**Table S2:** Profile used to generate simulated EBPR metagenomes using Grinder. All simulated metagenomes contained 100,000 reads. 454 metagenomes were generated with this command: grinder -reference\_file EBPRgenomes.fasta - abundance\_file EBPRprofile.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 EBPRgenomes.fasta -abundance\_file EBPRprofile.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.

|  |  |  |
| --- | --- | --- |
| Taxon | GenBank accession (chromosome) | Relative abundance (%) |
| Candidatus *Accumulibacter phosphatis* clade IIA str. UW-1 | NC\_013194.1 | 100 |