

Supplementary material- tables and figures

Abbreviations:

'*Candidatus* Phytoplasma species' were abbreviated as 'Ca. P. asteris' strain OY-M: OY-M; 'Ca. P. asteris' strain AY-WB: AY-WB; 'Ca. P. australiense': Paus and 'Ca. P. mali': Pmal. Locus tags (e.g. PAM_) are provided in brackets.

Supplementary Table 1 (ST1). Retron-related functions.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
	retron-type reverse transcriptase	342	-	471	-

Supplementary Table 2 (ST2). Genes involved in DNA replication.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>dnaA</i>	ATPase involved in DNA replication initiation	001	001	0001	193
<i>dnaB1</i>	Replicative DNA helicase	013	007	148	176
<i>dnaB2</i>	Replicative DNA helicase	673	068	822	070
<i>dnaB-like</i>	Replicative DNA helicase	074 388 550 523 570 645 686	179 220 284 617	037 073 094 361	420
<i>dnaC</i>	ATP-binding loader protein for DnaB	672	069	821	069
<i>dnaE</i>	DNA polymerase III, alpha subunit	591	129	535	697
<i>polC</i>	DNA polymerase III, alpha subunit	465	313	541	081 422
<i>holA</i>	DNA polymerase III, delta subunit	016	010	145	254
<i>holB</i>	DNA polymerase III, delta prime subunit	231	491	168	374
<i>dnaX</i>	DNA polymerase III, tau subunit	617	117	623	043
<i>dnaN</i>	DNA polymerase sliding clamp subunit	002	002	002	194
<i>dnaG</i>	DNA primase	524 549 569 572 627 644 685	108 178 219 285 616	614 360	305 415
<i>dnaD</i>	DNA replication protein BLAST	609	144	630	051
<i>priA</i>	Primosomal protein, replication factor Y	154	565	123	317
<i>ssb</i>	Single-stranded DNA binding protein	010 041 319	004 150 193	150 814	179 398

		324	232		
		359	271		
		364	378		
		396			
		410			
		512			
		535			
		564			
		655			
		699			
		726			
		759			
<i>rnhC</i>	Ribonuclease HIII	631	103	707	130
<i>lig</i>	NAD-dependent DNA ligase	438	321	770	275
<i>gyrA</i>	DNA gyrase subunit A (topoisomerase II)	499	254	214	196
<i>gyrB</i>	DNA gyrase subunit B (topoisomerase II)	498	255	213	195
<i>pmbA</i>	DNA gyrase modulator	764	332	702	324
<i>nrdA</i>	Ribonucleotide reductase, Coenzyme B12-dependent	054	025	056	187
<i>nrdF</i>	Ribonucleotide/diphosphate reductase, subunit beta	055	026	112	186
	putative telomere resolvase	-	-	-	103

Supplementary Table 3 (ST3). Proteins related to chromosome segregation.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>spoVG</i>	Regulatory protein SpoVG family	732	649	271	227
<i>smc</i>	Chromosome segregation ATPase	693	277	-	-
		348			
		037			
		516			
		380			

Supplementary Table 4 (ST4). Recombination-related functions.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>ruvA</i>	Holliday junction resolvosome DNA-binding subunit	-	-	-	168
<i>ruvB</i>	Holliday junction resolvosome helicase subunit	-	-	-	167
<i>ruvX</i>	Holliday junction resolvase-like protein	304	418	508	247
<i>recU</i>	Holliday junction-specific endonuclease	-	-	-	209
<i>recA</i>	RecA/RadA recombinase	-	-	-	135
<i>recG</i>	ATP-dependent RecG-like helicase	-	-	-	054
<i>recO</i>	Recombinational DNA repair protein O (RecF pathway)	-	-	-	303
<i>recR</i>	Recombinational DNA repair protein R	-	-	-	045

(RecF pathway)

<i>rmuC</i>	RmuC-family protein	270	450	642	-
<i>mgs1</i>	Recombination factor protein RarA	-	288	-	-

Supplementary Table 5 (ST5). DNA repair and degradation.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>uvrA</i>	Exonuclease ATPase subunit	450	336	699	-
<i>uvrB</i>	Helicase subunit of the DNA excision repair complex	763	399	453	-
<i>uvrC</i>	Helicase subunit of the DNA excision repair complex	433	398	452	-
<i>uvrD</i>	Superfamily I DNA and RNA helicases	315 355 413 505 527 559 621	085 115	693	434
<i>mutM</i>	Formamidopyrimidine-DNA glycolase (syn. nei, fbg)	674	067	823	071
<i>mutT</i>	NTP pyrophosphohydrolases including oxidative damage repair enzymes	476	302	776	108
<i>polA</i>	DNA polymerase I - 3'-5' exonuclease and polymerase domain	675 676	066	824	072
<i>xseA</i>	Exonuclease VII, large subunit	-	-	-	455
<i>tatD</i>	Mg-dependent DNase	605	140	690	152
<i>srmB</i>	Superfamily II DNA and RNA helicases	453 714	054 318	155 449	028 115 470
	Putative restriction endonuclease	777	-	-	-
<i>hsdM</i>	Type I restriction-modification system methyltransferase subunit	619	-	-	220
<i>hsdR</i>	Restriction enzymes type I helicase subunits and related helicases	618	-	-	-
<i>ung</i>	Uracil-DNA glycolase	163	556	521	230
<i>nfo</i>	Endonuclease IV	454	317	448	027 471

Supplementary Table 6 (ST6). Genes involved in modification and structure.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>topA</i>	Topoisomerase IA	279	442	634	075
<i>gyrA</i>	DNA gyrase, alpha subunit	499	254	214	196
<i>gyrB</i>	DNA gyrase, beta subunit	498	255	213	195

<i>himA</i>	Nucleotid DNA-binding protein, similar to integration host factor (IHF) and HU	043	192	042	119
		063	210	070	
		242	230	198	
		317	272	230	
		325	377	321	
		357	479	330	
		365		376	
		394		397	
		402		422	
		513		432	
		534		683	
		563		804	
		654			
		698			
758					
	N6 adenine-specific DNA methyltransferase	042	379	004	026
		299	424	043	243
		395		069	262
		409		199	472
		565		231	
				250	
				320	
				327	
				377	
				421	
				433	
				438	
				503	
				739	
		778			
		803			
-	C-5 cytosine-specific DNA methylase	004	-	-	-
	Putative methyltransferase			291	
				655	
				722	
				789	

Supplementary Table 7 (ST7). RNA polymerase and sigma factors.

Gene	Description	OY-M (PAM ₁)	AYWB (AYWB ₁)	Paus (PAa ₀)	Pmal (ATP ₀₀)
<i>rpoA</i>	DNA-directed RNA polymerase (α subunit)	227	495	560	367
<i>rpoB</i>	Bifunctional DNA-directed RNA polymerase, β and β' chain	260	461	665	390
<i>rpoC</i>	Bifunctional DNA-directed RNA polymerase, β and β' chain	261	460	664	391
<i>rpoZ</i>	DNA-directed RNA polymerase ω chain	736	654	106	448
<i>rpoE</i>	DNA-directed RNA polymerase, delta subunit	614	119	625	046

<i>rpoD</i>	DNA-dependent RNA polymerase sigma subunits ($\sigma_{70/32}$)	628	107	613	306
		408	194	258	397
		702	233		
		760	359		
			380		
	RNA polymerase sigma factor, fragment			395	
	RNA polymerase sigma factor			127	
<i>fliA/</i>	DNA-directed RNA polymerase	040	194	258	397
<i>rpoF</i>	specialized sigma subunit	320	206	316	
		323	354	409	
		360		723	
		363		790	
		511		815	
		536			
		656			
		700			

Supplementary Table 8 (ST8). Factors affecting the RNA polymerase.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>greA</i>	Transcription elongation factor	302	420	506	246
<i>nusA</i>	N utilization substance protein A	148	572	606	313
<i>nusB</i>	N utilization substance protein B, transcription termination factor	443	327	835	469 029
<i>nusG</i>	Transcription antitermination protein	225	466	670	385
<i>spoT</i>	Guanosine-3',5'-bis(diphosphate) 3'- pyrophosphohydrolase	126	596	767	181

Supplementary Table 9 (ST9). Transcriptional regulators.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>pepA</i>	Putative aminopeptidase (DNA-binding transcriptional repressor)	-	-	129	431
<i>hrcA</i>	Negative regulator of class I heat shock protein	706	059	557	204
	Putative cold shock protein (transcriptional regulator)	671	070	820	-
	Putative cold shock protein (transcriptional regulator)	-	-	-	295

Supplementary Table 10 (ST10). tRNA synthetases.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>pheT</i>	Phenylalanyl-tRNA synthetase β -chain	598	134	531	079
<i>pheS</i>	Phenylalanyl-tRNA synthetase α -chain	596	133	532	080
<i>thrS</i>	Threonyl-tRNA synthetase	745	663	018	165
<i>proS</i>	Prolyl-tRNA synthetase	246	475	678	435
<i>alaS</i>	Alanyl-tRNA synthetase	305	416	509	248
<i>hisS</i>	Histidyl-tRNA synthetase	127	594	485	270
<i>glyS</i>	Glycyl-tRNA synthetase β -chain	-	-	-	-
<i>glyQ</i>	Glycyl-tRNA synthetase α -chain	626	109	615	304
<i>argS</i>	Arginyl-tRNA synthetase	455	316	540	436
<i>glnS</i>	Glutamyl-tRNA synthetase	620	116	694	201
<i>aspS</i>	Aspartyl-tRNA synthetase	128	593	486	271
<i>leuS</i>	Leucyl-tRNA synthetase	738	656	104	446
<i>metG</i>	Methionyl-tRNA synthetase	233	489	128	376
<i>ileS</i>	Isoleucyl-tRNA synthetase	184	535	346	252
<i>cysS</i>	Cysteinyl-tRNA synthetase	141	579	499	335
<i>trpS</i>	Tryptophanyl-tRNA synthetase	466	312	542	092
<i>lysU</i>	Lysyl-tRNA synthetase (class II)	589	128	536	096
<i>gltX</i>	Glutamyl-tRNA synthetase	140	580	498	334
<i>serS</i>	Seryl-tRNA synthetase	083	632	596	132
<i>valS</i>	Valyl-tRNA synthetase	018	012	142	338
<i>tyrS</i>	Tyrosyl-tRNA synthetase, class Ib	469	309	546	114
<i>asnC</i>	asparaginyl-tRNA synthetase	754	671	026	158

Supplementary Table 11 (ST11). tRNAs predicted by tRNAScan-SE in the phytoplasma genomes (differences highlighted in bold letters).

Gene	Amino acid	OY-M	AYWB	Paus	Pmal
tRNA-Ala	Alanine	1	1	1	1
tRNA-Arg	Arginine	2	2	2	2
tRNA-Asn	Asparagine	1	1	1	1
tRNA-Asp	Aspartic acid	1	1	1	1
tRNA-Cys	Cysteine	1	1	1	1
tRNA-Gln	Glutamine	1	1	2	1
tRNA-Glu	Glutamic acid	1	1	1	1
tRNA-Gly	Glycine	2	2	2	2
tRNA-His	Histidine	1	1	2	1
tRNA-Ile	Isoleucine	2 ^{*1}	2	2	2
tRNA-Leu	Leucine	4	4	5	4
tRNA-Lys	Lysine	1	1	1	1
tRNA-Met	Methionine	3	3	3	3
tRNA-Phe	Phenylalanine	1	1	1	1
tRNA-Pro	Proline	1	1	1	1
tRNA-Ser	Serine	3	3 ^{*2}	3	3
tRNA-Thr	Threonine	2	2	2	2
tRNA-Trp	Tryptophan	1	1	1	1
tRNA-Tyr	Tyrosine	1	1	1	1

tRNA-Val	Valine	2	2	1	2
tRNA-OTHER		/	/	1 ^{*3}	/

*1 One additional tRNA was predicted at position 281032..281108 (this study)

*2 One additional tRNA was predicted at position 277264..277354 (this study)

*3 This tRNA is predicted as Pseudo-tRNA.

Supplementary Table 12 (ST12). Factors affecting the RNA polymerase.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>trmE</i>	tRNA modification GTPase	747	665	020	164
<i>trmD</i>	tRNA (Guanine-N(1)-)-methyltransferase	471	307	548	439
	tRNA/rRNA methyltransferase protein	672*	468	672	-
<i>spoU</i>	tRNA/rRNA methyltransferase (SpoU)	144	576	-	212
<i>miaA</i>	tRNA delta(2)-isopentenylpyrophosphate transferase	275	446	638	125
<i>truA</i>	Pseudouridylate synthase A	229	493	170	372
<i>truB</i>	tRNA pseudouridine 55 synthase	237	484	783	326
	Probable pseudouridine synthase	238	483	782	123
<i>rluA</i>	pseudouridylate synthase	131	590	489	274
<i>rimM</i>	16S rRNA processing protein	-	-	-	438
<i>ksgA</i>	Dimethyladenosine transferase	731	648	272	226
	Probable Dimethyladenosine transferase	306	415	-	279
<i>Pth</i>	peptidyl-tRNA hydrolase	152	567	610	223
<i>mnmA</i>	tRNA-specific 2-thiouridylase	125	597	766	182

* original annotation differs from this assignment

Supplementary Table 13 (ST13). Translation factors.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>infA</i>	Translation initiation factor IF-1	223	499	564	363
<i>infB</i>	Translation initiation factor IF-2	150	570	608	315
<i>infC</i>	Translation initiation factor IF-3	744	662	095	441
<i>tufB</i>	Elongation factor Tu	265	456	660	395
<i>tsf</i>	Elongation factor Ts (EF-Ts)	166	553	518	233
<i>lepA</i>	GTP-binding protein LepA (elongation factor)	445	330	222	289
<i>fusA</i>	Elongation factor G 1 (EF-G 1)	264	457	661	394
<i>efp</i>	Translation elongation factor P (EF-P)	276	445	637	124
<i>prfA</i>	Peptide chain release factor 1 (RF-1)	014	008	147	175
<i>prfB</i>	Peptide chain release factor 2 (RF-2)	473	305	550	99
<i>frr</i>	Ribosome recycling factor	168	551	516	235
<i>sua5</i>	Putative translation factor (SUA5)	015	009	146	174
<i>rbfA</i>	Ribosome-binding factor A	151	569	609	316

Supplementary Table 14 (ST14). Ribosomal proteins.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>rplA</i>	50S ribosomal protein L1	257	464	668	387
<i>rplB</i>	50S ribosomal protein L2	203	519	584	344
<i>rplC</i>	50S ribosomal protein L3	200	522	587	341
<i>rplD</i>	50S ribosomal protein L4	201	521	586	342
<i>rplE</i>	50S ribosomal protein L5	212	510	575	353
<i>rplF</i>	50S ribosomal protein L6	215	507	572	356
<i>rplI</i>	50S ribosomal protein L9	012	006	149	177
<i>rplJ</i>	50S ribosomal protein L10	258	463	667	388
<i>rplK</i>	50S ribosomal protein L11	256	465	669	386
<i>rplL</i>	50S ribosomal protein L7/L12	259	462	666	389
<i>rplM</i>	50S ribosomal protein L13	138	582	496	332
<i>rplN</i>	50S ribosomal protein L14	210	512	577	351
<i>rplO</i>	50S ribosomal protein L15	219	503	568	360
<i>rplP</i>	50S ribosomal protein L16	207	515	580	348
<i>rplQ</i>	50S ribosomal protein L17	228	494	559	368
<i>rplR</i>	50S ribosomal protein L18	216	506	571	357
<i>rplS</i>	50S ribosomal protein L19	470	308	547	440
<i>rplT</i>	50S ribosomal protein L20	742	660	097	443
<i>rplU</i>	50S ribosomal protein L21	086	629	594	284
<i>rplV</i>	50S ribosomal protein L22	205	517	582	346
<i>rplW</i>	50S ribosomal protein L23	202	520	585	343
<i>rplX</i>	50S ribosomal protein L24	211	511	576	352
<i>rpmA</i>	50S ribosomal protein L27	088	627	592	282
<i>rpmB</i>	50S ribosomal protein L28	106	603	715	278
<i>rpmC</i>	50S ribosomal protein L29	208	514	579	349
<i>rpmD</i>	50S ribosomal protein L30	218	504	569	359
<i>rpmE</i>	50S ribosomal protein L31	105	604	714	141
<i>rpmF</i>	50S ribosomal protein L32	198	525	589	308
<i>rpmG</i>	50S ribosomal protein L33	244 253	476	680	383
<i>rpmH</i>	50S ribosomal protein L34	247	474	677	378
<i>rpmI</i>	50S ribosomal protein L35	743	661	096	442
<i>rpmJ</i>	50S ribosomal protein L36	224	498	563	364
<i>rpsB</i>	30S ribosomal protein S2	165	554	519	232
<i>rpsC</i>	30S ribosomal protein S3	206	516	581	347
<i>rpsD</i>	30S ribosomal protein S4	586	241	088	310
<i>rpsE</i>	30S ribosomal protein S5	217	505	570	358
<i>rpsF</i>	30S ribosomal protein S6	009	003	152	180
<i>rpsG</i>	30S ribosomal protein S7	263	458	662	393
<i>rpsH</i>	30S ribosomal protein S8	214	508	573	355
<i>rpsI</i>	30S ribosomal protein S9	139	581	497	333
<i>rpsJ</i>	30S ribosomal protein S10	199	524	588	340
<i>rpsK</i>	30S ribosomal protein S11	226	496	561	366
<i>rpsL</i>	30S ribosomal protein S12	262	459	663	392
<i>rpsM</i>	30S ribosomal protein S13	225	497	562	365
<i>rpsN</i>	30S ribosomal protein S14	213	509	574	354
<i>rpsO</i>	30S ribosomal protein S15	136	585	494	269
<i>rpsP</i>	30S ribosomal protein S16	472	306	549	437

<i>rpsQ</i>	30S ribosomal protein S17	209	513	578	350
<i>rpsR</i>	30S ribosomal protein S18	011	005	150	178
<i>rpsS</i>	30S ribosomal protein S19	204	518	583	345
<i>rpsT</i>	30S ribosomal protein S20	081	633	599	133
<i>rpsU</i>	30S ribosomal protein S21	623	112	618	300

Supplementary Table 15 (ST15). Modifying and accessory factors.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>era</i>	GTP-binding protein Era (cell cycle/ribosome assembly)	625	110	616	302
<i>engA</i>	GTP-binding protein EngA (ribosome assembly)	240	481	780	121
<i>engB</i>	ribosome biogenesis GTP-binding protein	017	011	143	102
<i>engC</i>	GTPase EngC	182*	537	348	078
<i>engD</i>	GTP-dependent nucleic acid-binding protein EngD	183	536	347	251
<i>obgE</i>	GTPase ObgE	089	626	591	281
	ribosome biogenesis GTP-binding protein YlqF/GTPase	278*	443	635	076*

* original annotation differs from this assignment; this assignment is based on sequence homology and Pfam.

Supplementary Table 16 (ST16). Modifying and accessory factors.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
YkqC	RNase J1/J2	633*	101*	011*	211*

* original annotation differs from this assignment

Supplementary Table 17 (ST17). Heat shock proteins and chaperons.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>dnaJ</i>	Chaperone DnaJ	703	062	554	207
<i>dnaK</i>	Chaperone DnaK	704	061	555	206
<i>grpE</i>	Chaperone GrpE	705	060	556	205
<i>groEL</i>	Chaperonin 60kD subunit	121	600	761	185
<i>groES</i>	Chaperonin 10kD subunit	120	601	760	184
	Trigger factor (TF)	449	334	700	297
<i>lon</i>	ATP-dependent Lon protease	448	333	701	298
<i>ibpA</i>	Molecular chaperone	028	017	717	-

Supplementary Table 18 (ST18). Other proteins involved in translation.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>map</i>	Methionine aminopeptidase	222	500	565	362
<i>rnpA</i>	Ribonuclease P protein component	248	473	676	379
<i>pnp</i>	Polyribonucleotide nucleotidyltransferase	251	470	674	381
<i>pcnB</i>	Poly(A)polymerase	102	607	711	238
<i>smpB</i>	SsrA-binding protein	146	574	603	328

Supplementary Table 19 (ST19). Cell envelope related- proteins.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>mraW</i>	Methyltransferase involved in cell envelope biogenesis	735	652	107	449

Supplementary Table 20 (ST20). Proteins involved in lipopolysaccharide synthesis.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>rfaG</i>	Glycosyltransferase involved in LPS biosynthesis	008	-	-	083

Supplementary Table 21 (ST21). Proteins involved in cell division.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>ftsH</i>	Cell division protein FtsH homolog	591*	130	488*	273*
<i>ftsY</i>	Cell division protein FtsY homolog	064	679	827	074
<i>gidB</i>	Methyltransferase, glucose inhibited division protein B	267	454	645	-
<i>gidA</i>	Glucose inhibited division protein A	268	453	644	137

* original annotation differs from this assignment

Supplementary Table 22 (ST22). Immunodominant membrane proteins.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>amp</i>	antigenic membrane protein/ immunodominant membrane protein	122	599	762	-
<i>imp</i>	immunodominant membrane protein ArsC family/Spx protein	-	-	-	050

Supplementary Table 23 (ST23). Predicted integral membrane proteins caring a single transmembrane helix (TM) at least.

OY-M (PAM_)	TM(s)	AYWB (AYWB_)	TM(s)	Paus (PAa_0)	TM(s)	Pmal (ATP_00)	TM(s)
005	6	006	2	015	1	002	5
006	6	013	5	016	1	003	9
012	2	015	4	017	1	004	8
019	4	018	10	019	2	007	4
021	1	019	1	023	6	009	7
022	3	023	1	024	6	011*	1
027	2	024	2	027	1	012	2
029	1	027	3	047	1	013	4
030	10	029	6	048	1	014	3
031	1	042	1	065	2	015	6
046	2	052	13	080	2	017	2
048	1	053	6	081	1	018	6
057	7	055	1	083	2	019	12
058	3	063	1	086	1	020	1
061	2	073	1	089	10	021	1
065	1	080	1	090	3	022	1
066	2	081	2	092	2	023	2
068	1	082	1	098	6	032	6
077	3	083	7	109	3	033	1
078	6	084	1	110	12	034	2
082	1	091	1	111	1	035	1
092	1	092	2	112	1	036	1
094	19	093	6	113	2	038	1
095	1	094	6	114	6	039	1
096	4	096	1	115	5	040	1
102	1	105	1	116	1	041	1
107	1	120	6	119	1	047	7
109	1	121	1	120	7	048	1
111	1	124	2	125	2	050	1
114	2	125	6	130	2	056	1
119	6	132	3	132	1	058	1
126	1	135	4	133	6	061	3
130	2	145	1	134	6	066	6
134	5	146	1	136	2	067	6
153	4	148	1	137	2	068	1
156	1	149	1	139	4	076	1
157	1	152	1	141	5	077	1

158	7	153	1	149	2	082	6
162	3	155	1	153	2	084	6
169	9	157	1	154	1	085	6
173	1	158	1	156	1	086	1
176	6	159	1	157	1	087	1
177	4	160	1	158	1	088	4
180	9	161	1	160	1	098	3
186	10	162	7	162	1	101	4
189	6	166	2	163	1	103	1
190	6	167	1	165	10	104	13
191	1	173	1	168	1	107	12
196	1	177	1	171	11	110	6
220	10	183	2	173	9	111	6
232	1	185	3	177	5	127	1
235	2	186	1	178	5	128	1
241	1	187	1	180	1	129	2
243	5	188	1	186	2	134	6
249	7	189	1	192	1	136	1
252	11	190	1	202	1	138	2
254	3	202	1	203	1	143	2
258	1	211	1	204	1	145	1
269	2	212	1	205	2	146	1
270	1	214	1	218	1	149	1
272	1	218	1	219	1	150	2
277	1	224	1	220	2	151	13
280	12	225	1	221	1	160	6
282	12	228	2	223	6	161	6
286	8	229	1	234	1	169	1
288	1	236	1	235	1	173	5
289	1	237	1	238	2	177	2
297	1	242	10	241	1	183	1
298	1	243	3	242	2	188	1
306	7	256	2	243	1	191	5
307	2	257	2	244	1	192	1
308	6	261	2	246	1	203	7
311	2	262	5	251	1	221	10
312	1	263	1	266	6	222	8
313	7	265	5	267	5	228	8
314	1	269	1	268	1	229	2
316	1	274	1	269	2	236	9
326	1	275	1	270	8	241	1
327	2	276	2	312	1	242	1
329	1	279	2	313	1	253	5
347	1	292	1	314	1	259	1
349	2	294	1	318	7	265	2
351	2	297	1	329	1	267	1
352	1	300	1	333	1	272	2
353	6	303	1	336	1	273	2
354	1	314	6	337	1	276	3
366	1	315	6	339	1	279	7
367	2	316	1	345	10	280	5
369	1	319	2	380	1	291	6
378	1	320	6	381	1	292	6
379	2	329	1	382	1	293	2
382	1	342	1	383	2	299	2
383	2	345	2	385	2	309	5

392	1	351	1	389	1	311	10
403	1	353	2	390	1	312	3
404	1	357	1	393	1	318	7
405	2	358	4	398	1	320	1
412	1	366	1	407	7	322	4
414	1	368	1	416	1	327	1
415	4	369	1	417	1	330	5
416	1	371	1	418	1	331	2
417	2	373	2	436	1	361	9
418	2	376	1	438	1	371	9
419	1	385	2	440	1	375	1
755	1	392	1	446	2	379	1
756	1	404	3	450	6	380	7
761	2	405	2	457	2	382	1
436	5	408	3	467	1	384	3
437	1	409	1	481	1	388	1
444	1	413	6	483	9	396	1
446	2	414	2	484	9	400	1
457	6	415	7	487	1	401	3
458	2	425	1	488	2	404	1
460	3	426	1	492	6	405	1
461	1	432	2	501	1	406	1
462	2	433	1	502	1	412	2
475	1	435	11	515	9	413	1
477	1	439	12	522	2	416	1
479	1	441	12	526	1	427	7
483	2	444	1	530	4	429	4
485	1	448	1	533	3	433	5
487	5	450	1	538	5	444	6
489	1	452	2	539	2	453	1
490	5	455	7	541	1	456	1
494	1	463	1	543	5	459	1
495	1	467	3	552	1	460	1
507	1	468	1	553	1	463	1
508	6	469	10	558	1	464	2
509	1	471	2	567	10	465	1
510	2	472	7	590	3	466	6
515	2	477	6	597	1	475	2
517	1	479	1	598	1	476	1
528	1	488	2	600	1	477	1
529	3	490	1	604	6	478	1
530	3	529	1	626	7	479	12
531	2	530	6	629	1	480	6
532	1	531	6	633	12	481	2
539	1	533	11	635	1	483	6
541	1	534	6	636	1	484	3
555	2	539	9	640	1	485	4
556	1	543	5	641	1	486	2
557	7	544	6	642	1	489	7
558	1	550	9	643	2	491	4
561	1	557	2	648	1	494	8
562	1	559	1	649	1	495	9
575	1	561	8	671	3	496	5
580	1	562	1	673	9		
584	3	566	4	681	6		
585	10	568	1	685	1		

587	3	583	2	692	2
588	6	586	1	695	3
595	3	587	5	696	4
599	5	591	2	697	1
604	2	599	2	704	1
610	1	602	6	706	1
613	7	615	1	707	1
638	1	619	4	709	2
639	4	620	2	729	1
649	1	621	9	742	1
650	1	622	9	749	2
652	2	624	1	755	1
657	1	635	6	756	1
658	1	636	1	757	6
660	6	650	8	758	6
661	6	651	10	768	13
662	2	659	6	772	1
663	1	667	1	774	2
670	1	668	6	779	10
680	4	669	6	785	1
691	2			792	7
694	2			797	2
696	1			798	3
707	1			799	1
718	6			800	1
719	1			813	7
720	10			816	6
727	1			817	1
733	8			822	1
734	12			829	1
735	1			834	1
741	6			839	1
749	1				
751	6				
753	1				

Supplementary Table 24 (ST24). Predicted integral membrane proteins caring a single transmembrane helix (TM) and a signal peptide at least.

OY-M (PAM_)	TM(s)	AYWB (AYWB_)	TM(s)	Paus (PAa_0)	TM(s)	Pmal (ATP_00)	TM(s)
016	1	023	5	138	1	010	1
028	5	059	5	406	1	117	5
114	1	091	1	460	3	148	1
191	1	122	1	523	1	376	1
383	3	185	5	611	3	488	1
395	1	266	6	675	6		
428	1	295	1	762	1		
502	9	456	5	812	1		
625	1	464	2	818	1		
		497	5	828	1		
		502	1				
		750	5				

Supplementary Table 25 (ST25). Secretion apparatus.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>secA</i>	Preprotein translocase subunit SecA	474	304	551	100
<i>secE</i>	Preprotein translocase subunit SecE	254	467	671	384
<i>secY</i>	Preprotein translocase subunit SecY	220	502	567	361
<i>yidC</i>	Preprotein translocase subunit yidC	249	472	675	380

Supplementary Table 26 (ST26). Predicted secreted proteins.

OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
049			
069	022		
070	032	022	
125	033	030	
133	122	060	
160	127	064	
161	129	074	006
195	131	105	025
233	168	185	031
271	169	193	037
330	174	217	049
331	203	225	090
332	240	255	120
346	245	263	147
356	258	276	182
370	259	288	189
371	280	310	197
372	295	326	257
393	339	331	258
484	340	335	261
486	346	369	266
514	367	396	268
518	370	402	287
519	387	469	426
540	402	478	447
542	449	491	458
576	480	603	461
577	489	628	462
582	558	708	467
591	588	726	473
611	595	728	492
643	597	748	
653	638	766	
690	640	809	
710	645	837	
737	655		
765	658		

Supplementary Table 27 (ST27). Signal recognition particle (SRP) pathway associated proteins.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>ftsY</i>	Cell division protein, SRP docking protein	679	064	827	074
<i>ffh</i>	Signal recognition particle protein	678	065	826	073
<i>yidC</i>	Preprotein translocase subunit YidC	249	472	675	380

Supplementary Table 28 (ST28). Putative complete ABC transporter subunits with assignment.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>potA</i>	ABC-type spermidine/putrescine transport system, ATPase component	659	095	135	290
<i>potB</i>	ABC-type spermidine/putrescine transport system, permease component I	660	094	134	291
<i>potC</i>	ABC-type spermidine/putrescine transport system, permease component II	661	093	133	292
<i>potD</i>	ABC-type spermidine/putrescine transport system, periplasmic component	662	092	132	293
<i>znuA</i>	ABC-type Mn/Zn transport system, periplasmic component	092	624	481	492
<i>znuC</i>	ABC-type Mn/Zn transport system, ATPase component	093	623	482	493
<i>znuB</i>	ABC-type Mn/Zn transport system, permease component	094	622 621	483 484	494 495
<i>znuA2</i>	ABC-type Mn/Zn transport system, periplasmic component	/	/	/	006
<i>znuC2</i>	ABC-type Mn/Zn transport system, ATPase component	/	/	/	005
<i>znuB2</i>	ABC-type Mn/Zn transport system, permease component	/	/	/	004 003
<i>malK</i>	ABC-type sugar transport system (probably encoding maltose/maltodextrin transporter subunit, also similar to glycerol-3-phosphate transporter UgpC subunit), ATPase component	752	670	025	159
<i>malF</i>	ABC-type sugar transport system (probably encoding maltose/maltodextrin transporter subunit, also similar to glycerol-3-phosphate transporter UgpA subunit), permease component I	751	669	024	160
<i>malG</i>	ABC-type sugar transport system (probably encoding maltose/maltodextrin transporter subunit, also similar to glycerol-3-phosphate transporter UgpE subunit), permease component II	750	668	023	161

<i>malE</i>	ABC-type sugar transport system (probably encoding maltose/maltodextrin transporter subunit, also similar to glycerol-3-phosphate transporter UgpB subunit), periplasmic component	749	667	022	162
<i>dppF</i>	ABC-type dipeptide/oligopeptide transport system, ATPase component I	193*	527	753	065
<i>dppD</i>	ABC-type dipeptide/oligopeptide transport system, ATPase component II	192	528	754	064
<i>dppA</i>	ABC-type dipeptide/oligopeptide transport system, periplasmic component	191	529	755 756	068
<i>dppB</i>	ABC-type dipeptide/oligopeptide transport system, permease component I	190	530	757	067
<i>dppC</i>	ABC-type dipeptide/oligopeptide transport system, permease component II	189	531	758	066
<i>metN</i>	ABC-type methionine transport system, ATPase component	132	589	490	157
<i>metQ</i>	ABC-type methionine transport system, periplasmic component	133	588	491	192
<i>metI</i>	ABC-type methionine transport system, permease component	134	587*	492	191
<i>artM</i>	ABC-type amino acid transport system (probably arginine transporting), permease component I	490	262	450	/
<i>artI</i>	ABC-type amino acid transport system (probably arginine transporting), periplasmic component	489	263	267*	/
<i>artP</i>	ABC-type amino acid transport system (probably arginine transporting), ATPase component	488	264	775	/
<i>artQ</i>	ABC-type amino acid transport system (probably arginine transporting), permease component II	487	265	/	/
<i>artM2</i>	ABC-type amino acid transport system (probably arginine transporting), permease component I	077	/	/	/
<i>artI2</i>	ABC-type amino acid transport system (probably arginine transporting), periplasmic component	076*	/	/	/
<i>artP2</i>	ABC-type amino acid transport system (probably arginine transporting), ATPase component	079	634	/	/
	ABC-type amino acid transport system similar to ArtQ, permease and periplasmic component	078	635	/	/

* original annotation differs from this assignment

Supplementary Table 29 (ST29). Identified subunits of probably incomplete ABC transporters.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>dppF2</i>	ABC-type dipeptide/oligopeptide transport system, ATPase component I	026	/	718	/
<i>dppD2</i>	ABC-type dipeptide/oligopeptide transport system, ATPase component II	025	/	/	/
<i>dppB2</i>	ABC-type dipeptide/oligopeptide transport system, permease component I	022	/	/	/
<i>dppC2</i>	ABC-type dipeptide/oligopeptide transport system, permease component II	023 ^{*1}	/	/	/
<i>oppA</i>	ABC-type oligopeptide transport system, periplasmic component	/	/	/	463
<i>cbiQ</i>	ABC-type cobalt transport system, permease component	180	539	173	371
<i>cbiO</i>	ABC-type cobalt transport system, ATPase component	179 ^{*1}	540 541	174 175	370 369
<i>cbiQ2</i>	ABC-type cobalt transport system, permease component	^{*1}	015	139	/
<i>cbiO2</i>	ABC-type cobalt transport system, ATPase component	020	014	140	/
<i>artM</i>	ABC-type amino acid transport system (probably arginine transporting), permease component	494	/	/	/
<i>artI</i>	ABC-type amino acid transport system (probably arginine transporting), periplasmic component	495	/	/	/
	ABC-type amino acid transport system similar to ArtM, permease and periplasmic component	456	315	/	/
	ABC-type amino acid transport system, permease component		314 ^{*2}		
	ABC-type amino acid transport system similar to ArtI, permease and periplasmic component	457	/	/	/
<i>artM</i>	ABC-type amino acid transport system (probably arginine transporting), permease component	639	/	/	/
	ABC-type transport system, periplasmic component	640 ^{*2}	/	/	/
	ABC-type amino acid transport system, periplasmic component	641	/	/	/
<i>artM</i>	ABC-type amino acid transport system (probably arginine transporting), permease component	464	/	/	/
	ABC-type amino acid transport system similar to ArtM, permease and periplasmic component	588	125	/	/
	ABC-type amino acid transport system (periplasmic component), fragment-pseudo	/	/	013 ^{*2}	/
<i>artM</i>	ABC-type amino acid transport system	/	/	014	/

(permease component), fragment-pseudo

*¹ indicates that the subunit was identified by additional analysis but is not part of the current submitted annotation in the databases.

*² * original annotation differs from this assignment

Supplementary Table 30 (ST30). Putative thiamin transporter subunit.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
-	Putative thiamine transporter protein, Thia_YuaJ family	176*	544*	178*	309*

* original annotation differs from this assignment

Supplementary Table 31 (ST31). Symporters.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
		720			104
<i>mleP</i>	Malate (citrate)/Na ⁺ symporter	286	052 435	768	151 019 479

Supplementary Table 32 (ST32). Multidrug efflux pump proteins.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>mdlB</i>	multidrug efflux pump, ATP-binding and permease protein	059	028	114	111
<i>mdlA</i>	multidrug efflux pump, ATP-binding and permease protein	*	029	115	110
		280	441	633	
<i>norM</i>	Na ⁺ -driven multidrug efflux pump	282 734	439 651	165 110 171	107

* indicates that the subunit was identified by additional analysis; original annotation differs from this assignment

Supplementary Table 33 (ST33). P-type ATPases.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>mgtA</i>	P-type ATPase exporting cations (probably Mg)	585	242	089	311
	P-type ATPase exporting cations (probably calcium)	186	533	345	221
	P-type ATPase exporting cations	030 252	018 469	779 673	222
	P-type ATPase exporting cations (probably cadmium)	733	650	270	228

Supplementary Table 34 (ST34). Large-conductance mechanosensitive channel proteins.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>mscL</i>	large-conductance mechanosensitive channel	058	027	113	331

Supplementary Table 35 (ST35). Glycolysis and related genes.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
-	Had superfamily family phosphatase, subfamily IIIa	301	421	505	245
<i>Cof</i>	Had superfamily hydrolase, Subfamily IIb (sucrose-phosphate phosphatase)	171 593 634	548 100	010 513 534	106
<i>pgi</i>	glucose-6-phosphate isomerase	283	438	166	377
<i>pfkA</i>	6-phosphofructokinase	281	440	164	105
<i>fba</i>	Fructose-bisphosphate aldolase	172	547	512	109
<i>tpiA</i>	triosephosphate isomerase	170	549	514	166
<i>gapA</i>	glyceraldehyde-3-phosphate dehydrogenase	175	545	510	-
<i>pgk</i>	phosphoglycerate kinase	174	546	511	-
<i>pgm</i> (<i>gpml</i>)	Phosphoglyceromutase	285	436	060	-
<i>eno</i>	phosphopyruvate hydratase	284	437	059	-
<i>pykF</i>	pyruvate kinase	287	434	061	-
<i>dhaK</i>	kinase related to dihydroxyacetone kinase	665	090	819	277
<i>gtfA</i>	Sucrose phosphorylase (Glucosyltransferase-A)	723	-	221	-

Supplementary Table 36 (ST36). Deduced proteins involved in the formation of acetate from malate.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>mleP</i>	Malate (citrate)/Na ⁺ symporter	720 286	052 435	768	104 151 019 479
<i>sfcA</i> (<i>maeA</i>)	NAD ⁺ -dependent malic enzyme	721*	051	769	450*
<i>acoB</i> (<i>pdhB</i>)	thiamine pyrophosphate-dependent dehydrogenase, E1 component beta subunit	601	137	687	155
<i>acoA</i> (<i>pdhA</i>)	thiamine pyrophosphate-dependent dehydrogenase, E1 component alpha subunit (pyruvate dehydrogenase)	600	136	686	156
<i>aceF</i> (<i>pdhC</i>)	branched-chain alpha-keto acid dehydrogenase subunit E2 (lipoate acetyltransferase)	602	138	688	154
<i>Lpd</i> (<i>pdhD</i>)	Dihydrolipoamide dehydrogenase	603	139	689	153
<i>coaE</i>	coenzyme A kinase*	674	067	823	071
<i>hcaD</i>	NADH oxidase H ₂ O ₂ -forming	441	324	837*	288
pduL-like	CoA-phosphotransacetylase, similar to propanediol utilisation protein PduL	729*	646*	274*	224*
<i>ackA</i>	Acetate kinase	159	560	121	319
<i>eda</i>	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase	-	-	-	116
<i>acoB</i> (<i>pdhB</i>)	thiamine pyrophosphate-dependent dehydrogenase, E1 component beta subunit	601	137	687	155
<i>acoA</i> (<i>pdhA</i>)	thiamine pyrophosphate-dependent dehydrogenase, E1 component alpha subunit (pyruvate dehydrogenase)	600	136	686	156
<i>aceF</i> (<i>pdhC</i>)	branched-chain alpha-keto acid dehydrogenase subunit E2 (lipoate acetyltransferase)	602	138	688	154
<i>Lpd</i> (<i>pdhD</i>)	Dihydrolipoamide dehydrogenase	603	139	689	153
<i>coaE</i>	coenzyme A kinase*	674	067	823	071
<i>hcaD</i>	NADH oxidase H ₂ O ₂ -forming	441	324	837*	288
pduL-like	CoA-phosphotransacetylase, similar to propanediol utilisation protein PduL	729*	646*	274*	224*
<i>ackA</i>	Acetate kinase	159	560	121	319

* original annotation differs from this assignment

Supplementary Table 37 (ST37). NAD synthesis.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>nadE/ qns</i>	Glutamine-dependent NAD ⁺ synthetase	124	598	763	183

Supplementary Table 38 (ST38). Superoxide dismutase.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>sodA</i>	superoxide dismutase	442	326	836	468 030

Supplementary Table 39 (ST39). Lipoyl-protein ligases.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>lplA</i>	lipoate-protein ligase A	309	412	537	208

Supplementary Table 40 (ST40). Nucleotide metabolism.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>adk</i>	adenylate kinase	221	501	566	031 467
<i>gmk</i>	guanylate kinase	680 737	655	105	447
<i>pnp</i>	Polyribonucleotide nucleotidyltransferase	251	470	674	381
<i>nrdA</i>	Ribonucleotide reductase, Coenzyme B12-dependent	054	025	056	187
<i>nrdF</i>	Ribonucleotide/diphosphate reductase, subunit beta	055	026	112	186
<i>spoT</i>	Guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	126	596	767	181
<i>udk</i>	uridine kinase	142*	578	-	-
<i>pyrH</i>	Uridylate kinase	167	552	517	234
<i>pyrG</i>	CTP synthase	611	122	628	049
<i>cmk</i>	cytidylate kinase	239	482	781	122
<i>thyA</i>	thymidylate synthase	293	430	084	320
<i>tdk</i>	thymidine kinase	104	605	713	140
		230	074	071	
		344	181	169	373
<i>tmk</i>	Thymidylate kinase	374	222	304	403
		521	282	324	
			492	365	

				373	
				425	
				807	
				431	
				735	
				195	
				039	
				227	
<i>dut</i>	DUTPase	164	555	520	231
<i>hit</i>	diadenosine tetraphosphate hydrolase (AppppA hydrolase)	630	104	705	131
-	CMP/dCMP deaminase zinc-binding protein	103	606	712	139
	Putative IMP dehydrogenase/GMP reductase	-	-	048 068 203 381 417	-

* original annotation differs from this assignment

Supplementary Table 41 (ST41). Peptidases.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>pepP</i>	Xaa-Pro aminopeptidase	245	-	679	042
<i>pepV</i>	dipeptidase PepV	290	431	-	-
<i>oepF</i>	oligoendopeptidase F	178	542	176	-

Supplementary Table 42 (ST42). HflB and TldD proteins grouped by BLASTClust.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
		064			
		117			
		130			
		307	071		011
		316	096		034
		326	183	136	039
		326	187	235	146
		356	213	488	273
<i>hflB/ftsH</i>	ATP-dependent zinc metalloproteinase, transmembrane protein, HflB-like enzymes	366	229	523	382
		393	275	539	406
		403	409	799	464
		480	414		460
		532	591		487
		561			
		658			
		664*			
		695			

		713			
		727			
		762			
<i>tldD</i>	Zn-dependent protease	447*	331*	703	323

* original annotation differs from this assignment

Supplementary Table 43 (ST43). Amino acid synthesis and modification.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>metK</i>	S-Adenosylmethionine synthase; methionine adenosyltransferase	-	-	-	296
<i>asnB</i>	Asparagine synthase	594	130	-	-
<i>smtA</i>	SAM-dependent methyltransferase	303	419	507	-
<i>argE</i>	acetylornithine deacetylase	292	-	-	-

Supplementary Table 44 (ST44). Genes involved in lipid synthesis.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>cdsA</i>	Phosphatidate cytidyltransferase	169	550	515	236
<i>pgsA</i>	CDP-diacylglycerol-glycerol-3- phosphatidyltransferase	718	053	816	134
<i>pIsC</i>	Putative 1-acyl-sn-glycerol-3-phosphate acyltransferase	295	428	086	322
<i>pIsX</i>	Fatty acid/phospholipid synthesis protein	607	142	632	053
<i>pIsY</i>	acyl phosphate:glycerol-3-phosphate acyltransferase	436*	320*	266*	173*
<i>psD</i>	Phosphatidylserine decarboxylase proenzyme	612	121	627	048
<i>pssA</i>	CDP-diacylglycerol-serine O- phosphatidyltransferase	613	120	626	047
<i>gpsA</i>	glycerol 3-phosphate dehydrogenase	241	480	684	120

*The gene *pIsY* is annotated within the four genomes (and *A. laidlawii*, ACL_0547) as hypothetical protein.

Supplementary Table 45 (ST45). Genes involved in lipid synthesis.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>ribF</i>	Riboflavin kinase + FAD synthetase	451	-	-	-

Supplementary Table 46 (ST46). Genes involved in lipid synthesis.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>glyA</i>	serine hydroxymethyltransferase	181	538	172	142
<i>folk</i>	7,8-Dihydro-6-hydroxymethylpterin-pyrophosphokinase	580	249*	-	-
<i>folC</i>	Putative bifunctional protein: folylpolyglutamate synthase and dihydrofolate synthase	007	-	-	-
<i>folA</i>	dihydrofolate reductase	294	429	085	321
<i>folP</i>	dihydropteroate synthase	581	246*	-	-

* original annotation differs from this assignment

Supplementary Table 47 (ST47). Thiamine synthesis.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>thiJ</i>	4-methyl-5(B-hydroxyethyl)-thiazole monophosphate biosynthesis enzyme	137*	584	495*	237
<i>thil</i>	thiamine biosynthesis protein	143*	577	601	-

* original annotation differs from this assignment

Supplementary Table 48 (ST48). Pyridoxalphosphate.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>pdxK</i>	pyridoxal/pyridoxine/pyridoxamine kinase	434	-	-	-

Supplementary Table 49 (ST49). Proteins involved in in iron-sulfur cluster biosynthesis.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>(iscU)</i>	nifU-like protein, involved in Fe-S cluster formation	467 100 609	609	544 456	112
<i>(csdB)</i>	nifS-like protein (selenocysteine lyase)	468	310	545	113

Supplementary Table 50 (ST50). Acyl carrier protein metabolism.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>acpP</i>	Acyl carrier protein	739	657	099	445
<i>acpS</i>	Holo-(acyl-carrier-protein) synthase	440	323	838	294

Supplementary Table 51 (ST51). Phosphorus metabolic processes.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>ppa</i>	inorganic pyrophosphatase	145	575	602	329
<i>fba</i>	fructose/tagatose biphosphate aldolase	172	547	512	109
	exopolyphosphatase-related protein	746	664	019	163
	exopolyphosphatase-related protein	748	666	021	-
<i>hd</i>	superfamily phosphohydrolase	730	647	273	225
	phosphodiesterase	272	448	640	127
	Putative metallophosphoesterase	273*	447*	639	126*
<i>pgpB</i>	membrane-associated phospholipid phosphatase	005	-	-	085
<i>pldB</i>	Putative lysophospholipase	-	-	-	339
<i>pldB</i>	Putative lysophospholipase	-	-	-	396

* original annotation differs from the assignment

Supplementary Table 52 (ST52). Miscellaneous.

Gene	Description	OY-M (PAM_)	AYWB (AYWB_)	Paus (PAa_0)	Pmal (ATP_00)
<i>frvX</i>	endo-1,4-beta-glucanase-like protein	740	658	-	-
<i>trx</i>	Thioredoxin	236	485	784	325
	tengu-su inducer	765	168	-	-
	Zn-dependent hydrolase	637	098	006	210
<i>YjeE</i>	P-loop hydrolase	500	253	215	198
	Uncharacterised protein, DegV family	583	244	091	095
	Uncharacterised protein, DegV family	636	099	007	-
<i>gcp</i>	O-sialoglycoprotein endopeptidase	579	251	093	200
	Conserved hypothetical protein, similar to 3'-5' exoribonuclease YhaM	101	608	710	239
<i>tpm</i>	tetrapyrrole (Corrin/Porphyrin) methylase	232	490	167	375
	Conserved hypothetical protein	584	243	090	312
	glycoprotease family protein	501	252	216	199
	metalloprotein	624*	111	617	301*
	Nitroreductase	435	397	500	286
	Nitroreductase-like protein	-	-	-	287
<i>arsC</i>	Putative arsenate reductase related protein,thioredoxin family [hypoth. protein]	632	-	012	202

* original annotation differs from this assignment

Supplementary figure 1. Simplified formation of SAM, L-asparagine and L-ornithine

