Supplemental Table 1 List of reactions whose catalyzing enzymes abundance changed between 75 and 55 ℃ for the central metabolic network of *T. tengcongensis*

Reaction name	Reaction description	Reaction	Genes involved in the reaction	Enzyme	detected differential protein	data derivation
protein abundance decreasing from 75 to 55℃						
PPS	phosphoenolpyruvate synthase	atp[c] + h2o[c] + pyr[c] -> amp[c] + 2 h[c] + pep[c] + pi[c]	TTE0981	2.7.9.1	TTE0981	2DE
PTAr	phosphotransacetylase	accoa[c] + pi[c] <=> actp[c] + coa[c]	TTE1482	2.3.1.8	TTE1482	2DE
THDPS	tetrahydrodipicolinate succinylase	h2o[c] + succoa[c] + thdp[c] -> coa[c] + sl2a6o[c]	TTE0830	2.3.1.117	TTE0830	2DE
DHDPS	dihydrodipicolinate synthase	aspsa[c] + pyr[c] -> 23dhdp[c] + 2 h2o[c] + h[c]	TTE0832	4.2.1.52	TTE0832	2DE and iTRAQ
FBA	fructose bisphosphate aldolase	fdp[c] <=> dhap[c] + g3p[c]	TTE0137	4.1.2.13	TTE0137	2DE and iTRAQ
ICDHyr	isocitrate dehydrogenase NADP	icit[c] + nadp[c] <=> akg[c] + co2[c] + nadph[c]	TTE0387	1.1.1.42	TTE0387	iTRAQ
GLYCL	Glycine Cleavage System	gly[c] + nad[c] + thf[c] <=> co2[c] + mlthf[c] + nadh[c] + nh4[c]	(TTE0293 and TTE0294 and TTE0296 and TTE0088 and TTE1674)	1.4.4.2 and 2.1.2.10 and 1.8.1.4	TTE1674	iTRAQ
GLCabc	D glucose transport via ABC system	atp[c] + glc_D[e] + h2o[c] -> adp[c] + glc_D[c] + h[c] + pi[c]	((TTE1829 and TTE1830 and TTE1831 and TTE1979) or (TTE0290 and TTE0291 and TTE0292))		TTE1979	iTRAQ
ADSL1r	adenylsuccinate lyase	dcamp[c] <=> amp[c] + fum[c]	TTE1367	4.3.2.2	TTE1367	iTRAQ

ADSL2r	adenylosuccinate lyase	25aics[c] <=> aicar[c] + fum[c]	TTE1367	4.3.2.2	TTE1367	iTRAQ
OAADC	oxaloacetate decarboxylase	oaa[c] + h[c] -> pyr[c] + co2[c]	(TTE0252 and (TTE1208 or TTE1336))	4.1.1.3	TTE1336	iTRAQ
PRASCS	phosphoribosylaminoimidazolesuccinocarboxamide synthase	5aizc[c] + asp_L[c] + atp[c] <=> 25aics[c] + adp[c] + h[c] + pi[c]	TTE0588	6.3.2.6	TTE0588	iTRAQ
protein abundance increasing from 75 to 55℃						
ALADH	alanine dehydrogenase	ala_L[c] + nad[c] + h2o[c] -> h[c] + pyr[c] + nh4[c] + nadh[c]	TTE0161	1.4.1.1	TTE0161	2DE
PGK	phosphoglycerate kinase	13dpg[c] + adp[c] <=> 3pg[c] + atp[c]	TTE1761	2.7.2.3	TTE1761	2DE
THRDr	L threonine dehydrogenase	nad[c] + thr_L[c] <=> 2aobut[c] + h[c] + nadh[c]	TTE2405	1.1.1.103	TTE2405	2DE and iTRAQ
PFOR	pyruvate ferredoxin oxidoreductase	pyr[c] + coa[c] + fdxo[c] <=> co2[c] + fdxr[c] + h[c] + accoa[c]	((TTE0445 or TTE0961 or TTE2194) and (TTE1211 or TTE1342))	1.2.7.-	TTE1342, TTE0961	2DE and iTRAQ
GLUSy	glutamate synthase NADPH	akg[c] + gln_L[c] + h[c] + nadph[c] -> 2 glu_L[c] + nadp[c]	(TTE0567 or TTE0693)	1.4.1.13	TTE0567, TTE0693	2DE and iTRAQ
FNORr	ferredoxin-NADP reductase	fdxr[c] + h[c] + nadp[c] <=> fdxo[c] + nadph[c]	(TTE0566 or TTE0694)	1.18.1.2	TTE0694	iTRAQ
ADHEr	Acetaldehyde dehydrogenase	accoa[c] + 2 h[c] + 2 nadh[c] <=> coa[c] + etoh[c] + 2 nad[c]	TTE0695	1.2.1.10 and 1.1.1.1	TTE0695	iTRAQ
OFOR	2-ketoglutarate ferredoxin oxidoreductase	akg[c] + coa[c] + fdxo[c] -> co2[c] + fdxr[c] + h[c] + succoa[c]	(TTE0960 or TTE0961 or TTE1209 or TTE1210 or TTE1340 or TTE1341 or TTE1342 or TTE2198 or TTE2199)	1.2.7.3	TTE0960, TTE0961	iTRAQ
NADH11	NADH dehydrogenase	3 h[c] + nadh[c] + q[c] -> 2 h[e] + nad[c] + qh2[c]	(TTE0123 and TTE0124 and TTE0125 and TTE0127 and TTE0128 and TTE0890 and TTE0893 and TTE0894 and TTE2486)	1.6.5.3 and 1.6.99.3	TTE0890, TTE0893, TTE0894, TTE2486	iTRAQ

DHAD1	dihydroxy acid dehydratase 2 3 dihydroxy 3 methylbutanoate	23dhmb[c] -> 3mob[c] + h2o[c]	TTE0020	4.2.1.9	TTE0020	iTRAQ
DHAD2	Dihydroxy acid dehydratase 2 3 dihydroxy 3 methylpentanoate	23dhmp[c] -> 3mop[c] + h2o[c]	TTE0020	4.2.1.9	TTE0020	iTRAQ
TRPAS2	Tryptophanase L tryptophan	h2o[c] + trp_L[c] <=> indole[c] + nh4[c] + pyr[c]	TTE1602	4.1.99.1	TTE1602	iTRAQ
KARA1i	acetohydroxy acid isomeroreductase	alac_S[c] + h[c] + nadph[c] -> 23dhmb[c] + nadp[c]	TTE0015	1.1.1.86	TTE0015	iTRAQ
KARA2i	ketol acid reductoisomerase 2 Aceto 2 hydroxybutanoate	2ahbut[c] + h[c] + nadph[c] -> 23dhmp[c] + nadp[c]	TTE0015	1.1.1.86	TTE0015	iTRAQ
IPPS	2 isopropylmalate synthase	3mob[c] + accoa[c] + h2o[c] -> 3c3hmp[c] + coa[c] + h[c]	TTE0016	2.3.3.13	TTE0016	iTRAQ
CMS	citramalate synthase	pyr[c] + accoa[c] + h2o[c] -> coa[c] + citm[c] + h[c]	TTE0016	2.3.3.13	TTE0016	iTRAQ
NDPK1	nucleoside diphosphate kinase ATPGDP	atp[c] + gdp[c] <=> adp[c] + gtp[c]	TTE0747	2.7.4.6	TTE0747	iTRAQ
NDPK3	nucleoside diphosphate kinase ATPCDP	atp[c] + cdp[c] <=> adp[c] + ctp[c]	TTE0747	2.7.4.6	TTE0747	iTRAQ
ATPS4	ATP synthase four protons for one ATP	adp[c] + 4 h[e] + pi[c] -> atp[c] + h2o[c] + 3 h[c]	(TTE0630 and TTE0631 and TTE0633 and TTE0634 and TTE0635 and TTE0636 and TTE0637 and TTE0638)	3.6.3.14	TTE0637	iTRAQ
ALAR	alanine racemase	ala_L[c] <=> ala_D[c]	(TTE1207 or TTE2168)	5.1.1.1	TTE2168	iTRAQ
DHPS2	dihydropteroate synthase	4abz[c] + 6hmhptpp[c] -> dhpt[c] + h[c] + ppi[c]	TTE2370	2.5.1.15	TTE2370	iTRAQ
ASPK	aspartate kinase	asp_L[c] + atp[c] <=> 4pasp[c] + adp[c]	TTE1382	2.7.2.4	TTE1382	iTRAQ