Supplemental Material

Thin layer chromatography (TLC)

TLC is used to determine the nature of extracted biosurfactant. TLC of two bacterial isolate was carried out. BDB4 (as positive control) and DR1 as they were selected on the basis of screening tests.

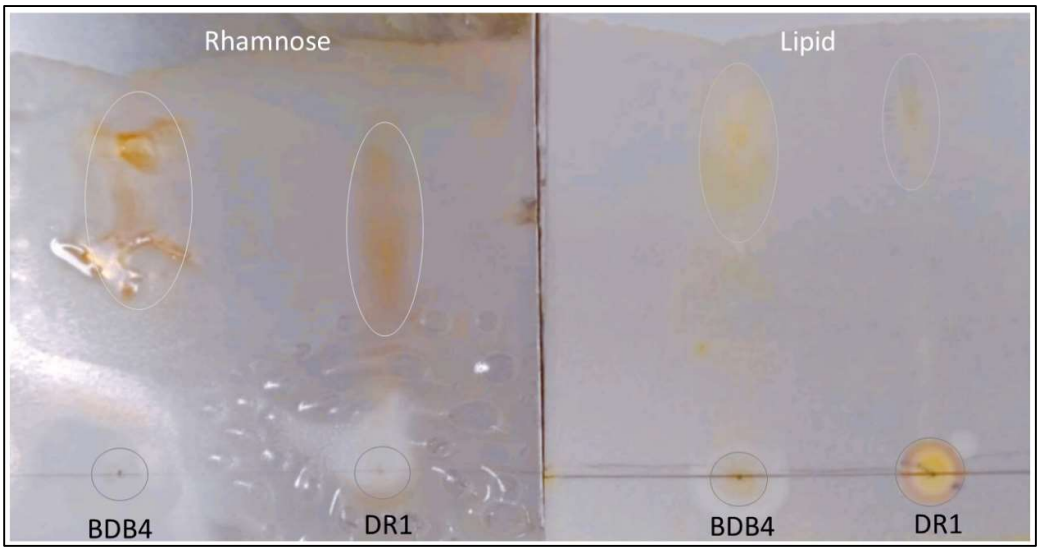


FIG S1. Thin layer chromatography of the extracted biosurfactant showed rhamnolipid. The left image displays brown spots, which test positive for rhamnose sugar upon treatment with orcinol. The right image shows yellow spots, indicating the lipid nature of the biosurfactant when treated with bromothymol blue.

Fourier Transform Infrared Spectroscopy (FTIR)

The presence of functional groups in the isolated biosurfactants is examined using FTIR analysis. Various peaks correspond to various functional groups. Below is information on the FTIR analysis of DR1 (Figure S2).

TABLE S1 Functional group prediction of *Acinetobacter oleivorans* DR1

Wavenumbers (cm−1)	Associated functional groups
3,417	–O–H
2,961	–CH2–CH3
1,660	C–O stretching in ester groups bonded to fatty acids
1,535	aromatic ring stretch
1,403	C–H bending
1,239	vibrations of –C–CH2 and –C–CH3 groups in the aliphatic chain
1,063	C–O–C vibration in cyclic structure of carbohydrate

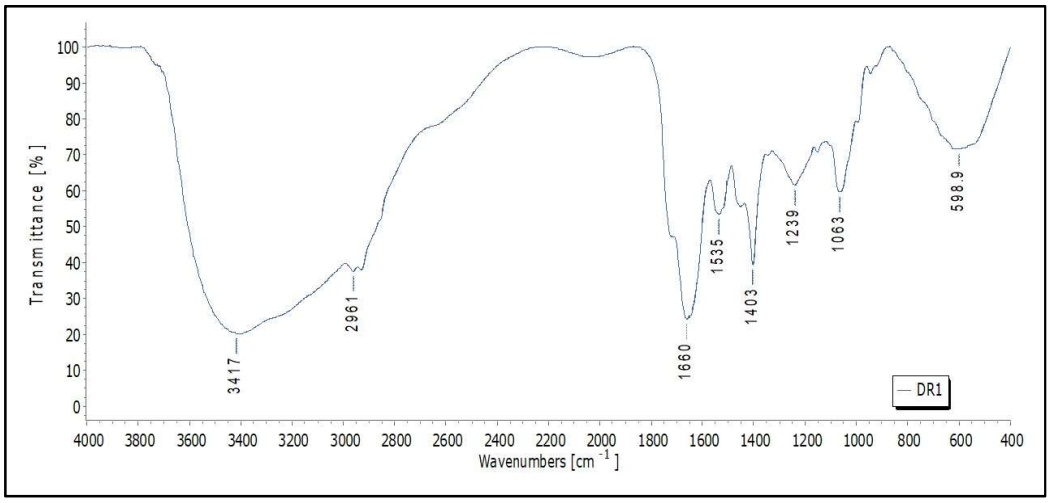
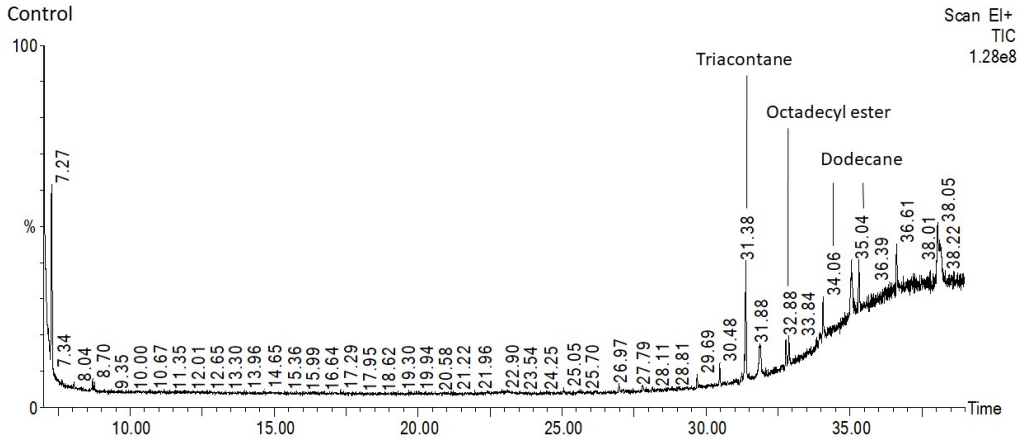
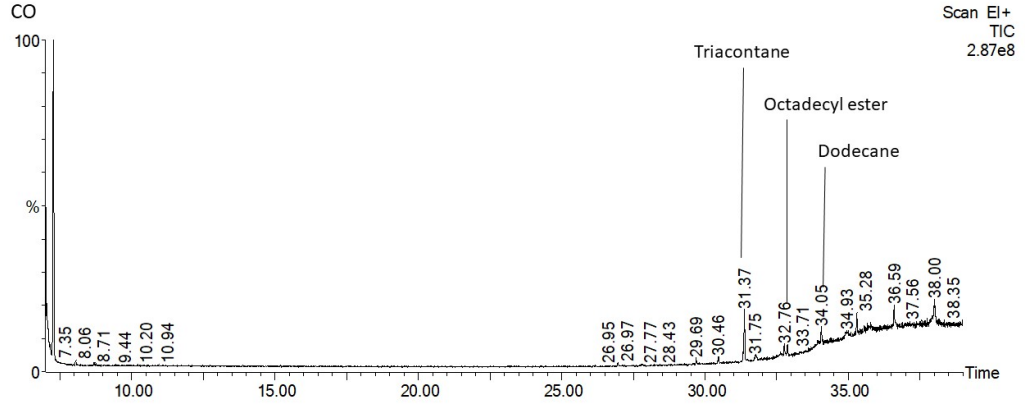
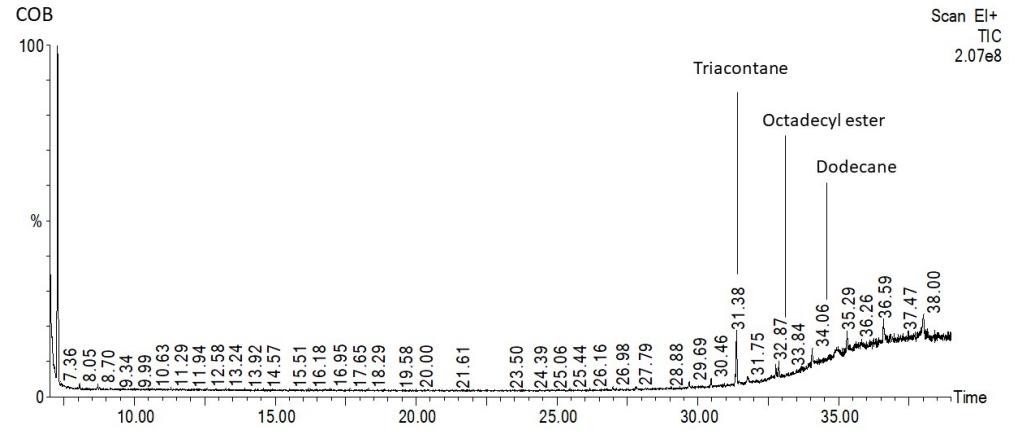


FIG S2 FTIR analysis of *Acinetobacter oleivorans* DR1

GCMS Chromatogram







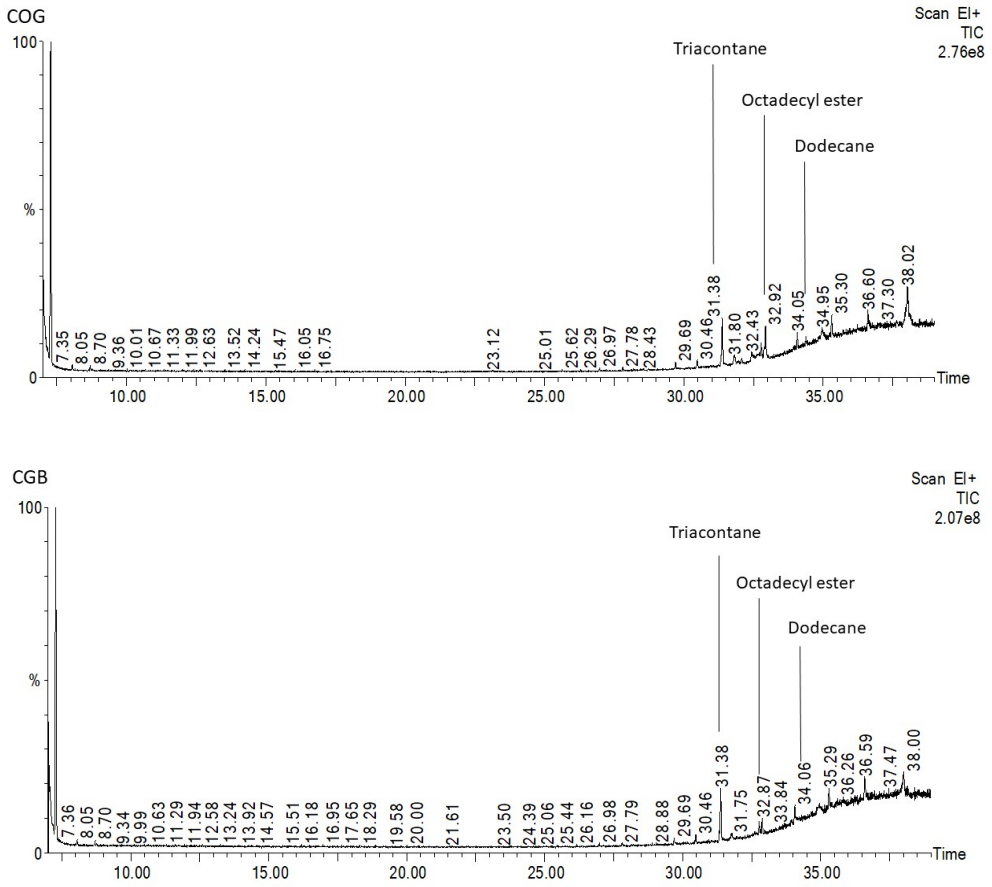


FIG S3 GC MS chromatogram of Control (0.1% crude oil with not bacterial inoculation), Treatments (0.1% crude oil with bacterial inoculation)- CO, COB, COG, and CGB. The most prominent hydrocarbons- Triacontane, Octadecyl esters, and Dodecane were shown and other peaks are not focused and not considered in the discussion of the present study.

Metabolomics of *Acinetobacter oleivorans* DR1.

In PLS-DA, the top 25 metabolites of negative mode are- N10 (Trifluoroacetic acid), N14 (L-Glutathione oxidized), N17 (Adenosine diphosphate ribose), N25 (UDP-N-acetylglucosamine), N23 (N-Acetyl-α-D-glucosamine 1-phosphate), N26 (Trifluoroacetic acid), N32 (L-(+)-Tartaric acid), N35 (Trifluoroacetic acid), N38 (Similar to: Gluconic acid; ΔMass: 67.9865 Da), N39 (α,α-Trehalose), N40 (L-Glutathione oxidized), N46 (D-(+)-Glucose), N54 (Itaconic acid), N59 (Itaconic acid), N61 (Similar to: Gluconic acid; ΔMass: 84.9767 Da), N63 (Trifluoroacetic acid), N65 (Glutaric acid), N66 (Glutaric acid), N73 (Citric acid), N78 (Similar to: Gluconic acid; ΔMass: 204.0435 Da), N91 (Similar to: Gluconic acid; ΔMass: 67.9867 Da), N249 (Similar to: (±)9-HpODE; ΔMass: -0.0554 Da), N267 (4-Dodecylbenzenesulfonic acid), N275 (4-

Dodecylbenzenesulfonic acid), and N301((2R)-3-{[(2-Aminoethoxy)(hydroxy)phosphoryl]oxy}-2-[(9Z)-9-hexadecenoyloxy]propyl (9Z)-9-hexadecenoate) (**Fig. S4)**

In PLS-DA positive mode, the top 20 metabolites are- N152 (Selodenoson), N378 (Similar to: N-{3-[3-({[4-(3-chloro-2-cyanophenoxy)phenyl]sulfonyl}amino)propoxy]phenyl}acetamide; ΔMass: 19.0315 Da), N107 (5-({[3-chloro-5-(trifluoromethyl)-2-pyridyl]methyl}thio)-4-pentyl-4H-1,2,4-triazol-3-ol), N383 (5-[(E)-2-Carboxyvinyl]-2-methoxyphenyl beta-D-glucopyranosiduronic acid), N379 (17-Methyl-3-(2,4-cyclopentadien-1-ylidene)-5alpha-androstane-17beta-ol), N376 (3-(2,4-Cyclopentadien-1-ylidene)-5alpha-androstan-17beta-ol), N147 (4-Vinylcyclohexene), N380 (2-({2-[(1-Benzylpiperidin-4-yl)amino]-2-oxoethyl}thio)acetic acid), N101 (meprobamate), N217 (N-Methyl-5-{5-[(2S)-1-(4-nitrobenzyl)-2-pyrrolidinyl]-1,2,4-oxadiazol-3-yl}-2-pyridinamine), N361 (Biotin), N352 (PENTOTHAL), N386 (2DF7X515LU), N157 (Indane), N156 (2,2,6,6-Tetramethyl-1-piperidinol), N230 (4-Vinylcyclohexene), N389 (Biphenyl), N316 (1,2,3,4-Tetramethyl-1,3-cyclopentadiene), N94 (Similar to: 8-(2,3-dihydroxy-3-methylbutyl)-7-methoxy-2H-chromen-2-one; ΔMass: 37.0876 Da) (**Fig. S5**).

The significantly induced metabolites of *Acinetobacter oleivorans* DR1 by the presence of crude oil in crude oil amended medium are- N20[Similar to: D-Glucose 6-phosphate; ΔMass: 119.9576 Da], N14 (L-Glutathione oxidized), N16 (α,α-Trehalose), N108 (Flavin mononucleotide), N81 (Succinic acid), N21 (D-Glucose 6-phosphate), N99 (Flavin adenine dinucleotide), N27 (Thiosulfic acid), N22 [Similar to: α,α-Trehalose; ΔMass: 45.8994 Da], N40 (L-Glutathione oxidized), N31 [Similar to: Cyclic ADP-ribose; ΔMass: 122.0463 Da], N18 [Similar to: UDP-N-acetylglucosamine; ΔMass: 1.1081 Da], N15 (cytidine 5′-monophosphate), N95 (isopropylmalic acid), N36 (Adenosine diphosphate), N24 (2-c-methyl-d-erythritol-2,4-cyclopyrophosphate), N23 (N-Acetyl-α-D-glucosamine 1-phosphate), N17 (Adenosine diphosphate ribose), N84 (Thymidine 5'-monophosphate). The metabolites of negative mode such as N32 (L-(+)-Tartaric acid) and N73 (Citric acid) are significantly high in crude oil + Glucose (COG) and crude oil + glucose + biosurfactant (COGB). These two metabolites are mainly formed by the presence of both glucose and crude oil. The four metabolites of negative mode – N46 (D-(+)-Glucose), N55 (alpha-ketoadipic acid), N91 [Similar to: Gluconic acid; ΔMass: 67.9867 Da] and N214 (epi-jasmonic acid) are significantly higher than crude oil amended

medium (CO and COB). Thus these four metabolites are mainly induced by the presence of glucose (**Fig. S6 A**).

While in the analysis of top 25 metabolites of positive mode, the metabolites which are mainly found to be produced by the presence of both crude oil + glucose are- N238 (IMINOCTADINE), N125 [Similar to: 4-morpholinobenzoic acid; ΔMass: 38.1442 Da], N339 (ampiroxicam), N131 (ethylestrenol), N180 (dictyoquinazol A), N263 (Bevenopran), N113 [Similar to: N-{4-[(2R,3R)-3-(Hydroxymethyl)-4-methyl-5-oxo-2-morpholinyl]phenyl}-2-methylbenzamide; ΔMass: -236.1168 Da], N119 (2-{[(2S)-1-Methoxy-1-oxo-2-hexanyl]amino}-2-oxoethanediazonium), N262 (2-[(3S)-1-(2-Thienylmethyl)-3-pyrrolidinyl]-1,3-benzothiazole), N124 [Similar to: 6-[(2E,6E)-7-(5-hydroxy-3-methyl-2-oxocyclopent-3-en-1-yl)-6-methylhepta-2,6-dien-2-yl]-3-methyl-5,6-dihydro-2H-pyran-2-one; ΔMass: -98.0748 Da], N116 (5,6-Dihydrothymidine), N195 (Eslicarbazepine acetate), N183 (Eterobarb), N121 (1-(beta-D-ribofuranosyl)thymine), N282 ((3Z,6E,8E,12Z,15Z,18Z)-3,6,8,12,15,18-Docosahexaen-10-ol), N120 (1,4-Dihydro-4-imino-1-Î²-D-ribofuranosyl-3-pyridinecarboxylic acid), and N338 (Ergocalciferol).

Some of the metabolites of positive mode which are significantly produced by the presence of crude oil but reduced by glucose are- N107 (5-({[3-chloro-5-(trifluoromethyl)-2-pyridyl]methyl}thio)-4-pentyl-4H-1,2,4-triazol-3-ol), N378 [Similar to: N-{3-[3-({[4-(3-chloro-2-cyanophenoxy)phenyl]sulfonyl}amino) propoxy]phenyl}acetamide; ΔMass: 19.0315 Da], N228 [Similar to: NP-006111; ΔMass: -80.0744 Da], N380 (2-({2-[(1-Benzylpiperidin-4-yl)amino]-2-oxoethyl}thio)acetic acid), N384 (1-Octadecyl Lysophosphatidic Acid), N385 (2DF7X515LU), N383 (5-[(E)-2-Carboxyvinyl]-2-methoxyphenyl beta-D-glucopyranosiduronic acid), and N364 (2-[(3S)-1-(2-Thienylmethyl)-3-pyrrolidinyl]-1,3-benzothiazole). The metabolites- N380, N384, N383 and 364 are more enhanced by the presence of biosurfactant (Fig. S6 B).

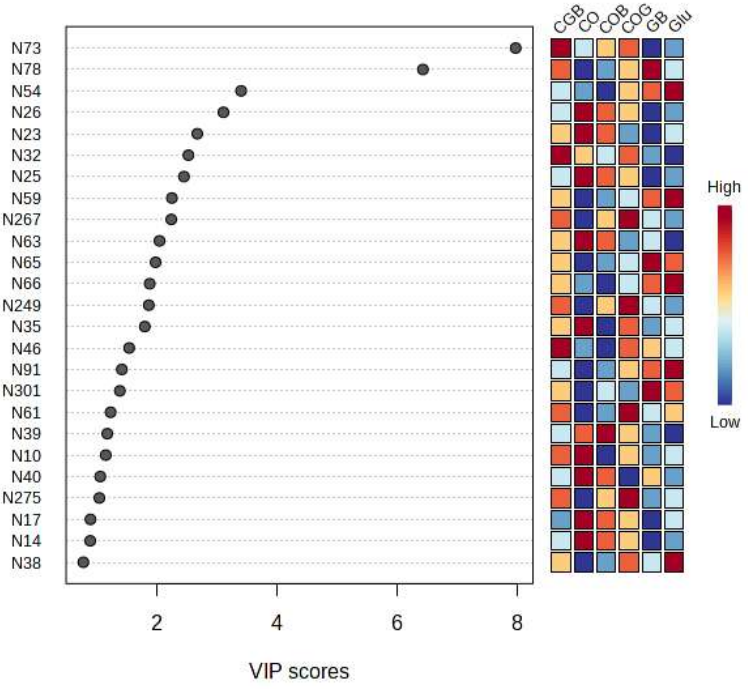


FIG S4 Partial Least Squares - Discriminant Analysis of top 25 metabolite (Negative mode).

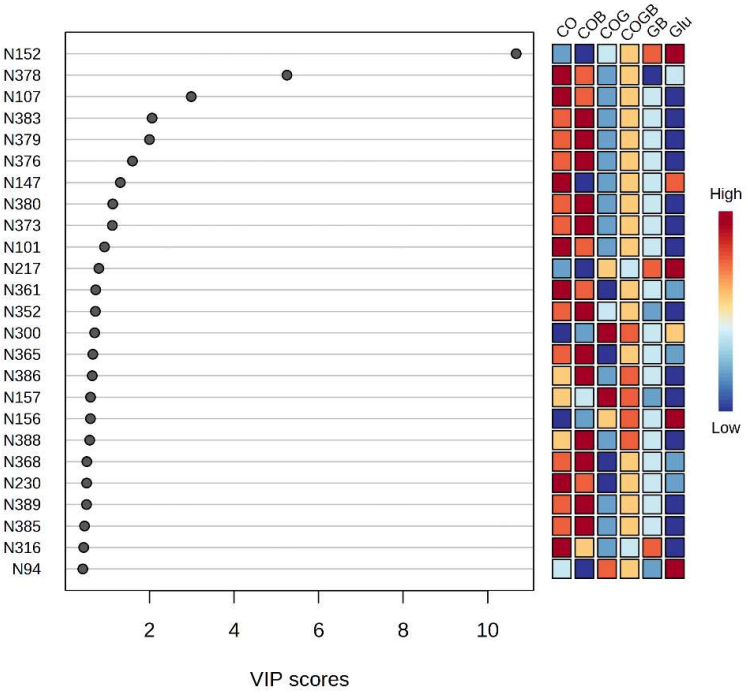


FIG S5 Partial Least Squares - Discriminant Analysis of top 25 metabolite (Positive mode).

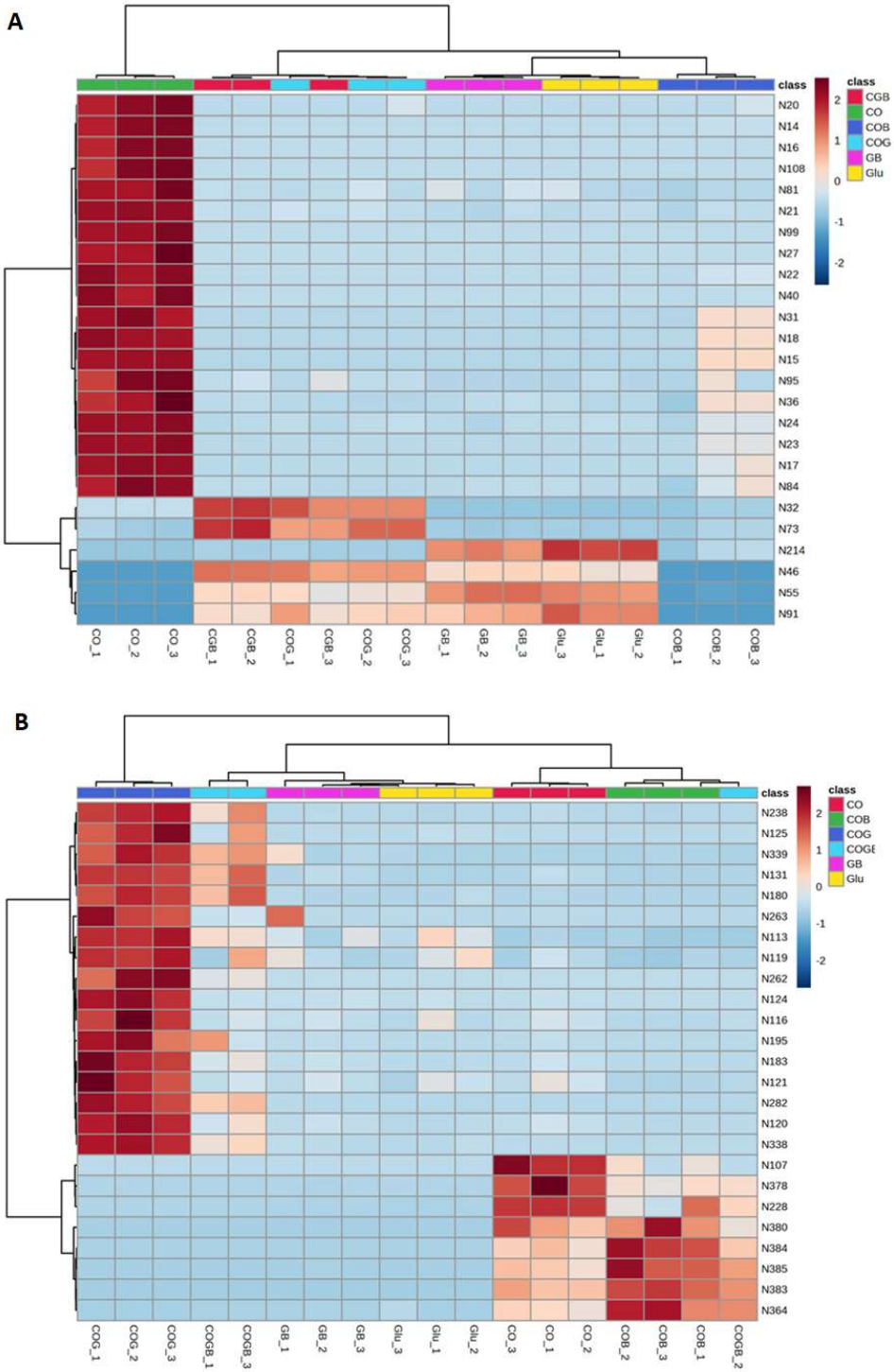
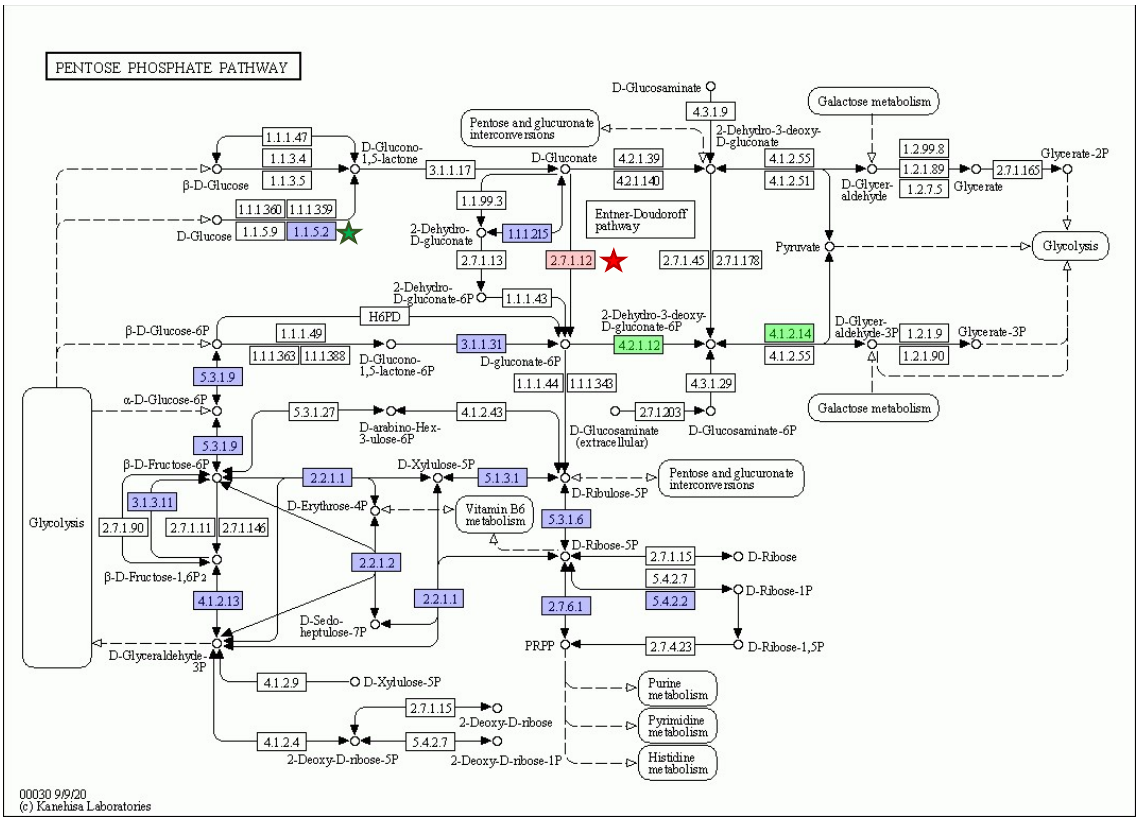


FIG S6 Heat map of top 25 metabolites. The details of metabolites have been described in the text. A. Negative ion mode. B. Positive ion mode.

A



B

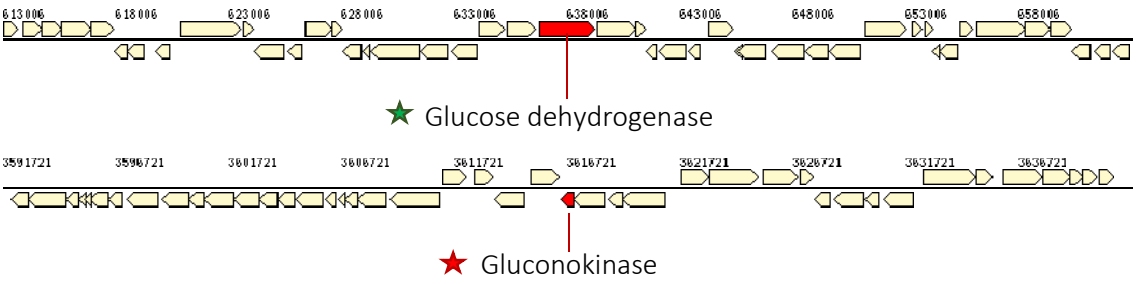


FIG S7 Genes annotated in the genome of *A. oleivorans* DR1 in the Kegg pentose phosphate pathway (A). The two genes *Gcd* (Glucose dehydrogenase) and *IdnK* (Gluconokinase) responsible for directing the glucose in to pentose phosphate pathway.

TABLE S2: List of important metabolites identified in different culture conditions.

SAMPLES LABELS	G AVERAGE	CO AVERAGE	COG AVERAGE	GB AVERAGE	COB AVERAGE	CGB AVERAGE
UDP-N-acetylglucosamine	20113225.26	25570021.63	21577384.19	7849687.172	5788017.625	8058459.922
L-Glutathione oxidized	42613.80009	117787991.5	47580.39956	42128.58386	1783432.287	43438.58925
cytidine 5-monophosphate	32681.90274	55260283.49	36490.94864	32244.21094	11057545.38	32515.973
Adenosine diphosphate ribose	16440.33558	114605821.5	27764.05171	15979.90676	12889393.33	16268.63269
UDP-N-acetylglucosamine	15464.64841	10800854.62	16784.30565	15083.37177	2064265.045	15383.42105
Guanosine monophosphate	26707.60761	47040221.94	29901.80855	26606.98244	26619913.87	27695.93392
D-Glucose 6-phosphate	2438886.259	51696175.08	3920199.6	1754514.907	1870481.415	2958109.09
N-Acetyl-D-glucosamine 1-phosphate	85882.60919	346634862.3	84538.413	54366.81476	35199927.7	90253.35129
Cyclic ADP-ribose	518809.994	57281317.22	594702.2751	708817.7923	10525634.93	820736.3188
L-(+)-Tartaric acid	179035.0227	37964122.18	191737218.6	313341.3526	9776718.238	217023607.7
2-Deoxypentose	66793.87748	568333.8674	173068.8628	59572.56209	38629.87279	572865.9309
Kojic acid	4288364.682	1358096.274	3631550.424	3932849.393	626492.7006	4834613.462
Adenosine diphosphate (ADP)	1131823.326	12358199.42	930033.5353	1324177.58	2595686.75	1178386.144
2-Hydroxyglutaric acid	9781230.818	9489013.619	12922786.41	7148227.979	2588236.042	13629680.95
Gluconic acid	69712016.03	26324.28251	62586592.43	36429203.2	62095.52975	42247128.31
Trehalose	503872.7143	113177601.8	1549440.108	589506.2739	129353158.7	1344000.021
D-Glucopyranosyl	3753025.541	58190.77608	14964576.52	5028477.919	121482.5748	15805444.03
2-Furoic acid	3572162.043	5036311.457	62258634.89	2472113.85	4109610.982	58952530.54
D-(+)-Glucose	389357520.5	2458511.008	611868484.5	417699148.6	1843216.028	637126791.4
1,4-D-xylobiose	302163.3849	50356.06606	435487.4492	415478.3852	107501.0643	1012129.908
D-Erythrose	20271900.72	467182.8038	22478445.77	12948866.63	299518.3309	35965803.59
isopropylmalic acid	35724393.51	1150695.673	5995086.279	26420929.24	248547.4145	20006696.62
Itaconic acid	211670483.9	5546374.168	140727391.2	149185392.7	2984313.504	51473076.45
alpha-ketoadipic acid	41307319.72	238724.6302	25707358.01	44543945.34	407143.1191	26425780.38
Adipic acid	1655397.028	2422796.826	1702130.57	1112605.902	673905.8805	1709740.877
threonic acid	11113011.15	1659983.63	16734824.88	8226083.595	735646.3449	12845594.99

Glutaric acid	147072297.3	214826.2207	90908576.39	148747787.2	232951.9618	95405712.37
alpha-Ketoglutaric acid	1072204.647	3073967.263	1250764.89	733449.131	211058.2704	1850785.808
DL-Malic acid	1416603.476	1029443.153	7908418.268	2116570.736	2037914.081	10828820.03
Pyrophosphoric Acid	110713572.5	89840632.58	164744381.3	120722202.1	140620994.2	166224356.7
1,2,3-cyclopropanetricarboxylic acid	1968680.066	997924.676	33179315.49	2903702.44	13680489.38	31894527.53
Adenosine diphosphate ribose	5972345.226	293498.6498	6882221.956	6070265.785	5826095.125	6344142.729
Vitamin C	9473084.636	160776.0377	6984317.582	7262302.896	221322.7073	9612923.929
Maleic acid	1339714.796	2149847.398	1750382.079	1414663.839	360553.1187	1370764.137
Succinic acid	2171345.279	29362775.86	2337756.517	3306719.225	773336.7181	2160728.776
Thymidine 5'-monophosphate	1141779.935	15064014.67	1019087.608	1206003.077	2255540.305	1169698.939
Citric acid	904207.9291	146732.0349	7795466.339	934024.7849	623226.3639	6105793.007
3,4-dihydroxyphenylacetic acid	6948769.739	1193323.782	10034276.08	5331875.038	1218472.019	9208724.276
isopropylmalic acid	79762.77224	2697144.809	124572.456	46722.64342	269939.6226	296283.7602
Flavin adenine dinucleotide (FAD)	70973.10218	23905699.32	77925.21052	68948.73269	124371.295	71652.6127
Flavin mononucleotide (FMN)	33989.02329	6583581.721	35068.77076	33979.16587	27318.59709	34503.1273
isopropylmalic acid	491257.5751	110964.6431	2257297.809	457151.4346	2309522.139	2718794.466
3-Anisic acid	9081647.845	3095540.34	7722454.795	5253022.47	3528156.661	8500718.445
Phthalic acid	423242.8083	326334.5836	284242.7685	1622063.642	445330.0837	448820.5319
Azelaic acid	9370168.907	1967581.4	9558152.484	4709251.945	5169631.234	8007005.817
16-Hydroxyhexadecanoic acid	110142.0241	8321667.478	123350.2759	109157.901	85858.55226	117714.866
Arabic acid	6359147.077	21017844.49	28333115.88	26470618.15	14981081.12	42097773.1
13S-hydroxyoctadecadienoic acid	1524961.541	97149.66107	1103843.596	1041173.117	1142281.761	3437690.974
16-Hydroxyhexadecanoic acid	954749.9203	60204.64721	1145030.538	1124841.052	583088.1669	1256532.215
3-oxopalmitic acid	784704.0498	152412.6513	1569334.885	1015051.965	731878.4026	2112939.862
Lauric acid ethyl ester	403960.5523	69892.36254	887437.9843	184468.5671	769453.0818	302125.0481
Oleic acid	903820.2236	76684.27109	1337073.471	1118032.921	759311.153	1478498.646
Palmitoleic acid	587695.4968	70094.14978	2031313.838	754394.0535	796809.065	4767586.155
Linoleic acid	616866.4558	41644.43597	572477.2613	494240.3252	811207.0543	1340260.873
Linoelaidic Acid	490354.513	57880.07858	298562.6685	516407.9828	238217.2039	1839874.047
Palmitic acid	3829245.469	1127347.865	16092248.83	3341852.36	4825292.463	3091398.759

Oleic acid	3137141.386	32791.32467	7993190.987	2144275.197	3237175.945	19434420.54
16-hydroxyphorbol 13-decanoate 12-palmitate	5594039.293	94997.65131	5645837.184	13905848.24	1435335.703	8942981.188
Methyl stearate	47812.70259	90648.78219	800547.066	66906.99037	748871.7293	1239264.618
Arabic acid	9328933.444	454564.7799	8248146.39	9663826.033	2134364.266	15082144.15
Stearic acid	11637327.04	859924.3111	22379442.66	9051383.926	11692759.54	12446838.84
dilauroyl peroxide	492004.558	80792.0648	302419.5458	494773.6673	646953.5222	1099396.064
lauric acid	3285488.35	66224.24633	1322022.445	2701813.857	2681686.958	3578880.394
Arachidic acid	108513.0648	33901.33201	614465.6943	77000.81706	292841.0093	476078.6941
1-palmitoyl-2-oleoyl-sn-glycero-3-phosphoethanolamine	9856607.768	210803.2844	2519454.085	12521231.51	10214763.93	7749387.233
Biotin	304685.7492	124099432.4	279115.8486	424453.536	63745519.16	54523708.3

TABLE S3 Genes involved in fatty acid synthesis

Gene ID	Gene Product Name	Gene Symbol	Amino Acid Sequence Length (aa)	Enzyme	KO
648059039	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.-)	*fabZ*	161	EC:4.2.1.59	K02372
648060944	3-ketoacyl-(acyl-carrier-protein) reductase	*fabG*	241	EC:1.1.1.100	K00059
648058954	3-ketoacyl-(acyl-carrier-protein) reductase	*fabG*	463	EC:1.1.1.100	K00059
648060946	3-oxoacyl-(acyl carrier protein) synthase I	*fabB*	400	EC:2.3.1.41	K00647
648060943	3-oxoacyl-(acyl carrier protein) synthase II	*fab*	408	EC:2.3.1.179	K09458
648060688	3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100)	*fabG*	244	EC:1.1.1.100	K00059
648059276	3-oxoacyl-[acyl-carrier-protein] reductase(3-ketoacyl-acyl carrier protein reductase)	*fabG*	245	EC:1.1.1.100	K00059
648059894	3-oxoacyl-[acyl-carrier-protein] reductase(3-ketoacyl-acyl carrier protein reductase)	*fabG*	245	EC:1.1.1.100	K00059

648058985	acetyl-CoA carboxylase, biotin carboxyl carrier protein	*accB, bccP*	139		K02160
648058135	acetyl-CoA carboxylase, carboxyl transferase, beta subunit	*accD*	298	EC:2.1.3.15	K01963
648060866	acetyl-coenzyme A carboxylase carboxyl transferase	*accA*	273	EC:2.1.3.15	K01962
648060062	acetyl/propionyl carboxylase subunit alpha		572	EC:6.4.1.2	K11263
648061262	AMP-binding enzyme family protein	*fadD*	559	EC:6.2.1.3	K01897
648059348	AMP-dependent synthetase and ligase		486	EC:6.2.1.3	K01897
648060648	Beta-ketoacyl synthase, N-terminal domain protein	*fabB*	409	EC:2.3.1.41	K00647
648058984	biotin carboxylase	*accC*	456	EC:6.4.1.2	K01961
648060934	Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9)	*fabI*	288	EC:1.3.1.9	K00208
648060689	malonyl CoA-acyl carrier protein transacylase	*fabD*	328	EC:2.3.1.39	K00645
648059299	putative long-chain-fatty-acid--CoA ligase-related protein	*fadD*	385	EC:6.2.1.3	K01897
648060074	short-chain dehydrogenase/reductase SDR	*fabG*	265	EC:1.1.1.100	K00059

TABLE S4 Genes for unsaturated fatty acids

Gene ID	Gene Product Name	Gene Symbol	Amino Acid Sequence Length (aa)	Enzyme	KO
648057950	acyl-CoA thioesterase II	*tesB*	290	EC:3.1.2	K10805
648058779	delta-9 desaturase	*desC*	323	EC:1.14.19.1	K00507
648058760	fatty acid desaturase		746		K22770
648061434	fatty acid desaturase	*desA3*	387	EC:1.14.19	K22769
648061435	flavodoxin reductase (ferredoxin-NADPH reductase) family protein 1		341		K22770
648058536	flavodoxin reductase (ferredoxin-NADPH reductase) family protein 1		355		K22770
648058537	Linoleoyl-CoA desaturase(Delta(6)-desaturase)	*desA3*	364	EC:1.14.19	K22769
648060452	multifunctional protein (Includes: acyl-CoA thioesterase I; protease I; lysophospholipasel(I))	*tesA*	207	EC:3.1.1.2	K10804
648058123	stearoyl-CoA desaturase	*desC*	390	EC:1.14.19.1	K00507

648058074	Thioesterase superfamily protein	*yciA*	138	EC:3.1.2	K10806

TABLE S5 Genes involved in fatty acid degradation

Gene ID	Gene Product Name	Gene Symbol	Amino Acid Sequence Length (aa)	Enzyme	KO
648061166	3-ketoacyl-CoA thiolase	*fadA*	390	EC:2.3.1.16	K00632
648060487	3-phenylpropionate dioxygenase ferredoxin	*hcaD*	403	EC:1.18.1.3	K00529
648059589	acetyl-CoA acetyltransferase	*atoB*	390	EC:2.3.1.9	K00626
648058150	acetyl-CoA acetyltransferase	*atoB*	401	EC:2.3.1.9	K00626
648060144	Acetyl-CoA acetyltransferase	*fadI*	402	EC:2.3.1.16	K00632
648059955	acetyl-CoA acetyltransferase	*dcaF*	401	EC:2.3.1.9	K00626
648058953	acetyl-CoA acetyltransferase	*atoB*	523	EC:2.3.1.9	K00626
648058158	acetyl-CoA acetyltransferase	*atoB*	391	EC:2.3.1.9	K00626
648060319	acyl coenzyme A dehydrogenase	*acd*	379	EC:1.3.8.7	K00249
648058642	acyl-CoA dehydrogenase	*fadE*	820	EC:1.3.99	K06445
648059675	Acyl-CoA dehydrogenase	*acd*	401	EC:1.3.8.7	K00249
648058033	acyl-CoA dehydrogenase	*acd*	387	EC:1.3.8.7	K00249
648061355	Acyl-CoA dehydrogenase	*bcd*	375	EC:1.3.8.1	K00248
648059263	Acyl-CoA dehydrogenase, C-terminal domain protein	*acd*	414	EC:1.3.8.7	K00249
648058288	alcohol dehydrogenase, class IV	*adh*	394	EC:1.1.1.1	K00001
648059676	alkane 1-monooxygenase	*alkM*	407	EC:1.14.15.3	K00496
648060245	alkane 1-monooxygenase	*alkM*	397	EC:1.14.15.3	K00496
648061262	AMP-binding enzyme family protein	*fadD*	559	EC:6.2.1.3	K01897
648059348	AMP-dependent synthetase and ligase	*fadD*	486	EC:6.2.1.3	K01897
648059286	beta-ketoadipyl CoA thiolase	*fadA, fadI*	404	EC:2.3.1.16	K00632
648059246	beta-ketoadipyl CoA thiolase	*fadA, fadI*	403	EC:2.3.1.16	K00632
648060497	enoyl-CoA hydratase	*paaF, echA*	262	EC:4.2.1.17	K01692
648059952	enoyl-CoA hydratase	*dcaE*	262	EC:4.2.1.17	K01692

648061354	enoyl-CoA hydratase	*paaF, echA*	257	EC:4.2.1.17	K01692
648060147	enoyl-CoA hydratase	*paaF, echA*	257	EC:4.2.1.17	K01692
648060806	glutaryl-CoA dehydrogenase	*gcdH*	403	EC:1.3.8.6	K00252
648061165	multifunctional fatty acid oxidation complex subunit alpha	*fadB*	717	EC:4.2.1.17	K01825
648058149	putative 3-hydroxybutyryl-CoA epimerase	*fadJ*	711	EC:4.2.1.17	K01782]
648058697	putative acyl coenzyme A dehydrogenase	*acd*	381	EC:1.3.8.7	K00249
648058904	putative alcohol dehydrogenase	*yiaY*	390	EC:1.1.1.1	K13954
648058964	putative iron-containing alcohol dehydrogenase	*adh*	385	EC:1.1.1.1	K00001
648059299	putative long-chain-fatty -acid--CoA ligase-related protein	*fadD*	385	EC:6.2.1.3	K01897
648060443	rubredoxin-NAD(+) reductase	*rubB, alkT*	393	EC:1.18.1.1	K05297
648059524	Zn-dependent alcohol dehydrogenase, class III	*frmA*	369	EC:1.1.1.1	K00121

TABLE S6 Genes for glycolysis/gluconeogenesis

Gene ID	Gene Product Name	Gene Symbol	Amino Acid Sequence Length (aa)	Enzyme	KO
648057704	acetate--CoA ligase	*acs*	649	EC:6.2.1.1	K01895
648061356	Acetyl-coenzyme A synthetase	*acs*	549	EC:6.2.1.1	K01895
648058288	alcohol dehydrogenase, class IV	*adh*	394	EC:1.1.1.1	K00001
648059616	dihydrolipoamide acetyltransferase	*aceF, pdhC*	496	EC:2.3.1.12	K00627
648058307	dihydrolipoamide dehydrogenase	*lpd*	477	EC:1.8.1.4	K00382
648058069	dihydrolipoamide dehydrogenase	*pdhD*	457	EC:1.8.1.4	K00382
648058432	fructose-1,6-bisphosphatase	*fbp*	323	EC:3.1.3.11	K03841

648059749	fructose-bisphosphate aldolase (EC 4.1.2.13)	*fda*	345	EC:4.1.2.13	K01624
648060473	galactose mutarotase	*galM*	381	EC:5.1.3.3	K01785
648061406	glucose-6-phosphate isomerase	*pgi*	556	EC:5.3.1.9	K01810
648058495	glyceraldehyde-3-phosphate dehydrogenase	*gap*	485	EC:1.2.1.12	K00134
648060278	glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase	*gapA*	339	EC:1.2.1.12	K00134
648058901	NAD-dependent aldehyde dehydrogenase	*aldB*	503	EC:1.2.1	K00138
648058341	phosphoenolpyruvate carboxykinase	*pckG*	610	EC:4.1.1.32	K01596
648058837	phosphoenolpyruvate synthase (EC 2.7.9.2)	*ppsA*	792	EC:2.7.9.2	K01007
648059751	phosphoglycerate kinase (EC 2.7.2.3)	*pgk*	395	EC:2.7.2.3	K00927
648061236	phosphoglycerate mutase (EC 5.4.2.1)	*gpmI*	515	EC:5.4.2.12	K15633
648060624	Phosphomannomutase/phosphoglucomutase(PMM /PGM)	*pmm-pgm*	472	EC:5.4.2.2	K15778
648059236	phosphopyruvate hydratase	*eno*	429	EC:4.2.1.11	K01689
648057576	putative alcohol dehydrogenase	*ahr*	342	EC:1.1.1.2	K12957
648058904	putative alcohol dehydrogenase	*yiaY*	390	EC:1.1.1.1	K13954
648058964	putative iron-containing alcohol dehydrogenase	*adh*	385	EC:1.1.1.1	K00001
648057686	pyruvate dehydrogenase subunit E1	*aceE*	905	EC:1.2.4.1	K00163
648057687	pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component	*aceF, pdhC*	655	EC:2.3.1.12	K00627
648059615	pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component	*lpd, pdhD*	467	EC:1.8.1.4	K00382
648061139	triosephosphate isomerase (EC 5.3.1.1)	*tpiA*	264	EC:5.3.1.1	K01803
648059403	Zn-dependent alcohol dehydrogenase	*yahK*	350	EC:1.1.1.2	K13979
648059524	Zn-dependent alcohol dehydrogenase, class III	*frmA*	369	EC:1.1.1.1	K00121

TABLE S7 Genes for pentose phosphate pathway.

Gene ID	Gene Product Name	Gene Symbol	Amino Acid Sequence Length (aa)	Enzyme	KO
648060980	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase	*eda*	209	EC:4.1.2.14	K01625
648058730	2-ketogluconate reductase(2KR) (2-ketoaldonatereductase)	*ghrB*	321	EC:1.1.1.215	K00090
648060981	6-phosphogluconate dehydratase (EC 4.2.1.12)	*edd*	617	EC:4.2.1.12	K01690
648058432	fructose-1,6-bisphosphatase	*fbp*	323	EC:3.1.3.11	K03841
648059749	fructose-bisphosphate aldolase (EC 4.1.2.13)	*fda*	345	EC:4.1.2.13	K01624
648060978	gluconate kinase	*gntK, idnK*	170	EC:2.7.1.12	K00851
648061406	glucose-6-phosphate isomerase	*pgi*	556	EC:5.3.1.9	K01810
648058870	hypothetical protein	*pgl*	411	EC:3.1.1.31	K07404
648060624	Phosphomannomutase/phosphoglucomutase(PMM /PGM)	*pmm-pgm*	472	EC:5.4.2.2	K15778
648059413	putative ribose-phosphate pyrophosphokinase	*prsA*	294	EC:2.7.6.1	K00948
648060467	Putative transketolase C-terminal section (TK)	*tktA, tktB*	334	EC:2.2.1.1	K00615
648058154	Quinoprotein glucose dehydrogenase-A precursor	*gcd*	801	EC:1.1.5.2	K00117
648059175	Quinoprotein glucose dehydrogenase-B precursor	*gcd*	479	EC:1.1.5.2	K00117
648059216	ribose-5-phosphate isomerase (EC 5.3.1.6)	*rpiA*	223	EC:5.3.1.6	K01807
648060677	ribose-phosphate pyrophosphokinase	*prs*	316	EC:2.7.6.1	K00948
648060823	ribulose-phosphate 3-epimerase	*rpe*	228	EC:5.1.3.1	K01783
648058950	transaldolase B	*talA, talB*	329	EC:2.2.1.2	K00616
648059775	transketolase	*tkt*	662	EC:2.2.1.1	K00615
648060468	transketolase, N-terminal subunit	*tktA, tktB*	283	EC:2.2.1.1	K00615

TABLE S8 Biotin metabolism

Gene ID	Gene Product Name	Gene Symbol	Amino Acid Sequence Length (aa)	Enzyme	KO
648059039	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.-)	*fabZ*	161	EC:4.2.1.59	K02372
648060944	3-ketoacyl-(acyl-carrier-protein) reductase	*fabG*	241	EC:1.1.1.100	K00059
648058954	3-ketoacyl-(acyl-carrier-protein) reductase	*fabG*	463	EC:1.1.1.100	K00059
648060946	3-oxoacyl-(acyl carrier protein) synthase I	*fabB*	400	EC:2.3.1.41	K00647
648060943	3-oxoacyl-(acyl carrier protein) synthase II	*fabF*	408	EC:2.3.1.179	K09458
648060688	3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100)	*fabG*	244	EC:1.1.1.100	K00059
648059894	3-oxoacyl-[acyl-carrier-protein] reductase(3-ketoacyl-acyl carrier protein reductase)	*fabG*	245	EC:1.1.1.100	K00059
648059276	3-oxoacyl-[acyl-carrier-protein] reductase(3-ketoacyl-acyl carrier protein reductase)	*fabG*	245	EC:1.1.1.100	K00059
648060699	8-amino-7-oxononanoate synthase	*bioF*	385	EC:2.3.1.47	K00652
648060700	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	*bioA*	426	EC:2.6.1.62	K00833
648060701	alpha/beta superfamily hydrolase/acyltransferase	*bioH*	243	EC:3.1.1.85	K02170
648060648	Beta-ketoacyl synthase, N-terminal domain protein	*fabB*	409	EC:2.3.1.41	K00647
648060711	Bifunctional protein birA	*birA*	250	EC:6.3.4.15	K03524
648059786	biotin synthase	*bioB*	329	EC:2.8.1.6	K01012
648060697	dithiobiotin synthetase	*bioD*	214	EC:6.3.3.3	K01935
648060934	Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9)	*fabI*	288	EC:1.3.1.9	K00208

648060698	putative biotin biosynthesis protein (BioC)	*bioC*	249	EC:2.1.1.197	K02169
648060074	short-chain dehydrogenase/reductase SDR	*fabG*	265	EC:1.1.1.100	K00059