|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Taxon** | **fna filename:** | **Abundance** | **% Abundance** | **Genus** | **% Abundance Genus** |
| Actinomyces oris strain T14V | GCF\_001553935.1\_ASM155393v1\_cds\_from\_genomic.fna | 0.03 | 3 | Actinomyces |  |
| Actinomyces sp. oral taxon 414 strain F0588 | GCF\_001278845.1\_ASM127884v1\_cds\_from\_genomic.fna | 0.067 | 6.7 | Actinomyces | 9.7 |
| Aggregatibacter actinomycetemcomitans strain 624 | GCF\_001594265.1\_ASM159426v1\_cds\_from\_genomic.fna | 0.04 | 4 | Aggregatibacter |  |
| Aggregatibacter aphrophilus strain W10433 | GCF\_001262035.1\_ASM126203v1\_cds\_from\_genomic.fna | 0.04 | 4 | Aggregatibacter | 8 |
| Agrobacterium tumefaciens strain A | GCF\_000971565.1\_ASM97156v1\_cds\_from\_genomic.fna | 0.03 | 3 | Agrobacterium | 3 |
| Bacillus subtilis BSn5 | GCF\_000186745.1\_ASM18674v1\_cds\_from\_genomic.fna | 0.03 | 3 | Bacillus | 3 |
| Capnocytophaga haemolytica strain CCUG 32990 | GCF\_001553545.1\_ASM155354v1\_cds\_from\_genomic.fna | 0.04 | 4 | Capnocytophaga |  |
| Capnocytophaga sp. oral taxon 323 strain F0383 | GCF\_001278825.1\_ASM127882v1\_cds\_from\_genomic.fna | 0.04 | 4 | Capnocytophaga | 8 |
| Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | GCF\_000007325.1\_ASM732v1\_cds\_from\_genomic.fna | 0.1 | 10 | Fusobacterium |  |
| Fusobacterium nucleatum subsp. polymorphum strain ChDC F306 | GCF\_001433955.1\_ASM143395v1\_cds\_from\_genomic.fna | 0.04 | 4 | Fusobacterium |  |
| Fusobacterium nucleatum subsp. vincentii 3\_1\_36A2 | GCF\_000162235.2\_ASM16223v2\_cds\_from\_genomic.fna | 0.007 | 0.7 | Fusobacterium | 14.7 |
| Leptotrichia buccalis DSM 113 | GCF\_000023905.1\_ASM2390v1\_cds\_from\_genomic.fna | 0.03 | 3 | Leptotrichia |  |
| Leptotrichia sp. oral taxon 847 | GCF\_001553645.1\_ASM155364v1\_cds\_from\_genomic.fna | 0.03 | 3 | Leptotrichia | 6 |
| Neisseria meningitidis MC58 chromosome | GCF\_000008805.1\_ASM880v1\_cds\_from\_genomic.fna | 0.03 | 3 | Neisseria |  |
| Neisseria sicca strain FDAARGOS\_2 | GCF\_002073715.1\_ASM207371v1\_cds\_from\_genomic.fna | 0.03 | 3 | Neisseria | 6 |
| Porphyromonas gingivalis ATCC 33277 DNA | GCF\_000010505.1\_ASM1050v1\_cds\_from\_genomic.fna | 0.03 | 3 | Porphyromonas | 3 |
| Prevotella dentalis DSM 3688 | GCF\_000242335.1\_ASM24233v3\_cds\_from\_genomic.fna | 0.03 | 3 | Prevotella |  |
| Prevotella denticola F0289 | GCF\_000193395.1\_ASM19339v1\_cds\_from\_genomic.fna | 0.03 | 3 | Prevotella | 6 |
| Rothia dentocariosa ATCC 17931 | GCF\_000164695.2\_ASM16469v2\_cds\_from\_genomic.fna | 0.04 | 4 | Rothia |  |
| Rothia mucilaginosa DNA complete genome strain: NUM-Rm6536 | GCF\_001548235.1\_ASM154823v1\_cds\_from\_genomic.fna | 0.001 | 0.1 | Rothia | 4.1 |
| Sphingomonas sp. MM-1 | GCF\_000347675.2\_ASM34767v2\_cds\_from\_genomic.fna | 0.03 | 3 | Sphingomonas | 3 |
| Staphylococcus epidermidis ATCC 12228 | GCF\_000007645.1\_ASM764v1\_cds\_from\_genomic.fna | 0.03 | 3 | Staphylococcus | 3 |
| Streptococcus cristatus AS 1.3089 | GCF\_000385925.1\_ASM38592v1\_cds\_from\_genomic.fna | 0.03 | 3 | Streptococcus |  |
| Streptococcus mitis B6 | GCF\_000027165.1\_ASM2716v1\_cds\_from\_genomic.fna | 0.01 | 1 | Streptococcus |  |
| Streptococcus mutans NN202DNA | GCF\_000091645.1\_ASM9164v1\_cds\_from\_genomic.fna | 0.005 | 0.5 | Streptococcus |  |
| Streptococcus mutans UA159 chromosome | GCF\_000007465.2\_ASM746v2\_cds\_from\_genomic.fna | 0.05 | 5 | Streptococcus |  |
| Streptococcus oralis Uo5 | GCF\_000253155.1\_ASM25315v1\_cds\_from\_genomic.fna | 0.07 | 7 | Streptococcus |  |
| Streptococcus sanguinis SK36 | GCF\_000014205.1\_ASM1420v1\_cds\_from\_genomic.fna | 0.03 | 3 | Streptococcus | 19.5 |
| Veillonella parvula DSM 2008 | GCF\_000024945.1\_ASM2494v1\_cds\_from\_genomic.fna | 0.03 | 3 | Veillonella | 3 |
|  | **TOTAL:** | **1** | **100** |  | **100** |