

Table S1. Differential operational taxonomic units (OTUs) (PSD vs Sham)

OTU ID	Phylum	Family	Genus	PSD-Mean (%)	PSD-Sd (%)	Sham-Mean (%)	Sham-Sd (%)	P value
OTU570	p__Bacteroidota	f__Prevotellaceae	g__Prevotellaceae_UCG-001	0.6372	0.6163	2.329	1.663	0.041
OTU992	p__Bacteroidota	f__Prevotellaceae	g__Alloprevotella	2.761	2.98	0	0	0.000
OTU551	p__Bacteroidota	f__Muribaculaceae	g__norank_f__Muribaculaceae	1.56	0.4433	0.8285	0.6768	0.031
OTU123	p__Bacteroidota	f__Prevotellaceae	g__Alloprevotella	0.08687	0.1178	1.547	1.291	0.002
OTU1035	p__Firmicutes	f__Lachnospiraceae	g__Lachnospiraceae_NK4A136_group	1.308	1.488	0.1388	0.1143	0.010
OTU110	p__Bacteroidota	f__Prevotellaceae	g__Prevotellaceae_NK3B31_group	0.02099	0.03409	1.311	1.009	0.001
OTU937	p__Firmicutes	f__Lachnospiraceae	g__unclassified_f__Lachnospiraceae	0.07346	0.1837	1.197	2.193	0.015
OTU1126	p__Firmicutes	f__Ruminococcaceae	g__Ruminococcus	0.249	0.6667	0.6145	0.4553	0.023
OTU88	p__Bacteroidota	f__Muribaculaceae	g__norank_f__Muribaculaceae	0	0	0.8547	1.76	0.001
OTU1003	p__Firmicutes	f__Oscillospiraceae	g__Intestinimonas	0.604	0.4386	0.232	0.1327	0.024
OTU621	p__Firmicutes	f__norank_o__Clostridia_UCG-014	g__norank_f__norank_o__Clostridia_UCG-014	0.4991	0.9219	0.05655	0.04907	0.016
OTU960	p__Firmicutes	f__Lachnospiraceae	g__Lachnospiraceae_NK4A136_group	0.09503	0.08075	0.4408	0.4151	0.040
OTU1138	p__Actinobacteriota	f__Eggerthellaceae	g__Adlercreutzia	0.3644	0.2213	0.1038	0.1295	0.005
OTU458	p__Bacteroidota	f__Muribaculaceae	g__norank_f__Muribaculaceae	0.4518	0.5485	0	0	0.005
OTU254	p__Firmicutes	f__Monoglobaceae	g__Monoglobus	0.3475	0.2219	0.09328	0.109	0.024
OTU839	p__Firmicutes	f__norank_o__Clostridia_UCG-014	g__norank_f__norank_o__Clostridia_UCG-014	0.302	0.1557	0.1067	0.07145	0.018
OTU577	p__Bacteroidota	f__Muribaculaceae	g__norank_f__Muribaculaceae	0.2723	0.1721	0.1242	0.0591	0.021
OTU510	p__Bacteroidota	f__Rikenellaceae	g__Alistipes	0.3399	0.2928	0.01982	0.03532	0.002
OTU507	p__Bacteroidota	f__Rikenellaceae	g__Alistipes	0.3142	0.1826	0.04431	0.04854	0.003
OTU1063	p__Bacteroidota	f__Muribaculaceae	g__norank_f__Muribaculaceae	0.08104	0.1001	0.239	0.2517	0.040
OTU999	p__Firmicutes	f__Ruminococcaceae	g__Ruminococcus	0.001166	0.003298	0.2705	0.553	0.039
OTU464	p__Firmicutes	f__Lachnospiraceae	g__Lachnoclostridium	0.008745	0.005252	0.2105	0.2179	0.027
OTU951	p__Firmicutes	f__norank_o__Clostridia_UCG-014	g__norank_f__norank_o__Clostridia_UCG-014	0.1685	0.1601	0.04664	0.07269	0.018
OTU1130	p__Bacteroidota	f__Prevotellaceae	g__Prevotellaceae_NK3B31_group	0.2111	0.4524	0	0	0.032
OTU77	p__Firmicutes	f__Lachnospiraceae	g__Blautia	0.002915	0.00554	0.1872	0.2729	0.011
OTU113	p__Firmicutes	f__Lachnospiraceae	g__Roseburia	0.002332	0.004318	0.186	0.2125	0.004
OTU766	p__Bacteroidota	f__Rikenellaceae	g__Alistipes	0.1312	0.07937	0.05306	0.0694	0.036
OTU667	p__Firmicutes	f__Lachnospiraceae	g__Lachnospiraceae_NK4A136_group	0.1667	0.1678	0.01458	0.01605	0.011
OTU1093	p__Firmicutes	f__Lachnospiraceae	g__Butyrivibrio	0.03032	0.05507	0.1475	0.2108	0.025
OTU180	p__Firmicutes	f__Lachnospiraceae	g__Ruminococcus_torques_group	0	0	0.1685	0.3539	0.032
OTU811	p__Firmicutes	f__Christensenellaceae	g__Christensenellaceae_R-7_group	0.1382	0.1533	0.01691	0.0169	0.023
OTU1030	p__Firmicutes	f__Oscillospiraceae	g__NK4A214_group	0.1096	0.1017	0.04023	0.02085	0.035
OTU28	p__Bacteroidota	f__Muribaculaceae	g__norank_f__Muribaculaceae	0	0	0.1306	0.1981	0.005
OTU94	p__Firmicutes	f__Ruminococcaceae	g__norank_f__Ruminococcaceae	0.001166	0.003298	0.1283	0.2278	0.046
OTU1048	p__Bacteroidota	f__Muribaculaceae	g__norank_f__Muribaculaceae	0.01691	0.01726	0.1114	0.07874	0.004
OTU797	p__Bacteroidota	f__Bacteroidaceae	g__Bacteroides	0.1178	0.1218	0.005247	0.007659	0.027
OTU521	p__Actinobacteriota	f__Eggerthellaceae	g__Enterorhabdus	0.07812	0.04273	0.03207	0.02912	0.027
OTU492	p__Actinobacteriota	f__Eggerthellaceae	g__Enterorhabdus	0.08512	0.04997	0.01341	0.01624	0.008
OTU57	p__Firmicutes	f__Lachnospiraceae	g__Anaerostipes	0.001166	0.003298	0.09387	0.2338	0.040
OTU847	p__Firmicutes	f__Anaerovoracaceae	g__Eubacterium_brachy_group	0.06938	0.03283	0.02274	0.0218	0.007
OTU382	p__Firmicutes	f__Lachnospiraceae	g__Marvinbryantia	0.002915	0.00554	0.0857	0.09532	0.025
OTU628	p__Firmicutes	f__Eubacterium_coprostanoligenes_group	g__norank_f__Eubacterium_coprostanoligenes_group	0	0	0.08512	0.1279	0.005
OTU915	p__Firmicutes	f__Lachnospiraceae	g__Lachnospiraceae_NK4A136_group	0.07288	0.1513	0.008745	0.02474	0.018
OTU1071	p__Firmicutes	f__Peptococcaceae	g__norank_f__Peptococcaceae	0.02157	0.01364	0.06005	0.03068	0.013
OTU603	p__Firmicutes	f__Ruminococcaceae	g__Ruminococcus	0.07579	0.1363	0.004664	0.01319	0.021
OTU616	p__Actinobacteriota	f__Eggerthellaceae	g__unclassified_f__Eggerthellaceae	0.07696	0.06891	0.000583	0.001649	0.001
OTU504	p__Actinobacteriota	f__Eggerthellaceae	g__Enterorhabdus	0.06646	0.08796	0.004664	0.007884	0.027
OTU787	p__Firmicutes	f__Christensenellaceae	g__Christensenellaceae_R-7_group	0.009328	0.02455	0.06005	0.07945	0.007
OTU1101	p__Actinobacteriota	f__Eggerthellaceae	g__Enterorhabdus	0.06238	0.0558	0.005247	0.002989	0.014
OTU1033	p__Actinobacteriota	f__Eggerthellaceae	g__Gordonibacter	0.05539	0.03842	0.009328	0.008636	0.004
OTU501	p__Actinobacteriota	f__Eggerthellaceae	g__unclassified_f__Eggerthellaceae	0.05131	0.03621	0.007579	0.007859	0.002
OTU477	p__Firmicutes	f__Monoglobaceae	g__Monoglobus	0.004664	0.01142	0.05306	0.07404	0.043
OTU93	p__Bacteroidota	f__Prevotellaceae	g__unclassified_f__Prevotellaceae	0	0	0.05306	0.08786	0.032
OTU802	p__Firmicutes	f__Ruminococcaceae	g__unclassified_f__Ruminococcaceae	0.002915	0.004947	0.04431	0.06482	0.022
OTU204	p__Firmicutes	f__Erysipelatoclostridiaceae	g__Erysipelatrichaceae_UCG-003	0	0	0.04664	0.06722	0.032
OTU87	p__Firmicutes	f__Lachnospiraceae	g__norank_f__Lachnospiraceae	0.005247	0.008055	0.04081	0.06276	0.037
OTU865	p__Actinobacteriota	f__Eggerthellaceae	g__unclassified_f__Eggerthellaceae	0.03032	0.01557	0.01224	0.01431	0.023
OTU542	p__Firmicutes	f__norank_o__RF39	g__norank_f__norank_o__RF39	0.03265	0.03894	0.008745	0.007659	0.039

OTU1095	p__Firmicutes	f__Lachnospiraceae	g__Roseburia	0	0	0.03906	0.07768	0.032
OTU19	p__Campilobacterota	f__Helicobacteraceae	g__Helicobacter	0	0	0.03848	0.08066	0.032
OTU758	p__Firmicutes	f__Anaerovoracaceae	g__Family_XIII_AD3011_group	0.02915	0.01448	0.009328	0.006107	0.002
OTU497	p__Firmicutes	f__Oscillospiraceae	g__unclassified_f__Oscillospiraceae	0.03148	0.03343	0.006996	0.009328	0.038
OTU661	p__Firmicutes	f__Anaerovoracaceae	g__Eubacterium_brachy_group	0.02624	0.01431	0.009328	0.01557	0.013
OTU978	p__Firmicutes	f__Christensenellaceae	g__Christensenellaceae_R-7_group	0.02099	0.009328	0.01049	0.008546	0.029
OTU761	p__Firmicutes	f__Erysipelotrichaceae	g__Dubosiella	0	0	0.03148	0.05083	0.013
OTU874	p__Firmicutes	f__Ruminococcaceae	g__Candidatus_Soleaferrea	0.02041	0.008614	0.01049	0.006941	0.042
OTU1010	p__Firmicutes	f__norank_o__RF39	g__norank_f__norank_o__RF39	0.02799	0.04866	0	0	0.032
OTU146	p__Firmicutes	f__Lachnospiraceae	g__Blautia	0	0	0.02565	0.02981	0.032
OTU6	p__Bacteroidota	f__Muribaculaceae	g__norank_f__Muribaculaceae	0	0	0.02565	0.04658	0.013
OTU133	p__Firmicutes	f__Anaerovoracaceae	g__Family_XIII_AD3011_group	0.002915	0.004947	0.02099	0.009972	0.002
OTU666	p__Firmicutes	f__norank_o__RF39	g__norank_f__norank_o__RF39	0.02157	0.02311	0.002332	0.002493	0.003
OTU854	p__Firmicutes	f__Peptococcaceae	g__norank_f__Peptococcaceae	0.01691	0.01026	0.006413	0.004273	0.012
OTU555	p__Actinobacteriota	f__Eggerthellaceae	g__DNF00809	0.01866	0.01616	0.002332	0.004986	0.004
OTU585	p__Bacteroidota	f__Muribaculaceae	g__norank_f__Muribaculaceae	0.01982	0.01776	0	0	0.001
OTU283	p__Actinobacteriota	f__Eggerthellaceae	g__Enterorhabdus	0.01924	0.04168	0	0	0.032
OTU450	p__Firmicutes	f__norank_o__Oscillospirales	g__norank_f__norank_o__Oscillospirales	0.01632	0.01115	0.002915	0.00347	0.010
OTU278	p__Firmicutes	f__Lachnospiraceae	g__Lachnospiraceae_UCG-001	0.01516	0.0136	0.002915	0.008245	0.028
OTU191	p__Bacteroidota	f__Tannerellaceae	g__Parabacteroides	0	0	0.01749	0.03434	0.032
OTU109	p__Actinobacteriota	f__Eggerthellaceae	g__Enterorhabdus	0.01341	0.01127	0.002915	0.004273	0.041
OTU1142	p__Bacteroidota	f__Muribaculaceae	g__norank_f__Muribaculaceae	0.01632	0.01596	0	0	0.001
OTU18	p__Firmicutes	f__Monoglobaceae	g__Monoglobus	0.000583	0.001649	0.01516	0.03361	0.044
OTU47	p__Firmicutes	f__Oscillospiraceae	g__norank_f__Oscillospiraceae	0.002332	0.003526	0.01341	0.009139	0.004
OTU669	p__Firmicutes	f__norank_o__RF39	g__norank_f__norank_o__RF39	0.01574	0.02696	0	0	0.013
OTU737	p__Firmicutes	f__Oscillospiraceae	g__UCG-005	0.003498	0.009894	0.01224	0.01474	0.042
OTU948	p__Deferribacterota	f__Deferribacteraceae	g__Mucispirillum	0.01224	0.007859	0.002915	0.00347	0.018
OTU260	p__Actinobacteriota	f__Eggerthellaceae	g__Enterorhabdus	0.01224	0.009308	0.002915	0.004947	0.048
OTU185	p__Firmicutes	f__Oscillospiraceae	g__UCG-005	0.002915	0.004947	0.01166	0.008989	0.028
OTU104	p__Firmicutes	f__UCG-010	g__norank_f__UCG-010	0	0	0.01399	0.009972	0.001
OTU509	p__Firmicutes	f__Ruminococcaceae	g__norank_f__Ruminococcaceae	0.001749	0.002414	0.01049	0.01136	0.011
OTU777	p__Proteobacteria	f__norank_o__Rhodospirillales	g__norank_f__norank_o__Rhodospirillales	0.01166	0.01271	0	0	0.013
OTU841	p__Firmicutes	f__norank_o__norank_c__Clostridia	g__norank_f__norank_o__norank_c__Clostridia	0.01049	0.01108	0.000583	0.001649	0.034
OTU478	p__Firmicutes	f__norank_o__norank_c__Clostridia	g__norank_f__norank_o__norank_c__Clostridia	0.008745	0.009796	0.001166	0.002159	0.035
OTU346	p__Actinobacteriota	f__Eggerthellaceae	g__Enterorhabdus	0.009911	0.01329	0	0	0.032
OTU545	p__Firmicutes	f__Erysipelatoclostridiaceae	g__Candidatus_Stoquefichus	0	0	0.008745	0.01257	0.013
OTU193	p__Firmicutes	f__Erysipelatoclostridiaceae	g__Erysipelatoclostridium	0	0	0.008162	0.01163	0.032
OTU827	p__Actinobacteriota	f__Eggerthellaceae	g__Parvibacter	0.008162	0.01108	0	0	0.013
OTU206	p__Firmicutes	f__Anaerofustaceae	g__Anaerofustis	0.006996	0.004986	0.001166	0.002159	0.011
OTU91	p__Elusimicrobiota	f__Elusimicrobiaceae	g__Elusimicrobium	0	0	0.007579	0.009308	0.012
OTU579	p__Firmicutes	f__Christensenellaceae	g__Christensenellaceae_R-7_group	0.006413	0.00347	0.000583	0.001649	0.004
OTU270	p__Actinobacteriota	f__Coriobacteriales_Incertae_Sedis	g__norank_f__Coriobacteriales_Incertae_Sedis	0.005247	0.006326	0	0	0.012
OTU1066	p__Firmicutes	f__Lachnospiraceae	g__norank_f__Lachnospiraceae	0.000583	0.001649	0.004081	0.003892	0.044
OTU490	p__Actinobacteriota	f__Actinomycetaceae	g__Actinomycetes	0.004664	0.006596	0	0	0.032
OTU453	p__Firmicutes	f__Ruminococcaceae	g__Paludicola	0.004664	0.006596	0	0	0.032
OTU117	p__Firmicutes	f__UCG-010	g__norank_f__UCG-010	0	0	0.004081	0.004622	0.012
OTU1100	p__Firmicutes	f__Lachnospiraceae	g__Acetatifactor	0.003498	0.004134	0	0	0.032
OTU823	p__Firmicutes	f__Lachnospiraceae	g__Lachnospiraceae_ND3007_group	0	0	0.002915	0.00347	0.032
OTU749	p__Firmicutes	f__Lachnospiraceae	g__unclassified_f__Lachnospiraceae	0	0	0.002915	0.00347	0.032
OTU81	p__Firmicutes	f__Lachnospiraceae	g__GCA-900066575	0.002332	0.002493	0	0	0.030

Table S2. Differential operational taxonomic units (OTUs) (EA vs PSD)

OUT ID	Phylum	Family	Genus	EA-Mean(%)	EA-Sd(%)	PSD-Mean(%)	PSD-Sd(%)	P value
OTU976	p__Bacteroidota	f__Muribaculaceae	g__norank_f__Muribaculaceae	0.8705	1.275	0.02857	0.06857	0.018
OTU518	p__Firmicutes	f__Monoglobaceae	g__Monoglobus	0.4612	0.3296	0.1417	0.1214	0.014
OTU415	p__Firmicutes	f__Lachnospiraceae	g__unclassified_f__Lachnospiraceae	0.4099	0.394	0.1154	0.2543	0.030
OTU1138	p__Actinobacteriota	f__Eggerthellaceae	g__Adlercreutzia	0.1149	0.1058	0.3644	0.2213	0.007
OTU893	p__Firmicutes	f__Lachnospiraceae	g__Eubacterium_ruminantium_group	0.3737	0.4893	0.04722	0.09104	0.034
OTU507	p__Bacteroidota	f__Rikenellaceae	g__Alistipes	0.1038	0.1051	0.3142	0.1826	0.014
OTU1110	p__Bacteroidota	f__Bacteroidaceae	g__Bacteroides	0.07346	0.03771	0.1638	0.07031	0.006
OTU1130	p__Bacteroidota	f__Prevotellaceae	g__Prevotellaceae_NK3B31_group	0	0	0.2111	0.4524	0.032
OTU789	p__Bacteroidota	f__Prevotellaceae	g__Alloprevotella	0.1528	0.3429	0	0	0.005
OTU555	p__Actinobacteriota	f__Eggerthellaceae	g__DNF00809	0.1049	0.08265	0.01866	0.01616	0.002
OTU305	p__Bacteroidota	f__Rikenellaceae	g__Alistipes	0.02041	0.0297	0.08454	0.07253	0.033
OTU492	p__Actinobacteriota	f__Eggerthellaceae	g__Enterorhabdus	0.01982	0.009894	0.08512	0.04997	0.010
OTU879	p__Firmicutes	f__Lachnospiraceae	g__norank_f__Lachnospiraceae	0.08512	0.08974	0.009911	0.01154	0.010
OTU123	p__Bacteroidota	f__Prevotellaceae	g__Alloprevotella	0.003498	0.009894	0.08687	0.1178	0.013
OTU1071	p__Firmicutes	f__Peptococcaceae	g__norank_f__Peptococcaceae	0.06122	0.0269	0.02157	0.01364	0.010
OTU616	p__Actinobacteriota	f__Eggerthellaceae	g__unclassified_f__Eggerthellaceae	0.004664	0.008269	0.07696	0.06891	0.003
OTU501	p__Actinobacteriota	f__Eggerthellaceae	g__unclassified_f__Eggerthellaceae	0.02507	0.03372	0.05131	0.03621	0.035
OTU1033	p__Actinobacteriota	f__Eggerthellaceae	g__Gordonibacter	0.01807	0.01071	0.05539	0.03842	0.048
OTU1043	p__Bacteroidota	f__Bacteroidaceae	g__Bacteroides	0.01166	0.0213	0.05947	0.05545	0.019
OTU472	p__Bacteroidota	f__Rikenellaceae	g__Alistipes	0.001166	0.003298	0.06472	0.08073	0.013
OTU382	p__Firmicutes	f__Lachnospiraceae	g__Marvinbryantia	0.05597	0.06337	0.002915	0.00554	0.049
OTU812	p__Desulfobacterota	f__Desulfovibrionaceae	g__Bilophila	0.03906	0.03934	0.005247	0.01127	0.017
OTU865	p__Actinobacteriota	f__Eggerthellaceae	g__unclassified_f__Eggerthellaceae	0.01108	0.00554	0.03032	0.01557	0.014
OTU1052	p__Firmicutes	f__Ruminococcaceae	g__Negativibacillus	0.01166	0.01537	0.02915	0.01943	0.029
OTU661	p__Firmicutes	f__Anaerovoracaceae	g__Eubacterium_brachy_group	0.01166	0.01087	0.02624	0.01431	0.039
OTU457	p__Firmicutes	f__Christensenellaceae	g__unclassified_f__Christensenellaceae	0.03673	0.02954	0	0	0.001
OTU946	p__Firmicutes	f__Lachnospiraceae	g__Lachnospiraceae_NK4A136_group	0.009328	0.02101	0.0239	0.0241	0.046
OTU480	p__Firmicutes	f__Ruminococcaceae	g__norank_f__Ruminococcaceae	0.02915	0.0244	0.002915	0.006567	0.010
OTU634	p__Firmicutes	f__Lachnospiraceae	g__norank_f__Lachnospiraceae	0.02449	0.0217	0.006996	0.01087	0.032
OTU626	p__Bacteroidota	f__Marinifilaceae	g__Odoribacter	0.03148	0.03979	0	0	0.013
OTU289	p__Desulfobacterota	f__Desulfovibrionaceae	g__norank_f__Desulfovibrionaceae	0.003498	0.009894	0.0274	0.03245	0.028
OTU978	p__Firmicutes	f__Christensenellaceae	g__Christensenellaceae_R-7_group	0.009328	0.01142	0.02099	0.009328	0.029
OTU972	p__Proteobacteria	f__norank_o__Rhodospirillales	g__norank_f__norank_o__Rhodospirillales	0.002332	0.002493	0.02332	0.03074	0.034
OTU974	p__Firmicutes	f__Oscillospiraceae	g__unclassified_f__Oscillospiraceae	0.01749	0.0102	0.00583	0.006941	0.033
OTU645	p__Firmicutes	f__Butyricocccaceae	g__Butyricoccus	0.01749	0.01189	0.00583	0.006941	0.042
OTU135	p__Bacteroidota	f__Muribaculaceae	g__norank_f__Muribaculaceae	0.004664	0.01319	0.01574	0.01865	0.032
OTU283	p__Actinobacteriota	f__Eggerthellaceae	g__Enterorhabdus	0	0	0.01924	0.04168	0.032
OTU605	p__Firmicutes	f__UCG-010	g__norank_f__UCG-010	0.01341	0.01041	0.004081	0.006799	0.027
OTU22	p__Firmicutes	f__norank_o__Clostridia_vadinBB60_group	g__norank_f__norank_o__Clostridia_vadinBB60_group	0	0	0.01516	0.03219	0.032
OTU999	p__Firmicutes	f__Ruminococcaceae	g__Ruminococcus	0.01399	0.02188	0.001166	0.003298	0.046
OTU109	p__Actinobacteriota	f__Eggerthellaceae	g__Enterorhabdus	0.001166	0.002159	0.01341	0.01127	0.016
OTU260	p__Actinobacteriota	f__Eggerthellaceae	g__Enterorhabdus	0	0	0.01224	0.009308	0.004
OTU676	p__Firmicutes	f__Lachnospiraceae	g__norank_f__Lachnospiraceae	0.01224	0.01831	0	0	0.013
OTU102	p__Actinobacteriota	f__Eggerthellaceae	g__Enterorhabdus	0.000583	0.001649	0.01108	0.008245	0.009
OTU117	p__Firmicutes	f__UCG-010	g__norank_f__UCG-010	0.009911	0.0142	0	0	0.013
OTU508	p__Firmicutes	f__norank_o__Clostridia_UCG-014	g__norank_f__norank_o__Clostridia_UCG-014	0.001166	0.003298	0.007579	0.007453	0.046
OTU103	p__Actinobacteriota	f__Eggerthellaceae	g__unclassified_f__Eggerthellaceae	0.000583	0.001649	0.006413	0.006075	0.034
OTU899	p__Firmicutes	f__Lachnospiraceae	g__unclassified_f__Lachnospiraceae	0.006996	0.007884	0	0	0.013
OTU256	p__Firmicutes	f__UCG-010	g__norank_f__UCG-010	0.000583	0.001649	0.00583	0.009245	0.049
OTU694	p__Firmicutes	f__norank_o__RF39	g__norank_f__norank_o__RF39	0.003498	0.004134	0	0	0.032
OTU155	p__Bacteroidota	f__Marinifilaceae	g__Odoribacter	0	0	0.003498	0.004134	0.032
OTU257	p__Firmicutes	f__Ruminococcaceae	g__norank_f__Ruminococcaceae	0	0	0.002915	0.00347	0.032

Table S3. Discriminative fecal metabolites (PSD vs Sham)

Metabolite name	FC(PSD/Sham)	Up/down regulation
11alpha-(chloromethyl)-1alpha,25-dihydroxyvitamin D3	1.31	↑
12a-Hydroxy-3-oxocholadienic acid	1.15	↑
(ent-16betaOH)-16,17-Dihydroxy-9(11)-kauren-19-oic acid	1.14	↑
5',8-Dihydroxy-3',4',7-trimethoxyflavan	1.13	↑
(-)-Folicanthine	1.12	↑
(ent-6alpha,7alpha,12alpha)-6,7,12-Trihydroxy-16-kauren-19-oic acid	1.12	↑
Diketopiperazine derivative of Quinaprilat	1.11	↑
3-Indoleacetic Acid	1.09	↑
PC(20:4/0:0)	1.07	↑
11-Dodecenoic acid	1.07	↑
Kojibiose	1.06	↑
(12S,15S)-15-O-Demethyl-10,29-dideoxy-11,12-dihydro-striatin C	1.06	↑
3b-Hydroxy-5-cholenic acid	1.06	↑
Ricinoleic Acid methyl ester	0.94	↓
ADMA	0.92	↓
Thr Cys Asn Glu	0.92	↓
(S)-b-aminoisobutyric acid	0.92	↓
Asteltoxin	0.92	↓
Trichocarposide	0.91	↓
Gamma-Hydroxyphenylbutazone	0.89	↓
COUMARINIC ACID METHYL ETHER	0.86	↓
N-Acetylputrescine	0.85	↓
Citric acid	0.85	↓
(+/-)-Aegeline	0.82	↓
Malvidin	0.81	↓
4-p-Coumaroyl-1,5-quinolactone	0.81	↓
5,7-dihydroxy-2-(1-hydroxy-3,5-dimethoxy-4-oxocyclohex-2-en-1-yl)-4H-chromen-4-one	0.80	↓
Cis-Resveratrol 3-O-glucuronide	0.80	↓
Estradiol	0.77	↓
Adenosine diphosphate ribose	0.72	↓
20-Hydroxy-leukotriene E4	0.70	↓
2-Hydroxyestradiol	0.66	↓
3,4,5-trihydroxy-6-(3-hydroxy-4-[(E)-2-[2,3,5-trihydroxy-4-(3-methylbut-2-en-1-yl)phenyl]ethenyl]phenoxy)oxane-2-carboxylic acid	0.66	↓
2-(2-Aminoethyl)indole	0.65	↓

Table S4. Discriminative fecal metabolites (EA vs PSD)

Metabolite name	FC(EA/PSD)	Up/down regulation
3-Methylthiopropylamine	2.24	↑
2-amino-4-([1-[(carboxymethyl)-C-hydroxycarbonimidoyl]-2-[[1-(2-hydroxyphenyl)-3-oxopropyl]sulfanyl]ethyl]-C-hydroxycarbonimidoyl)butanoic acid	1.84	↑
Cis-2,3-Dimethylthiirane	1.55	↑
Melledonal C	1.44	↑
N1,N12-Diacetylspermine	1.14	↑
Salpha-Pregnan-20alpha-ol-3-one	1.11	↑
Valyl-Isoleucine	1.09	↑
Ile Phe	1.09	↑
Safynol	1.08	↑
ADMA	1.08	↑
5-Methoxytryptophol	1.08	↑
SECURININE	1.07	↑
N,O-Didesmethylvenlafaxine	1.07	↑
Alpha-Pyrrolidinopentiophenone	1.06	↑
COTARNINE	1.06	↑
(R)-Sulcatol	1.05	↑
1-Pyrroline-5-carboxylic acid	1.04	↑
Acetylcholine	1.04	↑
Citrulline	1.04	↑
L-Glutamate	1.04	↑
Aminoethoxyacetic acid	1.04	↑
4-Methylene-L-glutamine	1.04	↑
11-peroxy-5Z,8Z,12E,14Z-eicosatetraenoate	0.96	↓
Yucalexin B22	0.96	↓
Arnidenediol	0.94	↓
Cardanolmonoene	0.94	↓
PC(20:4(0:0))	0.93	↓
Diketopiperazine derivative of Quinaprilat	0.93	↓
10-Hydroxymelleotide	0.93	↓
21-hydroxyallopregnanolone	0.92	↓
5,20-DiHETE	0.92	↓
Salpha-pregnane-3,20-dione	0.92	↓
TetraHCA	0.92	↓
1b-Hydroxycholic acid	0.92	↓
(ent-16betaOH)-16,17-Dihydroxy-9(11)-kauren-19-oic acid	0.92	↓
LysoPC(20:4(5Z,8Z,11Z,14Z))	0.90	↓
Deoxyguanosine	0.89	↓
Deuteroporphyrin IX	0.87	↓
4-Vinylphenol sulfate	0.82	↓
Isobutyl 2-furanpropionate	0.69	↓

Table S5. KEGG pathway analysis (PSD vs Sham)

Pathway ID	Pathway Description	Enriched Metabolites	P value
map04913	Ovarian steroidogenesis	2	0.015
map00140	Steroid hormone biosynthesis	2	0.037
map01070	Biosynthesis of plant hormones	2	0.041
map05208	Chemical carcinogenesis - reactive oxygen species	2	0.044
map05224	Breast cancer	1	0.038
map04929	GnRH secretion	1	0.045
map04075	Plant hormone signal transduction	1	0.046
map05215	Prostate cancer	1	0.050
map04917	Prolactin signaling pathway	1	0.050

Table S6. KEGG pathway analysis (EA vs PSD)

Pathway ID	Pathway Description	Enriched Metabolites	P value
map00140	Steroid hormone biosynthesis	3	0.008
map05033	Nicotine addiction	2	0.003
map04721	Synaptic vesicle cycle	2	0.004
map00660	C5-Branched dibasic acid metabolism	2	0.008
map00220	Arginine biosynthesis	2	0.008
map00250	Alanine, aspartate and glutamate metabolism	2	0.010
map04742	Taste transduction	2	0.011
map00332	Carbapenem biosynthesis	2	0.011
map05022	Pathways of neurodegeneration - multiple diseases	2	0.011
map04080	Neuroactive ligand-receptor interaction	2	0.017
map00997	Biosynthesis of various secondary metabolites - part 3	2	0.017
map00564	Glycerophospholipid metabolism	2	0.017
map00330	Arginine and proline metabolism	2	0.028
map02010	ABC transporters	2	0.035
map04810	Regulation of actin cytoskeleton	1	0.032
map04068	FoxO signaling pathway	1	0.032
map05016	Huntington disease	1	0.034
map05034	Alcoholism	1	0.036
map04724	Glutamatergic synapse	1	0.036
map04720	Long-term potentiation	1	0.037
map05017	Spinocerebellar ataxia	1	0.037
map05030	Cocaine addiction	1	0.037
map04911	Insulin secretion	1	0.037
map04725	Cholinergic synapse	1	0.037
map04072	Phospholipase D signaling pathway	1	0.038
map05231	Choline metabolism in cancer	1	0.038
map04540	Gap junction	1	0.038
map04730	Long-term depression	1	0.038
map04727	GABAergic synapse	1	0.038
map05031	Amphetamine addiction	1	0.038
map04713	Circadian entrainment	1	0.038
map05014	Amyotrophic lateral sclerosis	1	0.039
map04971	Gastric acid secretion	1	0.039
map04972	Pancreatic secretion	1	0.039
map04964	Proximal tubule bicarbonate reclamation	1	0.043
map04970	Salivary secretion	1	0.043
map00910	Nitrogen metabolism	1	0.046
map04723	Retrograde endocannabinoid signaling	1	0.046