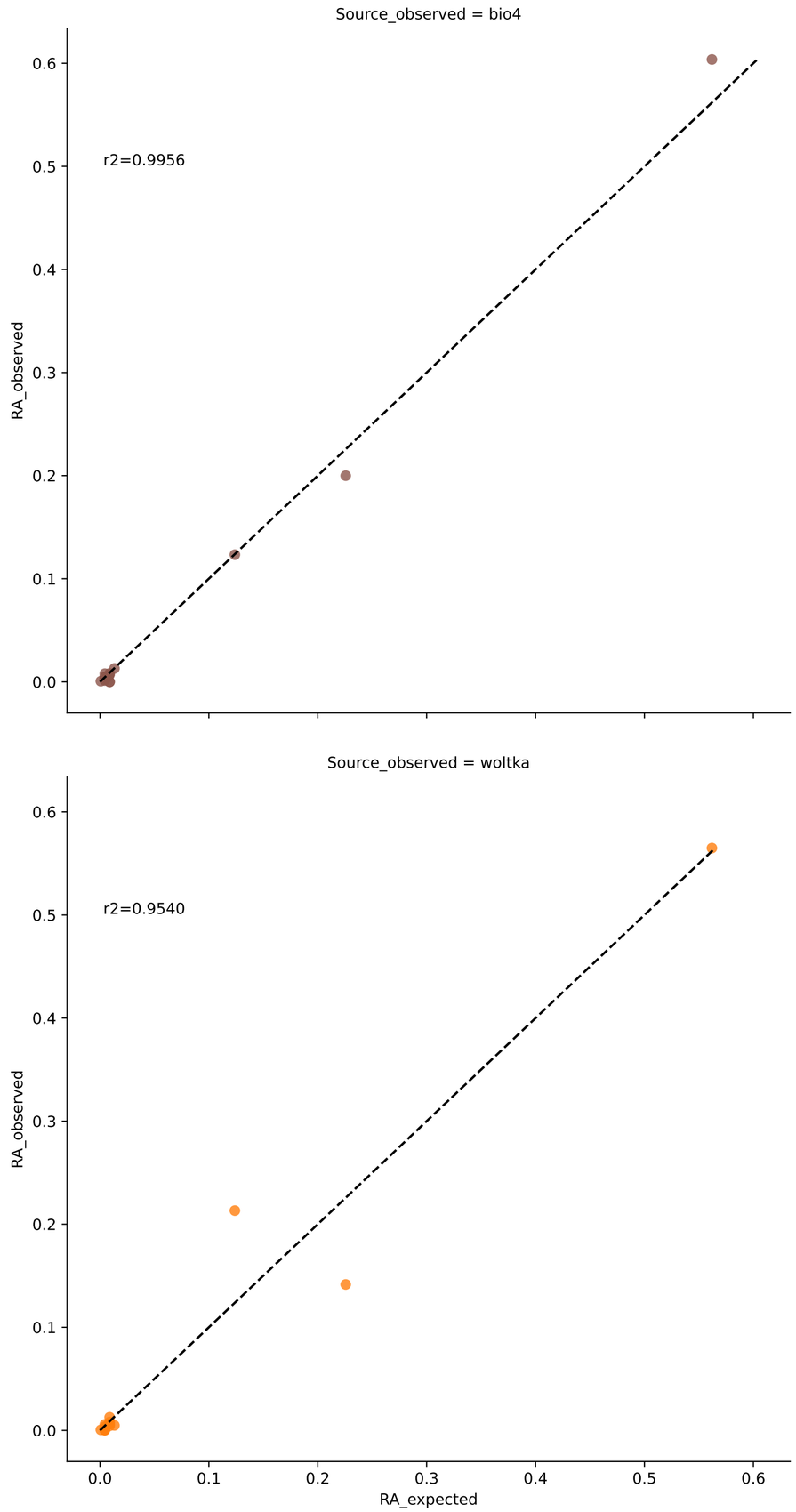

Expected vs. Observed Relative Abundance for S1 in Experiment camisimGI (Genus)
Source
woltka
Expected
bio4
jams
wgsa
Relative Abundance
10^{-1}
10^{-2}
10^{-3}
5.65e-01
2.13e-01
1.42e-01
1.27e-02
3.00e-03
1.60e-03
3.55e-03
5.95e-03
8.10e-03
5.83e-03
6.17e-03
4.38e-03
4.86e-03
1.68e-03
Achromobacter
Pseudomonas
Bordetella
Escherichia
Bacteroides
Butyrivibrio
Ruminococcus
Clostridium
Erysipelothrix
Bifidobacterium
Eubacterium
Burkholderia
Akkermansia
Odoribacter
Lachnoclostridium
Ruminiclostridium
Fermentimonas
Paraburkholderia
Genus


Expected vs. Observed Relative Abundance for S2 in Experiment camisimGI (Genus)
Source
Expected
woltka
bio4
jams
wgsa
Relative Abundance
10^{-1}
10^{-2}
1.47e-01
3.67e-01
7.97e-02
3.98e-03
8.76e-02
3.98e-03
2.91e-01
7.97e-03
1.20e-02
Achromobacter
Bordetella
Bacteroides
Butyrivibrio
Roseburia
Desulfovibrio
Clostridium
Parabacteroides
Ruminiclostridium
Genus

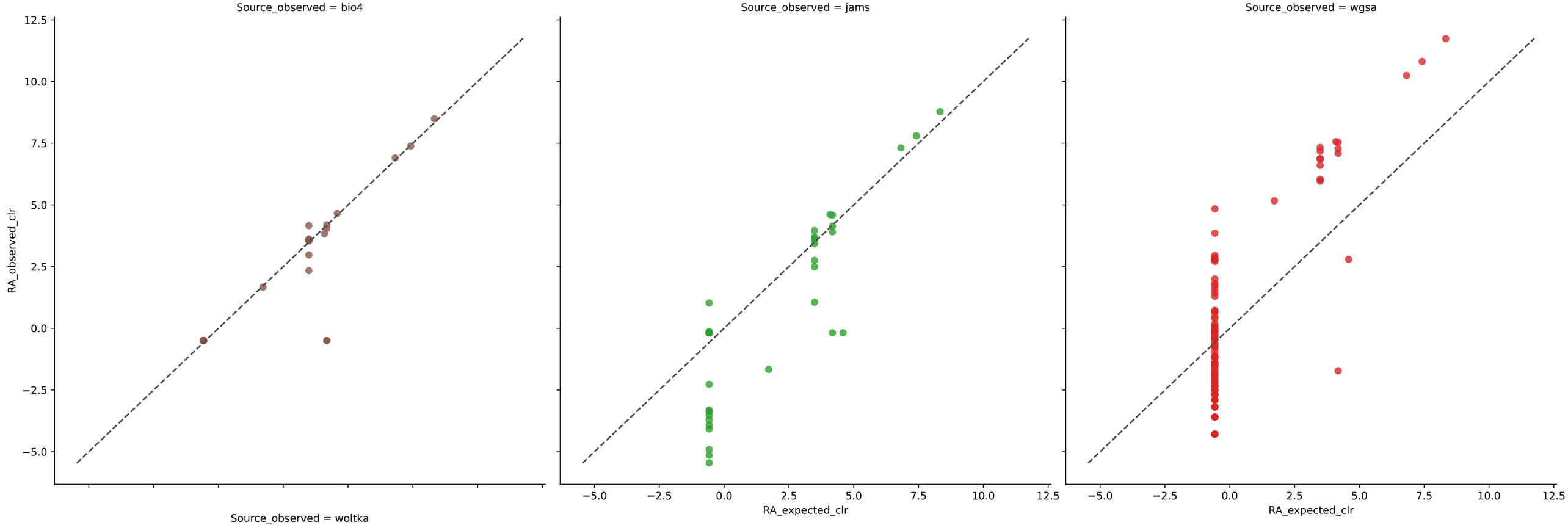

Expected vs. Observed Relative Abundance for S1 in Experiment camisimGI (Species)
Source
Expected
woltka
bio4
jams
wgsa
Relative Abundance
Species
Bordetella bronchiseptica
Bordetella parapertussis
Bordetella pertussis
Escherichia coli
Bacteroides thetaiotaomicron
Bacteroides fragilis
Ruminococcus vulgatus
Clostridium acetobutylicum
Clostridium botulinum
Clostridium butyricum
Clostridium cellulovorans
Clostridium pasteurianum
[Clostridium] sporogenes
[Clostridium] stercorarium
Clostridium tetani
Clostridium beijerinckii
Erysipelothrix rhusiopathiae
Clostridium scatologenes
Eubacterium limosum
Bifidobacterium animalis
Odoribacter splanchnicus
Bordetella holmesii
Lachnoclostridium phytofermentans
Clostridium aceticum
Achromobacter xylosoxidans
Burkholderia multivorans
Bordetella petrii
Clostridium saccharobutylicum
Butyrivibrio hungatei
Clostridium carboxidivorans
Akkermansia muciniphila
Bacteroides dorei
Bacteroides salanitronis
Bordetella bronchialis
Bordetella pseudohinzii
Fermentimonas caenicola

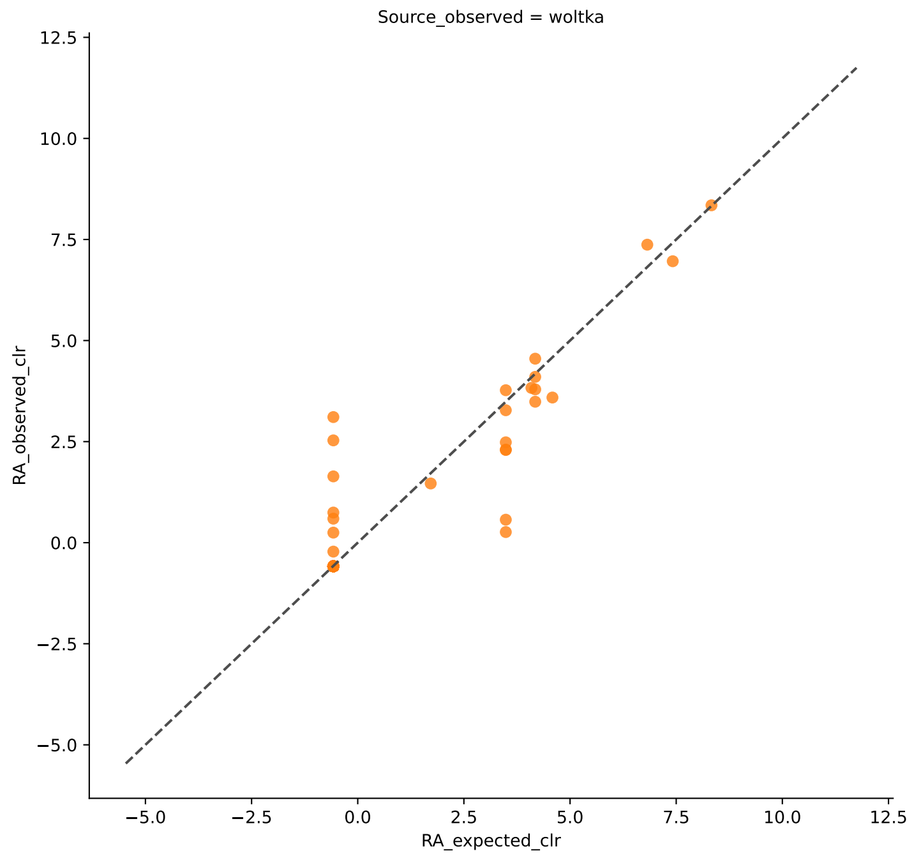

Expected vs. Observed Relative Abundance for S2 in Experiment camisimGI (Species)
Source
Expected
bio4
jams
wgsa
woltka
Relative Abundance
Species
3.67e-01
3.76e-02
2.39e-02
1.24e-01
1.26e-02
1.59e-02
8.51e-02
3.59e-02
1.47e-01
8.76e-02
1.81e-02
2.46e-03
5.50e-03
3.98e-03
3.98e-03
3.98e-03
2.54e-03
7.97e-03
7.50e-03
3.33e-03
3.98e-03
Bordetella bronchiseptica
Bordetella parapertussis
Bordetella pertussis
Bacteroides fragilis
Bacteroides thetaiotaomicron
Bacteroides vulgatus
Parabacteroides distasonis
Desulfovibrio africanus
Clostridium botulinum
Clostridium butyricum
Clostridium cellulovorans
Clostridium pasteurianum
Clostridium perfringens
Clostridium sporogenes
[Clostridium] stercorarium
Ruminiclostridium thermocellum
Clostridium scatologenes
Bordetella holmesii
Clostridium aceticum
Achromobacter xylosoxidans
Clostridium saccharobutylicum
Butyrivibrio hungatei
Clostridium carboxidivorans
Roseburia hominis
Bacteroides dorei
Parabacteroides sp. YL27

Bivariate Linear Regression for Sample S1 in Experiment camisimGI (Genus)



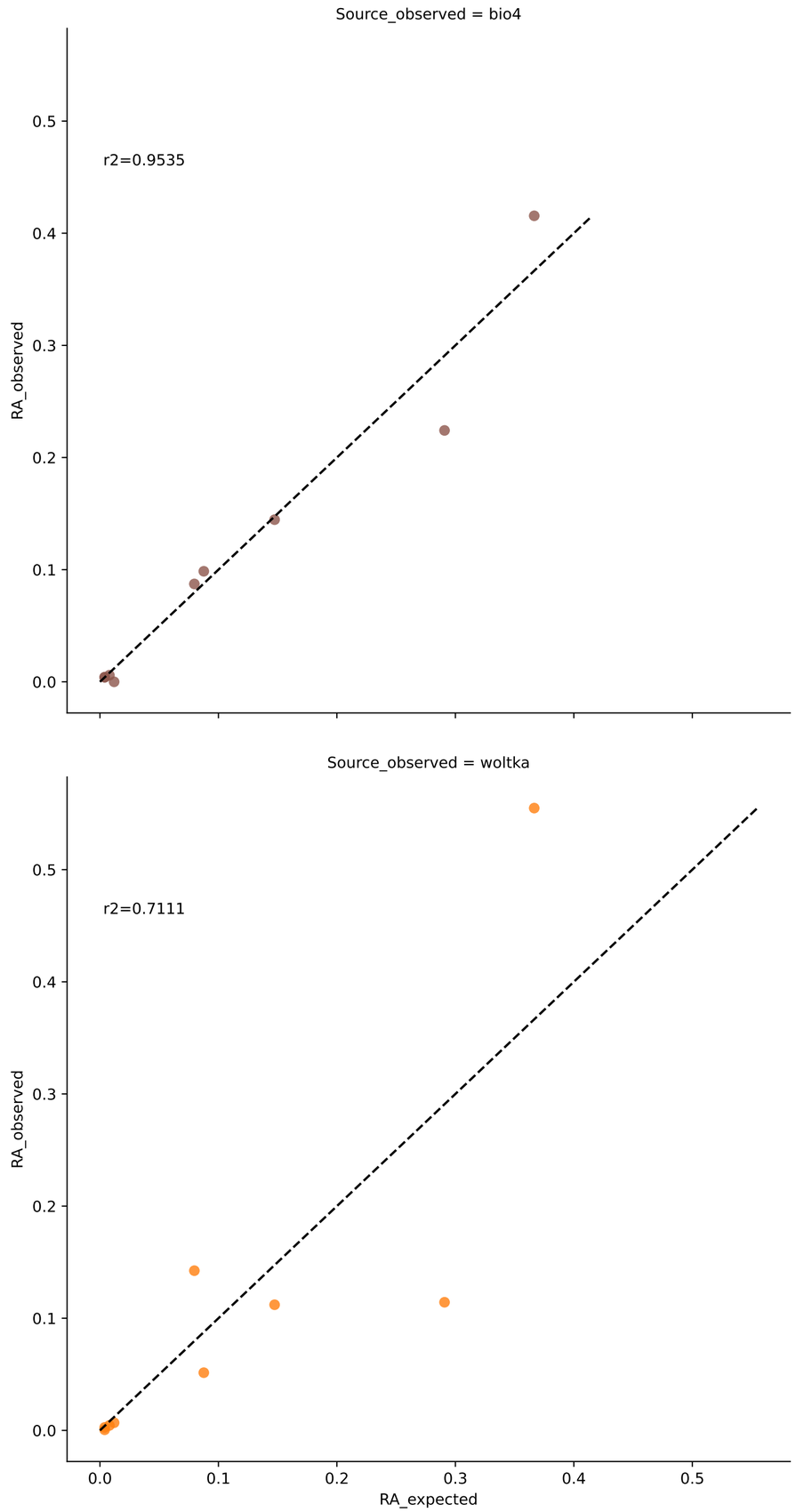
Bivariate Linear Regression for Sample S1 in Experiment camisimGI (Genus)



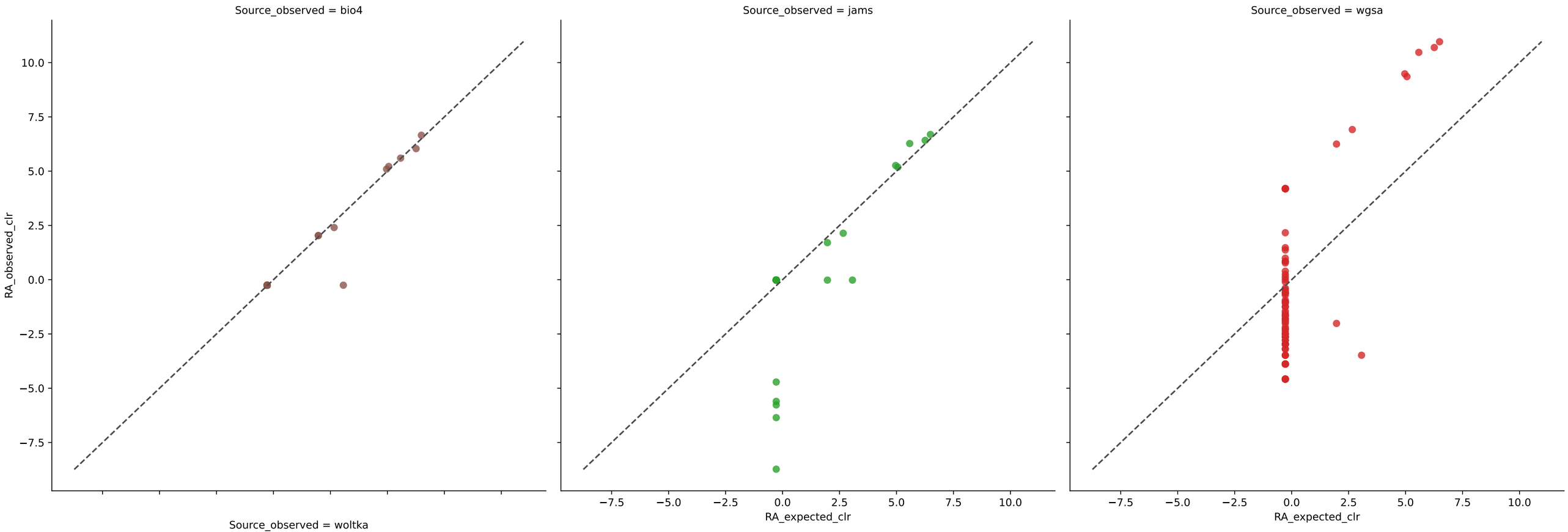


	R^2	MAE	AD	1-BC	RMSE
bio4	0.9957	0.0007	6.8349	0.9498	0.0042
jams	0.9986	0.0005	14.3745	0.9642	0.0020
wgsa	0.9992	0.0005	32.3711	0.9659	0.0020
woltka	0.9600	0.0015	7.5697	0.8866	0.0102

Bivariate Linear Regression for Sample S2 in Experiment camisimGI (Genus)

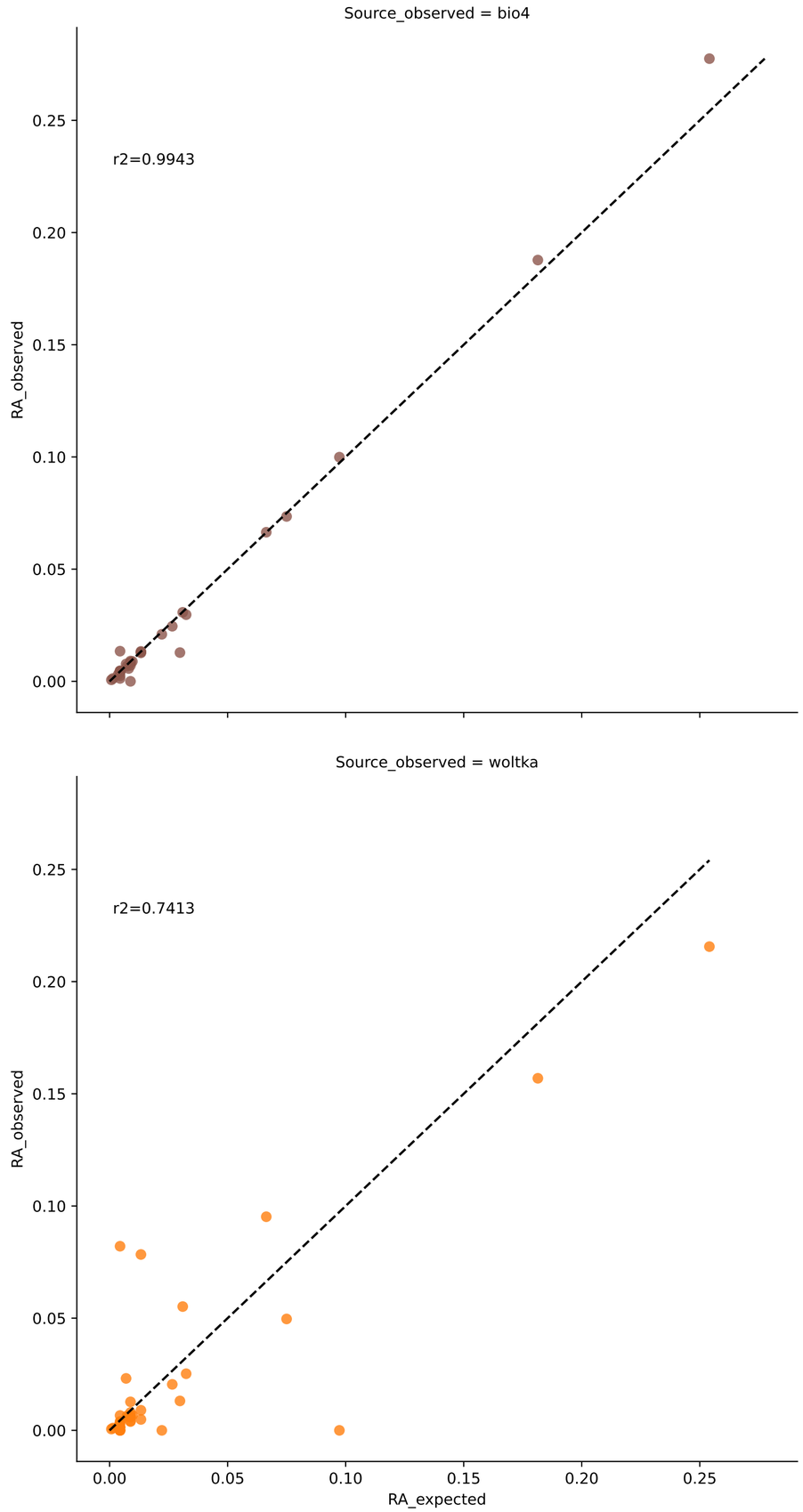


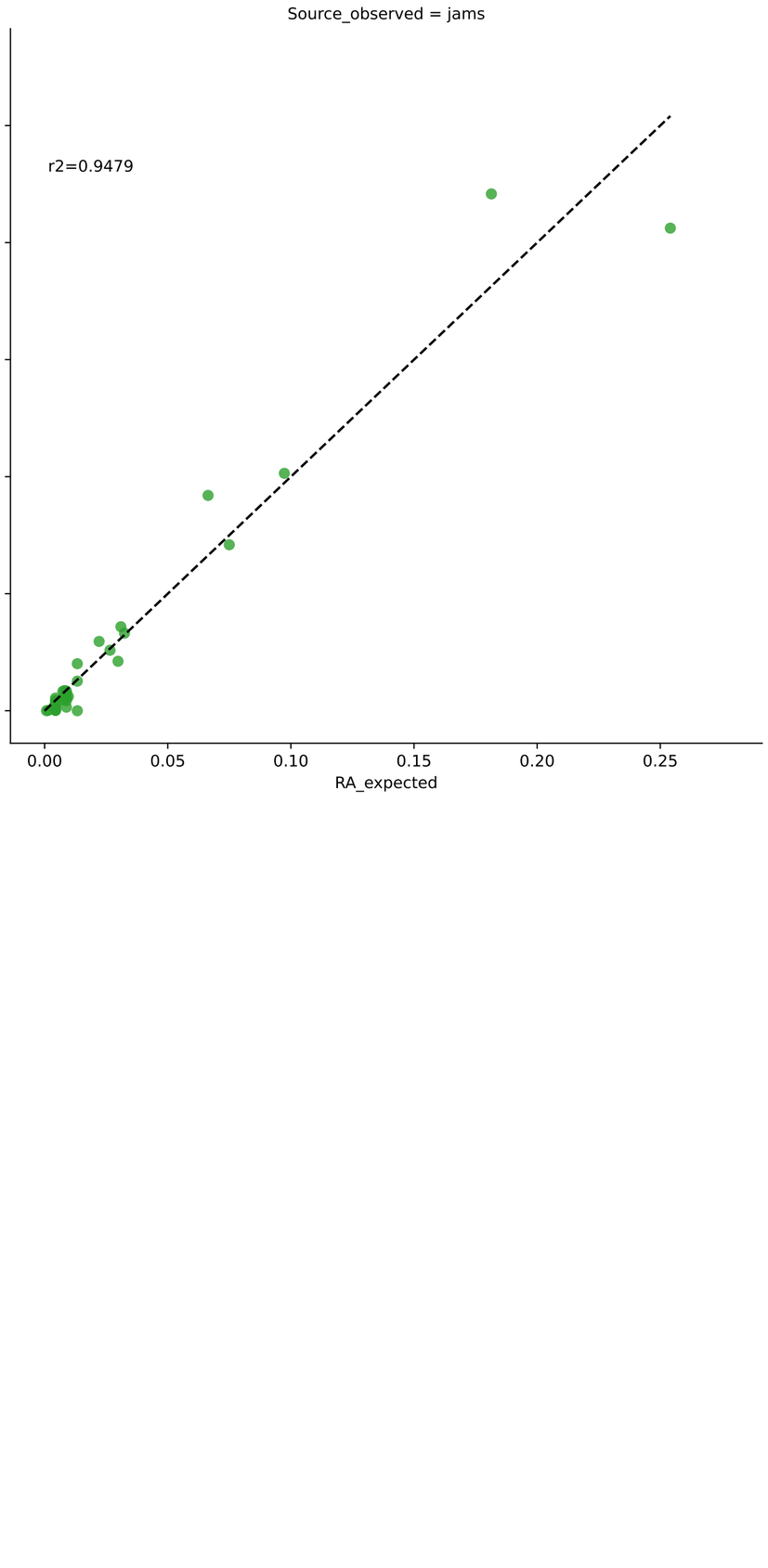
Bivariate Linear Regression for Sample S2 in Experiment camisimGI (Genus)

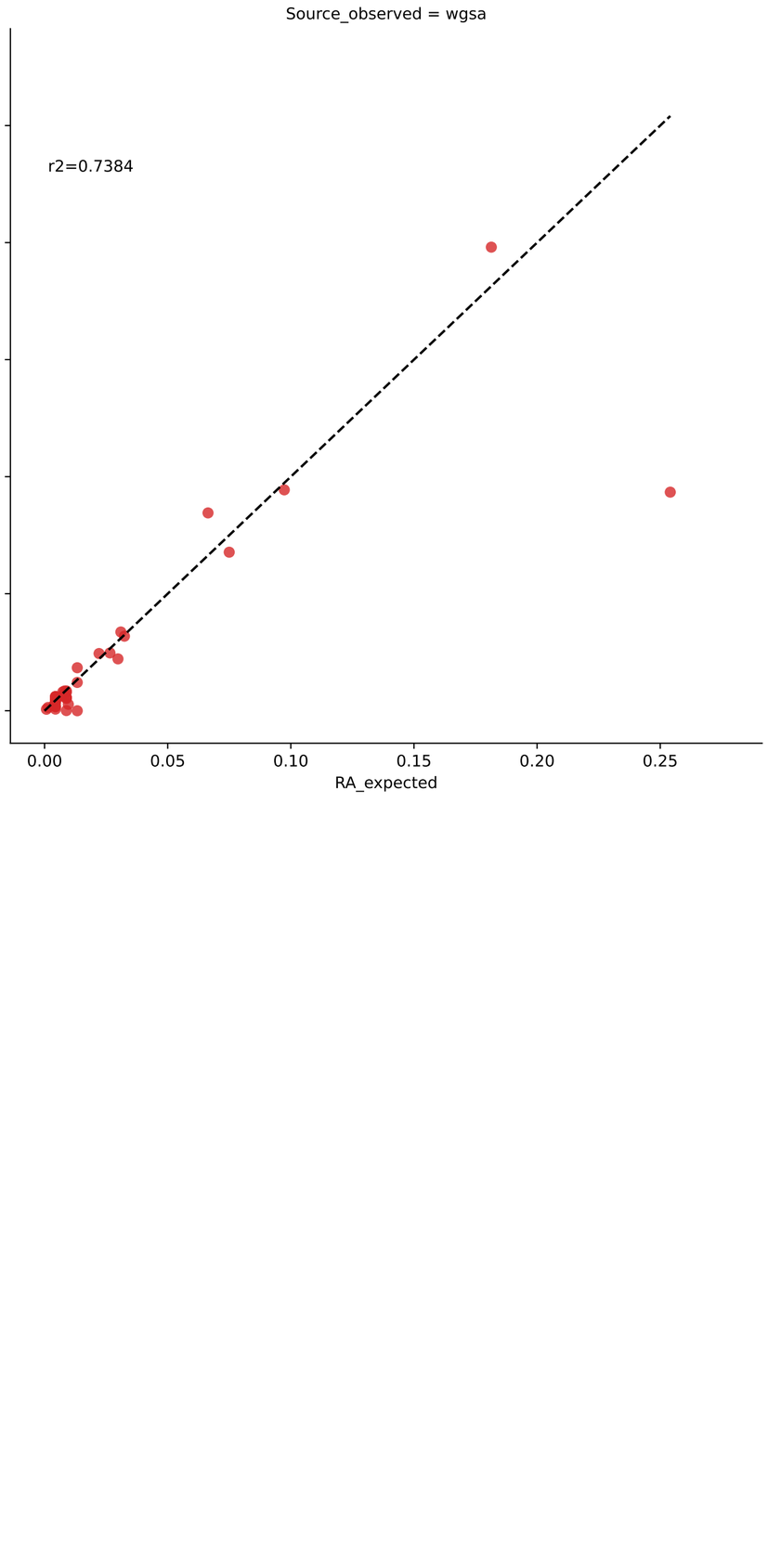


	R^2	MAE	AD	1-BC	RMSE
bio4	0.9718	0.0010	3.3618	0.9238	0.0070
jams	0.9680	0.0013	14.4887	0.9065	0.0075
wgsa	0.9768	0.0011	42.2811	0.9171	0.0064
woltka	0.7930	0.0035	3.8334	0.7408	0.0224

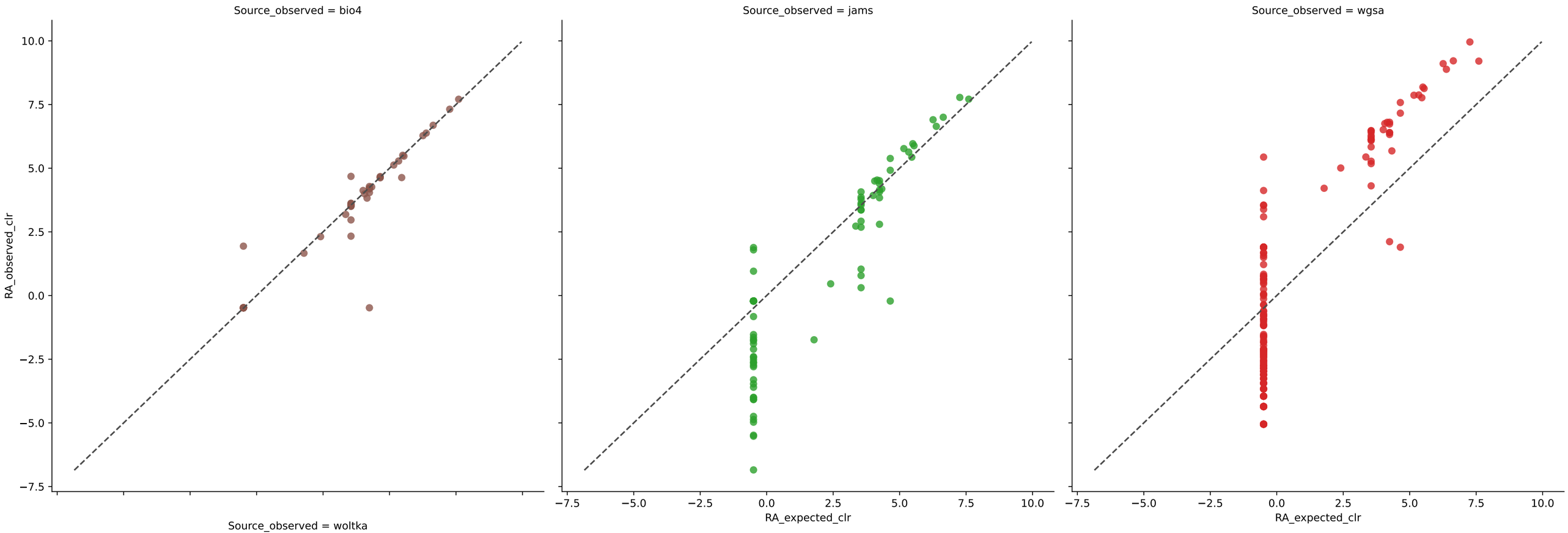
Bivariate Linear Regression for Sample S1 in Experiment camisimGI (Species)

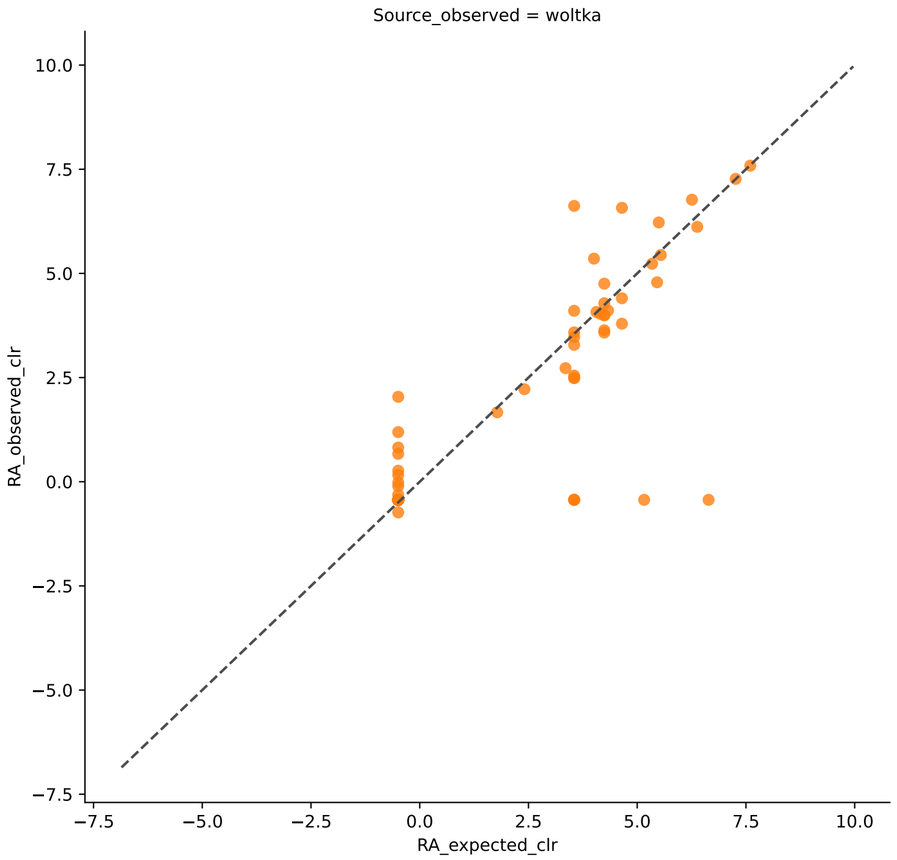






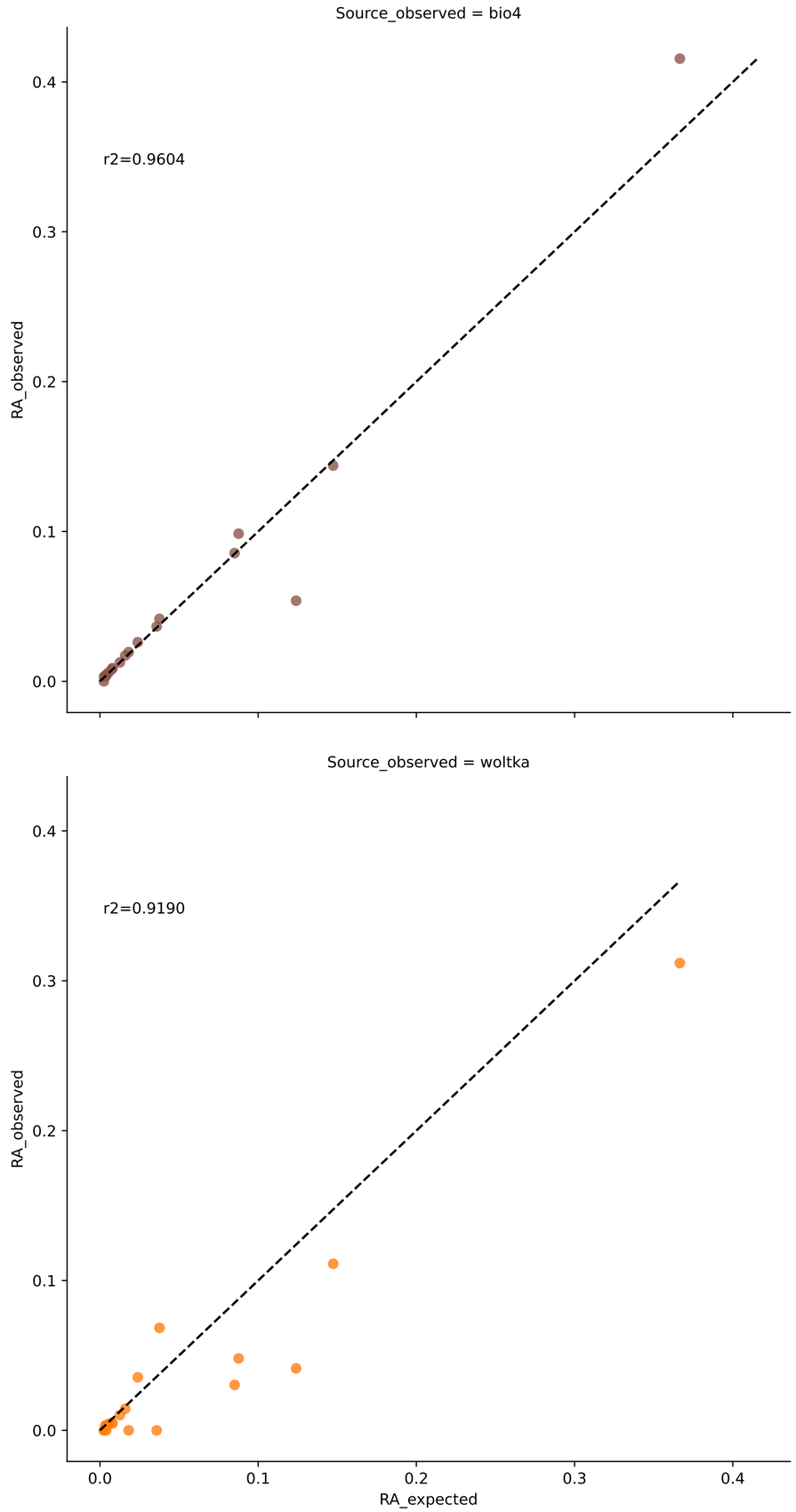
Bivariate Linear Regression for Sample S1 in Experiment camisimGI (Species)

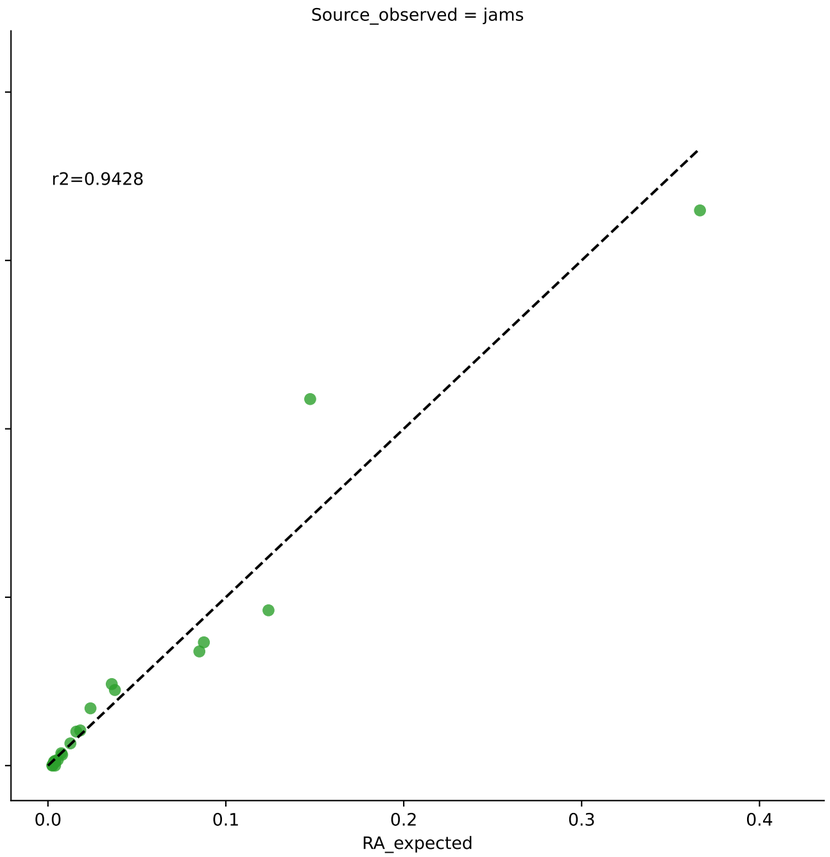


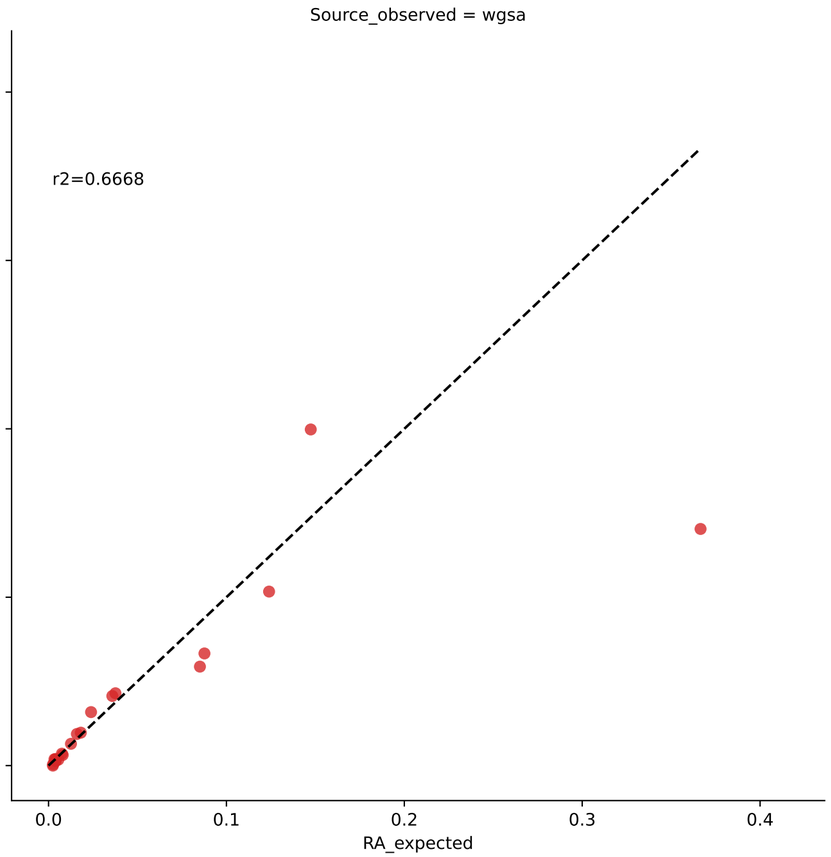


	R^2	MAE	AD	1-BC	RMSE
bio4	0.9945	0.0002	5.6885	0.9539	0.0017
jams	0.9575	0.0006	19.3401	0.8863	0.0037
wgsa	0.7889	0.0008	53.7532	0.8399	0.0085
woltka	0.7895	0.0014	13.5012	0.7257	0.0082

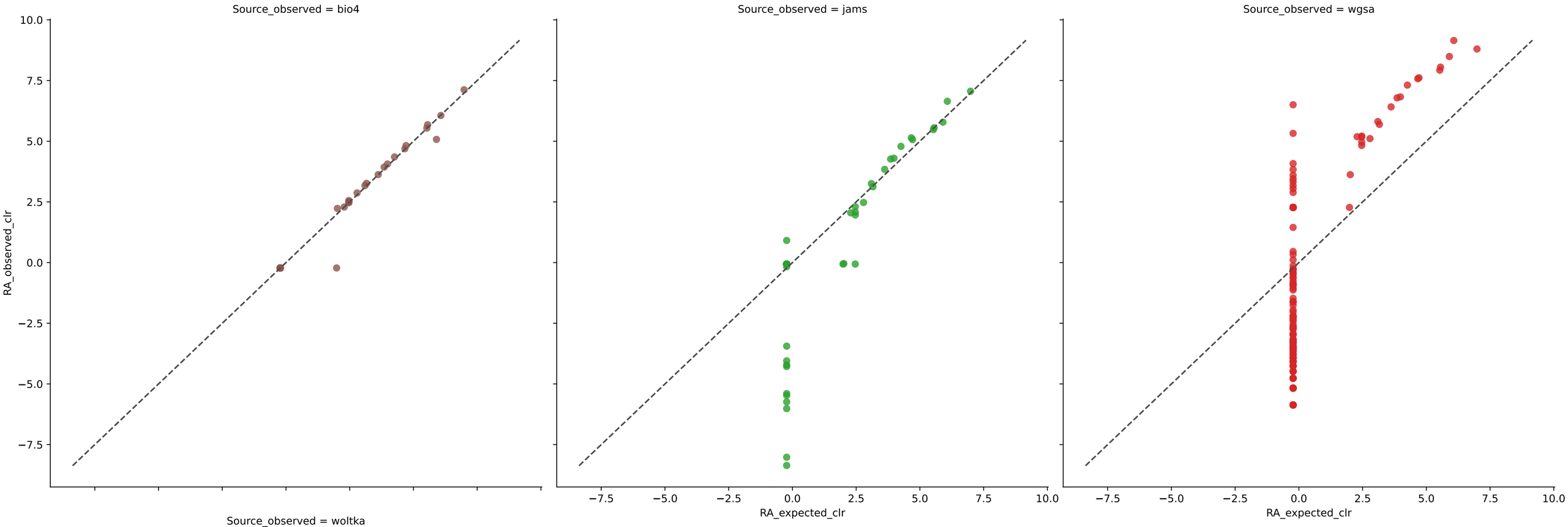
Bivariate Linear Regression for Sample S2 in Experiment camisimGI (Species)

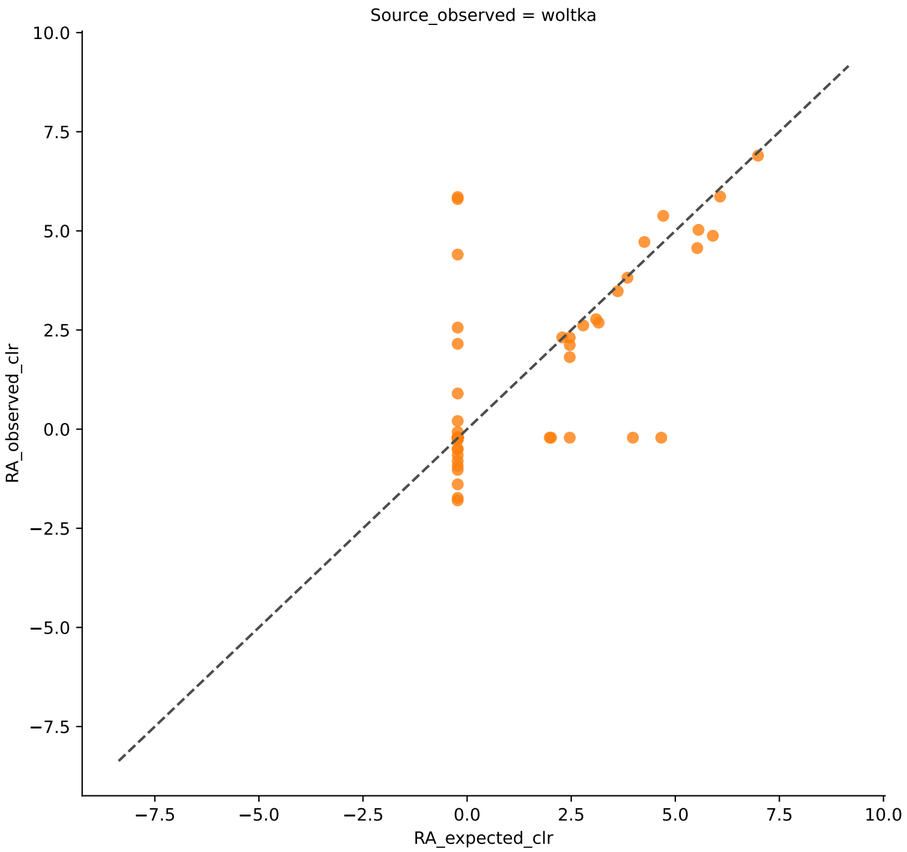






Bivariate Linear Regression for Sample S2 in Experiment camisimGI (Species)





	R^2	MAE	AD	1-BC	RMSE
bio4	0.9677	0.0004	2.3895	0.9254	0.0045
jams	0.9564	0.0006	18.1605	0.8856	0.0047
wgsa	0.7444	0.0011	64.1185	0.7742	0.0122
woltka	0.7760	0.0017	13.4128	0.6720	0.0106

Expected vs. Observed Relative Abundance for genus using bio4 in Experiment tourlousse

SampleID
expected
SRR17380244
SRR17380241
SRR17380242
SRR17380243
SRR17380246
SRR17380245

Relative Abundance

0.1
0.01
0.001

PSEUDOMONAS
ESCHERICHIA
BACTEROIDES
MEGASPHAERA
RUMINOCOCCUS
STAPHYLOCOCCUS
STREPTOCOCCUS
BACILLUS
LACTOBACILLUS
BIFIDOBACTERIUM
COLLINSELLA
MEGAMONAS
ANAEROSTIPES
AKKERMANSIA
PARABACTEROIDES
BLAUTIA
FLAVONIFRACTOR
LACHNOCLOSTRIDIUM
CUTIBACTERIUM
ENTEROCLOSTER

genus

Expected vs. Observed Relative Abundance for genus using jams in Experiment tourlousse

SampleID
expected
SRR17380244
SRR17380241
SRR17380242
SRR17380243
SRR17380246
SRR17380245

0.1
0.01
0.001
ive Abundance

PSEUDOMONAS
ESCHERICHIA
BACTEROIDES
MEGASPHAERA
RUMINOCOCCUS
STAPHYLOCOCCUS
STREPTOCOCCUS
BACILLUS
LACTOBACILLUS
BIFIDOBACTERIUM
COLLINSELLA
MEGAMONAS
ANAEROSTIPES
AKKERMANSIA
PARABACTEROIDES
BLAUTIA
FLAVONIFRACTOR
CUTIBACTERIUM
ENTEROCLOSTER

genus

Expected vs. Observed Relative Abundance for genus using wgsa in Experiment tourlousse

SampleID
expected
SRR17380244
SRR17380241
SRR17380242
SRR17380243
SRR17380246
SRR17380245

Relative Abundance
0.1
0.01
0.001

PSEUDOMONAS
ESCHERICHIA
BACTEROIDES
MEGASPHAERA
RUMINOCOCCUS
STAPHYLOCOCCUS
STREPTOCOCCUS
BACILLUS
LACTOBACILLUS
BIFIDOBACTERIUM
COLLINSELLA
MEGAMONAS
ANAEROSTIPES
AKKERMANSIA
PARABACTEROIDES
BLAUTIA
FLAVONIFRACTOR
Lachnoclostridium
Clostridioides
CUTIBACTERIUM
Mediterraneibacter
ENTEROCLOSTER

genus

Expected vs. Observed Relative Abundance for genus using woltka in Experiment tourlousse

SampleID
expected
SRR17380244
SRR17380241
SRR17380242
SRR17380243
SRR17380246
SRR17380245

Relative Abundance

0.1
0.01
0.001

PSEUDOMONAS
ESCHERICHIA
Shigella
BACTEROIDES
Prevotella
Roseburia
MEGASPHAERA
RUMINOCOCCUS
STAPHYLOCOCCUS
STREPTOCOCCUS
BACILLUS
Clostridium
LACTOBACILLUS
BIFIDOBACTERIUM
Eubacterium
Coprococcus
COLLINSELLA
MEGAMONAS
ANAEROSTIPES
AKKERMANSIA
PARABACTEROIDES
BLAUTIA
FLAVONIFRACTOR
Lachnoclostridium
Tyzzerella
CUTIBACTERIUM
ENTEROCLOSTER

genus

Expected vs. Observed Relative Abundance for species using bio4 in Experiment tourlousse

SampleID
expected
SRR17380246
SRR17380241
SRR17380244
SRR17380242
SRR17380243
SRR17380245

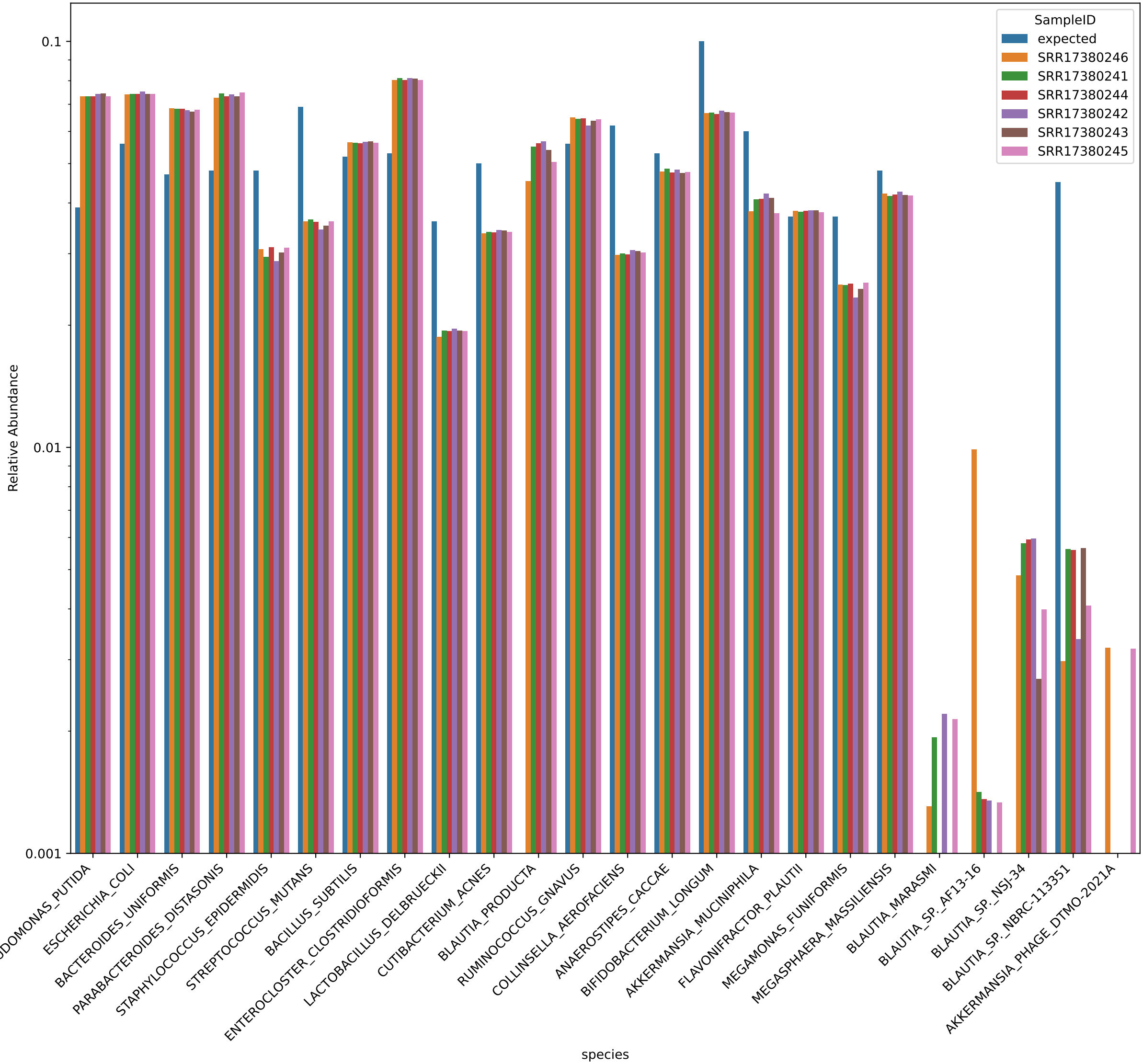
Relative Abundance

0.1
0.01
0.001

PSEUDOMONAS_PUTIDA
ESCHERICHIA_COLI
BACTEROIDES_UNIFORMIS
PARABACTEROIDES_DISTASONIS
STAPHYLOCOCCUS_EPIDERMIDIS
STREPTOCOCCUS_MUTANS
BACILLUS_SUBTILIS
ENTEROCLOSTER_CLOSTRIDIOFORMIS
LACTOBACILLUS_DELBRUECKII
CUTIBACTERIUM_ACNES
BLAUTIA_PRODUCTA
RUMINOCOCCUS_GNAVUS
COLLINSELLA_AEROFACIENS
ANAEROSTIPES_CACCAE
PSEUDOMONAS_PUTIDA_GROUP
MEGAMONAS_HYPERMEGALE
BACILLUS_MURIMARTINI
BIFIDOBACTERIUM_LONGUM
AKKERMANSIA_MUCINIPHILA
FLAVONIFRACTOR_PLAUTII
MEGAMONAS_FUNIFORMIS
MEGASPHAERA_MASSILIENSIS
MEGASPHAERA_SP._DISK-18
BACILLUS_INTESTINALIS
BLAUTIA_SP._NBRC-113351

species

Expected vs. Observed Relative Abundance for species using jams in Experiment tourlousse



Expected vs. Observed Relative Abundance for species using wgsa in Experiment tourlousse

SampleID
expected
SRR17380246
SRR17380241
SRR17380244
SRR17380242
SRR17380243
SRR17380245

Relative Abundance

0.1
0.01
0.001

PSEUDOMONAS_PUTIDA
ESCHERICHIA_COLI
BACTEROIDES_UNIFORMIS
PARABACTEROIDES_DISTASONIS
Megasphaera elsdenii
STAPHYLOCOCCUS_EPIDERMIDIS
STREPTOCOCCUS_MUTANS
BACILLUS_SUBTILIS
Clostridioides difficile
ENTEROCLOSTER_CLOSTRIDIOFORMIS
LACTOBACILLUS_DELBRUECKII
CUTIBACTERIUM_ACNES
Blautia producta
RUMINOCOCCUS_GNAVUS
COLLINSELLA_AEROFACIENS
ANAEROSTIPES_CACCAE
Enterocloster bolteae
BIFIDOBACTERIUM_LONGUM
AKKERMANSIA_MUCINIPHILA
FLAVONIFRACTOR_PLAUTII
MEGAMONAS_FUNIFORMIS
MEGASPHAERA_MASSILIENSIS
Blautia sp. YL58
Lachnoclostridium sp. YL32
Blautia argi
Megasphaera stantonii
BLAUTIA_SP._NBRC-113351

species

Expected vs. Observed Relative Abundance for species using woltka in Experiment tourlousse

SampleID
expected
SRR17380246
SRR17380241
SRR17380244
SRR17380242
SRR17380243
SRR17380245

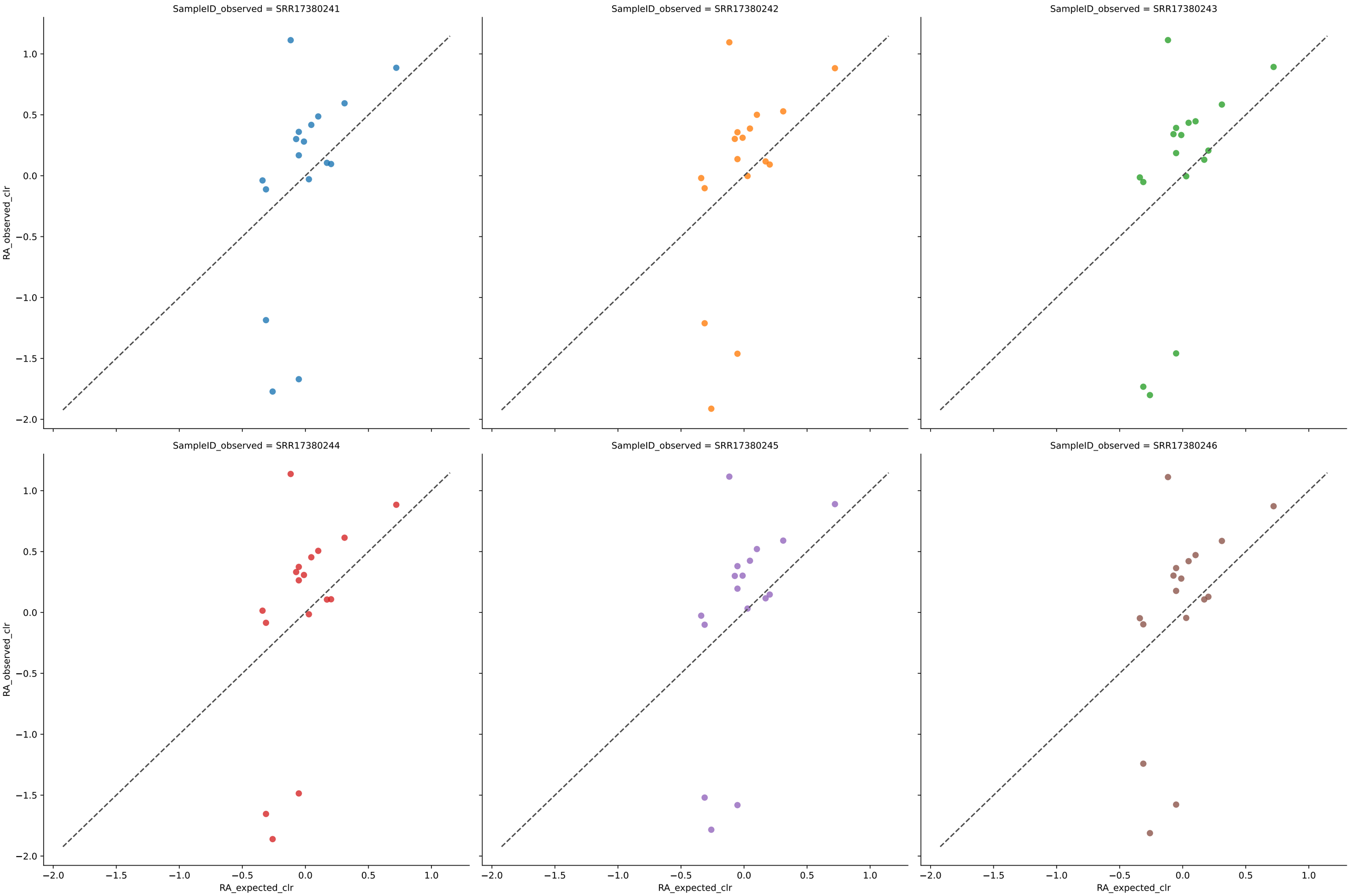
Relative Abundance

0.1
0.01
0.001

PSEUDOMONAS_PUTIDA
ESCHERICHIA_COLI
Shigella dysenteriae
Shigella flexneri
Bacteroides fragilis
Bacteroides thetaiotaomicron
BACTEROIDES_UNIFORMIS
PARABACTEROIDES_DISTASONIS
STAPHYLOCOCCUS_EPIDERMIDIS
STREPTOCOCCUS_MUTANS
Bacillus amyloliquefaciens
BACILLUS_SUBTILIS
ENTEROCLOSTER_CLOSTRIDIOFORMIS
LACTOBACILLUS_DELBRUECKII
Bifidobacterium breve
CUTIBACTERIUM_ACNES
Tyzzerella nexilis
Blautia producta
RUMINOCOCCUS_GNAVUS
Eubacterium ramulus
Bacteroides stercoris
COLLINSELLA_AEROFACIENS
ANAEROSTIPES_CACCAE
Clostridium bolteae
BIFIDOBACTERIUM_LONGUM
AKKERMANSIA_MUCINIPHILA
FLAVONIFRACTOR_PLAUTII
Bacteroides plebeius
Bacteroides coprocola
Bacteroides coprophilus
Prevotella stercorea
Parabacteroides johnsonii
MEGAMONAS_FUNIFORMIS
Bacillus velezensis
Parabacteroides gordonii
MEGASPHAERA_MASSILIENSIS
Anaerostipes sp. CAG:276
Collinsella sp. CAG:166
Akkermansia muciniphila CAG:154
Clostridium bolteae CAG:59
Clostridium clostridioforme CAG:132
Clostridium clostridioforme CAG:511
Staphylococcus sp. DORA_6_22
Bacillus sp. BSC154
Akkermansia sp. UNK.MGS-1
Staphylococcus sp. HMSC062B11
Akkermansia sp. 54_46
Akkermansia sp. Phil8
BLAUTIA_SP._NBRC-113351

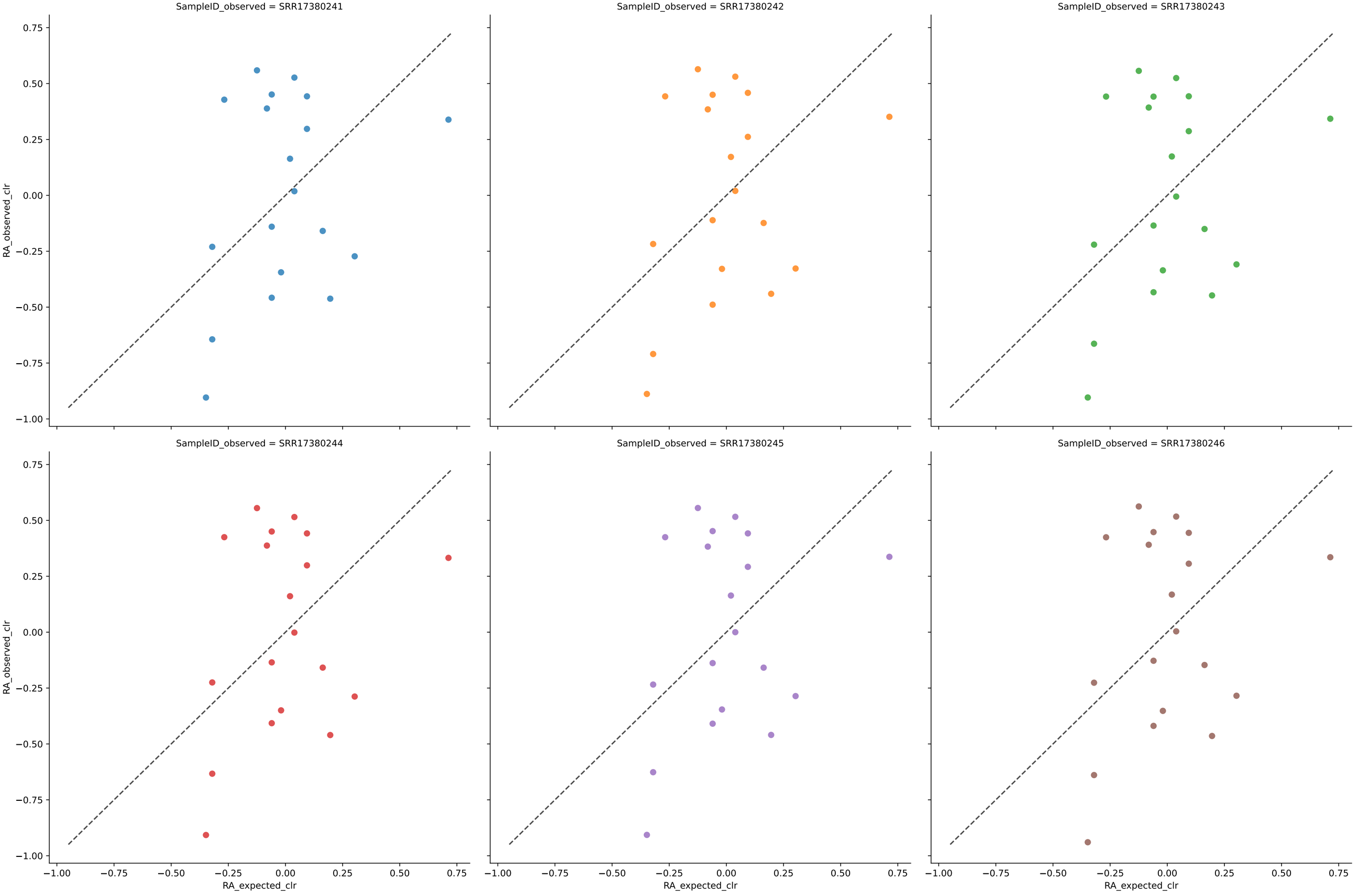
species

Expected vs. Observed Relative Abundance for genus using bio4 in Experiment tourlousse



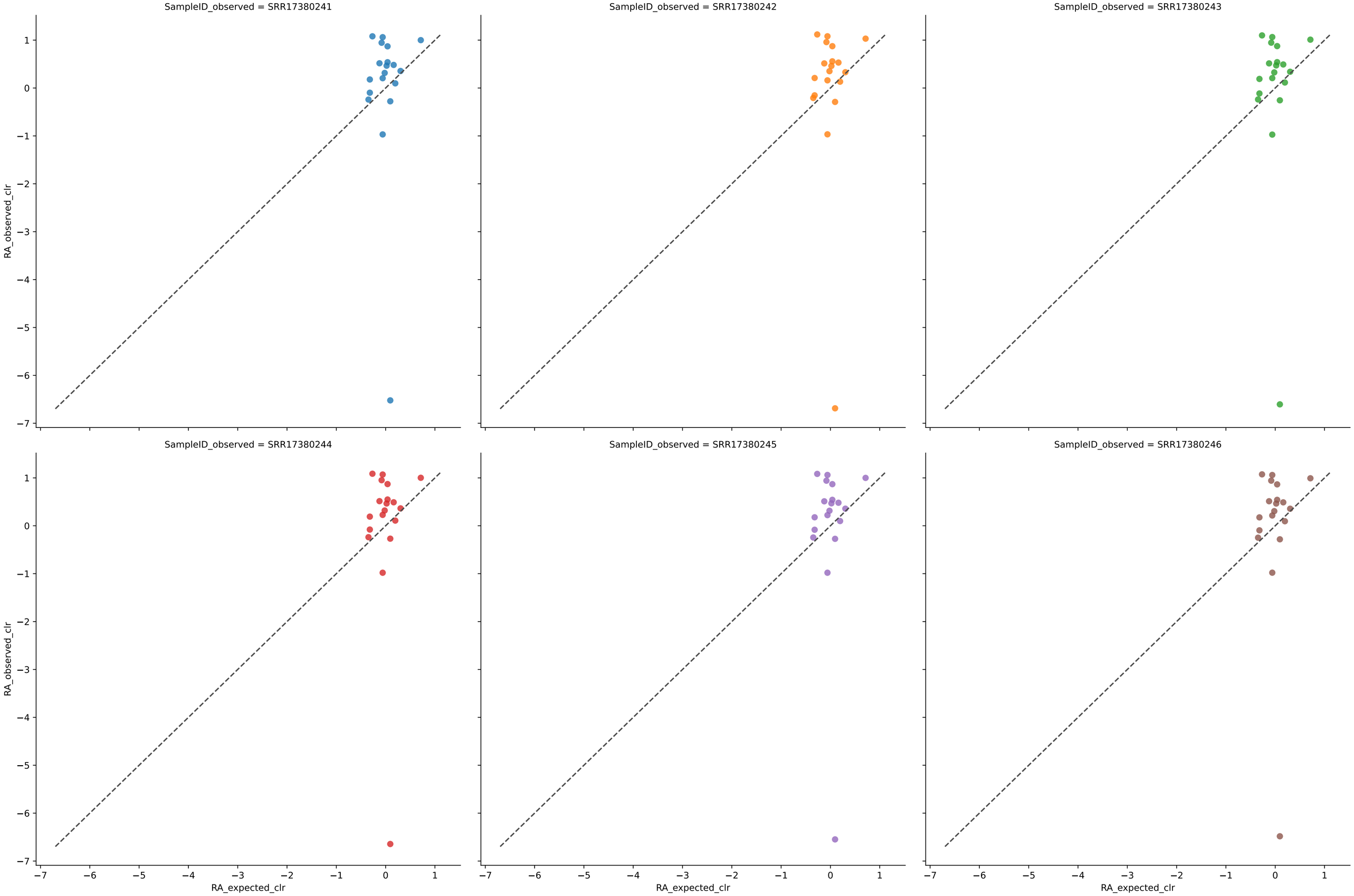
	R^2	MAE	AD	1-BC	RMSE
SRR17380241	0.2677	0.0179	2.8577	0.8333	0.0269
SRR17380242	0.2685	0.0175	2.8205	0.8367	0.0264
SRR17380243	0.2726	0.0175	2.9966	0.8362	0.0264
SRR17380244	0.2517	0.0187	3.0294	0.8264	0.0274
SRR17380245	0.2714	0.0179	2.9490	0.8333	0.0268
SRR17380246	0.2631	0.0178	2.8426	0.8342	0.0268
Average	0.2658	0.0179	2.9160	0.8333	0.0268

Expected vs. Observed Relative Abundance for genus using jams in Experiment tourlousse



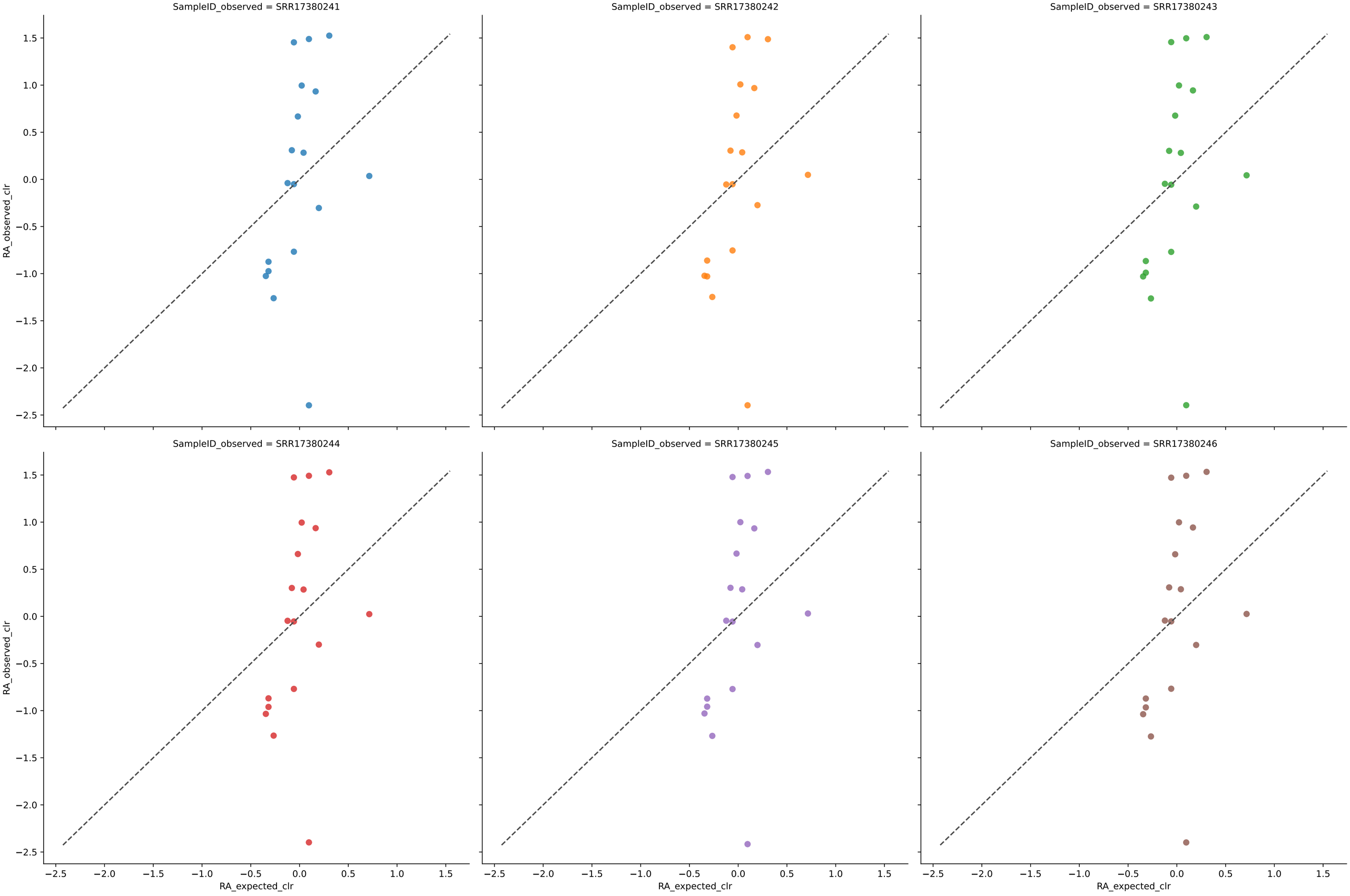
	R^2	MAE	AD	1-BC	RMSE
SRR17380241	0.0300	0.0199	1.8858	0.8103	0.0230
SRR17380242	0.0305	0.0199	1.9062	0.8103	0.0231
SRR17380243	0.0290	0.0199	1.8896	0.8097	0.0230
SRR17380244	0.0283	0.0198	1.8749	0.8109	0.0229
SRR17380245	0.0295	0.0197	1.8705	0.8115	0.0229
SRR17380246	0.0294	0.0199	1.8908	0.8102	0.0230
Average	0.0295	0.0199	1.8863	0.8105	0.0230

Expected vs. Observed Relative Abundance for genus using wgsa in Experiment tourlousse



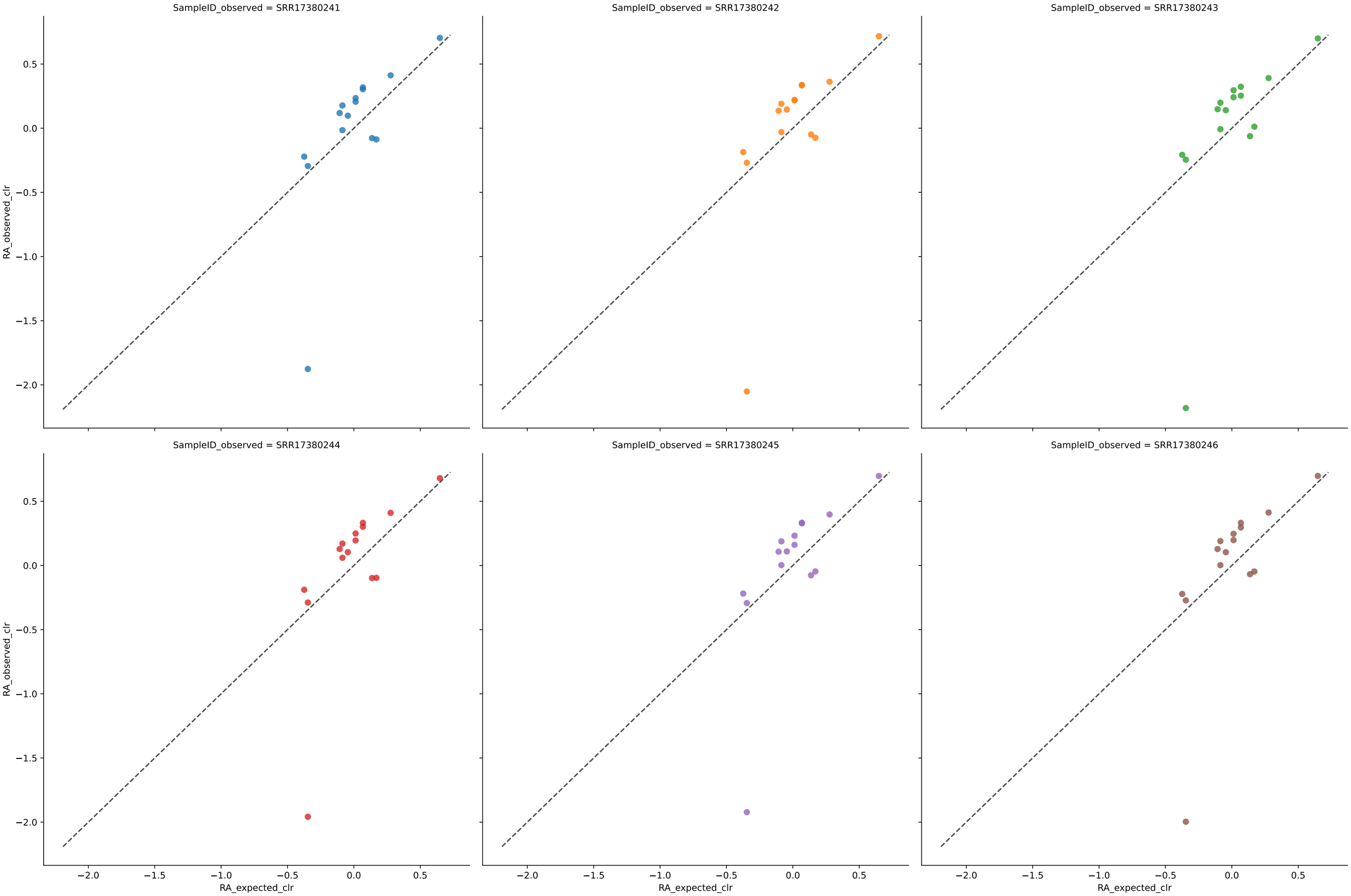
	R^2	MAE	AD	1-BC	RMSE
SRR17380241	0.0477	0.0229	7.1483	0.7491	0.0266
SRR17380242	0.0496	0.0231	7.3201	0.7457	0.0268
SRR17380243	0.0478	0.0229	7.2312	0.7489	0.0266
SRR17380244	0.0465	0.0229	7.2700	0.7490	0.0266
SRR17380245	0.0474	0.0228	7.1746	0.7497	0.0266
SRR17380246	0.0471	0.0228	7.1109	0.7495	0.0266
Average	0.0477	0.0229	7.2092	0.7486	0.0266

Expected vs. Observed Relative Abundance for genus using woltka in Experiment tourlousse



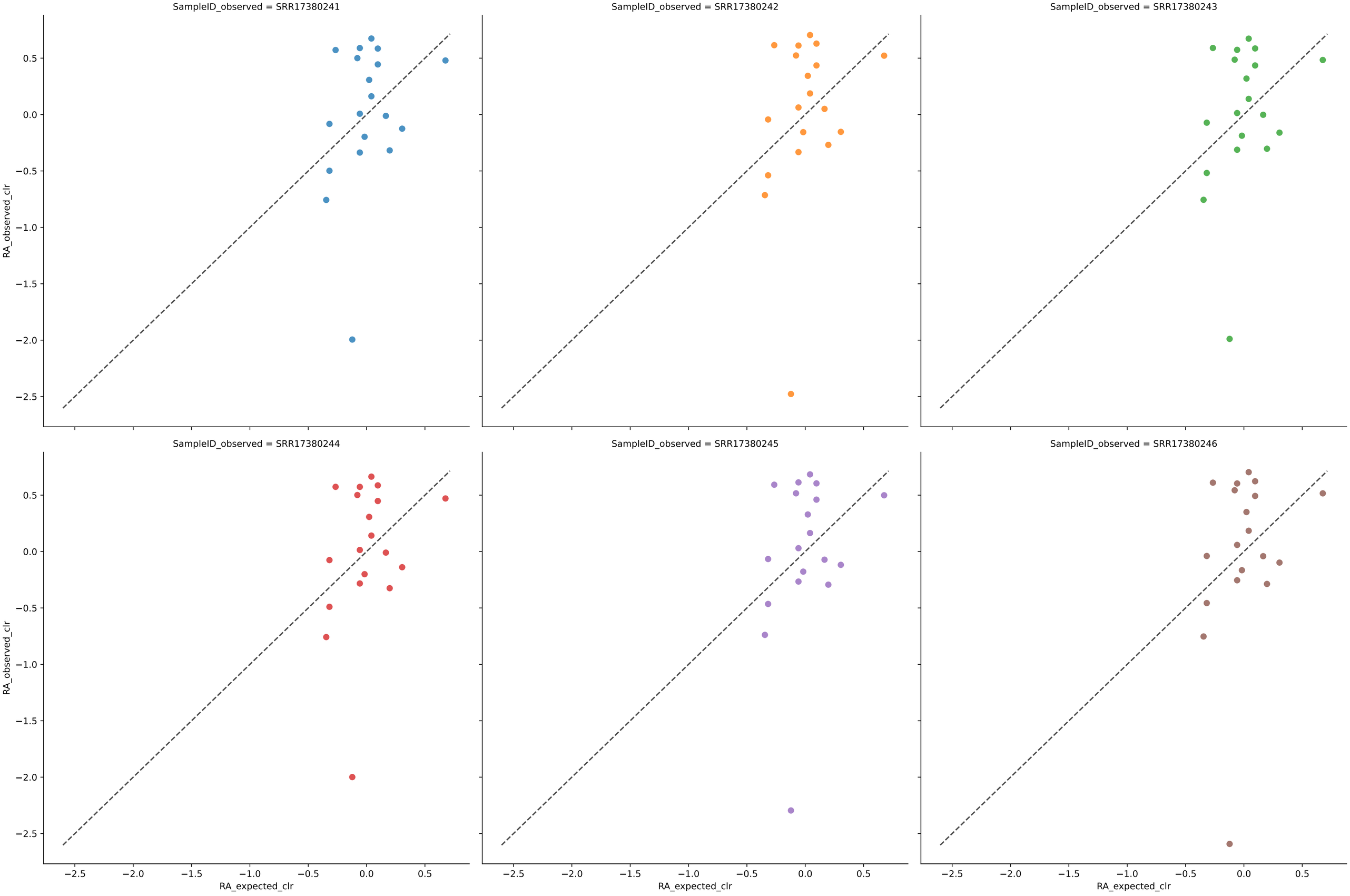
	R^2	MAE	AD	1-BC	RMSE
SRR17380241	0.0625	0.0338	4.1904	0.6493	0.0399
SRR17380242	0.0652	0.0336	4.1746	0.6512	0.0393
SRR17380243	0.0624	0.0339	4.1920	0.6489	0.0399
SRR17380244	0.0608	0.0340	4.2008	0.6477	0.0402
SRR17380245	0.0610	0.0341	4.2151	0.6474	0.0402
SRR17380246	0.0614	0.0340	4.2073	0.6476	0.0402
Average	0.0622	0.0339	4.1967	0.6487	0.0399

Expected vs. Observed Relative Abundance for species using bio4 in Experiment tourlousse



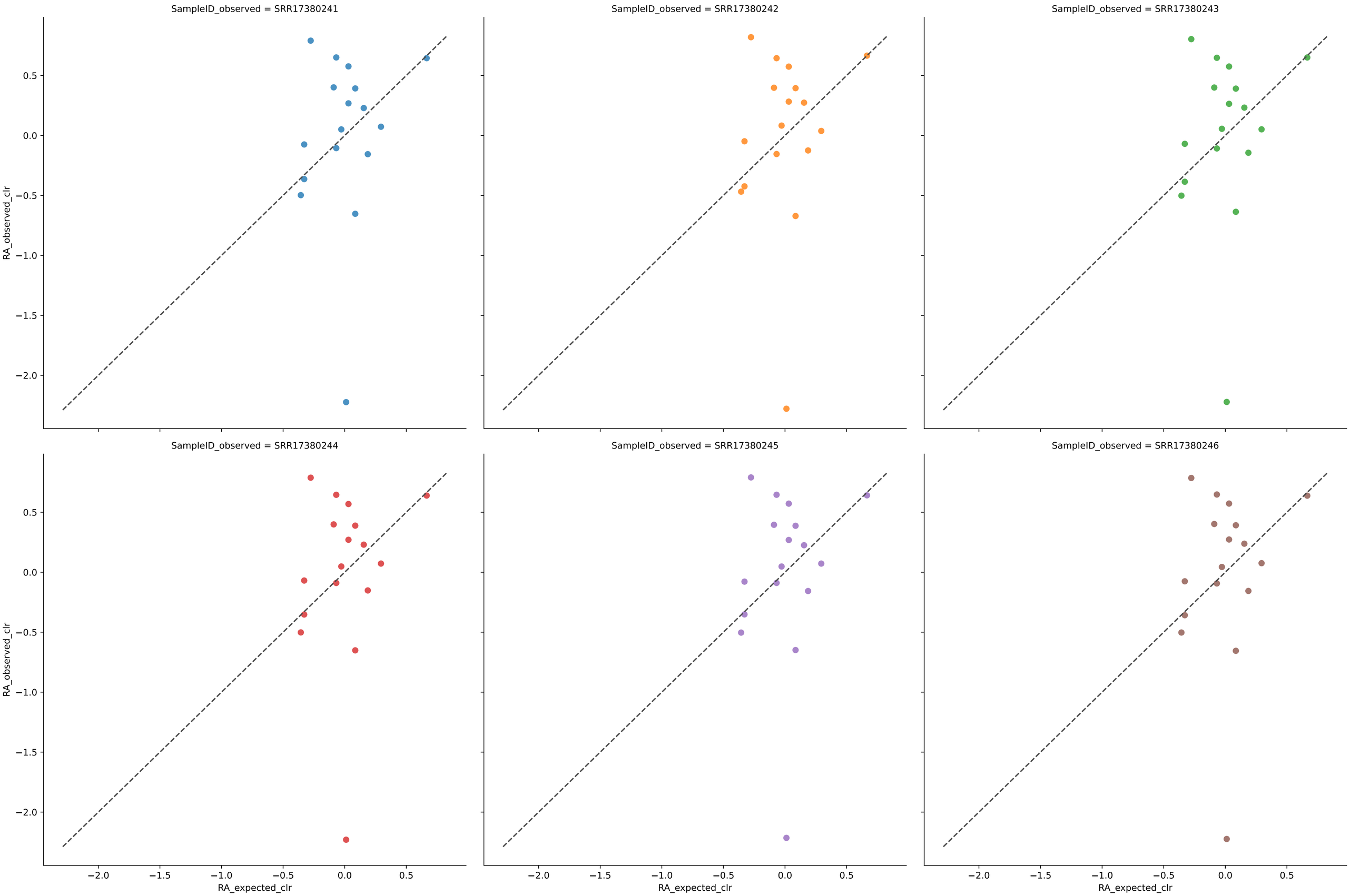
	R^2	MAE	AD	1-BC	RMSE
SRR17380241	0.6580	0.0115	1.6881	0.8978	0.0131
SRR17380242	0.6413	0.0115	1.8598	0.8980	0.0133
SRR17380243	0.6410	0.0115	1.9753	0.8984	0.0133
SRR17380244	0.6213	0.0120	1.7771	0.8932	0.0136
SRR17380245	0.6560	0.0114	1.7266	0.8985	0.0131
SRR17380246	0.6525	0.0114	1.7985	0.8988	0.0131
Average	0.6450	0.0115	1.8042	0.8975	0.0132

Expected vs. Observed Relative Abundance for species using jams in Experiment tourlousse



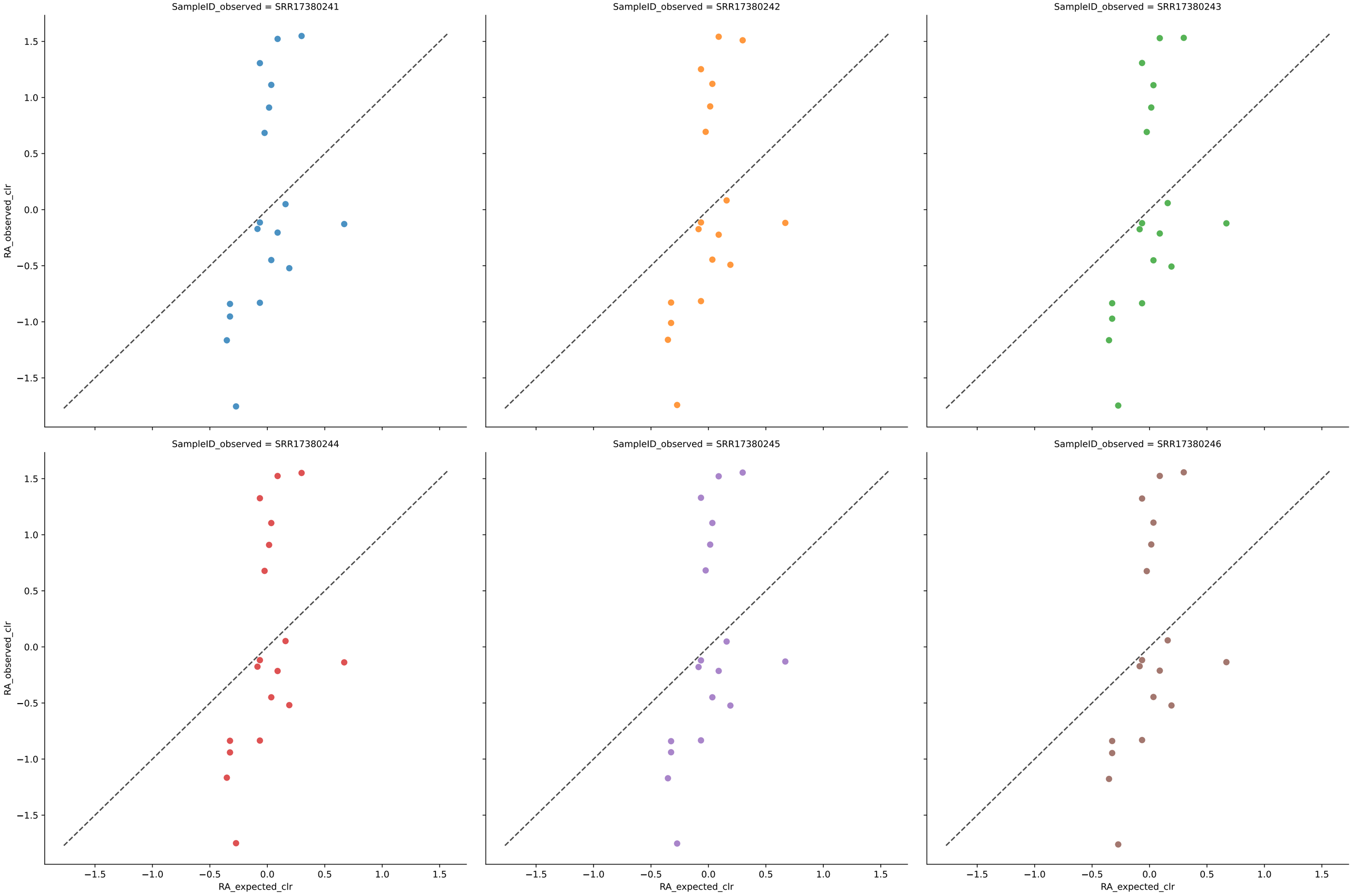
	R^2	MAE	AD	1-BC	RMSE
SRR17380241	0.0708	0.0196	2.5904	0.8046	0.0226
SRR17380242	0.0721	0.0197	2.9884	0.8033	0.0229
SRR17380243	0.0698	0.0196	2.5858	0.8045	0.0226
SRR17380244	0.0677	0.0195	2.5877	0.8050	0.0225
SRR17380245	0.0672	0.0197	2.8284	0.8026	0.0228
SRR17380246	0.0686	0.0198	3.0816	0.8014	0.0229
Average	0.0694	0.0196	2.7771	0.8036	0.0227

Expected vs. Observed Relative Abundance for species using wgsa in Experiment tourlousse



	R^2	MAE	AD	1-BC	RMSE
SRR17380241	0.0590	0.0211	2.8548	0.7685	0.0251
SRR17380242	0.0604	0.0212	2.9179	0.7665	0.0254
SRR17380243	0.0587	0.0211	2.8541	0.7685	0.0251
SRR17380244	0.0580	0.0210	2.8556	0.7692	0.0251
SRR17380245	0.0584	0.0210	2.8434	0.7693	0.0251
SRR17380246	0.0586	0.0210	2.8533	0.7691	0.0251
Average	0.0588	0.0211	2.8632	0.7685	0.0252

Expected vs. Observed Relative Abundance for species using woltka in Experiment tourlousse



	R^2	MAE	AD	1-BC	RMSE
SRR17380241	0.0578	0.0355	3.6808	0.6215	0.0395
SRR17380242	0.0587	0.0351	3.6547	0.6244	0.0390
SRR17380243	0.0573	0.0354	3.6761	0.6219	0.0394
SRR17380244	0.0566	0.0355	3.6851	0.6208	0.0396
SRR17380245	0.0569	0.0356	3.6902	0.6203	0.0396
SRR17380246	0.0572	0.0355	3.6944	0.6207	0.0396
Average	0.0574	0.0354	3.6802	0.6216	0.0394

Expected vs. Observed Relative Abundance for genus using bio4 in Experiment hilo

SampleID
expected
SRR11487931
SRR11487932
SRR11487934
SRR11487935
SRR11487933

Relative Abundance

0.1
0.01
0.001

ESCHERICHIA
BACTEROIDES
PREVOTELLA
ROSEBURIA
RUMINOCOCCUS
CLOSTRIDIUM
LACTOBACILLUS
BIFIDOBACTERIUM
EUBACTERIUM
COLLINSELLA
ANAEROSTIPES
FAECALIBACTERIUM
ALISTIPES
AKKERMANSIA
PARABACTEROIDES
BLAUTIA

genus

Expected vs. Observed Relative Abundance for genus using jams in Experiment hilo

SampleID
expected
SRR11487931
SRR11487932
SRR11487934
SRR11487935
SRR11487933

Relative Abundance

0.1
0.01
0.001

ESCHERICHIA
BACTEROIDES
PREVOTELLA
ROSEBURIA
RUMINOCOCCUS
CLOSTRIDIUM
LACTOBACILLUS
BIFIDOBACTERIUM
EUBACTERIUM
COLLINSELLA
ANAEROSTIPES
FAECALIBACTERIUM
ALISTIPES
AKKERMANSIA
PARABACTEROIDES
BLAUTIA
ANAEROBUTYRICUM

genus

Expected vs. Observed Relative Abundance for genus using wgsa in Experiment hilo

SampleID
expected
SRR11487931
SRR11487932
SRR11487934
SRR11487935
SRR11487933

Relative Abundance

0.1
0.01
0.001

Citrobacter
Enterobacter
ESCHERICHIA
Klebsiella
BACTEROIDES
PREVOTELLA
ROSEBURIA
RUMINOCOCCUS
Enterococcus
CLOSTRIDIUM
LACTOBACILLUS
BIFIDOBACTERIUM
EUBACTERIUM
COLLINSELLA
ANAEROSTIPES
FAECALIBACTERIUM
ALISTIPES
AKKERMANSIA
PARABACTEROIDES
BLAUTIA
Anaerobutyricum

genus

Expected vs. Observed Relative Abundance for genus using wol in Experiment hilo

SampleID
expected
SRR11487931
SRR11487932
SRR11487934
SRR11487935
SRR11487933

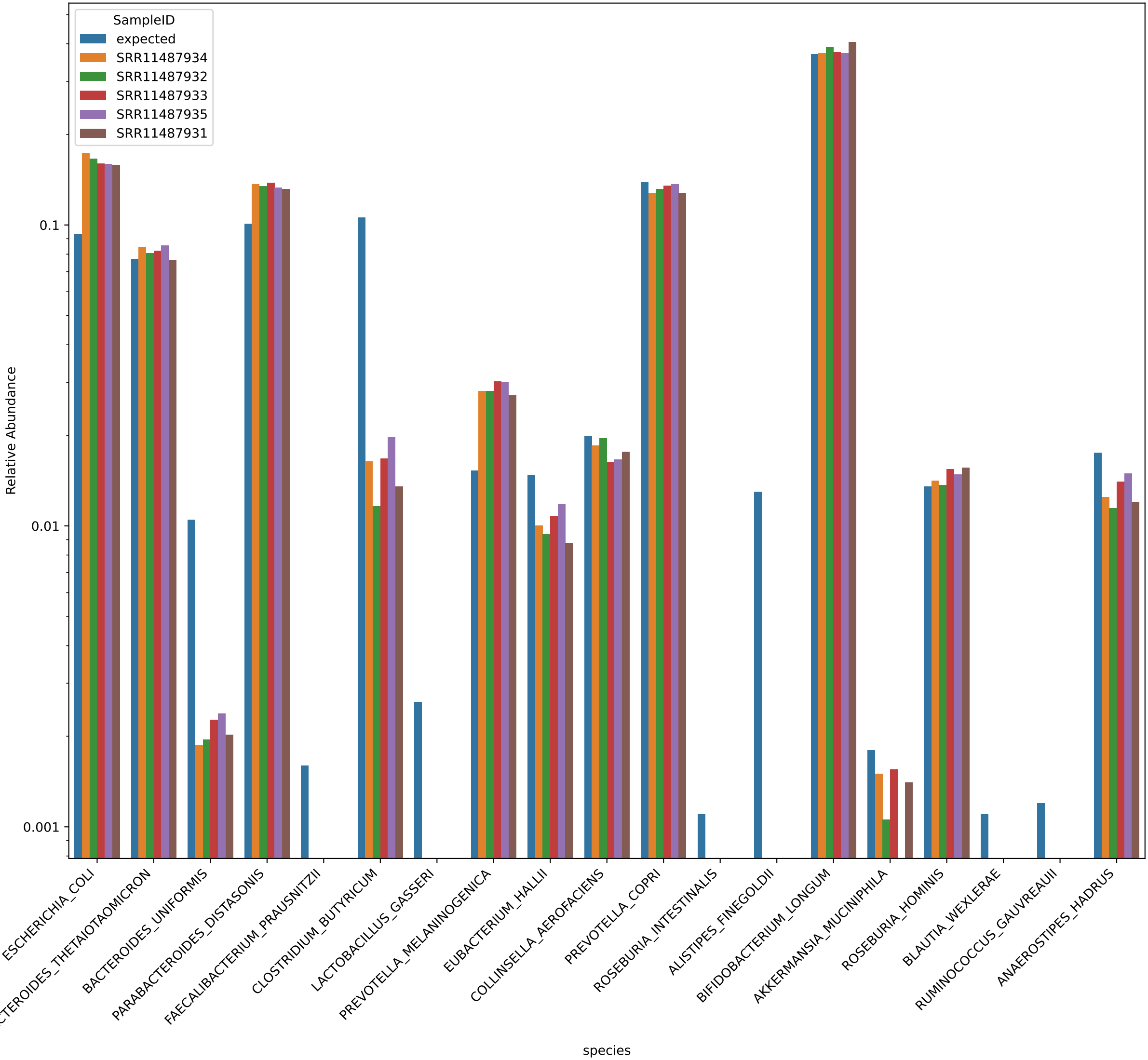
Relative Abundance

0.1
0.01
0.001

Citrobacter
ESCHERICHIA
Klebsiella
Kluyvera
Shigella
BACTEROIDES
PREVOTELLA
ROSEBURIA
RUMINOCOCCUS
CLOSTRIDIUM
LACTOBACILLUS
BIFIDOBACTERIUM
EUBACTERIUM
Obesumbacterium
COLLINSELLA
ANAEROSTIPES
FAECALIBACTERIUM
ALISTIPES
AKKERMANSIA
PARABACTEROIDES
BLAUTIA

genus

Expected vs. Observed Relative Abundance for species using bio4 in Experiment hilo



Expected vs. Observed Relative Abundance for species using jams in Experiment hilo

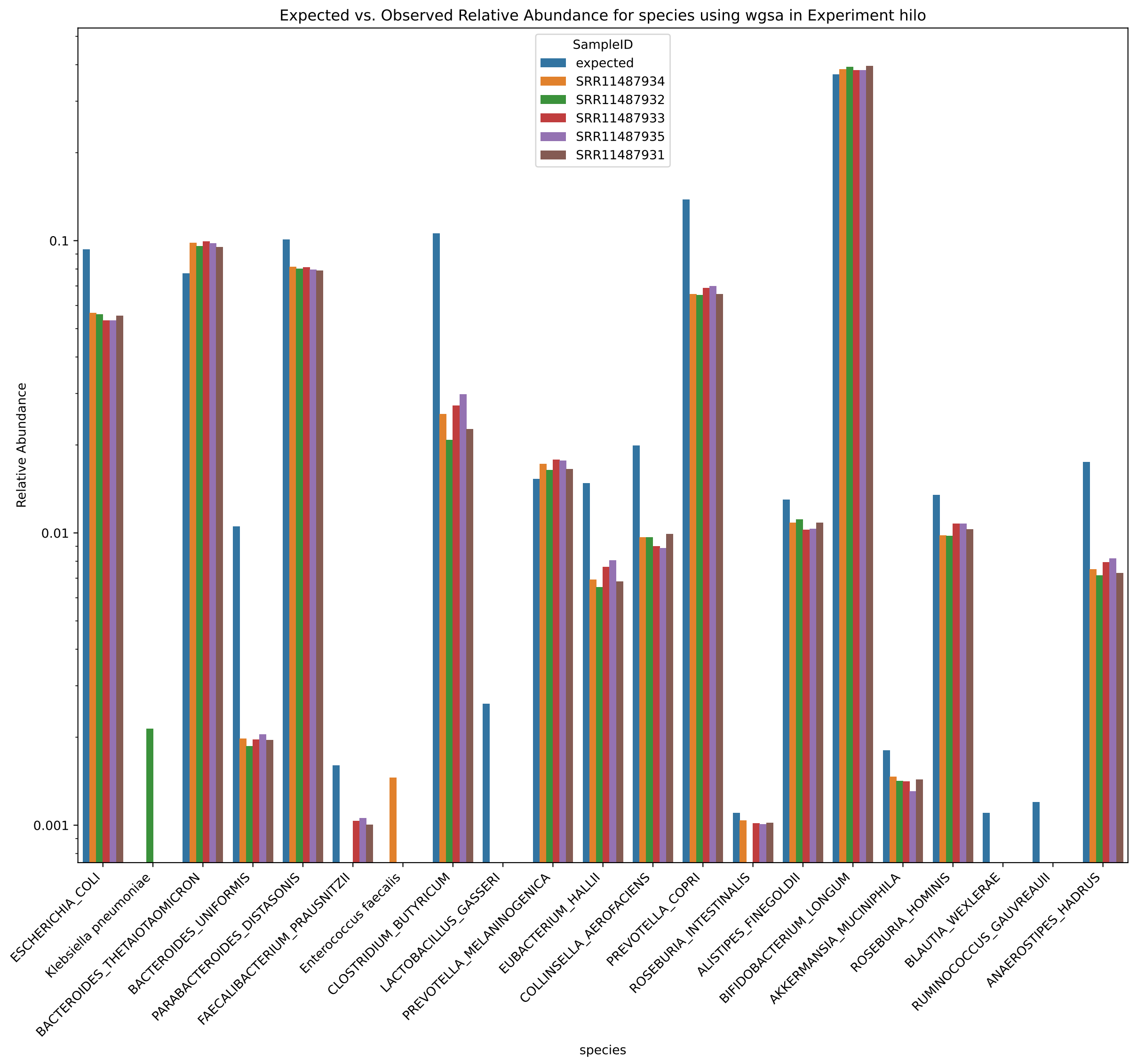
SampleID
expected
SRR11487934
SRR11487932
SRR11487933
SRR11487935
SRR11487931

Relative Abundance
0.1
0.01
0.001

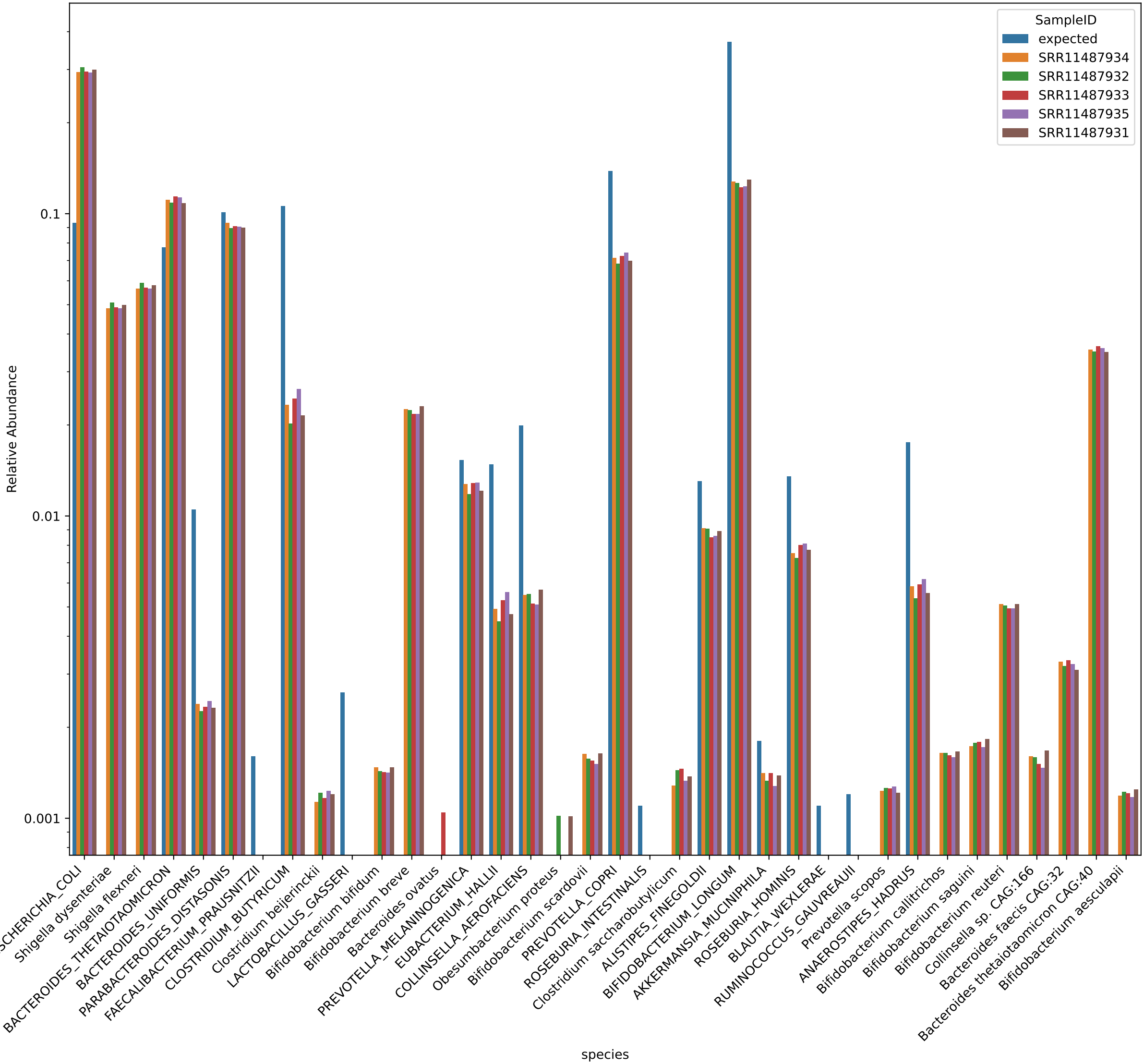
ESCHERICHIA_COLI
BACTEROIDES_THETAIOTAOMICRON
BACTEROIDES_UNIFORMIS
PARABACTEROIDES_DISTASONIS
FAECALIBACTERIUM_PRAUSNITZII
CLOSTRIDIUM_BUTYRICUM
LACTOBACILLUS_GASSERI
PREVOTELLA_MELANINOGENICA
EUBACTERIUM_HALLII
COLLINSELLA_AEROFACIENS
PREVOTELLA_COPRI
ROSEBURIA_INTESTINALIS
ALISTIPES_FINEGOLDII
BIFIDOBACTERIUM_LONGUM
AKKERMANSIA_MUCINIPHILA
ROSEBURIA_HOMINIS
BLAUTIA_WEXLERAE
RUMINOCOCCUS_GAUVREAUII
ANAEROSTIPES_HADRUS

species

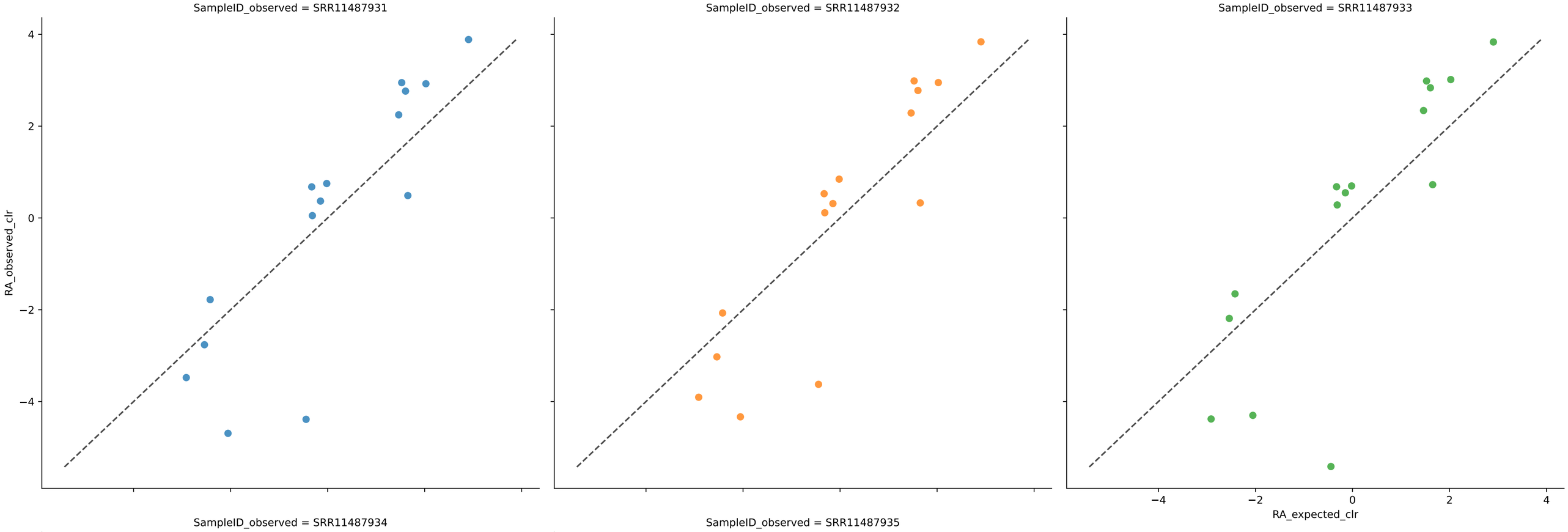
Expected vs. Observed Relative Abundance for species using wgsa in Experiment hilo



Expected vs. Observed Relative Abundance for species using wol in Experiment hilo

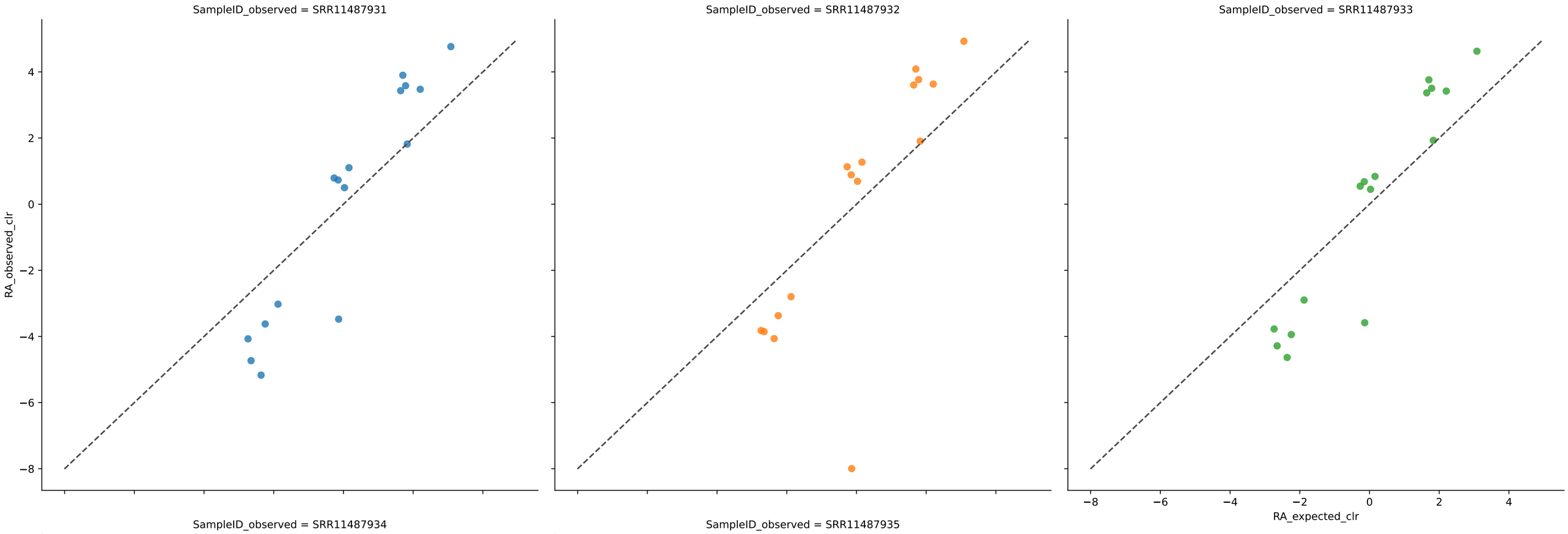


Expected vs. Observed Relative Abundance for genus using bio4 in Experiment Amos hilo



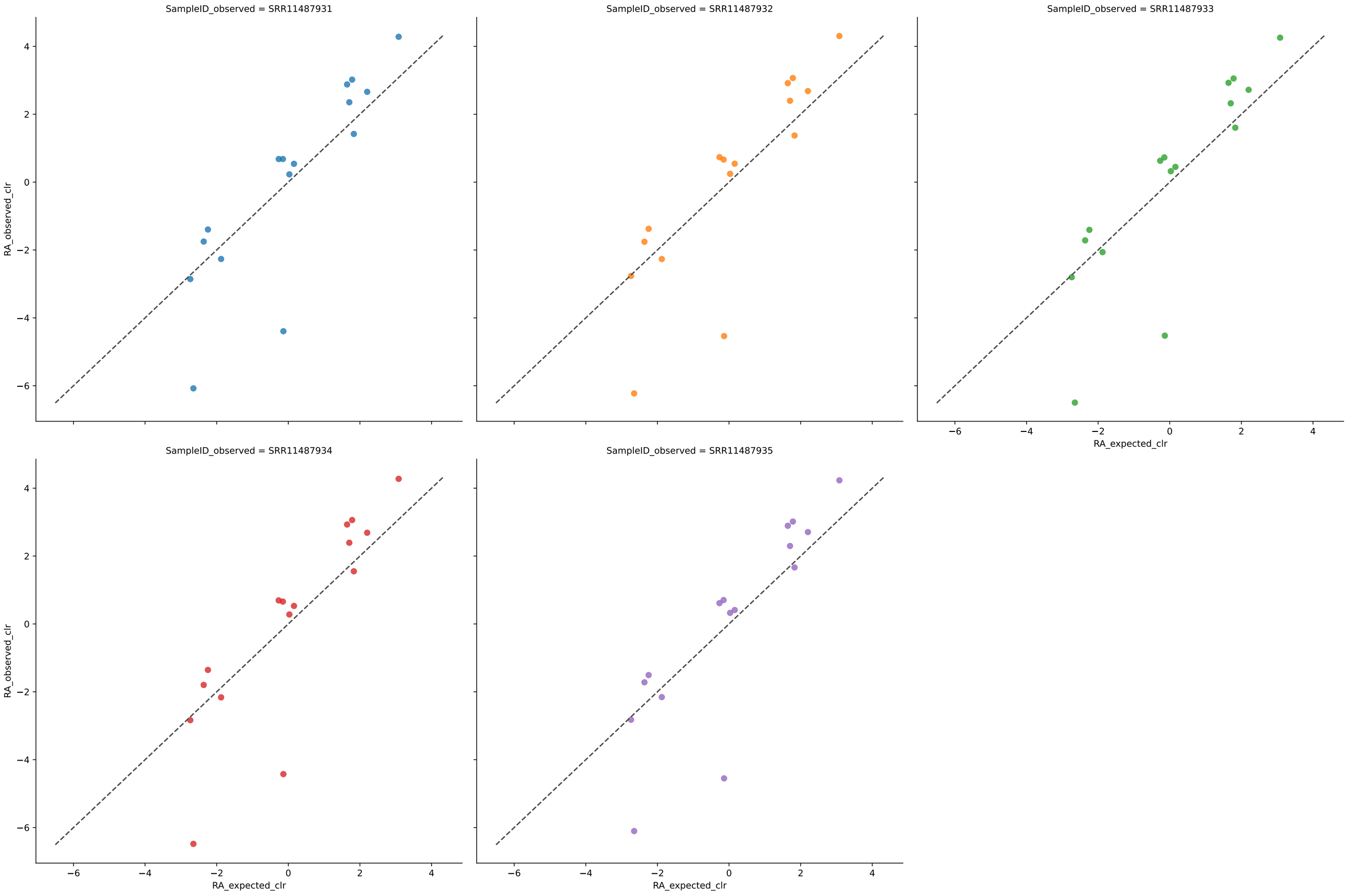
	R^2	MAE	AD	1-BC	RMSE
SRR11487931	0.9163	0.0178	5.6916	0.8663	0.0320
SRR11487932	0.9048	0.0174	5.1175	0.8693	0.0326
SRR11487933	0.9085	0.0162	6.4879	0.8781	0.0308
SRR11487934	0.8969	0.0160	5.6939	0.8798	0.0326
SRR11487935	0.9133	0.0152	5.4245	0.8859	0.0297
Average	0.9080	0.0165	5.6831	0.8759	0.0315

Expected vs. Observed Relative Abundance for genus using jams in Experiment Amos hilo



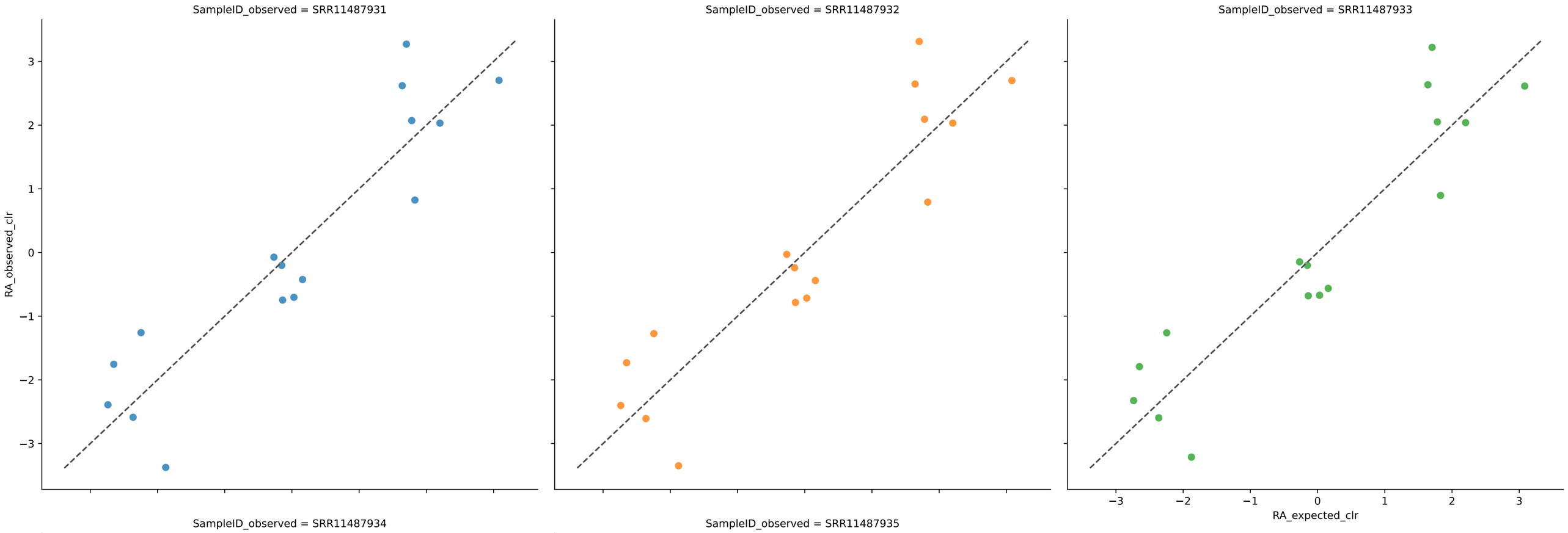
	R^2	MAE	AD	1-BC	RMSE
SRR11487931	0.9036	0.0219	6.8610	0.8241	0.0341
SRR11487932	0.8973	0.0221	9.6443	0.8223	0.0348
SRR11487933	0.9110	0.0206	6.3834	0.8339	0.0316
SRR11487934	0.9022	0.0215	6.4687	0.8270	0.0333
SRR11487935	0.9168	0.0204	6.9212	0.8356	0.0309
Average	0.9062	0.0213	7.2557	0.8286	0.0329

Expected vs. Observed Relative Abundance for genus using wgsa in Experiment Amos hilo

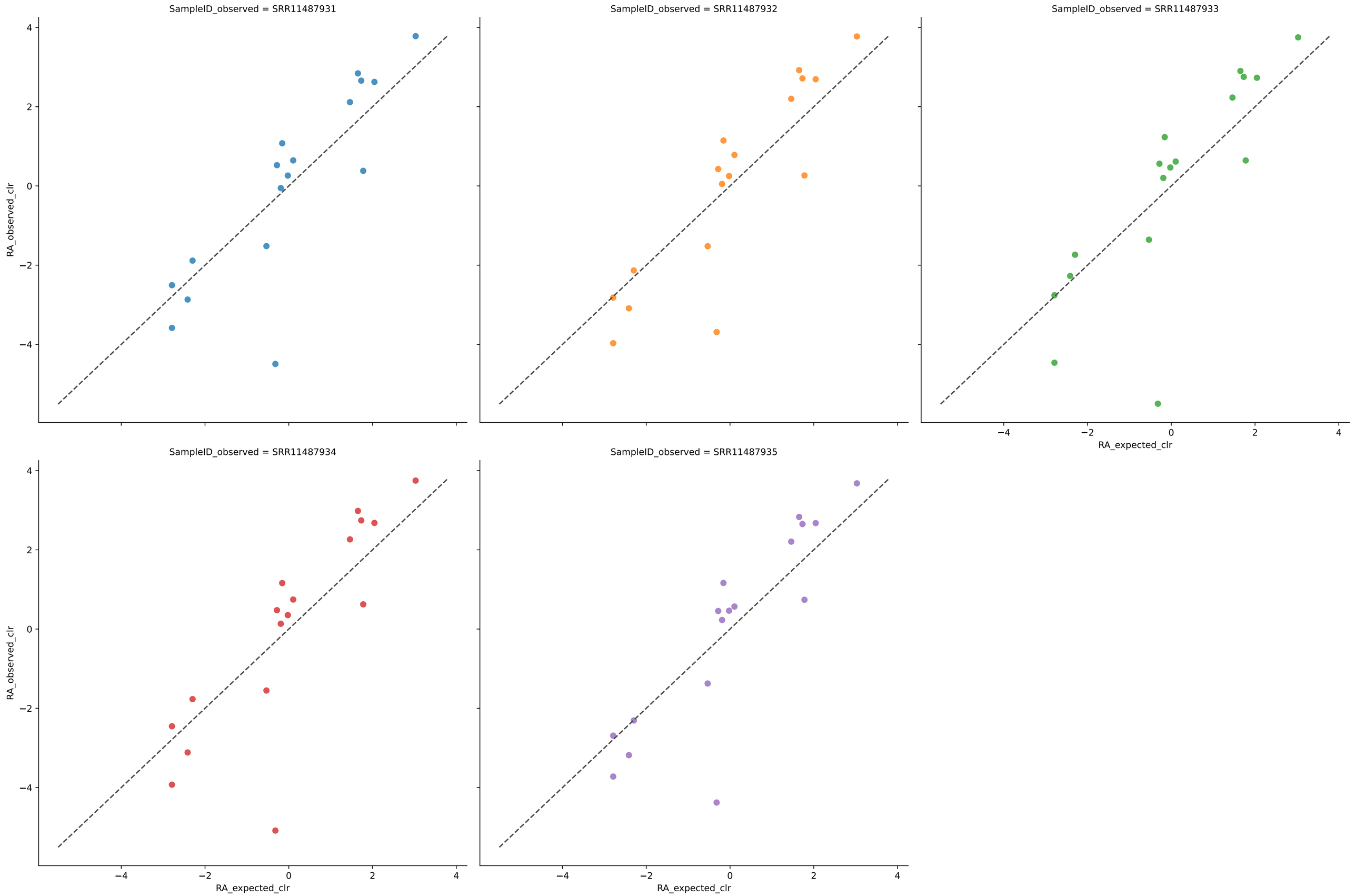


	R^2	MAE	AD	1-BC	RMSE
SRR11487931	0.9134	0.0195	6.1797	0.8316	0.0318
SRR11487932	0.9112	0.0196	6.4008	0.8305	0.0319
SRR11487933	0.9198	0.0187	6.5033	0.8385	0.0297
SRR11487934	0.9165	0.0189	6.4448	0.8365	0.0304
SRR11487935	0.9235	0.0183	6.2562	0.8420	0.0290
Average	0.9169	0.0190	6.3570	0.8358	0.0306

Expected vs. Observed Relative Abundance for genus using wol in Experiment Amos hilo

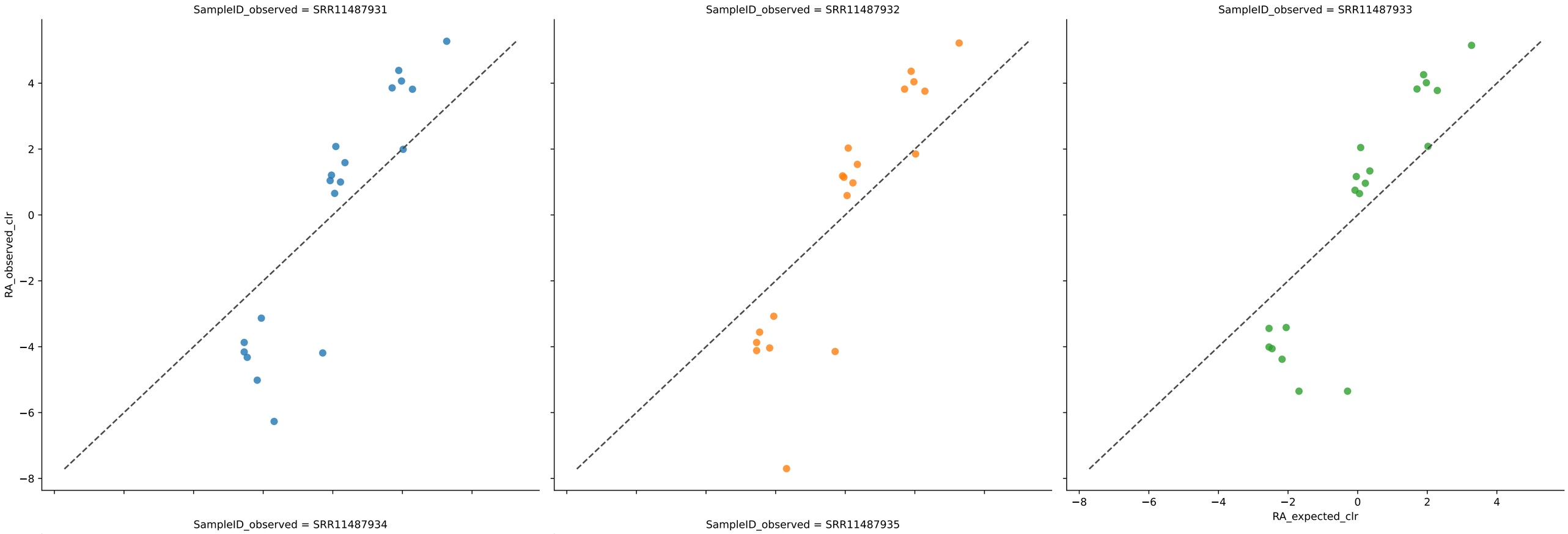


	R^2	MAE	AD	1-BC	RMSE
SRR11487931	0.3723	0.0425	3.1882	0.6373	0.0786
SRR11487932	0.3532	0.0434	3.2368	0.6289	0.0805
SRR11487933	0.3586	0.0427	3.0849	0.6355	0.0794
SRR11487934	0.3760	0.0420	3.1331	0.6418	0.0780
SRR11487935	0.3660	0.0422	3.0234	0.6404	0.0786
Average	0.3652	0.0426	3.1333	0.6368	0.0790



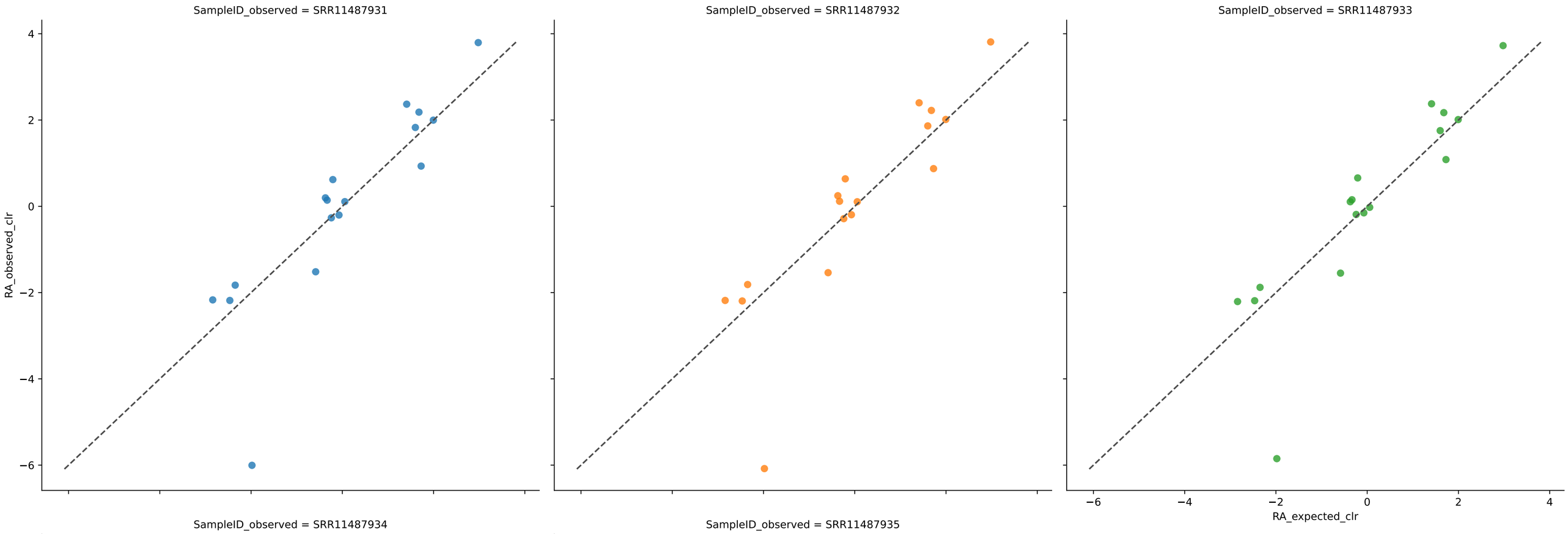
	R^2	MAE	AD	1-BC	RMSE
SRR11487931	0.9142	0.0169	5.2528	0.8563	0.0302
SRR11487932	0.9028	0.0164	4.8354	0.8604	0.0308
SRR11487933	0.9066	0.0152	6.2762	0.8708	0.0291
SRR11487934	0.8944	0.0161	5.8814	0.8626	0.0310
SRR11487935	0.9113	0.0145	5.1244	0.8766	0.0281
Average	0.9059	0.0158	5.4740	0.8653	0.0298

Expected vs. Observed Relative Abundance for species using jams in Experiment Amos hilo



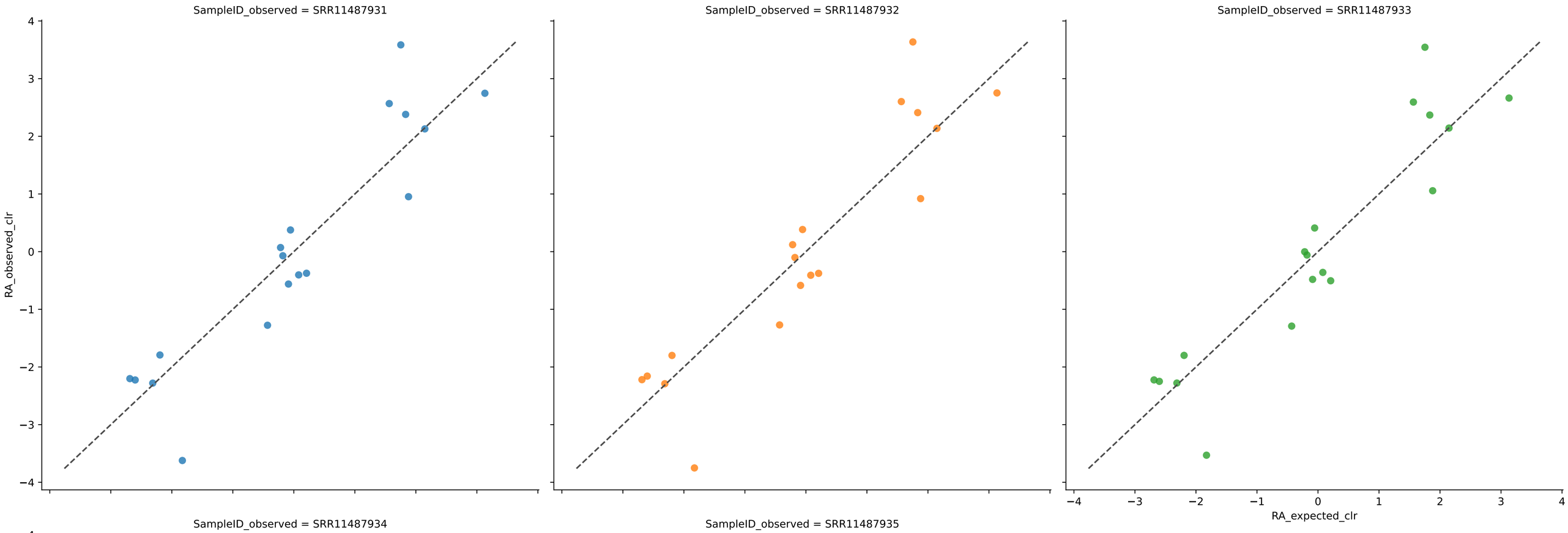
	R^2	MAE	AD	1-BC	RMSE
SRR11487931	0.9021	0.0191	9.1725	0.8156	0.0317
SRR11487932	0.8961	0.0194	9.5318	0.8132	0.0324
SRR11487933	0.9069	0.0184	8.8944	0.8227	0.0299
SRR11487934	0.8996	0.0189	7.5503	0.8170	0.0312
SRR11487935	0.9133	0.0180	8.8004	0.8255	0.0291
Average	0.9036	0.0188	8.7899	0.8188	0.0308

Expected vs. Observed Relative Abundance for species using wgsa in Experiment Amos hilo



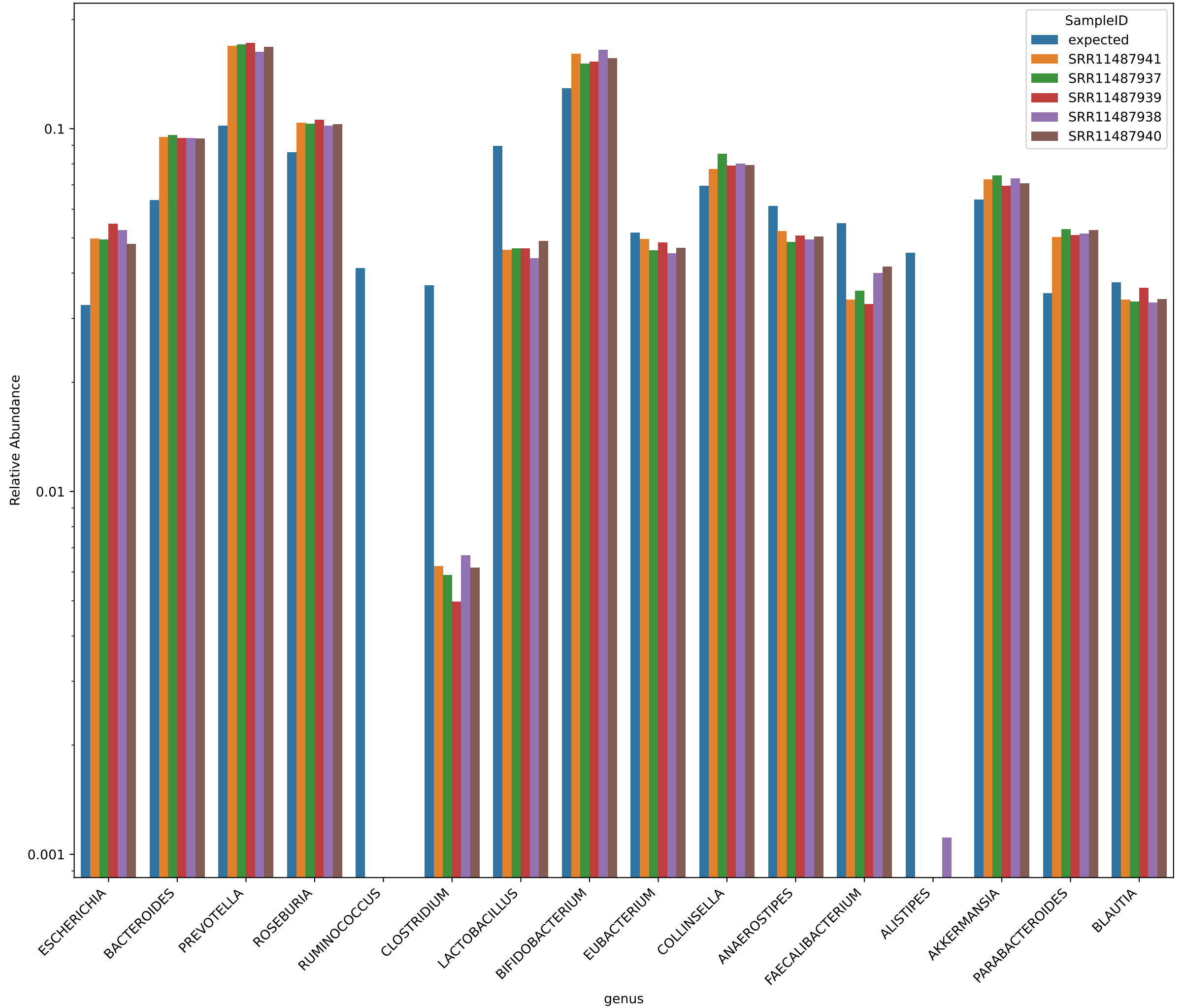
	R^2	MAE	AD	1-BC	RMSE
SRR11487931	0.9122	0.0180	4.6517	0.8276	0.0302
SRR11487932	0.9108	0.0180	4.7533	0.8279	0.0304
SRR11487933	0.9187	0.0171	4.4721	0.8366	0.0287
SRR11487934	0.9158	0.0173	4.4548	0.8343	0.0293
SRR11487935	0.9223	0.0168	4.4669	0.8392	0.0281
Average	0.9160	0.0175	4.5598	0.8331	0.0293

Expected vs. Observed Relative Abundance for species using wol in Experiment Amos hilo

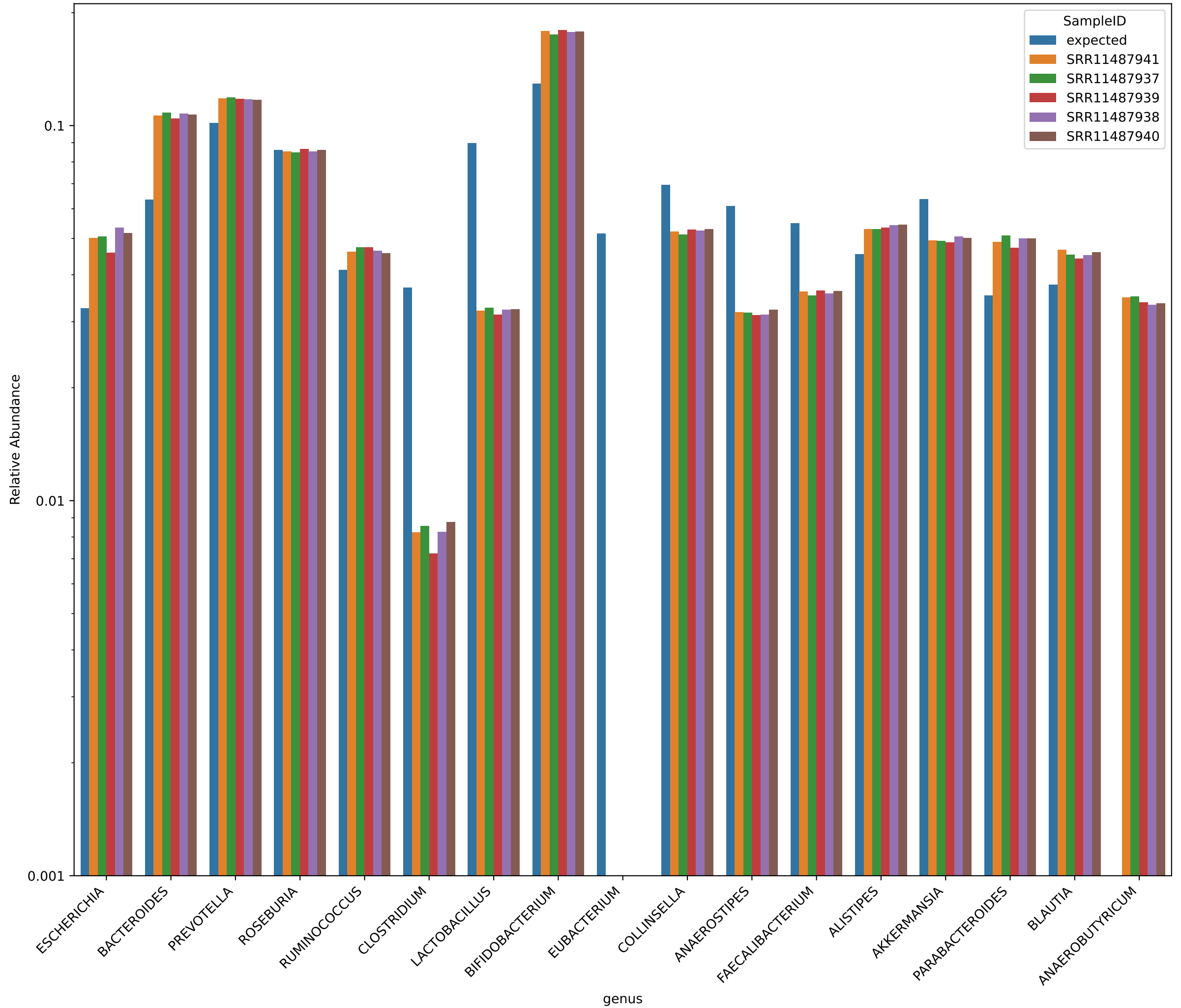


	R^2	MAE	AD	1-BC	RMSE
SRR11487931	0.2914	0.0391	3.3507	0.6019	0.0796
SRR11487932	0.2756	0.0399	3.4846	0.5938	0.0811
SRR11487933	0.2816	0.0391	3.2745	0.6021	0.0799
SRR11487934	0.2963	0.0386	3.3150	0.6080	0.0789
SRR11487935	0.2883	0.0387	3.2343	0.6071	0.0793
Average	0.2866	0.0391	3.3318	0.6026	0.0798

Expected vs. Observed Relative Abundance for genus using bio4 in Experiment mixed



Expected vs. Observed Relative Abundance for genus using jams in Experiment mixed



Expected vs. Observed Relative Abundance for genus using wgsa in Experiment mixed

SampleID
expected
SRR11487941
SRR11487937
SRR11487939
SRR11487938
SRR11487940

Relative Abundance
0.1
0.01
0.001

ESCHERICHIA
Vibrio
BACTEROIDES
PREVOTELLA
ROSEBURIA
RUMINOCOCCUS
Staphylococcus
CLOSTRIDIUM
LACTOBACILLUS
BIFIDOBACTERIUM
EUBACTERIUM
Coprococcus
COLLINSELLA
ANAEROSTIPES
FAECALIBACTERIUM
ALISTIPES
AKKERMANSIA
PARABACTEROIDES
BLAUTIA
Faecalicatena
Mediterraneibacter
Anaerobutyricum
Limosilactobacillus

genus

Expected vs. Observed Relative Abundance for genus using wol in Experiment mixed

SampleID
expected
SRR11487941
SRR11487937
SRR11487939
SRR11487938
SRR11487940

Relative Abundance
0.1
0.01
0.001

ESCHERICHIA
Shigella
BACTEROIDES
Butyrivibrio
PREVOTELLA
ROSEBURIA
RUMINOCOCCUS
CLOSTRIDIUM
LACTOBACILLUS
BIFIDOBACTERIUM
EUBACTERIUM
Coprococcus
COLLINSELLA
Dorea
ANAEROSTIPES
FAECALIBACTERIUM
ALISTIPES
AKKERMANSIA
PARABACTEROIDES
BLAUTIA
Fusicatenibacter
Lachnoclostridium
Tyzzerella

genus

Expected vs. Observed Relative Abundance for species using bio4 in Experiment mixed

SampleID
expected
SRR11487938
SRR11487940
SRR11487939
SRR11487941
SRR11487937

Relative Abundance

0.1
0.01
0.001

ESCHERICHIA_COLI
BACTEROIDES_THETAIOTAOMICRON
BACTEROIDES_UNIFORMIS
PARABACTEROIDES_DISTASONIS
FAECALIBACTERIUM_PRAUSNITZII
CLOSTRIDIUM_BUTYRICUM
LACTOBACILLUS_GASSERI
PREVOTELLA_MELANINOGENICA
EUBACTERIUM_HALLII
COLLINSELLA_AEROFACIENS
PREVOTELLA_COPRI
ROSEBURIA_INTESTINALIS
ALISTIPES_FINEGOLDII
BIFIDOBACTERIUM_LONGUM
AKKERMANSIA_MUCINIPHILA
ROSEBURIA_HOMINIS
BLAUTIA_WEXLERAE
RUMINOCOCCUS_GAUVREAUII
ANAEROSTIPES_HADRUS
LACTOBACILLUS_PARAGASSERI

species

Expected vs. Observed Relative Abundance for species using jams in Experiment mixed

SampleID
expected
SRR11487938
SRR11487940
SRR11487939
SRR11487941
SRR11487937

Relative Abundance
0.1
0.01
0.001

ESCHERICHIA_COLI
BACTEROIDES_THETAIOTAOMICRON
BACTEROIDES_UNIFORMIS
PARABACTEROIDES_DISTASONIS
FAECALIBACTERIUM_PRAUSNITZII
CLOSTRIDIUM_BUTYRICUM
LACTOBACILLUS_GASSERI
PREVOTELLA_MELANINOGENICA
LACTOBACILLUS_JOHNSONII
EUBACTERIUM_HALLII
COLLINSELLA_AEROFACIENS
PREVOTELLA_COPRI
ROSEBURIA_INTESTINALIS
ALISTIPES_FINEGOLDII
BIFIDOBACTERIUM_LONGUM
AKKERMANSIA_MUCINIPHILA
ROSEBURIA_HOMINIS
BLAUTIA_WEXLERAE
RUMINOCOCCUS_GAUVREAUII
LACTOBACILLUS_TAIWANENSIS
ANAEROSTIPES_HADRUS
LACTOBACILLUS_PARAGASSERI

species

Expected vs. Observed Relative Abundance for species using wgsa in Experiment mixed

SampleID
expected
SRR11487938
SRR11487940
SRR11487939
SRR11487941
SRR11487937

Relative Abundance

0.1
0.01
0.001

ESCHERICHIA_COLI
BACTEROIDES_THETAIOTAOMICRON
BACTEROIDES_UNIFORMIS
PARABACTEROIDES_DISTASONIS
FAECALIBACTERIUM_PRAUSNITZII
Staphylococcus aureus
CLOSTRIDIUM_BUTYRICUM
LACTOBACILLUS_GASSERI
Limosilactobacillus fermentum
Lactobacillus phage phiadh
PREVOTELLA_MELANINOGENICA
EUBACTERIUM_HALLII
Blautia obeum
COLLINSELLA_AEROFACIENS
PREVOTELLA_COPRI
ROSEBURIA_INTESTINALIS
ALISTIPES_FINEGOLDII
BIFIDOBACTERIUM_LONGUM
AKKERMANSIA_MUCINIPHILA
ROSEBURIA_HOMINIS
BLAUTIA_WEXLERAE
RUMINOCOCCUS_GAUVREAUII
ANAEROSTIPES_HADRUS
Blautia sp. YL58
Lactobacillus paragasseri
Blautia sp. SC05B48
Vibrio sp. Scap24
Faecalicatena sp. Marseille-Q4148

species

Expected vs. Observed Relative Abundance for species using wol in Experiment mixed

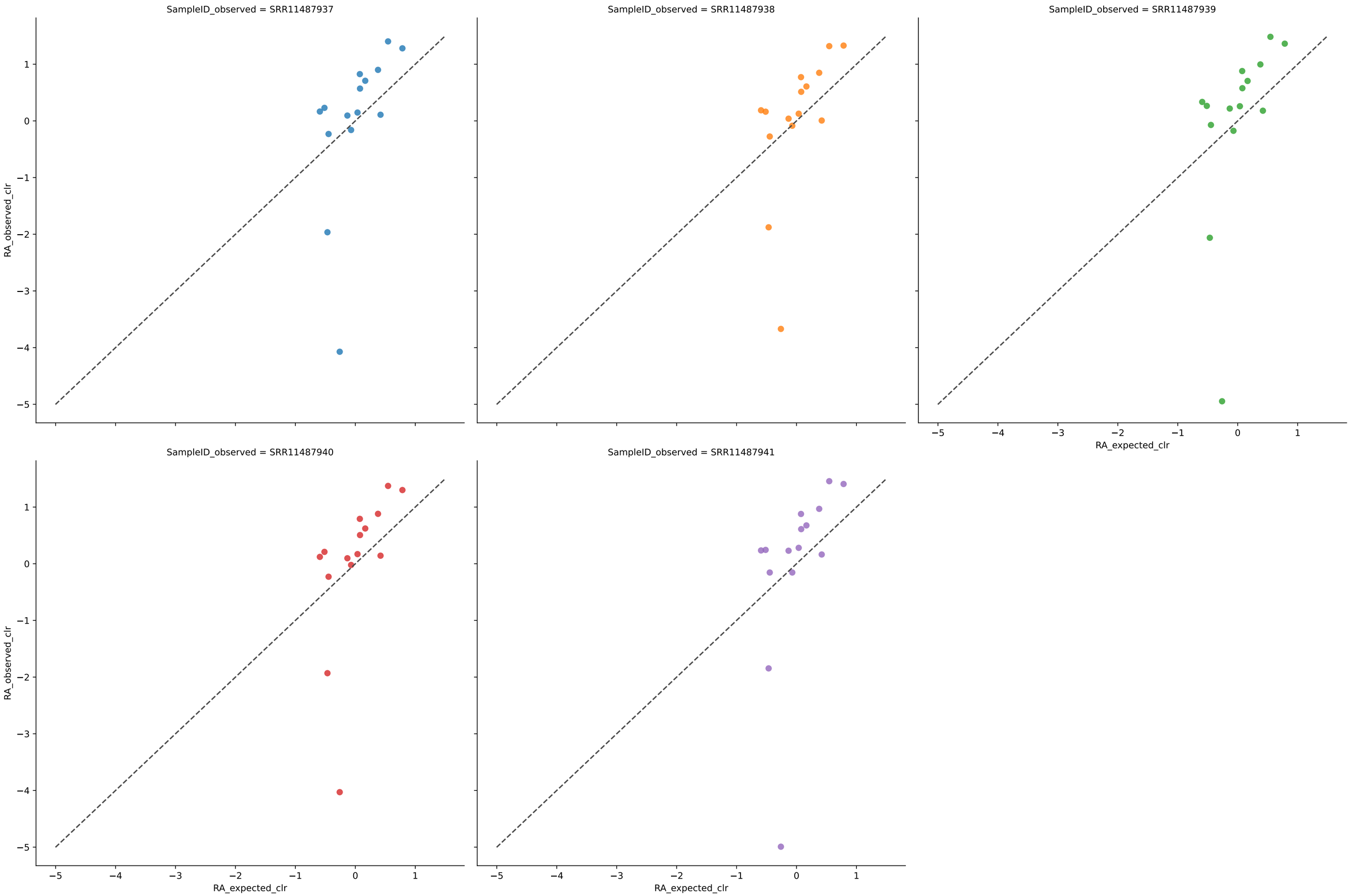
SampleID
expected
SRR11487938
SRR11487940
SRR11487939
SRR11487941
SRR11487937

Relative Abundance
0.1
0.01
0.001

species

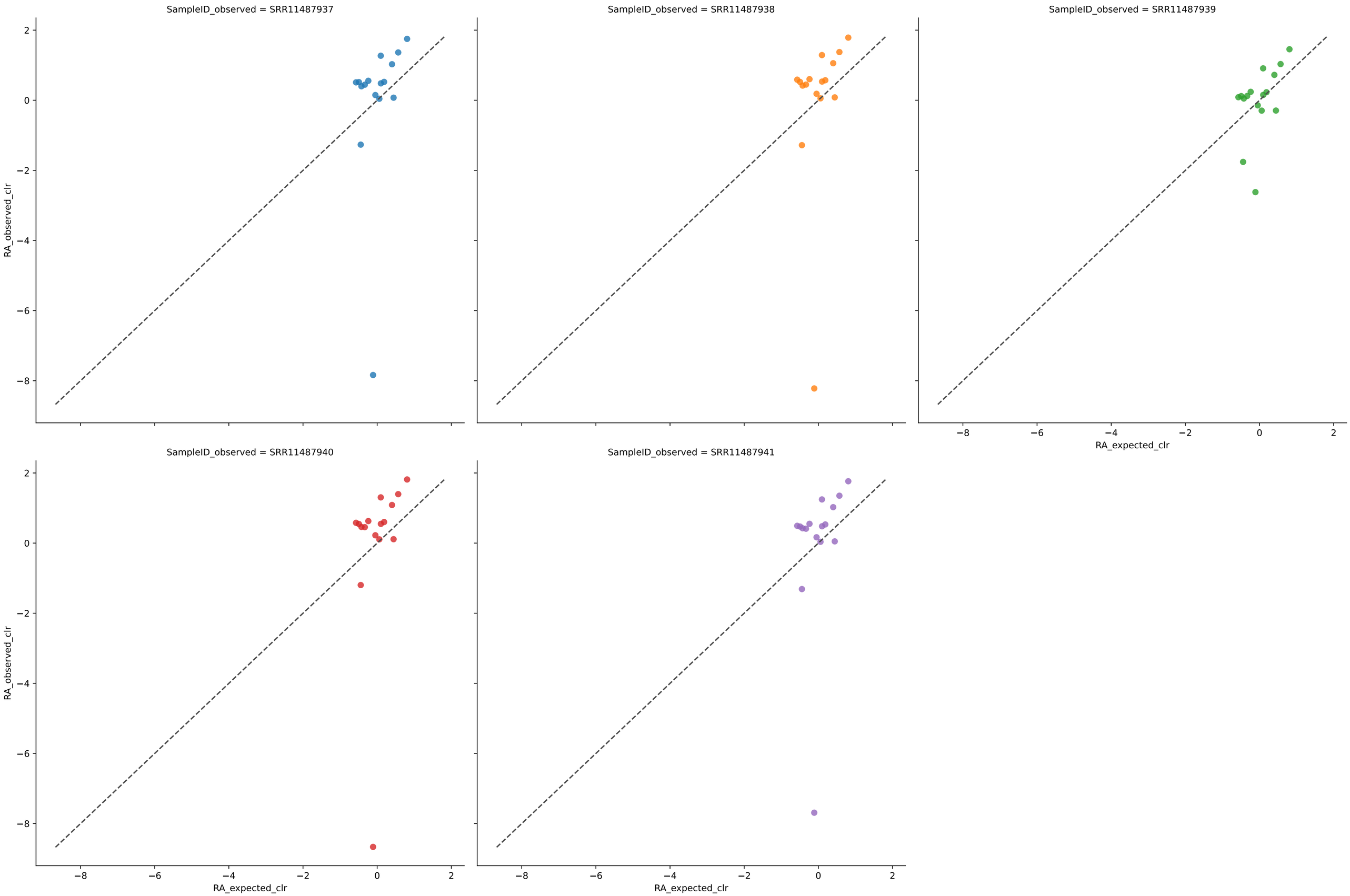
ESCHERICHIA_COLI
Shigella dysenteriae
Shigella flexneri
BACTEROIDES_THETAIOTAOMICRON
BACTEROIDES_UNIFORMIS
Bacteroides vulgatus
PARABACTEROIDES_DISTASONIS
FAECALIBACTERIUM_PRAUSNITZII
Blautia hansenii
CLOSTRIDIUM_BUTYRICUM
LACTOBACILLUS_GASSERI
Lactobacillus fermentum
Bifidobacterium breve
PREVOTELLA_MELANINOGENICA
Tyzzerella nexilis
Dorea formicigenerans
EUBACTERIUM_HALLII
Eubacterium ramulus
Eubacterium rectale
Eubacterium ventriosum
Blautia obeum
Butyrivibrio crossotus
Bacteroides stercoris
COLLINSELLA_AEROFACIENS
PREVOTELLA_COPRI
ROSEBURIA_INTESTINALIS
BIFIDOBACTERIUM_LONGUM
ALISTIPES_FINEGOLDII
AKKERMANSIA_MUCINIPHILA
ROSEBURIA_HOMINIS
Roseburia faecis
Alistipes shahii
Roseburia inulinivorans
Bacteroides pectinophilus
Coprococcus comes
Clostridium sp. M62/1
BLAUTIA_WEXLERAE
RUMINOCOCCUS_GAUVREAUII
Prevotella histicola
Prevotella fusca
Prevotella scopos
Ruminococcus faecis
ANAEROSTIPES_HADRUS
Fusicatenibacter saccharivorans
Bifidobacterium reuteri
Blautia sp. KLE 1732
Collinsella sp. CAG:166
Eubacterium sp. CAG:146
Akkermansia muciniphila CAG:154
Bacteroides faecis CAG:32
Bacteroides thetaiotaomicron CAG:40
Alistipes senegalensis
Akkermansia sp. UNK.MGS-1
Akkermansia sp. 54 46
Bacteroidales bacterium 55 9
Akkermansia sp. Phil8

Expected vs. Observed Relative Abundance for genus using bio4 in Experiment Amos mixed



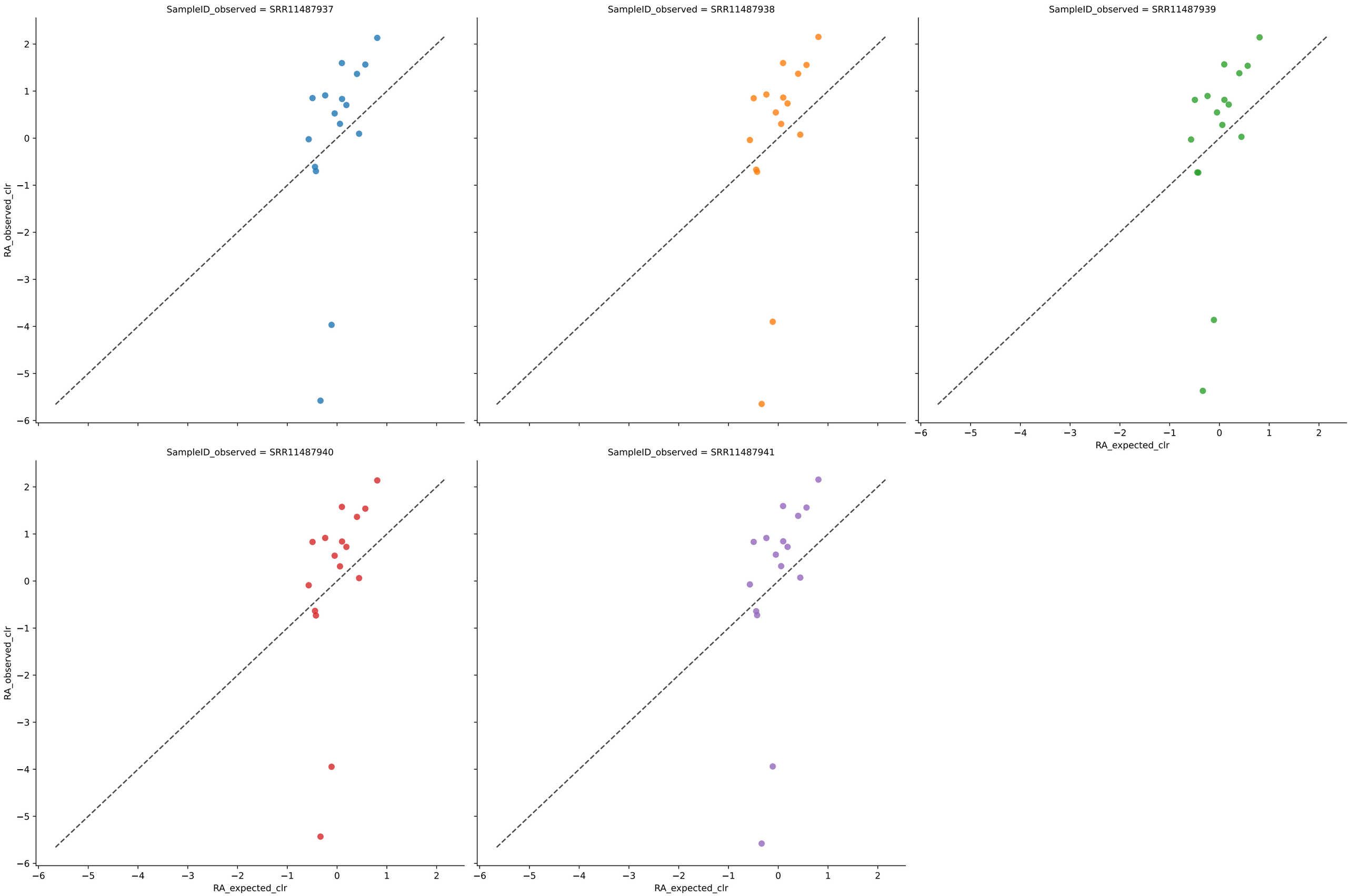
	R^2	MAE	AD	1-BC	RMSE
SRR11487937	0.6595	0.0241	4.5249	0.8155	0.0293
SRR11487938	0.6856	0.0238	4.1118	0.8178	0.0288
SRR11487939	0.6543	0.0237	5.3975	0.8188	0.0297
SRR11487940	0.6903	0.0226	4.4374	0.8273	0.0282
SRR11487941	0.6856	0.0235	5.3530	0.8203	0.0293
Average	0.6751	0.0235	4.7649	0.8199	0.0291

Expected vs. Observed Relative Abundance for genus using jams in Experiment Amos mixed



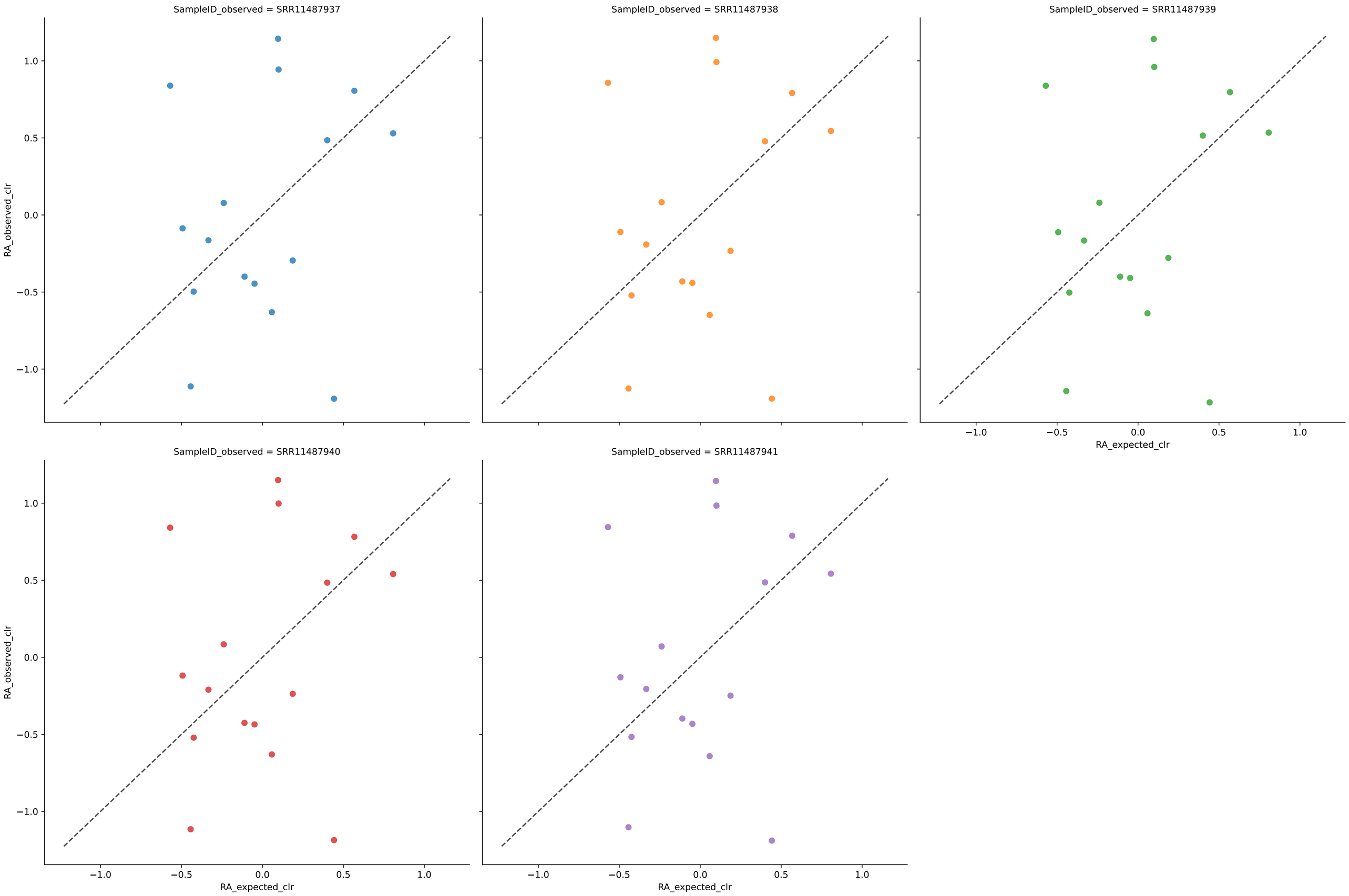
	R^2	MAE	AD	1-BC	RMSE
SRR11487937	0.5479	0.0239	8.2583	0.8032	0.0292
SRR11487938	0.5460	0.0239	8.6504	0.8036	0.0294
SRR11487939	0.5747	0.0234	3.4024	0.8067	0.0292
SRR11487940	0.5531	0.0236	9.0831	0.8060	0.0292
SRR11487941	0.5581	0.0237	8.1152	0.8045	0.0293
Average	0.5559	0.0237	7.5019	0.8048	0.0293

Expected vs. Observed Relative Abundance for genus using wgsa in Experiment Amos mixed



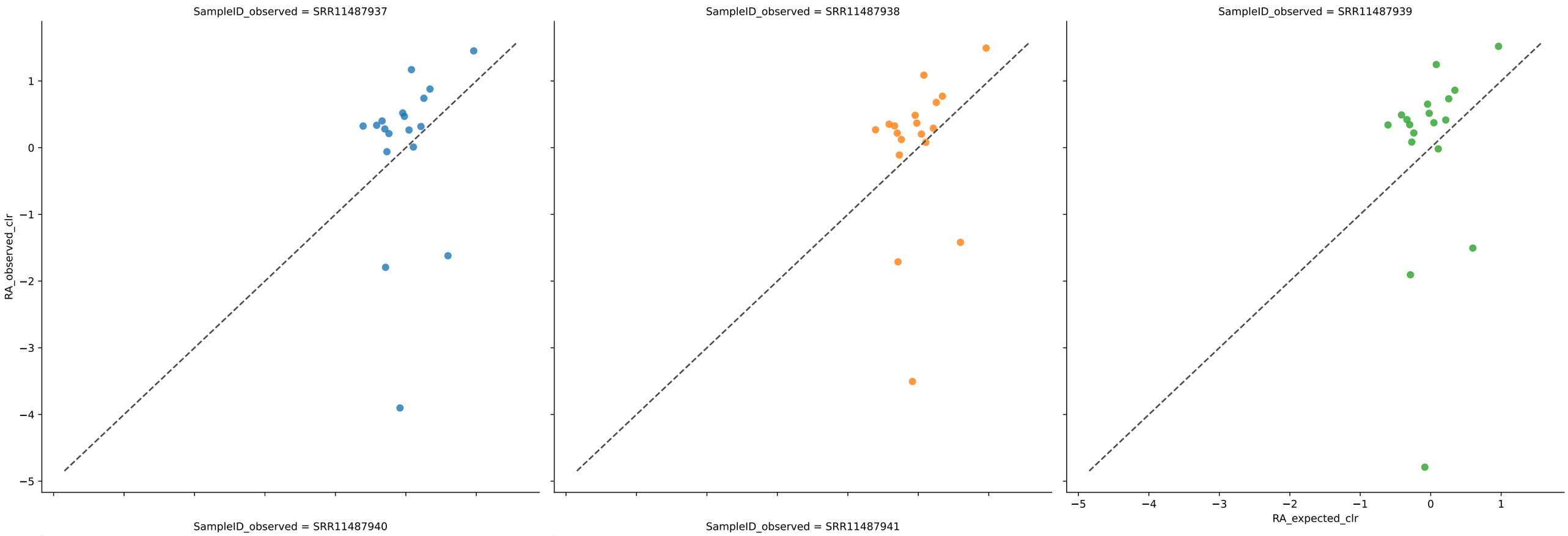
	R^2	MAE	AD	1-BC	RMSE
SRR11487937	0.6162	0.0271	7.2906	0.7596	0.0329
SRR11487938	0.6172	0.0272	7.3210	0.7596	0.0331
SRR11487939	0.6217	0.0271	7.0792	0.7598	0.0333
SRR11487940	0.6200	0.0271	7.1672	0.7602	0.0330
SRR11487941	0.6231	0.0271	7.2852	0.7601	0.0332
Average	0.6196	0.0271	7.2286	0.7599	0.0331

Expected vs. Observed Relative Abundance for genus using wol in Experiment Amos mixed



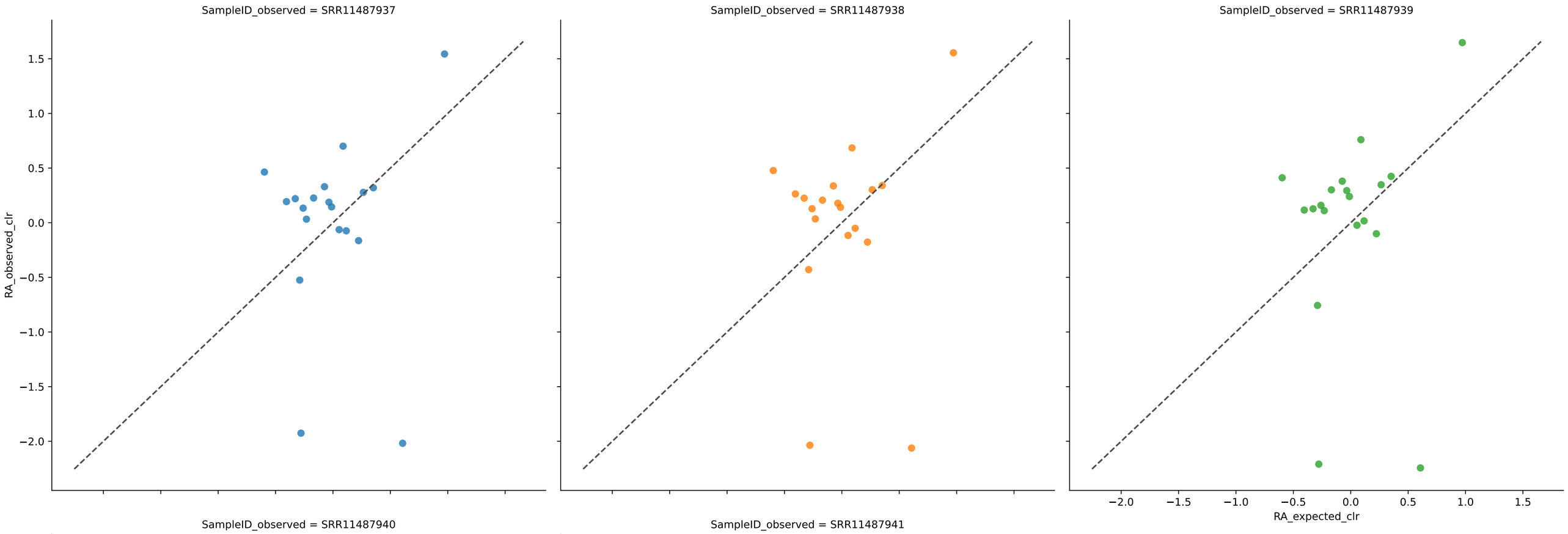
	R^2	MAE	AD	1-BC	RMSE
SRR11487937	0.0645	0.0319	2.8809	0.7349	0.0415
SRR11487938	0.0633	0.0324	2.9006	0.7305	0.0420
SRR11487939	0.0662	0.0317	2.8965	0.7363	0.0414
SRR11487940	0.0643	0.0324	2.8819	0.7307	0.0419
SRR11487941	0.0658	0.0321	2.8748	0.7333	0.0417
Average	0.0648	0.0321	2.8869	0.7331	0.0417

Expected vs. Observed Relative Abundance for species using bio4 in Experiment Amos mixed



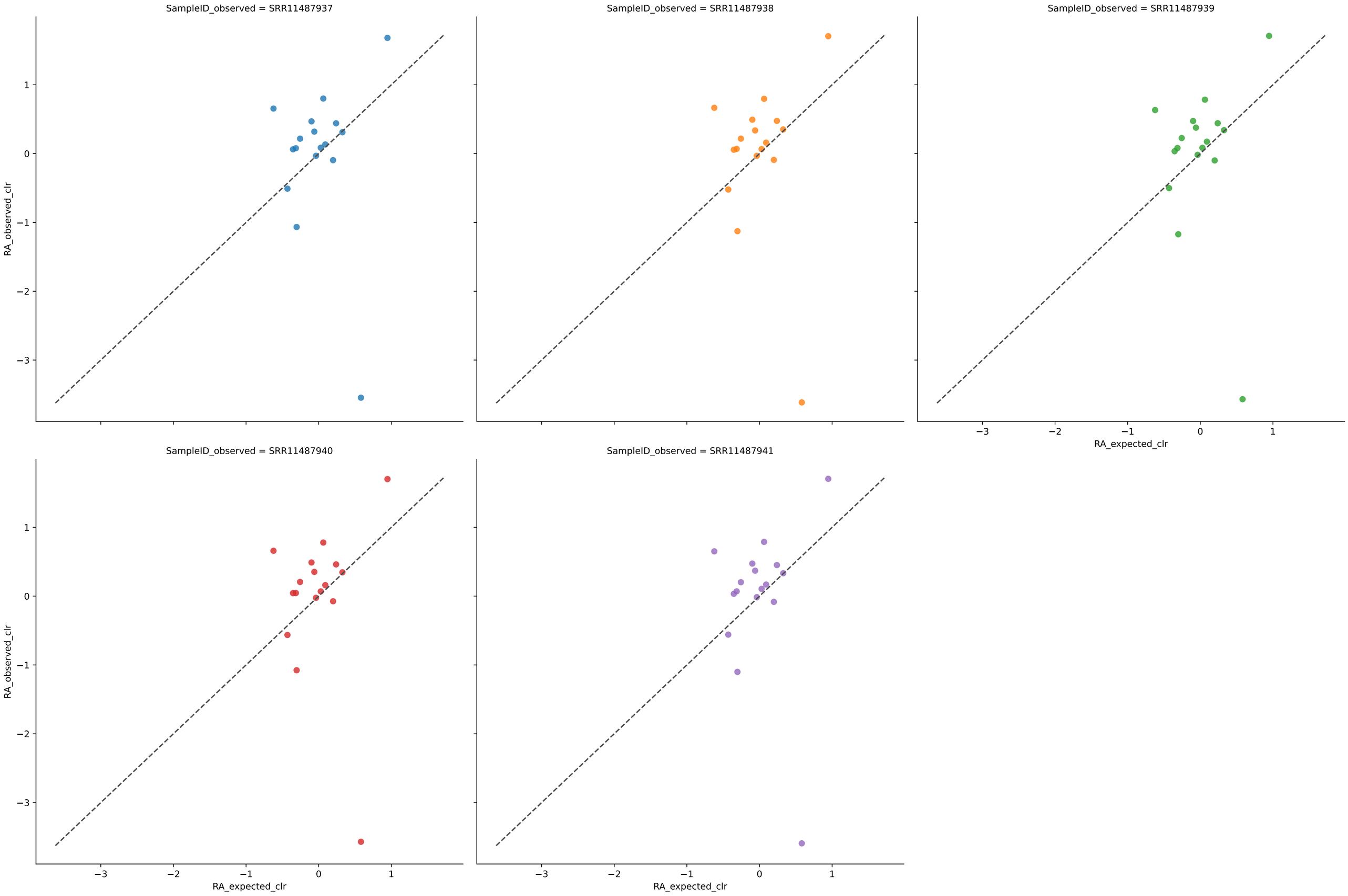
	R^2	MAE	AD	1-BC	RMSE
SRR11487937	0.2996	0.0223	5.1875	0.7909	0.0301
SRR11487938	0.3547	0.0218	4.7066	0.7964	0.0297
SRR11487939	0.2928	0.0219	5.9450	0.7946	0.0304
SRR11487940	0.3277	0.0211	5.0307	0.8025	0.0295
SRR11487941	0.3332	0.0217	5.8823	0.7966	0.0301
Average	0.3216	0.0217	5.3504	0.7962	0.0300

Expected vs. Observed Relative Abundance for species using jams in Experiment Amos mixed



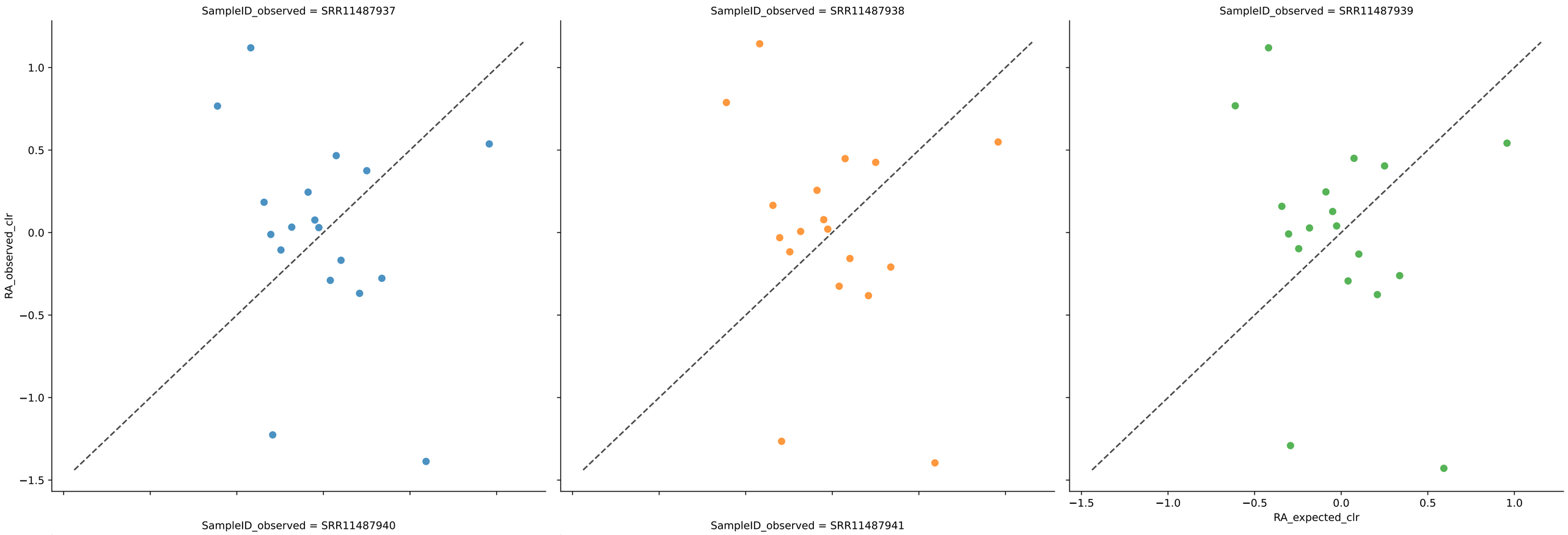
	R^2	MAE	AD	1-BC	RMSE
SRR11487937	0.3708	0.0199	3.6003	0.8015	0.0276
SRR11487938	0.3682	0.0200	3.6950	0.8008	0.0279
SRR11487939	0.4162	0.0191	3.9369	0.8061	0.0279
SRR11487940	0.3834	0.0197	3.4885	0.8044	0.0276
SRR11487941	0.3887	0.0196	3.6944	0.8037	0.0277
Average	0.3854	0.0197	3.6830	0.8033	0.0277

Expected vs. Observed Relative Abundance for species using wgsa in Experiment Amos mixed



	R^2	MAE	AD	1-BC	RMSE
SRR11487937	0.3833	0.0212	4.6362	0.7858	0.0296
SRR11487938	0.3924	0.0214	4.7186	0.7845	0.0298
SRR11487939	0.3983	0.0212	4.6751	0.7866	0.0298
SRR11487940	0.3953	0.0212	4.6599	0.7859	0.0297
SRR11487941	0.3961	0.0211	4.6848	0.7871	0.0297
Average	0.3931	0.0212	4.6749	0.7860	0.0297

Expected vs. Observed Relative Abundance for species using wol in Experiment Amos mixed



	R^2	MAE	AD	1-BC	RMSE
SRR11487937	0.0234	0.0274	3.2948	0.7069	0.0372
SRR11487938	0.0204	0.0276	3.3182	0.7037	0.0375
SRR11487939	0.0221	0.0271	3.3334	0.7102	0.0372
SRR11487940	0.0196	0.0275	3.2964	0.7046	0.0373
SRR11487941	0.0193	0.0274	3.2935	0.7059	0.0372
Average	0.0210	0.0274	3.3073	0.7062	0.0373