

Supplemental Materials

Table S1. General features of the *Pa.pacificus* genome with other Thermococcales strains.

Parameters	Strains		
	<i>Pa. pacificus</i>	<i>P. furiosus</i>	<i>T. onnurineus</i>
Genome size (bp)	1,859,370	1,908,256	1,847,607
Protein-coding regions (%)	78.11	92.5	90.1
GC content (%)	43.04	40.8	51.0
CDSs (no.)	2,001	2,065	1,976
tRNAs (no.)	46	46	46
rRNAs	5S (2), 7S, 16S, 32S	5S (2), 7S, 16S, 32S	5S (2), 7S, 16S, 32S

Table S2. *Pa.pacificus* genes discussed in the text.

TRMS, strain DY20341 grown with the elemental sulfur; TRM, strain DY20341 grown without sulfur. RPKM, reads per kb per million reads. The log2 ratio of TRMS-RPKM/TRM-RPKM.

Metabolic process		Gene ID	TRMS-RPKM	TRM-RPKM	log2(TRM S/TRM)	Predicted protein
Central metabolism	Pentose-phosphate metabolism	PAP_06885	2706	2923	-0.11	Ribulose biphosphate carboxylase(typeIII)
		PAP_04670	1601	1118	0.52	AMP phosphorylase (DeoA)
		PAP_04815	379	481	0.34	Ribose-1,5-bisphosphate isomerase (RBPI)
	Embden-Meyerhof pathway	PAP_01430	706	1271	-0.85	ADP-dependent glucokinase (GLK)
		PAP_01425	705	1174	-0.74	Phosphoglucose isomerase (PGI)
		PAP_04875	724	732	-0.02	ADP-dependent phosphofructokinase (PFK)
		PAP_03775	495	676	-0.45	Fructose-1,6-bisphosphate aldolase (FBA)
		PAP_09970	1092	950	0.20	Triosephosphate isomerase (TIM)
		PAP_09040	3732	1761	1.08	Glyceraldehyde-3-phosphate:ferredoxin oxidoreductase (GAPOR)
		PAP_03390	67	356	-2.41	Non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase (GAPN)
		PAP_02855	1803	1268	0.51	NAD(P)-dependent glyceraldehyde 3-phosphate dehydrogenase(GAPDH)
		PAP_01540	781	768	0.02	2-phosphoglycerate kinase(PGK)
		PAP_01310	1902	1236	0.62	Phosphoglycerate mutase (PGM)
		PAP_04825	1226	945	0.38	Phosphoglycerate mutase (PGM)
		PAP_04410	4896	3069	0.67	Enolase (ENO), phosphopyruvate hydratase
		PAP_08515	1342	1075	0.32	Pyruvate kinase (PYK)
		PAP_01340	411	712	-0.79	Phosphoenolpyruvate synthase (PPS)
		Metabolism of proteins	Utilization of proteins		327	334
PAP_05645	1074			1156	-0.11	
- 05675	624			684	-0.13	
			373	295	0.34	

		1042	1109	-0.09	
		605	641	-0.08	
		466	771	-0.73	
	PAP_00035	3261	3770	-0.21	Succinyl-CoA synthetase(SCS) ,subunit alpha
	PAP_05875	856	1344	0.67	Succinyl-CoA synthetase(SCS) , subunit beta
	PAP_04320	1908	2338	-0.29	Pyruvate:ferredoxin oxidoreductase (POR)
	-	9725	12723	-0.39	
	04330	6827	10624	-0.64	
	PAP_04305	1835	2656	-0.53	Ketoisovalerate oxidoreductase(VOR)
	-04315	10851	16844	-0.63	
		11573	21640	-0.90	
	PAP_05275	7806	11122	-0.51	Indolepyruvate oxidoreductase,alpha chain (IOR)
	PAP_05280	1704	3463	-1.02	Indolepyruvate oxidoreductase, beta chain (IOR)
	PAP_03610	8326	1974	2.08	Acetyl-CoA synthetase (ADP-forming) I ,alpha chain(ACS)
	PAP_05270	3547	4441	-0.32	Acetyl-CoA synthetase (ADP-forming) II 807,alpha chain(ACS)
	PAP_05870	2338	3209	-0.46	Acetyl-CoA synthetase (ADP-forming) ,alpha chain(ACS)
	PAP_06970	5283	5641	-0.09	Acetyl-CoA synthetase (ADP-forming),beta chain(ACS)
	PAP_03305	8371	5357	0.64	2-oxoglutarate oxidoreductase(OFOR)
	PAP_03310	5260	2616	1.01	2-oxoacid:ferredoxin oxidoreductase (KorAB)
	PAP_09030	582	1159	-0.99	Tungsten-containing aldehyde:ferredoxin oxidoreductase(AOR)
	PAP_08640	418	886	-1.08	Tungsten-containing formaldehyde:ferredoxin oxidoreductase (FOR)
	PAP_03980	699	966	-0.47	Fe-dependent alcohol dehydrogenase (ADH)
	PAP_00835	1634	988	0.73	Phosphoenolpyruvate (PEP) carboxylase (PC)
	PAP_02550	1738	1597	0.12	PEP carboxykinase (PCK)
	PAP_03770	3288	4048	-0.30	Pyruvate carboxylase (PVC)
	PAP_09695	172018	18247	-0.09	Glutamate dehydrogenase (GDH)
	PAP_06440	433	725	-0.71	Pyruvate formate lyase, alpha chain
	PAP_06540	804	1538	-0.94	Pyruvate formate lyase, beta chain
	PAP_03610	2612	2735	-0.07	Alanine aminotransferase (Ala AT)
Protease	PAP_01420	764	884	-0.21	Zn-dependent protease(membrane-bound)
	PAP_01675	1598	517	1.63	Peptidase S8 (extracellular)
	PAP_02280	232	529	-1.19	Transglutaminase-like enzyme, putative cysteine protease,YebA [Posttranslational modification, protein turnover, chaperones] (membrane-bound)

	PAP_03090	374	509	-0.44	Metalloprotease(intracellular)
	PAP_04200	102	372	-1.87	Metalloprotease(membrane-bound)
	PAP_04645				Serine protease (ClpP class)
	-	230	471	-1.03	[Posttranslational modification, protein
	PAP_04650	399	788	-0.98	turnover, chaperones] (membrane-bound)
	PAP_05230	99	340	-1.78	Zinc-dependent protease (intracellular)
	PAP_05570	77	428	-2.47	Protease (intracellular)
	PAP_09635	607	308	0.98	Peptidase (intracellular)
	PAP_09730	2802	2292	0.29	Protease (membrane-bound)
Peptidase	PAP_00355	2598	2211	0.23	Aminopeptidase (membrane-bound)
	PAP_01300	1234	1783	-0.53	Peptidase (extracellular)
	PAP_01620	749	887	-0.24	Dipeptidase (membrane-bound)
	PAP_02025	279	441	-0.66	Aminopeptidase YpdF (MP-, MA-, MS-, AP-, NP- specific)
	PAP_02935	3707	4371	-0.24	Aminopeptidase YpdF (MP-, MA-, MS-, AP-, NP- specific)
	PAP_02975	992	551	0.85	Peptidase (membrane-bound)
	PAP_03690	2436	3734	-0.62	Peptidase M50, zinc metallopeptidase (membrane-bound)
	PAP_04570	1165	1288	-0.14	Archaeal signal peptidase (membrane-bound)
	PAP_05440	4477	3383	0.40	Deblocking aminopeptidase (EC 3.4.11.-)
	PAP_06815	827	1105	-0.42	Prolyl endopeptidase (EC 3.4.21.26)
	PAP_07055	621	605	0.04	Pyrrolidone-carboxylate peptidase (EC 3.4.19.3)
	PAP_07075	1439	2572	-0.84	Thermostable carboxypeptidase 1 (EC 3.4.17.19)
	PAP_07630	1878	1682	0.16	Methionine aminopeptidase (EC 3.4.11.18)
	PAP_07645	1086	1071	0.02	Isoaspartyl aminopeptidase (EC 3.4.19.5)
	PAP_08040	873	972	-0.15	Deblocking aminopeptidase (EC 3.4.11.-)
	PAP_08100	413	679	-0.72	D-aminopeptidase
Amino-transferase	PAP_03885	204	310	-0.60	Histidinol-phosphate aminotransferase (EC 2.6.1.9)
	PAP_04390	17049	20334	-0.25	4-aminobutyrate aminotransferase
	PAP_04820	3749	8662	-1.21	Aspartate aminotransferase (AspB-4) (EC 2.6.1.1)
	PAP_04910	117	421	-1.85	Pyridoxal-phosphate dependent aminotransferase
	PAP_05920	7429	10788	-0.54	Aspartate aminotransferase (EC 2.6.1.1)
	PAP_06205	1912	1225	0.64	Aspartate aminotransferase (EC 2.6.1.1)
	PAP_06865	1322	1127	0.23	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16)
	PAP_08180	2612	2735	-0.07	Alanine aminotransferase
	PAP_09530	9579	7515	0.35	Serine-glyoxylate aminotransferase (EC 2.6.1.45)
	PAP_09565	209	445	-1.09	Glutamate aminotransferase

Metabolism of carbohydra tes	Transporter Amino acid degradation		532	653	-0.30	Dipeptide transport system (DppABCDF, APT)
		PAP_00150	251	388	-0.63	
		- 00170	153	354	-1.21	
			151	338	-1.16	
			3646	2687	0.44	
			117	295	-1.33	Branched-chain amino acid ABC transporter(LivKGFHM, AAT)
			26	137	-2.40	
		PAP_03900	39	203	-2.38	
		- 03925	95	279	-1.55	
			125	366	-1.55	
			146	295	-1.01	Proton/glutamate symport protein(GltT)
		PAP_03785	989	2629	-1.41	
		PAP_05545	94	413	-2.14	Sodium/proline symporter, SSF family(PutP)
		PAP_06890	225	1259	-2.48	Proline permease
		PAP_06940	1042	2141	-1.04	Aromatic amino acid permease(Cat-1)
		PAP_09570	160	438	-1.45	Alanine glycine permease(AGCS)
			198	729	-1.88	Dipeptide transport system (DppABCDF, APT)
		PAP_06335	48	244	-2.35	
		-	57	232	-2.03	
		06355	91	331	-1.86	
			193	528	-1.45	
			200	240	-0.26	Oligopeptide transport system, OPT family
			714	958	-0.42	
		PAP_10185	640	796	-0.31	
		- 10210	943	1111	-0.24	
			485	686	-0.50	
			4623	4306	0.10	Oligopeptide transporter, OPT family
		PAP_04080	6703	10018	-0.58	
		-	5031	5267	-0.07	
		PAP_04085				Glutamate dehydrogenase
		PAP_09695	182479	172018	-0.09	
	Starch degradation	PAP_00275	389	533	-0.45	α -amylase (extracellular) ,GH13 family
		PAP_01075	1124	921	0.29	Cyclodextrin glucosyltransferase (extracellular) , GH13 family
		PAP_09095	1159	907	0.35	α -amylase (intracellular) ,GH13 family
		PAP_09225	2120	1530	0.47	4- α - glucanotransferase (intracellular) , GH57 family
		PAP_04140	72	368	-2.35	α -galactosidase
	Maltose and trehalose degradation	PAP_04145	96	312	-1.70	β - galactosidase
		PAP_05120	7988	11334	-0.50	Trehalose synthase
		PAP_08185	460	918	-1.00	Glycosidase
		PAP_08190	654	1311	-1.00	Glycogen-debranching enzyme
		PAP_05485	9212	13542	-0.56	Amylopullulanase
	ABC-type transport systems		345	595	-0.79	Mal-I, malEFGK, transport maltotriose and longer oligomers
		PAP_04995	5972	5078	0.23	
		-	713	738	-0.05	
		05020	1307	1206	0.12	
			5086	5164	-0.02	

			890	1076	-0.27		
		PAP_05100	127	419	-1.72	Mal-II, transport maltooligosaccharides;	
		- 05110	34	128	-1.91		
			371	1019	-1.46		
		PAP_05125	3597	4390	-0.29	Mal-III, recognizes and transports maltose and trehalose;	
		- 05135	3137	2360	0.41		
			28993	18931	0.61		
		PAP_05160	182	672	-1.88	Mal-IV, malEFGK, transport maltotriose and longer oligomers	
		-	39	235	-2.59		
		05175	58	241	-2.05		
			82	403	-2.30		
		PAP_05160	709	772	-0.12	Sugar ABC-type transport system could transport sugar, eg. N-Acetyl-D-glucosamine and maltose.	
		-	64	210	-1.71		
		05175	75	202	-1.43		
			99	264	-1.42		
		PAP_06890	225	1259	-2.48	Proline permease	
		PAP_06940	1042	2141	-1.04	Aromatic amino acid permease	
		PAP_02220	15408	6805	1.18	C4-dicarboxylate ABC transporter substrate-binding protein;TRAP transporter solute receptor, TAXI family	
	PAP_10245	7903	4042	0.96	Anion permease; low-affinity inorganic phosphate transporter		
Glycerol degradation	PAP_03945	63	280	-2.15	Glycerol transport protein		
	PAP_02595	213	314	-0.56	Glycerol kinase		
	- 02605	90	375	-2.06	Glycerol-3-phosphate dehydrogenase		
		214	472	-1.14	Glycerophosphoryl diester phosphodiesteras (glpQKAD)		
	PAP_08525	152	330	-1.12	Glycerol kinase(glpK)		
	PAP_08540	81	279	-1.78	Glycerol-3-phosphate dehydrogenase(glpA)		
Nucleic acid biosyntheses	Purine Biosynthesis		275	678	-1.30	Phosphoribosylformylglycinamidine synthase, Pur LSPDETMCFOPC	
			89	179	-1.01		
			24	58	-1.27		
			132	308	-1.22		
			202	382	-0.92		
		PAP_00540	50	85	-0.77		
		-	59	159	-1.43		
		00605	26	87	-1.74		
			148	432	-1.55		
			60	199	1.73		
			178	153	0.22		
			26	27	-0.05		
			201	328	-0.71		
			69	217	-1.65		
	GMP synthase	PAP_00690	314	470	-0.58	GMP synthase	
		PAP_00695	123	247	-1.01	GMP synthase	
	Coenzyme biosynthesis	Riboflavin biosynthesis	PAP_00630	79	433	-2.45	Riboflavin synthase, RibDEBAH
			-	44	221	-2.33	
			00600	98	516	-2.40	
			51	143	-1.49		
	PAP_05950	123	257	-1.06	Riboflavin synthase, RibL		

Thiamin biosynthesis	PAP_03460	176	255	-0.53	Thiamin-monophosphate kinase(ThiL)
	PAP_03985	59	125	-1.08	Hydroxyethylthiazole kinase(ThiM)
	PAP_03990	37	115	-1.64	Thiamin phosphate synthase(ThiE)
	PAP_03995	74	221	-1.58	Bifunctional hydroxymethylpyrimidine kinase/phosphohydroxymethylpyrimidine kinase(ThiD)
	PAP_00665	150	255	-0.77	Thiamin (pyrimidine moiety) biosynthesis protein(ThiC) (Cys residues near extreme C-terminus)
	PAP_05095	34	128	-1.91	Thiamin ABC transport system
	- 05100	371	1019	-1.46	
	PAP_06425	3373	253	3.74	Cobalamin biosynthesis protein CobQ; 4Fe-4S ferredoxin type; iron-sulfur cluster binding domain
	PAP_06430	2931	276	3.41	Cobalamin biosynthesis protein CobQ; 4Fe-4S ferredoxin type; iron-sulfur cluster binding domain
	PAP_01095 - 01160	3434	1792	0.94	Membrane-bound proton-reducing H ₂ -evolving hydrogenase complexes (MBH1)
		1479	951	0.64	
		2178	1600	0.44	
		1266	777	0.70	
		2181	1254	0.80	
		2439	1518	0.68	
		2918	1756	0.73	
		9511	6318	0.59	
		1531	700	1.13	
		1988	1233	0.69	
		3249	2501	0.38	
		9654	7778	0.31	
		6292	6634	-0.08	
		3722	3997	-0.10	
Energy metabolism	Hydrogenase	387	388	0.00	Membrane-bound proton-reducing H ₂ -evolving hydrogenase complexes (MBH2)
		195	202	-0.05	
		182	208	-0.19	
		97	111	-0.19	
		132	169	-0.36	
		128	206	-0.69	
		163	207	-0.34	
		608	1038	-0.77	
		64	125	-0.97	
		106	157	-0.57	
		206	311	-0.59	
		364	627	-0.78	
		295	647	-1.13	
		206	319	-0.63	
		2448	1364	0.84	
		938	408	1.20	
		1214	398	1.61	
		915	216	2.08	
		02415	2716;	741;	
			982;	234;	
			4993;	807;	
	PAP_02355	1214	398	1.61	Membrane-bound NADP-reducing hydrogenase(MBX)
	-	915	216	2.08	
	02415	2716;	741;	1.87	
		982;	234;	2.07	
		4993;	807;	2.63	

		7346;	994;	2.89	
		2988;	502;	2.57	
		1490;	170;	3.13	
		1958;	322;	2.60	
		4088;	599;	2.77	
		2083	440	2.24	
	PAP_01490 - 01505	160; 85; 129; 118	513; 202; 331; 315	-1.68 -1.25 -1.36 -1.42	Cytoplasmic (Ni-Fe) hydrogenases (SHI,sulfl)
	PAP_03240 - 03255	8456; 5139; 5285; 8943	5100; 4213; 5334; 13605	0.73 0.29 -0.01 -0.61	Cytoplasmic (Ni-Fe) hydrogenases (SHII,sulflI)
Hydrogenase maturation	PAP_01595	32502	3010	3.43	Ni-Fe hydrogenase metallocenter assembly protein, HypF;
	PAP_04030	2840	883	1.69	hydrogenase expression/formation protein, HypE
	PAP_06285	7855	4813	0.71	hydrogenase isoenzymes formation protein, HypD
	PAP_06290	1187	388	1.61	Ni-Fe hydrogenase maturation protein,HypC
	PAP_08995	1873	478	1.97	Ni-Fe hydrogenase nickel incorporation protein ,HypA
	PAP_03260	585	669	-0.19	Hydrogenase maturation protease,HypD
	PAP_09005	1086	240	2.18	Hydrogenase maturation protease,HypI
Oxi-reductase	PAP_08740	65	216	-1.73	NADH-cytochrome b5, Heme/Steroid binding domain
	PAP_01510 - PAP_01525	55 399 392 89	61 589 1002 247	-0.15 -0.56 -1.35 -1.47	NADH-quinone oxidoreductase
	PAP_06370	208	341	-0.71	NAD(P)H-flavin oxidoreductase
	PAP_05150 - PAP_05155	79 84	270 289	-1.77 -1.78	Oxidoreductase, NAD(P)-binding domain
		508	509	0.00	
		5548	6880	-0.31	
ATP synthase	PAP_09395	906	1243	-0.46	
	-	1100	1234	-0.17	
	09435	1877	1862	0.01	V-type ATP synthase subunit(ATPVABCDEFGIK)
		347	249	0.48	
		4096	3136	0.39	
		3766	3080	0.29	
		1004	847	0.25	
Inorganic ion transport and metabolism		176	478	-1.44	
	PAP_05880	64	400	-2.64	
	-	309	928	-1.59	
	05910	191	411	-1.11	Facilitator transporter
		1057	2311	-1.12	
		40	102	-1.35	
		4394	10118	-1.20	

Cell motility and secretion	PAP_06115				
	-	51	168	-1.72	ABC-type multidrug transport system, permease and ATPase
	PAP_06120	98	271	-1.47	
	PAP_06800	514	928	-0.99	Sodium-driven multidrug efflux pump protein
	PAP_07815	43	411	-2.62	Low-affinity inorganic phosphate transporter
	PAP_08130				
	-	213	430	-1.01	ABC-type multidrug transport system, permease and ATPase
	PAP_08135	294	682	-1.21	
	PAP_01680	528	152	1.80	Nickel/Cobalt ABC transporter (cblMNQO)
	-	269	107	1.33	
	01695	307	179	0.78	
		581	474	0.29	
	PAP_08930	1268	714	0.83	EfeU-like ferrous iron transport permease
		131	887	-2.76	Flagella protein (flaABCDGHIJ)
		733	3983	-2.44	
		76	211	-1.47	
	PAP_04440	50	208	-2.06	
	-	14	33	-1.24	
	04485	55	112	-1.03	
		285	543	-0.93	
		149	377	-1.34	
		369	783	-1.09	
Sulfur metabolism	PAP_07020	498	746	-0.58	UDP-N-acetylglucosamine 2- epimerase(WecB)
	PAP_07025	1041	1014	0.04	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase(WecC)
	PAP_01275	4099	1723	1.25	Coenzyme A-dependent NAD(P)H elemental sulfur oxidoreductase(NSR)
	PAP_03325	2442	906	1.43	Pyridine nucleotide-disulfide oxidoreductase (NPSOR)
	PAP_00200				
	-	9127	2745	1.73	Ferredoxin-NADP ⁺ reductase (SuDHI)
	PAP_00205	8657	1899	2.19	
	PAP_01255	125	219	-0.81	Sulfate-transporting ATPase;sulfate transporter
	PAP_01260	250	522	-1.06	
	PAP_07225	7280	8810	-0.28	Glutarredoxin(pdo)
	PAP_08980	641	611	0.07	Glutarredoxin
	PAP_09885	1132	572	0.98	Sulfate adenylyltransferase(Sat)
	PAP_09900	282	269	0.07	Adenylylsulfate kinase(cysC)
	PAP_04545	1413	1282	0.14	PAPS reductase (cysH)
Cystein biosynthesis	PAP_05900	1057	2311	-1.13	Cysteine synthase(cysK,OASS)
	PAP_08745	87	631	-2.86	Cystathionine beta-synthase
	PAP_08750	144	631	-2.13	Cystathionine gamma-lyase
	PAP_06715	2586	2495	0.05	Cysteinyl-tRNA synthetase
	PAP_01245	2080	2938	-0.15	Cysteine desulfurase(SufS)

Fe-S cluster biogenesis	PAP_02345	308	586	-0.93	Fe-S cluster assembly ABC transporter (SufC)
	PAP_02350	866	1274	-0.56	Fe-S cluster containing protein(SufB)
	PAP_08965	6017	6692	-0.50	Cysteine desulfurase (iscS)
	PAP_08975	939	1100	-0.23	NifU-like Fe-S cluster assembly scaffold protein (IscU)
	PAP_09000	1086	240	2.18	Cytosolic Fe-S cluster carrier, Mrp/NBP35 ATP-binding protein
Fe-S cluster-containing proteins	PAP_06515	1980	101	4.29	Iron-molybdenum cofactor-binding protein
	PAP_06520	15920	212	6.23	Fe-Mo cluster-binding protein(SipA,PF2025)
	PAP_00320	228	110	1.05	Radical SAM protein, iron-sulphur containing
	- PAP_00330	36622	11960	1.61	
Iron uptake		3605	1311	1.46	
		1374	630	1.12	
	PAP_03965	61	145	-1.25	ABC-type iron (III) transporter ATPase(ABC.FEV.A)
	PAP_03970	73	162	-1.15	ABC-type iron (III) transporter permease(ABC.FEV.P)
	PAP_03975	542	667	-0.30	ABC-type iron (III) transporter Periplasmic binding protein(ABC.FEV.S)
	PAP_06035	3912	515	2.93	ABC-type iron(III)-siderophore transporter permease(ABC.FEV.P)
	PAP_06040	3065	430	2.83	ABC-type iron(III)-siderophore transporter ATPase(ABC.FEV.A)
	PAP_06225	5076	2237	1.18	Iron III ABC transporter Periplasmic binding protein (ABC.FEV.S)
	PAP_08650	378	261	0.53	ABC-type iron(III)-siderophore transporter ATPase (ABC.FEV.A)
	PAP_08655	454	237	0.94	ABC-type iron(III)-siderophore transporter permease (ABC.FEV.P)
	PAP_08660	1795	427	2.07	ABC-type iron (III) transporter Periplasmic binding protein (ABC.FEV.S)
	PAP_06060	5734	1852	1.63	Ferrous iron transporter (feoB)
	PAP_06065	283	138	1.04	Ferrous iron transporter (feoA)
	PAP_08930	1268	714	0.83	EfeU-like ferrous iron transport permease
	PAP_04295	90	316	-1.81	Low-affinity inorganic phosphate transporter (pltA)
	PAP_07815	43	264	-2.61	Low-affinity inorganic phosphate transporter
	PAP_10245	7903	4042	0.96	Low-affinity inorganic phosphate transporter
	PAP_03235	11891	27659	-1.22	Formate transporter
Storge	PAP_08895	715	891	-0.32	Iron storge protein, ferritin-like protein

	PAP_06370	208	341	-0.71	NADPH-flavin oxidoreductase
Regulators	PAP_02730	1095	541	1.02	Transcription termination protein NusA ,NusA-like transcription elongation factor,NusA superfamily
	PAP_09615	1638	786	1.06	XRE family transcriptional regulator, containing helix-turn-helix domain, COG1709 superfamily
	PAP_09880	199	90	1.14	CopG transcriptional regulator,RHH_1 superfamily
	PAP_05280	526	604	-0.20	TBP, TATA-box-binding protein(TON_1309)
	PAP_08070	742	2627	-1.82	Transcription regulator TrmB (TON_0332)
	PAP_04990	1439	944	-0.61	Transcription regulator TrmB(TON_1797)
	PAP_06755	287	325	-0.18	Transcription regulator AsnC-type (TON_0662)
	PAP_05565	77	428	-2.47	Transcription regulator AsnC-type (TON_1284)
	PAP_00110	340	276	0.30	Transcription regulator AsnC-type (TON_1510)
	PAP_08835	56	250	-2.15	ArsR-type transcription regulator, HTH motif
	PAP_06395	682	1689	-1.30	ArsR-type transcriptional regulator
	PAP_03045	48	114	-1.25	ArsR-type DNA binding domain (SurR, PF2051)
	PAP_07220	1521	1857	-0.28	ArsR-type DNA binding domain(PF0095)
	PAP_03325	2442	906	1.43	NAD(P)H:rubredoxin oxidoreductase (NROR)
Oxygen Detoxification	PAP_03330	2211	2988	-0.43	Rubrerhythrin
	PAP_03335	1148	1696	-0.56	Superoxide reductase (SOR)
	PAP_04835	1168	928	0.33	Heat shock protein
Stress responce	PAP_07685	1688	871	0.95	Heat shock protein
	PAP_08375	929	976	-0.07	Heat shock protein
	PAP_06790	216	663	-1.62	Heat shock regulator
	PAP_06210	41	133	-1.70	DNA repair and recombination protein RadB
	PAP_06965	1484	4458	-1.59	Restriction endonuclease
	PAP_07940	27	82	-1.60	CRISPR-associated protein(cas1.cas2,cas4a)
	-	117	347	-1.57	
	07950	53	104	-0.97	

	PAP_03320	2211	2988	-0.43	Rubrerythrin
	PAP_03360	709	895	-0.34	Rubrerythrin
	PAP_03370	57	123	-1.11	Rubrerythrin
	PAP_03375	281	224	0.33	Rubrerythrin
	PAP_03385	96	207	-1.11	Rubrerythrin
	PAP_03425	163	350	-1.10	Rubrerythrin
	PAP_03330	522	465	0.17	Rubredoxin
	PAP_03335	1148	1696	-0.56	Desulfoferrodoxin, ferrous iron-binding region
Others	PAP_06140 - 06190	9	19	-1.08	Hypothetical protein
		24	80	-1.74	
		112	387	-1.79	
		64	139	-1.12	
		26	67	-1.37	
		110	267	-1.28	
		67	286	-2.09	
		21	144	-2.78	
		35	166	-2.25	
		67	237	-1.82	
	PAP_07315- 07350	45	181	-2.01	Methyltransferase(UbiE)
		66	229	-1.79	
		11	21	-0.93	
		48	176	-1.87	
		85	164	-0.95	
		95	182	-0.94	
		35	68	-0.96	
		43	104	-1.27	
	PAP_06505	1141	553	1.04	Methyltransferase(UbiE)
	PAP_00080	2777	1209	1.20	(S)-2,3-di-O-geranylgeranylglycerol phosphate synthase (UbiA)
	PAP_04045	1170	136	3.10	Hypothetical protein
	PAP_09525	9740	2169	2.17	Ribonucleoside-diphosphate reductase
	PAP_09010	1420	381	1.90	Electron transporter; cytochrome complex assembly

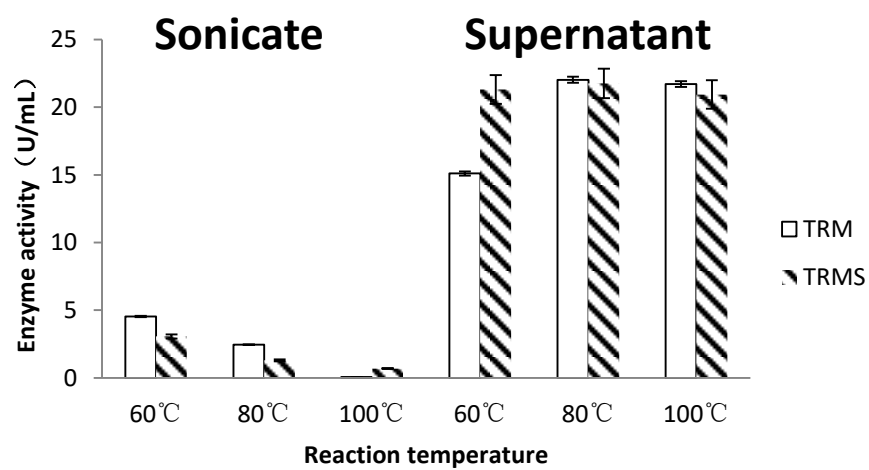


Figure S1. Protease activity at different temperature from cell sonicate or supernatant from strain DY20341 cultured in different medium TRM and TRMS