

Supporting Information for

Microbial diversity and secondary metabolism potential in relation to dark alterations in Paleolithic Lascaux Cave

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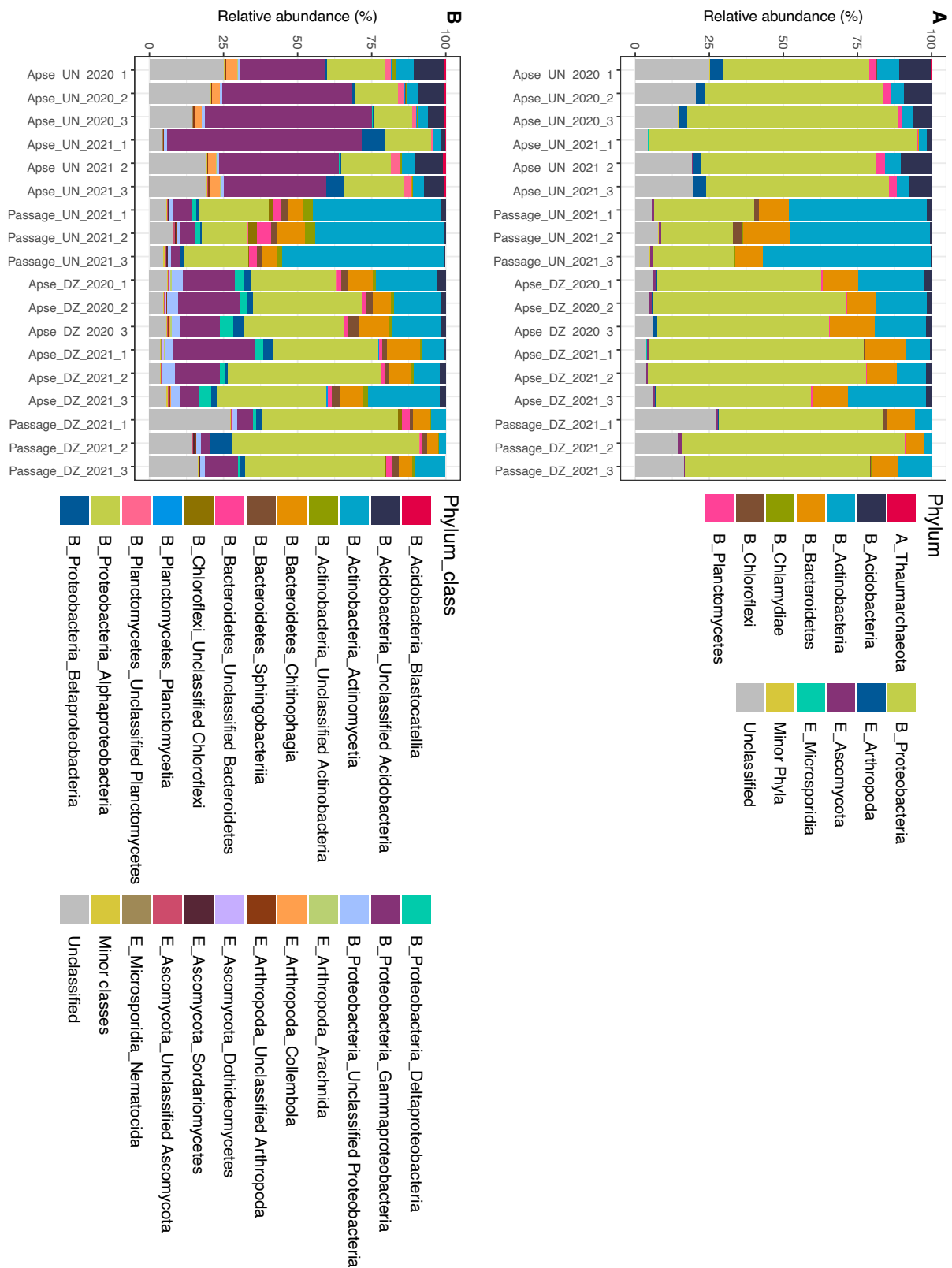
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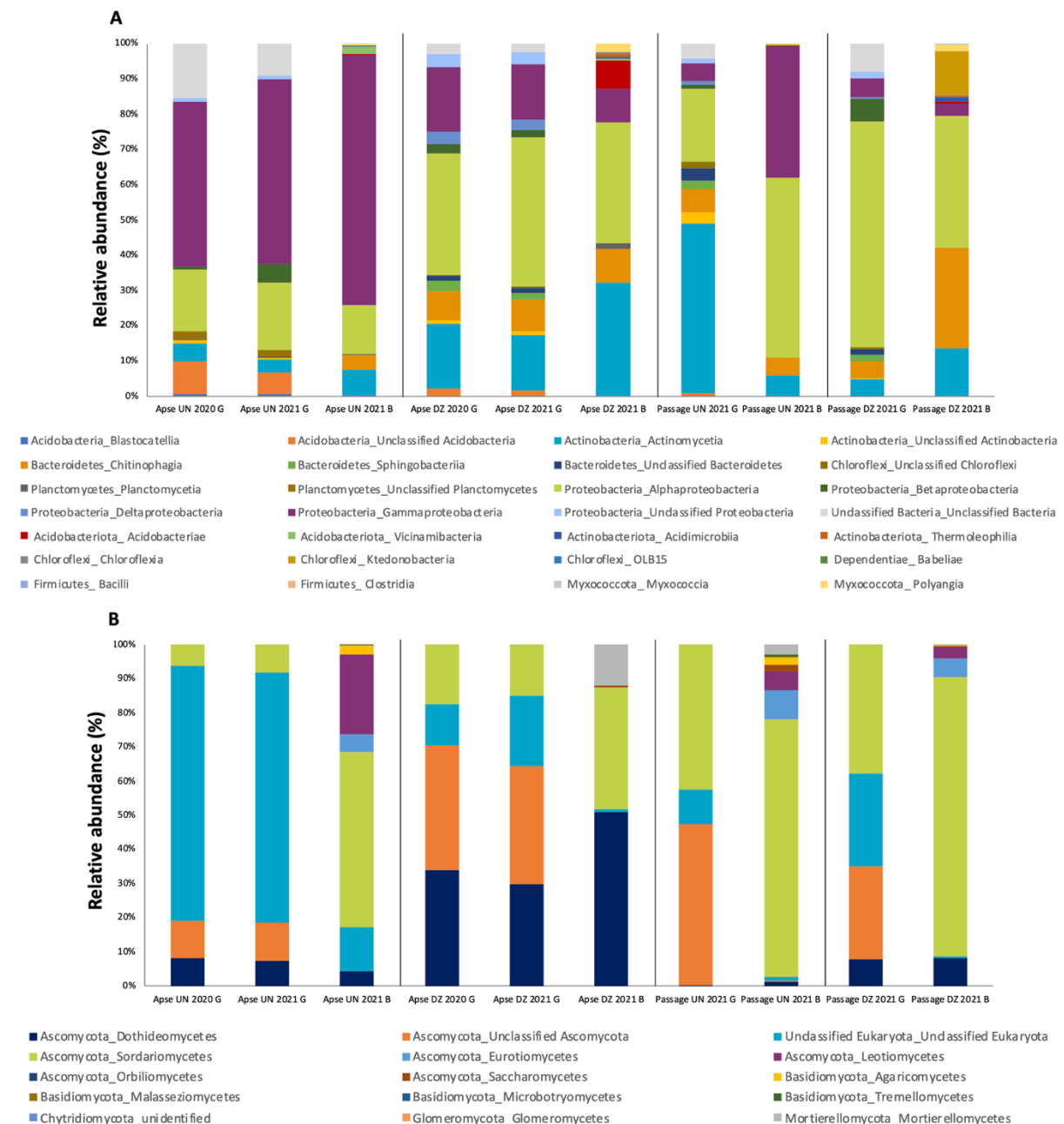
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Supplementary Figure 1. Relative abundance (% of sequences) of community taxa for each replicate at the **(A)** phylum and **(B)** class taxonomic levels. UN, unmarked surface; DZ, dark zone. Phyla or classes with a relative abundance <0.05% were considered as minor phyla or minor classes, respectively.



Supplementary Table 1. Metagenome characteristics before and after bio-informatic treatment. UN: Unmarked surfaces; DZ: Dark zones; Nb: number; ORF: Open Reading Frame; rRNA: ribosomal RNA; tRNA: transfer RNA; tmRNA: transfer-messenger RNA.

Sample	Nb raw reads	Mean quality score	% Bases ≥ 30	Nb cleaned reads	Nb Bacteria reads	Nb Archaea reads	Nb Eukaryota reads	Number of ORFs	Number of rRNAs	Number of tRNAs/tmRNAs
Apse_DZ_20	85,673,155	35.86	93.64	78,510,880	5,386,148	6.633	837.177	830.735	514	5.977
Apse_DZ_20	81,226,290	35.82	93.44	96,894,768	53,422,381	19.491	951.802	881.323	506	6.426
Apse_DZ_20	88,841,391	35.87	93.67	74,273,320	45,700,743	108.331	2,496,531	918.169	518	5.929
Apse_UN_20	102,718,931	36.01	94.33	81,440,904	55,412,434	9.66	604,451	885.744	528	4.86
Apse_UN_20	98,531,687	35.96	94.08	90,727,978	45,528,099	83.763	1,774,902	853.627	524	4.697
Apse_UN_20	66,825,010	36.00	94.28	60,997,870	49,293,283	79.499	1,893,948	779.836	490	4.019
Apse_DZ_21	98,486,488	35.88	93.65	89,278,002	53,844,638	8.354	856,427	728.927	488	5.131
Apse_DZ_21	104,961,917	35.75	93.04	95,557,330	54,382,377	7.051	435,671	833.271	538	6.065
Apse_DZ_21	140,424,511	35.98	94.15	132,209,678	54,368,032	19.507	769,913	758.261	486	5.564
Apse_UN_21	105,941,549	36.02	94.37	95,739,378	55,577,808	33.936	475,881	887.385	477	6.279
Apse_UN_21	92,595,905	35.90	93.90	86,021,596	48,824,622	113.186	1,879,684	888.181	462	6.111
Apse_UN_21	91,971,486	35.96	94.06	83,749,236	46,137,316	82.127	2,963,412	744.163	417	5.326
Passage_DZ_21	106,030,598	36.06	94.43	100,124,694	44,258,631	41.925	587,684	895.017	564	6.453
Passage_DZ_21	174,354,227	36.07	94.53	162,688,142	52,981,579	14.388	1,067,357	861.287	536	6.152
Passage_DZ_21	76,943,124	35.84	93.43	71,118,530	51,782,492	53.151	203,302	871.98	573	6.923
Passage_UN_21	142,219,108	35.87	93.68	128,964,288	54,888,846	33.842	388,215	651.108	491	4.076
Passage_UN_21	139,190,902	35.93	93.89	127,902,520	54,408,935	37.11	599,080	850.836	517	4.495
Passage_UN_21	109,737,221	35.95	93.99	100,947,270	53,742,721	77.092	661,644	910.773	533	5.049

Supplementary Table 2. Quality of metagenome assembly.

Characteristics	Results
Number of contigs	245692
Total length	2,000,301,993 bp
Longest contig	888686 bp
Shortest contig	2000 bp
N50	15821
N90	2842
Contigs at superkingdom (k) rank	196773 (80.1%), in 4 superkingdoms
Contigs at phylum (p) rank	179330 (73.0%), in 64 phyla
Contigs at class (c) rank	154005 (62.7%), in 96 classes
Contigs at order (o) rank	118396 (48.2%), in 217 orders
Contigs at family (f) rank	82624 (33.6%), in 345 families
Contigs at genus (g) rank	76655 (31.2%), in 644 genera
Contigs at species (s) rank	24710 (10.1%), in 747 species
Congruent	231460 (94.2%)
Disparity > 0	14233 (5.8%)
Disparity $\geq$ 0.25	7850 (3.2%)

N50: is the minimum contig length to cover 50% of the genome.

N90: is the minimum contig length to cover 90% of the genome.

Congruent means that all genes in the contig belong to the same taxa.

Disparity is the percentage of paired comparisons between genes that belong to different taxa.

Supplementary Table 3. Individual (A) and pooled (B) statistics of metagenomes.**A**

	Apse_UN_2020_1	Apse_UN_2020_2	Apse_UN_2020_3	Apse_DZ_2020_1	Apse_DZ_2020_2	Apse_DZ_2020_3
Number of reads	8.14E+07	9.07E+07	6.10E+07	7.85E+07	9.69E+07	7.43E+07
Number of bases	1.08E+10	1.20E+10	8.30E+09	1.07E+10	1.32E+10	9.96E+09
Number of ORFs	885744	853627	779836	830735	881323	918169
Number of rRNAs	528	524	490	514	506	518
Number of tRNAs/tmRNAs	4860	4697	4019	5977	6426	5929
ORFs by Aragorn	4860	4697	4019	5977	6426	5929
ORFs by Prodigal	880356	848406	775327	824244	874391	911722
ORFs by barrnap	528	524	490	514	506	518
Orphans (no hits)	173617	173573	162682	94852	88123	137914
No tax assigned (with hits)	3073	2739	2616	2513	2459	2816
KEGG annotations	450422	428560	387969	479048	515775	492072
COG annotations	598760	569797	514939	645923	697469	662857
Pfam annotations	458402	435016	393520	506753	548185	514970

	Apse_UN_2021_1	Apse_UN_2021_2	Apse_UN_2021_3	Apse_DZ_2021_1	Apse_DZ_2021_2	Apse_DZ_2021_3
Number of reads	9.57E+07	8.60E+07	8.37E+07	8.93E+07	9.56E+07	1.32E+08
Number of bases	1.29E+10	1.15E+10	1.12E+10	1.22E+10	1.29E+10	1.82E+10
Number of ORFs	651108	850836	910773	895017	861287	1071980
Number of rRNAs	491	517	533	564	536	573
Number of tRNAs/tmRNAs	4076	4495	5049	6453	6150	6923
ORFs by Aragorn	4076	4495	5049	6453	6150	6923
ORFs by Prodigal	646541	845824	905191	888000	854601	1064484
ORFs by barrnap	491	517	533	564	536	573
Orphans (no hits)	77270	170875	180929	100959	95453	186495
No tax assigned (with hits)	2145	2964	2758	2083	2713	3888
KEGG annotations	389268	427996	462535	522023	502454	561095
COG annotations	513486	569872	614236	701094	678341	756759
Pfam annotations	407158	435456	469084	552250	532870	579451

	Passage_UN_2021_1	Passage_UN_2021_2	Passage_UN_2021_3	Passage_DZ_2021_1	Passage_DZ_2021_2	Passage_DZ_2021_3
Number of reads	1.29E+08	1.28E+08	1.01E+08	1.00E+08	2.97E+08	7.11E+07
Number of bases	1.75E+10	1.71E+10	1.37E+10	1.44E+10	4.30E+10	9.57E+09
Number of ORFs	887385	888181	744163	728927	833271	758261
Number of rRNAs	477	462	417	488	538	486
Number of tRNAs/tmRNAs	6279	6110	5326	5131	6065	5564
ORFs by Aragorn	6279	6110	5326	5131	6065	5564
ORFs by Prodigal	880629	881609	738420	723308	826668	752211

ORFs by barrnap	477	462	417	488	538	486
Orphans (no hits)	94514	109745	89113	82657	94587	66844
No tax assigned (with hits)	4371	2966	2350	4235	4328	2801
KEGG annotations	524415	510343	431426	433564	497100	465658
COG annotations	708807	695279	587952	580263	665208	623425
Pfam annotations	549479	532336	448813	453932	519478	491541

B

	Apse_UN_2020	Apse_DZ_2020	Apse_UN_2021	Apse_DZ_2021	Passage_UN_2021	Passage_DZ_2021
Number of reads	2.33E+08	2.50E+08	2.66E+08	3.17E+08	3.58E+08	4.68E+08
Number of bases	3.11E+10	3.38E+10	3.56E+10	4.33E+10	4.83E+10	6.70E+10
Number of ORFs	2519207	2630227	2412717	2828284	2519729	2320459
Number of rRNAs	1542	1538	1541	1673	1356	1512
Number of tRNAs/tmRNAs	13576	18332	13620	19526	17715	16760
ORFs by Aragorn	13576	18332	13620	19526	17715	16760
ORFs by Prodigal	2504089	2610357	2397556	2807085	2500658	2302187
ORFs by barrnap	1542	1538	1541	1673	1356	1512
Orphans (no hits)	509872	320889	429074	382907	293372	244088
No tax assigned (with hits)	8428	7788	7867	8684	9687	11364
KEGG annotations	1266951	1486895	1279799	1585572	1466184	1396322
COG annotations	1683496	2006249	1697594	2136194	1992038	1868896
Pfam annotations	1286938	1569908	1311698	1664571	1530628	1464951

UN: Unmarked

DZ: Dark zone

_1 _2 and _3 refer to replicates

Supplementary Table 4. MAG taxonomic information. (p): phylum; (c): class; (o): order; (f): family; (g): genus.

MAG number	Domain	Phylum	Class	Order	Family	Genus	Final taxonomy
MAG1	Bacteria	Actinobacteria	Actinomycetia	Micrococcales	Microbacteriaceae	<i>Microbacterium</i>	(g) <i>Microbacterium</i>
MAG2	Bacteria	Actinobacteria	Actinomycetia	Not identified	Not identified	Not identified	(c) Actinomycetia
MAG3	Bacteria	Actinobacteria	Actinomycetia	Not identified	Not identified	Not identified	(c) Actinomycetia
MAG4	Bacteria	Actinobacteria	Thermoleophilia	Solirubrobacterales	Conexibacteraceae	<i>Conexibacter</i>	(g) <i>Conexibacter</i>
MAG5	Bacteria	Actinobacteria	Not identified	Not identified	Not identified	Not identified	(p) Actinobacteria
MAG6	Bacteria	Chlamydiae	Not identified	Not identified	Not identified	Not identified	(p) Chlamydiae
MAG7	Bacteria	Bacteroidetes	Chitinophagia	Chitinophagales	Chitinophagaceae	<i>Chitinophaga</i>	(g) <i>Chitinophaga</i>
MAG8	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	<i>Pedobacter</i>	(g) <i>Pedobacter</i>
MAG9	Bacteria	Proteobacteria	Alphaproteobacteria	Hyphomicrobiales	Hyphomicrobiaceae	<i>Hyphomicrobium</i>	(g) <i>Hyphomicrobium</i>
MAG10	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	<i>Brevundimonas</i>	(g) <i>Brevundimonas</i>
MAG11	Bacteria	Proteobacteria	Alphaproteobacteria	Hyphomicrobiales	Bradyrhizobiaceae	<i>Nitrobacter</i>	(g) <i>Nitrobacter</i>
MAG12	Bacteria	Proteobacteria	Alphaproteobacteria	Hyphomicrobiales	Not identified	Not identified	(o) Hyphomicrobiales
MAG13	Bacteria	Planctomycetes	Planctomycetia	Not identified	Not identified	Not identified	(c) Planctomycetia
MAG14	Bacteria	Actinobacteria	Actinomycetia	Corynebacteriales	Mycobacteriaceae	<i>Mycobacteroides</i>	(g) <i>Mycobacteroides</i>
MAG15	Bacteria	Proteobacteria	Alphaproteobacteria	Hyphomicrobiales	Xanthobacteraceae	<i>Labrys</i>	(g) <i>Labrys</i>
MAG16	Bacteria	Proteobacteria	Alphaproteobacteria	Hyphomicrobiales	Not identified	Not identified	(o) Hyphomicrobiales
MAG17	Bacteria	Acidobacteria	Not identified	Not identified	Not identified	Not identified	(p) Acidobacteria
MAG18	Bacteria	Actinobacteria	Actinomycetia	Streptomycetales	Streptomycetaceae	<i>Streptomyces</i>	(g) <i>Streptomyces</i>
MAG19	Bacteria	Actinobacteria	Actinomycetia	Corynebacteriales	Nocardiaceae	<i>Rhodococcus</i>	(g) <i>Rhodococcus</i>
MAG20	Bacteria	Proteobacteria	Alphaproteobacteria	Hyphomicrobiales	Not identified	Not identified	(o) Hyphomicrobiales
MAG21	Bacteria	Proteobacteria	Alphaproteobacteria	Hyphomicrobiales	Not identified	Not identified	(o) Hyphomicrobiales
MAG22	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Not identified	Not identified	(o) Rhodospirillales
MAG23	Bacteria	Planctomycetes	Not identified	Not identified	Not identified	Not identified	(p) Planctomycetes
MAG24	Bacteria	Not identified	Not identified	Not identified	Not identified	Not identified	(k) Bacteria
MAG25	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	<i>Olivibacter</i>	(g) <i>Olivibacter</i>
MAG26	Bacteria	Chlamydiae	Chlamydiia	Not identified	Not identified	Not identified	(c) Chlamydiia
MAG27	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	<i>Sphingomonas</i>	(g) <i>Sphingomonas</i>
MAG28	Bacteria	Proteobacteria	Alphaproteobacteria	Not identified	Not identified	Not identified	(c) Alphaproteobacteria
MAG29	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	<i>Stenotrophomonas</i>	(g) <i>Stenotrophomonas</i>
MAG30	Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Not identified	(f) Legionellaceae
MAG31	Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	<i>Legionella</i>	(g) <i>Legionella</i>
MAG32	Bacteria	Not identified	Not identified	Not identified	Not identified	Not identified	(f) Brucellaceae
MAG33	Bacteria	Not identified	Not identified	Not identified	Not identified	Not identified	(k) Bacteria
MAG34	Fungi	Ascomycota	Sordariomycota	Hypocreales	Not identified	Not identified	(o) Hypocreales
MAG35	Bacteria	Actinobacteria	Actinomycetia	Pseudonocardiales	Pseudonocardaceae	<i>Amycolatopsis</i>	(g) <i>Amycolatopsis</i>
MAG36	Bacteria	Actinobacteria	Actinomycetia	Not identified	Not identified	Not identified	(c) Actinomycetia
MAG37	Bacteria	Actinobacteria	Not identified	Not identified	Not identified	Not identified	(p) Actinobacteria
MAG38	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	<i>Olivibacter</i>	(g) <i>Olivibacter</i>
MAG39	Bacteria	Chloroflexi	Not identified	Not identified	Not identified	Not identified	(p) Chloroflexi

MAG40	Bacteria	Proteobacteria	Alphaproteobacteria	Hyphomicrobiales	Not identified	Not identified	(o) Hyphomicrobiales
MAG41	Bacteria	Proteobacteria	Alphaproteobacteria	Hyphomicrobiales	Not identified	Not identified	(o) Hyphomicrobiales
MAG42	Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Not identified	(f) Polyangiaceae
MAG43	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	<i>Luteimoas</i>	(g) <i>Luteimoas</i>
MAG44	Bacteria	Actinobacteria	Actinomycetia	Streptomycetales	Streptomycetaceae	<i>Streptomyces</i>	(g) <i>Streptomyces</i>
MAG45	Bacteria	Actinobacteria	Actinomycetia	Pseudonocardiales	Pseudonocardaceae	Not identified	(f) Pseudonocardaceae
MAG46	Bacteria	Actinobacteria	Actinomycetia	Not identified	Not identified	Not identified	(c) Actinomycetia
MAG47	Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	<i>Legionella</i>	(g) <i>Legionella</i>
MAG48	Bacteria	Bacteroidetes	Not identified	Not identified	Not identified	Not identified	(p) Bacteroidetes
MAG49	Bacteria	Proteobacteria	Not identified	Not identified	Not identified	Not identified	(p) Proteobacteria
MAG50	Bacteria	Not identified	Not identified	Not identified	Not identified	Not identified	(k) Bacteria
MAG51	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	<i>Ralstonia</i>	(g) <i>Ralstonia</i>
MAG52	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Not identified	(f) Xanthomonadaceae

Supplementary Table 5. Detailed information on selected functional genes.

Gene	KEGG number	Function	Hierarchical classes (KEGG)		
<i>prnA</i>	K14266	tryptophan 7-halogenase [EC:1.14.19.9]	Metabolism	Biosynthesis of other secondary metabolites	Staurosporine biosynthesis
<i>prnB</i>	K19981	monodechloroaminopyrrolnitrin synthase	Metabolism	Biosynthesis of other secondary metabolites	Staurosporine biosynthesis
<i>gcvP</i>	K00281	glycine dehydrogenase [EC:1.4.4.2]	Metabolism	Carbohydrate metabolism	Glyoxylate and dicarboxylate metabolism
<i>hcnA</i>	K10814	hydrogen cyanide synthase HcnA [EC:1.4.99.5]	Metabolism	Metabolism of other amino acids	Cyanoamino acid metabolism
<i>hcnB</i>	K10815	hydrogen cyanide synthase HcnB [EC:1.4.99.5]	Metabolism	Metabolism of other amino acids	Cyanoamino acid metabolism
<i>hcnC</i>	K10816	hydrogen cyanide synthase HcnC [EC:1.4.99.5]	Metabolism	Metabolism of other amino acids	Cyanoamino acid metabolism
<i>phzM</i>	K21103	phenazine-1-carboxylate N-methyltransferase [EC:2.1.1.327]	Metabolism	Biosynthesis of other secondary metabolites	Phenazine biosynthesis
<i>phzS</i>	K20940	5-methylphenazine-1-carboxylate 1-monooxygenase [EC:1.14.13.218]	Metabolism	Biosynthesis of other secondary metabolites	Phenazine biosynthesis
<i>tnr</i>	K17739	tetrahydroxynaphthalene reductase [EC:1.1.1.252]	Not Included in Pathway or Brite	Unclassified: metabolism	Unclassified: metabolism
<i>sdh</i>	K17740	scytalone dehydratase [EC:4.2.1.94]	Not Included in Pathway or Brite	Unclassified: metabolism	Unclassified: metabolism
<i>tyr</i>	K00505	tyrosinase [EC:1.14.18.1]	Metabolism	Amino acid metabolism	Tyrosine metabolism
<i>dod</i>	K10253	DOPA 4,5-dioxygenase [EC:1.14.99.-]	Not Included in Pathway or Brite	Unclassified: metabolism	Unclassified: metabolism
<i>dod</i>	K15777	4,5-DOPA dioxygenase extradiol [EC:1.13.11.-]	Metabolism	Biosynthesis of other secondary metabolites	Betalain biosynthesis
<i>pfmaG</i>	K17739	tetrahydroxynaphthalene reductase [EC:1.1.1.252]	Not Included in Pathway or Brite	Unclassified: metabolism	Unclassified: metabolism
<i>sdh1</i>	K17740	scytalone dehydratase [EC:4.2.1.94]	Not Included in Pathway or Brite	Unclassified: metabolism	Unclassified: metabolism
<i>lac</i>	K05909	laccase [EC:1.10.3.2]	Not Included in Pathway or Brite	Unclassified: metabolism	Unclassified: metabolism
<i>crtZ</i>	K02294	beta-carotene hydroxylase [EC:1.14.13.-]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>crtB</i>	K17841	15-cis-phytoene synthase	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis

<i>todA</i>	K17842	torulene dioxygenase [EC:1.13.11.59]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>Z-Iso</i>	K15744	zeta-carotene isomerase [EC:5.2.1.12]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>al-1</i>	K15745	phytoene desaturase (3,4- didehydrolycopene-forming) [EC:1.3.99.30]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>aog</i>	K14595	abscisate beta- glucosyltransferase [EC:2.4.1.263]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>crtX</i>	K14596	zeaxanthin glucosyltransferase [EC:2.4.1.276]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>cruC</i>	K14597	chlorobactene glucosyltransferase	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>cruD</i>	K14598	chlorobactene lauroyltransferase	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>crtNb</i>	K10210	diapolycopene oxygenase [EC:1.14.99.44]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>crtQ</i>	K10211	4,4'-diaponeurosporenoate glycosyltransferase [EC:2.4.1.-]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>crtO</i>	K10212	glycosyl-4,4'- diaponeurosporenoate acyltransferase [EC:2.3.1.-]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>pds</i>	K02293	15-cis-phytoene desaturase [EC:1.3.5.5]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>ccr2</i>	K09835	polycopene isomerase [EC:5.2.1.13]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>lut1</i>	K09837	carotenoid epsilon hydroxylase [EC:1.14.14.158]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>zep</i>	K09838	zeaxanthin epoxidase [EC:1.14.15.21]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis

<i>aba2</i>	K09841	xanthoxin dehydrogenase [EC:1.1.1.288]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>crtC</i>	K09844	carotenoid 1,2-hydratase [EC:4.2.1.131]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>crtD</i>	K09845	1-hydroxycarotenoid 3,4- desaturase [EC:1.3.99.27]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>crtF</i>	K09846	demethylspheroidene O- methyltransferase [EC:2.1.1.210]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>crtA</i>	K09847	spheroidene monooxygenase [EC:1.14.15.9]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>lcy1</i>	K06443	lycopene beta-cyclase [EC:5.5.1.19]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>crtB</i>	K02291	15-cis-phytoene synthase [EC:2.5.1.32]	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>crtW</i>	K02292	beta-carotene ketolase (CrtO type)	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis
<i>mnp1</i>	K20205	manganese peroxidase [EC:1.11.1.13]	Not Included in Pathway or Brite	Unclassified: metabolism	Enzymes with EC numbers
<i>mox</i>	K22348	manganese oxidase [EC:1.16.3.3]	Not Included in Pathway or Brite	Unclassified: metabolism	Enzymes with EC numbers
<i>pral</i>	K00481	p-hydroxybenzoate 3- monooxygenase [EC:1.14.13.2]	Metabolism	Xenobiotics biodegradation and metabolism	Benzoate degradation
<i>brcC</i>	K04112	benzoyl-CoA reductase subunit C [EC:1.3.7.8]	Metabolism	Xenobiotics biodegradation and metabolism	Benzoate degradation
<i>brcB</i>	K04113	benzoyl-CoA reductase subunit B [EC:1.3.7.8]	Metabolism	Xenobiotics biodegradation and metabolism	Benzoate degradation
<i>brcA</i>	K04114	benzoyl-CoA reductase subunit A [EC:1.3.7.8]	Metabolism	Xenobiotics biodegradation and metabolism	Benzoate degradation
<i>brcD</i>	K04115	benzoyl-CoA reductase subunit D [EC:1.3.7.8]	Metabolism	Xenobiotics biodegradation and metabolism	Benzoate degradation

<i>fadK</i>	K04116	cyclohexanecarboxylate-CoA ligase [EC:6.2.1.-]	Metabolism	Xenobiotics biodegradation and metabolism	Benzoate degradation
<i>thnJ</i>	K04118	pimeloyl-CoA dehydrogenase [EC:1.3.1.62]	Metabolism	Xenobiotics biodegradation and metabolism	Benzoate degradation
<i>badH</i>	K07535	2-hydroxycyclohexanecarboxyl-CoA dehydrogenase [EC:1.1.1.-]	Metabolism	Xenobiotics biodegradation and metabolism	Benzoate degradation
<i>menI</i>	K07536	2-ketocyclohexanecarboxyl-CoA hydrolase [EC:3.1.2.-]	Metabolism	Xenobiotics biodegradation and metabolism	Benzoate degradation
<i>cdh</i>	K07537	cyclohexa-1,5-dienecarbonyl-CoA hydratase [EC:4.2.1.100]	Metabolism	Xenobiotics biodegradation and metabolism	Benzoate degradation
<i>pcaF</i>	K07823	3-oxoadipyl-CoA thiolase [EC:2.3.1.174]	Metabolism	Xenobiotics biodegradation and metabolism	Benzoate degradation
<i>galB</i>	K10220	4-oxalomesaconate hydratase [EC:4.2.1.83]	Metabolism	Xenobiotics biodegradation and metabolism	Benzoate degradation
<i>gcdh</i>	K16173	glutaryl-CoA dehydrogenase (non-decarboxylating) [EC:1.3.99.32]	Metabolism	Xenobiotics biodegradation and metabolism	Benzoate degradation
<i>galD</i>	K16514	4-oxalomesaconate tautomerase [EC:5.3.2.8]	Metabolism	Xenobiotics biodegradation and metabolism	Benzoate degradation
<i>proH</i>	K16515	4-oxalomesaconate hydratase [EC:4.2.1.83]	Metabolism	Xenobiotics biodegradation and metabolism	Benzoate degradation
<i>chcA</i>	K19067	cyclohexane-1-carbonyl-CoA dehydrogenase [EC:1.3.8.11]	Metabolism	Xenobiotics biodegradation and metabolism	Benzoate degradation
<i>graF</i>	K20941	gamma-resorcyate decarboxylase [EC:4.1.1.103]	Metabolism	Xenobiotics biodegradation and metabolism	Benzoate degradation
<i>cgl</i>	K22270	3-hydroxybenzoate 6-monooxygenase [EC:1.14.13.24]	Metabolism	Xenobiotics biodegradation and metabolism	Benzoate degradation
<i>xamoE</i>	K22354	alkene monooxygenase beta subunit [EC:1.14.13.69]	Metabolism	Xenobiotics biodegradation and metabolism	Chloroalkane and chloroalkene degradation

<i>etnD</i>	K22356	alkene monooxygenase reductase	Metabolism	Xenobiotics biodegradation and metabolism	Chloroalkane and chloroalkene degradation
<i>xecA1</i>	K22363	2-hydroxypropyl-CoM lyase [EC:4.4.1.23]	Metabolism	Xenobiotics biodegradation and metabolism	Chloroalkane and chloroalkene degradation
<i>tfdA</i>	K06912	alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate dioxygenase [EC:1.14.11.-]	Metabolism	Xenobiotics biodegradation and metabolism	Chlorocyclohexane and chlorobenzene degradation
<i>pcpD</i>	K21607	tetrachlorobenzoquinone reductase [EC:1.1.1.404]	Metabolism	Xenobiotics biodegradation and metabolism	Chlorocyclohexane and chlorobenzene degradation
<i>phtD</i>	K04102	4,5-dihydroxyphthalate decarboxylase [EC:4.1.1.55]	Metabolism	Xenobiotics biodegradation and metabolism	Polycyclic aromatic hydrocarbon degradation
<i>ophB</i>	K18067	phthalate 4,5-cis-dihydrodiol dehydrogenase [EC:1.3.1.64]	Metabolism	Xenobiotics biodegradation and metabolism	Polycyclic aromatic hydrocarbon degradation
<i>pht3</i>	K18068	phthalate 4,5-dioxygenase [EC:1.14.12.7]	Metabolism	Xenobiotics biodegradation and metabolism	Polycyclic aromatic hydrocarbon degradation
<i>pht2</i>	K18069	phthalate 4,5-dioxygenase reductase component [EC:1.18.1.-]	Metabolism	Xenobiotics biodegradation and metabolism	Polycyclic aromatic hydrocarbon degradation
<i>tphA2I</i>	K18074	terephthalate 1,2-dioxygenase oxygenase component alpha subunit [EC:1.14.12.15]	Metabolism	Xenobiotics biodegradation and metabolism	Polycyclic aromatic hydrocarbon degradation
<i>tphBII</i>	K18076	1,2-dihydroxy-3,5-cyclohexadiene-1,4-dicarboxylate dehydrogenase [EC:1.3.1.53]	Metabolism	Xenobiotics biodegradation and metabolism	Polycyclic aromatic hydrocarbon degradation
<i>tphA1</i>	K18077	terephthalate 1,2-dioxygenase reductase component [EC:1.18.1.-]	Metabolism	Xenobiotics biodegradation and metabolism	Polycyclic aromatic hydrocarbon degradation
<i>padAd</i>	K18251	phthalate 3,4-dioxygenase subunit alpha [EC:1.14.12.-]	Metabolism	Xenobiotics biodegradation and metabolism	Polycyclic aromatic hydrocarbon degradation
<i>padAb</i>	K18252	phthalate 3,4-dioxygenase subunit beta [EC:1.14.12.-]	Metabolism	Xenobiotics biodegradation and metabolism	Polycyclic aromatic hydrocarbon degradation
<i>padAc1</i>	K18253	phthalate 3,4-dioxygenase ferredoxin component	Metabolism	Xenobiotics biodegradation and metabolism	Polycyclic aromatic hydrocarbon degradation

<i>padAd</i>	K18254	phthalate 3,4-dioxygenase ferredoxin reductase component [EC:1.18.1.3]	Metabolism	Xenobiotics biodegradation and metabolism	Polycyclic aromatic hydrocarbon degradation
<i>phnB</i>	K18257	cis-3,4-dihydrophenanthrene-3,4-diol dehydrogenase [EC:1.3.1.49]	Metabolism	Xenobiotics biodegradation and metabolism	Polycyclic aromatic hydrocarbon degradation
<i>phdK</i>	K18275	2-formylbenzoate dehydrogenase [EC:1.2.1.78]	Metabolism	Xenobiotics biodegradation and metabolism	Polycyclic aromatic hydrocarbon degradation
<i>pchf</i>	K05797	4-cresol dehydrogenase (hydroxylating) flavoprotein subunit [EC:1.17.9.1]	Metabolism	Xenobiotics biodegradation and metabolism	Toluene degradation
<i>bbsE</i>	K07543	benzylsuccinate CoA-transferase BbsE subunit [EC:2.8.3.15]	Metabolism	Xenobiotics biodegradation and metabolism	Toluene degradation
<i>bbsF</i>	K07544	benzylsuccinate CoA-transferase BbsF subunit [EC:2.8.3.15]	Metabolism	Xenobiotics biodegradation and metabolism	Toluene degradation
<i>bbsG</i>	K07545	(R)-benzylsuccinyl-CoA dehydrogenase [EC:1.3.8.3]	Metabolism	Xenobiotics biodegradation and metabolism	Toluene degradation
<i>bbsH</i>	K07546	E-phenyllitaconyl-CoA hydratase [EC:4.2.1.-]	Metabolism	Xenobiotics biodegradation and metabolism	Toluene degradation
<i>bbsC</i>	K07547	2-[hydroxy(phenyl)methyl]-succinyl-CoA dehydrogenase BbsC subunit [EC:1.1.1.35]	Metabolism	Xenobiotics biodegradation and metabolism	Toluene degradation
<i>bbsD</i>	K07548	2-[hydroxy(phenyl)methyl]-succinyl-CoA dehydrogenase BbsD subunit [EC:1.1.1.35]	Metabolism	Xenobiotics biodegradation and metabolism	Toluene degradation
<i>bbsA</i>	K07549	benzoylsuccinyl-CoA thiolase BbsA subunit [EC:2.3.1.-]	Metabolism	Xenobiotics biodegradation and metabolism	Toluene degradation
<i>bbsB</i>	K07550	benzoylsuccinyl-CoA thiolase BbsB subunit [EC:2.3.1.-]	Metabolism	Xenobiotics biodegradation and metabolism	Toluene degradation
<i>pchA</i>	K20199	4-hydroxybenzaldehyde dehydrogenase (NADP+) [EC:1.2.1.96]	Metabolism	Xenobiotics biodegradation and metabolism	Toluene degradation
<i>hipH</i>	K20218	4-hydroxyisophthalate hydroxylase	Metabolism	Xenobiotics biodegradation and metabolism	Toluene degradation

<i>poxD</i>	K16242	phenol hydroxylase P3 protein [EC:1.14.13.-]	Metabolism	Xenobiotics biodegradation and metabolism	Toluene degradation
<i>phyA</i>	K16243	phenol hydroxylase P1 protein	Metabolism	Xenobiotics biodegradation and metabolism	Toluene degradation
<i>poxC</i>	K16244	phenol hydroxylase P2 protein	Metabolism	Xenobiotics biodegradation and metabolism	Toluene degradation
<i>poxE</i>	K16245	phenol hydroxylase P4 protein	Metabolism	Xenobiotics biodegradation and metabolism	Toluene degradation
<i>poxF</i>	K16246	phenol hydroxylase P5 protein	Metabolism	Xenobiotics biodegradation and metabolism	Toluene degradation
