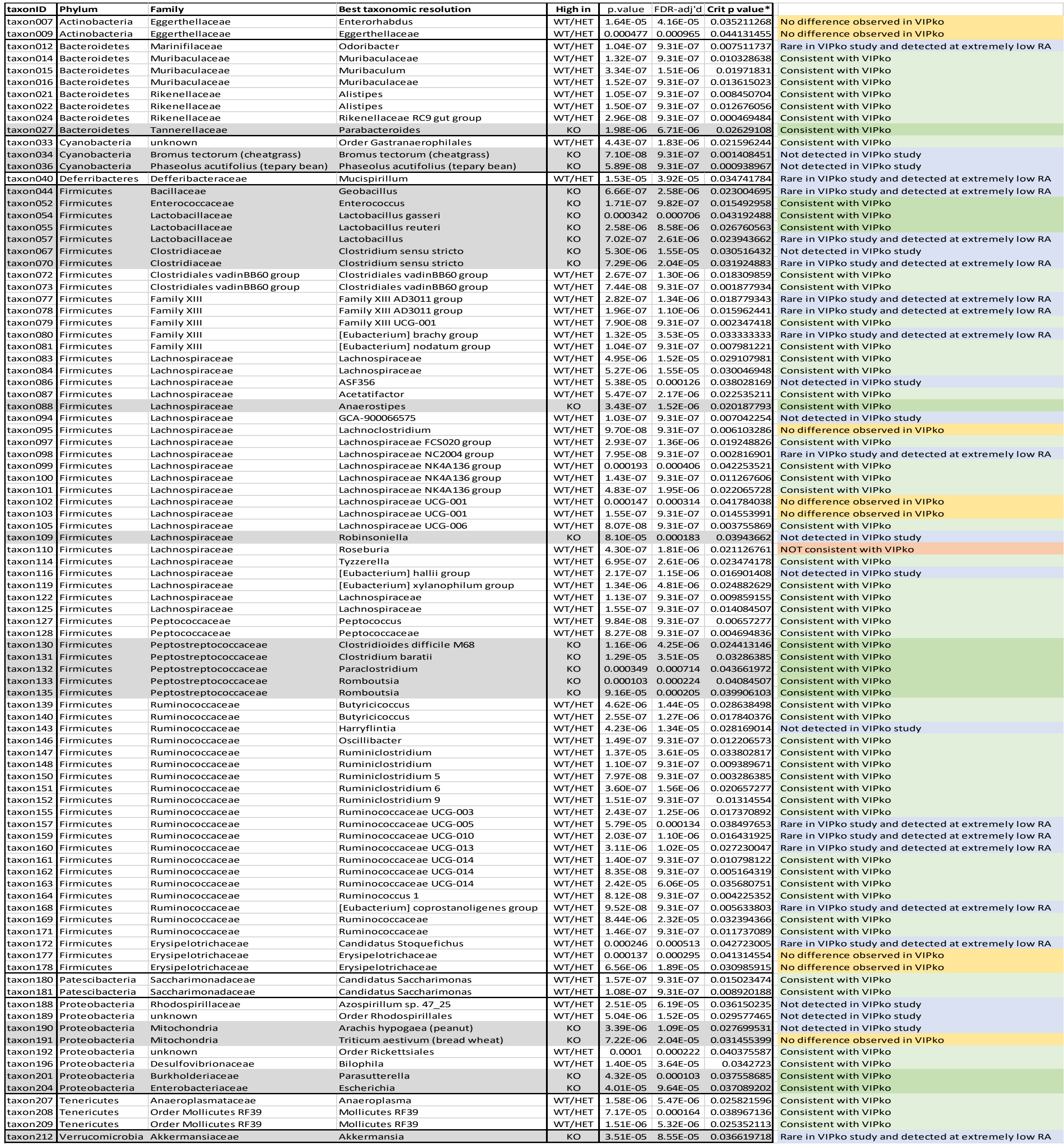
Table 2. Group sizes and sample coverage for the data presented.



taxonID	Phylum	Family	Best taxonomic resolution	High in	p.value	FDR-adj'd	Crit p value*	
taxon007	Actinobacteria	Eggerthellaceae	Enterorhabdus	WT/HET	1.64E-05	4.16E-05	0.035211268	No difference observed in VIPko
taxon009	Actinobacteria	Eggerthellaceae	Eggerthellaceae	WT/HET	0.000477	0.000965	0.044131455	No difference observed in VIPko
taxon012	Bacteroidetes	Marinifilaceae	Odoribacter	WT/HET	1.04E-07	9.31E-07	0.007511737	Rare in VIPko study and detected at extremely low RA
taxon014	Bacteroidetes	Muribaculaceae	Muribaculaceae	WT/HET	1.32E-07	9.31E-07	0.010328638	Consistent with VIPko
taxon015	Bacteroidetes	Muribaculaceae	Muribaculum	WT/HET	3.34E-07	1.51E-06	0.01971831	Consistent with VIPko
taxon016	Bacteroidetes	Muribaculaceae	Muribaculaceae	WT/HET	1.52E-07	9.31E-07	0.013615023	Consistent with VIPko
taxon021	Bacteroidetes	Rikenellaceae	Alistipes	WT/HET	1.05E-07	9.31E-07	0.008450704	Consistent with VIPko
taxon022	Bacteroidetes	Rikenellaceae	Alistipes	WT/HET	1.50E-07	9.31E-07	0.012676056	Consistent with VIPko
taxon024	Bacteroidetes	Rikenellaceae	Rikenellaceae RC9 gut group	WT/HET	2.96E-08	9.31E-07	0.000469484	Consistent with VIPko
taxon027	Bacteroidetes	Tannerellaceae	Parabacteroides	KO	1.98E-06	6.71E-06	0.02629108	Consistent with VIPko
taxon033	Cyanobacteria	unknown	Order Gastranaerophilales	WT/HET	4.43E-07	1.83E-06	0.021596244	Consistent with VIPko
taxon034	Cyanobacteria	Bromus tectorum (cheatgrass)	Bromus tectorum (cheatgrass)	KO	7.10E-08	9.31E-07	0.001408451	Not detected in VIPko study
taxon036	Cyanobacteria	Phaseolus acutifolius (tepary bean)	Phaseolus acutifolius (tepary bean)	KO	5.89E-08	9.31E-07	0.000938967	Not detected in VIPko study
taxon040	Deferribacteres	Defferibacteraceae	Mucispirillum	WT/HET	1.53E-05	3.92E-05	0.034741784	Rare in VIPko study and detected at extremely low RA
taxon044	Firmicutes	Bacillaceae	Geobacillus	KO	6.66E-07	2.58E-06	0.023004695	Rare in VIPko study and detected at extremely low RA
taxon052	Firmicutes	Enterococcaceae	Enterococcus	KO	1.71E-07	9.82E-07	0.015492958	Consistent with VIPko
taxon054	Firmicutes	Lactobacillaceae	Lactobacillus gasseri	KO	0.000342	0.000706	0.043192488	Consistent with VIPko
taxon055	Firmicutes	Lactobacillaceae	Lactobacillus reuteri	KO	2.58E-06	8.58E-06	0.026760563	Consistent with VIPko
taxon057	Firmicutes	Lactobacillaceae	Lactobacillus	KO	7.02E-07	2.61E-06	0.023943662	Rare in VIPko study and detected at extremely low RA
taxon067	Firmicutes	Clostridiaceae	Clostridium sensu stricto	KO	5.30E-06	1.55E-05	0.030516432	Not detected in VIPko study
taxon070	Firmicutes	Clostridiaceae	Clostridium sensu stricto	KO	7.29E-06	2.04E-05	0.031924883	Rare in VIPko study and detected at extremely low RA
taxon072	Firmicutes	Clostridiales vadinBB60 group	Clostridiales vadinBB60 group	WT/HET	2.67E-07	1.30E-06	0.018309859	Consistent with VIPko
taxon073	Firmicutes	Clostridiales vadinBB60 group	Clostridiales vadinBB60 group	WT/HET	7.44E-08	9.31E-07	0.001877934	Consistent with VIPko
taxon077	Firmicutes	Family XIII	Family XIII AD3011 group	WT/HET	2.82E-07	1.34E-06	0.018779343	Rare in VIPko study and detected at extremely low RA
taxon078	Firmicutes	Family XIII	Family XIII AD3011 group	WT/HET	1.96E-07	1.10E-06	0.015962441	Rare in VIPko study and detected at extremely low RA
taxon079	Firmicutes	Family XIII	Family XIII UCG-001	WT/HET	7.90E-08	9.31E-07	0.002347418	Consistent with VIPko
taxon080	Firmicutes	Family XIII	[Eubacterium] brachy group	WT/HET	1.32E-05	3.53E-05	0.033333333	Rare in VIPko study and detected at extremely low RA
taxon081	Firmicutes	Family XIII	[Eubacterium] nodatum group	WT/HET	1.04E-07	9.31E-07	0.007981221	Consistent with VIPko
taxon083	Firmicutes	Lachnospiraceae	Lachnospiraceae	WT/HET	4.95E-06	1.52E-05	0.029107981	Consistent with VIPko
taxon084	Firmicutes	Lachnospiraceae	Lachnospiraceae	WT/HET	5.27E-06	1.55E-05	0.030046948	Consistent with VIPko
taxon086	Firmicutes	Lachnospiraceae	ASF356	WT/HET	5.38E-05	0.000126	0.038028169	Not detected in VIPko study
taxon087	Firmicutes	Lachnospiraceae	Acetatifactor	WT/HET	5.47E-07	2.17E-06	0.022535211	Consistent with VIPko
taxon088	Firmicutes	Lachnospiraceae	Anaerostipes	KO	3.43E-07	1.52E-06	0.020187793	Consistent with VIPko
taxon094	Firmicutes	Lachnospiraceae	GCA-900066575	WT/HET	1.03E-07	9.31E-07	0.007042254	Not detected in VIPko study
taxon095	Firmicutes	Lachnospiraceae	Lachnoclostridium	WT/HET	9.70E-08	9.31E-07	0.006103286	No difference observed in VIPko
taxon097	Firmicutes	Lachnospiraceae	Lachnospiraceae FCS020 group	WT/HET	2.93E-07	1.36E-06	0.019248826	Consistent with VIPko
taxon098	Firmicutes	Lachnospiraceae	Lachnospiraceae NC2004 group	WT/HET	7.95E-08	9.31E-07	0.002816901	Rare in VIPko study and detected at extremely low RA
taxon099	Firmicutes	Lachnospiraceae	Lachnospiraceae NK4A136 group	WT/HET	0.000193	0.000406	0.042253521	Consistent with VIPko
taxon100	Firmicutes	Lachnospiraceae	Lachnospiraceae NK4A136 group	WT/HET	1.43E-07	9.31E-07	0.011267606	Consistent with VIPko
taxon101	Firmicutes	Lachnospiraceae	Lachnospiraceae NK4A136 group	WT/HET	4.83E-07	1.95E-06	0.022065728	Consistent with VIPko
taxon102	Firmicutes	Lachnospiraceae	Lachnospiraceae UCG-001	WT/HET	0.000147	0.000314	0.041784038	No difference observed in VIPko
taxon103	Firmicutes	Lachnospiraceae	Lachnospiraceae UCG-001	WT/HET	1.55E-07	9.31E-07	0.014553991	No difference observed in VIPko
taxon105	Firmicutes	Lachnospiraceae	Lachnospiraceae UCG-006	WT/HET	8.07E-08	9.31E-07	0.003755869	Consistent with VIPko
taxon109	Firmicutes	Lachnospiraceae	Robinsoniella	KO	8.10E-05	0.000183	0.03943662	Not detected in VIPko study
taxon110	Firmicutes	Lachnospiraceae	Roseburia	WT/HET	4.30E-07	1.81E-06	0.021126761	NOT consistent with VIPko
taxon114	Firmicutes	Lachnospiraceae	Tyzzerella	WT/HET	6.95E-07	2.61E-06	0.023474178	Consistent with VIPko
taxon116	Firmicutes	Lachnospiraceae	[Eubacterium] hallii group	WT/HET	2.17E-07	1.15E-06	0.016901408	Not detected in VIPko study
taxon119	Firmicutes	Lachnospiraceae	[Eubacterium] xylanophilum group	WT/HET	1.34E-06	4.81E-06	0.024882629	Consistent with VIPko
taxon122	Firmicutes	Lachnospiraceae	Lachnospiraceae	WT/HET	1.13E-07	9.31E-07	0.009859155	Consistent with VIPko
taxon125	Firmicutes	Lachnospiraceae	Lachnospiraceae	WT/HET	1.55E-07	9.31E-07	0.014084507	Consistent with VIPko
taxon127	Firmicutes	Peptococcaceae	Peptococcus	WT/HET	9.84E-08	9.31E-07	0.00657277	Consistent with VIPko
taxon128	Firmicutes	Peptococcaceae	Peptococcaceae	WT/HET	8.27E-08	9.31E-07	0.004694836	Consistent with VIPko
taxon130	Firmicutes	Peptostreptococcaceae	Clostridioides difficile M68	KO	1.16E-06	4.25E-06	0.024413146	Consistent with VIPko
taxon131	Firmicutes	Peptostreptococcaceae	Clostridium baratii	KO	1.29E-05	3.51E-05	0.03286385	Consistent with VIPko
taxon132	Firmicutes	Peptostreptococcaceae	Paraclostridium	KO	0.000349	0.000714	0.043661972	Consistent with VIPko
taxon133	Firmicutes	Peptostreptococcaceae	Romboutsia	KO	0.000103	0.000224	0.04084507	Consistent with VIPko
taxon135	Firmicutes	Peptostreptococcaceae	Romboutsia	KO	9.16E-05	0.000205	0.039906103	Consistent with VIPko
taxon139	Firmicutes	Ruminococcaceae	Butyricicoccus	WT/HET	4.62E-06	1.44E-05	0.028638498	Consistent with VIPko
taxon140	Firmicutes	Ruminococcaceae	Butyricicoccus	WT/HET	2.55E-07	1.27E-06	0.017840376	Consistent with VIPko
taxon143	Firmicutes	Ruminococcaceae	Harryflintia	WT/HET	4.23E-06	1.34E-05	0.028169014	Not detected in VIPko study
taxon146	Firmicutes	Ruminococcaceae	Oscillibacter	WT/HET	1.49E-07	9.31E-07	0.012206573	Consistent with VIPko
taxon147	Firmicutes	Ruminococcaceae	Ruminiclostridium	WT/HET	1.37E-05	3.61E-05	0.033802817	Consistent with VIPko
taxon148	Firmicutes	Ruminococcaceae	Ruminiclostridium	WT/HET	1.10E-07	9.31E-07	0.009389671	Consistent with VIPko
taxon150	Firmicutes	Ruminococcaceae	Ruminiclostridium 5	WT/HET	7.97E-08	9.31E-07	0.003286385	Consistent with VIPko
taxon151	Firmicutes	Ruminococcaceae	Ruminiclostridium 6	WT/HET	3.60E-07	1.56E-06	0.020657277	Consistent with VIPko
taxon152	Firmicutes	Ruminococcaceae	Ruminiclostridium 9	WT/HET	1.51E-07	9.31E-07	0.01314554	Consistent with VIPko
taxon155	Firmicutes	Ruminococcaceae	Ruminococcaceae UCG-003	WT/HET	2.43E-07	1.25E-06	0.017370892	Consistent with VIPko
taxon157	Firmicutes	Ruminococcaceae	Ruminococcaceae UCG-005	WT/HET	5.79E-05	0.000134	0.038497653	Rare in VIPko study and detected at extremely low RA
taxon159	Firmicutes	Ruminococcaceae	Ruminococcaceae UCG-010	WT/HET	2.03E-07	1.10E-06	0.016431925	Rare in VIPko study and detected at extremely low RA
taxon160	Firmicutes	Ruminococcaceae	Ruminococcaceae UCG-013	WT/HET	3.11E-06	1.02E-05	0.027230047	Rare in VIPko study and detected at extremely low RA
taxon161	Firmicutes	Ruminococcaceae	Ruminococcaceae UCG-014	WT/HET	1.40E-07	9.31E-07	0.010798122	Consistent with VIPko
taxon162	Firmicutes	Ruminococcaceae	Ruminococcaceae UCG-014	WT/HET	8.35E-08	9.31E-07	0.005164319	Consistent with VIPko
taxon163	Firmicutes	Ruminococcaceae	Ruminococcaceae UCG-014	WT/HET	2.42E-05	6.06E-05	0.035680751	Consistent with VIPko
taxon164	Firmicutes	Ruminococcaceae	Ruminococcus 1	WT/HET	8.12E-08	9.31E-07	0.004225352	Consistent with VIPko
taxon168	Firmicutes	Ruminococcaceae	[Eubacterium] coprostanoligenes group	WT/HET	9.52E-08	9.31E-07	0.005633803	Rare in VIPko study and detected at extremely low RA
taxon169	Firmicutes	Ruminococcaceae	Ruminococcaceae	WT/HET	8.44E-06	2.32E-05	0.032394366	Consistent with VIPko
taxon171	Firmicutes	Ruminococcaceae	Ruminococcaceae	WT/HET	1.46E-07	9.31E-07	0.011737089	Consistent with VIPko
taxon172	Firmicutes	Erysipelotrichaceae	Candidatus Stoquefichus	WT/HET	0.000246	0.000513	0.042723005	Rare in VIPko study and detected at extremely low RA
taxon177	Firmicutes	Erysipelotrichaceae	Erysipelotrichaceae	WT/HET	0.000137	0.000295	0.041314554	No difference observed in VIPko
taxon178	Firmicutes	Erysipelotrichaceae	Erysipelotrichaceae	WT/HET	6.56E-06	1.89E-05	0.030985915	No difference observed in VIPko
taxon180	Patescibacteria	Saccharimonadaceae	Candidatus Saccharimonas	WT/HET	1.57E-07	9.31E-07	0.015023474	Consistent with VIPko
taxon181	Patescibacteria	Saccharimonadaceae	Candidatus Saccharimonas	WT/HET	1.08E-07	9.31E-07	0.008920188	Consistent with VIPko
taxon188	Proteobacteria	Rhodospirillaceae	Azospirillum sp. 47_25	WT/HET	2.51E-05	6.19E-05	0.036150235	Not detected in VIPko study
taxon189	Proteobacteria	unknown	Order Rhodospirillales	WT/HET	5.04E-06	1.52E-05	0.029577465	Not detected in VIPko study
taxon190	Proteobacteria	Mitochondria	Arachis hypogaea (peanut)	KO	3.39E-06	1.09E-05	0.027699531	Not detected in VIPko study
taxon191	Proteobacteria	Mitochondria	Triticum aestivum (bread wheat)	KO	7.22E-06	2.04E-05	0.031455399	No difference observed in VIPko
taxon192	Proteobacteria	unknown	Order Rickettsiales	WT/HET	0.0001	0.000222	0.040375587	Consistent with VIPko
taxon196	Proteobacteria	Desulfovibrionaceae	Bilophila	WT/HET	1.40E-05	3.64E-05	0.0342723	Consistent with VIPko
taxon201	Proteobacteria	Burkholderiaceae	Parasutterella	KO	4.32E-05	0.000103	0.037558685	Consistent with VIPko
taxon204	Proteobacteria	Enterobacteriaceae	Escherichia	KO	4.01E-05	9.64E-05	0.037089202	Consistent with VIPko
taxon207	Tenericutes	Anaeroplasmataceae	Anaeroplasma	WT/HET	1.58E-06	5.47E-06	0.025821596	Consistent with VIPko
taxon208	Tenericutes	Order Mollicutes RF39	Mollicutes RF39	WT/HET	7.17E-05	0.000164	0.038967136	Consistent with VIPko
taxon209	Tenericutes	Order Mollicutes RF39	Mollicutes RF39	WT/HET	1.51E-06	5.32E-06	0.025352113	Consistent with VIPko
taxon212	Verrucomicrobia	Akkermansiaceae	Akkermansia	KO	3.51E-05	8.55E-05	0.036619718	Rare in VIPko study and detected at extremely low RA