**Figure 9 – Source data**. 16S rRNA gene sequence datasets used to analyze the sources of Melainabacteria.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QIIME ID | Title in QIIME database | Region | Cyano Seqs | Total Seqs | Ref |
| **Host associated** | | | | | |
| 317 | The influence of sex handedness and washing on the diversity of hand surface bacteria S1\_V183 | NA | 1 | 460244 | [[1](#_ENREF_1)] |
| 77 | A core gut microbiome in obese and lean twins | V2 | 81 | 1039357 | [[2](#_ENREF_2)] |
| 314 | Characterization of airborne microbial communities at a high elevation site and their potential to act as atmospheric ice nuclei | V2 | 0 | 4786 | [[3](#_ENREF_3)] |
| 316 | Bacterial communities of disease vectors sampled across time space and species | V2 | 10 | 177977 | [[4](#_ENREF_4)] |
| 450 | Bacterial Community Variation in Human Body Habitats Across Space and Time | V2 | 4 | 352051 | [[5](#_ENREF_5)] |
| 449 | V2 | 589 | 792256 |
| 460 | Comparison of T5KO and wildtype mice | V2 | 13 | 18251 | [[6](#_ENREF_6)] |
| 393 | Forensic identification using skin bacterial communities | V2 | 0 | 17615 | [[7](#_ENREF_7)] |
| 232 | V2 | 0 | 119805 |
| 459 | The effect of diet on the human gut microbiome: a metagenomic analysis in humanized gnotobiotic mice. | V2 | 0 | 20415 | [[8](#_ENREF_8)] |
| 454 | V2 | 1 | 33530 |
| 458 | NA | 0 | 93080 |
| 457 | V2 | 0 | 156891 |
| 455 | V2 | 0 | 286779 |
| 456 | V2 | 0 | 352772 |
| 453 | V2 | 76 | 416083 |
| 452 | V2 | 0 | 484260 |
| 451 | Crawford mice | NA | 34 | 144845 | [[9](#_ENREF_9)] |
| 391 | Burmese python gut microbiome | V2 | 2 | 319182 | [[10](#_ENREF_10)] |
| 721 | Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample | V4 | 162851 | 22302948 | [[11](#_ENREF_11)] |
| 722 | V4 | 0 | 36395009 |
| 509 | Vaginal microbiome of reproductive age women | V13 | 0 | 823722 | [[12](#_ENREF_12)] |
| 395 | Delivery mode effects on newborn microbiota | V2 | 54 | 156602 | [[13](#_ENREF_13)] |
| 486 | Composition, variability, and temporal stability of the intestinal microbiota of the elderly. | V4 | 0 | 2637162 | [[14](#_ENREF_14)] |
| 101 | Succession of microbial consortia in the developing infant gut microbiome | V2 | 0 | 313172 | [[15](#_ENREF_15)] |
| 496 | Impact of diet in shaping gut microbiota revealed by a comparative study in children from Europe and rural Africa | V56 | 0 | 7596 | [[16](#_ENREF_16)] |
| 494 | Incomplete recovery and individualized responses of the human distal gut microbiota to repeated antibiotic perturbation | V13 | 10758 | 2445577 | [[17](#_ENREF_17)] |
| 349 | Human oral, gut, and plaque microbiota in patients with atherosclerosis | V2 | 50 | 381870 | [[18](#_ENREF_18)] |
| 495 | Resistant Starches Types 2 and 4 Have Differential Effects on the Composition of the Fecal Microbiota in Human Subjects | V13 | 29 | 929198 | [[19](#_ENREF_19)] |
| 929 | Bacterial communities associated with the lichen symbiosis | V4 | 0 | 16743 | [[20](#_ENREF_20)] |
| 524 | Disordered Microbial Communities in the Upper Respiratory Tract of Cigarette Smokers | V2 | 11 | 729003 | [[21](#_ENREF_21)] |
| 966 | Characterization of Bacteria in Biopsies of Colon and Stools by High Throughput Sequencing of the V2 Region of Bacterial 16S rRNA Gene in Human | V2 | 3 | 78190 | [[22](#_ENREF_22)] |
| 625 | Diet drives convergence in gut microbiome functions across mammalian phylogeny and within humans | V2 | 33 | 69097 | [[23](#_ENREF_23)] |
| 626 | V2 | 163 | 160692 |
| 550 | Moving pictures of the human microbiome | V4 | 0 | 68666081 | [[24](#_ENREF_24)] |
| 1010 | Linking Long-Term Dietary Patterns with Gut Microbial Enterotypes | V2 | 709 | 352652 | [[25](#_ENREF_25)] |
| 742 | The antibacterial lectin RegIII promotes the spatial segregation of microbiota and host in the intestine | V13 | 11 | 104551 | [[26](#_ENREF_26)] |
| 1335 | restroom surface metagenome | V2 | 54 | 378334 | [[27](#_ENREF_27)] |
| 1345 | Architectural design influences the diversity and structure of the built environment microbiome | V2 | 0 | 65571 | [[28](#_ENREF_28)] |
| 850 | Human gut microbiome viewed across age and geography |  | 0 | 1092569420 | [[29](#_ENREF_29)] |
| 967 | Improved detection of bifidobacteria with optimised 16S rRNA gene based pyrosequencing | V35 | 0 | 37977 | [[30](#_ENREF_30)] |
| 1192 | Zebrafish gut metagenome | V3 | 0 | 92463 | [[31](#_ENREF_31)] |
| 802 | MyD88-dependent signaling modulates virus susceptibility and gut microbial ecology | V2 | 620 | 339416 | [[32](#_ENREF_32)] |
| 909 | Progression of NAFLD is driven by inflammasome-mediated dysbiosis | V2 | 192 | 369519 | [[33](#_ENREF_33)] |
| 1011 | Linking Long-Term Dietary Patterns with Gut Microbial Enterotypes | V2 | 4203 | 898799 | [[25](#_ENREF_25)] |
| 867 | Finland | V2 | 182 | 929870 | [[34](#_ENREF_34)] |
| NA | UKTwins | V2 | 1138 | 2685624 | NA |
| 968 | HMP production phase 1 | V13 | 287 | 23724484 | [[35](#_ENREF_35)] |
| 969 | HMP production phase 1 | V35 | 2800 | 36784860 |
| 933 | Latitudinal surveys of algal-associated microorganisms | V4 | 0 | 70989436 | NA |
| **Environment** | | | | | |
| 103 | Pyrosequencing-based assessment of soil pH as a predictor of soil bacterial community structure at the continental scale | V2 | 0 | 139612 | [[36](#_ENREF_36)] |
| 104 | Soil bacterial diversity in the Arctic is not fundamentally different from that found in other biomes | V2 | 0 | 94065 | [[37](#_ENREF_37)] |
| 130 | Bacterial community structure across groundwater arsenic gradients | V2 | 1 | 31500 | [[38](#_ENREF_38)] |
| 213 | Shifts in bacterial community structure associated with inputs of low molecular weight carbon compounds to soil | V2 | 0 | 62742 |  |
| 397 | Plot-scale manipulations of organic matter inputs to soils correlate with shifts in microbial community composition in a lowland tropical rainforest | V2 | 5 | 37836 | [[39](#_ENREF_39)] |
| 619 | NEON: Directions and resources for long-term monitoring in soil microbial ecology | V4 | 87 | 372622 | NA |
| 721 | Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample | V4 | 531 | 13854938 | [[40](#_ENREF_40)] |
| 816 | The effects of soil bacterial community structure on decomposition in a tropical rain forest | V2 | 0 | 1396 | [[41](#_ENREF_41)] |
| 928 | Examining the global dominant archaeal populations in soil | V4 | 15 | 14402 | [[42](#_ENREF_42)] |
| 1005 | Uncovering the mechanistic basis for soil microbial community response to altered precipitation patterns | V6 | 125 | 177838 | NA |
| 1038 | Oregon Transect | V4 | 0 | 3869679 | NA |
| 1031 | Alder/Fir | V4 | 0 | 1863345 | NA |
| 1039 | Jurelevicius Rio de Janeiro Coastline | V4 | 0 | 6377665 | NA |
| 1037 | LTSP 16S | V4 | 0 | 4464143 | NA |
| 1197, 1046, 1198 | Jansson Gulf Oil Spill Sediments | V4 | 0 | 76309188 | NA |

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