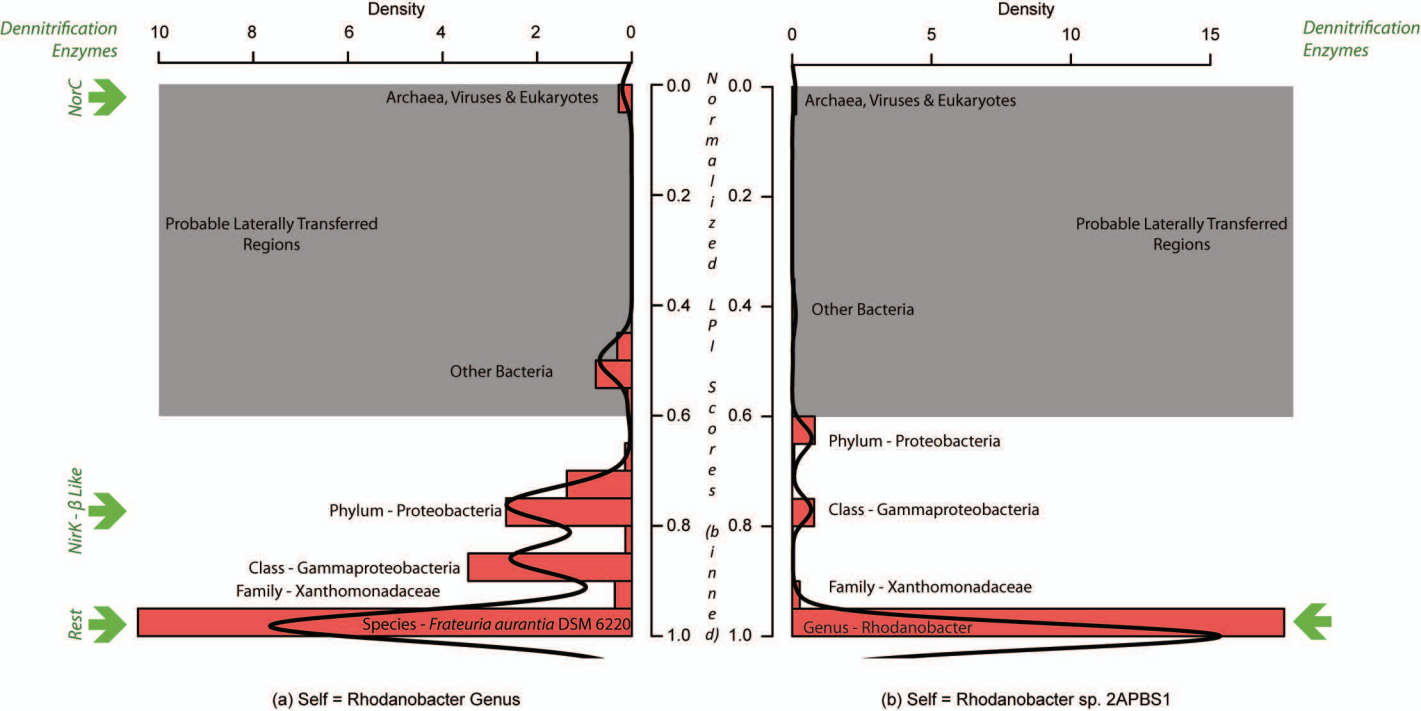
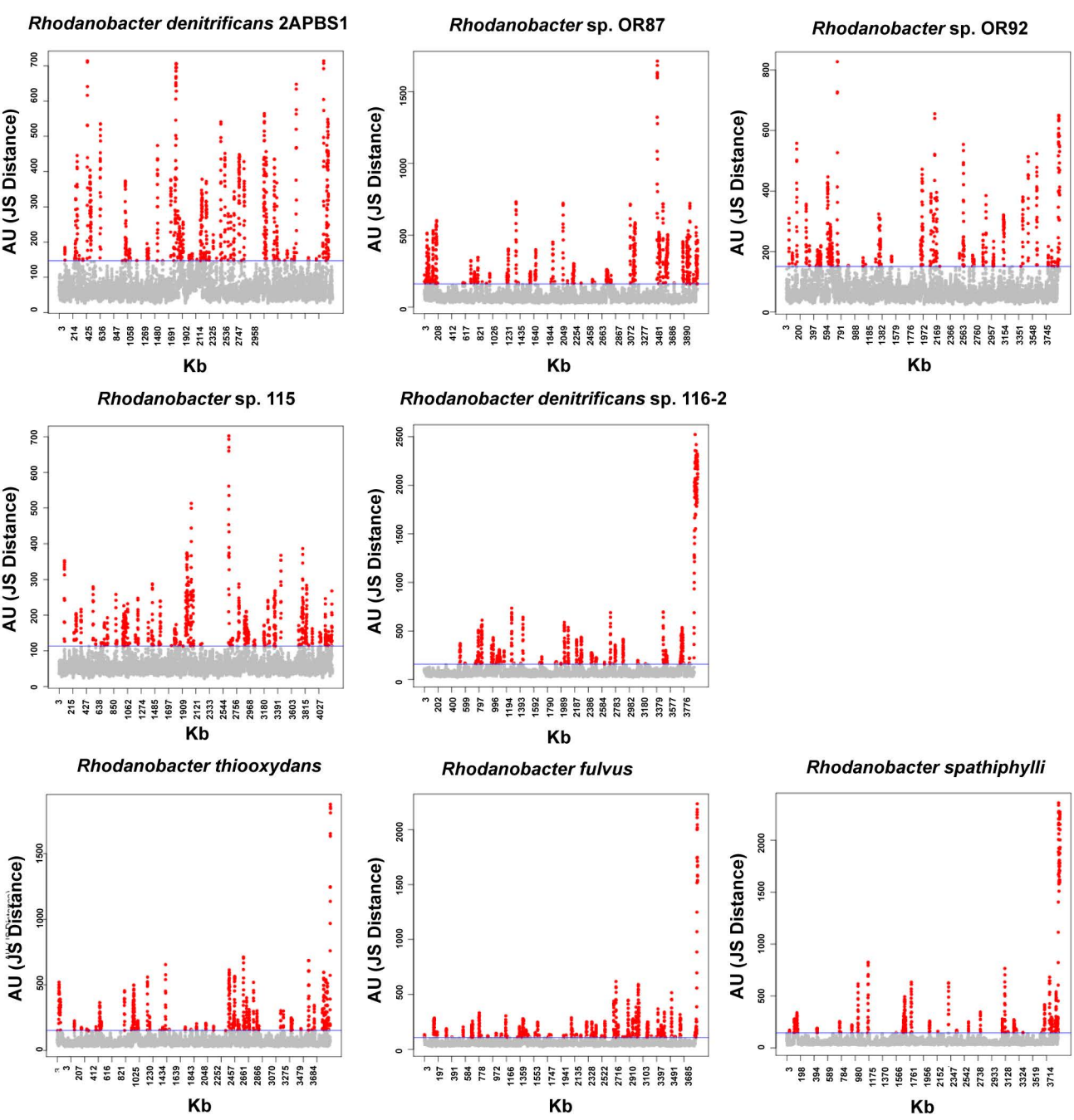
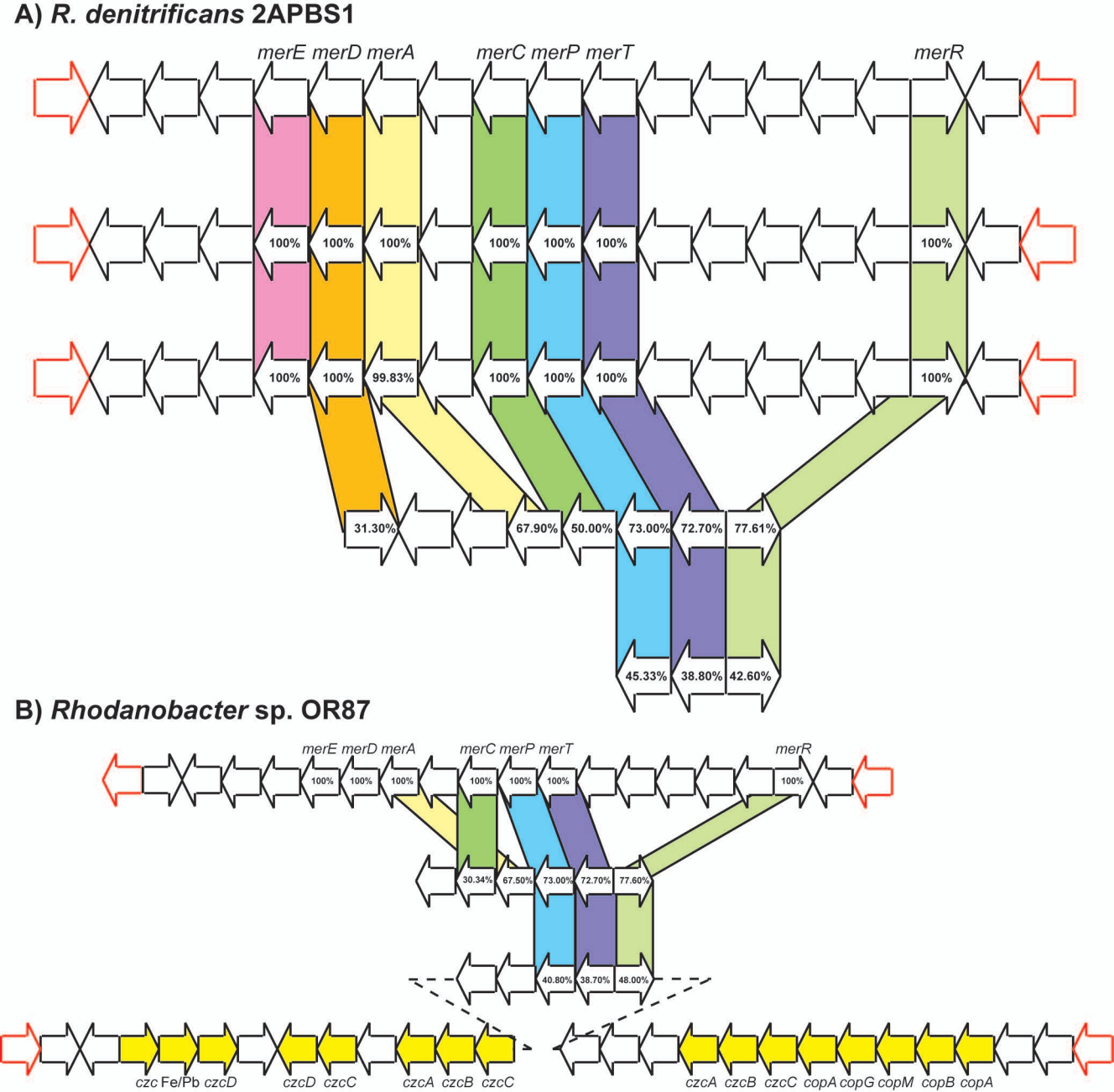


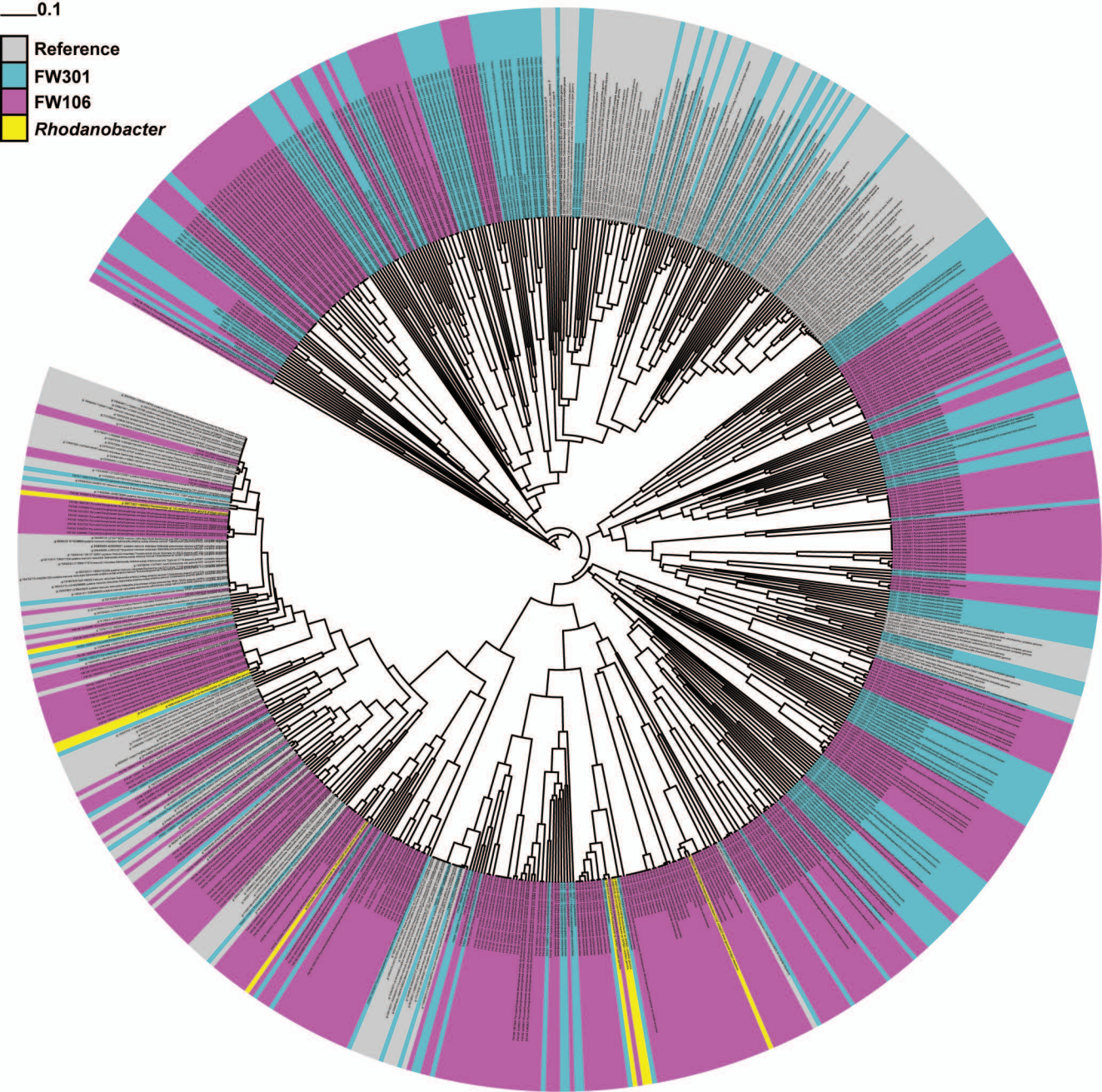
(a) Self = Rhodanobacter Genus

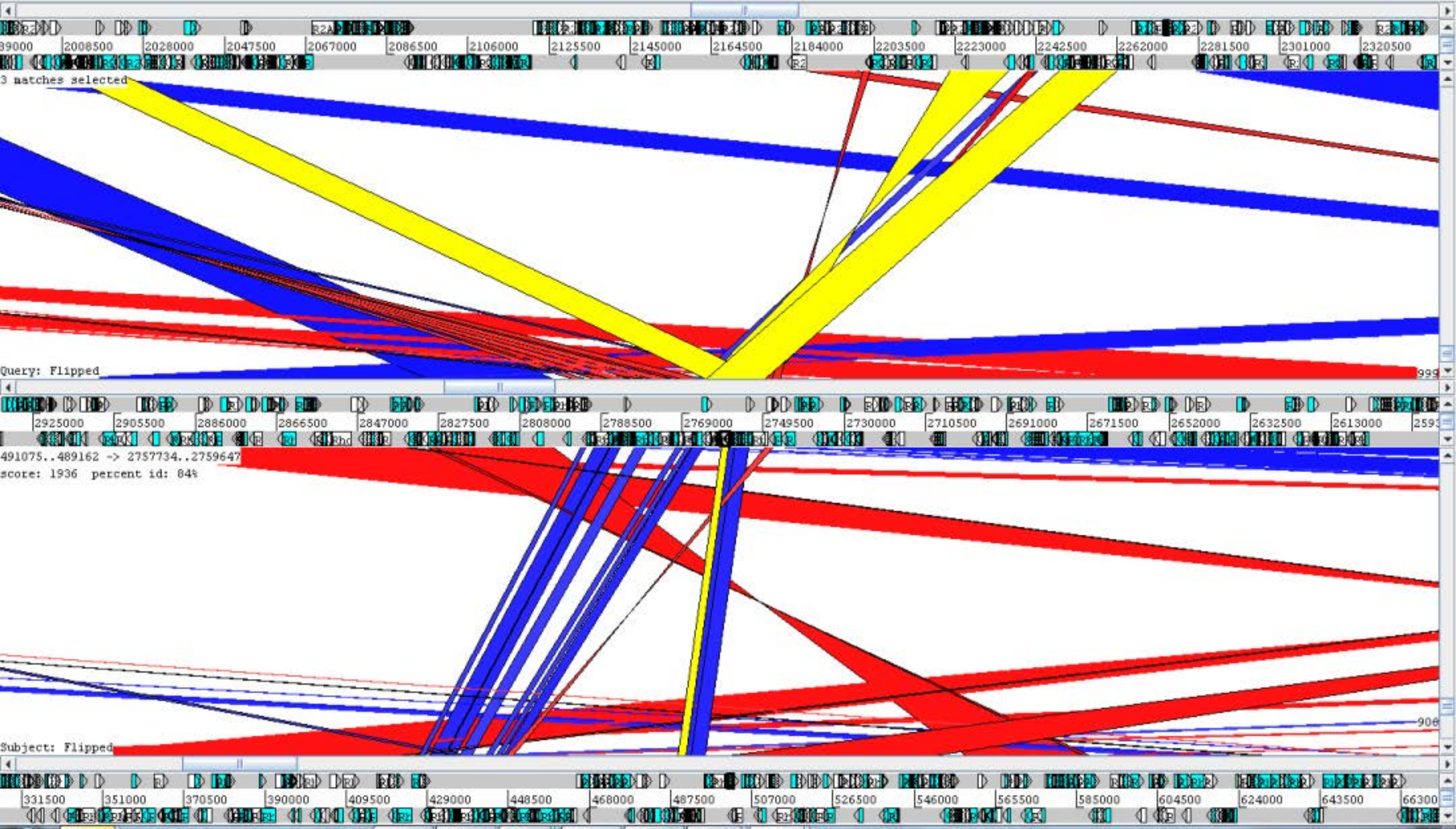
(b) Self = Rhodanobacter sp. 2APBS1


Rhodanobacter denitrificans 2APBS1
Rhodanobacter sp. OR87
Rhodanobacter sp. OR92
Rhodanobacter sp. 115
Rhodanobacter denitrificans sp. 116-2
Rhodanobacter thiooxydans
Rhodanobacter fulvus
Rhodanobacter spathiphylli
AU (JS Distance)
Kb


A) R2APBS1_2892
gi|505071441 Nitrate/nitrite transporter Thioalkalivibrio nitratireducens
gi|489385671 nitrate/nitrite antiporter Pseudomonas stutzeri
gi|627772427 antiporter Pseudomonas stutzeri
FW301 17473811
gi|121602919|4014217−4015884 Polaromonas naphthalenivorans CJ
FW106 10320282 Major Facilitator Superfamily
FW106 10194711 Major Facilitator Superfamily
FW106 10311941 Major Facilitator Superfamily
FW106 10358971 Major Facilitator Superfamily
FW106 10413941 Major Facilitator Superfamily
FW106 10465272 Major Facilitator Superfamily
FW106 10489551 Major Facilitator Superfamily
FW106 100021120 Major Facilitator Superfamily
gb|AJXW01000003.1|19759−18104 Rhodanobacter thiooxydans
2585741338 RhoFW104T7 00833 MFS Rhodanobacter sp. FW104−T
2585807183 RhoFW510R12 04787 MFS Rhodanobacter sp. FW510−R1
2522340129 RHOOR444DRAFT 02427 MFS Rhodanobacter sp. OR444
2585738089 RhoFW104R5 07407 MFS Rhodanobacter sp. FW104−R
2585729585 RhoFW104R3 06366 MFS Rhodanobacter sp. FW104−R
2510413925 Nitrate/Nitrite transporter Rhodanobacter sp. OR87
2510321964 Nitrate/Nitrite transporter Rhodanobacter sp. OR92
gb|CP003470.1|3019956−3021611 Rhodanobacter sp. 2APBS
gb|AJXV01000003.1|70895−72550 Rhodanobacter sp. 116−2
gi|518167602 MFS transporter Stenotrophomonas maltophilia
gi|655456675 nitrate/nitrite transporter NarK Thermomonas fusca
2585796483 RhoFW510T8 02422 nitrite ext prot Rhodanobacter sp. FW510−T8
2585790838 RhoFW104R8 00189 nitrite ext prot Rhodanobacter sp. FW104−R
2585811014 RhoFW510R12 08626 nitrite ext prot Rhodanobacter sp. FW512−R1
2585813359 RhoFW510R10 02318 nitrite ext prot Rhodanobacter sp. FW510−R1
0.01
B) R2APBS1_2893
2538848278 UU9 06324 major facilitator superfamily protein Rhodanobacter fulvus Jip2
2585796477 RhoFW510T8 02416 Nitrate/nitrite transporter Rhodanobacter sp. FW510−T8
2585733454 RhoFW104R5 02763 Nitrate/nitrite transporter Rhodanobacter sp. FW104−R5
2585813353 RhoFW510R10 02312 Nitrate/nitrite transporter Rhodanobacter sp. FW510−R10
2585741337 RhoFW104T7 00832 Nitrate/nitrite transporter Rhodanobacter sp. FW104−T7
2585729586 RhoFW104R3 06367 Nitrate/nitrite transporter Rhodanobacter sp. FW104−R3
2585738090 RhoFW104R5 07408 Nitrate/nitrite transporter Rhodanobacter sp. FW104−R5
2585807184 RhoFW510R12 04788 Nitrate/nitrite transporter Rhodanobacter sp. FW510−R12
2522340128 RHOOR444DRAFT 02426 Nitrate/nitrite transporter Rhodanobacter sp. OR444
FW301 11867741 Major Facilitator Superfamily
gb|CP002986.1|c2525128−2523797 Stenotrophomonas maltophilia JV3
FW106 100021122 Nitrate/nitrite transporter
FW106 10537861 Major Facilitator Superfamily
gb|AJXW01000003.1|16617−17939 Rhodanobacter thiooxydans LCS2
gb|AJXV01000003.1|69396−70718 Rhodanobacter sp. 116−2
gi|469816339|c3023115−3021793 Rhodanobacter sp. 2APBS1
2510413926 Nitrate/nitrite transporter Rhodanobacter sp. OR87
2510321965 Nitrate/nitrite transporter Rhodanobacter sp. OR92
0.1


A) R. denitrificans 2APBS1
merE merD merA
merC merP merT
merR
100%
100%
100%
100%
100%
100%
100%
100%
100%
100%
100%
99.83%
100%
100%
100%
100%
31.30%
67.90%
50.00%
73.00%
72.70%
77.61%
45.33%
38.80%
42.60%
B) Rhodanobacter sp. OR87
merE merD merA
merC merP merT
merR
100%
100%
100%
100%
100%
100%
100%
30.34%
67.50%
73.00%
72.70%
77.60%
40.80%
38.70%
48.00%
czc Fe/Pb czcD
czcD czcC
czcA czcB czcC
czcA czcB czcC copA copG copM copB copA


0.1
Reference
FW301
FW106
Rhodanobacter


3 matches selected
Query: Flipped
491075..489162 -> 2757734..2759647
score: 1936 percent id: 84%
Subject: Flipped

1) *R. denitrificans* 2APBS1
2) *R.* sp. FW104-R5
3) *R.* sp. OR87
4) *R.* sp. OR92
5) *R.* sp. 115
6) *R.* sp. 116
7) *R.* sp. FW104-R3
8) *R.* sp. OR444
9) *R.* sp. FW104-R8
10) *R.* sp. FW104-T7
11) *R.* sp. FW510-T8
12) *R.* sp. FW510-R12
13) *R.* sp. FW510-R10
14) *R. fulvus* Jip2
15) *R. thiooxydans* LCS2

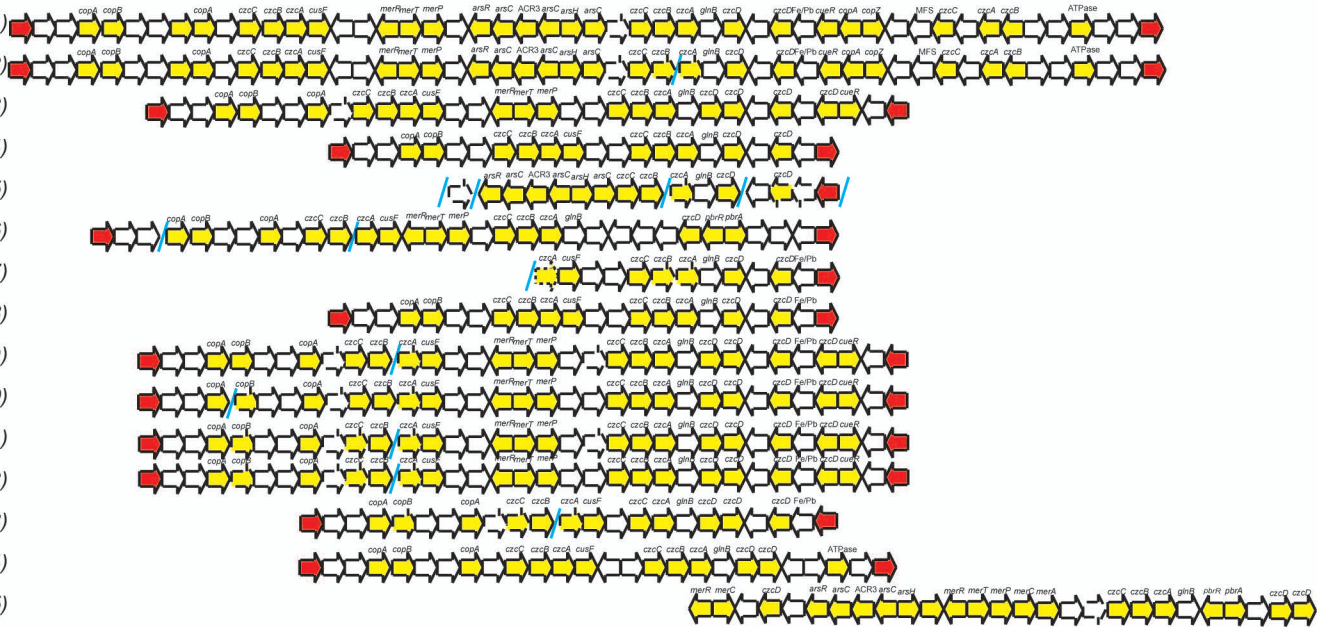


Table S1. 16S Samples from 100 OR-IFRC Wells Project with Significant Hits to *Rhodanobacter* 16S Sequences. *Rhodanobacter* sequences were obtained from the Ribosomal Database and compared to OR-IFRC 100 Well Survey 16S samples using BlastN. Only hits resulting in >97% identity between the query and well sequence were counted.

Area[a]	Well	# Blast Hits to *Rhodanobacter* >97% identity	%Sequences Assigned to *Rhodanobacter*
1	FW-021	40076	10.8
2	TPB16	79	0.0
3	FW-104	7016	1.9
3	FW-106	125277	33.8
3	FW-109-40	25231	6.8
3	FW-109-35	1570	0.4
3	FW-126	18	0.0
3	GW-101	0	0.0
5	FW-511	2451	0.7
-	GW-314	52	0.0
-	GW-705	17	0.0
Background	FW-300	27	0.0
Background	FW-301	292	0.1
Background	FW-303	123	0.0
NT3-NT8	GW-056	16	0.0
NT3-NT8	GW-057	21	0.0
NT3-NT8	GW-089	25	0.0
NT3-NT8	GW-162	5	0.0
NT3-NT8	GW-228	13	0.0
NT3-NT8	GW-621	86	0.0
NT3-NT8	GW-654	17	0.0
NT3-NT8	GW-683	28	0.0
NT3-NT8	GW-685	29	0.0
NT3-NT8	GW-694	4	0.0

NT3-NT8	GW-704	52	0.0
NT3-NT8	GW-706	46	0.0
NT3-NT8	GW-714	10	0.0
NT3-NT8	GW-715	12	0.0
NT3-NT8; Waste Management	GW-098	174	0.0
NT3-NT8; Waste Management	GW-363	299	0.1
NT3-NT8; Waste Management	GW-636	34	0.0
NT3-NT8; Waste Management	GW-639	16	0.0
NT3-NT8; Waste Management	GW-641	245	0.1
NT3-NT8; Waste Management	GW-921	167	0.0
NT3-NT8; Waste Management	GW-925	21	0.0
Y-12 East	GW-148	164	0.0
Y-12 East	GW-151	1813	0.5
Y-12 East	GW-198	33	0.0
Y-12 East	GW-199	24	0.0
Y-12 East	GW-220	218	0.1
Y-12 East	GW-223	28	0.0
Y-12 East	GW-271	12	0.0
Y-12 East	GW-283	33	0.0
Y-12 East	GW-383	80	0.0
Y-12 East	GW-384	132	0.0
Y-12 East	GW-385	6	0.0
Y-12 East	GW-60-1A	13	0.0
Y-12 East	GW-658	32	0.0
Y-12 East	GW-750	260	0.1
Y-12 East	GW-753	13	0.0
Y-12 East	GW-754	17	0.0
Y-12 East	GW-755	59	0.0
Y-12 East	GW-760	3	0.0
Y-12 East	GW-761	28	0.0

Y-12 East	GW-763	110	0.0
Y-12 East	GW-764	1615	0.4
Y-12 East	GW-765	40	0.0
Y-12 East	GW-773	42	0.0
Y-12 East	GW-775	23	0.0
Y-12 East	GW-779	16	0.0
Y-12 East	GW-782	16	0.0
Y-12 East	GW-803	114	0.0
Y-12 East	GW-804	17	0.0
Y-12 East	GW-928	30	0.0
Y-12 East	GW-929	80	0.0
Y-12 East Secure	GW-350	13	0.0
Y-12 West	DP16D	988	0.3
Y-12 West	FW-021	29003	7.8
Y-12 West	FW-104	9172	2.5
Y-12 West	FW-106	124	0.0
Y-12 West	FW-109-35	53187	14.3
Y-12 West	FW-109-40	21984	5.9
Y-12 West	FW-126	0	0.0
Y-12 West	FW-215	208	0.1
Y-12 West	FW-233-17-	111	0.0
Y-12 West	FW-410-28	8143	2.2
Y-12 West	FW-507	0	0.0
Y-12 West	FW-510	18928	5.1
Y-12 West	FW-511	14924	4.0
Y-12 West	FW-602-2-2	70	0.0
Y-12 West	FW-603	388	0.1
Y-12 West	GW-066	8	0.0
Y-12 West	GW-084	5	0.0
Y-12 West	GW-085	875	0.2

Y-12 West	GW-086	342	0.1
Y-12 West	GW-101	47	0.0
Y-12 West	GW-105	288	0.1
Y-12 West	GW-107	29	0.0
Y-12 West	GW-115	50	0.0
Y-12 West	GW-122	64	0.0
Y-12 West	GW-123	14	0.0
Y-12 West	GW-125	7	0.0
Y-12 West	GW-127	45	0.0
Y-12 West	GW-190	28	0.0
Y-12 West	GW-246	67	0.0
Y-12 West	GW-247	156	0.0
Y-12 West	GW-345	46	0.0
Y-12 West	GW-346	48	0.0
Y-12 West	GW-526	0	0.0
Y-12 West	GW-531	25	0.0
Y-12 West	GW-533	21	0.0
Y-12 West	GW-537	32	0.0
Y-12 West	GW-631	77	0.0
Y-12 West	GW-736	49	0.0
Y-12 West	GW-737	50	0.0
Y-12 West	GW-800	14	0.0
Y-12 West	PTMW-02	2407	0.6
Y-12 West	TPB16	108	0.0

[a] OR-IFRC is divided into areas containing wells. Background represents uncontaminated background site ~1 km from former S-3 waste disposal ponds. Area 3 is located at the base of the contaminated groundwater plume emanating from the S-3 ponds. Area 1 is a contaminated plot located immediately south of Area 3 and the S-3 ponds. Area 2 is a contaminated site west of Area 1, Areas 4 is located west of Area 3 and Area 5 is located east of Area 3 and the S-3 ponds upstream of the contaminant plums.

Table S2. Predicted Lateral Transfer of Metal Resistance Genes in *R. denitrificans* 2APBS1 Detected by Alien Hunter, DarkHorse and GOHTAM. Genes are listed in order of appearance in the genome.

Locus Tag	Gene	Alien Hunter	DarkHorse	GOHTAM	Source of LGT Event (DarkHorse)
R2APBS1_0160	*arsR*	NO	NO	NO	*Hyphomicrobium denitrificans* 1NES1
R2APBS1_0352	*nitR*	NO	YES	NO	*Methyloversatilis universalis* FAM5
R2APBS1_0926	*nitR*	YES	YES	YES	*Sulfuricella denitrificans* skB26
R2APBS1_1288	*copA*	NO	NO	NO	*Sulfuricella denitrificans* skB26
R2APBS1_1289	*copB*	NO	YES	NO	*Sulfuricella denitrificans* skB26
R2APBS1_1290	*copM*	NO	NO	NO	*Alicycliphilus denitrificans* BC
R2APBS1_1291	*copG*	NO	YES	NO	*Herbaspirillum* sp. GW103
R2APBS1_1293	*czcC*	NO	NO	NO	*Cupriavidus basilensis* OR16
R2APBS1_1294	*czcB*	NO	NO	NO	*Ralstonia* sp. 5_7_47FAA
R2APBS1_1295	*czcA*	NO	NO	NO	*Cupriavidus basilensis* OR16
R2APBS1_1299	*chrF*	NO	YES	YES	*Burkholderia terrae* BS001
R2APBS1_1300	*chrB*	NO	NO	NO	*Burkholderia terrae* BS001
R2APBS1_1302	*chrA*	NO	YES	NO	*Burkholderia terrae* BS001
R2APBS1_1407	*arsH*	NO	YES	NO	*Burkholderia terrae* BS001
R2APBS1_1408	*arsC*	NO	NO	NO	*Burkholderia ambifaria* MEX-5
R2APBS1_1409	*arsB*	NO	YES	NO	*Burkholderia terrae* BS001
R2APBS1_1410	*arsR*	NO	NO	NO	*Oxalobacteraceae* bacterium IMCC9480
R2APBS1_1712	*copA*	YES	NO	YES	*Ferrimonas balearica* DSM 9799
R2APBS1_1713	*copB*	YES	YES	YES	*Klebsiella* sp. ND3
R2APBS1_1714	*copM*	YES	NO	YES	*Alishewanella aestuarii* B11
R2APBS1_1715	*copG*	YES	YES	YES	*Escherichia coli* UMNF18
R2APBS1_1719	*czcC*	YES	NO	NO	*Alishewanella aestuarii* B11
R2APBS1_1720	*czcB*	YES	NO	NO	*Alishewanella* sp. HW16

R2APBS1_1721	*czcA*	YES	NO	NO	*Alishewanella aestuarii* B11
R2APBS1_1729	*arsR*	YES	YES	YES	*Alishewanella agri* BL06
R2APBS1_1730	*arsC*	YES	YES	YES	*Alishewanella aestuarii* B11
R2APBS1_1731	*arsB*	YES	YES	YES	*Alishewanella aestuarii* B11
R2APBS1_1732	*arsC*	YES	NO	YES	*Pseudomonas* sp. Ag1
R2APBS1_1733	*arsH*	YES	YES	YES	*Pseudomonas aeruginosa* NCMG1179
R2APBS1_1735	*czcC*	YES	NO	NO	*Pseudomonas aeruginosa* 39016
R2APBS1_1736	*czcB*	YES	NO	NO	*Burkholderiales* bacterium JOSHI_001
R2APBS1_1737	*czcA*	YES	NO	NO	*Burkholderiales* bacterium JOSHI_001
R2APBS1_1748	*czcC*	YES	NO	NO	*Hydrocarboniphaga effusa* AP103
R2APBS1_1750	*czcA*	YES	YES	NO	*Hydrocarboniphaga effusa* AP103
R2APBS1_1751	*czcB*	YES	NO	NO	*Hydrocarboniphaga effusa* AP103
R2APBS1_2038	*czcC*	YES	YES	NO	*Stenotrophomonas maltophilia* D457
R2APBS1_2040	*czcA*	YES	YES	NO	*Stenotrophomonas maltophilia* D457
R2APBS1_2095	*merE*	YES	NO	NO	*Stenotrophomonas maltophilia* D457
R2APBS1_2096	*merD*	YES	NO	YES	*Stenotrophomonas maltophilia* D457
R2APBS1_2097	*merA*	YES	NO	YES	*Stenotrophomonas maltophilia* D457
R2APBS1_2099	*merC*	YES	NO	YES	*Stenotrophomonas maltophilia* D457
R2APBS1_2100	*merP*	YES	YES	NO	*Stenotrophomonas maltophilia* D457
R2APBS1_2101	*merT*	YES	NO	YES	*Stenotrophomonas maltophilia* D457
R2APBS1_2107	*merR*	YES	NO	NO	*Stenotrophomonas maltophilia* D457
R2APBS1_3418	*czcB*	NO	YES	NO	*Stenotrophomonas maltophilia* D457
R2APBS1_3419	*czcA*	NO	YES	NO	*Stenotrophomonas maltophilia* D457
R2APBS1_3784	*merR*	NO	NO	YES	*Congregibacter litoralis* KT71
R2APBS1_3785	*merT*	NO	YES	YES	*Hyphomicrobium denitrificans* 1NES1
R2APBS1_3786	*merP*	NO	NO	NO	*Methyloversatilis universalis* FAM5
R2APBS1_3788	*merA*	NO	NO	NO	*Sulfuricella denitrificans* skB26

R2APBS1_3791	*merR*	**NO**	**NO**	**NO**	*Sulfuricella denitrificans* skB26

Table S3. Assembly Statistics of Isolated *Rhodanobacter* Strains.

A)

Strain Name	kmer	# contigs	# scaffolds	NCBI Project ID	IMG Genome ID
FW104-R3	75	4635	2149	PRJNA255803	2585427563
FW104-R5	55	4950	1253	PRJNA255806	2585427564
FW104-T7	55	471	129	PRJNA255808	2585427565
FW104-R8	75	175	73	PRJNA255809	2585427584
FW510-T8	67	214	108	PRJNA255810	2585427585
FW510-R10	67	182	81	PRJNA255812	2585427588
FW510_R12	55	3156	711	PRJNA255897	2585427587

B)

Strain Name	Genome Size (bp)	Gene Count	GC%	%Genes Assigned to COG's	%Genes Assigned to KEGG
FW104-R3	5159882	7765	68	31.41	12.13
FW104-R5	7813723	9812	68	39.58	14.79
FW104-T7	4134736	3754	67	67.47	27.54
FW104-R8	3723194	3360	68	69.17	28.11
FW510-T8	3724196	3407	68	69.71	28.27
FW510-R10	3907877	3602	68	66.94	26.96
FW510-R12	7867162	8636	68	49.73	19.53