

Supplementary file 2. CO-MO (Species level) Metastat analysis

Taxa	mean. CO.	varianc e.CO.	standar d.error. CO.	mean. MO.	varianc e.MO.	standar d.error. MO.	p.value	q.v alu e
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales; f_Lachnospiraceae;g_Blautia;s_Clostridiales_bacteri um_VE202-06	0.0297 006558 205442	0.0003 949325 954371	0.0062 843662 802003	0.1332 102314 40598	0.0019 414146 574876	0.0155 780882 070284	0.0009 990009 990009	0.03505 079487 35694
k_Bacteria;p_Firmicutes;c_Erysipelotrichia;o_Erysip elotrichales;f_Erysipelotrichaceae;g_Incertae_Sedis;s_ _Erysipelotrichaceae_bacterium_21_3	0.0082 590667 207132	5.4705 978595 7856e-	0.0023 389309 223614	0.0862 306632 4482	0.0010 032582 641788	0.0111 985393 25392	0.0009 990009 990009	0.03505 079487 35694
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales ;f_Ruminococcaceae;g_Anaerotruncus;s_Anaerotru ncus_sp_G32012	0.3733 020827 11393	0.0120 594424 337851	0.0347 267079 260115	0.0254 402509 629312	0.0010 769471 887408	0.0116 025169 076628	0.0009 990009 990009	0.03505 079487 35694
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f _Lactobacillaceae;g_Lactobacillus;s_mouse_gut_me tagenome	0.1620 469019 82967	0.0147 450566 12961	0.0383 992924 582746	0.0446 345074 8912	0.0006 034182 769860	0.0086 848882 90776	0.0009 990009 990009	0.03505 079487 35694
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Sta phylococcaceae;g_Staphylococcus;s_Staphylococcus _sp_SV3	0.0013 787245 837214	5.4233 695079 1425e-	0.0007 364352 997999	0.0003 194477 024526	4.4403 088434 7641e-	0.0002 355925 731924	0.0014 907850 854524	0.04922 866393 69432

	2	06	39	29	07	82	8	
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales	0	0	0	0.0047	6.0596	0.0027	0.0009	0.03505
;f_Clostridiaceae_1;g_Clostridium_sensu_stricto_1;s_				265284	278816	521872	990009	079487
Clostridium_butyricum				095966	8386e-	850707	990009	35694
				9	05		99	
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Bifi	0	0	0	0.0184	0.0025	0.0177	0.0009	0.03505
dobacteriales;f_Bifidobacteriaceae;g_Gardnerella;s_				339298	179395	409822	990009	079487
Gardnerella_vaginalis_0288E				455473	982262	100775	990009	35694
					8		99	
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Baci	0	0	0	0.0022	1.1635	0.0012	0.0009	0.03505
llaceae;g_Bacillus;s_Bacillus_coagulans				876146	285508	059895	990009	079487
				406336	6545e-	059998	990009	35694
				6	05	7	99	
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f	0	0	0	0.0018	9.4782	0.0010	0.0009	0.03505
_Lactobacillaceae;g_Lactobacillus;s_Lactobacillus_s				885411	988334	884793	990009	079487
p._EMML_3041				624956	7759e-	770139	990009	35694
					06	6	99	
k_Bacteria;p_Proteobacteria;c_Gammaproteobacter	0	0	0	0.0049	5.8500	0.0027	0.0009	0.03505
ia;o_Pseudomonadales;f_Moraxellaceae;g_Acinet				386482	757666	041809	990009	079487
bacter;s_Acinetobacter_calcoaceticus				725421	832e-	681221	990009	35694
				1	05	4	99	
k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacter	0	0	0	0.0039	8.1057	0.0031	0.0009	0.03505
oidales;f_Prevotellaceae;g_Prevotella;s_Prevotella_b				066130	743142	831144	990009	079487
ivia				833885	5383e-	957128	990009	35694
				5	05	5	99	

k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales; f_Clostridiaceae_1;g_Clostridium_sensu_stricto_6;s_ Clostridium_sp._M2_40	0	0	0	0.0009 669075 438176 45	1.8543 958619 5214e- 06	0.0004 814555 875093 95	0.0009 990009 990009 99	0.03505 079487 35694
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Pae nibacillaceae;g_Thermobacillus;s_Thermobacillus_co mposti_KWC4	0	0	0	0.0011 283422 121477 7	4.4731 992287 3044e- 06	0.0007 477632 670780 94	0.0009 990009 990009 99	0.03505 079487 35694
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_ _Lactobacillaceae;g_Lactobacillus;s_Lactobacillus_pl antarum	0	0	0	0.0009 188239 978885 86	4.7694 885288 0136e- 06	0.0007 721308 607355 17	0.0009 990009 990009 99	0.03505 079487 35694
k_Bacteria;p_Proteobacteria;c_Epsilonproteobacteri a;o_Campylobacteriales;f_Helicobacteraceae;g_Woli nella;s_Wolinella_succinogenes	0	0	0	0.0005 189914 851385 94	8.3797 076976 1856e- 07	0.0003 236454 019760 39	0.0009 990009 990009 99	0.03505 079487 35694
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Pae nibacillaceae;g_Paenibacillus;s_Bacillus_sp._DB10320 10	0	0	0	0.0006 701439 954522 89	1.2586 859185 7098e- 06	0.0003 966556 943009 55	0.0009 990009 990009 99	0.03505 079487 35694
k_Bacteria;p_Proteobacteria;c_Gammaproteobacter ia;o_Enterobacteriales;f_Enterobacteriaceae;g_Arse nophonus;s_secondary_endosymbiont_of_Bemisia_ta baci	0	0	0	0.0013 333333 333333 3	1.4222 222222 2222e- 05	0.0013 333333 333333 3	0.0009 990009 990009 99	0.03505 079487 35694