Table S4a. Correlation coeffencicies of CRC affecting bacteria species with their associated metabolites.

Type	Species	Metabolites	pvalue
Tumor promoting bacteria	Alistipes_finegoldii	X23.4_476.011mz_pos	0.000000387
Tumor promoting bacteria	Alistipes_finegoldii	X21.4_494.68mz_pos	0.000232816
Tumor promoting bacteria	Alistipes_finegoldii	X24.5_504.692mz_pos	0.000162744
Tumor promoting bacteria	Alistipes_finegoldii	X26.1_509.03mz_pos	0.000793675
Tumor promoting bacteria	Alistipes_finegoldii	X26.3_514.705mz_pos	0.000881926
Tumor promoting bacteria	Bilophila_wadsworthia	X23.4_476.011mz_pos	0.0000445
Tumor promoting bacteria	Fusobacterium_nucleatum	X21.2_512.336mz_neg	0.000581862
Tumor promoting bacteria	Fusobacterium_nucleatum	X19.2_536.299mz_neg	0.000431165
Tumor promoting bacteria	Fusobacterium_sp._oral_taxon_370	X21.2_512.336mz_neg	0.000850936
Tumor promoting bacteria	Fusobacterium_sp._oral_taxon_370	X19.2_536.299mz_neg	0.0000961
Tumor promoting bacteria	Odoribacter_splanchnicus	X23.4_476.011mz_pos	0.00000193
Tumor promoting bacteria	Odoribacter_splanchnicus	X21.4_494.68mz_pos	0.0000338
Tumor promoting bacteria	Odoribacter_splanchnicus	X24.8_495.024mz_pos	0.000618015
Tumor promoting bacteria	Odoribacter_splanchnicus	X22.9_499.686mz_pos	0.000395014
Tumor promoting bacteria	Odoribacter_splanchnicus	X24.5_504.692mz_pos	0.000898428
Tumor promoting bacteria	Odoribacter_splanchnicus	X26.1_509.03mz_pos	0.0000538
Tumor promoting bacteria	Odoribacter_splanchnicus	X24.5_509.699mz_pos	0.000471107
Tumor promoting bacteria	Odoribacter_splanchnicus	X22.8_514.027mz_pos	0.000873131
Tumor promoting bacteria	Odoribacter_splanchnicus	X28.1_519.043mz_pos	0.00036497
Tumor promoting bacteria	Odoribacter_splanchnicus	X22.8_519.703mz_pos	0.000941545
Tumor promoting bacteria	Odoribacter_splanchnicus	X27.6_534.052mz_pos	0.000351569
Tumor promoting bacteria	Odoribacter_splanchnicus	X24.1_539.384mz_pos	0.000829119
Tumor promoting bacteria	Odoribacter_splanchnicus	X22.5_543.378mz_pos	0.000446579
Tumor promoting bacteria	Odoribacter_splanchnicus	X25.7_544.056mz_pos	0.000751099
Tumor promoting bacteria	Odoribacter_splanchnicus	X27.3_549.062mz_pos	0.000605254
Tumor promoting bacteria	Odoribacter_splanchnicus	X26.9_563.068mz_pos	0.00078505
Tumor promoting bacteria	Odoribacter_splanchnicus	X28.6_568.075mz_pos	0.00028924
Tumor promoting bacteria	Odoribacter_splanchnicus	X29.9_587.088mz_pos	0.000433112
Tumor promoting bacteria	Odoribacter_splanchnicus	X28_597.091mz_pos	0.000744256
Tumor promoting bacteria	Odoribacter_splanchnicus	X21.3_635.934mz_pos	0.000546533
Tumor promoting bacteria	Parvimonas_micra	X26.9_483.368mz_pos	0.000267309
Tumor promoting bacteria	Parvimonas_sp._oral_taxon_110	X26.9_483.368mz_pos	0.00000626
Tumor promoting bacteria	Peptostreptococcus_stomatis	X29.6_447.311mz_neg	0.00014658
Tumor promoting bacteria	Peptostreptococcus_stomatis	X19.2_536.299mz_neg	0.0000327
Tumor promoting bacteria	Peptostreptococcus_stomatis	X23.5_714.829mz_pos	0.000873348
Tumor promoting bacteria	[Clostridium]_scindens	X9.9_193.09mz_neg	0.000489135
Tumor promoting bacteria	[Clostridium]_scindens	X27.4_355.227mz_pos	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X34.2_382.183mz_pos	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X9.9_386.067mz_neg	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X25.9_398.179mz_neg	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X7_461.195mz_pos	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X20.1_462.141mz_neg	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X22_471.005mz_pos	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X28.6_475.116mz_neg	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X20.6_476.358mz_pos	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X28.5_477.13mz_pos	0.000812702
Tumor promoting bacteria	[Clostridium]_scindens	X21.4_494.68mz_pos	0.00000613
Tumor promoting bacteria	[Clostridium]_scindens	X22.8_514.027mz_pos	0.000249066
Tumor promoting bacteria	[Clostridium]_scindens	X34.3_531.178mz_neg	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X21.6_542.426mz_pos	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X34.3_567.155mz_neg	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X41.9_572.415mz_pos	0.0000614
Tumor promoting bacteria	[Clostridium]_scindens	X41.8_572.415mz_pos	0.00000953
Tumor promoting bacteria	[Clostridium]_scindens	X25.4_629.391mz_neg	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X34.3_631.103mz_neg	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X16.7_646.473mz_pos	0.000469578
Tumor promoting bacteria	[Clostridium]_scindens	X34.3_694.016mz_neg	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X25.1_702.536mz_pos	0.000179331
Tumor promoting bacteria	[Clostridium]_scindens	X22.1_732.546mz_pos	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X26.2_776.038mz_pos	0.000964522

Tumor promoting bacteria	[Clostridium]_scindens	X25.7_776.038mz_pos	0.0000131
Tumor promoting bacteria	[Clostridium]_scindens	X26.5_804.604mz_pos	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X19_877.609mz_pos	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X19.5_938.662mz_pos	0.000351401
Tumor promoting bacteria	[Clostridium]_scindens	X27.2_950.698mz_pos	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X19.2_982.688mz_pos	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X26.4_994.724mz_pos	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X26_1038.751mz_pos	0.000552826
Tumor promoting bacteria	[Clostridium]_scindens	X20_1040.729mz_pos	0.0000097
Tumor promoting bacteria	[Clostridium]_scindens	X14_432.109mz_neg	0.000552826
Anti-tumor bacteria	Bifidobacterium_longum	X16_223.134mz_neg	0.000388097
Anti-tumor bacteria	Bifidobacterium_longum	X16_289.106mz_neg	0.000534335
Anti-tumor bacteria	Bifidobacterium_longum	X18.4_616.463mz_pos	0.000969352
Anti-tumor bacteria	Parabacteroides_distasonis	X23.4_476.011mz_pos	0.00000476
Anti-tumor bacteria	Parabacteroides_distasonis	X23.2_490.686mz_pos	0.000515566
Anti-tumor bacteria	Parabacteroides_distasonis	X21.4_494.68mz_pos	0.0000253
Anti-tumor bacteria	Parabacteroides_distasonis	X24.8_495.024mz_pos	0.000325704
Anti-tumor bacteria	Parabacteroides_distasonis	X22.9_499.686mz_pos	0.000396069
Anti-tumor bacteria	Parabacteroides_distasonis	X26.1_509.03mz_pos	0.000156007
Anti-tumor bacteria	Parabacteroides_distasonis	X24.5_509.699mz_pos	0.000740044
Anti-tumor bacteria	Parabacteroides_distasonis	X22.8_514.027mz_pos	0.00085905
Anti-tumor bacteria	Parabacteroides_distasonis	X26.3_514.705mz_pos	0.000707717
Anti-tumor bacteria	Parabacteroides_distasonis	X28.1_519.043mz_pos	0.000627966
Anti-tumor bacteria	Parabacteroides_distasonis	X27.6_534.052mz_pos	0.000633274
Anti-tumor bacteria	Parabacteroides_distasonis	X22.5_543.378mz_pos	0.00027199
Anti-tumor bacteria	Parabacteroides_distasonis	X28.6_568.075mz_pos	0.000701341
Anti-tumor bacteria	Parabacteroides_distasonis	X29.9_587.088mz_pos	0.000884732
others	Clostridiales_bacterium_VE202-26	X9.9_193.09mz_neg	0.0000443
others	Enterocloster_clostridioformis	X9.9_193.09mz_neg	0.000980048
others	Faecalibacillus_faecis	X9.9_193.09mz_neg	0.000373195
others	Firmicutes_bacterium_CAG:341	X9.9_193.09mz_neg	0.000122172
others	Hungatella_hathewayi	X9.9_193.09mz_neg	0.000983322
others	Lachnospiraceae_bacterium_5_1_57FAA	X9.9_193.09mz_neg	0.000320883
others	Bifidobacterium_bifidum	X16_223.134mz_neg	0.000786618
others	Human_endogenous_retrovirus_W	X16_223.134mz_neg	0.000774975
others	Bifidobacterium_bifidum	X16_289.106mz_neg	0.000716336
others	Amedibacterium_intestinale	X27.4_355.227mz_pos	0.0000982
others	Clostridiales_bacterium_VE202-01	X27.4_355.227mz_pos	2.81E-09
others	Clostridiales_bacterium_VE202-26	X27.4_355.227mz_pos	0.000661026
others	Clostridioides_difficile	X27.4_355.227mz_pos	0.0000379
others	Erysipelatoclostridium_ramosum	X27.4_355.227mz_pos	0.000236163
others	Erysipelatoclostridium_sp._An15	X27.4_355.227mz_pos	0.0000291
others	Erysipelatoclostridium_sp._An173	X27.4_355.227mz_pos	0.000000174
others	Erysipelotrichaceae_bacterium	X27.4_355.227mz_pos	0.000924475
others	Faecalibacillus_faecis	X27.4_355.227mz_pos	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X27.4_355.227mz_pos	0.000107763
others	Amedibacterium_intestinale	X34.2_382.183mz_pos	0.0000982
others	Clostridiales_bacterium_VE202-01	X34.2_382.183mz_pos	2.81E-09
others	Clostridiales_bacterium_VE202-26	X34.2_382.183mz_pos	0.000661026
others	Clostridioides_difficile	X34.2_382.183mz_pos	0.0000379
others	Erysipelatoclostridium_ramosum	X34.2_382.183mz_pos	0.000236163
others	Erysipelatoclostridium_sp._An15	X34.2_382.183mz_pos	0.0000291
others	Erysipelatoclostridium_sp._An173	X34.2_382.183mz_pos	0.000000174
others	Erysipelotrichaceae_bacterium	X34.2_382.183mz_pos	0.000924475
others	Faecalibacillus_faecis	X34.2_382.183mz_pos	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X34.2_382.183mz_pos	0.000107763
others	Amedibacterium_intestinale	X9.9_386.067mz_neg	0.0000982
others	Clostridiales_bacterium_VE202-01	X9.9_386.067mz_neg	2.81E-09
others	Clostridiales_bacterium_VE202-26	X9.9_386.067mz_neg	0.000661026
others	Clostridioides_difficile	X9.9_386.067mz_neg	0.0000379
others	Erysipelatoclostridium_ramosum	X9.9_386.067mz_neg	0.000236163
others	Erysipelatoclostridium_sp._An15	X9.9_386.067mz_neg	0.0000291
others	Erysipelatoclostridium_sp._An173	X9.9_386.067mz_neg	0.000000174

others	Erysipelotrichaceae_bacterium	X9.9_386.067mz_neg	0.000924475
others	Faecalibacillus_faecis	X9.9_386.067mz_neg	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X9.9_386.067mz_neg	0.000107763
others	Amedibacterium_intestinale	X25.9_398.179mz_neg	0.0000982
others	Clostridiales_bacterium_VE202-01	X25.9_398.179mz_neg	2.81E-09
others	Clostridiales_bacterium_VE202-26	X25.9_398.179mz_neg	0.000661026
others	Clostridioides_difficile	X25.9_398.179mz_neg	0.0000379
others	Erysipelatoclostridium_ramosum	X25.9_398.179mz_neg	0.000236163
others	Erysipelatoclostridium_sp._An15	X25.9_398.179mz_neg	0.0000291
others	Erysipelatoclostridium_sp._An173	X25.9_398.179mz_neg	0.000000174
others	Erysipelotrichaceae_bacterium	X25.9_398.179mz_neg	0.000924475
others	Faecalibacillus_faecis	X25.9_398.179mz_neg	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X25.9_398.179mz_neg	0.000107763
others	Amedibacterium_intestinale	X7_461.195mz_pos	0.0000982
others	Clostridiales_bacterium_VE202-01	X7_461.195mz_pos	2.81E-09
others	Clostridiales_bacterium_VE202-26	X7_461.195mz_pos	0.000661026
others	Clostridioides_difficile	X7_461.195mz_pos	0.0000379
others	Erysipelatoclostridium_ramosum	X7_461.195mz_pos	0.000236163
others	Erysipelatoclostridium_sp._An15	X7_461.195mz_pos	0.0000291
others	Erysipelatoclostridium_sp._An173	X7_461.195mz_pos	0.000000174
others	Erysipelotrichaceae_bacterium	X7_461.195mz_pos	0.000924475
others	Faecalibacillus_faecis	X7_461.195mz_pos	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X7_461.195mz_pos	0.000107763
others	Amedibacterium_intestinale	X20.1_462.141mz_neg	0.0000982
others	Clostridiales_bacterium_VE202-01	X20.1_462.141mz_neg	2.81E-09
others	Clostridiales_bacterium_VE202-26	X20.1_462.141mz_neg	0.000661026
others	Clostridioides_difficile	X20.1_462.141mz_neg	0.0000379
others	Erysipelatoclostridium_ramosum	X20.1_462.141mz_neg	0.000236163
others	Erysipelatoclostridium_sp._An15	X20.1_462.141mz_neg	0.0000291
others	Erysipelatoclostridium_sp._An173	X20.1_462.141mz_neg	0.000000174
others	Erysipelotrichaceae_bacterium	X20.1_462.141mz_neg	0.000924475
others	Faecalibacillus_faecis	X20.1_462.141mz_neg	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X20.1_462.141mz_neg	0.000107763
others	Amedibacterium_intestinale	X22_471.005mz_pos	0.0000982
others	Clostridiales_bacterium_VE202-01	X22_471.005mz_pos	2.81E-09
others	Clostridiales_bacterium_VE202-26	X22_471.005mz_pos	0.000661026
others	Clostridioides_difficile	X22_471.005mz_pos	0.0000379
others	Erysipelatoclostridium_ramosum	X22_471.005mz_pos	0.000236163
others	Erysipelatoclostridium_sp._An15	X22_471.005mz_pos	0.0000291
others	Erysipelatoclostridium_sp._An173	X22_471.005mz_pos	0.000000174
others	Erysipelotrichaceae_bacterium	X22_471.005mz_pos	0.000924475
others	Faecalibacillus_faecis	X22_471.005mz_pos	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X22_471.005mz_pos	0.000107763
others	Amedibacterium_intestinale	X28.6_475.116mz_neg	0.0000982
others	Clostridiales_bacterium_VE202-01	X28.6_475.116mz_neg	2.81E-09
others	Clostridiales_bacterium_VE202-26	X28.6_475.116mz_neg	0.000661026
others	Clostridioides_difficile	X28.6_475.116mz_neg	0.0000379
others	Erysipelatoclostridium_ramosum	X28.6_475.116mz_neg	0.000236163
others	Erysipelatoclostridium_sp._An15	X28.6_475.116mz_neg	0.0000291
others	Erysipelatoclostridium_sp._An173	X28.6_475.116mz_neg	0.000000174
others	Erysipelotrichaceae_bacterium	X28.6_475.116mz_neg	0.000924475
others	Faecalibacillus_faecis	X28.6_475.116mz_neg	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X28.6_475.116mz_neg	0.000107763
others	Alistipes_communis	X23.4_476.011mz_pos	3.66E-08
others	Alistipes_dispar	X23.4_476.011mz_pos	0.00015587
others	Alistipes_finegoldii_CAG:68	X23.4_476.011mz_pos	0.000135187
others	Alistipes_ihumii	X23.4_476.011mz_pos	0.00000765
others	Alistipes_indistinctus	X23.4_476.011mz_pos	0.000255082
others	Alistipes_onderdonkii	X23.4_476.011mz_pos	0.0000031
others	Alistipes_provencensis	X23.4_476.011mz_pos	0.0000472
others	Alistipes_putredinis	X23.4_476.011mz_pos	0.000129767
others	Alistipes_putredinis_CAG:67	X23.4_476.011mz_pos	0.000173359
others	Alistipes_senegalensis	X23.4_476.011mz_pos	0.000163049

others	Alistipes_shahii	X23.4_476.011mz_pos	0.000000958
others	Alistipes_sp._56_sp_Nov_56_25	X23.4_476.011mz_pos	0.000395059
others	Alistipes_sp._58_9_plus	X23.4_476.011mz_pos	0.000311167
others	Alistipes_sp._AF14-19	X23.4_476.011mz_pos	0.0000055
others	Alistipes_sp._CAG:268	X23.4_476.011mz_pos	0.000029
others	Alistipes_sp._CAG:29	X23.4_476.011mz_pos	0.00019956
others	Alistipes_sp._HGB5	X23.4_476.011mz_pos	0.000000597
others	Bacteroidaceae_bacterium	X23.4_476.011mz_pos	0.0000516
others	Bacteroidales_bacterium	X23.4_476.011mz_pos	0.00000202
others	Bacteroides_acidifaciens	X23.4_476.011mz_pos	0.0000306
others	Bacteroides_caccae	X23.4_476.011mz_pos	0.0000115
others	Bacteroides_cellulosilyticus	X23.4_476.011mz_pos	0.0000164
others	Bacteroides_clarus	X23.4_476.011mz_pos	0.00000429
others	Bacteroides_clarus_CAG:160	X23.4_476.011mz_pos	0.00000676
others	Bacteroides_congonensis	X23.4_476.011mz_pos	0.0000885
others	Bacteroides_eggerthii	X23.4_476.011mz_pos	0.00000515
others	Bacteroides_faecis	X23.4_476.011mz_pos	0.0000136
others	Bacteroides_faecis_CAG:32	X23.4_476.011mz_pos	0.0000494
others	Bacteroides_finegoldii	X23.4_476.011mz_pos	0.0000593
others	Bacteroides_finegoldii_CAG:203	X23.4_476.011mz_pos	0.000069
others	Bacteroides_fluxus	X23.4_476.011mz_pos	0.00000187
others	Bacteroides_ilei	X23.4_476.011mz_pos	0.0000851
others	Bacteroides_intestinalis	X23.4_476.011mz_pos	0.000246617
others	Bacteroides_nordii	X23.4_476.011mz_pos	0.0000619
others	Bacteroides_ovatus	X23.4_476.011mz_pos	0.000148039
others	Bacteroides_salyersiae	X23.4_476.011mz_pos	0.000174985
others	Bacteroides_sp._2_2_4	X23.4_476.011mz_pos	0.0000321
others	Bacteroides_sp._3_1_19	X23.4_476.011mz_pos	0.00000509
others	Bacteroides_sp._3_1_40A	X23.4_476.011mz_pos	0.000731975
others	Bacteroides_sp._44_46	X23.4_476.011mz_pos	0.00000366
others	Bacteroides_sp._4_1_36	X23.4_476.011mz_pos	0.00000288
others	Bacteroides_sp._9_1_42FAA	X23.4_476.011mz_pos	0.000178045
others	Bacteroides_sp._AM16-15	X23.4_476.011mz_pos	0.0000623
others	Bacteroides_sp._AM26-11	X23.4_476.011mz_pos	0.000210582
others	Bacteroides_sp._CAG:633	X23.4_476.011mz_pos	0.0000879
others	Bacteroides_sp._CAG:754	X23.4_476.011mz_pos	0.0000725
others	Bacteroides_sp._D2	X23.4_476.011mz_pos	0.0000995
others	Bacteroides_sp._D20	X23.4_476.011mz_pos	0.000000978
others	Bacteroides_sp._D22	X23.4_476.011mz_pos	0.000522127
others	Bacteroides_sp._HPS0048	X23.4_476.011mz_pos	0.000116192
others	Bacteroides_sp._NMBE5	X23.4_476.011mz_pos	1.9E-10
others	Bacteroides_sp._OF03-11BH	X23.4_476.011mz_pos	0.00000466
others	Bacteroides_sp._OF04-15BH	X23.4_476.011mz_pos	0.000149929
others	Bacteroides_sp._OM08-17BH	X23.4_476.011mz_pos	0.0000108
others	Bacteroides_stercoris	X23.4_476.011mz_pos	0.0000695
others	Bacteroides_stercoris_CAG:120	X23.4_476.011mz_pos	0.00000651
others	Bacteroides_thetaiotaomicron	X23.4_476.011mz_pos	0.00000416
others	Bacteroides_uniformis	X23.4_476.011mz_pos	0.000000575
others	Bacteroides_xylanisolvens	X23.4_476.011mz_pos	0.000419175
others	Bacteroidetes_bacterium_ADurb.BinA104	X23.4_476.011mz_pos	0.000232949
others	Barnesiella_intestinihominis	X23.4_476.011mz_pos	0.000155133
others	Butyricimonas_faecalis	X23.4_476.011mz_pos	0.0000339
others	Butyricimonas_faecihominis	X23.4_476.011mz_pos	0.00000409
others	Butyricimonas_paravirosa	X23.4_476.011mz_pos	0.0000946
others	Butyricimonas_sp._Marseille-P3923	X23.4_476.011mz_pos	0.00000248
others	Butyricimonas_virosa	X23.4_476.011mz_pos	0.0000827
others	Clostridiales_bacterium_59_14	X23.4_476.011mz_pos	0.000216966
others	Coprobacter_fastidiosus	X23.4_476.011mz_pos	0.000529565
others	Coprobacter_secundus	X23.4_476.011mz_pos	0.000000342
others	Cronobacter_sakazakii	X23.4_476.011mz_pos	0.000803201
others	Desulfovibrio_fairfieldensis	X23.4_476.011mz_pos	0.000201863
others	Desulfovibrio_legallii	X23.4_476.011mz_pos	0.0000146
others	Desulfovibrio_piger	X23.4_476.011mz_pos	0.000692565

others	Enterobacter_hormaechei	X23.4_476.011mz_pos	0.00021778
others	Erysipelatoclostridium_ramosum	X23.4_476.011mz_pos	0.000608748
others	Eubacterium_sp._45_250	X23.4_476.011mz_pos	0.000459415
others	Firmicutes_bacterium_CAG:103	X23.4_476.011mz_pos	0.000447385
others	Firmicutes_bacterium_CAG:124	X23.4_476.011mz_pos	0.000301852
others	Firmicutes_bacterium_CAG:129	X23.4_476.011mz_pos	0.000214362
others	Firmicutes_bacterium_CAG:129_59_24	X23.4_476.011mz_pos	0.0000568
others	Firmicutes_bacterium_CAG:170	X23.4_476.011mz_pos	0.000448731
others	Firmicutes_bacterium_CAG:176_63_11	X23.4_476.011mz_pos	0.000772856
others	Firmicutes_bacterium_CAG:24053_14	X23.4_476.011mz_pos	0.0000307
others	Firmicutes_bacterium_CAG:466	X23.4_476.011mz_pos	0.000728712
others	Firmicutes_bacterium_CAG:83	X23.4_476.011mz_pos	0.000251494
others	Intestinimonas_butyriciproducens	X23.4_476.011mz_pos	0.000369213
others	Methanobrevibacter_smithii	X23.4_476.011mz_pos	0.000714593
others	Parabacteroides_bouchesdurhonensis	X23.4_476.011mz_pos	0.00059477
others	Parabacteroides_goldsteinii	X23.4_476.011mz_pos	0.000221186
others	Parabacteroides_johnsonii	X23.4_476.011mz_pos	0.00000112
others	Parabacteroides_massiliensis	X23.4_476.011mz_pos	0.0000184
others	Parabacteroides_merdae	X23.4_476.011mz_pos	0.00000658
others	Parabacteroides_sp._20_3	X23.4_476.011mz_pos	0.0000399
others	Parabacteroides_sp._AM58-2XD	X23.4_476.011mz_pos	0.00032565
others	Parabacteroides_sp._CAG:409	X23.4_476.011mz_pos	0.000327283
others	Parabacteroides_sp._D13	X23.4_476.011mz_pos	0.00000178
others	Parabacteroides_sp._TM07-1AC	X23.4_476.011mz_pos	0.000200907
others	Paraprevotella_clara	X23.4_476.011mz_pos	0.0000511
others	Paraprevotella_clara_CAG:116	X23.4_476.011mz_pos	0.00000139
others	Paraprevotella_xylaniphila	X23.4_476.011mz_pos	0.0000293
others	Phascolarctobacterium_succinatutens	X23.4_476.011mz_pos	0.000358421
others	Phocaeicola_dorei	X23.4_476.011mz_pos	0.000713804
others	Prevotella_bivia	X23.4_476.011mz_pos	0.0000233
others	Prevotella_intermedia	X23.4_476.011mz_pos	0.000929236
others	Prevotella_marseillensis	X23.4_476.011mz_pos	0.000193247
others	Prevotella_rara	X23.4_476.011mz_pos	0.000381681
others	Prevotella_sp._CAG:891	X23.4_476.011mz_pos	0.000506141
others	Prevotella_sp._MGM2	X23.4_476.011mz_pos	0.000276786
others	Prevotella_sp._P3-122	X23.4_476.011mz_pos	0.0000451
others	Rikenellaceae_bacterium	X23.4_476.011mz_pos	0.000000951
others	Ruthenibacterium_lactatiformans	X23.4_476.011mz_pos	0.000574391
others	Salmonella_enterica	X23.4_476.011mz_pos	0.000446965
others	Streptococcus_pneumoniae	X23.4_476.011mz_pos	0.000282439
others	uncultured_Bacteroides_sp.	X23.4_476.011mz_pos	0.0000953
others	Amedibacterium_intestinale	X20.6_476.358mz_pos	0.0000982
others	Clostridiales_bacterium_VE202-01	X20.6_476.358mz_pos	2.81E-09
others	Clostridiales_bacterium_VE202-26	X20.6_476.358mz_pos	0.000661026
others	Clostridioides_difficile	X20.6_476.358mz_pos	0.0000379
others	Erysipelatoclostridium_ramosum	X20.6_476.358mz_pos	0.000236163
others	Erysipelatoclostridium_sp._An15	X20.6_476.358mz_pos	0.0000291
others	Erysipelatoclostridium_sp._An173	X20.6_476.358mz_pos	0.000000174
others	Erysipelotrichaceae_bacterium	X20.6_476.358mz_pos	0.000924475
others	Faecalibacillus_faecis	X20.6_476.358mz_pos	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X20.6_476.358mz_pos	0.000107763
others	Clostridiales_bacterium_VE202-01	X28.5_477.13mz_pos	0.00000191
others	Clostridiales_bacterium_VE202-26	X28.5_477.13mz_pos	0.000626054
others	Clostridioides_difficile	X28.5_477.13mz_pos	0.000825165
others	Clostridium_sp._CAG:169	X28.5_477.13mz_pos	0.000144458
others	Erysipelatoclostridium_sp._An15	X28.5_477.13mz_pos	0.0000151
others	Erysipelatoclostridium_sp._An173	X28.5_477.13mz_pos	0.00000117
others	Faecalibacillus_faecis	X28.5_477.13mz_pos	0.000137414
others	Lachnospiraceae_bacterium_5_1_57FAA	X28.5_477.13mz_pos	0.000474585
others	Prevotella_intermedia	X26.9_483.368mz_pos	0.000791742
others	Bacteroides_eggerthii	X23.2_490.686mz_pos	0.000351714
others	Bacteroides_sp._3_1_19	X23.2_490.686mz_pos	0.00038014
others	Bacteroides_sp._NMBE5	X23.2_490.686mz_pos	0.00045569

others	Parabacteroides_merdae	X23.2_490.686mz_pos	0.000959236
others	Parabacteroides_sp._D13	X23.2_490.686mz_pos	0.000506827
others	Paraprevotella_clara_CAG:116	X23.2_490.686mz_pos	0.000502848
others	Alistipes_communis	X21.4_494.68mz_pos	0.000782917
others	Alistipes_ihumii	X21.4_494.68mz_pos	0.000547848
others	Alistipes_onderdonkii	X21.4_494.68mz_pos	0.000636042
others	Alistipes_sp._AF14-19	X21.4_494.68mz_pos	0.000237341
others	Alistipes_sp._HGB5	X21.4_494.68mz_pos	0.000363221
others	Bacteroidaceae_bacterium	X21.4_494.68mz_pos	0.000166383
others	Bacteroidales_bacterium	X21.4_494.68mz_pos	0.0000957
others	Bacteroides_caccae	X21.4_494.68mz_pos	0.000126971
others	Bacteroides_cellulosilyticus	X21.4_494.68mz_pos	0.000289405
others	Bacteroides_clarus	X21.4_494.68mz_pos	0.000493953
others	Bacteroides_clarus_CAG:160	X21.4_494.68mz_pos	0.000288205
others	Bacteroides_congonensis	X21.4_494.68mz_pos	0.000215344
others	Bacteroides_eggerthii	X21.4_494.68mz_pos	0.0000785
others	Bacteroides_faecis	X21.4_494.68mz_pos	0.0000616
others	Bacteroides_finegoldii	X21.4_494.68mz_pos	0.000713623
others	Bacteroides_fluxus	X21.4_494.68mz_pos	0.000289987
others	Bacteroides_ovatus	X21.4_494.68mz_pos	0.000251035
others	Bacteroides_sp._2_2_4	X21.4_494.68mz_pos	0.0000695
others	Bacteroides_sp._3_1_19	X21.4_494.68mz_pos	0.0000135
others	Bacteroides_sp._3_1_40A	X21.4_494.68mz_pos	0.000098
others	Bacteroides_sp._44_46	X21.4_494.68mz_pos	0.000536114
others	Bacteroides_sp._4_1_36	X21.4_494.68mz_pos	0.000172942
others	Bacteroides_sp._4_3_47FAA	X21.4_494.68mz_pos	0.000505528
others	Bacteroides_sp._9_1_42FAA	X21.4_494.68mz_pos	0.0000542
others	Bacteroides_sp._AM16-15	X21.4_494.68mz_pos	0.0000556
others	Bacteroides_sp._AM26-11	X21.4_494.68mz_pos	0.000201777
others	Bacteroides_sp._AM28-6	X21.4_494.68mz_pos	0.00069271
others	Bacteroides_sp._CAG:633	X21.4_494.68mz_pos	0.0000695
others	Bacteroides_sp._CAG:754	X21.4_494.68mz_pos	0.000291265
others	Bacteroides_sp._D20	X21.4_494.68mz_pos	0.0000161
others	Bacteroides_sp._D22	X21.4_494.68mz_pos	0.0000658
others	Bacteroides_sp._NMBE5	X21.4_494.68mz_pos	0.000104227
others	Bacteroides_sp._OF03-11BH	X21.4_494.68mz_pos	0.000373521
others	Bacteroides_stercoris	X21.4_494.68mz_pos	0.000567863
others	Bacteroides_thetaiotaomicron	X21.4_494.68mz_pos	0.000472705
others	Bacteroides_uniformis	X21.4_494.68mz_pos	0.0000247
others	Bacteroides_xylanisolvens	X21.4_494.68mz_pos	0.000372556
others	Bacteroidetes_bacterium_ADurb.BinA104	X21.4_494.68mz_pos	0.000101002
others	Blautia_hansenii	X21.4_494.68mz_pos	0.000603006
others	Blautia_producta	X21.4_494.68mz_pos	0.000688257
others	Blautia_sp._Marseille-P3201T	X21.4_494.68mz_pos	0.0008456
others	Butyricimonas_faecalis	X21.4_494.68mz_pos	0.000485957
others	Butyricimonas_faecihominis	X21.4_494.68mz_pos	0.0000396
others	Butyricimonas_sp._Marseille-P3923	X21.4_494.68mz_pos	0.000141806
others	Clostridiales_bacterium_VE202-01	X21.4_494.68mz_pos	0.000163674
others	Clostridioides_difficile	X21.4_494.68mz_pos	0.000777628
others	Coprobacter_fastidiosus	X21.4_494.68mz_pos	0.000747298
others	Coprobacter_secundus	X21.4_494.68mz_pos	0.000841376
others	Dorea_sp._D27	X21.4_494.68mz_pos	0.000121936
others	Erysipelatoclostridium_ramosum	X21.4_494.68mz_pos	0.0000288
others	Erysipelatoclostridium_sp._An15	X21.4_494.68mz_pos	0.0000682
others	Erysipelatoclostridium_sp._An173	X21.4_494.68mz_pos	0.000281047
others	Lachnospiraceae_bacterium_5_1_57FAA	X21.4_494.68mz_pos	0.000125555
others	Lachnospiraceae_bacterium_6_1_63FAA	X21.4_494.68mz_pos	0.000664878
others	Parabacteroides_johnsonii	X21.4_494.68mz_pos	0.000158902
others	Parabacteroides_merdae	X21.4_494.68mz_pos	0.000185766
others	Parabacteroides_sp._20_3	X21.4_494.68mz_pos	0.0000227
others	Parabacteroides_sp._D13	X21.4_494.68mz_pos	0.0000482
others	Paraprevotella_clara	X21.4_494.68mz_pos	0.000362892
others	Phocaeicola_dorei	X21.4_494.68mz_pos	0.000126509

others	Phocaeicola_vulgatus	X21.4_494.68mz_pos	0.000202661
others	Prevotella_bivia	X21.4_494.68mz_pos	0.0000333
others	Prevotella_intermedia	X21.4_494.68mz_pos	0.000319938
others	Shigella_flexneri	X21.4_494.68mz_pos	0.000994577
others	uncultured_Bacteroides_sp.	X21.4_494.68mz_pos	0.000140887
others	Bacteroides_eggerthii	X24.8_495.024mz_pos	0.000211876
others	Bacteroides_faecis	X24.8_495.024mz_pos	0.000982299
others	Bacteroides_sp._3_1_19	X24.8_495.024mz_pos	0.000191926
others	Bacteroides_sp._NMBE5	X24.8_495.024mz_pos	0.0000361
others	Bacteroides_stercoris	X24.8_495.024mz_pos	0.000858282
others	Parabacteroides_merdae	X24.8_495.024mz_pos	0.000398945
others	Parabacteroides_sp._20_3	X24.8_495.024mz_pos	0.000999516
others	Parabacteroides_sp._D13	X24.8_495.024mz_pos	0.000209759
others	Paraprevotella_clara	X24.8_495.024mz_pos	0.000697734
others	Paraprevotella_clara_CAG:116	X24.8_495.024mz_pos	0.0000499
others	Paraprevotella_xylaniphila	X24.8_495.024mz_pos	0.000609684
others	Prevotella_bivia	X24.8_495.024mz_pos	0.000952543
others	Bacteroides_sp._3_1_19	X22.9_499.686mz_pos	0.000136178
others	Bacteroides_sp._NMBE5	X22.9_499.686mz_pos	0.000371589
others	Butyricimonas_faecihominis	X22.9_499.686mz_pos	0.000992573
others	Parabacteroides_sp._D13	X22.9_499.686mz_pos	0.000629281
others	Alistipes_communis	X24.5_504.692mz_pos	0.000166373
others	Alistipes_ihumii	X24.5_504.692mz_pos	0.000254131
others	Alistipes_indistinctus	X24.5_504.692mz_pos	0.000656826
others	Alistipes_onderdonkii	X24.5_504.692mz_pos	0.000726132
others	Alistipes_shahii	X24.5_504.692mz_pos	0.000420513
others	Alistipes_sp._AF14-19	X24.5_504.692mz_pos	0.00088918
others	Alistipes_sp._HGB5	X24.5_504.692mz_pos	0.000178379
others	Bacteroides_eggerthii	X24.5_504.692mz_pos	0.000701252
others	Bacteroides_fluxus	X24.5_504.692mz_pos	0.000362137
others	Bacteroides_sp._44_46	X24.5_504.692mz_pos	0.000387592
others	Bacteroides_sp._D20	X24.5_504.692mz_pos	0.000279725
others	Bacteroides_sp._NMBE5	X24.5_504.692mz_pos	0.000055
others	Bacteroides_stercoris_CAG:120	X24.5_504.692mz_pos	0.000737599
others	Bacteroides_uniformis	X24.5_504.692mz_pos	0.000262456
others	Butyricimonas_faecihominis	X24.5_504.692mz_pos	0.000436346
others	Clostridiales_bacterium_VE202-01	X24.5_504.692mz_pos	0.000529536
others	Desulfovibrio_legallii	X24.5_504.692mz_pos	0.000750348
others	Firmicutes_bacterium_CAG:24053_14	X24.5_504.692mz_pos	0.00085144
others	Paraprevotella_clara_CAG:116	X24.5_504.692mz_pos	0.000279787
others	Rikenellaceae_bacterium	X24.5_504.692mz_pos	0.000489212
others	Alistipes_ihumii	X26.1_509.03mz_pos	0.000745179
others	Alistipes_sp._AF14-19	X26.1_509.03mz_pos	0.000633543
others	Alistipes_sp._HGB5	X26.1_509.03mz_pos	0.000436554
others	Bacteroides_faecis	X26.1_509.03mz_pos	0.000624275
others	Bacteroides_sp._3_1_19	X26.1_509.03mz_pos	0.0000835
others	Bacteroides_sp._4_1_36	X26.1_509.03mz_pos	0.000908415
others	Bacteroides_sp._D20	X26.1_509.03mz_pos	0.000309698
others	Bacteroides_sp._NMBE5	X26.1_509.03mz_pos	0.00015681
others	Bacteroides_uniformis	X26.1_509.03mz_pos	0.0004387
others	Butyricimonas_faecalis	X26.1_509.03mz_pos	0.000877486
others	Butyricimonas_faecihominis	X26.1_509.03mz_pos	0.000110851
others	Parabacteroides_sp._20_3	X26.1_509.03mz_pos	0.000345465
others	Parabacteroides_sp._D13	X26.1_509.03mz_pos	0.000251671
others	Paraprevotella_clara_CAG:116	X26.1_509.03mz_pos	0.000361764
others	Prevotella_bivia	X26.1_509.03mz_pos	0.000998916
others	Bacteroides_caccae	X24.5_509.699mz_pos	0.000849861
others	Bacteroides_sp._3_1_19	X24.5_509.699mz_pos	0.000410771
others	Bacteroides_sp._NMBE5	X24.5_509.699mz_pos	0.000021
others	Parabacteroides_merdae	X24.5_509.699mz_pos	0.000613595
others	Parabacteroides_sp._D13	X24.5_509.699mz_pos	0.000507127
others	Paraprevotella_clara_CAG:116	X24.5_509.699mz_pos	0.00013234
others	Paraprevotella_xylaniphila	X24.5_509.699mz_pos	0.000549849

others	Amedibacterium_intestinale	X22.8_514.027mz_pos	0.00040322
others	Bacteroidales_bacterium	X22.8_514.027mz_pos	0.000856633
others	Bacteroides_sp._3_1_19	X22.8_514.027mz_pos	0.000353054
others	Bacteroides_sp._AM16-15	X22.8_514.027mz_pos	0.000772476
others	Bacteroides_sp._NMBE5	X22.8_514.027mz_pos	0.000409592
others	Blautia_sp._Marseille-P3201T	X22.8_514.027mz_pos	0.00057685
others	Clostridioides_difficile	X22.8_514.027mz_pos	0.000751909
others	Erysipelatoclostridium_sp._An15	X22.8_514.027mz_pos	0.000447135
others	Intestinibacter_bartlettii	X22.8_514.027mz_pos	0.000282196
others	Lachnospiraceae_bacterium_5_1_57FAA	X22.8_514.027mz_pos	0.000222015
others	Lachnospiraceae_bacterium_6_1_63FAA	X22.8_514.027mz_pos	0.000423294
others	Parabacteroides_merdae	X22.8_514.027mz_pos	0.000455062
others	Parabacteroides_sp._20_3	X22.8_514.027mz_pos	0.000985353
others	Peptostreptococcaceae_bacterium	X22.8_514.027mz_pos	0.0000597
others	Prevotella_intermedia	X22.8_514.027mz_pos	0.000476531
others	uncultured_Bacteroides_sp.	X22.8_514.027mz_pos	0.000770087
others	Alistipes_ihumii	X26.3_514.705mz_pos	0.000480135
others	Alistipes_indistinctus	X26.3_514.705mz_pos	0.000831906
others	Alistipes_onderdonkii	X26.3_514.705mz_pos	0.000754885
others	Bacteroidales_bacterium	X26.3_514.705mz_pos	0.000624263
others	Bacteroides_eggerthii	X26.3_514.705mz_pos	0.000701272
others	Bacteroides_sp._3_1_19	X26.3_514.705mz_pos	0.00072793
others	Coprobacter_secundus	X26.3_514.705mz_pos	0.000613667
others	Parabacteroides_sp._D13	X26.3_514.705mz_pos	0.000566295
others	Paraprevotella_clara	X26.3_514.705mz_pos	0.000564362
others	Paraprevotella_clara_CAG:116	X26.3_514.705mz_pos	0.0000505
others	Paraprevotella_xylaniphila	X26.3_514.705mz_pos	0.000320385
others	Bacteroides_caccae	X28.1_519.043mz_pos	0.000735419
others	Bacteroides_sp._3_1_19	X28.1_519.043mz_pos	0.00037083
others	Bacteroides_sp._NMBE5	X28.1_519.043mz_pos	0.0000468
others	Bacteroides_stercoris	X28.1_519.043mz_pos	0.000946482
others	Parabacteroides_merdae	X28.1_519.043mz_pos	0.000474456
others	Parabacteroides_sp._D13	X28.1_519.043mz_pos	0.00035902
others	Paraprevotella_clara	X28.1_519.043mz_pos	0.000733103
others	Paraprevotella_clara_CAG:116	X28.1_519.043mz_pos	0.0000805
others	Paraprevotella_xylaniphila	X28.1_519.043mz_pos	0.000384942
others	Prevotella_sp._CAG:891	X28.1_519.043mz_pos	0.000657322
others	Bacteroides_sp._3_1_19	X22.8_519.703mz_pos	0.000919577
others	Bacteroides_sp._NMBE5	X22.8_519.703mz_pos	0.0000373
others	Parabacteroides_merdae	X22.8_519.703mz_pos	0.000874345
others	Paraprevotella_clara_CAG:116	X22.8_519.703mz_pos	0.000235708
others	Paraprevotella_xylaniphila	X22.8_519.703mz_pos	0.000837452
others	Amedibacterium_intestinale	X34.3_531.178mz_neg	0.0000982
others	Clostridiales_bacterium_VE202-01	X34.3_531.178mz_neg	2.81E-09
others	Clostridiales_bacterium_VE202-26	X34.3_531.178mz_neg	0.000661026
others	Clostridioides_difficile	X34.3_531.178mz_neg	0.0000379
others	Erysipelatoclostridium_ramosum	X34.3_531.178mz_neg	0.000236163
others	Erysipelatoclostridium_sp._An15	X34.3_531.178mz_neg	0.0000291
others	Erysipelatoclostridium_sp._An173	X34.3_531.178mz_neg	0.000000174
others	Erysipelotrichaceae_bacterium	X34.3_531.178mz_neg	0.000924475
others	Faecalibacillus_faecis	X34.3_531.178mz_neg	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X34.3_531.178mz_neg	0.000107763
others	Bacteroides_caccae	X27.6_534.052mz_pos	0.000715823
others	Bacteroides_sp._3_1_19	X27.6_534.052mz_pos	0.000365582
others	Bacteroides_sp._NMBE5	X27.6_534.052mz_pos	0.0000323
others	Bacteroides_stercoris	X27.6_534.052mz_pos	0.000987658
others	Parabacteroides_merdae	X27.6_534.052mz_pos	0.000476079
others	Parabacteroides_sp._D13	X27.6_534.052mz_pos	0.000384145
others	Paraprevotella_clara	X27.6_534.052mz_pos	0.00078406
others	Paraprevotella_clara_CAG:116	X27.6_534.052mz_pos	0.0000929
others	Paraprevotella_xylaniphila	X27.6_534.052mz_pos	0.000399652
others	Prevotella_sp._CAG:891	X27.6_534.052mz_pos	0.000664055
others	Fusobacterium_pseudoperiodonticum	X19.2_536.299mz_neg	0.000123234

others	Bacteroides_sp._3_1_19	X24.1_539.384mz_pos	0.000913223
others	Bacteroides_sp._NMBE5	X24.1_539.384mz_pos	0.0000269
others	Parabacteroides_merdae	X24.1_539.384mz_pos	0.000830644
others	Paraprevotella_clara_CAG:116	X24.1_539.384mz_pos	0.000190233
others	Paraprevotella_xylaniphila	X24.1_539.384mz_pos	0.0007068
others	Prevotella_sp._CAG:891	X24.1_539.384mz_pos	0.000834384
others	Amedibacterium_intestinale	X21.6_542.426mz_pos	0.0000982
others	Clostridiales_bacterium_VE202-01	X21.6_542.426mz_pos	2.81E-09
others	Clostridiales_bacterium_VE202-26	X21.6_542.426mz_pos	0.000661026
others	Clostridioides_difficile	X21.6_542.426mz_pos	0.0000379
others	Erysipelatoclostridium_ramosum	X21.6_542.426mz_pos	0.000236163
others	Erysipelatoclostridium_sp._An15	X21.6_542.426mz_pos	0.0000291
others	Erysipelatoclostridium_sp._An173	X21.6_542.426mz_pos	0.000000174
others	Erysipelotrichaceae_bacterium	X21.6_542.426mz_pos	0.000924475
others	Faecalibacillus_faecis	X21.6_542.426mz_pos	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X21.6_542.426mz_pos	0.000107763
others	Bacteroides_eggerthii	X22.5_543.378mz_pos	0.000161605
others	Bacteroides_faecis	X22.5_543.378mz_pos	0.000638737
others	Bacteroides_sp._3_1_19	X22.5_543.378mz_pos	0.000209274
others	Bacteroides_sp._AM16-15	X22.5_543.378mz_pos	0.000995176
others	Bacteroides_sp._AM26-11	X22.5_543.378mz_pos	0.000369334
others	Bacteroides_sp._NMBE5	X22.5_543.378mz_pos	0.000335807
others	Bacteroides_stercoris	X22.5_543.378mz_pos	0.000896963
others	Coprobacter_fastidiosus	X22.5_543.378mz_pos	0.000761775
others	Parabacteroides_johnsonii	X22.5_543.378mz_pos	0.000699738
others	Parabacteroides_merdae	X22.5_543.378mz_pos	0.000164539
others	Parabacteroides_sp._20_3	X22.5_543.378mz_pos	0.000381104
others	Parabacteroides_sp._D13	X22.5_543.378mz_pos	0.000227157
others	Paraprevotella_clara	X22.5_543.378mz_pos	0.000687816
others	Paraprevotella_clara_CAG:116	X22.5_543.378mz_pos	0.000180864
others	Phocaeicola_vulgatus	X22.5_543.378mz_pos	0.00090115
others	Prevotella_bivia	X22.5_543.378mz_pos	0.000851319
others	Bacteroides_sp._3_1_19	X25.7_544.056mz_pos	0.000766591
others	Bacteroides_sp._NMBE5	X25.7_544.056mz_pos	0.0000317
others	Parabacteroides_merdae	X25.7_544.056mz_pos	0.000671126
others	Parabacteroides_sp._D13	X25.7_544.056mz_pos	0.000841295
others	Paraprevotella_clara_CAG:116	X25.7_544.056mz_pos	0.000168999
others	Paraprevotella_xylaniphila	X25.7_544.056mz_pos	0.000475742
others	Prevotella_sp._CAG:891	X25.7_544.056mz_pos	0.00065608
others	Bacteroidales_bacterium_KA00251	X27.3_549.062mz_pos	0.000890245
others	Bacteroides_caccae	X27.3_549.062mz_pos	0.000737885
others	Bacteroides_sp._3_1_19	X27.3_549.062mz_pos	0.000681554
others	Bacteroides_sp._NMBE5	X27.3_549.062mz_pos	0.0000438
others	Parabacteroides_merdae	X27.3_549.062mz_pos	0.000534433
others	Parabacteroides_sp._D13	X27.3_549.062mz_pos	0.000589509
others	Paraprevotella_clara	X27.3_549.062mz_pos	0.000889925
others	Paraprevotella_clara_CAG:116	X27.3_549.062mz_pos	0.0000769
others	Paraprevotella_xylaniphila	X27.3_549.062mz_pos	0.000399492
others	Prevotella_sp._CAG:891	X27.3_549.062mz_pos	0.000500494
others	Bacteroidales_bacterium_KA00251	X26.9_563.068mz_pos	0.000863573
others	Bacteroides_caccae	X26.9_563.068mz_pos	0.000810444
others	Bacteroides_sp._3_1_19	X26.9_563.068mz_pos	0.00098682
others	Bacteroides_sp._NMBE5	X26.9_563.068mz_pos	0.0000308
others	Parabacteroides_merdae	X26.9_563.068mz_pos	0.000685576
others	Parabacteroides_sp._D13	X26.9_563.068mz_pos	0.000865038
others	Paraprevotella_clara_CAG:116	X26.9_563.068mz_pos	0.000108125
others	Paraprevotella_xylaniphila	X26.9_563.068mz_pos	0.000447447
others	Prevotella_sp._CAG:891	X26.9_563.068mz_pos	0.000398023
others	Amedibacterium_intestinale	X34.3_567.155mz_neg	0.0000982
others	Clostridiales_bacterium_VE202-01	X34.3_567.155mz_neg	2.81E-09
others	Clostridiales_bacterium_VE202-26	X34.3_567.155mz_neg	0.000661026
others	Clostridioides_difficile	X34.3_567.155mz_neg	0.0000379
others	Erysipelatoclostridium_ramosum	X34.3_567.155mz_neg	0.000236163

others	Erysipelatoclostridium_sp._An15	X34.3_567.155mz_neg	0.0000291
others	Erysipelatoclostridium_sp._An173	X34.3_567.155mz_neg	0.000000174
others	Erysipelotrichaceae_bacterium	X34.3_567.155mz_neg	0.000924475
others	Faecalibacillus_faecis	X34.3_567.155mz_neg	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X34.3_567.155mz_neg	0.000107763
others	Bacteroidales_bacterium_KA00251	X28.6_568.075mz_pos	0.000156614
others	Bacteroides_caccae	X28.6_568.075mz_pos	0.000832615
others	Bacteroides_ilei	X28.6_568.075mz_pos	0.00088044
others	Bacteroides_sp._3_1_19	X28.6_568.075mz_pos	0.000396887
others	Bacteroides_sp._AM16-15	X28.6_568.075mz_pos	0.000974229
others	Bacteroides_sp._NMBE5	X28.6_568.075mz_pos	0.0000275
others	Bacteroides_sp._OF04-15BH	X28.6_568.075mz_pos	0.000726112
others	Bacteroides_stercoris	X28.6_568.075mz_pos	0.000527501
others	Bacteroides_stercoris_CAG:120	X28.6_568.075mz_pos	0.000677491
others	Methanobrevibacter_smithii	X28.6_568.075mz_pos	0.000848424
others	Parabacteroides_merdae	X28.6_568.075mz_pos	0.00069684
others	Parabacteroides_sp._CAG:409	X28.6_568.075mz_pos	0.000817142
others	Parabacteroides_sp._D13	X28.6_568.075mz_pos	0.00031115
others	Paraprevotella_clara	X28.6_568.075mz_pos	0.00043493
others	Paraprevotella_clara_CAG:116	X28.6_568.075mz_pos	0.0000289
others	Paraprevotella_xylaniphila	X28.6_568.075mz_pos	0.000156185
others	Prevotella_bivia	X28.6_568.075mz_pos	0.000887081
others	Prevotella_sp._CAG:891	X28.6_568.075mz_pos	0.000361095
others	Clostridiales_bacterium_VE202-26	X41.9_572.415mz_pos	0.00000743
others	Dorea_sp._D27	X41.9_572.415mz_pos	0.000926141
others	Erysipelatoclostridium_sp._An15	X41.9_572.415mz_pos	0.000068
others	Erysipelatoclostridium_sp._An173	X41.9_572.415mz_pos	0.000647254
others	Lachnospiraceae_bacterium_5_1_57FAA	X41.9_572.415mz_pos	0.0000542
others	Blautia_producta	X41.8_572.415mz_pos	0.000851419
others	Clostridiales_bacterium_VE202-01	X41.8_572.415mz_pos	0.0000351
others	Clostridiales_bacterium_VE202-26	X41.8_572.415mz_pos	0.00000394
others	Clostridioides_difficile	X41.8_572.415mz_pos	0.00033941
others	Dorea_sp._D27	X41.8_572.415mz_pos	0.000261635
others	Erysipelatoclostridium_ramosum	X41.8_572.415mz_pos	0.000387476
others	Erysipelatoclostridium_sp._An15	X41.8_572.415mz_pos	0.0000736
others	Erysipelatoclostridium_sp._An173	X41.8_572.415mz_pos	0.00000918
others	Lachnospiraceae_bacterium_5_1_57FAA	X41.8_572.415mz_pos	0.0000151
others	Sutterella_sp._AM11-39	X41.8_572.415mz_pos	0.00029884
others	Bacteroidales_bacterium_KA00251	X29.9_587.088mz_pos	0.000566318
others	Bacteroides_caccae	X29.9_587.088mz_pos	0.000647311
others	Bacteroides_sp._3_1_19	X29.9_587.088mz_pos	0.000562561
others	Bacteroides_sp._NMBE5	X29.9_587.088mz_pos	0.0001179
others	Bacteroides_sp._OF04-15BH	X29.9_587.088mz_pos	0.000795978
others	Methanobrevibacter_smithii	X29.9_587.088mz_pos	0.000712419
others	Parabacteroides_merdae	X29.9_587.088mz_pos	0.000479369
others	Parabacteroides_sp._CAG:409	X29.9_587.088mz_pos	0.000730331
others	Parabacteroides_sp._D13	X29.9_587.088mz_pos	0.000419011
others	Paraprevotella_clara	X29.9_587.088mz_pos	0.00069802
others	Paraprevotella_clara_CAG:116	X29.9_587.088mz_pos	0.0000661
others	Paraprevotella_xylaniphila	X29.9_587.088mz_pos	0.000309011
others	Prevotella_sp._CAG:891	X29.9_587.088mz_pos	0.000347005
others	Bacteroidales_bacterium_KA00251	X28_597.091mz_pos	0.000608847
others	Bacteroides_caccae	X28_597.091mz_pos	0.000615772
others	Bacteroides_sp._NMBE5	X28_597.091mz_pos	0.000121319
others	Parabacteroides_merdae	X28_597.091mz_pos	0.000715752
others	Parabacteroides_sp._D13	X28_597.091mz_pos	0.000833222
others	Paraprevotella_clara	X28_597.091mz_pos	0.000761471
others	Paraprevotella_clara_CAG:116	X28_597.091mz_pos	0.0000732
others	Paraprevotella_xylaniphila	X28_597.091mz_pos	0.00013867
others	Prevotella_sp._CAG:891	X28_597.091mz_pos	0.000369241
others	Bacteroides_sp._NMBE5	X18.4_616.463mz_pos	0.000612236
others	Amedibacterium_intestinale	X25.4_629.391mz_neg	0.0000982
others	Clostridiales_bacterium_VE202-01	X25.4_629.391mz_neg	2.81E-09

others	Clostridiales_bacterium_VE202-26	X25.4_629.391mz_neg	0.000661026
others	Clostridioides_difficile	X25.4_629.391mz_neg	0.0000379
others	Erysipelatoclostridium_ramosum	X25.4_629.391mz_neg	0.000236163
others	Erysipelatoclostridium_sp._An15	X25.4_629.391mz_neg	0.0000291
others	Erysipelatoclostridium_sp._An173	X25.4_629.391mz_neg	0.000000174
others	Erysipelotrichaceae_bacterium	X25.4_629.391mz_neg	0.000924475
others	Faecalibacillus_faecis	X25.4_629.391mz_neg	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X25.4_629.391mz_neg	0.000107763
others	Amedibacterium_intestinale	X34.3_631.103mz_neg	0.0000982
others	Clostridiales_bacterium_VE202-01	X34.3_631.103mz_neg	2.81E-09
others	Clostridiales_bacterium_VE202-26	X34.3_631.103mz_neg	0.000661026
others	Clostridioides_difficile	X34.3_631.103mz_neg	0.0000379
others	Erysipelatoclostridium_ramosum	X34.3_631.103mz_neg	0.000236163
others	Erysipelatoclostridium_sp._An15	X34.3_631.103mz_neg	0.0000291
others	Erysipelatoclostridium_sp._An173	X34.3_631.103mz_neg	0.000000174
others	Erysipelotrichaceae_bacterium	X34.3_631.103mz_neg	0.000924475
others	Faecalibacillus_faecis	X34.3_631.103mz_neg	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X34.3_631.103mz_neg	0.000107763
others	Clostridiales_bacterium_VE202-01	X16.7_646.473mz_pos	0.000202478
others	Erysipelatoclostridium_sp._An15	X16.7_646.473mz_pos	0.000104902
others	Erysipelatoclostridium_sp._An173	X16.7_646.473mz_pos	0.0000752
others	Lachnospiraceae_bacterium_5_1_57FAA	X16.7_646.473mz_pos	0.000414862
others	Amedibacterium_intestinale	X34.3_694.016mz_neg	0.0000982
others	Clostridiales_bacterium_VE202-01	X34.3_694.016mz_neg	2.81E-09
others	Clostridiales_bacterium_VE202-26	X34.3_694.016mz_neg	0.000661026
others	Clostridioides_difficile	X34.3_694.016mz_neg	0.0000379
others	Erysipelatoclostridium_ramosum	X34.3_694.016mz_neg	0.000236163
others	Erysipelatoclostridium_sp._An15	X34.3_694.016mz_neg	0.0000291
others	Erysipelatoclostridium_sp._An173	X34.3_694.016mz_neg	0.000000174
others	Erysipelotrichaceae_bacterium	X34.3_694.016mz_neg	0.000924475
others	Faecalibacillus_faecis	X34.3_694.016mz_neg	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X34.3_694.016mz_neg	0.000107763
others	Clostridiales_bacterium_VE202-26	X25.1_702.536mz_pos	0.0000373
others	Erysipelatoclostridium_sp._An173	X25.1_702.536mz_pos	0.000949987
others	Lachnospiraceae_bacterium_5_1_57FAA	X25.1_702.536mz_pos	0.000673879
others	Amedibacterium_intestinale	X22.1_732.546mz_pos	0.0000982
others	Clostridiales_bacterium_VE202-01	X22.1_732.546mz_pos	2.81E-09
others	Clostridiales_bacterium_VE202-26	X22.1_732.546mz_pos	0.000661026
others	Clostridioides_difficile	X22.1_732.546mz_pos	0.0000379
others	Erysipelatoclostridium_ramosum	X22.1_732.546mz_pos	0.000236163
others	Erysipelatoclostridium_sp._An15	X22.1_732.546mz_pos	0.0000291
others	Erysipelatoclostridium_sp._An173	X22.1_732.546mz_pos	0.000000174
others	Erysipelotrichaceae_bacterium	X22.1_732.546mz_pos	0.000924475
others	Faecalibacillus_faecis	X22.1_732.546mz_pos	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X22.1_732.546mz_pos	0.000107763
others	Amedibacterium_intestinale	X25.7_776.038mz_pos	0.000205757
others	Clostridiales_bacterium_VE202-26	X25.7_776.038mz_pos	0.000428271
others	Intestinibacter_bartlettii	X25.7_776.038mz_pos	0.0000274
others	Lachnospiraceae_bacterium_5_1_57FAA	X25.7_776.038mz_pos	0.000165168
others	Peptostreptococcaceae_bacterium	X25.7_776.038mz_pos	0.000274962
others	Amedibacterium_intestinale	X26.5_804.604mz_pos	0.0000982
others	Clostridiales_bacterium_VE202-01	X26.5_804.604mz_pos	2.81E-09
others	Clostridiales_bacterium_VE202-26	X26.5_804.604mz_pos	0.000661026
others	Clostridioides_difficile	X26.5_804.604mz_pos	0.0000379
others	Erysipelatoclostridium_ramosum	X26.5_804.604mz_pos	0.000236163
others	Erysipelatoclostridium_sp._An15	X26.5_804.604mz_pos	0.0000291
others	Erysipelatoclostridium_sp._An173	X26.5_804.604mz_pos	0.000000174
others	Erysipelotrichaceae_bacterium	X26.5_804.604mz_pos	0.000924475
others	Faecalibacillus_faecis	X26.5_804.604mz_pos	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X26.5_804.604mz_pos	0.000107763
others	Amedibacterium_intestinale	X19_877.609mz_pos	0.0000982
others	Clostridiales_bacterium_VE202-01	X19_877.609mz_pos	2.81E-09
others	Clostridiales_bacterium_VE202-26	X19_877.609mz_pos	0.000661026

others	Clostridioides_difficile	X19_877.609mz_pos	0.0000379
others	Erysipelatoclostridium_ramosum	X19_877.609mz_pos	0.000236163
others	Erysipelatoclostridium_sp._An15	X19_877.609mz_pos	0.0000291
others	Erysipelatoclostridium_sp._An173	X19_877.609mz_pos	0.000000174
others	Erysipelotrichaceae_bacterium	X19_877.609mz_pos	0.000924475
others	Faecalibacillus_faecis	X19_877.609mz_pos	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X19_877.609mz_pos	0.000107763
others	Amedibacterium_intestinale	X19.5_938.662mz_pos	0.000292248
others	Clostridiales_bacterium_VE202-01	X19.5_938.662mz_pos	0.00000213
others	Clostridioides_difficile	X19.5_938.662mz_pos	0.000312775
others	Clostridium_sp._AT4	X19.5_938.662mz_pos	0.000276508
others	Dorea_sp._D27	X19.5_938.662mz_pos	0.000710786
others	Erysipelatoclostridium_ramosum	X19.5_938.662mz_pos	0.0000318
others	Erysipelatoclostridium_sp._An15	X19.5_938.662mz_pos	0.0000678
others	Erysipelatoclostridium_sp._An173	X19.5_938.662mz_pos	0.0000873
others	Lachnospiraceae_bacterium_5_1_57FAA	X19.5_938.662mz_pos	0.000836637
others	Amedibacterium_intestinale	X27.2_950.698mz_pos	0.0000982
others	Clostridiales_bacterium_VE202-01	X27.2_950.698mz_pos	2.81E-09
others	Clostridiales_bacterium_VE202-26	X27.2_950.698mz_pos	0.000661026
others	Clostridioides_difficile	X27.2_950.698mz_pos	0.0000379
others	Erysipelatoclostridium_ramosum	X27.2_950.698mz_pos	0.000236163
others	Erysipelatoclostridium_sp._An15	X27.2_950.698mz_pos	0.0000291
others	Erysipelatoclostridium_sp._An173	X27.2_950.698mz_pos	0.000000174
others	Erysipelotrichaceae_bacterium	X27.2_950.698mz_pos	0.000924475
others	Faecalibacillus_faecis	X27.2_950.698mz_pos	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X27.2_950.698mz_pos	0.000107763
others	Amedibacterium_intestinale	X19.2_982.688mz_pos	0.0000982
others	Clostridiales_bacterium_VE202-01	X19.2_982.688mz_pos	2.81E-09
others	Clostridiales_bacterium_VE202-26	X19.2_982.688mz_pos	0.000661026
others	Clostridioides_difficile	X19.2_982.688mz_pos	0.0000379
others	Erysipelatoclostridium_ramosum	X19.2_982.688mz_pos	0.000236163
others	Erysipelatoclostridium_sp._An15	X19.2_982.688mz_pos	0.0000291
others	Erysipelatoclostridium_sp._An173	X19.2_982.688mz_pos	0.000000174
others	Erysipelotrichaceae_bacterium	X19.2_982.688mz_pos	0.000924475
others	Faecalibacillus_faecis	X19.2_982.688mz_pos	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X19.2_982.688mz_pos	0.000107763
others	Amedibacterium_intestinale	X26.4_994.724mz_pos	0.0000982
others	Clostridiales_bacterium_VE202-01	X26.4_994.724mz_pos	2.81E-09
others	Clostridiales_bacterium_VE202-26	X26.4_994.724mz_pos	0.000661026
others	Clostridioides_difficile	X26.4_994.724mz_pos	0.0000379
others	Erysipelatoclostridium_ramosum	X26.4_994.724mz_pos	0.000236163
others	Erysipelatoclostridium_sp._An15	X26.4_994.724mz_pos	0.0000291
others	Erysipelatoclostridium_sp._An173	X26.4_994.724mz_pos	0.000000174
others	Erysipelotrichaceae_bacterium	X26.4_994.724mz_pos	0.000924475
others	Faecalibacillus_faecis	X26.4_994.724mz_pos	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X26.4_994.724mz_pos	0.000107763
others	Amedibacterium_intestinale	X26_1038.751mz_pos	0.0000982
others	Clostridiales_bacterium_VE202-01	X26_1038.751mz_pos	2.81E-09
others	Clostridiales_bacterium_VE202-26	X26_1038.751mz_pos	0.000661026
others	Clostridioides_difficile	X26_1038.751mz_pos	0.0000379
others	Erysipelatoclostridium_ramosum	X26_1038.751mz_pos	0.000236163
others	Erysipelatoclostridium_sp._An15	X26_1038.751mz_pos	0.0000291
others	Erysipelatoclostridium_sp._An173	X26_1038.751mz_pos	0.000000174
others	Erysipelotrichaceae_bacterium	X26_1038.751mz_pos	0.000924475
others	Faecalibacillus_faecis	X26_1038.751mz_pos	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X26_1038.751mz_pos	0.000107763
others	Blautia_producta	X20_1040.729mz_pos	0.000877877
others	Clostridiales_bacterium_VE202-01	X20_1040.729mz_pos	0.0000401
others	Clostridiales_bacterium_VE202-26	X20_1040.729mz_pos	0.00000397
others	Clostridioides_difficile	X20_1040.729mz_pos	0.000362537
others	Dorea_sp._D27	X20_1040.729mz_pos	0.000268934
others	Erysipelatoclostridium_ramosum	X20_1040.729mz_pos	0.000406664
others	Erysipelatoclostridium_sp._An15	X20_1040.729mz_pos	0.0000786

others	Erysipelatoclostridium_sp._An173	X20_1040.729mz_pos	0.0000103
others	Lachnospiraceae_bacterium_5_1_57FAA	X20_1040.729mz_pos	0.0000158
others	Sutterella_sp._AM11-39	X20_1040.729mz_pos	0.000262191
others	Amedibacterium_intestinale	X14_432.109mz_neg	0.0000982
others	Clostridiales_bacterium_VE202-01	X14_432.109mz_neg	2.81E-09
others	Clostridiales_bacterium_VE202-26	X14_432.109mz_neg	0.000661026
others	Clostridioides_difficile	X14_432.109mz_neg	0.0000379
others	Erysipelatoclostridium_ramosum	X14_432.109mz_neg	0.000236163
others	Erysipelatoclostridium_sp._An15	X14_432.109mz_neg	0.0000291
others	Erysipelatoclostridium_sp._An173	X14_432.109mz_neg	0.000000174
others	Erysipelotrichaceae_bacterium	X14_432.109mz_neg	0.000924475
others	Faecalibacillus_faecis	X14_432.109mz_neg	0.000386653
others	Lachnospiraceae_bacterium_5_1_57FAA	X14_432.109mz_neg	0.000107763
others	Bacteroidales_bacterium_KA00251	X21.3_635.934mz_pos	0.0000175
others	Bacteroides_ilei	X21.3_635.934mz_pos	0.000348037
others	Bacteroides_sp._3_1_19	X21.3_635.934mz_pos	0.000953838
others	Bacteroides_sp._NMBE5	X21.3_635.934mz_pos	0.0000877
others	Bacteroides_sp._OF04-15BH	X21.3_635.934mz_pos	0.000401382
others	Bacteroides_stercoris	X21.3_635.934mz_pos	0.000483549
others	Bacteroides_stercoris_CAG:120	X21.3_635.934mz_pos	0.000406466
others	Methanobrevibacter_smithii	X21.3_635.934mz_pos	0.00097126
others	Parabacteroides_sp._CAG:409	X21.3_635.934mz_pos	0.000481461
others	Parabacteroides_sp._D13	X21.3_635.934mz_pos	0.000640588
others	Paraprevotella_clara	X21.3_635.934mz_pos	0.00047228
others	Paraprevotella_clara_CAG:116	X21.3_635.934mz_pos	0.0000279
others	Paraprevotella_xylaniphila	X21.3_635.934mz_pos	0.000167047
others	Prevotella_sp._CAG:891	X21.3_635.934mz_pos	0.0003158
others	Bacteroidales_bacterium_KA00251	X23.5_714.829mz_pos	0.00086088
others	Prevotella_sp._885	X23.5_714.829mz_pos	0.000475227