

**Supplementary file 1. CO-MO(Genus level ) Metastat analysis**

Taxa	mean.C O.	variance. CO.	standard .error.C O.	mean.M O.	variance. MO.	standard .error.M O.	p.value	q.v alu e
k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o _Bacteroidales;f_Rikenellaceae;g_Alistipes	0.09217 9909722 8342	0.00082 1157249 999059	0.00906 1772729 43357	0.01074 5502167 2486	0.00010 9719987 929871	0.00370 3376633 72683	0.00099 9000999 000999	0.042583 3361015 169
k_Bacteria;p_Firmicutes;c_Erysipelotrichia;o _Erysipelotrichales;f_Erysipelotrichaceae;g_ Turicibacter	0.00252 8762454 82506	2.28313 0634354 05e-06	0.00047 7821162 607314	0.01842 2381578 9401	0.00015 2079386 07379	0.00436 0037070 8543	0.00099 9000999 000999	0.042583 3361015 169
k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o _Bacteroidales;f_Prevotellaceae;g_Alloprev otella	0.04008 6683336 4502	0.00050 9583522 418577	0.00713 8511906 68319	0.00876 0890904 63499	5.27191 1650623 36e-05	0.00256 7078020 48929	0.00099 9000999 000999	0.042583 3361015 169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clo stridiales;f_Lachnospiraceae;g_Acetatifactor	0.00333 3960261 55412	6.79246 4284493 67e-06	0.00082 4164078 596833	0.02381 8841909 4337	0.00012 0580845 713174	0.00388 2345388 31191	0.00099 9000999 000999	0.042583 3361015 169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clo stridiales;f_Lachnospiraceae;g_Roseburia	0.05317 2212196 6488	0.00077 4204258 637177	0.00879 8887762 87763	0.00430 1393952 02664	2.89903 4196933 84e-05	0.00190 3626209 67649	0.00099 9000999 000999	0.042583 3361015 169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clo stridiales;f_Ruminococcaceae;g_Ruminococ cus	0.02611 4110211 373	0.00029 7308613 905474	0.00545 2601341 61185	0.00155 2696955 415	3.56427 3181270 34e-06	0.00066 7483443 733845	0.00099 9000999 000999	0.042583 3361015 169
k_Bacteria;p_Proteobacteria;c_Alphaproteo bacteria;o_Rhodospirillales;f_Acetobacterac	0 0	0 0	0 0	0.01436 6222642	0.00042 7803174	0.00731 2687386	0.00099 9000999	0.042583 3361015

eae;g_Acetobacter				0816	506014	53936	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Dorea	0.00014	1.32931	3.64597	0.00121	1.04565	0.00036	0.00099	0.042583
	5529217	1765121	2799022	1831927	0741344	1533321	9000999	3361015
	880315	3e-08	65e-05	68812	21e-06	656562	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Marvinbryantia	0.00651	1.89586	0.00137	0.00028	1.44655	0.00013	0.00099	0.042583
	7697744	0820933	6902618	6285860	3101509	4469006	9000999	3361015
	79074	91e-05	53695	813824	55e-07	722253	000999	169
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Thalassospira	0.00293	3.53386	0.00059	0.00019	1.59501	0.00014	0.00099	0.042583
	2710296	4497986	4463161	8945521	5718797	1200908	9000999	3361015
	35925	09e-06	010511	794757	71e-07	22998	000999	169
k_Bacteria;p_Firmicutes;c_Erysipelotrichia;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Holdemania	2.11841	2.03919	1.42800	0.00039	1.53214	0.00013	0.00099	0.042583
	6000202	5406913	3994011	5704073	5291341	8390086	9000999	3361015
	73e-05	56e-09	77e-05	165591	99e-07	862372	000999	169
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Paenibacillaceae;g_Aneurinibacillus	0	0	0	0.00164	5.53631	0.00083	0.00099	0.042583
				9981450	9543393	1889381	9000999	3361015
				58877	33e-06	422895	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Caldicoprobacteraceae;g_Caldicoprobacter	0	0	0	0.00132	3.28197	0.00064	0.00099	0.042583
				5168065	6986782	0505365	9000999	3361015
				12972	36e-06	588607	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Syntrophomonadaceae;g_Dethiobacter	0	0	0	0.00067	8.54572	0.00032	0.00099	0.042583
				0187236	1020469	6835605	9000999	3361015
				908555	12e-07	092016	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Gracilibacteraceae;g_Gracilibacter	0	0	0	0.00067	9.04364	0.00033	0.00099	0.042583
				3114589	7191847	6222530	9000999	3361015
				106748	22e-07	324918	000999	169

k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae_1;g_Candidatus_Arthromitus	0.00048	1.49962	0.00012	1.33926	1.43489	1.33926	0.00099	0.042583
	4435414	3309688	2459107	1798896	7732786	1798896	9000999	3361015
	541867	65e-07	855996	45e-05	68e-09	45e-05	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Family_XI;g_Sedimentibacter	0	0	0	0.00056	6.06196	0.00027	0.00099	0.042583
				3334213	1966913	5271728	9000999	3361015
				836161	93e-07	636313	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Family_XIV;g_Anaerobranca	0	0	0	0.00047	7.30064	0.00030	0.00099	0.042583
				8347727	7192636	2089539	9000999	3361015
				755804	81e-07	554021	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Syntrophomonadaceae;g_Syntrophomonas	0	0	0	0.00031	2.15526	0.00016	0.00099	0.042583
				9444891	3352349	4136503	9000999	3361015
				001596	87e-07	8752	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;s_bacterium_enrichment_culture_clone_BBMC-9	0	0	0	0.00027	1.45408	0.00013	0.00099	0.042583
				2857184	4714004	4818614	9000999	3361015
				206236	32e-07	905561	000999	169
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Delftia	0	0	0	6.26532	5.21842	2.55402	0.00099	0.042583
				9929112	8122064	3326553	9000999	3361015
				05e-05	52e-09	74e-05	000999	169
k_Bacteria;p_Actinobacteria;c_Actinobacteriales;o_Bifidobacteriales;f_Bifidobacteriaceae;g_Gardnerella	0	0	0	0.00036	7.55959	0.00030	0.00099	0.042583
				3808409	9214730	7400374	9000999	3361015
				212514	26e-07	404665	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Dehalobacter	0	0	0	0.00015	6.81841	9.23201	0.00099	0.042583
				7412939	1888470	7580457	9000999	3361015
				50675	31e-08	64e-05	000999	169
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria	0	0	0	8.46196	1.31004	4.04667	0.00099	0.042583

bacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Desulfovibrio				6185148	5512371	3807541	9000999	3361015
				4e-05	21e-08	21e-05	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Cellulosilyticum	0	0	0	0.00019	7.08457	9.41048	0.00099	0.042583
				0856790	3939953	2147553	9000999	3361015
				151943	91e-08	54e-05	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae_1;g_Clostridium_sensu_stricto_12	0	0	0	0.00010	2.41899	5.49885	0.00099	0.042583
				3720737	1842594	4247244	9000999	3361015
				370813	88e-08	24e-05	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Acetivibrio	0	0	0	0.00012	3.83223	6.92119	0.00099	0.042583
				4791582	3154595	3136478	9000999	3361015
				980224	18e-08	69e-05	000999	169
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Lactococcus	0	0	0	0.00019	1.43655	0.00013	0.00099	0.042583
				3829967	6961155	4003589	9000999	3361015
				594806	49e-07	558055	000999	169
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Pasteuriaceae;g_Pasteuria	0	0	0	6.34362	1.02327	3.57644	0.00099	0.042583
				5916636	4251365	0708591	9000999	3361015
				83e-05	39e-08	08e-05	000999	169
k_Bacteria;p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Atopobium	0	0	0	6.13118	7.86221	3.13492	0.00099	0.042583
				4046816	9129051	8055205	9000999	3361015
				05e-05	9e-09	55e-05	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Thermoanaerobacterales;f_Thermoanaerobacteraceae;g_Gelria	0	0	0	8.30456	1.50022	4.33045	0.00099	0.042583
				9343339	4290152	0741771	9000999	3361015
				15e-05	59e-08	28e-05	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Desulfitobact	0	0	0	3.64173	3.84598	2.19259	0.00099	0.042583
				9925654	8534524	7926696	9000999	3361015

erium				65e-05	21e-09	84e-05	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Cryptanaerobacter	0	0	0	6.38726	9.18448	3.38830	0.00099	0.042583
				4821984	8240198	4930234	9000999	3361015
				32e-05	76e-09	06e-05	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae_1;g_Clostridium_sensu_stricto_6	0	0	0	5.93154	1.00351	3.54173	0.00099	0.042583
				5098223	2633730	7980374	9000999	3361015
				68e-05	11e-08	37e-05	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Defluviitaleaceae;g_Defluviitalea	0	0	0	5.95793	6.77480	2.91006	0.00099	0.042583
				1876356	5707964	9953618	9000999	3361015
				31e-05	49e-09	92e-05	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Gracilibacteraceae;g_Lutispora	0	0	0	3.14542	3.08972	1.96523	0.00099	0.042583
				6180185	8448120	8041599	9000999	3361015
				78e-05	71e-09	77e-05	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Family_XI;g_Tissierella	0	0	0	4.30656	4.60262	2.39859	0.00099	0.042583
				7039175	1411685	8916994	9000999	3361015
				88e-05	97e-09	56e-05	000999	169
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Paenibacillaceae;g_Thermobacillus	0	0	0	6.64610	1.20209	3.87635	0.00099	0.042583
				0884370	3240247	9826318	9000999	3361015
				91e-05	93e-08	91e-05	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae_2;g_Alkaliphilus	0	0	0	3.23574	3.59372	2.11947	0.00099	0.042583
				8874520	3697753	0363602	9000999	3361015
				02e-05	05e-09	97e-05	000999	169
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Chromatiales;f_Ectothiorhodospiraceae;g_Thioalkalispira	0	0	0	4.63238	8.37227	3.23501	0.00099	0.042583
				3901403	1186270	7617083	9000999	3361015
				33e-05	01e-09	02e-05	000999	169

k_Bacteria;p_Actinobacteria;c_Nitriliruptoria;o_Nitriliruptorales;f_Nitriliruptoraceae;g_Nitriliruptor	0	0	0	6.63489	3.07339	6.19818	0.00099	0.042583
				1010493	8585932	3792383	9000999	3361015
				64e-05	88e-08	14e-05	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Family_XI;g_Peptoniphilus	0	0	0	4.89008	5.70979	2.67156	0.00099	0.042583
				4369265	7074600	2528418	9000999	3361015
				02e-05	99e-09	76e-05	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;s_bacterium_enrichment_culture_clone_LDC-11	0	0	0	3.12512	2.45367	1.75131	0.00099	0.042583
				9169331	2368547	1069080	9000999	3361015
				67e-05	36e-09	59e-05	000999	169
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_vadinBB60;g_Clostridiales_bacterium_JN18_A56_K	0	0	0	4.37050	4.85577	2.46368	0.00099	0.042583
				2955377	9467436	1053686	9000999	3361015
				48e-05	74e-09	93e-05	000999	169
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	0	0	0	4.68701	1.46808	4.28381	0.00099	0.042583
				0255913	7867258	8196508	9000999	3361015
				7e-05	93e-08	42e-05	000999	169
k_Bacteria;p_Proteobacteria;c_Epsilonproteobacteria;o_Epsilonproteobacteria;f_Synergistaceae;g_Synergista	0	0	0	5.22340	1.05484	3.63120	0.00099	0.042583

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obacteria;o__Campylobacteriales;f__Helicobac				1874468	9674793	1032015	9000999	3361015
teraceae;g__Wolinella				48e-05	01e-08	81e-05	000999	169
k__Bacteria;p__Proteobacteria;c__Gammaprot	0	0	0	3.70115	8.51763	3.26298	0.00099	0.042583
eobacteria;o__Enterobacteriales;f__Enterobact				2596513	5540941	0911096	9000999	3361015
eriaceae;g__Morganella				32e-05	65e-09	03e-05	000999	169
k__Bacteria;p__Proteobacteria;c__Gammaprot	0	0	0	3.83664	9.30227	3.40996	0.00099	0.042583
eobacteria;o__Xanthomonadales;f__Nevskiace				0071839	6266569	2658624	9000999	3361015
ae;g__Nevskia				64e-05	34e-09	24e-05	000999	169

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