

Table S1. Parameters for reference gene (FunGene) database construction and gene-targeted assembly for each protein of interest.

FunGene Database	Protein	Minimum HMM score	Minimum length (aa)	Minimum HMM coverage (%)	Number of FunGene sequences	Number of dereplicated sequences	Minimum length (aa)
Chloramphenicol efflux pump	CmlA	298	390	80	3747	491	150
Dfra1	Dfra1	100	135	80	4659	211	50
Dfra12	Dfra12	90	130	80	26637	1252	50
IntI	IntI	90	315	80	9418	2562	150
RepA	RepA	400	220	80	387	31	150
Resfam_AAC6-Ia	AAC6-Ia	100	170	80	757	112	100
Resfam_AdeB	AdeB	1400	1000	80	53493	10025	150
Resfam_ANT3	ANT3	310	245	80	7806	790	150
Resfam_ANT6	ANT6	130	260	80	4097	1066	150
Resfam_ANT9	ANT9	400	245	80	4044	41	150
Resfam_Chloramphenicol Acetyltransferase CAT	CAT	195	200	80	9996	1299	150
Resfam_ClassA	ClassA	179	275	80	34258	5713	150
Resfam_ClassB	ClassB	76	255	80	9853	2087	150
Resfam_ClassC	ClassC	400	370	80	12916	3641	150
Resfam_ermB	Resfam_ermB	400	200	80	2090	182	100
Resfam_ermC	Resfam_ermC	265	200	80	7173	246	100
Resfam_MexC	MexC	300	340	80	2569	720	150
Resfam_MexE	MexE	400	390	80	1567	665	150
Resfam_Quinolone Resistance Protein Qnr	Qnr	230	200	80	2562	558	100
Resfam_tetA	TetA	680	390	80	2060	70	150
Resfam_tetD	TetD	795	350	80	261	9	150
Resfam_tetX	TetX	300	360	80	227	112	150
Resfam_TolC	TolC	350	430	80	19431	3189	150
Resfam_vanA	VanA	700	300	80	250	28	150
Resfam_vanC	VanC	730	300	80	35	29	150
Resfam_vanH	VanH	500	280	80	438	61	150
Resfam_vanT	VanT	600	650	80	304	97	150
Resfam_vanW	VanW	130	220	80	1311	423	150
Resfam_vanX	VanX	100	150	80	16689	2340	100
Resfam_vanY	VanY	220	300	80	250	35	150
Resfam_vanZ	VanZ	80	120	80	1042	189	100
StrA	StrA	400	230	80	4286	154	150
StrB	StrB	159	230	80	4695	222	150
tet_sul2	Sul2	200	245	80	9031	298	150
TetM	TetM	1175	600	80	5531	543	150
TetQ	TetQ	650	600	80	242	70	150
TetW	TetW	1260	600	80	345	169	150

Table S2. Sequencing depth and Nonpareil-estimated coverage of *Centralia* metagenomes.

Site name	Fire History	Sequencing depth (Gbases)	Coverage (%)
Cen01	Recovered	23	58.96
Cen03	Recovered	26	49.49
Cen04	Recovered	25	38.32
Cen05	Recovered	25	45.97
Cen06	Fire-affected	22	54.23
Cen07	Recovered	21	53.26
Cen10	Fire-affected	36	89.96
Cen12	Fire-affected	24	88.63
Cen14	Fire-affected	24	82.79
Cen15	Fire-affected	20	76.48
Cen16	Fire-affected	51	76.30
Cen17	Reference	24	29.12

Table S3. Sample site characteristics and measured soil geochemical data.

Sample	latitude	longitude	Soil temperature (°C)	Classification	Date since fire (Elick 2011)	Organic matter (500°C)	NO3- (ppm)	NH4- (ppm)	pH	S (ppm)	K (ppm)	Ca (ppm)	Mg (ppm)	Fe (ppm)	As (ppm)	Soil Moisture (%)
Cen01	40 47.926	076 20.357	14.1	Recovered	1982	3.9	0.7	2.2	4.7	1	35	194	61	48.6	2.63	7
Cen03	40 47.881	076 20.468	14.7	Recovered	2002	48.9	0.3	3.2	4.5	4	31	1416	241	54.7	7.1	5
Cen04	40 47.870	076 20.489	13.3	Recovered	1999	12.8	0.8	5	4.6	23	34	103	46	167.2	3.6	4
Cen05	40 47.831	076 20.572	14.0	Recovered	2009	25.4	5.7	5	4.1	6	43	63	43	164.5	1.75	27
Cen06	40 47.849	076 20.506	24.1	Fire affected	2014	11.9	0.8	3.2	4.7	4	46	111	52	75.6	2.05	17
Cen07	40 48.086	076 20.736	13.5	Recovered	2005	6	0.7	4	4.6	14	40	78	37	108.9	5.56	242
Cen10	40 48.062	076 20.582	54.2	Fire affected	2007	24.5	98.4	120.6	4	21	57	245	70	508	3.79	111
Cen12	40 48.078	076 20.589	32.0	Fire affected	2009	6	0.2	2	4.8	7	24	51	30	150.3	3.9	70
Cen14	40 48.040	076 20.469	34.1	Fire affected	2002	21.9	0.9	2.7	5	5	58	394	64	102.7	2.97	64
Cen15	40 48.045	076 20.489	38.9	Fire affected	2002	9.6	1.1	4	5.2	13	44	224	50	93.3	2.25	119
Cen16	40 48.048	076 20.487	21.7	Fire affected	2002	10.6	0.5	1.2	5.6	8	33	497	56	80.8	3.57	78
Cen17	40 47.998	076 20.416	12.1	Reference	NA	6.1	0.1	3.3	5.7	6	99	652	73	48.6	1.99	27

Table S4. Spearman's rank correlation between relative abundance of ARGs and soil temperature. Significant differences are bolded.

Gene	Spearman's rho	p value
AAC6-Ia	0.119326331	0.711849439
ClassA	-0.594405594	0.0457531
ClassB	-0.741258741	0.00817064
ClassC	-0.035212141	0.91348822
CEP	0.204271555	0.524238954
intI	-0.013986014	0.973693904
adeB	-0.045765054	0.887688984
tolC	-0.697619343	0.011658884
sul2	0.542908013	0.068150085
dfra12	-0.706293706	0.013286114
vanA	-0.108581603	0.736943708
vanH	-0.169018276	0.59949787
vanX	-0.125874126	0.699712221
vanZ	-0.270429867	0.39525819

Table S5. Correlations between ARG phylum and Proteobacteria class normalized abundances and soil temperature. Spearman's rank correlations with *rplB*-normalized abundance and soil temperature. Significant correlations ($p < 0.05$) are bolded.

Gene	Phylum	Spearman's rho	p value
ClassA	Acidobacteria	-0.045765054	0.887688984
ClassA	Actinobacteria	0.66567352	0.018134057
ClassA	Alphaproteobacteria	-0.293706294	0.354332534
ClassA	Betaproteobacteria	-0.8048763	0.001588848
ClassA	Deltaproteobacteria	-0.425485705	0.167901396
ClassA	Gammaproteobacteria	-0.448469578	0.143665129
ClassB	Acidobacteria	-0.440559441	0.15421575
ClassB	Alphaproteobacteria	-0.004160459	0.989761605
ClassB	Bacteroidetes	-0.086009076	0.790410909
ClassB	Betaproteobacteria	0.043671315	0.892800448
ClassB	Deltaproteobacteria	0.550736912	0.063497906
ClassB	Gammaproteobacteria	-0.384615385	0.218387427
ClassB	Gemmatimonadetes	0.393041832	0.206255757
ClassB	Verrucomicrobia	0.263402795	0.408125175
dfra12	Acidithiobacillia	-0.354787438	0.257796301
dfra12	Actinobacteria	0.070727811	0.827099003
dfra12	Alphaproteobacteria	-0.734265734	0.009052097
dfra12	Bacteroidetes	-0.683115531	0.014338998
dfra12	Betaproteobacteria	-0.690018571	0.013012243
dfra12	C. Peregrinibacteria	-0.305699203	0.333893136
dfra12	Deinococcus-Thermus	-0.082610537	0.798539196
dfra12	Deltaproteobacteria	-0.514830787	0.08675862
dfra12	Firmicutes	-0.608391608	0.040002049
dfra12	Gammaproteobacteria	0.202797203	0.528100237
dfra12	Microgenomates	0.108237592	0.737751195
dfra12	Parcubacteria	-0.330442147	0.294152738
dfra12	Verrucomicrobia	-0.156042125	0.628187113
intI	Acidithiobacillia	0.043671315	0.892800448
intI	Betaproteobacteria	-0.475524476	0.121319356
intI	Chlorobi	0.241900526	0.448765409
intI	Chloroflexi	0.06425264	0.842745428
intI	Cyanobacteria	0.366606083	0.241141519
intI	Deltaproteobacteria	-0.364273764	0.244376487
intI	Gammaproteobacteria	-0.496503497	0.104092833
intI	Gemmatimonadetes	0.319717875	0.311035387
intI	Nitrospirae	0.517482517	0.088650879
intI	Planctomycetes	0.458947427	0.133408824
intI	Verrucomicrobia	0.104011487	0.747690649

Table S6. Correlations between ARG phylum and Proteobacteria class relative abundances and soil temperature. Spearman's rank correlations with relative abundance and soil temperature. Significant correlations ($p < 0.05$) are bolded.

Gene	Phylum	Spearman's rho	p value
ClassA	Acidobacteria	-0.045765054	0.887688984
ClassA	Actinobacteria	0.66567352	0.018134057
ClassA	Alphaproteobacteria	-0.293706294	0.354332534
ClassA	Betaproteobacteria	-0.8048763	0.001588848
ClassA	Deltaproteobacteria	-0.425485705	0.167901396
ClassA	Gammaproteobacteria	-0.448469578	0.143665129
ClassB	Acidobacteria	-0.440559441	0.15421575
ClassB	Alphaproteobacteria	-0.004160459	0.989761605
ClassB	Bacteroidetes	-0.086009076	0.790410909
ClassB	Betaproteobacteria	0.043671315	0.892800448
ClassB	Deltaproteobacteria	0.550736912	0.063497906
ClassB	Gammaproteobacteria	-0.384615385	0.218387427
ClassB	Gemmatimonadetes	0.393041832	0.206255757
ClassB	Verrucomicrobia	0.263402795	0.408125175
dfra12	Acidithiobacillia	-0.354787438	0.257796301
dfra12	Actinobacteria	0.070727811	0.827099003
dfra12	Alphaproteobacteria	-0.734265734	0.009052097
dfra12	Bacteroidetes	-0.683115531	0.014338998
dfra12	Betaproteobacteria	-0.690018571	0.013012243
dfra12	C. Peregrinibacteria	-0.305699203	0.333893136
dfra12	Deinococcus-Thermus	-0.082610537	0.798539196
dfra12	Deltaproteobacteria	-0.514830787	0.08675862
dfra12	Firmicutes	-0.608391608	0.040002049
dfra12	Gammaproteobacteria	0.202797203	0.528100237
dfra12	Microgenomates	0.108237592	0.737751195
dfra12	Parcubacteria	-0.330442147	0.294152738
dfra12	Verrucomicrobia	-0.156042125	0.628187113
intI	Acidithiobacillia	0.043671315	0.892800448
intI	Betaproteobacteria	-0.475524476	0.121319356
intI	Chlorobi	0.241900526	0.448765409
intI	Chloroflexi	0.06425264	0.842745428
intI	Cyanobacteria	0.366606083	0.241141519
intI	Deltaproteobacteria	-0.364273764	0.244376487
intI	Gammaproteobacteria	-0.496503497	0.104092833
intI	Gemmatimonadetes	0.319717875	0.311035387
intI	Nitrospirae	0.517482517	0.088650879
intI	Planctomycetes	0.458947427	0.133408824
intI	Verrucomicrobia	0.104011487	0.747690649
rplB	Acidobacteria	-0.412587413	0.184480685
rplB	Actinobacteria	0.195804196	0.542873521
rplB	Alphaproteobacteria	0.251748252	0.430115289
rplB	Aquificae	-0.84354992	0.000564148
rplB	Bacteroidetes	-0.53522454	0.072939241
rplB	Betaproteobacteria	-0.664335664	0.022159207
rplB	Caldiserica	0.043671315	0.892800448
rplB	C. Saccharibacteria	0.17935393	0.577012393
rplB	Chlamydiae	-0.128974244	0.689537493
rplB	Chlorobi	0.137295163	0.67047431
rplB	Chloroflexi	0.727272727	0.010000917
rplB	Cyanobacteria	0.082610537	0.798539196
rplB	Deltaproteobacteria	-0.485927542	0.109227185

rplB	Dictyoglomi	-0.480384461	0.113937412
rplB	Elusimicrobia	0.431410581	0.161423074
rplB	Epsilonproteobacteria	-0.530263793	0.076151068
rplB	Firmicutes	0.223776224	0.48491114
rplB	Gammaproteobacteria	0.251748252	0.430115289
rplB	Gemmatimonadetes	-0.433566434	0.161446426
rplB	Ignavibacteriae	0.004160459	0.989761605
rplB	metagenomes	-0.188811189	0.557827775
rplB	Nitrospirae	-0.119326331	0.711849439
rplB	Planctomycetes	0.083916084	0.800197518
rplB	Synergistetes	0.197187988	0.53902672
rplB	Thermobaculum	0.626433696	0.029292738
rplB	Thermodesulfobacteria	-0.470131923	0.122998942
rplB	Thermotogae	-0.218356573	0.49536676
rplB	Verrucomicrobia	-0.34965035	0.266004309
rplB	Viridiplantae	0.480384461	0.113937412
