

1 **Table S4. *H. volcanii* genes with growth phase-dependent above-average**
 2 **translational efficiency^{*1}**

identifier	putative function	length (bp)	translational repression factor					
			exp			stat		
			∅	SD	n	∅	SD	n
Exponential growth phase overtranslation								
<u>AA - amino acid metabolism</u>								
432H12	aspartokinase LysC	901	0.3	0.3	3	0.7	0.3	3
437F10	beta-eliminating lyase TnaA	1267	0.2	0.1	4	0.6	0.3	3
441B11	IGP synthase cyclase subunit HisF	678	0.5	0.1	4	1.5	0.5	2
	NADPH:quinone oxidoreductase Qor	582						
441C11	aspartokinase LysC	729	0.4	0.3	2	1.2	0.6	3
441F5	D-3-phosphoglycerate dehydrogenase SerA	796	0.5	0.1	4	0.9	0.2	3
	conserved hypothetical protein	666						
446B6	O-acetylserine lyase CysM	909	0.1	0.0	2	1.0	0.4	2
447F4	aminotransferase, class V superfamily Csd	761	0.3	0.1	4	0.6	0.2	3
448H10	glutamate synthase large subunit GltA	1469	0.3	0.1	3	0.6	0.2	3
452H2	glutamate dehydrogenase GdhB	2628	0.4	0.1	3	0.8	0.1	2
454E4	argininosuccinate synthase ArgG	1068	0.5	0.1	4	0.9	0.3	3
454G5	serine hydroxymethyltransferase GlyA	1068	0.5	0.2	4	1.1	0.4	3
<u>CHM - carbohydrate metabolism</u>								
445G2	polysaccharide deacetylase domain protein	218	0.5	0.2	2	0.9	0.2	3
454B11	acetoin dehydrogenase AcoA	855	0.1	0.1	2	0.4	0.2	3
<u>CIM - central intermediary metabolism</u>								
441D1	NAD-dependent malate dehydrogenase Mdh	1604	0.4	0.1	3	1.0	0.6	3
443B7	succinyl-CoA synthase, alpha subunit SucD	745	0.4	0.0	4	0.7	0.3	3
	succinyl-CoA synthase, beta subunit SucC	741						
449B11	pyruvate ferredoxin oxidoreductase subunit alpha PorA	1626	0.3	0.1	2	0.6	0.2	3
<u>COM - coenzyme metabolism</u>								
444F11	isochorismatase family protein family	944	0.4	0.1	4	0.8	0.3	3
<u>CP - cellular processes</u>								
454B5	cell division protein FtsH	1216	0.4	0.1	3	0.8	0.2	3
456H3	ATP-dependent protease, putative	1561	0.5	0.0	4	1.0	0.6	3
457F11	peptidylprolyl isomerase PpiB2	254	0.4	0.1	2	0.7	0.3	3
	tellurite resistance protein TehB	197						
<u>EM - energy metabolism</u>								
433C1	cytochrome c oxidase subunit I-like protein CtaD	1159	0.5	0.2	4	0.9	0.3	3
434B6	H ⁺ -transporting ATP synthase subunit I Atpl	1027	0.4	0.1	4	0.8	0.4	3
	hypothetical protein	519						
<u>LIP - lipid metabolism</u>								
447D1	3-hydroxybutyryl-CoA dehydrogenase Hbd1	810	0.3	0.1	3	0.8	0.3	3
<u>MIS - miscellaneous</u>								
438B7	phospho-adenyl-sulfate Reductase NodP	835	0.3	0.1	3	0.5	0.1	3
	phospho-adenyl-sulfate Reductase NodP	735						
449F5	dehydrogenase homolog	115	0.4	0.1	2	1.3	0.5	2
457F5	oxidoreductase Aad	706	0.4	0.1	3	0.7	0.3	3
	sporulation control protein Alr4153	651						
458E5	putative peptidase	876	0.4	0.2	3	0.8	0.2	3
<u>NUM - nucleotide metabolism</u>								

439D9	inosine monophosphate dehydrogenase-GMP reductase	798	0.4	0.1	4	0.9	0.3	3
	AT hook motif domain protein	663						
442F2	phosphoribosylformylglycinamide synthase I PurQ	675	0.4	0.0	2	1.4	0.3	2
<u>REG - gene regulation</u>								
432G1	LtrC-like protein LtrC	452	0.4	0.3	2	2.0	0.2	2
	hypothetical protein Vng7115	409						
447A5	2-domain regulatory protein Prp2	1019	0.5	0.2	4	1.0	0.5	3
450G2	sugar-specific transcriptional regulator TrmB	1140	0.4	0.0	2	0.7	0.1	2
<u>RRR - replication, repair, recombination</u>								
440H6	DNA gyrase, A subunit GyrA	1421	0.4	0.1	3	0.8	0.3	3
460C5	DNA polymerase B PolB1	1523	0.4	0.1	3	0.7	0.1	3
<u>SIG - signal transduction</u>								
451B12	MCP domain signal transducer Htr4	1218	0.5	0.2	3	1.1	0.7	2
<u>TC - transcription</u>								
435H3	transcription factor B Tfb	958	0.4	0.1	4	0.8	0.2	3
456D3	transcription factor B Tfb	638	0.4	0.1	4	1.0	0.1	3
<u>TL - translation</u>								
435H4	translation initiation factor 2, subunit alpha Eif2A	801	0.4	0.1	4	0.8	0.3	3
448H7	ribosomal protein L24 RplX	399	0.5	0.1	2	2.2	1.0	2
	conserved hypothetical protein	396						
	hypothetical protein	396						
459F10	tyrosyl-tRNA synthetase TyrS	871	0.4	0.1	3	0.7	0.2	3
	lipase-esterase	608						
<u>TP - small molecule transport</u>								
436D4	dipeptide ABC transporter ATP-binding DppD	1535	0.3	0.1	4	0.6	0.3	3
438B3	ferrichrome-binding protein (Vng2549C)	797	0.5	0.4	4	1.2	0.6	2
439F6	ferrichrome-binding protein	1248	0.2	0.0	2	2.0	0.8	3
441H2	cationic amino acid transporter Cat-1	880	0.5	0.1	3	1.4	0.6	3
444H6	oligopeptide ABC transporter, solute-binding protein OppA	1412	0.3	0.1	4	0.6	0.2	3
	hypothetical protein	1359						
449H12	ABC transport protein inner membrane component	894	0.5	0.3	3	2.2	1.4	2
	ABC transport protein inner membrane component	544						
452D5	ABC transporter permease protein MacB	1143	0.5	0.1	4	1.4	0.5	3
455A2	amino acid ABC transporter (substrate-binding protein)	921	0.3	0.1	3	0.7	0.1	3
459H9	ferrichrome-binding protein (Vng2549C)	1115	0.5	0.2	3	1.1	0.3	3
<u>CHY - conserved hypothetical protein, HY - hypothetical protein, NOF - no function assigned to experimentally identified protein; no homology to annotated genes</u>								
434A7			0.4	0.3	3	1.2	0.1	3
434G7	homolog 1 to rad50 ATPase	1196	0.5	0.1	4	0.8	0.3	3
	homolog 1 to rad50 ATPase	1160						
434H4	homolog 1 to rad50 ATPase	1196	0.5	0.1	4	1.0	0.5	3
	homolog 1 to rad50 ATPase	1160						
436A5			0.5	0.2	3	1.2	0.7	3
436D3	hypothetical protein	972	0.5	0.3	4	1.3	0.9	3
	glucose dehydrogenase OxrA	786						
	sigma-70 region 4 like DNA binding protein	495						
	hypothetical protein	492						
	hypothetical protein	476						
441D2	membrane protein, putative	781	0.4	0.2	4	1.0	0.4	3
	precorrin-8W decarboxylase CbiT	620						
441H3	replication protein A	1213	0.4	0.1	4	0.7	0.2	3

442F5	conserved hypothetical protein sugar-specific transcriptional regulator TrmB	519 300	0.4	0.1	3	0.9	0.0	2
443C7	hypothetical protein rrnB0067 hypothetical protein rrnB0068 hypothetical protein rrnB0068	448 417 313	0.4	0.2	2	0.9	0.3	3
444B11	hypothetical protein conserved protein mannose-1-phosphate guanylyltransferase ManC conserved hypothetical protein	780 576 507 402	0.3	0.2	3	1.0	0.4	3
444F5	hypothetical protein membrane protein Pan1 conserved hypothetical protein	1536 724 555	0.3	0.0	3	0.6	0.4	3
445F1			0.5	0.2	3	1.2	0.2	2
445H1	hypothetical protein Vng6400h	1078	0.5	0.2	4	1.1	0.4	2
446D1			0.3	0.1	4	0.5	0.1	3
448E7			0.3	0.4	2	1.0	0.2	3
450B1	predicted phospho-2-dehydro-3-deoxyheptonate aldolase tryptophan synthase, alpha subunit TrpA	729 511	0.5	0.1	4	0.9	0.2	2
451F9	hypothetical protein endonuclease III NthA1	670 530	0.5	0.3	3	1.2	0.1	2
455A10	circadian regulator	741	0.5	0.1	4	1.0	0.3	3
457B9	HD domain protein small conductance mechanosensitive ion channel	813 463	0.4	0.1	3	0.9	0.1	2
458F2	conserved hypothetical protein conserved hypothetical protein Hypothetical protein Vng6400h	558 415 309	0.4	0.1	4	0.8	0.2	3
459C2	mRNA 3'-end processing factor Epf1 geranylgeranyl reductase family subfamily	735 593	0.2	0.0	2	0.6	0.2	3
460B2	conserved hypothetical protein serine hydroxymethyltransferase GlyA	668 516	0.4	0.1	4	1.0	0.3	3

Stationary growth phase overtranslation

CP - cellular processes

435H5	protein kinase Prk	1185	2.3	2.1	3	0.4	0.1	3
444E6	kinase anchor protein PrkA	1167	1.4	0.9	2	0.4	0.1	3

EM - energy metabolism

450E9	halocyanin precursor-like HcpB natural resistance-associated macrophage protein family	687 342	0.9	0.2	2	0.2	0.2	2
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MIS - miscellaneous

433F2	glycosyltransferase stage V sporulation protein R-like SpoVR	907 542	2.3	1.4	3	0.5	0.1	3
442E3	urease, alpha subunit UreC	1075	0.9	0.4	3	0.4	0.2	3

CHY - conserved hypothetical protein, HY - hypothetical protein, NOF - no function assigned to experimentally identified protein; no homology to annotated genes

443E2	stage V sporulation protein R-like SpoVR glycosyltransferase	956 588	1.2	0.9	2	0.4	0.1	3
444D11	stage V sporulation protein R-like SpoVR glycosyltransferase	713 619	1.1	0.5	3	0.5	0.2	3
456A7	hypothetical protein lipoprotein, putative lipoprotein, putative	1440 1058 441	0.8	0.2	3	0.5	0.2	3

1 *¹All genes are tabulated which have a “translational repression factor” of ≤ 0.5 differentially in exponential
2 phase (upper part) or in stationary phase (lower part). The translational repression factor is the quotient of
3 free RNA to polysome-bound RNA (normalized to the average of all genes). The identifier is the clone
4 designation in the onefold coverage genome library used to generate the shotgun DNA microarray
5 (Zaigler et al. 2003). The “putative functions” are derived from blast searches against public databases.
6 The “length” is the partial or total length of the gene which is present in the respective clone. The columns
7 \bar{x} , SD and n list average value, standard deviation and number of biological replicates included in the
8 analysis.