

1 **Table S2. *H. salinarum* genes with constitutive non-average translational**  
 2 **efficiency<sup>\*1</sup>**

ORF	gene product	translational repression factor			transcript level					
		exp			stat					
		∅	SD	n	∅	SD	n	∅	SD	n
<b>Constitutive overtranslation</b>										
<u>AA - amino acid metabolism</u>										
OE5206R	carbamate kinase	<b>0.4</b>	0.2	4	<b>0.5</b>	0.1	3	<b>1.4</b>	0.3	3
OE5208R	arginine deiminase	<b>0.3</b>	0.1	4	<b>0.3</b>	0.0	3	<b>1.3</b>	0.1	3
<u>CP - cellular processes</u>										
OE3541R	probable heat shock protein	<b>0.4</b>	0.1	4	<b>0.5</b>	0.1	3	<b>4.7</b>	1.4	3
OE3925R	thermosome beta chain	<b>0.2</b>	0.1	4	<b>0.3</b>	0.0	3	<b>0.2</b>	0.0	3
OE4122R	thermosome alpha chain	<b>0.2</b>	0.1	4	<b>0.4</b>	0.2	3	<b>0.2</b>	0.0	3
OE5212F_a	SMC-like protein Sph1	<b>0.4</b>	0.2	4	<b>0.4</b>	0.0	3	<b>2.9</b>	1.5	3
OE5212F_b	SMC-like protein Sph1	<b>0.4</b>	0.2	3	<b>0.3</b>	0.1	3	<b>4.5</b>	1.9	3
<u>MIS - miscellaneous</u>										
OE2708R	superoxide dismutase 1 (Mn containing)	<b>0.4</b>	0.1	4	<b>0.5</b>	0.2	3	<b>0.2</b>	0.1	3
OE3112R	AAA-type ATPase (transitional ATPase homolog)	<b>0.3</b>	0.2	4	<b>0.5</b>	0.0	2	<b>0.6</b>	0.1	3
OE3356F	AAA-type ATPase (transitional ATPase homolog)	<b>0.3</b>	0.2	3	<b>0.5</b>	0.0	3	<b>0.9</b>	0.1	3
OE5082R	AAA-type ATPase (transitional ATPase homolog)	<b>0.4</b>	0.2	4	<b>0.4</b>	0.0	3	<b>0.8</b>	0.1	3
OE5160F	glycerol dehydrogenase	<b>0.5</b>	0.4	4	<b>0.3</b>	0.0	3	<b>1.1</b>	0.3	3
<u>TC - transcription</u>										
OE1478R	transcription initiation factor TFB	<b>0.4</b>	0.2	4	<b>0.3</b>	0.1	3	<b>0.7</b>	0.1	3
<u>TP - small molecule transport</u>										
OE1781F	probable ABC-type transport system ATP-binding protein	<b>0.4</b>	0.1	4	<b>0.3</b>	0.1	3			0
<u>CHY - conserved hypothetical protein, HY - hypothetical protein, NOF - no function assigned to experimentally identified protein</u>										
OE1782F	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>0.5</b>	0.1	3	<b>0.7</b>	0.1	3
OE1783F	conserved hypothetical protein	<b>0.3</b>	0.0	4	<b>0.5</b>	0.1	3	<b>0.8</b>	0.2	3
OE2585R	conserved hypothetical protein	<b>0.5</b>	0.1	4	<b>0.4</b>	0.1	3			0
orf178-02		<b>0.5</b>	0.1	4	<b>0.3</b>	0.0	3			0

3

4 <sup>\*1</sup>All genes are tabulated which have a “translational repression factor” of ≤0.5 in exponential phase  
 5 and in stationary phase. The translational repression factor is the quotient of free RNA to polysome-  
 6 bound RNA (normalized to the average of all genes). If available, also the relative transcript levels of  
 7 these genes are listed (Quotient stationary phase / exponential phase). ORF numbers and gene  
 8 products were taken from the genome website www.halolex.mpg.de. The columns ∅, SD and n list  
 9 average value, standard deviation and number of repetitions.