

In silico* analysis of pathogenic islands and metabolic pathways for understanding infection biology and lifestyle of *Clostridium chauvoei

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SUPPLEMENTARY MATERIAL

In Silico Characterization of Pathogenic Islands and Pathways in *Clostridium chauvoei* for Understanding Infection Biology and Lifestyle

Supplementary Table 1. The genes in pathogenic islands of *Clostridium chauvoei* strain SBP 07/09

S. No.	Island No.	Gene No.	Gene start	Gene end
1	CCPI1	CCPI-G1	537993	538685
2	CCPI1	CCPI-G2	538814	539695
3	CCPI1	CCPI-G3	539725	540570
4	CCPI1	CCPI-G4	540600	540890
5	CCPI1	CCPI-G5	540920	541813
6	CCPI1	CCPI-G6	541843	542688
7	CCPI1	CCPI-G7	542718	543599
8	CCPI1	CCPI-G8	543629	543895
9	CCPI1	CCPI-G9	543925	544794
10	CCPI1	CCPI-G10	544995	545177

11	CCPI2	CCPI-G11	725827	726444
12	CCPI2	CCPI-G12	726661	727899
13	CCPI2	CCPI-G13	728033	729511
14	CCPI2	CCPI-G14	729710	730927
15	CCPI2	CCPI-G15	730914	734408
16	CCPI2	CCPI-G16	734484	734621
17	CCPI2	CCPI-G17	734944	735627
18	CCPI2	CCPI-G18	736027	736170
19	CCPI2	CCPI-G19	736268	737347
20	CCPI2	CCPI-G20	737553	738326
21	CCPI3	CCPI-G21	1322471	1323061
22	CCPI3	CCPI-G22	1323145	1323228
23	CCPI3	CCPI-G23	1323225	1324277
24	CCPI3	CCPI-G24	1324600	1326144
25	CCPI3	CCPI-G25	1326343	1326603
26	CCPI3	CCPI-G26	1326764	1327024
27	CCPI3	CCPI-G27	1327111	1327329
28	CCPI3	CCPI-G28	1327469	1328899
29	CCPI4	CCPI-G29	1811552	1812190
30	CCPI4	CCPI-G30	1812183	1812341
31	CCPI4	CCPI-G31	1812579	1812968
32	CCPI4	CCPI-G32	1813075	1813194
33	CCPI4	CCPI-G33	1813350	1813580
34	CCPI4	CCPI-G34	1813567	1813764
35	CCPI4	CCPI-G35	1813766	1815070
36	CCPI4	CCPI-G36	1815072	1815932
37	CCPI4	CCPI-G37	1816080	1816571

38	CCPI4	CCPI-G38	1816751	1816942
39	CCPI4	CCPI-G39	1817007	1817180
40	CCPI4	CCPI-G40	1817292	1817483
41	CCPI4	CCPI-G41	1817656	1818030
42	CCPI4	CCPI-G42	1818150	1819055
43	CCPI5	CCPI-G43	2258243	2259109
44	CCPI5	CCPI-G44	2259311	2260849
45	CCPI5	CCPI-G45	2261086	2261832
46	CCPI5	CCPI-G46	2261907	2263082
47	CCPI5	CCPI-G47	2263292	2264290
48	CCPI5	CCPI-G48	2264342	2265382
49	CCPI5	CCPI-G49	2265571	2266947
50	CCPI5	CCPI-G50	2267198	2268835
51	CCPI6	CCPI-G51	2610857	2612245
52	CCPI6	CCPI-G52	2612383	2612703
53	CCPI6	CCPI-G53	2612737	2613054
54	CCPI6	CCPI-G54	2613177	2614076
55	CCPI6	CCPI-G55	2614134	2615489
56	CCPI6	CCPI-G56	2615697	2616890
57	CCPI6	CCPI-G57	2617045	2618682
58	CCPI6	CCPI-G58	2618851	2619567
59	CCPI6	CCPI-G59	2619737	2623213
60	CCPI6	CCPI-G60	2623235	2625475
61	CCPI6	CCPI-G61	2625547	2626854
62	CCPI6	CCPI-G62	2627524	2628012
63	CCPI6	CCPI-G63	2628795	2629430
64	CCPI6	CCPI-G64	2629832	2631070

65	CCPI6	CCPI-G65	2631310	2631723
66	CCPI7	CCPI-G66	2786754	2788193
67	CCPI7	CCPI-G67	2788324	2789244
68	CCPI7	CCPI-G68	2789423	2790862
69	CCPI8	CCPI-G69	2830535	2831566
70	CCPI8	CCPI-G70	2831568	2832362
71	CCPI8	CCPI-G71	2832375	2833421
72	CCPI8	CCPI-G72	2833553	2835190
73	CCPI8	CCPI-G73	2836209	2838836
74	CCPI8	CCPI-G74	2839404	2839628
75	CCPI8	CCPI-G75	2839797	2839892
76	CCPI8	CCPI-G76	2840050	2841300
77	CCPI8	CCPI-G77	2841653	2842345
78	CCPI8	CCPI-G78	2842931	2843410
79	CCPI8	CCPI-G79	2843456	2844100
80	CCPI8	CCPI-G80	2844210	2844851
81	CCPI8	CCPI-G81	2844935	2845432

Supplementary Table 2. The functions predicted by different tools for genes present in pathogenic islands of *Clostridium chauvoei* strain SBP 07/09

S. No	Island No.	Gene No.	Tools	Function
1	CCPI1	CCPI-G1	BLAST	hypothetical protein
			InterPro	No match found
			KEGG	No match found
2	CCPI1	CCPI-G2	BLAST	Rpn family recombination-promoting nuclease/putative transposase

			InterPro	Recombination-promoting nuclease RpnA
			KEGG	No match found
3	CCPI1	CCPI-G3	BLAST	Rpn family recombination-promoting nuclease/putative transposase
			InterPro	Recombination-promoting nuclease RpnA
			KEGG	No match found
4	CCPI1	CCPI-G4	BLAST	hypothetical protein
			InterPro	No match found
			KEGG	No match found
5	CCPI1	CCPI-G5	BLAST	Rpn family recombination-promoting nuclease/putative transposase
			InterPro	Recombination-promoting nuclease RpnA
			KEGG	No match found
6	CCPI1	CCPI-G6	BLAST	Rpn family recombination-promoting nuclease/putative transposase
			InterPro	No match found
			KEGG	No match found
7	CCPI1	CCPI-G7	BLAST	Rpn family recombination-promoting nuclease/putative transposase
			InterPro	Recombination-promoting nuclease RpnA
			KEGG	No match found
8	CCPI1	CCPI-G8	BLAST	hypothetical protein

			InterPro	No match found
			KEGG	No match found
9	CCPI1	CCPI-G9	BLAST	Rpn family recombination-promoting nuclease/putative transposase
			InterPro	Recombination-promoting nuclease RpnA
			KEGG	No match found
10	CCPI1	CCPI-G10	BLAST	PspC domain-containing protein
			InterPro	Recombination-promoting nuclease RpnA
			KEGG	pspC; phage shock protein C
11	CCPI2	CCPI-G11	BLAST	phosphate propanoyltransferase
			InterPro	Phosphate propanoyltransferase
			KEGG	K15024; putative phosphotransacetylase [EC:2.3.1.8]
12	CCPI2	CCPI-G12	BLAST	IS256 family transposase
			InterPro	Transposase, mutator type
			KEGG	No match found
13	CCPI2	CCPI-G13	BLAST	FAD-binding protein
			InterPro	FAD-dependent oxidoreductase SdhA/FrdA/AprA
			KEGG	No match found
14	CCPI2	CCPI-G14	BLAST	exonuclease SbcCD subunit D
			InterPro	Nuclease SbcCD subunit D
			KEGG	sbcD, mre11; DNA repair protein

				SbcD/Mre11
15	CCPI2	CCPI-G15	BLAST	AAA family ATPase
			InterPro	No match found
			KEGG	sbcC, rad50; DNA repair protein SbcC/Rad50
16	CCPI2	CCPI-G16	BLAST	hypothetical protein
			InterPro	No match found
			KEGG	No match found
17	CCPI2	CCPI-G17	BLAST	pseudouridine synthase
			InterPro	Pseudouridine synthase, RsuA/RluB/E/F
			KEGG	rluF; 23S rRNA pseudouridine2604 synthase [EC:5.4.99.21]
18	CCPI2	CCPI-G18	BLAST	hypothetical protein
			InterPro	No match found
			KEGG	No match found
19	CCPI2	CCPI-G19	BLAST	hypothetical protein C6H62_03430
			InterPro	Transcription regulator HTH, AraC- type
			KEGG	No match found
20	CCPI2	CCPI-G20	BLAST	DUF4046 domain-containing protein
			InterPro	No match found
			KEGG	No match found
21	CCPI3	CCPI-G21	BLAST	CDP-diacylglycerol--glycerol-3- phosphate 3-phosphatidyltransferase

			InterPro	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
			KEGG	pgsA, PGS1; CDP-diacylglycerol---glycerol-3-phosphate 3-phosphatidyltransferase [EC:2.7.8.5]
22	CCPI3	CCPI-G22	BLAST	No match found
			InterPro	No match found
			KEGG	No match found
23	CCPI3	CCPI-G23	BLAST	recombinase RecA
			InterPro	DNA recombination and repair protein RecA
			KEGG	recA; recombination protein RecA
24	CCPI3	CCPI-G24	BLAST	ribonuclease Y
			InterPro	Ribonuclease Y
			KEGG	rny; ribonuclease Y [EC:3.1.-.-]
25	CCPI3	CCPI-G25	BLAST	stage V sporulation protein S
			InterPro	Sporulation stage V, protein S
			KEGG	spoVS; stage V sporulation protein S
26	CCPI3	CCPI-G26	BLAST	HPr family phosphocarrier protein
			InterPro	Phosphocarrier protein HPr
			KEGG	ptsH; phosphocarrier protein HPr
27	CCPI3	CCPI-G27	BLAST	DUF378 domain-containing protei
			InterPro	Protein of unknown function DUF378

			KEGG	K09779; uncharacterized protein
28	CCPI3	CCPI-G28	BLAST	adenylosuccinate lyase
			InterPro	Adenylosuccinate lyase
			KEGG	purB, ADSL; adenylosuccinate lyase [EC:4.3.2.2]
29	CCPI4	CCPI-G29	BLAST	tyrosine-type recombinase/integrase
			InterPro	No match found
			KEGG	No match found
30	CCPI4	CCPI-G30	BLAST	hypothetical protein
			InterPro	No match found
			KEGG	No match found
31	CCPI4	CCPI-G31	BLAST	ArpU family phage packaging/lysis transcriptional regulator
			InterPro	Putative autolysin regulatory protein ArpU-like
			KEGG	No match found
32	CCPI4	CCPI-G32	BLAST	Hypothetical protein CCH01_014020
			InterPro	No match found
			KEGG	No match found
33	CCPI4	CCPI-G33	BLAST	hypothetical protein
			InterPro	No match found
			KEGG	No match found
34	CCPI4	CCPI-G34	BLAST	hypothetical protein

			InterPro	No match found
			KEGG	No match found
35	CCPI4	CCPI-G35	BLAST	replicative DNA helicase
			InterPro	DNA helicase, DnaB type
			KEGG	dnaB; replicative DNA helicase [EC:5.6.2.3]
36	CCPI4	CCPI-G36	BLAST	hypothetical protein
			InterPro	No match found
			KEGG	No match found
37	CCPI4	CCPI-G37	BLAST	Putative Conserved domain protein
			InterPro	No match found
			KEGG	No match found
38	CCPI4	CCPI-G38	BLAST	hypothetical protein
			InterPro	No match found
			KEGG	No match found
39	CCPI4	CCPI-G39	BLAST	hypothetical protein
			InterPro	No match found
			KEGG	No match found
40	CCPI4	CCPI-G40	BLAST	helix-turn-helix transcriptional regulator
			InterPro	No match found
			KEGG	No match found
41	CCPI4	CCPI-G41	BLAST	helix-turn-helix transcriptional regulator

			InterPro	No match found
			KEGG	No match found
42	CCPI4	CCPI-G42	BLAST	DUF4236 domain-containing protein
			InterPro	No match found
			KEGG	No match found
43	CCPI5	CCPI-G43	BLAST	DegV family protein
			InterPro	DegV domain-containing
			KEGG	No match found
44	CCPI5	CCPI-G44	BLAST	Putative=2,3-bisphosphoglycerate-independent phosphoglycerate mutase
			InterPro	Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent
			KEGG	gpmI; 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [EC:5.4.2.12]
45	CCPI5	CCPI-G45	BLAST	Putative Triosephosphate isomerase
			InterPro	Triosephosphate isomerase
			KEGG	TPI, tpiA; triosephosphate isomerase (TIM) [EC:5.3.1.1]
46	CCPI5	CCPI-G46	BLAST	phosphoglycerate kinase
			InterPro	Phosphoglycerate kinase
			KEGG	PGK, pgk; phosphoglycerate kinase [EC:2.7.2.3]

47	CCPI5	CCPI-G47	BLAST	type I glyceraldehyde-3-phosphate dehydrogenase
			InterPro	Glyceraldehyde-3-phosphate dehydrogenase, type I
			KEGG	GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [EC:1.2.1.12]
48	CCPI5	CCPI-G48	BLAST	Putative Transcriptional regulator
			InterPro	Bacterial SorC Transcriptional Regulators
			KEGG	cggR; central glycolytic genes regulator
49	CCPI5	CCPI-G49	BLAST	RNA polymerase factor sigma-54
			InterPro	RNA polymerase sigma factor 54
			KEGG	rpoN; RNA polymerase sigma-54 factor
50	CCPI5	CCPI-G50	BLAST	Transposase DDE domain protein
			InterPro	IS1182 transposase
			KEGG	K07487; transposase
51	CCPI6	CCPI-G51	BLAST	sigma 54-interacting transcriptional regulator
			InterPro	No match found
			KEGG	No match found
52	CCPI6	CCPI-G52	BLAST	PTS lactose/cellobiose transporter subunit IIA
			InterPro	Phosphotransferase system, lactose/cellobiose-type IIA subunit

			KEGG	celC, chbA; cellobiose PTS system EIIA component [EC:2.7.1.196 2.7.1.205]
53	CCPI6	CCPI-G53	BLAST	Putative Lichenan-specific phosphotransferase enzyme iib component
			InterPro	PTS system sugar-specific EIIB domain-containing protein
			KEGG	celA, chbB; cellobiose PTS system EIIB component [EC:2.7.1.196 2.7.1.205]
54	CCPI6	CCPI-G54	BLAST	PEP phosphonomutase
			InterPro	No match found
			KEGG	No match found
55	CCPI6	CCPI-G55	BLAST	PTS sugar transporter subunit IIC
			InterPro	Phosphotransferase system, cellobiose-type IIC component
			KEGG	celB, chbC; cellobiose PTS system EIIC component
56	CCPI6	CCPI-G56	BLAST	ROK family transcriptional regulator
			InterPro	ROK family
			KEGG	No match found
57	CCPI6	CCPI-G57	BLAST	Transposase DDE domain protein
			InterPro	IS1182 transposase
			KEGG	K07487; transposase
58	CCPI6	CCPI-G58	BLAST	class B sortase

			InterPro	Sortase B family
			KEGG	srtB; sortase B [EC:3.4.22.71]
59	CCPI6	CCPI-G59	BLAST	alpha-L-fucosidase
			InterPro	Glycoside hydrolase, family 29
			KEGG	FUCA; alpha-L-fucosidase [EC:3.2.1.51]
60	CCPI6	CCPI-G60	BLAST	glycoside hydrolase family 16 protein
			InterPro	Glycosyl Hydrolase Family 16
			KEGG	No match found
61	CCPI6	CCPI-G61	BLAST	PTS sugar transporter subunit IIC
			InterPro	Phosphotransferase system, cellobiose-type IIC component
			KEGG	celB, chbC; cellobiose PTS system EIIC component
62	CCPI6	CCPI-G62	BLAST	amidohydrolase family protein
			InterPro	Metallo-dependent Hydrolases
			KEGG	No match found
63	CCPI6	CCPI-G63	BLAST	hypothetical protein
			InterPro	No match found
			KEGG	No match found
64	CCPI6	CCPI-G64	BLAST	IS256 family transposase
			InterPro	Transposase, mutator type
			KEGG	K07493; putative transposase

65	CCPI6	CCPI-G65	BLAST	hypothetical protein
			InterPro	No match found
			KEGG	No match found
66	CCPI7	CCPI-G66	BLAST	DDE-type integrase/transposase/recombinase
			InterPro	No match found
			KEGG	No match found
67	CCPI7	CCPI-G67	BLAST	sugar ABC transporter permease
			InterPro	ABC transporter permease component
			KEGG	ngcF; N-acetylglucosamine transport system permease protein
68	CCPI7	CCPI-G68	BLAST	DDE-type integrase/transposase/recombinase
			InterPro	No match found
			KEGG	No match found
69	CCPI8	CCPI-G69	BLAST	anaerobic sulfite reductase subunit AsrA
			InterPro	Sulphite reductase, subunit A
			KEGG	asrA; anaerobic sulfite reductase subunit A
70	CCPI8	CCPI-G70	BLAST	anaerobic sulfite reductase subunit AsrB
			InterPro	Sulphite reductase, subunit B
			KEGG	asrB; anaerobic sulfite reductase subunit B

71	CCPI8	CCPI-G71	BLAST	sulfite reductase subunit C
			InterPro	Sulphite reductase, subunit C
			KEGG	asrC; anaerobic sulfite reductase subunit C
72	CCPI8	CCPI-G72	BLAST	Transposase DDE domain protein
			InterPro	IS1182 transposase
			KEGG	K07487; transposase
73	CCPI8	CCPI-G73	BLAST	hypothetical protein BTM20_13170
			InterPro	No match found
			KEGG	No match found
74	CCPI8	CCPI-G74	BLAST	transcriptional regulator
			InterPro	No match found
			KEGG	No match found
75	CCPI8	CCPI-G75	BLAST	MarR family transcriptional regulator
			InterPro	No match found
			KEGG	No match found
76	CCPI8	CCPI-G76	BLAST	MFS transporter
			InterPro	Major facilitator superfamily
			KEGG	No match found
77	CCPI8	CCPI-G77	BLAST	YjjG family noncanonical pyrimidine nucleotidase
			InterPro	Pyrimidine 5'-nucleotidase YjjG

			KEGG	E3.8.1.2; 2-haloacid dehalogenase [EC:3.8.1.2]
78	CCPI8	CCPI-G78	BLAST	23S rRNA (pseudouridine(1915)-N(3))- methyltransferase RlmH
			InterPro	RNA methyltransferase RlmH
			KEGG	rlmH; 23S rRNA (pseudouridine1915- N3)-methyltransferase [EC:2.1.1.177]
79	CCPI8	CCPI-G79	BLAST	Hsp20 family protein
			InterPro	No match found
			KEGG	No match found
80	CCPI8	CCPI-G80	BLAST	lactate utilization protein
			InterPro	Uncharacterised conserved protein UCP020269
			KEGG	No match found
81	CCPI8	CCPI-G81	BLAST	SEC-C metal-binding domain-containing protein
			InterPro	No match found
			KEGG	No match found

Supplementary Table 3: The number of genes according to their functions in pathogenic islands of *C. chauvoei* strain SBP 07/09

S. No.	Pathogenic Island No.	No. of genes	No. of Genes with Functions			No. of Hypothetical Proteins			No. of Genes with No Function		
			BLASTp	InterPro	BlastKOALA	BLASTp	InterPro	BlastKOALA	BLASTp	InterPro	BlastKOALA
1	CCPI1	10	7	6	1	3	0	0	0	4	9
2	CCPI2	10	6	6	4	4	0	0	0	4	6
3	CCPI3	8	6	6	6	1	1	1	1	1	1
4	CCPI4	14	5	2	1	9	0	0	0	12	13
5	CCPI5	8	8	8	8	0	0	0	0	0	1
6	CCPI6	15	13	11	8	2	0	0	0	4	7
7	CCPI7	3	3	1	1	0	0	0	0	2	2
8	CCPI8	13	12	7	6	1	1	0	0	5	7
Total		81	60	47	35	20	2	1	1	32	46

Supplementary Table 4: The metabolic pathway analysis predicted using KEGG Mapper and BioCyc Pathway Tools in *C. chauvoei* strain SBP 07/09

S. no	Gene no.	Gene name	Gene synonym	Pathways predicted through KEGG Mapper based on KO IDs	KEGG pathways related to <i>Clostridium</i>	BioCyc pathways related to <i>Clostridium</i>
1	CCPI-G10	pspC; phage shock protein C	PspC domain-containing protein	K03973	-	-
2	CCPI-G11	putative phosphotransacetylase [EC:2.3.1.8]	phosphate propanoyltransferase	K15024 - Taurine and hypotaurine metabolism; Pyruvate metabolism; Propanoate metabolism; Carbon fixation pathways in prokaryotes; Metabolic pathways; Microbial metabolism in diverse environments; Carbon metabolism	Pyruvate metabolism; Propanoate metabolism	L-threonine degradation I, S-propane-1,2-diol degradation
3	CCPI-G14	sbcD, mre11; DNA repair protein SbcD/Mre11	exonuclease SbcCD subunit D	K03547	-	-
4	CCPI-G15	sbcC, rad50; DNA repair protein SbcC/Rad50	AAA family ATPase	K03546	-	ATP biosynthesis
5	CCPI-G17	rluF; 23S rRNA pseudouridine2604 synthase [EC:5.4.99.21]	pseudouridine synthase	K06182	-	-
6	CCPI-G21	pgsA, PGS1; CDP-diacylglycerol---glycerol-3-phosphate 3-phosphatidyltransferase	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	K00995 - Glycerophospholipid metabolism; Metabolic pathways	-	cardiolipin biosynthesis I, cardiolipin biosynthesis III

		[EC:2.7.8.5]				
7	CCPI-G23	recA; recombination protein RecA	recombinase RecA	K03553 - Homologous recombination	Homologous recombination	-
8	CCPI-G24	rny; ribonuclease Y [EC:3.1.-.-]	ribonuclease Y	K18682 - RNA degradation	RNA degradation	-
9	CCPI-G25	spoVS; stage V sporulation protein S	stage V sporulation protein S	K06416	-	-
10	CCPI-G26	ptsH; phosphocarrier protein HPr	HPr family phosphocarrier protein	K02784 - Phosphotransferase system (PTS)	Phosphotransferase system (PTS)	-
11	CCPI-G27	uncharacterized protein	DUF378 domain-containing protein	K09779	-	-
12	CCPI-G28	purB, ADSL; adenylosuccinate lyase [EC:4.3.2.2]	adenylosuccinate lyase	K01756 - Purine metabolism; Alanine, aspartate and glutamate metabolism; Metabolic pathways; Biosynthesis of secondary metabolites; Nucleotide metabolism; Biosynthesis of cofactors	-	adenosine ribonucleotides <i>de novo</i> biosynthesis, inosine-5'-phosphate biosynthesis II
13	CCPI-G35	dnaB; replicative DNA helicase [EC:5.6.2.3]	replicative DNA helicase	K02314 - DNA replication; Cell cycle - Caulobacter	-	-
14	CCPI-G44	gpmI; 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [EC:5.4.2.12]	Putative=2,3-bisphosphoglycerate-independent phosphoglycerate mutase	K15633 - Glycolysis / Gluconeogenesis; Glycine, serine and threonine metabolism; Methane metabolism; Metabolic pathways; Biosynthesis of secondary metabolites; Microbial metabolism in diverse environments; Carbon metabolism; Biosynthesis of amino acids	Glycolysis / Gluconeogenesis	gluconeogenesis I, glycolysis IV, glycolysis I (from glucose 6-phosphate)

15	CCPI-G45	TPI, tpiA; triosephosphate isomerase (TIM) [EC:5.3.1.1]	Putative Triosephosphate isomerase	K01803 - Glycolysis / Gluconeogenesis; Fructose and mannose metabolism; Inositol phosphate metabolism; Carbon fixation in photosynthetic organisms; Metabolic pathways; Biosynthesis of secondary metabolites; Microbial metabolism in diverse environments; Carbon metabolism; Biosynthesis of amino acids	Glycolysis / Gluconeogenesis	glycolysis I (from glucose 6- phosphate), gluconeogenesis I, glycolysis IV
16	CCPI-G46	PGK, pgk; phosphoglycerate kinase [EC:2.7.2.3]	phosphoglycerate kinase	K00927 - Glycolysis / Gluconeogenesis; Carbon fixation in photosynthetic organisms; Metabolic pathways; Biosynthesis of secondary metabolites; Microbial metabolism in diverse environments; Carbon metabolism; Biosynthesis of amino acids; HIF-1 signaling pathway	Glycolysis / Gluconeogenesis	glycolysis I (from glucose 6- phosphate), gluconeogenesis I, glycolysis IV
17	CCPI-G47	GAPDH, gapA; glyceraldehyde 3- phosphate dehydrogenase (phosphorylating) [EC:1.2.1.12]	type I glyceraldehyde- 3-phosphate dehydrogenase	K00134 - Glycolysis / Gluconeogenesis; Carbon fixation in photosynthetic organisms; Metabolic pathways; Biosynthesis of secondary metabolites; Microbial metabolism in diverse environments; Carbon metabolism; Biosynthesis of amino acids;	Glycolysis / Gluconeogenesis	glycolysis I (from glucose 6- phosphate), gluconeogenesis I, glycolysis IV

				HIF-1 signaling pathway; Alzheimer disease; Pathogenic Escherichia coli infection; Salmonella infection; Diabetic cardiomyopathy		
18	CCPI- G48	cggR; central glycolytic genes regulator	Putative Transcriptional regulator	K05311	-	-
19	CCPI- G49	rpoN; RNA polymerase sigma-54 factor	RNA polymerase factor sigma-54	K03092 - Two-component system; Flagellar assembly; Biofilm formation - Vibrio cholerae	-	-
20	CCPI- G50	transposase	Transposase DDE domain protein	K07487	-	-
21	CCPI- G52	celC, chbA; cellobiose PTS system EIIA component [EC:2.7.1.196 2.7.1.205]	PTS lactose/cellobiose transporter subunit IIA	K02759 - Starch and sucrose metabolism; Phosphotransferase system (PTS)	Phosphotransferase system (PTS)	
22	CCPI- G53	celA, chbB; cellobiose PTS system EIIB component [EC:2.7.1.196 2.7.1.205]	Putative Lichenan- specific phosphotransferase enzyme iib component	K02760 - Starch and sucrose metabolism; Phosphotransferase system (PTS)	Phosphotransferase system (PTS)	-
23	CCPI- G55	celB, chbC; cellobiose PTS system EIIC component	PTS sugar transporter subunit IIC	K02761- Starch and sucrose metabolism; Phosphotransferase system (PTS)	Phosphotransferase system (PTS)	-
24	CCPI- G57	K07487; transposase	Transposase DDE domain protein	K07487	-	-
25	CCPI-	srtB; sortase B	class B sortase	K08600	-	-

	G58	[EC:3.4.22.71]				
26	CCPI-G59	FUCA; alpha-L-fucosidase [EC:3.2.1.51]	alpha-L-fucosidase	K01206 - Other glycan degradation; Lysosome	-	-
27	CCPI-G61	celB, chbC; cellobiose PTS system EIIC component	PTS sugar transporter subunit IIC	K02761 - Starch and sucrose metabolism; Phosphotransferase system (PTS)	Phosphotransferase system (PTS)	-
28	CCPI-G64	K07493; putative transposase	IS256 family transposase	K07493	-	-
29	CCPI-G67	ngcF; N-acetylglucosamine transport system permease protein	sugar ABC transporter permease	K10201 - ABC transporters	ABC transporters	-
30	CCPI-G69	asrA; anaerobic sulfite reductase subunit A	anaerobic sulfite reductase subunit AsrA	K16950 - Sulfur metabolism; Metabolic pathways; Microbial metabolism in diverse environments	-	-
31	CCPI-G70	asrB; anaerobic sulfite reductase subunit B	anaerobic sulfite reductase subunit AsrB	K16951 - Sulfur metabolism; Metabolic pathways; Microbial metabolism in diverse environments	-	-
32	CCPI-G71	asrC; anaerobic sulfite reductase subunit C	sulfite reductase subunit C	K00385 - Sulfur metabolism; Metabolic pathways; Microbial metabolism in diverse environments	-	-
33	CCPI-G72	transposase	Transposase DDE domain protein	K07487	-	-

34	CCPI-G77	E3.8.1.2; 2-haloacid dehalogenase [EC:3.8.1.2]	YjjG family noncanonical pyrimidine nucleotidase	K01560 - Chlorocyclohexane and chlorobenzene degradation; Chloroalkane and chloroalkene degradation; Metabolic pathways; Microbial metabolism in diverse environments	-	-
35	CCPI-G78	rlmH; 23S rRNA (pseudouridine1915-N3)-methyltransferase [EC:2.1.1.177]	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH	K00783	-	-
36	CCPI-G80	-	lactate utilization protein	-	-	pyruvate fermentation to S-lactate, gluconeogenesis I

Supplementary Table 5: The category of the pathways based on biological relevance and evidence in *C. chauvoei* strain SBP 07/09

S. No	Pathways	Category
1	(S)-propane-1,2-diol degradation	Consistent
2	[2Fe-2S] iron-sulfur cluster biosynthesis	Consistent
3	2-deoxy- α -D-ribose 1-phosphate degradation	Consistent
4	2-methyladeninyl adenosylcobamide biosynthesis from adenosylcobinamide-GDP	Consistent
5	2-O- α -mannosyl-D-glycerate degradation	False positive
6	3-dehydroquinate biosynthesis I	Consistent
7	4-deoxy-L-threo-hex-4-enopyranuronate degradation	Consistent
8	5-aminoimidazole ribonucleotide biosynthesis I	Consistent
9	5-aminoimidazole ribonucleotide biosynthesis II	Missing
10	5-hydroxybenzimidazolyl adenosylcobamide biosynthesis from adenosylcobinamide-GDP	Missing
11	5-methoxy-6-methylbenzimidazolyl adenosylcobamide biosynthesis from adenosylcobinamide-GDP	Missing
12	5-methoxybenzimidazolyl adenosylcobamide biosynthesis from adenosylcobinamide-GDP	Missing
13	5-methylbenzimidazolyl adenosylcobamide biosynthesis from adenosylcobinamide-GDP	Consistent
14	5-oxo-L-proline metabolism	Consistent
15	acetate and ATP formation from acetyl-CoA I	Consistent
16	acetyl-CoA fermentation to butanoate II	Missing

17	acyl carrier protein activation	Consistent
18	acyl-[acyl-carrier protein] thioesterase pathway	Missing
19	adenine and adenosine salvage I	Consistent
20	adenine and adenosine salvage III	Consistent
21	adeninyl adenosylcobamide biosynthesis from adenosylcobinamide-GDP	Consistent
22	adenosine deoxyribonucleotides de novo biosynthesis II	Consistent
23	adenosine nucleotides degradation II	Consistent
24	adenosine ribonucleotides de novo biosynthesis	Consistent
25	adenosylcobalamin biosynthesis from adenosylcobinamide-GDP I	Consistent
26	adenosylcobalamin salvage from cobalamin	Consistent
27	adenosylcobinamide-GDP biosynthesis from cobyrinate a,c-diamide	Partially consistent
28	adenosylcobinamide-GDP salvage from cobinamide I	Consistent
29	alanine racemization	Consistent
30	ammonia assimilation cycle III	Consistent
31	arsenate detoxification I	Partially consistent
32	ATP biosynthesis	Consistent
33	base-degraded thiamine salvage	Consistent
34	benzimidazolyl adenosylcobamide biosynthesis from adenosylcobinamide-GDP	Consistent
35	biotin biosynthesis from 8-amino-7-oxononanoate I	Partially consistent
36	biotin-carboxyl carrier protein assembly	Consistent

37	bis(guanylyl molybdenum cofactor) biosynthesis	Consistent
38	bis(guanylyl molybdopterin) cofactor sulfurylation	Poor topological match
39	bis(guanylyl tungstenpterin) cofactor biosynthesis	Poor topological match
40	cardiolipin biosynthesis I	Partially consistent
41	cardiolipin biosynthesis III	Partially consistent
42	CDP-diacylglycerol biosynthesis I	Consistent
43	choline degradation III	Consistent
44	chorismate biosynthesis from 3-dehydroquinate	Consistent
45	chorismate biosynthesis I	Consistent
46	CMP phosphorylation	Consistent
47	cob(II)yrinate a,c-diamide biosynthesis I (early cobalt insertion)	Consistent
48	coenzyme A biosynthesis I (prokaryotic)	Consistent
49	creatinine degradation I	Consistent
50	cyanophycin metabolism	Not reported
51	cytidylyl molybdenum cofactor sulfurylation	Poor topological match
52	D-arabinose degradation I	Consistent
53	D-galactose degradation I (Leloir pathway)	Consistent
54	dipyrromethane cofactor biosynthesis	Poor topological match
55	di-trans,poly-cis-undecaprenyl phosphate biosynthesis	Consistent
56	D-mannose degradation	Missing
57	D-sorbitol degradation I	Missing
58	ethanol degradation I	Consistent

59	ethanol degradation II	Poor topological match
60	fatty acid biosynthesis initiation (type II)	Consistent
61	fatty acid elongation -- saturated	Consistent
62	fatty acid β -oxidation I (generic)	Consistent
63	flavin biosynthesis I (bacteria and plants)	Consistent
64	folate polyglutamylation	Consistent
65	folate transformations III (E. coli)	Not reported
66	formate assimilation into 5,10-methylenetetrahydrofolate	Consistent
67	fucose degradation	Consistent
68	GDP-L-fucose biosynthesis I (from GDP-D-mannose)	Consistent
69	GDP-mannose biosynthesis	Partially consistent
70	gluconeogenesis I	Consistent
71	glucose and glucose-1-phosphate degradation	Consistent
72	glutathione biosynthesis	Consistent
73	glycerol and glycerophosphodiester degradation	Consistent
74	glycerol degradation I	Consistent
75	glycerophosphodiester degradation	Consistent
76	glycine biosynthesis I	Consistent
77	glycogen biosynthesis I (from ADP-D-Glucose)	Consistent
78	glycogen degradation II	Consistent
79	glycolysis I (from glucose 6-phosphate)	Consistent
80	glycolysis IV	Consistent
81	guanine and guanosine salvage I	Consistent
82	guanine and guanosine salvage II	Consistent

83	guanosine deoxyribonucleotides de novo biosynthesis II	Consistent
84	guanosine nucleotides degradation III	Consistent
85	guanosine ribonucleotides de novo biosynthesis	Consistent
86	guanylyl molybdenum cofactor biosynthesis	Consistent
87	heme b biosynthesis I (aerobic)	Poor topological match
88	heme b biosynthesis II (oxygen-independent)	Consistent
89	hydrogen production III	Partially consistent
90	hydroxymethylpyrimidine salvage	Consistent
91	inosine 5'-phosphate degradation	Consistent
92	inosine-5'-phosphate biosynthesis II	Consistent
93	L-alanine biosynthesis III	Consistent
94	L-ascorbate degradation I (bacterial, anaerobic)	Consistent
95	L-asparagine biosynthesis II	Consistent
96	L-cysteine biosynthesis V (mycobacteria)	Not reported
97	L-glutamate biosynthesis I	Consistent
98	L-glutamate biosynthesis III	Consistent
99	L-glutamine biosynthesis I	Consistent
100	L-glutamine degradation I	Consistent
101	L-glutamine degradation II	Consistent
102	L-histidine biosynthesis	Missing
103	L-homoserine biosynthesis	Consistent
104	lipoprotein posttranslational modification	Consistent
105	L-isoleucine biosynthesis I (from threonine)	Consistent
106	L-isoleucine degradation I	Consistent

107	L-lysine biosynthesis III	Consistent
108	L-phenylalanine biosynthesis I	Not reported
109	L-proline biosynthesis I (from L-glutamate)	Consistent
110	L-serine degradation	Consistent
111	L-threonine degradation I	Consistent
112	methylerythritol phosphate pathway I	Consistent
113	molybdenum cofactor biosynthesis	Consistent
114	molybdopterin biosynthesis	Poor topological match
115	N ¹⁰ -formyl-tetrahydrofolate biosynthesis	Missing
116	N ⁶ -L-threonylcarbamoyladenosine ³⁷ -modified tRNA biosynthesis	Consistent
117	N-acetylglucosamine degradation I	Consistent
118	N-acetylneuraminate and N-acetylmannosamine degradation I	Consistent
119	NAD de novo biosynthesis I (from aspartate)	Missing
120	NAD salvage pathway II (PNC IV cycle)	Consistent
121	NAD salvage pathway III (to nicotinamide riboside)	Consistent
122	NADH repair (prokaryotes)	Partially consistent
123	NADP biosynthesis	Consistent
124	NADPH repair (prokaryotes)	Partially consistent
125	nitrate reduction IV (dissimilatory)	Partially consistent
126	nitrate reduction V (assimilatory)	Partially consistent
127	octanoyl-[acyl-carrier protein] biosynthesis (mitochondria, yeast)	Not reported
128	oleandomycin activation/inactivation	Missing

129	oleate β -oxidation	Consistent
130	palmitate biosynthesis (type II fatty acid synthase)	Not reported
131	palmitoleate biosynthesis I (from (5Z)-dodec-5-enoate)	Missing
132	pentose phosphate pathway (non-oxidative branch) I	Consistent
133	peptidoglycan biosynthesis I (meso-diaminopimelate containing)	Consistent
134	peptidoglycan maturation (meso-diaminopimelate containing)	Consistent
135	phosphatidylglycerol biosynthesis II (non-plastidic)	Missing
136	phosphatidylserine and phosphatidylethanolamine biosynthesis I	Consistent
137	phosphopantothenate biosynthesis I	Consistent
138	ppGpp metabolism	Partially consistent
139	PRPP biosynthesis	Consistent
140	purine deoxyribonucleosides degradation I	Consistent
141	purine deoxyribonucleosides salvage	Consistent
142	purine nucleotides degradation II (aerobic)	Consistent
143	purine ribonucleosides degradation	Consistent
144	putrescine biosynthesis III	Consistent
145	pyridoxal 5'-phosphate salvage I	Partially consistent
146	pyrimidine deoxyribonucleosides degradation	Consistent
147	pyrimidine deoxyribonucleosides salvage	Consistent
148	pyrimidine deoxyribonucleotide phosphorylation	Consistent

149	pyrimidine deoxyribonucleotides de novo biosynthesis I	Consistent
150	pyrimidine deoxyribonucleotides dephosphorylation	Consistent
151	pyrimidine nucleobases salvage I	Consistent
152	pyrimidine nucleobases salvage II	Consistent
153	pyrimidine ribonucleosides degradation	Consistent
154	pyrimidine ribonucleosides salvage I	Consistent
155	pyruvate fermentation to (S)-lactate	Consistent
156	pyruvate fermentation to acetate IV	Consistent
157	pyruvate fermentation to butanoate	Consistent
158	pyruvate fermentation to ethanol I	Consistent
159	queuosine biosynthesis	Missing
160	queuosine biosynthesis III (queuosine salvage)	Partially consistent
161	reactive oxygen species degradation	Consistent
162	ribose phosphorylation	Consistent
163	S-adenosyl-L-methionine biosynthesis	Consistent
164	S-adenosyl-L-methionine cycle I	Missing
165	S-methyl-5'-thioadenosine degradation IV	Consistent
166	spermidine biosynthesis I	Consistent
167	spermidine biosynthesis III	Consistent
168	stearate biosynthesis II (bacteria and plants)	Missing
169	superoxide radicals degradation	Consistent
170	superpathway of 5-aminoimidazole ribonucleotide biosynthesis	Missing
171	superpathway of adenosine nucleotides de novo biosynthesis II	Consistent
172	superpathway of coenzyme A biosynthesis I	Consistent

	(bacteria)	
173	superpathway of guanosine nucleotides de novo biosynthesis II	Consistent
174	superpathway of L-phenylalanine biosynthesis	Consistent
175	superpathway of N-acetylglucosamine, N-acetylmannosamine and N-acetylneuraminate degradation	Consistent
176	superpathway of purine deoxyribonucleosides degradation	Consistent
177	superpathway of pyrimidine deoxyribonucleoside salvage	Consistent
178	superpathway of pyrimidine deoxyribonucleosides degradation	Consistent
179	superpathway of pyrimidine nucleobases salvage	Consistent
180	superpathway of pyrimidine ribonucleosides degradation	Consistent
181	tetrahydrofolate biosynthesis	Consistent
182	tetrahydrofolate salvage from 5,10-methenyltetrahydrofolate	Partially consistent
183	thiamine diphosphate biosynthesis I (E. coli)	Consistent
184	thiamine diphosphate biosynthesis II (Bacillus)	Consistent
185	thiamine diphosphate biosynthesis III (Staphylococcus)	Consistent
186	thiamine diphosphate salvage II	Partially consistent
187	thiamine diphosphate salvage III	Partially consistent
188	thiamine diphosphate salvage IV (yeast)	Not reported

189	thiamine formation from pyrithiamine and oxythiamine (yeast)	Missing
190	thiamine phosphate formation from pyrithiamine and oxythiamine (yeast)	Not reported
191	thiamine salvage II	Missing
192	thiamine salvage III	Missing
193	thiamine salvage IV (yeast)	Missing
194	thioredoxin pathway	Consistent
195	thiosulfate oxidation III (multienzyme complex)	Poor topological match
196	thymine degradation	Consistent
197	tRNA charging	Consistent
198	tRNA processing	Consistent
199	tRNA-uridine 2-thiolation and selenation (bacteria)	Partially consistent
200	UDP-N-acetyl-D-glucosamine biosynthesis I	Consistent
201	UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)	Consistent
202	UDP- α -D-galactose biosynthesis	Consistent
203	UDP- α -D-glucose biosynthesis	Consistent
204	UMP biosynthesis III	Consistent
205	uracil degradation I (reductive)	Consistent
206	urea cycle	Consistent
207	UTP and CTP de novo biosynthesis	Consistent
208	UTP and CTP dephosphorylation I	Consistent
209	xanthine and xanthosine salvage	Consistent
210	β -alanine biosynthesis III	Consistent

Consistent: Pathways that are well-documented in the literature and present in standard metabolic databases, indicating strong biological support and reliable reconstruction.

Partially Consistent: Pathways with some supporting evidence from literature or databases but missing key enzymatic steps or essential branches, suggesting incomplete or truncated reconstructions.

Poor Topological Match: Pathways whose reaction sequence or overall structure significantly deviates from canonical versions, indicating likely prediction or annotation errors.

Missing: Pathways are known in curating databases or literature for the organism but not inferred in the current reconstruction, suggesting annotation gaps or tool limitations.

Not Reported: Pathways computationally inferred but lacking evidence in literature or databases, possibly representing novel findings or spurious predictions.

False Positive: Pathways established in other organisms but unlikely to be biologically relevant in the studied organism, often due to misannotation or overly broad inference rules.

Supplementary Table 6: The genes from pathogenic islands of *C. chauvoei* strain SBP 07/09 present within BioCyc pathways.

S. No.	Gene No	Protein function	BioCyc Pathways
1	CCPI-G1	Hypothetical protein	-
2	CCPI-G2	Rpn family recombination-promoting nuclease/putative transposase	-
3	CCPI-G3	Rpn family recombination-promoting nuclease/putative transposase	-
4	CCPI-G4	Hypothetical protein	-
5	CCPI-G5	Rpn family recombination-promoting nuclease/putative transposase	-
6	CCPI-G6	Rpn family recombination-promoting nuclease/putative transposase	-
7	CCPI-G7	Rpn family recombination-promoting nuclease/putative transposase	-
8	CCPI-G8	Hypothetical protein	-
9	CCPI-G9	Rpn family recombination-promoting nuclease/putative transposase	-

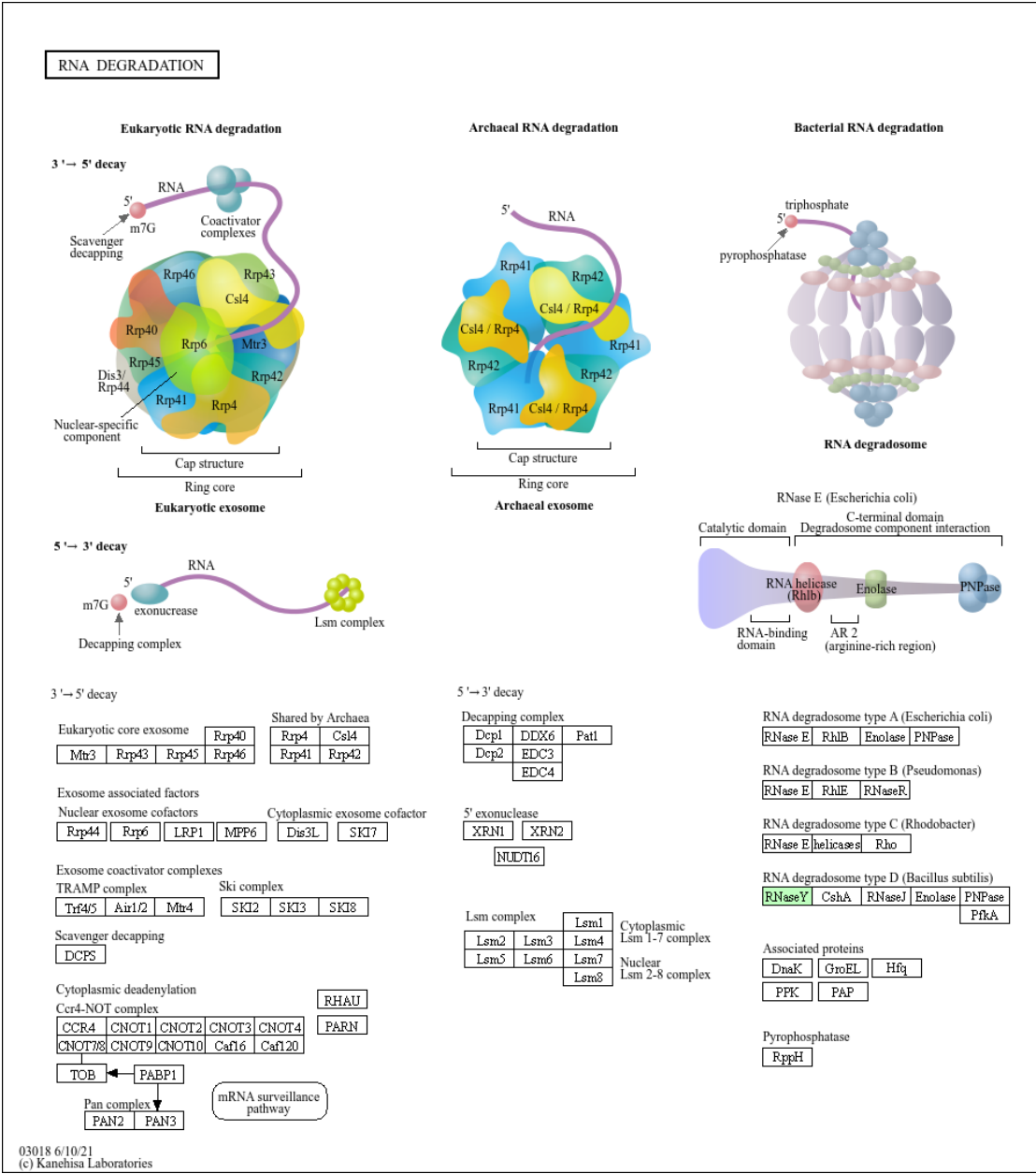
10	CCPI-G10	PspC domain-containing protein	-
11	CCPI-G11	Phosphate propanoyltransferase	L-threonine degradation I, S-propane-1,2-diol degradation
12	CCPI-G12	IS256 family transposase	-
13	CCPI-G13	FAD-binding protein	-
14	CCPI-G14	Exonuclease SbcCD subunit D	
15	CCPI-G15	AAA family ATPase	ATP biosynthesis
16	CCPI-G16	Hypothetical protein	-
17	CCPI-G17	Pseudouridine synthase	-
18	CCPI-G18	Hypothetical protein	-
19	CCPI-G19	Hypothetical protein C6H62_03430	-
20	CCPI-G20	DUF4046 domain-containing protein	-
21	CCPI-G21	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	Cardiolipin biosynthesis I, Cardiolipin biosynthesis III
22	CCPI-G22	No match found	
23	CCPI-G23	Recombinase RecA	-
24	CCPI-G24	Ribonuclease Y	-
25	CCPI-G25	Stage V sporulation protein S	-
26	CCPI-G26	HPr family phosphocarrier protein	-
27	CCPI-G27	DUF378 domain-containing protein	-
28	CCPI-G28	Adenylosuccinate lyase	Adenosine ribonucleotides <i>de novo</i> biosynthesis, inosine-5'-phosphate biosynthesis II
29	CCPI-G29	Tyrosine-type recombinase/integrase	-
30	CCPI-G30	Hypothetical protein	-
31	CCPI-G31	ArpU family phage packaging/lysis transcriptional regulator	-

32	CCPI-G32	Hypothetical protein CCH01_014020	-
33	CCPI-G33	Hypothetical protein	-
34	CCPI-G34	Hypothetical protein	-
35	CCPI-G35	Replicative DNA helicase	-
36	CCPI-G36	Hypothetical protein	-
37	CCPI-G37	Putative Conserved domain protein	-
38	CCPI-G38	Hypothetical protein	-
39	CCPI-G39	Hypothetical protein	-
40	CCPI-G40	Helix-turn-helix transcriptional regulator	-
41	CCPI-G41	Helix-turn-helix transcriptional regulator	-
42	CCPI-G42	DUF4236 domain-containing protein	-
43	CCPI-G43	DegV family protein	-
44	CCPI-G44	Putative=2,3-bisphosphoglycerate-independent phosphoglycerate mutase	Gluconeogenesis I, Glycolysis IV, Glycolysis I (from glucose 6-phosphate)
45	CCPI-G45	Putative Triosephosphate isomerase	Glycolysis I (from glucose 6-phosphate), Gluconeogenesis I, Glycolysis IV
46	CCPI-G46	Phosphoglycerate kinase	Glycolysis I (from glucose 6-phosphate), Gluconeogenesis I, Glycolysis IV
47	CCPI-G47	Type I glyceraldehyde-3-phosphate dehydrogenase	Glycolysis I (from glucose 6-phosphate), Gluconeogenesis I, Glycolysis IV
48	CCPI-G48	Putative Transcriptional regulator	-
49	CCPI-G49	RNA polymerase factor sigma-54	-
50	CCPI-G50	Transposase DDE domain protein	-

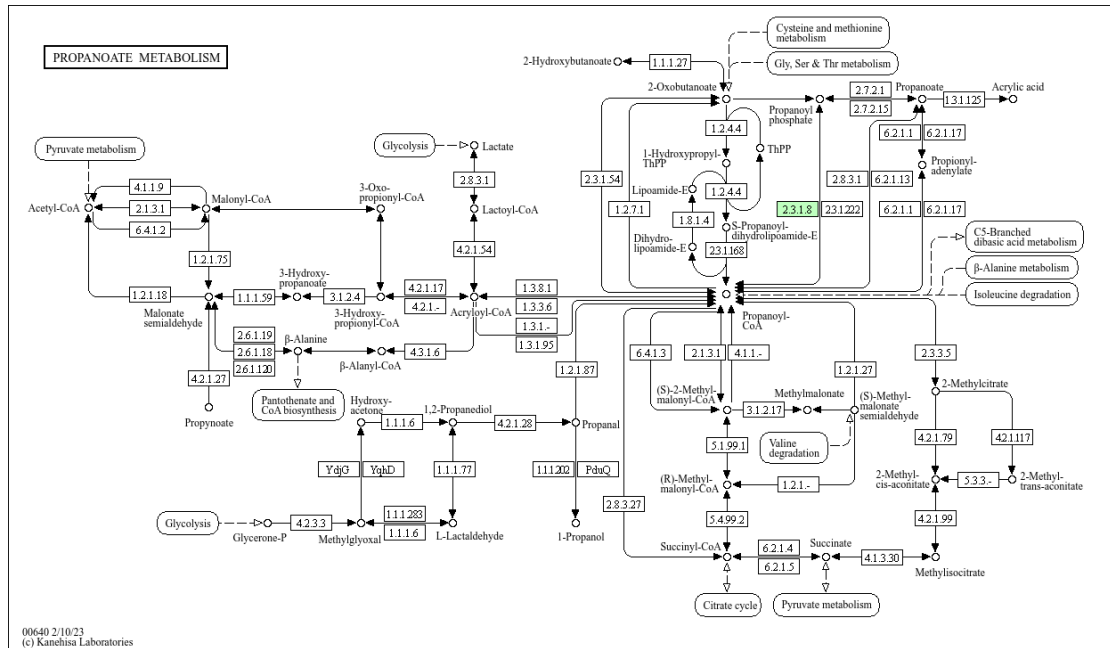
51	CCPI-G51	Sigma 54-interacting transcriptional regulator	-
52	CCPI-G52	PTS lactose/cellobiose transporter subunit IIA	-
53	CCPI-G53	Putative Lichenan-specific phosphotransferase enzyme iib component	-
54	CCPI-G54	PEP phosphonmutase	-
55	CCPI-G55	PTS sugar transporter subunit IIC	-
56	CCPI-G56	ROK family transcriptional regulator	-
57	CCPI-G57	Transposase DDE domain protein	-
58	CCPI-G58	Class B sortase	-
59	CCPI-G59	Alpha-L-fucosidase	-
60	CCPI-G60	Glycoside hydrolase family 16 protein	-
61	CCPI-G61	PTS sugar transporter subunit IIC	-
62	CCPI-G62	Amidohydrolase family protein	-
63	CCPI-G63	Hypothetical protein	-
64	CCPI-G64	IS256 family transposase	-
65	CCPI-G65	Hypothetical protein	-
66	CCPI-G66	DDE-type Integrase/transposase/recombinase	-
67	CCPI-G67	Sugar ABC transporter permease	-
68	CCPI-G68	DDE-type Integrase/transposase/recombinase	-
69	CCPI-G69	Anaerobic sulfite reductase subunit AsrA	-
70	CCPI-G70	Anaerobic sulfite reductase subunit AsrB	-

71	CCPI-G71	Sulfite reductase subunit C	-
72	CCPI-G72	Transposase DDE domain protein	-
73	CCPI-G73	Hypothetical protein BTM20_13170	-
74	CCPI-G74	Transcriptional regulator	-
75	CCPI-G75	MarR family transcriptional regulator	-
76	CCPI-G76	MFS transporter	-
77	CCPI-G77	YjjG family noncanonical pyrimidine nucleotidase	-
78	CCPI-G78	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH	-
79	CCPI-G79	Hsp20 family protein	-
80	CCPI-G80	Lactate utilization protein	Pyruvate fermentation to S-lactate, Gluconeogenesis I
81	CCPI-G81	SEC-C metal-binding domain-containing protein	-

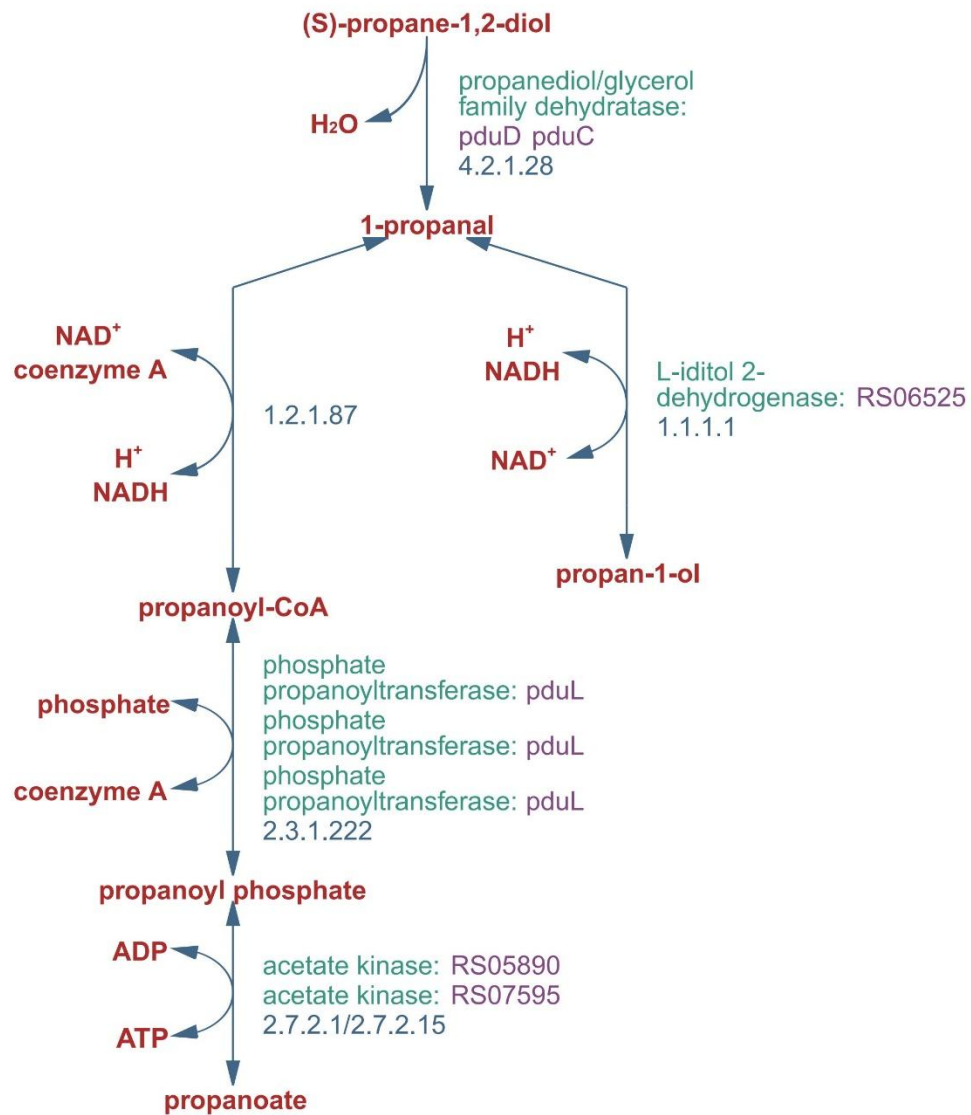
Supplementary figures: KEGG & BioCyc pathways



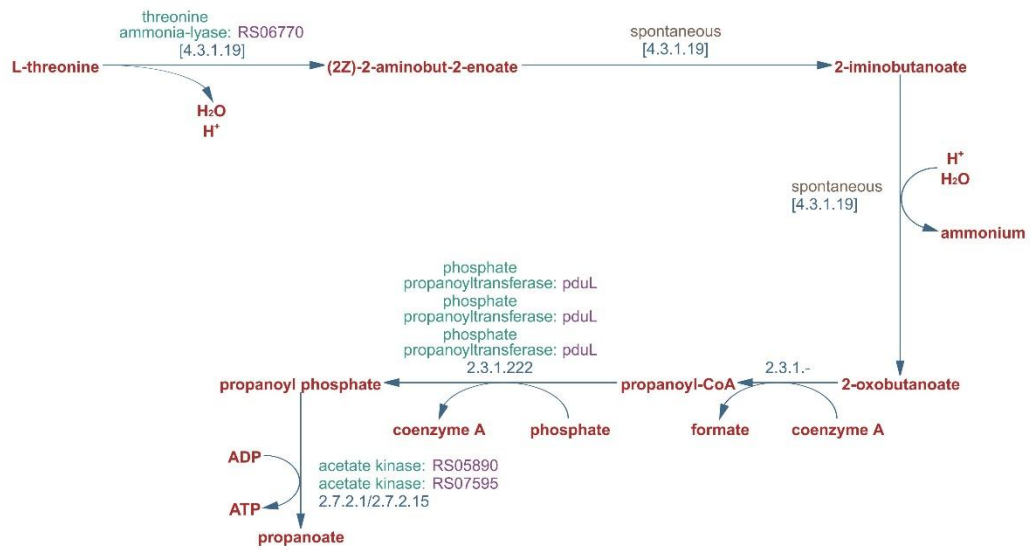
Supplementary Figure 1: This figure shows the RNA degradation pathway mapped and derived from KEGG with highlighted genes related to the pathogenicity islands of *C. chauvoei*.



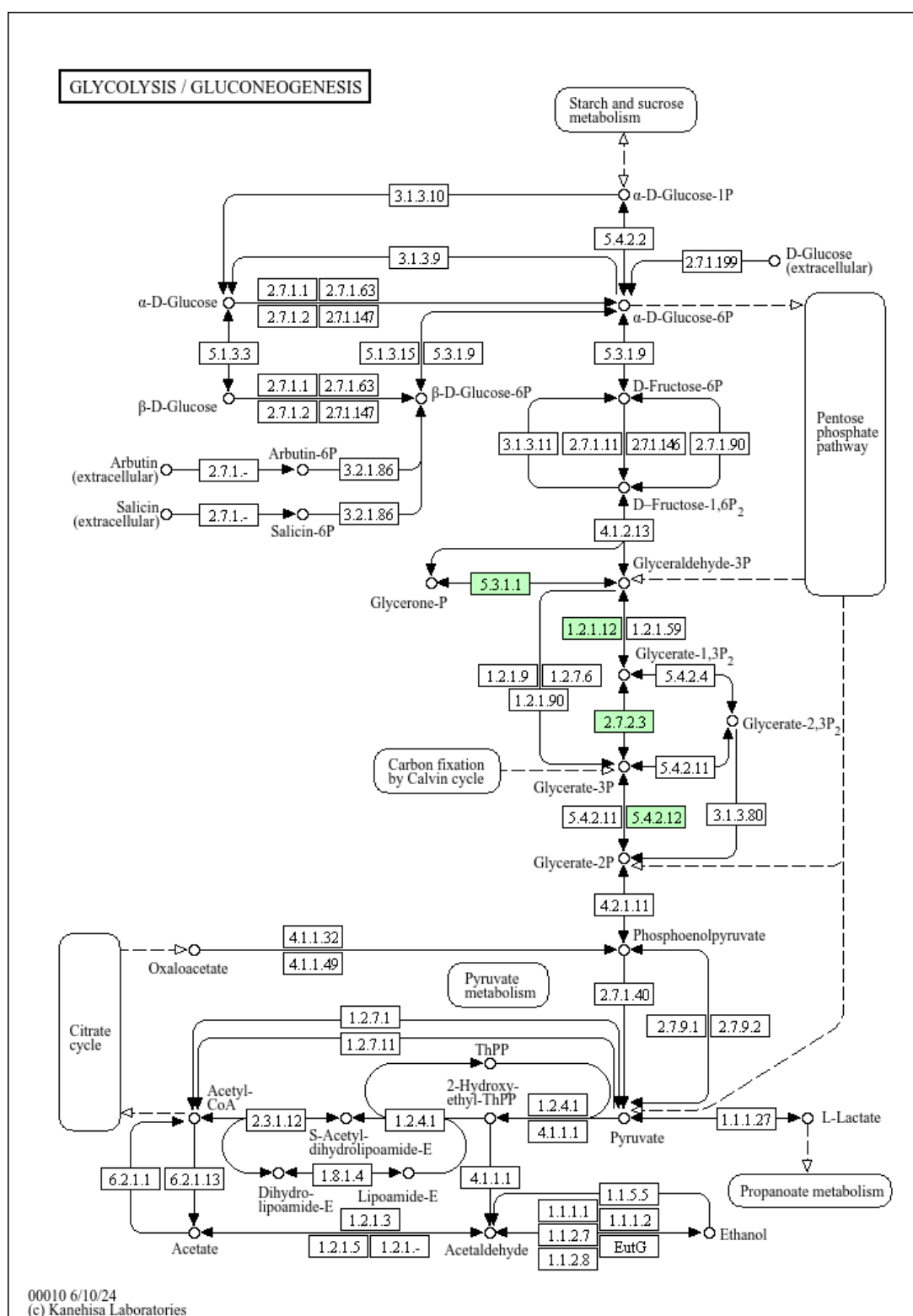
Supplementary Figure 4: This figure shows the propanoate metabolism pathway mapped and derived from KEGG with highlighted genes related to the pathogenicity islands of *C. chauvoei*.

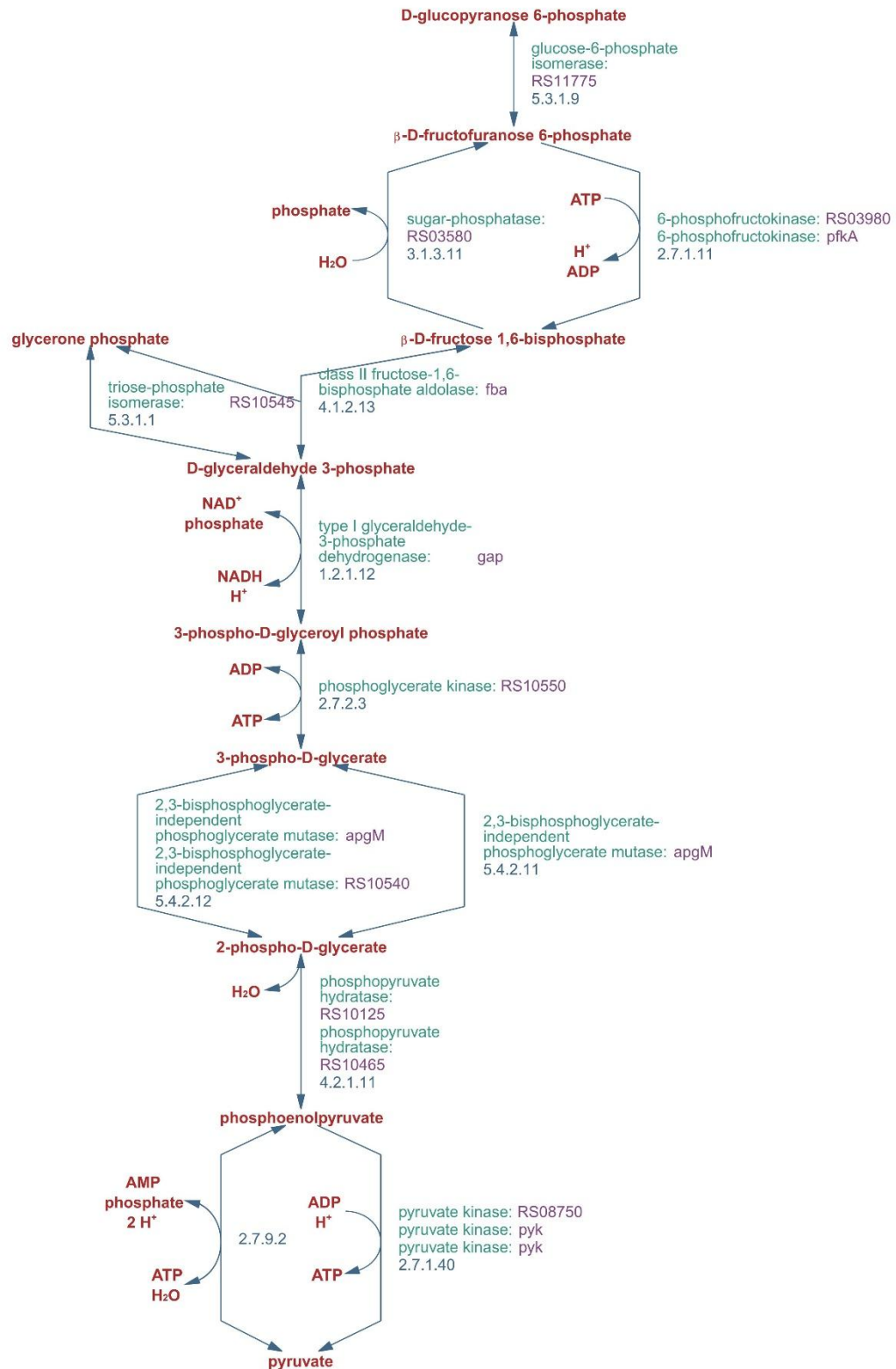


Supplementary Figure 5: This figure shows the propane-1,2 diol degradation pathway in *C. chauvoei* by Pathway tools/BioCyc.

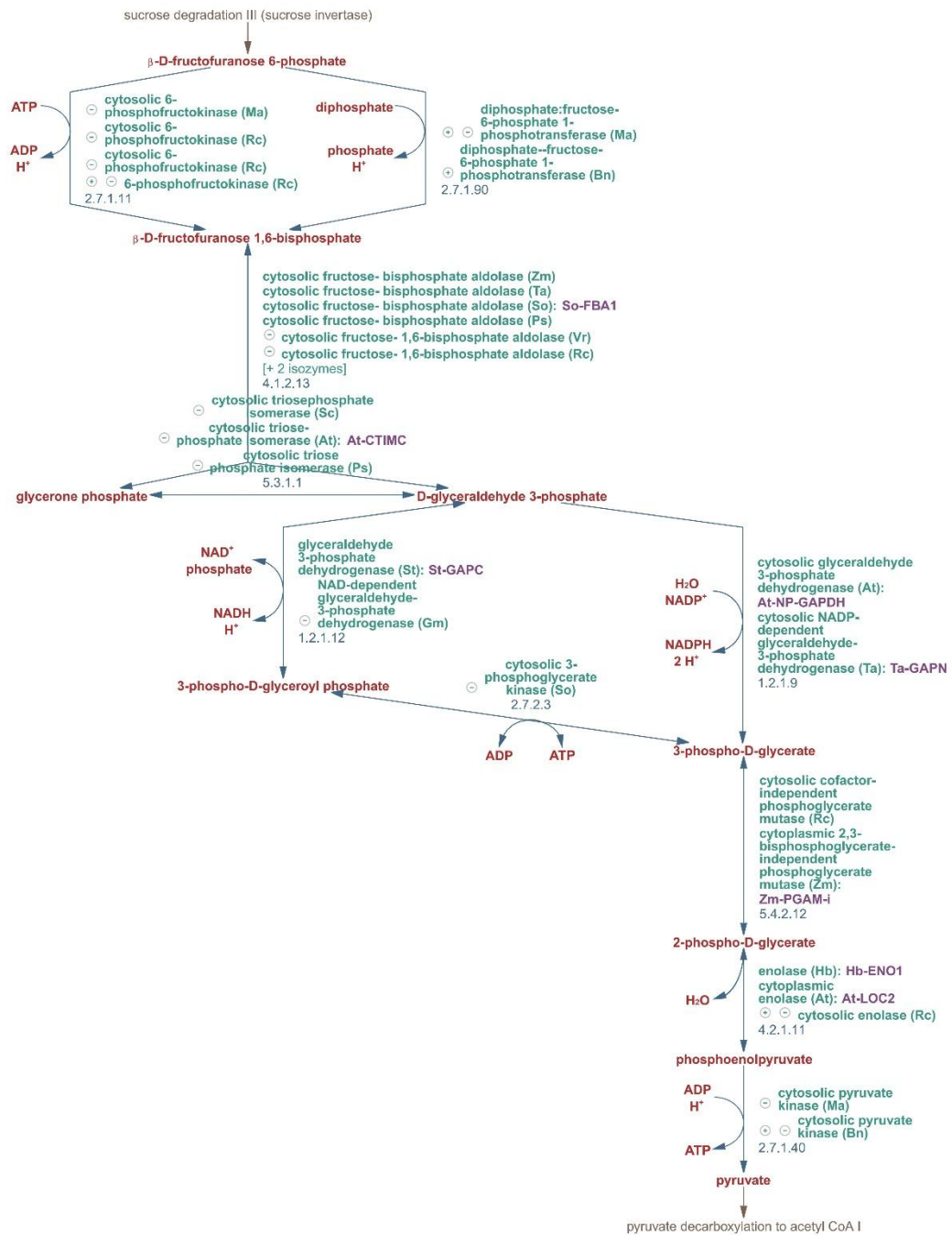


Supplementary Figure 6: This figure shows the L-threonine degradation pathway in *C. chauvoei* by Pathway tools/BioCyc.

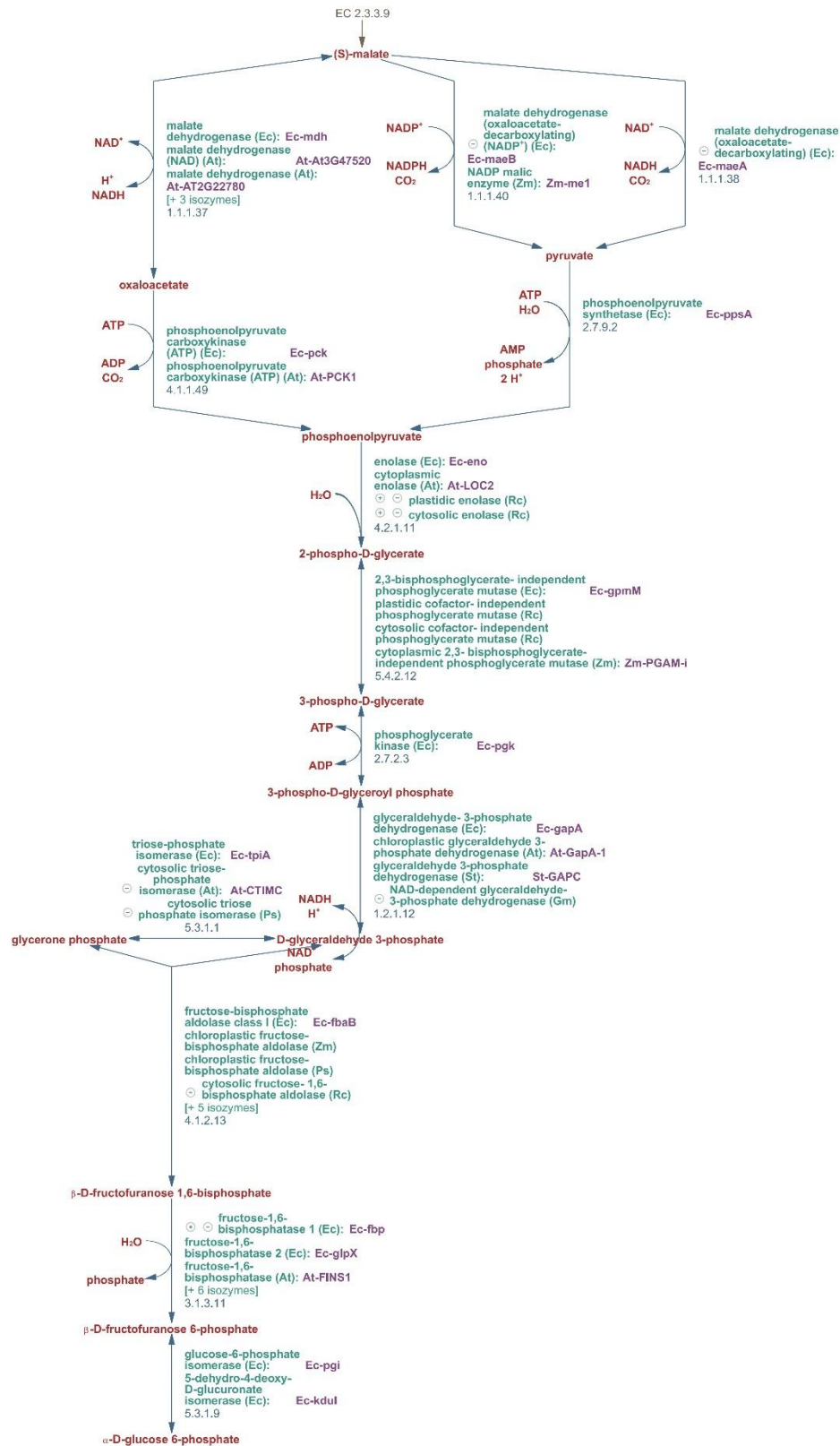




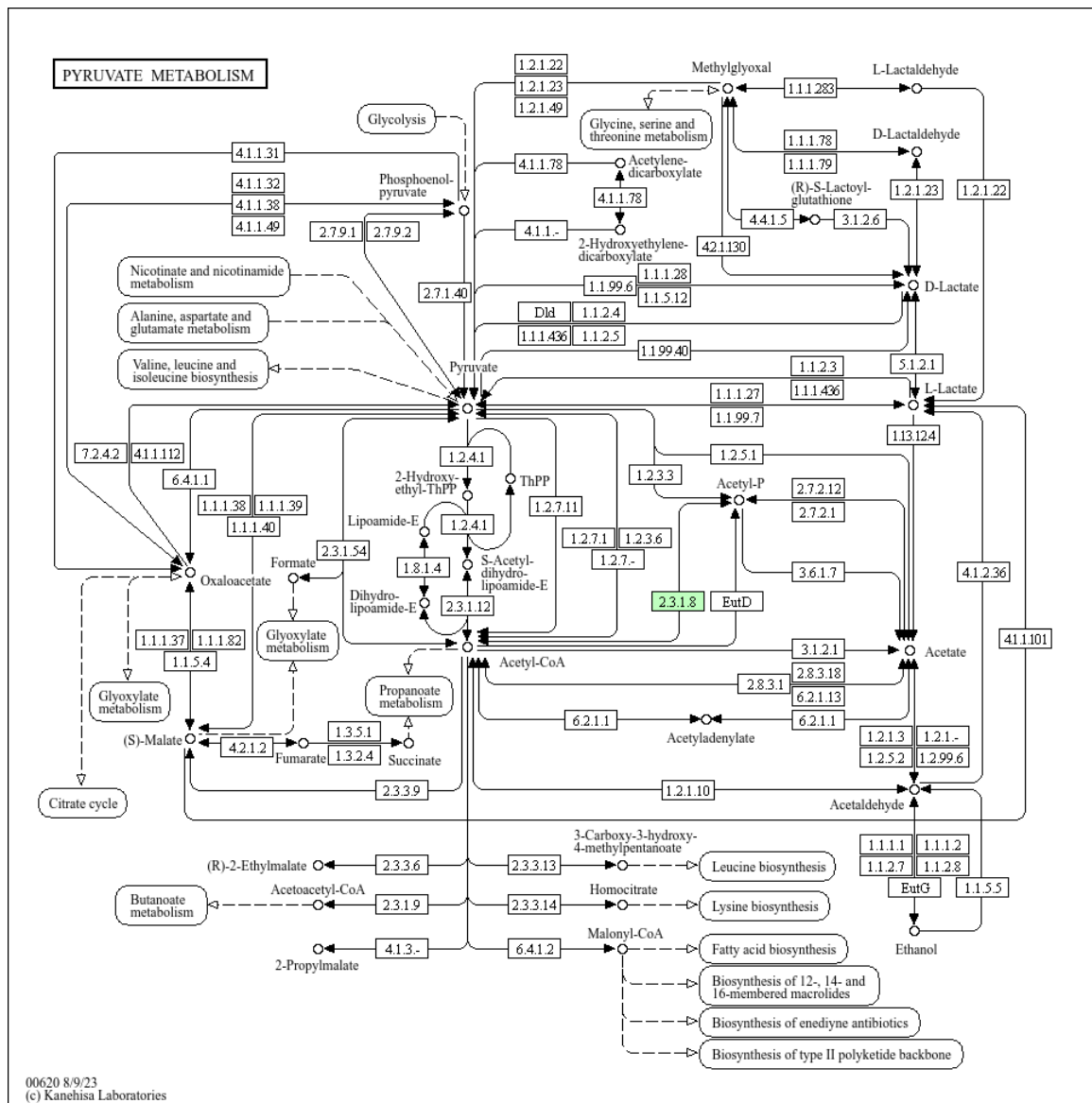
Supplementary Figure 8: This figure shows the glycolysis I pathway in *C. chauvoei* by Pathway tools/BioCyc



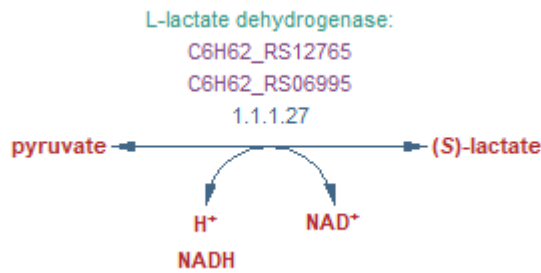
Supplementary Figure 9: This figure shows the glycolysis IV pathway in *C. chauvoei* by Pathway tools/BioCyc



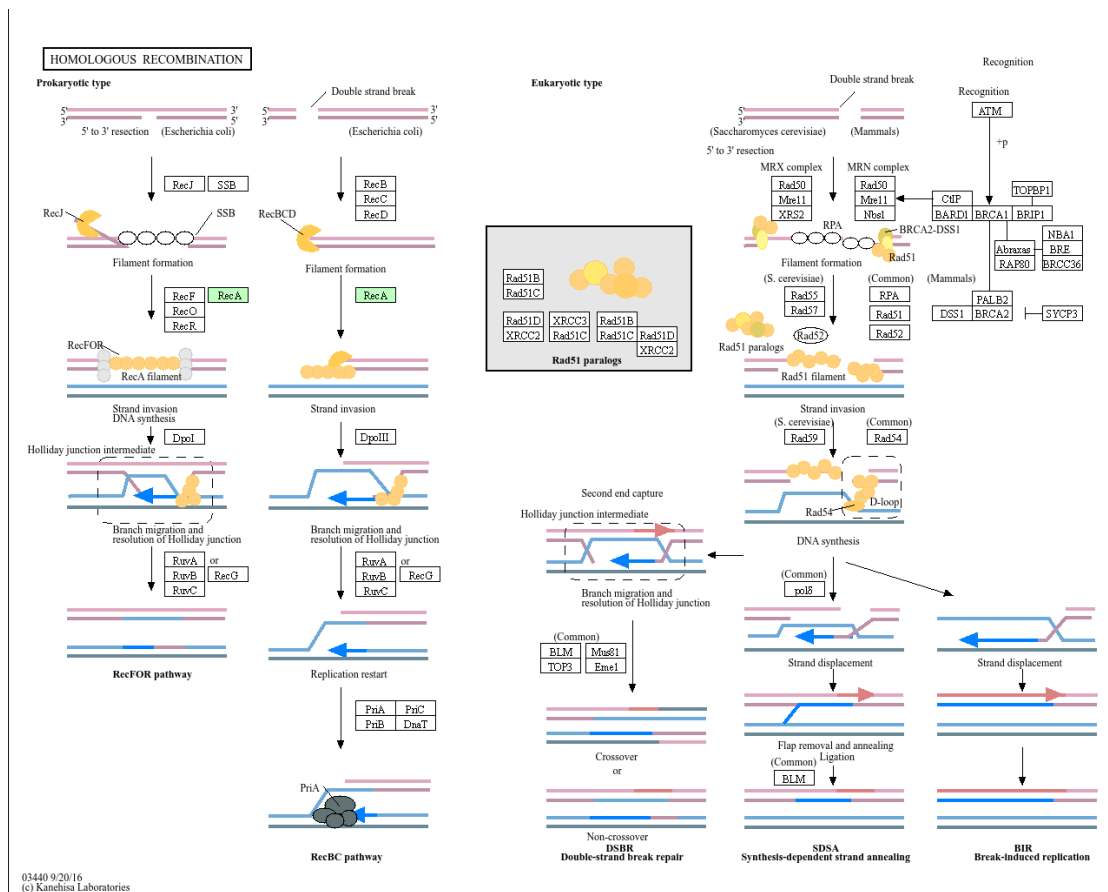
Supplementary Figure 10: This figure shows the gluconeogenesis pathway in *C. chauvoei* by Pathway tools/BioCyc.



Supplementary Figure 11: This figure shows the pyruvate metabolism pathway mapped and derived from KEGG with highlighted genes related to the pathogenicity islands of *C. chauvoei*.



Supplementary Figure 12: This figure shows the pyruvate fermentation to lactate pathway in *C. chauvoei* by Pathway tools/BioCyc.



Supplementary Figure 13: This figure shows the Homologous recombination pathway mapped and derived from KEGG with highlighted genes related to the pathogenicity islands of *C. chauvoei*.