

1 **Table S5. *H. volcanii* genes with constitutive non-average translational**
 2 **efficiency^{*1}**

identifier	putative function	length (bp)	translational repression factor					
			exp			stat		
			∅	SD	n	∅	SD	n
Constitutive undertranslation								
<u>AA - amino acid metabolism</u>								
436G3	branched-chain amino acid aminotransferase IlvE1	512	3.3	0.8	4	2.9	1.4	3
	rieske [2Fe-2S] domain containing oxidoreductase	426						
	GtrA-like family protein	320						
<u>COM - coenzyme metabolism</u>								
457D5	NAD+ synthetase NadE	480	2.8	1.8	3	2.1	0.5	3
<u>ISH - transposases and ISH-encoded proteins</u>								
435B10	transposase Tnp	999	2.6	0.4	4	3.0	1.1	3
435E12	transposase Tnp	519	3.8	0.9	3	2.5	0.9	3
	tryptophanyl-tRNA synthetase TrpS	468						
438E1	transposase Tnp	999	3.6	1.2	4	4.8	0.8	3
447C11	transposase Tnp	287	2.4	1.1	2	3.2	1.3	3
449G12	transposase Tnp	372	3.2	1.1	2	3.8	2.7	2
452F5	transposase Tnp	999	3.0	0.6	4	4.0	1.7	3
453G11	transposase Tnp	384	4.2	2.9	4	3.5	0.9	3
454C9	transposase Tnp	537	3.3	1.0	4	4.3	1.1	3
457D3	transposase	324	2.8	1.6	3	2.3	0.8	3
<u>MIS - miscellaneous</u>								
432H4	conditioned medium-induced protein 9-related protein	288	2.9	1.3	4	3.1	1.3	3
	conserved hypothetical protein	224						
	cold shock transcription regulator protein CspD1	195						
438F2	nonhistone chromosomal protein MC1	237	6.6	0.5	2	4.9	0.8	3
	dihydroorotate oxidase PyrD	186						
447D4	conditioned medium-induced protein 9-related protein	288	3.0	1.1	4	4.7	2.2	3
	cold shock transcription regulator protein CspD1	192						
448A8	rhodanese-like domain protein	366	2.2	0.9	4	2.8	1.8	3
	translation initiation factor SUI1, putative	294						
	hypothetical protein	221						
<u>TP - small molecule transport</u>								
439E10	multi antimicrobial extrusion drug-sodium antiporter MatE	518	3.7	1.4	2	2.9	0.8	3
<u>CHY - conserved hypothetical protein, HY - hypothetical protein, NOF - no function assigned to experimentally identified protein; no homology to annotated genes</u>								
431E9	hypothetical protein	949	5.8	1.1	4	5.7	2.2	3
	transposase Cap8H	840						
431G4	conserved hypothetical protein	613	3.9	2.9	2	2.3	1.1	3
	hypothetical protein	351						
432B7	cyanoglobin GlnN	363	4.0	1.5	4	3.3	2.3	3
	putative transcription factor TFIIIB repeat	230						
432C2			8.0	3.7	4	13.7	10.7	3
432E2			13.3	4.4	4	16.2	7.2	3
432F1			8.9	4.8	4	13.8	8.7	3
433A2	hypothetical protein	560	14.3	13.9	4	8.0	3.2	3
	transposase Cap8H	443						

434D8	conserved protein	1314	7.7	4.5	3	9.5	10.9	2
435E2	hypothetical protein	1723	3.0	1.0	4	2.7	1.3	3
	acyl-CoA thioester hydrolase Act	483						
	conserved hypothetical protein	456						
	uncharacterized ACR, COG1259 superfamily	444						
436C6	hypothetical protein	1049	9.6	1.8	4	11.8	10.0	3
	dihydrofolate reductase FolA	419						
436E3	hypothetical protein Vng6148h	816	2.6	0.6	3	2.3	0.3	3
436H11	hypothetical protein Vng6148h	842	2.1	0.4	3	2.2	0.0	3
	SNF2 family N-terminal domain protein	540						
438H5	conserved hypothetical protein	386	4.0	2.9	4	7.2	5.1	3
441D12	conserved protein	318	4.5		2	3.1	0.9	2
443B3	hypothetical protein Vng6406H	931	3.1	0.1	2	2.1	0.2	3
443C3			4.6	1.1	3	3.8	1.2	3
446H9			9.0	3.4	4	12.1	6.2	3
447A6	membrane protein, putative	883	2.5	1.1	2	2.9	1.8	3
447B12	hypothetical protein	277	19.0	10.0	4	23.1	20.1	3
	transposase Cap8H	160						
448E3			10.9	9.8	4	6.0	3.9	3
448F9			24.8	18.0	4	36.6	24.9	3
450H8	conserved hypothetical protein	414	3.6	3.0	4	2.6	1.6	3
	3-ketoacyl-CoA thiolase AcaB2	394						
451C1	hypothetical protein	1691	8.6	1.3	3	9.3	4.2	2
452E9			6.4	4.5	4	12.8	10.6	3
453F7			12.2	3.4	4	17.7	9.9	3
456E3	conserved hypothetical protein	537	3.8	0.4	3	4.2	1.3	3
459B12	conserved hypothetical protein	648	2.1	1.0	4	3.1	1.7	3

Constitutive overtranslation

AA - amino acid metabolism

438C6	3-isopropylmalate dehydratase, large subunit LeuC	1252	0.4	0.1	4	0.3	0.2	3
	3-isopropylmalate dehydratase, small subunit LeuD	609						
440H4	aspartate aminotransferase AvtA4	1041	0.4	0.0	4	0.4	0.2	3
457A1	beta-eliminating lyase TnaA	1407	0.3	0.1	4	0.5	0.1	3
457E2	glutamate synthase large subunit GltA	1699	0.3	0.1	4	0.4	0.1	3

CHM - carbohydrate metabolism

437A5	L-lactate dehydrogenase	510	0.4	0.1	4	0.5	0.1	3
	ferritin-like domain subfamily	453						
440F5	glucoamylase	877	0.3	0.1	3	0.4	0.3	3
454E2	NAD dependent epimerase-dehydratase family	1026	0.4	0.1	2	0.4	0.0	3

CIM - central intermediary metabolism

432H8	aldehyde ferredoxin oxidoreductase Aor2	1042	0.5	0.1	4	0.4	0.1	2
437H9	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	1217	0.3	0.1	4	0.3	0.1	3
438C2	pyruvate dehydrogenase E1 alpha subunit PdhA2	816	0.4	0.1	4	0.5	0.2	3
	pyruvate dehydrogenase PdhB	505						
439F10	succinate dehydrogenase flavoprotein subunit SdhA	1148	0.3	0.1	4	0.5	0.2	3
444C5	2,3-bisphosphoglycerate-independent PGA mutase	1645	0.4	0.1	3	0.5	0.2	3
445F10	acetate-CoA ligase AcsA	760	0.5	0.1	4	0.5	0.2	3
	bacterio-opsin activator-like protein Boa	711						
446B3	succinate dehydrogenase iron-sulfur protein SdhB	661	0.3	0.0	4	0.4	0.0	3
449A6	glycolate oxidase subunit GlcD	1061	0.5	0.2	4	0.5	0.2	3
450C10	acetate--CoA ligase AcsA	438	0.4	0.0	2	0.5	0.1	3

	bacterio-opsin activator-like protein Boa	247						
	acyl-coenzyme A synthetase ACS5	222						
457C3	aconitate hydratase 1 AcnA	509	0.3	0.1	4	0.4	0.2	3
	thioredoxin	261						
458A10	pyruvate dehydrogenase PdhB	492	0.4	0.2	4	0.4	0.2	3
	pyruvate dehydrogenase E1 alpha subunit PdhA2	294						
460E10	succinyl-Coa synthetase Acs3	961	0.4	0.1	4	0.4	0.1	3
	cobyrinic acid ac-diamide synthase Pta	682						
<u>COM - coenzyme metabolism</u>								
447G2	precorrin-3B C17-methyltransferase CobH	746	0.3	0.1	4	0.5	0.4	3
431B8	cobalamin biosynthesis CbiL	540	0.3	0.1	3	0.4	0.1	3
	precorrin-8W decarboxylase CbiT	506						
	cobalamin biosynthesis precorrin-3 methylase CbiF	294						
<u>CP - cellular processes</u>								
446A11	general stress protein 69 Gsp	963	0.4	0.1	4	0.5	0.1	3
452G11	cell division control protein 48 Cdc48	1118	0.3	0.1	4	0.4	0.2	3
	hypothetical protein RrnAC1529	579						
<u>EM - energy metabolism</u>								
439A6	V-type ATPase, subunit A	1210	0.4	0.0	4	0.4	0.1	3
444H1	V-type ATPase, subunit A	736	0.4	0.1	4	0.4	0.1	3
	V-type ATPase, subunit C	557						
448F1	V-type ATPase, subunit A	809	0.3	0.1	4	0.4	0.1	3
448G5	V-type ATPase, subunit A	1461	0.3	0.1	4	0.3	0.1	3
449E6	V-type ATPase, subunit A	918	0.4	0.1	4	0.3	0.2	3
<u>LIP - lipid metabolism</u>								
454A12	3-hydroxybutyryl-CoA dehydrogenase HBD2	1159	0.4	0.1	4	0.5	0.3	3
<u>MIS - miscellaneous</u>								
432H9	sulfatase arylsulfatase A-like	937	0.4	0.1	4	0.5	0.1	3
	glutamate-cysteine ligase family 2 GCS2	462						
436A2	N-acyl-L-amino acid amidohydrolase	920	0.4	0.1	4	0.4	0.2	3
	hypothetical protein	887						
	oligopeptide ABC transporter peptide-binding protein	688						
440B1	cobalamin biosynthesis CbiG	632	0.3	0.1	4	0.3	0.1	3
	precorrin-3B C17-methyltransferase CobH	528						
441B2	phenylacetic acid degradation protein PaaA	683	0.3	0.1	4	0.4	0.1	3
447H5	4-aminobutyrate aminotransferase GabT	629	0.5	0.2	3	0.5	0.1	3
	mRNA 3'-end processing factor-like Epf2	502						
448C2	catalase-peroxidase HPI KatG	480	0.3	0.1	4	0.4	0.1	3
450C2	mandelate racemase - muconate lactonizing enzyme	975	0.3	0.1	4	0.4	0.1	3
451A6	mandelate racemase - muconate lactonizing enzyme, N-terminal domain protein	1062	0.3	0.1	4	0.4	0.2	3
452B2	hydantoinase	1375	0.3	0.1	4	0.3	0.1	3
452C2	phenylacetic acid degradation protein PaaA	852	0.3	0.1	4	0.3	0.1	3
454A2	aldehyde ferredoxin oxidoreductase Aor	1643	0.3	0.1	2	0.3	0.0	3
455G2	4-aminobutyrate aminotransferase GabT	1326	0.4	0.2	3	0.5	0.1	3
455H3	catalase-peroxidase HPI KatG	713	0.3	0.1	3	0.4	0.1	3
	N5,N10-methylenetetrahydromethanopterin reductase	647						
456A8	hydantoinase	474	0.5	0.2	4	0.4	0.2	3
458G9	phenylacetic acid degradation protein PaaA	564		0.2	4	0.3	0.1	3
	transcription regulator Boa-12	441						
459G4	cobalamin biosynthesis CbiG	981	0.4	0.1	4	0.3	0.1	3

RRR - replication, repair, recombination

434D1	DNA topoisomerase VI, B subunit Top6B	1539	0.3	0.1	4	0.2	0.0	3
440A10	excinuclease ABC, B subunit UvrB	1323	0.5	0.2	3	0.5	0.0	3
440G11	DNA polymerase B PolB1	1359	0.4	0.1	4	0.4	0.2	3
448H1	DNA topoisomerase I TopA	587	0.4	0.1	3	0.5	0.1	3
455A6	DNA gyrase, B subunit GyrB	856	0.3	0.1	4	0.3	0.1	3
	DNA topoisomerase VI, B subunit Top6B	542						
457G12	excinuclease ABC, B subunit UvrB	1487	0.4	0.1	3	0.5	0.2	3

SIG - signal transduction

439G2	HTR-like protein HtlD	1492	0.5	0.1	3	0.5	0.1	3
455G7	heme-based aerotactic transducer HemAT Htr10	571	0.5	0.1	4	0.4	0.2	3

TC - transcription

433F10	DNA-directed RNA polymerase subunit B RpoB2	1566	0.4	0.1	4	0.3	0.1	3
438E9	DNA-directed RNA polymerase RpoE	573	0.3	0.1	4	0.4	0.1	3
444B9	DNA-directed RNA polymerase, subunit A" RpoA2	1029	0.5	0.1	4	0.4	0.1	3
	DNA-directed RNA polymerase subunit A' RpoA1	799						
445H3	DNA-directed RNA polymerase subunit A' RpoA1	987	0.3	0.1	4	0.5	0.3	3
	DNA-directed RNA polymerase beta subunit RpoB	440						
447C10	DNA-directed RNA polymerase RpoE	569	0.4	0.1	4	0.4	0.2	3
	translation initiation factor eIF-2 subunit gamma Eif2G	511						
	predicted RNA-binding protein containing PIN domain	390						
460G3	DNA-directed RNA polymerase subunit B RpoB2	1528	0.3	0.1	4	0.4	0.0	3

TL - translation

433D2	isoleucyl-tRNA synthetase IleS	1113	0.4	0.1	4	0.4	0.1	3
436E1	ribosomal protein L22 RplV	462	0.3	0.1	4	0.3	0.2	3
	ribosomal protein S19 RpsS	423						
	ribosomal protein L2 RplB	359						
440C3	translation initiation factor eIF-2 subunit gamma Eif2G	1034	0.3	0.1	4	0.4	0.1	3
446A3	ribosomal protein L14p Rpl14P	372	0.4	0.1	4	0.5	0.4	3
446E8	ribosomal protein L32E Rpl32e	672	0.4	0.1	4	0.5	0.3	3
	ribosomal protein L19e	385						
451H10	leucyl-tRNA synthetase LeuS	1431	0.3	0.1	4	0.4	0.1	3
	hypothetical protein	1431						
455D12	ribosomal protein L6p Rpl6p	537	0.4	0.1	4	0.4	0.2	3
	ribosomal protein S8 RpsH	393						
	ribosomal protein L32E Rpl32e	367						
460C6	phenylalanyl-tRNA synthetase alpha chain PheS	1334	0.4	0.2	3	0.3	0.0	2

TP - small molecule transport

432D5	dipeptide ABC transporter ATP-binding DppF	1274	0.4	0.0	4	0.4	0.1	3
438H12	oligopeptide ABC transporter MII9136, peptide-binding	988	0.4	0.1	4	0.4	0.2	3
	dipeptide transport system permease protein MII9135	510						
439C3	dipeptide transport system permease protein MII9134	900	0.4	0.1	4	0.4	0.1	3
	dipeptide transport system permease protein MII9135	739						
	hypothetical protein	543						
444G10	dipeptide ABC transporter ATP-binding DppD	1245	0.4	0.2	4	0.4	0.1	3
449H2	oligopeptide ABC transporter peptide-binding protein	748	0.3	0.1	4	0.3	0.2	3
	dipeptide ABC transporter permease DppB2	561						
455F7	oligopeptide ABC transporter MII9136, peptide-binding	1516	0.3	0.0	4	0.4	0.2	3
455H8	dipeptide transport system permease protein MII9135	918	0.4	0.1	4	0.4	0.2	3
	oligopeptide ABC transporter MII9136, peptide-binding	514						
456A3	dipeptide transport system permease protein MII9135	815	0.3	0.0	4	0.4	0.1	3

460H7	oligopeptide ABC transporter peptide-binding protein	753	0.3	0.0	4	0.4	0.2	3
	dipeptide ABC transporter permease DppB2	502						
<u>CHY - conserved hypothetical protein, HY - hypothetical protein, NOF - no function assigned to experimentally identified protein; no homolgy to annotated genes</u>								
435C3	protein of unknown function (DUF917) superfamily	1089	0.4	0.1	4	0.4	0.1	3
	protein of unknown function (DUF917) superfamily	518						
439A9	hypothetical protein	714	0.4	0.1	4	0.4	0.2	3
	L-carnitine dehydratase/bile acid-inducible protein F	671						
446D1			0.3	0.1	4	0.5	0.1	3
446H2	mRNA 3'-end processing factor-like Epf2	965	0.3	0.0	4	0.4	0.1	3
448G7			0.3	0.1	2	0.5	0.1	3
450A5	hypothetical protein rrnAC1828	1209	0.4	0.1	4	0.5	0.2	3
	FeS assembly protein SufB	418						
452G2	endonuclease Staphylococcal nuclease-like ComA	820	0.4	0.1	2	0.5	0.2	3
452H12			0.3	0.2	2	0.4	0.0	2
453C4	hypothetical protein rrnAC1529	762	0.4	0.1	4	0.4	0.3	3
	cell division control protein 48 Cdc48	593						
455E4			0.5	0.1	4	0.5	0.2	3
459A5	oxidoreductase MviM3	948	0.4	0.3	3	0.5	0.3	3
	conserved hypothetical protein	670						

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2 [†]All genes are tabulated which have a “translational repression factor” of ≤ 0.5 or ≥ 2.0 in exponential

3 phase and in stationary phase. The translational repression factor is the quotient of free RNA to

4 polysome-bound RNA (normalized to the average of all genes). The identifier is the clone designation

5 in the onefold coverage genome library used to generate the shotgun DNA microarray (Zaigler et al.

6 2003). The “putative functions” are derived from blast searches against public databases. The “length”

7 is the partial or total length of the gene which is present in the respective clone. The columns $\bar{\phi}$, SD

8 and n list average value, standard deviation and number of biological replicates included in the

9 analysis.