**Table S1:** Profile used to generate simulated AMD metagenomes using Grinder. All simulated metagenomes contained 100,000 reads. 454 metagenomes were generated with this command: grinder -reference\_file AMDgenomes.fasta - abundance\_file AMDprofile.txt -total\_reads 100000 -read\_dist [one of 100, 150, 200, 250, 300, 400, or 600] normal 50 -homopolymer\_dist balzer. All 454 read length distributions were normal with a standard deviation of 50 bp. Illumina metagenomes were generated with this command: grinder -reference\_file AMDgenomes.fasta -abundance\_file AMDprofile.txt -total\_reads 100000 -read\_dist [one of 100, 150, 200, 250, or 300] -md poly4 3e-3 3.3e-8. All Illumina read length distributions were uniform with all reads having exactly the average read length.

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| --- | --- | --- |
| Taxon | GenBank accession (chromosome) | Relative abundance (%) |
| *Leptospirillum* sp. Group II 'CF-1' | NZ\_CP012147.1 | 65 |
| *Ferroplasma acidarmanus* fer1 | NC\_021592.1 | 35 |