

Table S1. Genome features of the ten sequenced *Shewanella* organisms used in the study

Species or strain	Genome Size ^a	Number of genes	Protein coding genes (%coding)	tRNAs & rRNAs	Partially shared genes ^b (%)	Strain specific genes ^b (%)	Accession Number
<i>S. oneidensis</i> MR1	5,131,416	4,561; 184	4,318 (83); 149 (69)	130	1,401 (33.4)	628 (14.9)	AE014299; AE014300
<i>S. sp.</i> W3-18-1	4,708,380	4,217	4,044 (85)	129	1,624 (40.1)	258 (6.4)	CP000503
<i>S. putrefaciens</i> CN-32	4,659,620	4,134	3,972 (85)	129	1,623 (40.9)	180 (4.5)	CP000681
<i>S. sp.</i> MR-7	4,799,109	4,178; 8	4,006 (85); 8 (56)	144	1,691 (42.4)	162 (4.0)	CP000444; CP000445
<i>S. sp.</i> MR-4	4,706,287	4,084	3,924 (85)	141	1,661 (42.4)	91 (2.3)	CP000446
<i>S. sp.</i> ANA-3	5,251,146	4,268; 251	4111 (85); 249 (83)	135	1,762 (40.3)	442 (10.1)	CP000469; CP000470
<i>S. denitrificans</i> OS217	4,545,906	3,905	3,754 (84)	127	737 (19.7)	827 (22.2)	CP000302
<i>S. frigidimarina</i> NCIMB400	4,845,257	4,199	4,029 (84)	133	1,097 (27.5)	726 (18.2)	CP000447
<i>S. loihica</i> PV-4	4,602,594	3,993	3,859 (85)	124	1,196 (30.9)	494 (12.8)	CP000606
<i>S. amazonensis</i> SB2B	4,306,142	3,785	3,645 (88)	130	1,250 (32.4)	440 (11.4)	CP000507
Isolate	Place of isolation						
<i>S. oneidensis</i> MR-1	Freshwater sediments, Lake Oneida, NY, USA						
<i>Shewanella sp.</i> W3-18-1	Marine sediments, Pacific Ocean (630 m, 5-6 cm core), WA, USA						
<i>S. putrefaciens</i> CN-32	Subsurface sandstone, New Mexico, NM, USA						
<i>Shewanella sp.</i> MR-7	60 m depth, anoxic, Black Sea						
<i>Shewanella sp.</i> MR-4	5 m depth, oxic, Black Sea						
<i>Shewanella sp.</i> ANA-3	Arsenic treated wood in brackish estuary, Woods Hole, MA, USA						
<i>S. denitrificans</i> OS217	Marine oxic/anoxic zone, Gotland Deep, Baltic Sea						
<i>S. frigidimarina</i> NCIMB 400	Marine, North Sea, UK						
<i>S. loihica</i> PV-4	Marine, Naha Vents, Hawaii						
<i>S. amazonensis</i> SB2B	Marine sediments, Amazon River delta, Brazil						

^a Genome size was computed as the sum of chromosome and plasmid.

^b Only orthologous genes outside of the core were considered in this analysis.