

Supplementary Table S1. The number of genes from each COG pathway identified in the *Geobacter anodireducens* SD-1, *G. soli* GSS01, *G. sulfurreducens* PCA, and *G. metallireducens* GS-15 genomes using the Function Category Comparison tool on the IMG/MER website.

*These results are based on computer annotations and might not be completely accurate.

Functional category	SD-1	GSS01	PCA	GS-15
Archaeal/Vacuolar-type H ⁺ ATPase subunits	8	8	1	1
F0F1-type ATP synthase subunits	9	9	9	9
NADH:Ubiquinone oxidoreductase subunits	28	28	28	30
Pyruvate decarboxylation	13	13	17	18
TCA cycle	16	18	19	28
Arginine biosynthesis	9	10	9	10
Histidine biosynthesis	14	14	13	13
Isoleucine biosynthesis	6	6	7	7
Leucine biosynthesis	10	10	12	12
Methionine biosynthesis	9	10	10	12
Phenylalanine/tyrosine biosynthesis	13	12	12	12
Proline biosynthesis	3	3	3	3
Threonine biosynthesis	4	4	4	5
Tryptophan biosynthesis	17	16	15	16
Valine biosynthesis	10	10	11	11
Purine biosynthesis	13	15	16	15
Purine salvage	3	3	3	3
Pyrimidine biosynthesis	14	14	14	14
Pyrimidine salvage	4	5	5	4
Thymidylate biosynthesis	5	6	5	5
Entner-Doudoroff pathway	1	1	1	3
Gluconeogenesis	13	13	12	14
Glycolysis	13	13	12	14
Pentose phosphate pathway	5	5	5	8
Biotin biosynthesis	5	5	5	5
Cobalamin biosynthesis	15	17	15	15
Coenzyme A biosynthesis	5	7	7	7
FAD biosynthesis	5	7	7	7
Heme biosynthesis	10	12	13	12
Menaquinone biosynthesis	11	10	10	14
NAD biosynthesis	4	6	7	7
Pyridoxal phosphate biosynthesis	2	3	4	4
Riboflavin biosynthesis	3	4	4	4
Thiamine biosynthesis	11	13	12	14
Ubiquinone biosynthesis	15	14	16	17
Deoxyxylulose pathway of terpenoid biosynthesis	5	6	6	6
Fatty acid biosynthesis	18	23	18	57
Aminoacyl-tRNA synthetases and alternate systems for amino acid activation	24	24	24	25
Ribosomal proteins - large subunit	33	33	31	31
Ribosomal proteins - small subunit	20	20	19	20
Translation factors and enzymes involved in translation	20	20	20	21
Basal transcription factors	6	9	7	8
DNA-dependent RNA polymerase subunits	9	10	8	10
Transcriptional regulators	52	55	58	57
Basal replication machinery	16	16	18	23
DNA polymerase III subunits	5	4	4	4

Lipid A biosynthesis	9	11	11	11
Flagellum structure and biogenesis	28	29	29	25
Preprotein translocase subunits	9	7	8	8
Multisubunit NA⁺/H⁺ antiporter	12	12	11	6

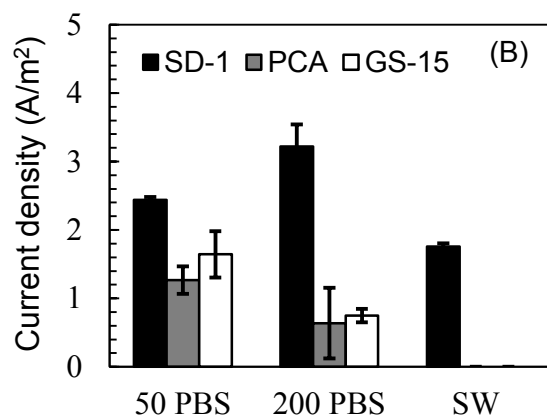
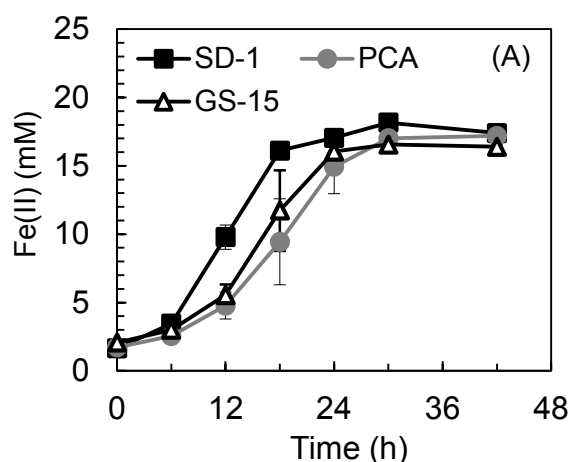


Figure 1. (A) Iron reduction of *G. anodireducens* SD-1, *G. sulfurreducens* PCA and *G. metallireducens* GS-15 in basal medium with Fe(III) citrate (20 mM) as electron acceptor and acetate (1 g/L) as electron donor.¹ (B) Maximum current densities generated by strains SD-1, PCA, GS-15 using different buffers: 50 mM phosphate buffer solution (PBS), 200 mM PBS, and saline water (SW, 50 mM PBS with 3.8% NaCl).²

1 D. Sun, A. Wang, S. Cheng, M. Yates and B. E. Logan, International journal of systematic and evolutionary microbiology, 2014, 64, 3485-3491.

2 D. Sun, D. Call, A. Wang, S. Cheng and B. E. Logan, Environmental microbiology reports, 2014, 6, 723-729.