

Table S1 Meaningful SNPs from saliva screened according to selection criteria

| SNP         | chr.<br>exposure | pos.exposure | effect_allele.<br>exposure | other_allele.<br>exposure | eaf.<br>exposure | beta.<br>exposure | se.exposure | pval.<br>exposure | samplesize.<br>exposure | exposure                                                                                                                                                | id.exposure                       | maf    | R2        | F.value   | mr_keep.<br>exposure | pval_origin.<br>exposure |
|-------------|------------------|--------------|----------------------------|---------------------------|------------------|-------------------|-------------|-------------------|-------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------|--------|-----------|-----------|----------------------|--------------------------|
| rs73547069  | 19               | 41163234     | G                          | A                         | 0.3              | 0.124             | 0.02225     | 2.84E-08          | 1898                    | k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Streptococcaceae g__Streptococcus s__Streptococcus_infantis_l_mgs_1798                       | pheno.1000.assoc.linear.gz.raw.gz | 0.3    | 0.0064579 | 12.323802 | TRUE                 | Reported                 |
| rs11001287  | 10               | 75075572     | C                          | A                         | 0.3183           | -0.1227           | 0.02235     | 4.61E-08          | 1888                    | k__Bacteria p__Bacteroidota c__Bacteroidia o__Bacteroidales f__Porphyromonadaceae g__Porphyromonas s__Porphyromonas_catoniae_mgs_3071                   | pheno.1110.assoc.linear.gz.raw.gz | 0.3183 | 0.0065335 | 12.403308 | TRUE                 | Reported                 |
| rs9668910   | 12               | 97704823     | G                          | T                         | 0.2744           | 0.1326            | 0.02267     | 5.79E-09          | 1881                    | k__Bacteria p__Spirochaetota c__Spirochaetia o__Treponematales f__Treponemataceae g__Treponema_B s__Treponema_B_denticola_mgs_3534                      | pheno.1343.assoc.linear.gz.raw.gz | 0.2744 | 0.0070016 | 13.248804 | TRUE                 | Reported                 |
| rs7112471   | 11               | 14233717     | C                          | T                         | 0.3543           | 0.1308            | 0.02209     | 3.82E-09          | 1897                    | k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Enterobacterales f__Pasteurellaceae g__Aggregatibacter s__unclassified_mgs_2536                 | pheno.1348.assoc.linear.gz.raw.gz | 0.3543 | 0.0078279 | 14.950979 | TRUE                 | Reported                 |
| rs12843069  | X                | 5416233      | A                          | G                         | 0.2671           | 0.1303            | 0.02258     | 9.36E-09          | 1902                    | k__Bacteria p__Firmicutes c__Clostridia o__Peptostreptococcales f__Filifactoraceae g__Peptoanaerobacter s__unclassified_mgs_555                         | pheno.1385.assoc.linear.gz.raw.gz | 0.2671 | 0.0066472 | 12.714155 | TRUE                 | Reported                 |
| rs1629126   | 1                | 53099456     | T                          | C                         | 0.241            | 0.126             | 0.02199     | 1.19E-08          | 1915                    | k__Bacteria p__Spirochaetota c__Spirochaetia o__Treponematales f__Treponemataceae g__Treponema_D s__unclassified_mgs_79                                 | pheno.1548.assoc.linear.gz.raw.gz | 0.241  | 0.005808  | 11.175697 | TRUE                 | Reported                 |
| rs7112471   | 11               | 14233717     | C                          | T                         | 0.3543           | 0.1241            | 0.02224     | 2.73E-08          | 1900                    | k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Enterobacterales f__Pasteurellaceae g__Aggregatibacter s__unclassified_mgs_1980                 | pheno.177.assoc.linear.gz.raw.gz  | 0.3543 | 0.0070465 | 13.469231 | TRUE                 | Reported                 |
| rs1343652   | 10               | 97699551     | A                          | C                         | 0.3577           | -0.1299           | 0.02281     | 1.44E-08          | 1903                    | k__Bacteria p__Bacteroidota c__Bacteroidia o__Flavobacteriales f__Flavobacteriaceae g__Capnocytophaga s__Capnocytophaga_sputigena_mgs_3341              | pheno.188.assoc.linear.gz.raw.gz  | 0.3577 | 0.0077536 | 14.854832 | TRUE                 | Reported                 |
| rs1850921   | 17               | 22533151     | C                          | T                         | 0.4799           | -0.1542           | 0.02263     | 1.28E-11          | 1912                    | k__Bacteria p__Firmicutes c__Bacilli o__Erysipelotrichales f__Erysipelatoclostridiaceae g__Eggerthia                                                    | pheno.2010.assoc.linear.gz.raw.gz | 0.4799 | 0.0118696 | 22.943277 | TRUE                 | Reported                 |
| rs1243689   | 14               | 20592046     | A                          | G                         | 0.3334           | -0.128            | 0.02275     | 2.13E-08          | 1910                    | k__Bacteria p__Firmicutes c__Bacilli o__Staphylococcales f__Gemellaceae g__Gemella s__unclassified_mgs_1413                                             | pheno.2040.assoc.linear.gz.raw.gz | 0.3334 | 0.0072825 | 13.996954 | TRUE                 | Reported                 |
| rs11068121  | 12               | 116647726    | T                          | C                         | 0.4057           | -0.1325           | 0.0224      | 3.93E-09          | 1907                    | k__Bacteria p__Firmicutes c__Bacilli o__Staphylococcales f__Gemellaceae g__Gemella s__unclassified_mgs_2314                                             | pheno.2072.assoc.linear.gz.raw.gz | 0.4057 | 0.0084659 | 16.265215 | TRUE                 | Reported                 |
| rs186022    | 8                | 17693261     | T                          | C                         | 0.3564           | -0.1268           | 0.02231     | 1.51E-08          | 1908                    | k__Bacteria p__Bacteroidota c__Bacteroidia o__Flavobacteriales f__Flavobacteriaceae g__Capnocytophaga s__Capnocytophaga_haemolytica_mgs_801             | pheno.2241.assoc.linear.gz.raw.gz | 0.3564 | 0.007376  | 14.163167 | TRUE                 | Reported                 |
| rs5771402   | 22               | 15357296     | A                          | T                         | 0.3705           | 0.1391            | 0.02252     | 7.90E-10          | 1906                    | k__Bacteria p__Patescibacteria c__Saccharimonadia o__Saccharimonadales f__Saccharimonadaceae g__Saccharimonas s__unclassified_mgs_271                   | pheno.2253.assoc.linear.gz.raw.gz | 0.3705 | 0.0090254 | 17.34094  | TRUE                 | Reported                 |
| rs6503138   | 17               | 8682242      | C                          | G                         | 0.4358           | -0.1236           | 0.02244     | 4.18E-08          | 1908                    | k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Streptococcaceae g__Streptococcus s__Streptococcus_sanguinis_mgs_1844                        | pheno.2350.assoc.linear.gz.raw.gz | 0.4358 | 0.0075125 | 14.427302 | TRUE                 | Reported                 |
| rs6952495   | 7                | 33914260     | C                          | T                         | 0.4073           | -0.1333           | 0.02228     | 2.58E-09          | 1907                    | k__Bacteria p__Firmicutes c__Negativicutes o__Selenomonadales f__Selenomonadaceae g__Centipeda s__Centipeda_artemidis_mgs_219                           | pheno.2368.assoc.linear.gz.raw.gz | 0.4073 | 0.0085791 | 16.484528 | TRUE                 | Reported                 |
| rs12557603  | X                | 23143242     | C                          | G                         | 0.3956           | 0.1249            | 0.0226      | 3.79E-08          | 1906                    | k__Bacteria p__Firmicutes c__Bacilli o__Erysipelotrichales f__Erysipelotrichaceae g__Solobacterium s__unclassified_mgs_2939                             | pheno.2405.assoc.linear.gz.raw.gz | 0.3956 | 0.0074599 | 14.31049  | TRUE                 | Reported                 |
| rs9668910   | 12               | 97704823     | G                          | T                         | 0.2744           | 0.1236            | 0.02232     | 3.47E-08          | 1906                    | k__Bacteria p__Bacteroidota c__Bacteroidia o__Bacteroidales f__Bacteroidaceae g__Bacteroides s__Bacteroides_pyogenes_A_mgs_637                          | pheno.2414.assoc.linear.gz.raw.gz | 0.2744 | 0.0060834 | 11.65374  | TRUE                 | Reported                 |
| rs6552264   | 4                | 177767524    | T                          | C                         | 0.4332           | 0.1252            | 0.02256     | 3.26E-08          | 1903                    | k__Bacteria p__Firmicutes c__Clostridia o__Lachnospirales f__Lachnospiraceae g__Catonella s__unclassified_mgs_3151                                      | pheno.2471.assoc.linear.gz.raw.gz | 0.4332 | 0.0076976 | 14.746706 | TRUE                 | Reported                 |
| rs6503138   | 17               | 8682242      | C                          | G                         | 0.4358           | -0.1238           | 0.02244     | 3.96E-08          | 1902                    | k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Streptococcaceae g__Streptococcus s__Streptococcus_sanguinis_mgs_1697                        | pheno.2513.assoc.linear.gz.raw.gz | 0.4358 | 0.0075369 | 14.42882  | TRUE                 | Reported                 |
| rs11244913  | 10               | 126258624    | G                          | T                         | 0.4465           | -0.1269           | 0.02272     | 2.68E-08          | 1904                    | k__Bacteria p__Firmicutes c__Clostridia o__Lachnospirales f__Lachnospiraceae g__Lachnoanaerobaculum s__Lachnoanaerobaculum_sp000296385_mgs_3537         | pheno.2587.assoc.linear.gz.raw.gz | 0.4465 | 0.0079596 | 15.260666 | TRUE                 | Reported                 |
| rs5842      | 16               | 75229126     | T                          | A                         | 0.4739           | -0.1268           | 0.02278     | 2.94E-08          | 1895                    | k__Bacteria p__Campylobacterota c__Campylobacteria o__Campylobacterales f__Campylobacteraceae g__Campylobacter_A s__unclassified_mgs_2769               | pheno.2597.assoc.linear.gz.raw.gz | 0.4739 | 0.0080172 | 15.299245 | TRUE                 | Reported                 |
| rs2901982   | 18               | 55698707     | C                          | T                         | 0.4115           | 0.1245            | 0.02266     | 4.48E-08          | 1898                    | k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Enterobacterales f__Pasteurellaceae g__Aggregatibacter s__Aggregatibacter_sp000466335_mgs_2447  | pheno.273.assoc.linear.gz.raw.gz  | 0.4115 | 0.0075073 | 14.341548 | TRUE                 | Reported                 |
| rs6037790   | 20               | 4240829      | C                          | T                         | 0.2491           | 0.1275            | 0.0227      | 2.25E-08          | 1905                    | k__Bacteria p__Firmicutes c__Clostridia o__Lachnospirales f__Lachnospiraceae g__Lachnoanaerobaculum s__Lachnoanaerobaculum_sp000287675_mgs_978          | pheno.2757.assoc.linear.gz.raw.gz | 0.2491 | 0.0060814 | 11.643785 | TRUE                 | Reported                 |
| rs17691375  | 5                | 136104051    | A                          | G                         | 0.2681           | -0.1272           | 0.02255     | 1.96E-08          | 1906                    | k__Bacteria p__Firmicutes c__Bacilli o__Staphylococcales f__Gemellaceae g__Gemella s__unclassified_mgs_2104                                             | pheno.2758.assoc.linear.gz.raw.gz | 0.2681 | 0.0063497 | 12.167074 | TRUE                 | Reported                 |
| rs1334218   | 13               | 53985560     | G                          | C                         | 0.347            | 0.1242            | 0.02238     | 3.28E-08          | 1901                    | k__Bacteria p__Campylobacterota c__Campylobacteria o__Campylobacterales f__Campylobacteraceae g__Campylobacter_A s__unclassified_mgs_3093               | pheno.2839.assoc.linear.gz.raw.gz | 0.347  | 0.0069906 | 13.368647 | TRUE                 | Reported                 |
| rs10139564  | 14               | 20681626     | C                          | A                         | 0.4274           | -0.126            | 0.02265     | 3.02E-08          | 1902                    | k__Bacteria p__Firmicutes c__Clostridia o__Lachnospirales f__Lachnospiraceae g__Oribacterium s__unclassified_mgs_388                                    | pheno.2859.assoc.linear.gz.raw.gz | 0.4274 | 0.0077706 | 14.879847 | TRUE                 | Reported                 |
| rs11186611  | 10               | 91549918     | C                          | T                         | 0.2556           | 0.1266            | 0.02249     | 2.05E-08          | 1896                    | k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Streptococcaceae g__Streptococcus s__unclassified_mgs_2776                                   | pheno.289.assoc.linear.gz.raw.gz  | 0.2556 | 0.0060991 | 11.622552 | TRUE                 | Reported                 |
| rs7908470   | 10               | 19414207     | C                          | T                         | 0.2107           | -0.1289           | 0.02201     | 5.54E-09          | 1905                    | k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Streptococcaceae g__Streptococcus s__unclassified_mgs_564                                    | pheno.298.assoc.linear.gz.raw.gz  | 0.2107 | 0.0055264 | 10.575186 | TRUE                 | Reported                 |
| rs116088775 | 1                | 96147995     | G                          | A                         | 0.3345           | 0.1232            | 0.02248     | 4.75E-08          | 1895                    | k__Bacteria p__Spirochaetota c__Spirochaetia o__Treponematales f__Treponemataceae g__Treponema_D s__unclassified_mgs_2715                               | pheno.3062.assoc.linear.gz.raw.gz | 0.3345 | 0.0067576 | 12.879262 | TRUE                 | Reported                 |
| rs1334218   | 13               | 53985560     | G                          | C                         | 0.347            | 0.1266            | 0.02254     | 2.26E-08          | 1893                    | k__Bacteria p__Campylobacterota c__Campylobacteria o__Campylobacterales f__Campylobacteraceae g__Campylobacter_A s__unclassified_mgs_3153               | pheno.3088.assoc.linear.gz.raw.gz | 0.347  | 0.0072634 | 13.835586 | TRUE                 | Reported                 |
| rs7228635   | 18               | 64502408     | A                          | G                         | 0.3214           | -0.1259           | 0.02275     | 3.57E-08          | 1896                    | k__Bacteria p__Patescibacteria c__Saccharimonadia o__Saccharimonadales f__Saccharimonadaceae g__unclassified_mgs_377                                    | pheno.3170.assoc.linear.gz.raw.gz | 0.3214 | 0.0069142 | 13.186647 | TRUE                 | Reported                 |
| rs12707372  | 7                | 137715827    | G                          | T                         | 0.4585           | 0.1264            | 0.02244     | 2.04E-08          | 1890                    | k__Bacteria p__Actinobacteriota c__Actinobacteria o__Actinomycetales f__Actinomycetaceae g__Pauljensenia s__Pauljensenia_sp000308055_mgs_1404           | pheno.3209.assoc.linear.gz.raw.gz | 0.4585 | 0.0079334 | 15.098129 | TRUE                 | Reported                 |
| rs4593315   | 5                | 109224389    | T                          | C                         | 0.2269           | 0.1334            | 0.02305     | 8.41E-09          | 1865                    | k__Bacteria p__Patescibacteria c__Saccharimonadia o__Saccharimonadales f__Saccharimonadaceae g__TM7x s__unclassified_mgs_3359                           | pheno.3393.assoc.linear.gz.raw.gz | 0.2269 | 0.0062433 | 11.704277 | TRUE                 | Reported                 |
| rs6631405   | X                | 31792860     | A                          | G                         | 0.3943           | -0.1282           | 0.02297     | 2.76E-08          | 1867                    | k__Bacteria p__Patescibacteria c__Saccharimonadia o__Saccharimonadales f__Saccharimonadaceae g__unclassified_mgs_834 s__unclassified_mgs_834            | pheno.3400.assoc.linear.gz.raw.gz | 0.3943 | 0.0078504 | 14.756796 | TRUE                 | Reported                 |
| rs3128691   | 1                | 202223455    | C                          | A                         | 0.2731           | -0.1345           | 0.0231      | 6.82E-09          | 1861                    | k__Bacteria p__Patescibacteria c__Saccharimonadia o__Saccharimonadales f__Saccharimonadaceae g__TM7x s__unclassified_mgs_386                            | pheno.3406.assoc.linear.gz.raw.gz | 0.2731 | 0.0071824 | 13.448717 | TRUE                 | Reported                 |
| rs6950804   | 7                | 82198562     | T                          | C                         | 0.2339           | -0.1427           | 0.02297     | 6.49E-10          | 1861                    | k__Bacteria p__Patescibacteria c__Saccharimonadia o__Saccharimonadales f__Saccharimonadaceae g__TM7x s__unclassified_mgs_386                            | pheno.3406.assoc.linear.gz.raw.gz | 0.2339 | 0.0072978 | 13.666397 | TRUE                 | Reported                 |
| rs4457930   | 14               | 103160256    | A                          | G                         | 0.2736           | -0.1223           | 0.02212     | 3.63E-08          | 1915                    | k__Bacteria p__Spirochaetota c__Spirochaetia o__Treponematales f__Treponemataceae g__unclassified_mgs_2387 s__unclassified_mgs_2387                     | pheno.3432.assoc.linear.gz.raw.gz | 0.2736 | 0.0059453 | 11.44141  | TRUE                 | Reported                 |
| rs2448227   | 12               | 77984335     | T                          | C                         | 0.2982           | 0.1244            | 0.02218     | 2.38E-08          | 1851                    | k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Burkholderiales f__Burkholderiaceae g__Dakarella                                                | pheno.3512.assoc.linear.gz.raw.gz | 0.2982 | 0.0064773 | 12.054546 | TRUE                 | Reported                 |
| rs2245108   | 1                | 69222857     | C                          | G                         | 0.4068           | -0.1241           | 0.02245     | 3.70E-08          | 1915                    | k__Bacteria p__Firmicutes c__Clostridia o__Eubacteriales f__Eubacteriaceae g__Pseudoramibacter                                                          | pheno.3584.assoc.linear.gz.raw.gz | 0.4068 | 0.0074329 | 14.325531 | TRUE                 | Reported                 |
| rs12442073  | 15               | 58466159     | A                          | G                         | 0.3901           | 0.1263            | 0.0216      | 5.89E-09          | 1902                    | k__Bacteria p__Firmicutes c__Bacilli o__Staphylococcales f__Gemellaceae g__Gemella s__Gemella_haemolysans_B_mgs_2903                                    | pheno.388.assoc.linear.gz.raw.gz  | 0.3901 | 0.0075905 | 14.532287 | TRUE                 | Reported                 |
| rs12123637  | 1                | 14827392     | C                          | T                         | 0.2637           | -0.1253           | 0.02281     | 4.49E-08          | 1894                    | k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Enterobacterales f__Pasteurellaceae g__Haemophilus_D s__Haemophilus_D_parainfluenzae_A_mgs_3345 | pheno.463.assoc.linear.gz.raw.gz  | 0.2637 | 0.0060967 | 11.605773 | TRUE                 | Reported                 |
| rs11037188  | 11               | 42967315     | C                          | G                         | 0.2697           | -0.1291           | 0.02262     | 1.31E-08          | 1904                    | k__Bacteria p__Bacteroidota c__Bacteroidia o__Bacteroidales f__Bacteroidaceae g__Prevotella s__Prevotella_aurantiaca_mgs_2854                           | pheno.479.assoc.linear.gz.raw.gz  | 0.2697 | 0.0065655 | 12.57002  | TRUE                 | Reported                 |
| rs4911713   | 22               | 15406720     | C                          | A                         | 0.4077           | 0.1591            | 0.02249     | 2.11E-12          | 1891                    | k__Bacteria p__Firmicutes c__Negativicutes o__Veillonellales f__Veillonellaceae g__F0422 s__unclassified_mgs_392                                        | pheno.589.assoc.linear.gz.raw.gz  | 0.4077 | 0.0122251 | 23.379045 | TRUE                 | Reported                 |
| rs4706262   | 6                | 69659643     | C                          | T                         | 0.2379           | -0.1256           | 0.02255     | 2.93E-08          | 1908                    | k__Bacteria p__Bacteroidota c__Bacteroidia o__Bacteroidales f__Bacteroidaceae g__Prevotella s__unclassified_mgs_3522                                    | pheno.63.assoc.linear.gz.raw.gz   | 0.2379 | 0.0057203 | 10.965539 | TRUE                 | Reported                 |
| rs7112471   | 11               | 14233717     | C                          | T                         | 0.3543           | 0.1289            | 0.02235     | 9.37E-09          | 1896                    | k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Enterobacterales f__Pasteurellaceae g__Aggregatibacter s__unclassified_mgs_2851                 | pheno.641.assoc.linear.gz.raw.gz  | 0.3543 | 0.0076022 | 14.508815 | TRUE                 | Reported                 |
| rs9975931   | 21               | 24645277     | A                          | T                         | 0.201            | -0.1281           | 0.02263     | 1.72E-08          | 1909                    | k__Bacteria p__Fusobacteriota c__Fusobacteriia o__Fusobacteriales f__Leptotrichiaceae g__Leptotrichia_A s__Leptotrichia_A_sp000469505_mgs_2741          | pheno.653.assoc.linear.gz.raw.gz  | 0.201  | 0.0052707 | 10.104548 | TRUE                 | Reported                 |
| rs16835168  | 1                | 237363880    | T                          | C                         | 0.3042           | 0.1258            | 0.02258     | 2.90E-08          | 1896                    | k__Bacteria p__Bacteroidota c__Bacteroidia o__Bacteroidales f__Bacteroidaceae g__Prevotella s__Prevotella_multiformis_mgs_380                           | pheno.724.assoc.linear.gz.raw.gz  | 0.3042 | 0.0066994 | 12.774214 | TRUE                 | Reported                 |
| rs7112471   | 11               | 14233717     | C                          | T                         | 0.3543           | 0.1245            | 0.0227      | 4.71E-08          | 1895                    | k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Enterobacterales f__Pasteurellaceae g__Aggregatibacter s__Aggregatibacter_sp000466335_mgs_1486  | pheno.817.assoc.linear.gz.raw.gz  | 0.3543 | 0.007092  | 13.521107 | TRUE                 | Reported                 |
| rs4842768   | 12               | 91465582     | C                          | A                         | 0.382            | -0.1377           | 0.02233     | 8.46E-10          | 1905                    | k__Bacteria p__Firmicutes c__Clostridia o__4C28d-15 f__CAG-917 g__unclassified_mgs_2636 s__unclassified_mgs_2636                                        | pheno.844.assoc.linear.gz.raw.gz  | 0.382  | 0.0089526 | 17.190721 | TRUE                 | Reported                 |
| rs2254290   | 6                | 13346428     | T                          | C                         | 0.4219           | -0.124            | 0.02239     | 3.49E-08          | 1897                    | k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Enterobacterales f__Pasteurellaceae g__Haemophilus_A s__Haemophilus_A_sputorum_mgs_975          | pheno.938.assoc.linear.gz.raw.gz  | 0.4219 | 0.0075004 | 14.320716 | TRUE                 | Reported                 |
| rs72622121  | 3                | 2152415      | G                          | T                         | 0.3044           | 0.1242            | 0.02264     | 4.66E-08          | 1901                    | k__Bacteria p__Firmicutes c__Clostridia o__TANB77 f__CAG-508 g__CAG-793 s__unclassified_mgs_2346                                                        | pheno.979.assoc.linear.gz.raw.gz  | 0.3044 | 0.0065325 | 12.486729 | TRUE                 | Reported                 |
| rs7628864   | 3                | 86801468     | A                          | G                         | 0.399            | 0.1277            | 0.02285     | 2.66E-08          | 1873                    | k__Bacteria p__Firmicutes c__Clostridia o__Lachnospirales f__Lachnospiraceae g__F0428                                                                   | pheno.99.assoc.linear.gz.raw.gz   | 0.399  | 0.0078209 | 14.748331 | TRUE                 | Reported                 |

Table S2 Meaningful SNPs from tongue screened according to selection criteria

| SNP         | chr.<br>exposure | pos.<br>exposure | effect_allele.<br>exposure | other_allele.<br>exposure | eaf.<br>exposure | beta.<br>exposure | se.exposure | pval.<br>exposure | samplesize.<br>exposure | exposure                                                                                                                                                | id.exposure                                         | maf | R2 | F.value  | mr_keep.<br>exposure | pval_origin.<br>exposure |
|-------------|------------------|------------------|----------------------------|---------------------------|------------------|-------------------|-------------|-------------------|-------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------|-----|----|----------|----------------------|--------------------------|
| rs17135209  | 10               | 3400341          | T                          | C                         | 0.3832           | 0.122             | 0.02219     | 4.34E-08          | 1984                    | k_Bacterialp__Proteobacteria[c__Gammaproteobacteria]o__Enterobacteriales[f__Pasteurellaceae]g__Haemophilus_D[s__unclassified_mgs_1145                   | pheno.1056.assoc.linear. 0.3832 0.0070359 14.043961 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs36067748  | 3                | 1802482          | C                          | T                         | 0.276            | -0.1201           | 0.02194     | 4.97E-08          | 2000                    | k_Bacterialp__Firmicutes[c__Negativicutes]o__Veillonellales[f__Veillonellaceae]g__Veillonella[s__unclassified_mgs_1075                                  | pheno.1057.assoc.linear. 0.276 0.0057645 11.584302  |     |    | 15.00252 | TRUE                 | Reported                 |
| rs11923281  | 3                | 45272013         | T                          | C                         | 0.4623           | 0.1232            | 0.02235     | 4.03E-08          | 1988                    | k_Bacterialp__Firmicutes[c__Bacilli]o__Erysipelotrichales[f__Erysipelotrichaceae]g__Solobacterium[s__unclassified_mgs_2613                              | pheno.1267.assoc.linear. 0.4623 0.007546 15.100252  |     |    | 15.00252 | TRUE                 | Reported                 |
| rs1913263   | 12               | 16352362         | A                          | G                         | 0.4923           | -0.1382           | 0.02188     | 3.34E-10          | 1998                    | k_Bacterialp__Firmicutes[c__Bacilli]o__Lactobacillales[f__Streptococcaceae]g__Streptococcus[s__unclassified_mgs_934                                     | pheno.1284.assoc.linear. 0.4923 0.0095474 19.240214 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs58459070  | 6                | 109938114        | A                          | C                         | 0.2242           | 0.1241            | 0.02217     | 2.45E-08          | 1995                    | k_Bacterialp__Firmicutes[c__Bacilli]o__Lactobacillales[f__Streptococcaceae]g__Streptococcus[s__unclassified_mgs_2744                                    | pheno.1287.assoc.linear. 0.2242 0.0053575 10.73493  |     |    | 15.00252 | TRUE                 | Reported                 |
| rs926132    | 21               | 15273270         | G                          | A                         | 0.3058           | 0.1265            | 0.02224     | 1.48E-08          | 2000                    | k_Bacterialp__Firmicutes[c__Clostridia]o__Lachnospirales[f__Lachnospiraceae]g__Oribacterium[s__Oribacterium_sinus_mgs_3034                              | pheno.1293.assoc.linear. 0.3058 0.0067941 13.667508 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs1202601   | 1                | 230885125        | G                          | A                         | 0.4214           | 0.1311            | 0.02214     | 3.78E-09          | 1984                    | k_Bacterialp__Bacteroidota[c__Bacteroidia]o__Bacteroidales[f__Bacteroidaceae]g__Prevotella[s__Prevotella_sp000467895_mgs_1817                           | pheno.1354.assoc.linear. 0.4214 0.0083812 16.752023 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs730756    | 22               | 48279116         | T                          | C                         | 0.2597           | 0.1276            | 0.02231     | 1.24E-08          | 1987                    | k_Bacterialp__Bacteroidota[c__Bacteroidia]o__Flavobacteriales[f__Weekseellaceae]g__unclassified_mgs_1950[s__unclassified_mgs_1950                       | pheno.139.assoc.linear. 0.2597 0.0062605 12.505441  |     |    | 15.00252 | TRUE                 | Reported                 |
| rs17135209  | 10               | 3400341          | T                          | C                         | 0.3832           | 0.127             | 0.02221     | 1.24E-08          | 1983                    | k_Bacterialp__Proteobacteria[c__Gammaproteobacteria]o__Enterobacteriales[f__Pasteurellaceae]g__Haemophilus_D                                            | pheno.13.assoc.linear. 0.3832 0.0076244 15.220037   |     |    | 15.00252 | TRUE                 | Reported                 |
| rs17135209  | 10               | 3400341          | T                          | C                         | 0.3832           | 0.1293            | 0.02232     | 8.08E-09          | 1988                    | k_Bacterialp__Proteobacteria[c__Gammaproteobacteria]o__Enterobacteriales[f__Pasteurellaceae]g__Haemophilus_D[s__Haemophilus_D_paininfluenzae_L_mgs_3228 | pheno.1516.assoc.linear. 0.3832 0.0079031 15.820568 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs10971443  | 9                | 33202603         | C                          | A                         | 0.3616           | 0.1277            | 0.02222     | 1.05E-08          | 1978                    | k_Bacterialp__Proteobacteria[c__Gammaproteobacteria]o__Burkholderiales[f__Neisseriaceae]g__Simonsiella[s__Simonsiella_muelleri_mgs_3058                 | pheno.1548.assoc.linear. 0.3616 0.0075289 14.990019 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs1913263   | 12               | 16352362         | A                          | G                         | 0.4923           | -0.1225           | 0.02221     | 3.95E-08          | 1995                    | k_Bacterialp__Firmicutes[c__Bacilli]o__Lactobacillales[f__Streptococcaceae]g__Streptococcus[s__Streptococcus_infantis_H_mgs_68                          | pheno.1550.assoc.linear. 0.4923 0.0075013 15.063176 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs9320838   | 6                | 121680161        | G                          | A                         | 0.4673           | -0.1213           | 0.02188     | 3.33E-08          | 1993                    | k_Bacterialp__Firmicutes[c__Bacilli]o__Lactobacillales[f__Streptococcaceae]g__Streptococcus[s__unclassified_mgs_2460                                    | pheno.1584.assoc.linear. 0.4673 0.0073254 14.692457 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs7294985   | 12               | 16349610         | G                          | A                         | 0.495            | -0.148            | 0.0218      | 1.50E-11          | 1993                    | k_Bacterialp__Firmicutes[c__Bacilli]o__Lactobacillales[f__Streptococcaceae]g__Streptococcus[s__unclassified_mgs_2460                                    | pheno.1584.assoc.linear. 0.495 0.0109509 22.04466   |     |    | 15.00252 | TRUE                 | Reported                 |
| rs3775944   | 4                | 10018350         | G                          | T                         | 0.4861           | -0.1268           | 0.02155     | 4.69E-09          | 1987                    | k_Bacterialp__Firmicutes[c__Clostridia]o__Lachnospirales[f__Lachnospiraceae]g__Lachnoanaerobaculum[s__Lachnoanaerobaculum_umeaense_mgs_772              | pheno.158.assoc.linear. 0.4861 0.0080329 16.074445  |     |    | 15.00252 | TRUE                 | Reported                 |
| rs17135209  | 10               | 3400341          | T                          | C                         | 0.3832           | 0.1236            | 0.02216     | 2.78E-08          | 1988                    | k_Bacterialp__Proteobacteria[c__Gammaproteobacteria]o__Enterobacteriales[f__Pasteurellaceae]g__Haemophilus_D[s__unclassified_mgs_2986                   | pheno.1620.assoc.linear. 0.3832 0.0072217 14.446537 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs6908390   | 6                | 25609528         | T                          | C                         | 0.2406           | 0.1219            | 0.02221     | 4.63E-08          | 1990                    | k_Bacterialp__Bacteroidota[c__Bacteroidia]o__Flavobacteriales[f__Flavobacteriaceae]g__Capnocytophaga[s__Capnocytophaga_sp002209445_mgs_3500             | pheno.1677.assoc.linear. 0.2406 0.00543 10.853871   |     |    | 15.00252 | TRUE                 | Reported                 |
| rs6490533   | 13               | 20247566         | G                          | C                         | 0.4258           | -0.1319           | 0.02217     | 3.17E-09          | 1990                    | k_Bacterialp__Bacteroidota[c__Bacteroidia]o__Flavobacteriales[f__Flavobacteriaceae]g__Capnocytophaga[s__Capnocytophaga_sp002209445_mgs_3500             | pheno.1677.assoc.linear. 0.4258 0.0085072 17.057495 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs34131705  | 17               | 66574767         | G                          | A                         | 0.3485           | 0.1315            | 0.02201     | 2.73E-09          | 1995                    | k_Bacterialp__Firmicutes[c__Bacilli]o__RF39[f__unclassified_mgs_1766                                                                                    | pheno.168.assoc.linear. 0.3485 0.0078523 15.773559  |     |    | 15.00252 | TRUE                 | Reported                 |
| rs7294985   | 12               | 16349610         | G                          | A                         | 0.495            | -0.1238           | 0.02186     | 1.73E-08          | 1980                    | k_Bacterialp__Firmicutes[c__Bacilli]o__Lactobacillales[f__Streptococcaceae                                                                              | pheno.1691.assoc.linear. 0.495 0.0076625 15.273365  |     |    | 15.00252 | TRUE                 | Reported                 |
| rs7294985   | 12               | 16349610         | G                          | A                         | 0.495            | -0.1251           | 0.02162     | 8.43E-09          | 1995                    | k_Bacterialp__Firmicutes[c__Bacilli]o__Lactobacillales[f__Streptococcaceae]g__Streptococcus[s__Streptococcus_pseudopneumoniae_A_mgs_1809                | pheno.1699.assoc.linear. 0.495 0.0078242 15.716646  |     |    | 15.00252 | TRUE                 | Reported                 |
| rs1568075   | 3                | 7141230          | G                          | T                         | 0.3061           | -0.1225           | 0.02231     | 4.52E-08          | 1993                    | k_Bacterialp__Bacteroidota[c__Bacteroidia]o__Bacteroidales[f__Bacteroidaceae]g__Prevotella[s__unclassified_mgs_2853                                     | pheno.1747.assoc.linear. 0.3061 0.0063747 12.773533 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs12387128  | X                | 118369469        | A                          | C                         | 0.3324           | -0.1314           | 0.02163     | 1.50E-09          | 1992                    | k_Bacterialp__Fusobacteriota[c__Fusobacteriales]o__Fusobacteriales[f__Leptotrichiaceae]g__Leptotrichia_A                                                | pheno.1829.assoc.linear. 0.3324 0.007663 15.367101  |     |    | 15.00252 | TRUE                 | Reported                 |
| rs2584298   | 18               | 75647489         | G                          | T                         | 0.4735           | -0.1234           | 0.02215     | 2.90E-08          | 1996                    | k_Bacterialp__Firmicutes[c__Bacilli]o__Lactobacillales[f__Streptococcaceae]g__Streptococcus[s__unclassified_mgs_3493                                    | pheno.1905.assoc.linear. 0.4735 0.0075924 15.255054 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs4990850   | 15               | 93152812         | A                          | T                         | 0.2396           | -0.1225           | 0.02235     | 4.80E-08          | 1977                    | k_Bacterialp__Bacteroidota[c__Bacteroidia]o__Bacteroidales[f__Bacteroidaceae]g__F0040[s__unclassified_mgs_2335                                          | pheno.1939.assoc.linear. 0.2396 0.005468 10.85874   |     |    | 15.00252 | TRUE                 | Reported                 |
| rs7972928   | 12               | 7697208          | C                          | A                         | 0.3576           | -0.1303           | 0.0223      | 5.89E-09          | 1974                    | k_Bacterialp__Actinobacteriota[c__Coriobacteriales]o__Coriobacteriales[f__Atopobiaceae]g__Lancefieldella[s__unclassified_mgs_2666                       | pheno.2003.assoc.linear. 0.3576 0.0078005 15.503501 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs7294985   | 12               | 16349610         | G                          | A                         | 0.495            | -0.1192           | 0.02175     | 4.80E-08          | 1992                    | k_Bacterialp__Firmicutes[c__Bacilli]o__Lactobacillales[f__Streptococcaceae]g__Streptococcus[s__Streptococcus_infantis_L_mgs_1798                        | pheno.2082.assoc.linear. 0.495 0.0071036 14.237319  |     |    | 15.00252 | TRUE                 | Reported                 |
| rs17135209  | 10               | 3400341          | T                          | C                         | 0.3832           | 0.1292            | 0.02228     | 7.79E-09          | 1979                    | k_Bacterialp__Proteobacteria[c__Gammaproteobacteria]o__Enterobacteriales[f__Pasteurellaceae]g__Haemophilus_D[s__unclassified_mgs_3550                   | pheno.208.assoc.linear. 0.3832 0.0078909 15.724329  |     |    | 15.00252 | TRUE                 | Reported                 |
| rs263894    | 5                | 165724519        | A                          | G                         | 0.4256           | 0.1241            | 0.02218     | 2.52E-08          | 1994                    | k_Bacterialp__Firmicutes[c__Clostridia]o__Lachnospirales[f__Lachnospiraceae]g__Oribacterium[s__unclassified_mgs_2037                                    | pheno.2130.assoc.linear. 0.4256 0.0075299 15.113377 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs6725231   | 2                | 58562595         | G                          | A                         | 0.2803           | -0.1312           | 0.02181     | 2.14E-09          | 2000                    | k_Bacterialp__Firmicutes[c__Negativicutes]o__Veillonellales[f__Veillonellaceae]g__Veillonella[s__Veillonella_rogosae_mgs_2008                           | pheno.214.assoc.linear. 0.2803 0.006945 13.973154   |     |    | 15.00252 | TRUE                 | Reported                 |
| rs7294985   | 12               | 16349610         | G                          | A                         | 0.495            | -0.1241           | 0.0221      | 2.26E-08          | 1995                    | k_Bacterialp__Firmicutes[c__Bacilli]o__Lactobacillales[f__Streptococcaceae]g__Streptococcus[s__unclassified_mgs_1210                                    | pheno.2225.assoc.linear. 0.495 0.0076996 15.464443  |     |    | 15.00252 | TRUE                 | Reported                 |
| rs994834    | 2                | 58567530         | G                          | T                         | 0.2827           | -0.1257           | 0.02174     | 8.48E-09          | 1999                    | k_Bacterialp__Firmicutes[c__Negativicutes]o__Veillonellales[f__Veillonellaceae]g__Veillonella[s__Veillonella_rogosae_mgs_1856                           | pheno.2232.assoc.linear. 0.2827 0.0064081 12.879447 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs17135209  | 10               | 3400341          | T                          | C                         | 0.3832           | 0.1303            | 0.02227     | 5.64E-09          | 1984                    | k_Bacterialp__Proteobacteria[c__Gammaproteobacteria]o__Enterobacteriales[f__Pasteurellaceae]g__Haemophilus_A[s__Haemophilus_A_sputorum_mgs_3223         | pheno.2270.assoc.linear. 0.3832 0.0080258 16.035849 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs17135209  | 10               | 3400341          | T                          | C                         | 0.3832           | 0.1314            | 0.02221     | 3.91E-09          | 1982                    | k_Bacterialp__Proteobacteria[c__Gammaproteobacteria]o__Enterobacteriales[f__Pasteurellaceae]g__Haemophilus[s__Haemophilus_haemolyticus_mgs_3201         | pheno.2301.assoc.linear. 0.3832 0.0081619 16.293523 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs17135209  | 10               | 3400341          | T                          | C                         | 0.3832           | 0.1225            | 0.02222     | 4.02E-08          | 1984                    | k_Bacterialp__Proteobacteria[c__Gammaproteobacteria]o__Enterobacteriales[f__Pasteurellaceae]g__Haemophilus_D[s__unclassified_mgs_3140                   | pheno.244.assoc.linear. 0.3832 0.0070937 14.160136  |     |    | 15.00252 | TRUE                 | Reported                 |
| rs17135209  | 10               | 3400341          | T                          | C                         | 0.3832           | 0.1227            | 0.02229     | 4.14E-08          | 1979                    | k_Bacterialp__Proteobacteria[c__Gammaproteobacteria]o__Enterobacteriales[f__Pasteurellaceae]g__Haemophilus_D[s__Haemophilus_D_paininfluenzae_A_mgs_3466 | pheno.2465.assoc.linear. 0.3832 0.0071169 14.170903 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs17135209  | 10               | 3400341          | T                          | C                         | 0.3832           | 0.1215            | 0.02207     | 4.16E-08          | 1984                    | k_Bacterialp__Proteobacteria[c__Gammaproteobacteria]o__Enterobacteriales[f__Pasteurellaceae]g__Aggregatibacter[s__unclassified_mgs_108                  | pheno.2502.assoc.linear. 0.3832 0.0069783 13.928275 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs263894    | 5                | 165724519        | A                          | G                         | 0.4256           | 0.1239            | 0.02218     | 2.69E-08          | 1993                    | k_Bacterialp__Firmicutes[c__Clostridia]o__Lachnospirales[f__Lachnospiraceae]g__Oribacterium[s__Oribacterium_sinus_mgs_2094                              | pheno.255.assoc.linear. 0.4256 0.0075057 15.056772  |     |    | 15.00252 | TRUE                 | Reported                 |
| rs1913263   | 12               | 16352362         | A                          | G                         | 0.4923           | -0.1303           | 0.02204     | 4.00E-09          | 1999                    | k_Bacterialp__Firmicutes[c__Bacilli]o__Lactobacillales[f__Streptococcaceae]g__Streptococcus[s__Streptococcus_infantis_mgs_1655                          | pheno.262.assoc.linear. 0.4923 0.008487 17.093677   |     |    | 15.00252 | TRUE                 | Reported                 |
| rs62208757  | 20               | 56930856         | C                          | T                         | 0.4707           | 0.1261            | 0.02215     | 1.44E-08          | 1992                    | k_Bacterialp__Firmicutes[c__Bacilli]o__Erysipelotrichales[f__Erysipelotrichaceae]g__Solobacterium[s__unclassified_mgs_3390                              | pheno.2649.assoc.linear. 0.4707 0.0079233 15.8933   |     |    | 15.00252 | TRUE                 | Reported                 |
| rs3796835   | 4                | 10009906         | C                          | T                         | 0.4234           | -0.1217           | 0.02154     | 1.84E-08          | 1992                    | k_Bacterialp__Firmicutes[c__Clostridia]o__Lachnospirales[f__Lachnospiraceae]g__Oribacterium[s__unclassified_mgs_1411                                    | pheno.2673.assoc.linear. 0.4234 0.0072316 14.495787 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs3914801   | 2                | 35748897         | C                          | T                         | 0.2468           | -0.1233           | 0.02225     | 3.43E-08          | 1990                    | k_Bacterialp__Patescibacteria[c__Saccharimonadia]o__Saccharimonadales[f__Saccharimonadaceae]g__TM7x[s__unclassified_mgs_3200                            | pheno.2846.assoc.linear. 0.2468 0.0056521 11.300291 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs1913263   | 12               | 16352362         | A                          | G                         | 0.4923           | -0.1255           | 0.02205     | 1.47E-08          | 1994                    | k_Bacterialp__Firmicutes[c__Bacilli]o__Lactobacillales[f__Streptococcaceae]g__Streptococcus[s__unclassified_mgs_2667                                    | pheno.285.assoc.linear. 0.4923 0.0078733 15.807989  |     |    | 15.00252 | TRUE                 | Reported                 |
| rs17135209  | 10               | 3400341          | T                          | C                         | 0.3832           | 0.1239            | 0.02219     | 2.66E-08          | 1984                    | k_Bacterialp__Proteobacteria[c__Gammaproteobacteria]o__Enterobacteriales[f__Pasteurellaceae]g__Haemophilus_D[s__Haemophilus_D_paininfluenzae_A_mgs_3080 | pheno.286.assoc.linear. 0.3832 0.0072568 14.488025  |     |    | 15.00252 | TRUE                 | Reported                 |
| rs10989486  | 9                | 101390873        | C                          | G                         | 0.3772           | 0.1237            | 0.02195     | 2.01E-08          | 1985                    | k_Bacterialp__Firmicutes[c__Clostridia]o__TANB77[f__CAG-508]g__CAG-793[s__unclassified_mgs_1414                                                         | pheno.2994.assoc.linear. 0.3772 0.0071894 14.35972  |     |    | 15.00252 | TRUE                 | Reported                 |
| rs962895    | 6                | 164023029        | C                          | T                         | 0.3331           | -0.1241           | 0.02219     | 2.55E-08          | 1987                    | k_Bacterialp__Patescibacteria[c__Saccharimonadia]o__Saccharimonadales[f__Saccharimonadaceae]g__unclassified_mgs_1558[s__unclassified_mgs_1558           | pheno.3117.assoc.linear. 0.3331 0.0068424 13.675753 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs6711520   | 2                | 35777899         | T                          | G                         | 0.2398           | -0.124            | 0.02244     | 3.73E-08          | 1975                    | k_Bacterialp__Patescibacteria[c__Saccharimonadia]o__Saccharimonadales[f__Saccharimonadaceae]g__TM7x[s__unclassified_mgs_2908                            | pheno.3139.assoc.linear. 0.2398 0.005606 11.122924  |     |    | 15.00252 | TRUE                 | Reported                 |
| rs7579383   | 2                | 35783862         | C                          | T                         | 0.2413           | -0.1235           | 0.02243     | 4.18E-08          | 1978                    | k_Bacterialp__Patescibacteria[c__Saccharimonadia]o__Saccharimonadales[f__Saccharimonadaceae]g__TM7x[s__unclassified_mgs_386                             | pheno.3196.assoc.linear. 0.2413 0.0055846 11.097123 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs6711520   | 2                | 35777899         | T                          | G                         | 0.2398           | -0.1234           | 0.02232     | 3.69E-08          | 1975                    | k_Bacterialp__Patescibacteria[c__Saccharimonadia]o__Saccharimonadales[f__Saccharimonadaceae]g__TM7x[s__unclassified_mgs_572                             | pheno.3198.assoc.linear. 0.2398 0.0055518 11.014944 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs7579383   | 2                | 35783862         | C                          | T                         | 0.2413           | -0.1303           | 0.02233     | 6.18E-09          | 1980                    | k_Bacterialp__Patescibacteria[c__Saccharimonadia]o__Saccharimonadales[f__Saccharimonadaceae]g__TM7x[s__unclassified_mgs_689                             | pheno.3216.assoc.linear. 0.2413 0.0062165 12.373163 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs138204206 | 2                | 4995200          | A                          | C                         | 0.2842           | 0.1356            | 0.02226     | 1.33E-09          | 1976                    | k_Bacterialp__Patescibacteria[c__Saccharimonadia]o__Saccharimonadales[f__Saccharimonadaceae]g__unclassified_mgs_1065                                    | pheno.3233.assoc.linear. 0.2842 0.0074811 14.878992 |     |    | 15.00252 | TRUE                 | Reported                 |
| rs9453106   | 6                | 64900266         | C                          | A                         | 0.4742           | 0.1291            | 0.02219     | 6.93E-09          | 1981                    | k_Bacterialp__Actinobacteriota[c__Actinobacteria]o__Mycobacteriales[f__Mycobacteriaceae]g__Corynebacterium                                              | pheno.327.assoc.linear. 0.4742 0.0083112 16.585746  |     |    | 15.00252 | TRUE                 | Reported                 |
| rs11858584  | 15               |                  |                            |                           |                  |                   |             |                   |                         |                                                                                                                                                         |                                                     |     |    |          |                      |                          |