SUPPLEMENTARY ONLINE INFORMATION

Patterns of endemism and niche adaptation in coalbed microbial communities

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Running title: *Coalbed microbial communities*

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SUPPLEMENTARY FIGURES, TABLES, AND FILES

Supplementary Figure 1 Rarefaction curves for coal samples collected using different sampling methods (cores, cuttings, drilling fluids). Horizontal axis shows number of reads sampled; vertical axis indicates accumulation of OTUs. Curves that became horizontal with increasing sequencing depth indicate that full sampling depth had been reached.

Supplementary Figure 2 Bray-Curtis dissimilarities between coal samples (microbial communities) across all sampling locations based on non-metric multidimensional scaling (NMDS). Microbial communities partitioned by coal rank: sub-bituminous (blue), high volatile bituminous (orange), and volatile bituminous (green).

Supplementary Figure 3 Distribution of indicator values and p-values for all OTUs in the dataset (A). Number of abundant, intermediate, and rare indicator OTUs for each indicator group (B).

Supplementary Table 1 Sample information. Sample ID based on 4-digit identifier. First digit specifies drilling method used: coal core, CR; coal cutting, CT; drilling fluid, DF; or production waters, PW. Second digit specifies well number. Third digit specifies coal rank: high volatile bituminous, HB; volatile bituminous, VB; or subbituminous, SB. Fourth digit specifies sample depth.

Supplementary Table 2 Sample diversity estimates for pyrotag datasets. Total OTU counts, Shannon and Simpson diversity metrics, and Chao1 richness estimates for each sample collected. Diversity metrics calculated from OTU table rarified to 1,050 reads. Shannon and Simpson indices consider both OTU (97% similarity cutoff) richness and evenness. Inverse Simpson indices are reported. Chao1 indices consider OTU richness.

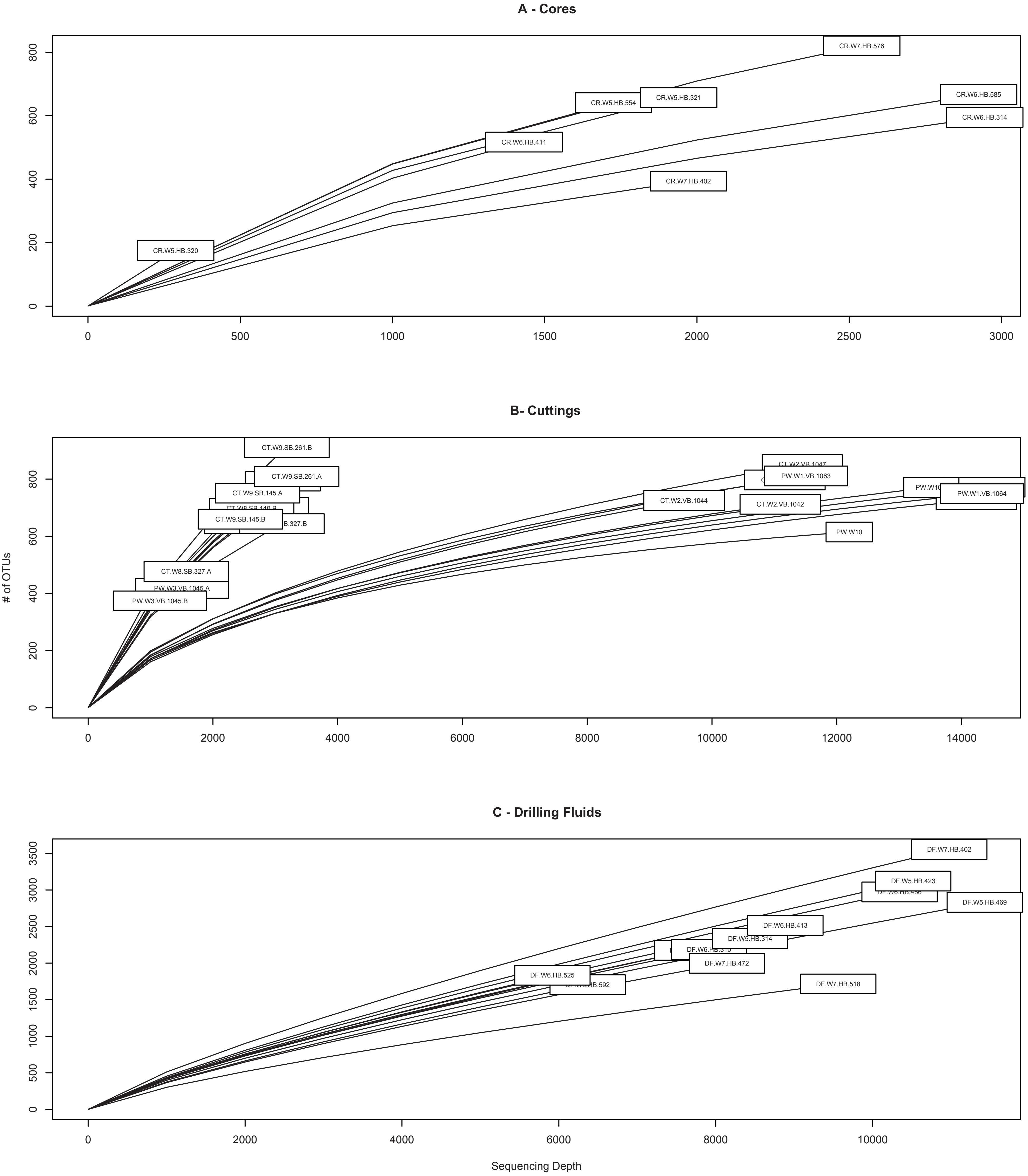
Supplementary Table 3 Metagenomic binning statistics. Genome completeness based on number of 107 single-copy TIGRFAM marker genes recovered. Genome contamination based on the number of single-copy TIGRFAM markers found in duplicate.

Supplementary Table 4 Aromatic compound degradation coding sequences annotated in the Celeribacter sp. population genome (Bin 1).

Supplementary File 1 Bin 1 ORF annotations. ORF annotations based on best BLASTP hits (e-value E-6) against the RefSeq database.

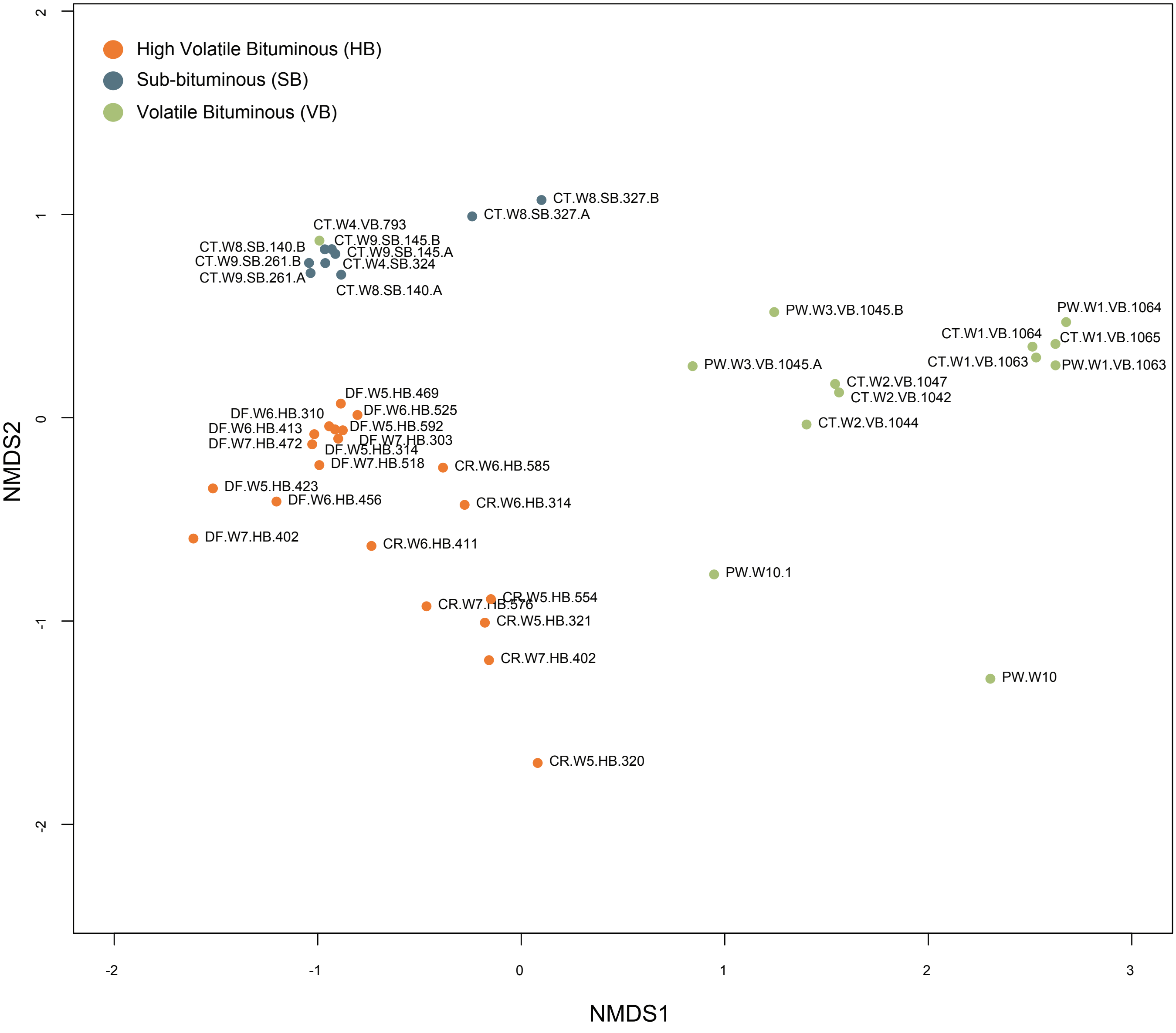
Supplementary File 2 (A) MetaCyc pathway table for *Paraccocus N5*, *S. mucosus*, *C. baekdonensis*, and Bin 1 (*Celeribacter* sp.) pathway/genome databases (PGDBs). (B) MetaCyc pathways and supporting reactions for Bin 1 (*Celeribacter* sp.*)* PGDB. Pathways were inferred using MetaPathways from annotated open reading frames and manual curation.

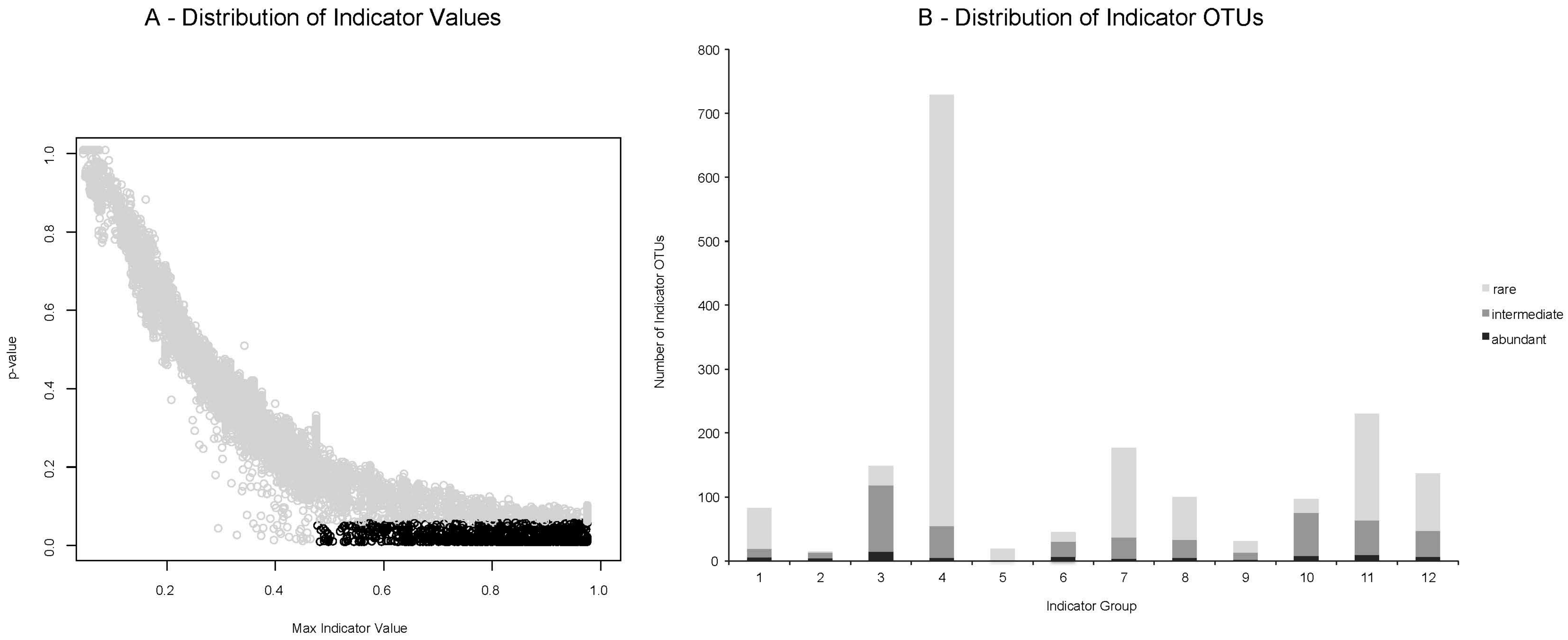
Supplementary File 3 Variable genomic regions in Bin 1 population genome.



Supplementary Figure 1 Rarefaction curves for coal samples collected using different sampling methods (cores, cuttings, drilling fluids).

Supplementary Figure 2: NMDS/Bray - Stress = 0.127





A - Distribution of Indicator Values

B - Distribution of Indicator OTUs

Supplmentary Figure 3 Distribution of indicator values and p-values for all OTUs

Table S1 Sample Information

Sample ID	Collection Method	Well No.	Coal Rank	Formation	Total reads[a]	Pressure (kPa)	Temperature (°C)	Salinity (TDS)	Depth (m)
Cores									
CR-W5-HB-320	Core	5	High Volatile Bituminous C	Horseshoe Canyon	288	2,500	22	2,000	320.70
CR-W5-HB-321	Core	5	High Volatile Bituminous C	Horseshoe Canyon	1940	2,500	22	2,000	321.96
CR-W5-HB-554	Core	5	High Volatile Bituminous C	Horseshoe Canyon	1726	2,500	22	2,000	544.50
CR-W6-HB-314	Core	6	High Volatile Bituminous C	Horseshoe Canyon	2945	2,500	22	2,000	314.60
CR-W6-HB-411	Core	6	High Volatile Bituminous C	Horseshoe Canyon	1432	2,500	22	2,000	411.60
CR-W6-HB-585	Core	6	High Volatile Bituminous C	Horseshoe Canyon	2925	2,500	22	2,000	585.00
CR-W7-HB-402	Core	7	High Volatile Bituminous C	Horseshoe Canyon	1972	2,500	22	2,000	402.00
CR-W7-HB-576	Core	7	High Volatile Bituminous C	Horseshoe Canyon	2541	2,500	22	2,000	576.26
Drilling Fluids (core-associated)									
DF-W5-HB-314	Drilling Fluid	5	High Volatile Bituminous C	Horseshoe Canyon	7311	2,500	22	2,000	314
DF-W5-HB-423	Drilling Fluid	5	High Volatile Bituminous C	Horseshoe Canyon	9038	2,500	22	2,000	423
DF-W5-HB-469	Drilling Fluid	5	High Volatile Bituminous C	Horseshoe Canyon	10056	2,500	22	2,000	469
DF-W5-HB-592	Drilling Fluid	5	High Volatile Bituminous C	Horseshoe Canyon	5503	2,500	22	2,000	592
DF-W6-HB-310	Drilling Fluid	6	High Volatile Bituminous C	Horseshoe Canyon	6841	2,500	22	2,000	310
DF-W6-HB-413	Drilling Fluid	6	High Volatile Bituminous C	Horseshoe Canyon	7669	2,500	22	2,000	413
DF-W6-HB-456	Drilling Fluid	6	High Volatile Bituminous C	Horseshoe Canyon	8903	2,500	22	2,000	456
DF-W6-HB-525	Drilling Fluid	6	High Volatile Bituminous C	Horseshoe Canyon	4972	2,500	22	2,000	525
DF-W7-HB-303	Drilling Fluid	7	High Volatile Bituminous C	Horseshoe Canyon	6623	2,500	22	2,000	303
DF-W7-HB-402	Drilling Fluid	7	High Volatile Bituminous C	Horseshoe Canyon	9351	2,500	22	2,000	402
DF-W7-HB-472	Drilling Fluid	7	High Volatile Bituminous C	Horseshoe Canyon	7134	2,500	22	2,000	472
DF-W7-HB-518	Drilling Fluid	7	High Volatile Bituminous C	Horseshoe Canyon	8759	2,500	22	2,000	518
Cuttings									
CT-W1-VB-1063	Cutting	1	Volatile Bituminous A or B	Upper Mannville	11168	10,150	35-40	60,000	1063
CT-W1-VB-1064	Cutting	1	Volatile Bituminous A or B	Upper Mannville	14372	10,150	35-40	60,000	1,064.40
CT-W1-VB-1065	Cutting	1	Volatile Bituminous A or B	Upper Mannville	14237	10,150	35-40	60,000	1,065.70
CT-W2-VB-1042	Cutting	2	Volatile Bituminous A or B	Upper Mannville	11094	10,150	32-35	60,000	1,042.30
CT-W2-VB-1044	Cutting	2	Volatile Bituminous A or B	Upper Mannville	9551	10,150	32-35	60,000	1,044.90
CT-W2-VB-1047	Cutting	2	Volatile Bituminous A or B	Upper Mannville	11450	10,150	32-35	60,000	1,047.10
CT-W4-VB-793	Cutting	4	Volatile Bituminous A or B	Horseshoe Canyon	3106	1,000	22	10,000	793
CT-W4-SB-324	Cutting	4	Sub-bituminous	Scollard (Ardley)	1572	1,000	22	2,000	324
CT-W8-SB-140.A	Cutting	8	Sub-bituminous	Horseshoe Canyon	3120	1,000	20	1,000	140
CT-W8-SB-140.B	Cutting	8	Sub-bituminous	Belly River	2462	1,000	20	1,000	140
CT-W8-SB-327.A	Cutting	8	Sub-bituminous	Belly River	2856	1,500	20	1,000	327
CT-W8-SB-327.B	Cutting	8	Sub-bituminous	Belly River	2620	4,500	20	1,000	327
CT-W9-SB-145.A	Cutting	9	Sub-bituminous	Belly River	2714	1,000	20	1,000	145
CT-W9-SB-145.B	Cutting	9	Sub-bituminous	Belly River	2440	1,000	20	1,000	145
CT-W9-SB-261.A	Cutting	9	Sub-bituminous	Belly River	3342	1,000	20	1,000	261
CT-W9-SB-261.B	Cutting	9	Sub-bituminous	Belly River	3186	1,000	20	1,000	261
Production Waters (cutting-associated)									
PW-W1-VB-1063	Production Water	1	Volatile Bituminous A or B	Upper Mannville	11507	10,150	35-40	60,000	1,063
PW-W1-VB-1064	Production Water	1	Volatile Bituminous A or B	Upper Mannville	14328	10,150	35-40	60,000	1,064.40
PW-W3-VB-1045.A	Production Water	3	Volatile Bituminous A or B	Upper Mannville	1504	9,000-10,000	41	50,000-60,000	1,045.50
PW-W3-VB-1045.B	Production Water	3	Volatile Bituminous A or B	Upper Mannville	1151	9,000-10,000	41	50,000-60,001	1,045.50
PW-W10-VB.A	Production Water	10	Volatile Bituminous A or B	Upper Mannville	12201	-	-	-	-
PW-W10-VB.B	Production Water	10	Volatile Bituminous A or B	Upper Mannville	13516	-	-	-	-

[a] Singletons removed

Table S2 Sample Diversity Estimates

Sample	Total OTUs	Rarified OTUs	Shannon	Simpson	Chao1
Cores					
CR-W5-HB-554	641	501	5.49	78.13	1207
CR-W7-HB-576	820	508	5.37	58.00	1421
CR-W5-HB-321	657	473	5.28	59.16	1018
CR-W6-HB-411	517	450	5.25	66.07	1208
CR-W6-HB-585	667	365	4.64	30.73	1228
CR-W6-HB-314	595	310	4.16	12.05	792
CR-W7-HB-402	394	275	3.96	12.93	687
CR-W5-HB-320*	175	-	-	-	-
Drilling fluids					
DF-W6-HB-456	1785	456	5.20	59.01	1559
DF-W7-HB-402	1257	357	4.49	25.88	1032
DF-W7-HB-472	1533	380	4.48	20.35	1193
DF-W6-HB-310	1085	334	4.32	17.71	943
DF-W6-HB-525	891	342	4.32	18.85	1088
DF-W5-HB-314	1189	344	4.25	17.42	1001
DF-W7-HB-303	984	285	4.20	18.17	893
DF-W6-HB-413	1418	323	4.17	13.11	914
DF-W5-HB-592	790	282	4.06	17.21	805
DF-W5-HB-469	1470	361	3.79	5.97	1237
DF-W7-HB-518	916	248	3.77	14.07	678
DF-W5-HB-423	989	294	3.75	9.54	1017
Cuttings					
CT-W9-SB-261.B	910	451	5.03	39.59	1364
CT-W8-SB-140.A	702	413	4.85	29.62	1020
CT-W9-SB-261.A	809	394	4.79	32.08	1325
CT-W4-SB-324	793	393	4.78	28.04	1021
CT-W8-SB-140.B	698	399	4.77	27.53	1179
CT-W9-SB-145.A	751	411	4.73	25.74	1096
CT-W8-SB-327.B	644	389	4.66	22.27	1151
CT-W8-SB-327.A	477	365	4.62	22.35	853
CT-W9-SB-145.B	660	394	4.55	20.98	1122
CT-W4-VB-793	645	357	4.37	17.51	874
CT-W1-VB-1063	797	220	3.52	10.61	595
CT-W2-VB-1047	852	210	3.31	8.70	626
CT-W1-VB-1064	772	192	3.24	9.96	665
CT-W2-VB-1044	725	202	3.18	6.59	571
CT-W1-VB-1065	728	182	3.17	8.89	522
CT-W2-VB-1042	712	185	3.15	8.60	450
Production Waters					
PW-W3-VB-1045.B	771	373	4.70	25.94	735
PW-W3-VB-1045.A	615	349	4.38	14.29	739
PW-W1-VB-1063	811	206	3.34	10.72	656
PW-W10-VB.A	418	185	3.18	6.22	461
PW-W1-VB-1064	749	199	3.17	8.79	542
PW-W10-VB.B	374	224	3.07	4.34	494

Notes: Diversity metrics calcualted from OTU table rarified to 1,050 reads. *Sample contained <1,050 reac

Table S3 MaxBin Summary and Marker Predictions

Bin Statistics		**Bin001**	**Bin002**
	Coverage	17.53	3.84
	Genome completeness	99%	63%
	Genome contamination	8%	33%
	Genome size	4,691,774 bp	2,943,087 bp
	GC content	60%	50%
	Predicted ORFs	4755	3812
	Total marker	115	89
	Unique marker	106	67
	Taxonomic classification, sister lineage (PhyloSift)	*C. baekdonensis*	*A. dehalogenens*
TIGRFAM Accession	*Product*	*Single-copy genes*	
PGK	N/A	1	1
Ribosomal_L23	ribosomal protein L23	1	-
Ribosomal_L5	ribosomal protein L5	1	2
Ribosomal_L3	ribosomal protein L3	1	-
Ribosomal_L6	ribosomal protein L6	2	-
Ribosomal_S17	ribosomal protein S17	1	3
Ribosomal_S9	ribosomal protein S9	1	1
Ribosomal_S8	ribosomal protein S8	1	1
Ribosomal_S11	ribosomal protein S11	2	1
Ribosomal_S13	ribosomal protein S13	1	2
Ribosomal_L10	ribosomal protein L10	1	1
Ribosomal_L4	ribosomal protein L4	1	-
tRNA-synt_1d	tRNA synthetases class I	1	1
GrpE	protein GrpE	1	1
Methyltransf_5	methyltransferase	1	2
TIGR00001	ribosomal protein L35	1	1
TIGR00002	ribosomal protein S16	2	1
TIGR00009	ribosomal protein L28	1	-
TIGR00012	ribosomal protein L29	1	3
TIGR00019	peptide chain release factor 1	1	-
TIGR00029	ribosomal protein S20	1	-
TIGR00043	probable rRNA maturation factor YbeY	1	3
TIGR00059	ribosomal protein L17	1	3
TIGR00060	ribosomal protein L18	1	-
TIGR00061	ribosomal protein L21	1	-
TIGR00062	ribosomal protein L27	1	-
TIGR00064	signal recognition particle-docking protein FtsY	1	1
TIGR00082	ribosome-binding factor A	1	-
TIGR00086	SsrA-binding protein	1	-
TIGR00092	GTP-binding protein YchF	2	1
TIGR00115	trigger factor	1	1
TIGR00116	translation elongation factor Ts	1	-
TIGR00152	dephospho-CoA kinase	1	-
TIGR00158	ribosomal protein L9	1	1
TIGR00165	ribosomal protein S18	1	1
TIGR00166	ribosomal protein S6	1	1
TIGR00168	translation initiation factor IF-3	1	-
TIGR00234	tyrosine--tRNA ligase	1	1

TIGR00337	CTP synthase	1	-
TIGR00344	alanine--tRNA ligase	1	1
TIGR00362	chromosomal replication initiator protein DnaA	1	1
TIGR00389	glycine--tRNA ligase	1	-
TIGR00392	isoleucine--tRNA ligase	1	1
TIGR00396	leucine--tRNA ligase	1	1
TIGR00409	proline--tRNA ligase		-
TIGR00414	serine--tRNA ligase	1	1
TIGR00418	threonine--tRNA ligase	1	1
TIGR00420	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	1	1
TIGR00422	valine--tRNA ligase	2	1
TIGR00435	cysteine--tRNA ligase	1	-
TIGR00436	GTP-binding protein Era	1	-
TIGR00442	histidine--tRNA ligase	1	1
TIGR00459	aspartate--tRNA ligase	1	1
TIGR00460	methionyl-tRNA formyltransferase	1	1
TIGR00468	phenylalanine--tRNA ligase, alpha subunit	1	1
TIGR00472	phenylalanine--tRNA ligase, beta subunit	1	1
TIGR00487	translation initiation factor IF-2	1	-
TIGR00496	ribosome recycling factor	1	-
TIGR00575	DNA ligase, NAD-dependent	1	1
TIGR00631	excinuclease ABC subunit B	1	1
TIGR00663	DNA polymerase III, beta subunit	1	1
TIGR00755	ribosomal RNA small subunit methyltransferase A	1	1
TIGR00810	preprotein translocase, SecG subunit	1	-
TIGR00855	ribosomal protein L7/L12	1	1
TIGR00922	transcription termination/antitermination factor NusG	2	-
TIGR00952	ribosomal protein S15	1	-
TIGR00959	signal recognition particle protein	2	1
TIGR00963	preprotein translocase, SecA subunit	1	-
TIGR00964	preprotein translocase, SecE subunit	2	-
TIGR00967	preprotein translocase, SecY subunit	1	1
TIGR00981	ribosomal protein S12	1	1
TIGR01009	ribosomal protein S3	1	2
TIGR01011	ribosomal protein S2	1	1
TIGR01017	ribosomal protein S4	2	1
TIGR01021	ribosomal protein S5	1	-
TIGR01024	ribosomal protein L19	1	-
TIGR01029	ribosomal protein S7	1	2
TIGR01030	ribosomal protein L34	1	-
TIGR01031	ribosomal protein L32	1	1
TIGR01032	ribosomal protein L20	1	1
TIGR01044	ribosomal protein L22	1	2
TIGR01049	ribosomal protein S10	1	-
TIGR01050	ribosomal protein S19	1	2
TIGR01059	DNA gyrase, B subunit	1	-
TIGR01063	DNA gyrase, A subunit	1	-
TIGR01066	ribosomal protein L13	1	1
TIGR01067	ribosomal protein L14	1	3
TIGR01071	ribosomal protein L15	1	1
TIGR01079	ribosomal protein L24	1	1

TIGR01164	ribosomal protein L16	1	3
TIGR01169	ribosomal protein L1	1	1
TIGR01171	ribosomal protein L2	1	1
TIGR01391	DNA primase	1	3
TIGR01393	elongation factor 4	1	1
TIGR01632	ribosomal protein L11	1	1
TIGR01953	transcription termination factor NusA	1	-
TIGR02012	protein RecA	1	-
TIGR02013	DNA-directed RNA polymerase, beta subunit	1	1
TIGR02027	DNA-directed RNA polymerase, alpha subunit	1	1
TIGR02191	ribonuclease III	1	-
TIGR02350	chaperone protein DnaK	1	1
TIGR02387	DNA-directed RNA polymerase, gamma subunit	1	-
TIGR02397	DNA polymerase III, subunit gamma and tau	1	-
TIGR02432	tRNA(Ile)-lysidine synthetase	1	-
TIGR02729	Obg family GTPase CgtA	1	1
TIGR03263	guanylate kinase	1	-
TIGR03594	ribosome-associated GTPase EngA	1	2

Eugenol Degradation

Locus Tag	Gene Annotation
missing	Eugenol hydroxylase
29_19	coniferyl aldehyde dehydrogenase

Ferulic Acid Degradation

Locus Tag	Gene Annotation
5_29	feruloyl-CoA synthetase
5_24	enoyl-CoA hydratase
74_6	3-ketoacyl-CoA thiolase

Vanillin and Vanillate Degradation I

Locus Tag	Gene Annotation
missing	vanillin degydrogenase

Vanillate

Locus Tag	Gene Annotation
8_28	vanillate O-demethylase oxidoreductase
8_29	3-oxoacyl-ACP reductase
8_30	aromatic-ring-hydroxylating dioxygenase

Protocatechuate Degradation II (ortho-cleavage pathway)

Locus Tag	Gene Annotation
0_83	putative protein, gamma-carboxymuconolactone decarboxylase
17_16	putative carboxymuconolactone decarboxylase family protein
67_12	carboxymuconolactone decarboxylase
0_47	4-carboxymuconolactone decarboxylase
5_30	amidohydrolase
5_31	acyl-CoA dehydrogenase
5_32	transcriptional regulator
5_33	4-hydroxybenzoate 3-monooxygenase
5_34	3-carboxy-cis,cis-muconate cycloisomerase
5_35	protocatechuate 3,4-dioxygenase subunit alpha
5_36	protocatechuate 3,4-dioxygenase subunit beta
5_37	4-carboxymuconolactone decarboxylase
5_38	3-oxoadipate enol-lactonase

Benzoate Degradation I (aerobic)

Locus Tag	Gene Annotation
13_57	1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase
13_58	2-chlorobenzoate 1,2-dioxygenase, electron transfer subunit

13_59	benzoate 1,2-dioxygenase subunit beta
13_60	benzoate 1,2-dioxygenase subunit alpha

Catechol Degradation to 2-oxopent-4-enoate I

Locus Tag	Gene Annotation
108_4	metapyrocatechase (catechol 2,3-dioxygenase)
38_16	alpha/beta hydrolase
38_17	paraquat-inducible protein A
38_18	paraquat-inducible protein B
38_19	paraquat-inducible protein B
38_20	hypothetical protein
38_21	alkyl hydroperoxide reductase
38_22	hypothetical protein
38_23	catechol 2,3 dioxygenase
38_24	ATP:cob(I)alamin adenosyltransferase
38_25	2-hydroxymuconic semialdehyde dehydrogenase
38_26	2-oxopent-4-enoate hydratase
38_27	acetaldehyde dehydrogenase
38_28	4-hyroxy-2-oxovalerate aldolase
38_29	4-oxalocrotonate decarboxylase
38_30	oxalocrotonate tautomerase
38_31	antibiotic biosynthesis monooxygenase
38_32	GntR family transcriptional regulator
38_33	ArsR family transcriptional regulator
62_5	catechol 2,3 dioxygenase

Anthranilate Degradation II (aerobic)

Locus Tag	Gene Annotation
27_10	2-aminobenzoate-CoA ligase
missing	2-aminobenzoyl-CoA monooxygenase

2-amino-3-carboxymuconate semialdehyde Degradation to 2-oxopentenoate

Locus Tag	Gene Annotation
38_25	2-hydroxymuconic semialdehyde dehydrogenase
38_29	4-oxalocrotonate decarboxylase
74_3	putative 2-amino-3-carboxymuconate-6-semialdehyde decarboxylase

Gentisate Degradation I

Locus Tag	Gene Annotation
5_14	maleylpyruvate isomerase
5_15	gentisate 1,2-dioxygenase
59_18	gentisate 1,2-dioxygenase

5_16	maleylacetoacetate isomerase
5_17	fumarylacetoacetate hydrolase
5_18	3-hydroxybenzoate 6-hydroxylase

Salicylate Degradation I

Locus Tag	Gene Annotation
36_1	Salicylate hydroxylase
39_8	salicylate 1-monooxygenase
84_9	salicylate 1-monooxygenase

Phenylacetate Degradation I (aerobic)

Locus Tag	Gene Annotation
298_0	putative phenylacetate-coenzyme A ligase
459_0	phenylacetyl-CoA ligase (phenylacetic acid catabolism)
74_5	aromatic compound degradation protein PaaI
74_6	3-ketoacyl-CoA thiolase
68_1	PaaX family transcriptional regulator
68_2	acetyl-CoA acetyltransferase
68_3	phenylacetate-CoA oxygenase subunit PaaA
68_4	phenylacetate-CoA oxygenase subunit PaaB
68_5	phenylacetate-CoA oxygenase, PaaI subunit
68_6	phenylacetate-CoA oxygenase, PaaJ subunit
68_7	phenylacetate-CoA oxygenase/reductase, PaaK subunit
68_8	enoyl-CoA hydratase
68_9	phenylacetic acid degradation protein PaaY
68_10	TetR family transcriptional regulator
68_11	phenylacetate-CoA ligase
68_12	phenylacetic acid degradation protein PaaD
68_13	enoyl-CoA hydratase
68_14	phenylacetic acid degradation protein K
68_15	ABC transporter substrate-binding protein
68_16	ABC transporter permease

Biphenyl Degradation

Locus Tag	Gene Annotation
102_0	biphenyl 2,3-dioxygenase
67_7	biphenyl 2,3-dioxygenase
67_8	3-(3-hydroxyphenyl)propionate hydroxylase
67_9	3-(3-hydroxyphenyl)propionate hydroxylase
67_10	5-carboxymethyl-2-hydroxymuconate isomerase
67_11	transcriptional regulator
67_12	carboxymuconolactone decarboxylase

67_13	Glutathione S-transferase
67_14	hypothetical protein
67_15	phage integrase

3-oxoadipate Degradation

Locus Tag	Gene Annotation
68_2	beta-ketoadipyl CoA thiolase
5_40	acetyl-CoA acetyltransferase
5_41	3-oxoadipate CoA-transferase subunit B
5_42	3-oxoadipate CoA-transferase subunit A

2-oxopentenoate Degradation

Locus Tag	Gene Annotation
108_1	4-hyroxy-2-oxovalerate/4-hydroxy-2-oxopentanoic acid aldolase
108_2	acetaldehyde dehydrogenase
108_3	2-keto-4-pentenoate hydratase
108_4	putative 3,4-dihydroxyphenylacetate 2,3-dioxygenase
108_5	monooxygenase
108_6	2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase
38_28	putative 4-hydroxy-2-oxovalerate aldolase
4_60	acetaldehyde dehydrogenase 2
121_3	2-keto-4-pentenoate hydratase
246_0	4-hydroxy 2-oxovalerate aldolase