

1 **Table S1. *H. salinarum* genes with growth phase-dependent above-average**  
 2 **translational efficiencies<sup>\*1</sup>**

ORF	gene product	translational repression factor						transcript level		
		exp			stat			stat/exp		
		∅	SD	n	∅	SD	n	∅	SD	n
<b>Stationary growth phase overtranslation</b>										
OE3542R	hypothetical protein	<b>0.5</b>	0.1	4	<b>0.2</b>	0.0	3	<b>2.6</b>	0.3	3
<b>Exponential growth phase overtranslation</b>										
<u>AA - amino acid metabolism</u>										
OE1270F	glutamate dehydrogenase	<b>0.3</b>	0.2	4	<b>0.6</b>	0.2	3	<b>0.4</b>	0.1	3
OE1916F	cysteine synthase CysK1	<b>0.4</b>	0.1	4	<b>0.9</b>	0.1	3	<b>0.5</b>	0.0	3
OE3331R	anthranilate synthase beta chain	<b>0.5</b>	0.2	4	<b>1.0</b>	0.2	2			0
OE3959R	branched-chain-amino-acid transaminase	<b>0.3</b>	0.1	4	<b>0.6</b>	0.1	2			0
OE5205R_a	ornithine carbamoyltransferase, catabolic	<b>0.3</b>	0.1	4	<b>0.6</b>	0.1	3	<b>0.9</b>	0.2	3
OE5205R_b	ornithine carbamoyltransferase, catabolic	<b>0.3</b>	0.1	4	<b>0.7</b>	0.1	2	<b>1.1</b>	0.2	3
<u>CHP - chaperones</u>										
OE1737R	DnaK-type molecular chaperone Hsp70	<b>0.4</b>	0.1	4	<b>0.9</b>	0.3	3	<b>0.5</b>	0.1	3
<u>CIM - central intermediary metabolism</u>										
OE1500R	pyruvate, water dikinase (PEP synthase)	<b>0.4</b>	0.1	4	<b>0.9</b>	0.0	3	<b>0.2</b>	0.0	3
OE3195F	succinate-CoA ligase (ADP-forming) beta chain	<b>0.3</b>	0.2	4	<b>1.0</b>	0.2	3	<b>0.3</b>	0.0	3
OE3196F	succinate--CoA ligase (ADP-forming) alpha chain	<b>0.3</b>	0.1	4	<b>0.9</b>	0.0	3	<b>0.6</b>	0.5	3
OE3308F	malate dehydrogenase (oxaloacetate decarboxylating)	<b>0.4</b>	0.1	4	<b>0.9</b>	0.2	3	<b>0.7</b>	0.0	3
OE3634F	isocitrate dehydrogenase (NADP+)	<b>0.4</b>	0.1	4	<b>0.9</b>	0.2	2	<b>0.4</b>	0.0	3
OE4613F	aconitate hydratase	<b>0.3</b>	0.1	4	<b>0.7</b>	0.2	3	<b>0.5</b>	0.1	3
<u>COM - coenzyme metabolism</u>										
OE2057F	thiamin biosynthesis protein ThiC	<b>0.4</b>	0.1	4	<b>1.1</b>	0.1	3	<b>0.3</b>	0.0	3
OE3207F	probable precorrin-8W decarboxylase	<b>0.4</b>	0.1	4	<b>0.8</b>	0.1	3	<b>0.1</b>	0.0	3
OE3209F	probable precorrin-2 C20-methyltransferase	<b>0.4</b>	0.2	4	<b>0.8</b>	0.1	3	<b>0.2</b>	0.1	3
OE3524F	pyridoxine biosynthesis protein	<b>0.4</b>	0.1	4	<b>0.7</b>	0.2	3	<b>0.5</b>	0.0	3
<u>CP - cellular processes</u>										
OE1076F	cell division control protein Cdc6 homolog	<b>0.3</b>	0.1	4	<b>1.1</b>	0.3	2			0
OE1275F	proteasome alpha chain	<b>0.4</b>	0.1	4	<b>0.7</b>	0.1	2	<b>0.5</b>	0.1	3
OE1512R	segregation and condensation protein ScpA	<b>0.3</b>	0.1	4	<b>0.8</b>	0.0	2	<b>1.1</b>	0.1	3
OE1515R_a	structural-maintenance-of-chromosomes protein	<b>0.3</b>	0.2	4	<b>0.9</b>	0.1	2	<b>1.2</b>	0.2	3
OE1515R_b	structural-maintenance-of-chromosomes protein	<b>0.4</b>	0.2	4	<b>1.1</b>	0.3	2	<b>1.8</b>	0.1	3
OE1515R_c	structural-maintenance-of-chromosomes protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.3	2	<b>1.7</b>	0.1	3
OE1515R_d	structural-maintenance-of-chromosomes protein	<b>0.4</b>	0.2	4	<b>1.0</b>	0.1	2	<b>3.7</b>	1.9	3
OE1515R_e	structural-maintenance-of-chromosomes protein	<b>0.4</b>	0.2	4	<b>1.2</b>	0.3	2	<b>2.9</b>	1.0	3
OE1559R	cell division protein FtsZ1	<b>0.3</b>	0.1	4	<b>1.3</b>	0.5	2			0
OE2296F	proteasome beta chain	<b>0.4</b>	0.2	3	<b>0.8</b>	0.1	2	<b>0.8</b>	0.1	3
OE3693F	peptidylprolyl isomerase	<b>0.4</b>	0.1	4	<b>1.0</b>	0.1	3	<b>0.5</b>	0.2	3
OE3718F	cell division protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.1	3	<b>1.1</b>	0.2	3
OE4184F	cell division control protein Cdc6 homolog	<b>0.3</b>	0.1	4	<b>1.0</b>	0.1	2			0
OE5019F	cell division control protein Cdc6 homolog	<b>0.4</b>	0.2	4	<b>1.0</b>	0.1	3	<b>1.1</b>	0.1	3
OE5069F	cell division control protein Cdc6 C-terminal region homolog	<b>0.5</b>	0.1	4	<b>1.0</b>	0.1	2			0
OE5142F	cell division protein FtsZ5	<b>0.4</b>	0.1	4	<b>0.9</b>	0.0	3			0
OE5381F	cell division control protein Cdc6 homolog (pseudogene, N-terminal part, interrupted by frameshift)	<b>0.3</b>	0.1	4	<b>1.0</b>	0.2	3			0
OE6037R	cell division control protein Cdc6 homolog	<b>0.4</b>	0.1	4	<b>1.3</b>	0.6	2			0

OE7115F	cell division control protein Cdc6 homolog	<b>0.4</b>	0.2	4	<b>1.0</b>	0.0	2	<b>1.1</b>	0.2	3
<u>EM - energy metabolism</u>										
OE1979R	cytochrome-c oxidase chain I	<b>0.4</b>	0.1	4	<b>1.0</b>	0.2	3	<b>1.2</b>	0.2	3
OE3984R	H <sup>+</sup> -transporting two-sector ATPase chain B.a	<b>0.3</b>	0.1	4	<b>1.0</b>	0.1	3			0
OE3985R	H <sup>+</sup> -transporting two-sector ATPase chain A.a	<b>0.5</b>	0.1	4	<b>1.1</b>	0.3	3	<b>0.2</b>	0.0	3
OE3987R	H <sup>+</sup> -transporting two-sector ATPase chain C.a	<b>0.5</b>	0.2	4	<b>0.9</b>	0.1	3	<b>0.2</b>	0.1	3
OE3989R	H <sup>+</sup> -transporting two-sector ATPase chain K.a	<b>0.5</b>	0.1	4	<b>1.1</b>	0.1	3	<b>0.1</b>	0.0	3
OE7066F	cytochrome d ubiquinol oxidase chain II	<b>0.5</b>	0.2	4	<b>0.9</b>	0.1	2	<b>0.9</b>	0.3	3
OE7084F	thioredoxin	<b>0.3</b>	0.1	4	<b>0.9</b>	0.0	2	<b>0.9</b>	0.1	3
<u>ISH - transposases and ISH-encoded proteins</u>										
OE1058R	probable transposase (ISH1)	<b>0.5</b>	0.3	3	<b>0.9</b>	0.1	2			0
OE5062R	IS1341-type transposase (TCE31)	<b>0.4</b>	0.1	4	<b>1.2</b>	0.3	2	<b>0.6</b>	0.0	3
OE5063R	probable IS200-type transposase (TCE31)	<b>0.4</b>	0.1	3	<b>1.1</b>	0.4	2	<b>0.7</b>	0.1	3
OE5102R	probable IS1341-type transposase (ISH12)	<b>0.4</b>	0.3	4	<b>1.0</b>	0.2	3			0
OE5104R	probable IS200-type transposase (ISH12)	<b>0.5</b>	0.3	4	<b>1.0</b>	0.1	2	<b>1.3</b>	0.3	3
OE5180F	probable transposase (TCE33)	<b>0.5</b>	0.2	4	<b>0.9</b>	0.0	2			0
OE5233F	probable transposase (ISH5)	<b>0.4</b>	0.2	4	<b>1.0</b>	0.0	3	<b>0.9</b>	0.1	3
OE5260F	probable transposase (ISH10)	<b>0.4</b>	0.1	4	<b>1.1</b>	0.0	2			0
OE5338R	transposase homolog (ISH8/ISH26) (nonfunctional, C-terminal part, interrupted by ISH1)	<b>0.5</b>	0.2	4	<b>0.9</b>	0.1	3	<b>1.1</b>	0.3	3
OE5339R	probable transposase (ISH1)	<b>0.4</b>	0.1	4	<b>0.8</b>	0.2	2	<b>1.1</b>	0.2	3
OE5393F	insertion element protein (ISH2)	<b>0.4</b>	0.1	4	<b>1.2</b>	0.3	2			0
OE5407F	probable transposase (ISH8/ISH26)	<b>0.4</b>	0.1	4	<b>1.1</b>	0.1	2	<b>1.2</b>	0.3	3
OE5418F	insertion element protein (ISH2)	<b>0.4</b>	0.1	4	<b>1.1</b>	0.3	2	<b>0.7</b>	0.2	3
OE6012F	probable transposase (ISH6/ISHS1)	<b>0.4</b>	0.1	4	<b>1.2</b>	0.2	2			0
OE6075R	probable transposase (ISH8/ISH26)	<b>0.5</b>	0.2	4	<b>0.9</b>	0.2	3			0
OE6089R	IS1341-type transposase (TCE32)	<b>0.5</b>	0.2	4	<b>1.0</b>	0.2	3	<b>0.7</b>	0.1	3
OE6126R	insertion element protein (ISH2)	<b>0.4</b>	0.1	4	<b>1.0</b>	0.1	3	<b>0.9</b>	0.2	3
OE6133R	probable transposase (ISH10)	<b>0.5</b>	0.2	4	<b>0.9</b>	0.1	2	<b>1.1</b>	0.3	3
OE6165R	probable transposase (ISH3/ISH27)	<b>0.3</b>	0.1	4	<b>1.0</b>	0.1	3			0
OE6277R	transposase homolog (TCE33) (nonfunctional, N-terminal part)	<b>0.3</b>	0.1	4	<b>0.9</b>	0.1	2	<b>0.7</b>	0.1	3
OE6296R	probable transposase (ISH8/ISH26)	<b>0.5</b>	0.3	3	<b>0.9</b>	0.2	2	<b>1.4</b>	0.3	3
OE6353F	insertion element protein (ISH2)	<b>0.4</b>	0.1	4	<b>1.0</b>	0.2	2	<b>0.9</b>	0.2	3
OE7006R	probable transposase (ISH7/ISH24)	<b>0.4</b>	0.2	4	<b>1.0</b>	0.0	2	<b>1.0</b>	0.2	3
OE7019F	probable transposase (ISH8/ISH26)	<b>0.4</b>	0.1	4	<b>1.2</b>	0.5	2	<b>0.7</b>	0.1	3
OE7052F	probable transposase (ISH5)	<b>0.3</b>	0.1	4	<b>1.0</b>	0.2	2	<b>1.0</b>	0.1	3
OE7159R	probable transposase (ISH7/ISH24)	<b>0.4</b>	0.1	4	<b>1.0</b>	0.1	2	<b>1.1</b>	0.3	3
OE7170R_a	probable transposase (ISH4/ISH23/ISH50)	<b>0.4</b>	0.1	4	<b>0.9</b>	0.2	2			0
OE7170R_b	probable transposase (ISH4/ISH23/ISH50)	<b>0.4</b>	0.2	4	<b>1.0</b>	0.3	2	<b>0.6</b>	0.1	3
<u>LIP - lipid metabolism</u>										
OE4500R	probable acyl/butyryl-CoA dehydrogenase	<b>0.4</b>	0.2	4	<b>0.9</b>	0.0	2	<b>0.5</b>	0.1	3
OE7093R	isopentenyl-diphosphate delta-isomerase	<b>0.3</b>	0.1	4	<b>1.2</b>	0.5	2	<b>0.8</b>	0.1	2
<u>MIS - miscellaneous</u>										
OE2378R	ParA domain protein (fla operon protein ParA1)	<b>0.4</b>	0.1	4	<b>1.0</b>	0.3	2	<b>0.5</b>		1
OE2386R	p-nitrophenylphosphatase homolog	<b>0.3</b>	0.1	4	<b>0.8</b>	0.1	2	<b>0.7</b>	0.2	2
OE2674R	rRNA (adenine-N6,N6-)-dimethyltransferase	<b>0.5</b>	0.1	4	<b>0.9</b>	0.2	2	<b>0.8</b>	0.2	3
OE2689F	fibrillarin	<b>0.4</b>	0.1	4	<b>0.9</b>	0.1	2			0
OE2853R	probable peptidylprolyl isomerase	<b>0.4</b>	0.2	4	<b>0.9</b>	0.1	3	<b>0.3</b>	0.0	3
OE3101R	bacterioopsin activator	<b>0.4</b>	0.1	4	<b>0.8</b>	0.1	3			0
OE3218F	cobalamin operon protein	<b>0.3</b>	0.1	4	<b>0.9</b>	0.2	3	<b>0.2</b>	0.1	3
OE3339R	AAA-type ATPase (transitional ATPase homolog)	<b>0.5</b>	0.2	4	<b>1.0</b>	0.2	2	<b>0.6</b>	0.1	2

OE3349F	coenzyme F420-quinone oxidoreductase 42K chain	<b>0.3</b>	0.1	4	<b>0.6</b>	0.1	2	<b>0.6</b>	0.1	3
OE3356F	AAA-type ATPase (transitional ATPase homolog)	<b>0.4</b>	0.1	4	<b>1.5</b>	0.4	2			0
OE3544F	probable oxidoreductase (ferredoxin reductase homolog)	<b>0.5</b>	0.1	4	<b>0.9</b>	0.1	3	<b>0.7</b>	0.1	3
OE3971R	ParA domain protein	<b>0.4</b>	0.1	4	<b>1.1</b>	0.2	2			0
OE4263F	conserved hem operon protein	<b>0.4</b>	0.1	4	<b>1.3</b>	0.4	2			0
OE4438F	leucyl aminopeptidase	<b>0.4</b>	0.2	4	<b>1.2</b>	0.2	3	<b>0.3</b>	0.1	3
OE4509F	nonhistone chromosomal protein	<b>0.4</b>	0.2	3	<b>0.8</b>	0.1	2	<b>0.9</b>	0.2	2
OE5094F	diaminobutyrate-pyruvate aminotransferase (siderophore biosynthesis protein)	<b>0.4</b>	0.2	4	<b>1.1</b>	0.1	2	<b>1.6</b>	0.3	3
OE5095F	L-2,4-diaminobutyrate decarboxylase (siderophore biosynthesis protein)	<b>0.5</b>	0.2	4	<b>0.9</b>	0.1	3	<b>1.4</b>	0.2	2
OE5096F	siderophore biosynthesis protein	<b>0.5</b>	0.1	4	<b>0.9</b>	0.1	2	<b>0.8</b>	0.2	3
OE5097F	siderophore biosynthesis protein (malonyl-CoA decarboxylase homolog)	<b>0.4</b>	0.2	4	<b>1.1</b>	0.3	2	<b>1.1</b>	0.1	3
OE5099F	siderophore biosynthesis protein	<b>0.5</b>	0.2	4	<b>0.9</b>	0.1	2			0
OE5112R	gas-vesicle operon protein GvpM2	<b>0.5</b>	0.2	4	<b>0.9</b>	0.1	3			0
OE5113R	gas-vesicle operon protein GvpL2	<b>0.5</b>	0.1	4	<b>1.0</b>	0.1	2	<b>0.9</b>	0.1	3
OE5114R	gas-vesicle operon protein GvpK2	<b>0.4</b>	0.2	4	<b>1.2</b>	0.0	3	<b>1.0</b>	0.2	3
OE5116R	gas-vesicle operon protein GvpJ2	<b>0.4</b>	0.2	4	<b>0.8</b>	0.1	2	<b>1.3</b>	0.4	3
OE5121R	gas-vesicle operon protein GvpG2	<b>0.4</b>	0.1	4	<b>0.9</b>	0.1	2	<b>0.7</b>	0.0	2
OE5123R	gas-vesicle operon protein GvpE2 (probable activator)	<b>0.5</b>	0.1	4	<b>0.9</b>	0.2	3	<b>1.0</b>	0.1	3
OE5125F	gas-vesicle protein GvpA2	<b>0.4</b>	0.2	4	<b>0.9</b>	0.1	3	<b>0.9</b>	0.1	3
OE5127F	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.0</b>	0.2	2	<b>0.7</b>	0.2	3
OE5128F	gas-vesicle operon protein GvpN2	<b>0.4</b>	0.2	4	<b>1.2</b>	0.5	2	<b>1.8</b>	0.4	3
OE5129F	gas-vesicle operon protein GvpO2	<b>0.5</b>	0.2	4	<b>0.8</b>	0.1	2			0
OE5186R	catalase (including: peroxidase)	<b>0.2</b>	0.1	4	<b>0.7</b>	0.1	3	<b>0.6</b>	0.1	3
OE5189F	probable acyl-CoA transferase (3-oxoacid CoA-transferase homolog)	<b>0.5</b>	0.1	4	<b>1.6</b>	0.2	2	<b>0.8</b>	0.1	3
OE5192R	alkaline phosphatase	<b>0.3</b>	0.1	4	<b>1.0</b>	0.0	3	<b>2.5</b>	0.4	3
OE5337R	probable ATP-dependent helicase (nonfunctional, C-terminal part, interrupted by ISH8)	<b>0.5</b>	0.2	4	<b>1.5</b>	0.3	2	<b>0.9</b>	0.0	3
OE5436R	probable arsenate reductase	<b>0.3</b>	0.1	4	<b>1.1</b>	0.2	2			0
OE6311F	AAA-type ATPase (transitional ATPase homolog)	<b>0.4</b>	0.1	4	<b>1.0</b>	0.2	2			0
OE7010R	ParA domain protein (nonfunctional, N-terminal part, interrupted by ISH7)	<b>0.4</b>	0.1	4	<b>1.0</b>	0.0	2			0
OE7024R	gas-vesicle operon protein GvpK1	<b>0.4</b>	0.2	4	<b>0.9</b>	0.1	2	<b>0.8</b>	0.0	3
OE7026R	gas-vesicle operon protein GvpJ1	<b>0.5</b>	0.2	4	<b>1.3</b>	0.3	2			0
OE7028R	gas-vesicle operon protein GvpH1	<b>0.5</b>	0.2	4	<b>0.9</b>	0.0	2	<b>0.9</b>	0.2	3
OE7036F_a	gas-vesicle protein GvpC1	<b>0.5</b>	0.2	4	<b>0.9</b>	0.1	2			0
OE7036F_b	gas-vesicle protein GvpC1	<b>0.4</b>	0.1	4	<b>0.8</b>	0.1	2			0
OE7037F	gas-vesicle operon protein GvpN	<b>0.4</b>	0.1	4	<b>1.3</b>	0.3	2			0
OE7038F	gas-vesicle operon protein GvpO1	<b>0.5</b>	0.2	4	<b>1.0</b>	0.2	2	<b>0.6</b>	0.0	3
<u>NUM - nucleotide metabolism</u>										
OE2667F	nucleoside-diphosphate kinase	<b>0.4</b>	0.1	4	<b>1.8</b>	0.9	2	<b>0.5</b>	0.1	3
OE5201F	aspartate carbamoyltransferase catalytic chain	<b>0.3</b>	0.1	4	<b>1.1</b>	0.4	2	<b>0.2</b>	0.1	2
OE5202F	aspartate carbamoyltransferase regulatory chain	<b>0.2</b>	0.1	4	<b>1.0</b>	0.3	2	<b>0.2</b>	0.0	3
<u>REG - gene regulation</u>										
OE5209R	transcription regulator ArcR	<b>0.4</b>	0.2	4	<b>0.8</b>	0.2	3	<b>1.2</b>	0.1	3
OE5443F	probable transcription regulator	<b>0.4</b>	0.2	4	<b>1.0</b>	0.2	2	<b>0.7</b>	0.1	3
<u>RRR - replication, repair, recombination</u>										
OE4282F	single-stranded-DNA-specific exonuclease	<b>0.4</b>	0.1	4	<b>1.1</b>	0.3	2	<b>0.7</b>	0.0	3
OE4293R	DNA-directed DNA-polymerase type III chain 2 (intein-containing)	<b>0.4</b>	0.1	4	<b>0.9</b>	0.0	2			0
OE4466R	DNA repair protein	<b>0.3</b>	0.1	4	<b>0.6</b>	0.2	3	<b>0.4</b>	0.1	3

OE6036F_a	probable DNA-directed DNA polymerase type II	<b>0.4</b>	0.2	4	<b>1.1</b>	0.1	2			0
OE6036F_b	probable DNA-directed DNA polymerase type II	<b>0.5</b>	0.2	4	<b>1.1</b>	0.3	2	<b>1.0</b>	0.1	3
OE7114F	probable DNA-directed DNA polymerase type II	<b>0.5</b>	0.3	3	<b>0.9</b>	0.1	3			0
OE7194F	plasmid replication protein RepJ	<b>0.4</b>	0.1	4	<b>1.4</b>	0.2	2			0
<u>SEC - protein secretion</u>										
OE1347R	type II secretion system protein GspE1	<b>0.5</b>	0.2	4	<b>1.0</b>	0.2	2	<b>0.8</b>	0.1	3
OE4450R	signal recognition particle 54K protein	<b>0.3</b>	0.1	4	<b>1.0</b>	0.2	2	<b>0.7</b>	0.3	2
<u>SIG - signal transduction</u>										
OE1536R	transducer protein Htr14	<b>0.4</b>	0.1	4	<b>1.0</b>	0.1	2	<b>1.1</b>		1
OE2195F	transducer protein Htr18	<b>0.4</b>	0.1	4	<b>0.9</b>	0.2	3	<b>0.6</b>	0.2	3
OE2406R	protein-glutamate O-methyltransferase CheR	<b>0.4</b>	0.1	4	<b>1.3</b>	0.5	2			0
OE2415R	taxis sensor histidine kinase CheA	<b>0.2</b>	0.1	4	<b>0.6</b>	0.1	3	<b>0.5</b>	0.1	3
OE2416R	protein-glutamate methylesterase CheB	<b>0.3</b>	0.1	4	<b>0.7</b>	0.3	2	<b>0.5</b>	0.0	3
OE2474R	transducer protein HtrXIII	<b>0.4</b>	0.2	4	<b>0.9</b>	0.1	2	<b>0.6</b>	0.1	3
OE2996R	transducer protein Htr9 (HtpIII)	<b>0.5</b>	0.3	3	<b>0.9</b>	0.1	3			0
OE3070R	transducer protein HtrXII	<b>0.4</b>	0.2	4	<b>1.0</b>	0.2	3	<b>0.6</b>	0.1	3
OE3150R_a	transducer protein HemAT	<b>0.4</b>	0.1	4	<b>1.2</b>	0.1	2	<b>0.9</b>	0.0	3
OE3150R_b	transducer protein HemAT	<b>0.4</b>	0.1	4	<b>1.0</b>	0.1	2	<b>0.6</b>	0.1	3
OE3167F_a	transducer protein HtrVIII	<b>0.4</b>	0.2	4	<b>1.0</b>	0.1	3	<b>0.7</b>	0.1	3
OE3167F_b	transducer protein HtrVIII	<b>0.4</b>	0.2	4	<b>1.1</b>	0.3	2	<b>0.7</b>	0.1	3
OE3347F	Transducer protein HtrI	<b>0.3</b>	0.1	4	<b>1.0</b>	0.1	3			0
OE3436R_a	transducer protein Htr17	<b>0.5</b>	0.1	4	<b>1.2</b>	0.2	3	<b>0.8</b>	0.2	3
OE3436R_b	transducer protein Htr17	<b>0.4</b>	0.1	4	<b>1.0</b>	0.2	2			0
OE3473F	transducer protein HtrVII	<b>0.4</b>	0.0	4	<b>1.4</b>	0.8	2	<b>1.1</b>	0.2	3
OE3474R	transducer protein CosT	<b>0.5</b>	0.2	4	<b>1.1</b>	0.2	3	<b>0.7</b>	0.1	3
OE3481R_a	transducer protein HtrII	<b>0.3</b>	0.1	4	<b>2.0</b>	1.4	3			0
OE3481R_b	transducer protein HtrII	<b>0.4</b>	0.1	4	<b>0.9</b>	0.3	3	<b>0.7</b>	0.0	2
OE3611R_a	transducer protein BasT	<b>0.4</b>	0.2	4	<b>1.0</b>	0.2	2	<b>0.6</b>	0.1	2
OE3611R_b	transducer protein BasT	<b>0.5</b>	0.1	3	<b>1.0</b>	0.4	2	<b>0.7</b>	0.1	2
OE5243F_a	transducer protein Car	<b>0.3</b>	0.2	4	<b>0.7</b>	0.1	2	<b>0.4</b>	0.1	3
OE5243F_b	transducer protein Car	<b>0.4</b>	0.1	4	<b>1.0</b>	0.2	2	<b>0.8</b>	0.0	3
OE7042R	probable signal-transducing histidine kinase / response regulator	<b>0.5</b>	0.1	4	<b>0.9</b>	0.2	2	<b>0.9</b>	0.2	2
<u>TC - transcription</u>										
OE2631F	DNA-directed RNA polymerase chain D	<b>0.4</b>	0.2	4	<b>0.9</b>	0.0	3	<b>0.3</b>	0.1	3
OE2637F	DNA-directed RNA polymerase chain N	<b>0.3</b>	0.1	4	<b>0.8</b>	0.1	3			0
OE4146F	TATA-binding transcription initiation factor	<b>0.3</b>	0.1	4	<b>1.0</b>	0.3	2	<b>0.6</b>	0.1	3
OE4740R	DNA-directed RNA polymerase chain A'	<b>0.2</b>	0.0	3	<b>0.7</b>	0.1	3	<b>0.4</b>	0.1	3
OE4743R	DNA-directed RNA polymerase chain H	<b>0.4</b>	0.1	4	<b>0.7</b>	0.2	3	<b>0.3</b>	0.0	3
OE6026R	transcription initiation factor TFB	<b>0.4</b>	0.1	4	<b>1.4</b>	0.2	2			0
OE6071R	transcription initiation factor TFB	<b>0.4</b>	0.1	4	<b>1.2</b>	0.5	2			0
OE6127F	TATA-binding transcription initiation factor (nonfunctional, C-terminal part, interrupted by ISH2)	<b>0.4</b>	0.3	3	<b>0.9</b>	0.2	2	<b>0.9</b>	0.2	2
OE6140R	transcription initiation factor TFB	<b>0.4</b>	0.1	4	<b>1.0</b>	0.1	2	<b>1.2</b>	0.3	3
OE7059R_a	TATA-binding transcription initiation factor (nonfunctional, C-terminal part, interrupted by ISH2)	<b>0.3</b>	0.1	4	<b>0.9</b>	0.1	2	<b>0.8</b>	0.1	3
OE7059R_b	TATA-binding transcription initiation factor (nonfunctional, C-terminal part, interrupted by ISH2)	<b>0.4</b>	0.2	4	<b>1.1</b>	0.1	2	<b>0.9</b>	0.2	3
OE7062R	TATA-binding transcription initiation factor (nonfunctional, N-terminal part, interrupted by ISH2)	<b>0.4</b>	0.2	4	<b>0.9</b>	0.1	3	<b>0.7</b>	0.1	3
OE7146R	transcription initiation factor TFB (nonfunctional, C-terminal part, interrupted by ISH8)	<b>0.5</b>	0.1	4	<b>0.9</b>	0.1	2			0
OE7214R	TATA-binding transcription initiation factor	<b>0.4</b>	0.2	4	<b>1.0</b>	0.3	2	<b>0.7</b>	0.0	2

TL - translation

OE1821R	ribosomal protein L36a.eR (HLA)	<b>0.3</b>	0.1	4	<b>0.7</b>	0.3	3			0
OE2165R	ribosomal protein S15	<b>0.4</b>	0.1	4	<b>1.2</b>	0.1	2	<b>0.2</b>	0.1	3
OE2600R	ribosomal protein L12	<b>0.3</b>	0.0	4	<b>0.9</b>	0.2	3			0
OE2601R	ribosomal protein L10	<b>0.4</b>	0.2	4	<b>1.0</b>	0.2	3	<b>0.2</b>	0.0	3
OE2602R	ribosomal protein L1	<b>0.4</b>	0.2	4	<b>1.0</b>	0.0	3	<b>0.2</b>	0.1	3
OE2629F	ribosomal protein S11	<b>0.2</b>	0.1	4	<b>1.0</b>	0.7	2	<b>0.2</b>	0.0	3
OE2632F	ribosomal protein L18.eR	<b>0.5</b>	0.2	4	<b>0.9</b>	0.2	3	<b>0.2</b>	0.0	3
OE2641F	ribosomal protein S2	<b>0.4</b>	0.1	4	<b>0.9</b>	0.1	3	<b>0.2</b>	0.0	3
OE2664F	ribosomal protein S28.eR	<b>0.4</b>	0.1	4	<b>1.1</b>	0.2	3	<b>0.5</b>	0.1	3
OE3388F	ribosomal protein L3	<b>0.4</b>	0.0	4	<b>1.0</b>	0.3	3			0
OE3392F	ribosomal protein L2	<b>0.3</b>	0.0	4	<b>0.9</b>	0.2	3	<b>0.2</b>	0.1	3
OE3393F	ribosomal protein S19	<b>0.2</b>	0.0	4	<b>1.0</b>	0.1	3	<b>0.2</b>	0.1	3
OE3394F	ribosomal protein L22	<b>0.2</b>	0.0	4	<b>1.2</b>	0.2	2	<b>0.2</b>	0.0	3
OE3395F	ribosomal protein S3	<b>0.4</b>	0.2	4	<b>0.8</b>	0.1	3	<b>0.1</b>	0.0	3
OE3396F	ribosomal protein L29	<b>0.3</b>	0.1	4	<b>1.1</b>	0.1	3	<b>0.3</b>	0.0	3
OE3402F	ribosomal protein L14	<b>0.3</b>	0.1	4	<b>0.9</b>	0.2	3	<b>0.2</b>	0.1	3
OE3404F	ribosomal protein L24	<b>0.4</b>	0.1	4	<b>1.1</b>	0.2	2			0
OE3405F	ribosomal protein S4.eR	<b>0.4</b>	0.1	4	<b>1.0</b>	0.4	2	<b>0.1</b>	0.0	2
OE3411F	ribosomal protein L6	<b>0.2</b>	0.0	4	<b>0.9</b>	0.2	2	<b>0.1</b>	0.0	3
OE3412F	ribosomal protein L32.eR	<b>0.2</b>	0.0	4	<b>1.0</b>	0.2	2	<b>0.2</b>	0.1	3
OE3413F	ribosomal protein L19.eR	<b>0.3</b>	0.1	4	<b>1.0</b>	0.0	2	<b>0.2</b>	0.1	3
OE3414F	ribosomal protein L18	<b>0.4</b>	0.2	4	<b>1.0</b>	0.1	3	<b>0.2</b>	0.0	3
OE3416F	ribosomal protein L30	<b>0.2</b>	0.1	4	<b>1.1</b>	0.1	2	<b>0.3</b>	0.0	3
OE3487R	translation initiation factor aIF-5A	<b>0.4</b>	0.1	4	<b>1.0</b>	0.2	3	<b>0.4</b>	0.0	3
OE4459R	ribosomal protein L31.eR	<b>0.4</b>	0.1	4	<b>0.9</b>	0.1	3			0
OE4460R	ribosomal protein L39.eR	<b>0.3</b>	0.1	3	<b>0.9</b>	0.2	3	<b>0.3</b>	0.1	3
OE4721R	translation elongation factor aEF-1 alpha chain	<b>0.3</b>	0.1	4	<b>0.5</b>	0.1	3	<b>0.2</b>	0.0	3
OE4736R	ribosomal protein S12	<b>0.4</b>	0.1	4	<b>0.9</b>	0.3	2	<b>0.3</b>	0.0	3
OE5203F	arginine-tRNA ligase	<b>0.3</b>	0.2	3	<b>0.7</b>	0.1	3	<b>0.8</b>	0.2	3

TP - small molecule transport

OE3910R	probable ABC-type transport system periplasmic substrate-binding protein	<b>0.3</b>	0.1	4	<b>1.0</b>	0.0	2	<b>0.4</b>	0.2	3
OE4301R	ABC-type transport system ATP-binding protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.1	3	<b>0.2</b>	0.0	3
OE4302R	ABC-type oligopeptide transport system ATP-binding protein	<b>0.4</b>	0.2	4	<b>1.1</b>	0.2	2	<b>0.1</b>	0.0	3
OE5101R	probable cationic amino acid transport protein	<b>0.5</b>	0.2	4	<b>1.5</b>	0.1	2	<b>0.7</b>	0.0	3
OE5132F	probable phosphate transport protein	<b>0.4</b>	0.1	4	<b>1.1</b>	0.1	2			0
OE5146R	ABC-type transport system ATP-binding protein	<b>0.5</b>	0.1	4	<b>1.6</b>	0.4	2			0
OE5147R	probable ABC-type transport system periplasmic substrate-binding protein	<b>0.4</b>	0.1	4	<b>1.1</b>	0.1	2			0
OE5168F	probable ABC-type transport system permease protein (sugar / sn-glycerol-3-phosphate transport protein)	<b>0.5</b>	0.2	4	<b>0.9</b>	0.2	2	<b>4.6</b>	1.9	3
OE5204R	probable Na <sup>+</sup> /H <sup>+</sup> -exchanging protein	<b>0.5</b>	0.1	4	<b>1.0</b>	0.2	3	<b>0.5</b>	0.0	3
OE5223R	ABC-type transport system ATP-binding protein (nonfunctional, C-terminal part, interrupted by ISH3)	<b>0.4</b>	0.2	4	<b>0.9</b>	0.1	3	<b>1.0</b>	0.1	3
OE5245F	ABC-type transport system ATP-binding protein	<b>0.4</b>	0.2	4	<b>1.0</b>	0.2	2	<b>0.7</b>	0.1	3
OE5255R	probable transport protein	<b>0.4</b>	0.2	4	<b>1.0</b>	0.1	2	<b>0.9</b>	0.1	3
OE5264F	ABC-type transport system ATP-binding protein	<b>0.4</b>	0.1	4	<b>1.2</b>	0.3	2			0
OE5268R	ABC-type transport system ATP-binding protein	<b>0.3</b>	0.1	4	<b>1.1</b>	0.1	3	<b>0.8</b>	0.1	3
OE5270R	ABC-type transport system permease protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.0	2	<b>0.8</b>	0.2	3
OE5272R	ABC-type transport system permease protein	<b>0.4</b>	0.2	4	<b>1.0</b>	0.0	2	<b>1.0</b>	0.1	3
OE5273R	ABC-type transport system periplasmic substrate-	<b>0.4</b>	0.2	4	<b>1.0</b>	0.0	2	<b>0.6</b>	0.1	3

binding protein										
OE5307F	ABC-type transport system ATP-binding protein	<b>0.4</b>	0.1	4	<b>1.1</b>	0.2	2	<b>0.6</b>	0.0	3
<u>CHY - conserved hypothetical protein, HY - hypothetical protein, NOF - no function assigned to experimentally identified protein</u>										
OE1231R	hypothetical protein	<b>0.5</b>	0.2	4	<b>1.0</b>	0.2	2	<b>0.7</b>	0.1	3
OE1293F	hypothetical protein (overlaps real protein)	<b>0.4</b>	0.2	4	<b>0.9</b>	0.1	2			0
OE1564R	Na <sup>+</sup> /Ca <sup>2+</sup> -exchanging protein homolog	<b>0.4</b>	0.2	4	<b>1.3</b>	0.5	2	<b>0.8</b>	0.1	3
OE2027F	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.3</b>	0.2	2	<b>0.8</b>	0.1	3
OE2044F	conserved hypothetical protein	<b>0.4</b>	0.2	4	<b>1.2</b>	0.6	2	<b>0.7</b>	0.1	3
OE2120F	conserved hypothetical protein	<b>0.3</b>	0.1	4	<b>1.3</b>	0.3	2	<b>0.7</b>	0.2	3
OE2160R	hypothetical protein	<b>0.3</b>	0.1	4	<b>0.8</b>	0.2	3	<b>0.3</b>	0.1	3
OE3050F	conserved hypothetical protein	<b>0.4</b>	0.2	4	<b>1.1</b>	0.1	2	<b>0.8</b>	0.1	3
OE3075R	hypothetical protein	<b>0.5</b>	0.2	4	<b>1.0</b>	0.2	2	<b>0.8</b>	0.1	3
OE3367F	DnaJ N-terminal domain protein	<b>0.4</b>	0.1	4	<b>1.3</b>	0.1	2	<b>0.7</b>	0.1	2
OE3398F	conserved hypothetical protein	<b>0.2</b>	0.0	4	<b>1.0</b>	0.2	2	<b>0.1</b>	0.0	3
OE3617F	conserved hypothetical protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.3	2	<b>1.0</b>	0.3	2
OE3815R	conserved hypothetical protein	<b>0.5</b>	0.1	4	<b>1.0</b>	0.2	3			0
OE4027F	conserved hypothetical protein	<b>0.4</b>	0.2	4	<b>1.0</b>	0.2	3	<b>0.8</b>	0.1	3
OE4393R	transport protein homolog	<b>0.4</b>	0.1	4	<b>1.3</b>	0.1	2	<b>0.5</b>	0.1	3
OE4627F	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.0</b>	0.3	2			0
OE4713R	conserved hypothetical protein	<b>0.5</b>	0.1	4	<b>1.0</b>	0.1	3	<b>1.2</b>	0.4	3
OE5018R	hypothetical protein	<b>0.5</b>	0.2	4	<b>0.9</b>	0.1	2	<b>0.8</b>	0.1	3
OE5022F	conserved hypothetical protein	<b>0.4</b>	0.2	4	<b>1.0</b>	0.0	2	<b>1.1</b>	0.2	3
OE5029R	hypothetical protein	<b>0.5</b>	0.2	4	<b>1.1</b>	0.3	2	<b>0.6</b>	0.0	3
OE5030R	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.5</b>	0.2	2			0
OE5031R	conserved hypothetical protein	<b>0.3</b>	0.1	4	<b>0.9</b>	0.1	3			0
OE5032R	hypothetical protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.2	3			0
OE5036F	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.0</b>	0.2	3	<b>1.2</b>	0.0	3
OE5039R	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.3</b>	0.0	2	<b>0.9</b>	0.0	3
OE5043R	conserved hypothetical protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.1	2	<b>1.1</b>	0.3	3
OE5048F	conserved hypothetical protein	<b>0.5</b>	0.1	4	<b>1.4</b>	0.3	2	<b>0.9</b>	0.1	3
OE5055F	cationic amino acid transport protein homolog	<b>0.4</b>	0.0	3	<b>1.2</b>	0.2	2	<b>1.1</b>	0.1	3
OE5065R	conserved hypothetical protein	<b>0.3</b>	0.1	3	<b>1.2</b>	0.1	2			0
OE5068F	conserved hypothetical protein	<b>0.5</b>	0.0	3	<b>1.1</b>	0.1	2	<b>1.8</b>	0.4	3
OE5070R	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.7</b>	0.2	2			0
OE5074R	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.1</b>	0.2	2	<b>0.9</b>	0.1	3
OE5076R	hypothetical protein	<b>0.4</b>	0.2	4	<b>1.0</b>	0.1	3	<b>0.8</b>	0.1	3
OE5078F	sodium-dependent phosphate transport protein homolog	<b>0.4</b>	0.1	4	<b>1.0</b>	0.1	2	<b>1.0</b>	0.1	3
OE5090F	hypothetical protein	<b>0.4</b>	0.1	4	<b>0.9</b>	0.0	2	<b>1.6</b>	0.3	3
OE5093F	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.0</b>	0.3	2	<b>0.8</b>	0.0	3
OE5106F	TrkA domain protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.1	2	<b>0.7</b>	0.0	3
OE5110F	conserved hypothetical protein	<b>0.5</b>	0.1	4	<b>1.4</b>	0.6	2	<b>1.2</b>	0.4	3
OE5130F	TrkA domain protein	<b>0.3</b>	0.1	4	<b>1.1</b>	0.0	3			0
OE5134F	probable transport protein	<b>0.5</b>	0.3	3	<b>1.3</b>	0.3	3	<b>0.9</b>	0.4	3
OE5138F	conserved hypothetical protein	<b>0.3</b>	0.1	4	<b>0.9</b>	0.1	3			0
OE5141R	conserved hypothetical protein	<b>0.3</b>	0.1	4	<b>0.9</b>	0.1	2	<b>0.8</b>	0.1	3
OE5157F	conserved hypothetical protein	<b>0.5</b>	0.2	4	<b>1.0</b>	0.2	2	<b>0.9</b>	0.2	3
OE5158F	hypothetical protein	<b>0.4</b>	0.1	4	<b>0.9</b>	0.0	3	<b>1.2</b>		1
OE5163R	hypothetical protein (overlaps a more likely protein)	<b>0.4</b>	0.2	4	<b>0.9</b>	0.1	3	<b>1.1</b>	0.6	3
OE5165R	hypothetical protein	<b>0.5</b>	0.1	4	<b>1.4</b>	0.4	2	<b>0.7</b>	0.0	3
OE5176R	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.0</b>	0.1	2	<b>0.7</b>	0.1	3

OE5178F	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.3</b>	0.2	2	<b>0.9</b>	0.1	3
OE5188F	protein kinase weak homolog	<b>0.4</b>	0.2	4	<b>1.0</b>	0.1	2	<b>1.4</b>	0.4	3
OE5190R	hydrogenase expression/formation protein homolog	<b>0.5</b>	0.2	4	<b>0.9</b>	0.1	2	<b>1.3</b>	0.2	3
OE5193F	hemolysin homolog	<b>0.5</b>	0.2	4	<b>1.3</b>	0.4	2	<b>1.1</b>	0.1	3
OE5198R	conserved hypothetical protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.1	2			0
OE5210F	hypothetical protein	<b>0.5</b>	0.2	4	<b>1.2</b>	0.1	2	<b>0.9</b>	0.1	3
OE5219F	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.1</b>	0.0	2	<b>1.4</b>	0.5	3
OE5222R	hypothetical protein	<b>0.5</b>	0.2	4	<b>0.9</b>	0.1	3			0
OE5235F	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.0</b>	0.3	2	<b>0.8</b>	0.0	3
OE5249F	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>0.9</b>	0.1	2			0
OE5254F	conserved hypothetical protein	<b>0.5</b>	0.2	4	<b>0.9</b>	0.1	3			0
OE5265F	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.3</b>	0.3	2	<b>1.0</b>	0.2	3
OE5286R	ATP-dependent RNA helicase homolog	<b>0.4</b>	0.2	3	<b>1.0</b>	0.2	2	<b>0.9</b>	0.2	2
OE5296F	hypothetical protein	<b>0.5</b>	0.2	4	<b>1.2</b>	0.1	2	<b>0.8</b>	0.1	3
OE5297F	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.5</b>	0.3	2			0
OE5303F	predicted orf	<b>0.5</b>	0.2	4	<b>0.8</b>	0.1	2	<b>0.8</b>	0.1	2
OE5308F	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.4</b>	0.3	2			0
OE5314F	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.1</b>	0.2	2	<b>0.9</b>	0.3	3
OE5315R	hypothetical protein	<b>0.5</b>	0.2	4	<b>0.9</b>	0.1	2	<b>0.8</b>	0.2	3
OE5325F	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.5</b>	0.3	2	<b>1.0</b>	0.2	3
OE5335R	nuclease chain B homolog	<b>0.5</b>	0.2	4	<b>1.0</b>	0.1	2	<b>0.8</b>	0.1	3
OE5345R	hypothetical protein	<b>0.4</b>	0.1	4	<b>0.9</b>	0.1	3	<b>0.9</b>	0.2	3
OE5349R	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.1</b>	0.2	2			0
OE5350R	conserved hypothetical protein	<b>0.3</b>	0.1	4	<b>1.1</b>	0.4	3			0
OE5360F	conserved hypothetical protein (nonfunctional, N-terminal part, interrupted by ISH3)	<b>0.3</b>	0.1	4	<b>0.9</b>	0.1	3	<b>0.7</b>	0.1	3
OE5361R	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.0</b>	0.2	2	<b>0.8</b>	0.0	2
OE5365R	conserved hypothetical protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.1	2	<b>0.7</b>	0.1	3
OE5366R	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.0</b>	0.2	2			0
OE5386R	deoxyhypusine synthase homolog (nonfunctional, central part)	<b>0.5</b>	0.3	4	<b>0.9</b>	0.1	2	<b>1.0</b>	0.2	3
OE5389F	conserved hypothetical protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.3	2	<b>0.9</b>	0.1	3
OE5391F	conserved hypothetical protein	<b>0.5</b>	0.2	4	<b>1.0</b>	0.2	2	<b>1.1</b>	0.1	3
OE5394R	conserved hypothetical protein (nonfunctional, N-terminal part, interrupted by ISH2)	<b>0.4</b>	0.2	4	<b>0.9</b>	0.1	2	<b>0.8</b>	0.0	3
OE5396R	hypothetical protein	<b>0.4</b>	0.1	4	<b>0.8</b>	0.0	3	<b>0.8</b>	0.1	3
OE5399R	hypothetical protein	<b>0.4</b>	0.2	4	<b>1.0</b>	0.3	2	<b>0.7</b>	0.0	3
OE5404F	hypothetical protein	<b>0.3</b>	0.1	4	<b>0.9</b>	0.1	3			0
OE5405F	hypothetical protein	<b>0.5</b>	0.2	4	<b>0.9</b>	0.2	2	<b>0.7</b>	0.1	3
OE5413F	conserved hypothetical protein	<b>0.5</b>	0.2	4	<b>0.9</b>	0.0	2	<b>1.2</b>	0.2	3
OE5417R	conserved hypothetical protein	<b>0.5</b>	0.1	4	<b>1.3</b>	0.3	2			0
OE5430F	hypothetical protein	<b>0.5</b>	0.1	3	<b>0.9</b>	0.0	2	<b>0.7</b>	0.0	3
OE5434R	conserved hypothetical protein	<b>0.5</b>	0.2	4	<b>0.9</b>	0.1	2	<b>0.8</b>	0.1	3
OE5444F	probable methyltransferase (phosphatidylethanolamine N-methyltransferase homolog)	<b>0.4</b>	0.1	4	<b>0.9</b>	0.2	2	<b>0.6</b>	0.0	3
OE6002R	hypothetical protein	<b>0.4</b>	0.1	4	<b>0.9</b>	0.2	2			0
OE6005R	hypothetical protein	<b>0.5</b>	0.2	4	<b>1.1</b>	0.3	3			0
OE6008R_a	ParA domain protein	<b>0.4</b>	0.2	4	<b>1.0</b>	0.0	2	<b>0.8</b>	0.1	3
OE6008R_b	ParA domain protein	<b>0.3</b>	0.1	4	<b>1.0</b>	0.1	3			0
OE6010F	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.5</b>	0.7	2	<b>0.7</b>	0.1	3
OE6020R	hypothetical protein	<b>0.5</b>	0.3	3	<b>1.0</b>	0.2	2	<b>1.0</b>	0.2	3
OE6022R	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.0</b>	0.2	2	<b>0.7</b>	0.1	3

OE6023R	conserved hypothetical protein	<b>0.5</b>	0.1	2	<b>1.3</b>	0.4	2			0
OE6027R	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.4</b>	0.4	2			0
OE6032F	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.2</b>	0.4	2	<b>1.3</b>	0.3	3
OE6038R	hypothetical protein	<b>0.5</b>	0.2	4	<b>0.9</b>	0.2	3	<b>1.3</b>	0.2	3
OE6049R	conserved hypothetical protein	<b>0.5</b>	0.2	4	<b>0.9</b>	0.2	2	<b>1.1</b>	0.1	3
OE6051F	conserved hypothetical protein	<b>0.5</b>	0.2	4	<b>0.9</b>	0.2	2	<b>1.2</b>	0.2	3
OE6052R	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.2</b>	0.3	2			0
OE6066R	hypothetical protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.1	3	<b>0.9</b>	0.3	3
OE6069R	conserved hypothetical protein	<b>0.5</b>	0.1	4	<b>1.1</b>	0.0	2	<b>0.7</b>	0.1	3
OE6073R	conserved hypothetical protein	<b>0.5</b>	0.2	4	<b>1.2</b>	0.5	2	<b>0.7</b>	0.1	3
OE6083R	conserved hypothetical protein	<b>0.5</b>	0.1	4	<b>0.9</b>	0.2	2			0
OE6084R	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>0.9</b>	0.0	2	<b>0.7</b>	0.1	3
OE6088R	hypothetical protein	<b>0.4</b>	0.1	4	<b>0.9</b>	0.2	2	<b>0.6</b>	0.0	3
OE6092R	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.1</b>	0.2	2	<b>0.4</b>		1
OE6095R	conserved hypothetical protein	<b>0.5</b>	0.1	4	<b>1.2</b>	0.3	2	<b>0.6</b>	0.1	3
OE6097R	conserved hypothetical protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.1	3	<b>0.7</b>	0.1	3
OE6099F	hypothetical protein	<b>0.5</b>	0.2	4	<b>1.2</b>	0.1	2	<b>0.8</b>	0.1	3
OE6102R	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.0</b>	0.1	2	<b>0.9</b>	0.1	3
OE6104R	conserved hypothetical protein	<b>0.5</b>	0.1	4	<b>0.9</b>	0.2	2	<b>0.7</b>	0.1	3
OE6112F	hypothetical protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.2	2	<b>0.7</b>	0.0	2
OE6115F	conserved hypothetical protein	<b>0.5</b>	0.2	4	<b>0.9</b>	0.1	2	<b>0.8</b>	0.1	3
OE6118F	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.2</b>	0.4	2			0
OE6120F	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.0</b>	0.0	3	<b>0.8</b>	0.1	3
OE6121F	hypothetical protein	<b>0.5</b>	0.2	4	<b>0.9</b>	0.2	3	<b>0.6</b>	0.2	3
OE6128R	hypothetical protein	<b>0.5</b>	0.1	4	<b>1.1</b>	0.1	2	<b>0.8</b>		1
OE6138F	conserved hypothetical protein	<b>0.5</b>	0.2	4	<b>1.0</b>	0.3	2	<b>0.8</b>	0.1	3
OE6145R	signal-transducing histidine kinase homolog	<b>0.5</b>	0.1	4	<b>0.9</b>	0.2	2			0
OE6147R	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.1</b>	0.2	2	<b>0.9</b>	0.2	3
OE6150R	conserved hypothetical protein	<b>0.5</b>	0.2	4	<b>1.0</b>	0.0	2	<b>0.9</b>	0.2	3
OE6152R	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.1</b>	0.0	2	<b>0.6</b>	0.0	3
OE6154F	hypothetical protein	<b>0.3</b>	0.1	4	<b>1.0</b>	0.1	2	<b>0.8</b>	0.1	3
OE6161R	conserved hypothetical protein (nonfunctional, C-terminal part, interrupted by ISH3)	<b>0.4</b>	0.2	4	<b>1.0</b>	0.2	2	<b>0.8</b>	0.1	3
OE6170R	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.2</b>	0.4	2	<b>0.6</b>	0.1	3
OE6278R	protein kinase AfsK homolog	<b>0.4</b>	0.1	4	<b>1.2</b>	0.3	2			0
OE6280R	hypothetical protein	<b>0.5</b>	0.2	4	<b>1.0</b>	0.2	2	<b>0.9</b>	0.3	3
OE6301F	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.2</b>	0.5	2	<b>0.9</b>	0.1	3
OE6303F	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.1</b>	0.3	3	<b>0.8</b>	0.1	3
OE6315F	conserved hypothetical protein	<b>0.5</b>	0.1	4	<b>1.5</b>	0.6	2	<b>0.8</b>	0.0	2
OE6321R	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.0</b>	0.0	2			0
OE6323R	hypothetical protein	<b>0.4</b>	0.2	4	<b>1.0</b>	0.2	2	<b>0.8</b>		1
OE6329R	hypothetical protein	<b>0.5</b>	0.3	4	<b>0.9</b>	0.1	3	<b>0.9</b>	0.3	3
OE6340R	conserved hypothetical protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.0	2	<b>0.8</b>	0.1	3
OE6357F	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.2</b>	0.4	2	<b>0.7</b>	0.1	3
OE7001R	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.0</b>	0.1	3	<b>1.1</b>	0.2	3
OE7009F	conserved hypothetical protein (encoded by ISH7/ISH24 subtype 1)	<b>0.4</b>	0.1	4	<b>0.9</b>	0.1	3			0
OE7015F	conserved hypothetical protein (nonfunctional, N-terminal part, interrupted by ISH3)	<b>0.5</b>	0.2	4	<b>1.4</b>	0.6	2	<b>0.9</b>	0.2	3
OE7020F	hypothetical protein	<b>0.4</b>	0.3	3	<b>0.9</b>	0.2	2	<b>1.0</b>	0.3	3
OE7043R	predicted orf	<b>0.5</b>	0.1	4	<b>0.9</b>	0.2	2			0
OE7056F	predicted orf	<b>0.4</b>	0.1	4	<b>1.0</b>	0.2	2	<b>0.7</b>	0.1	3



OE7057F	conserved hypothetical protein	<b>0.5</b>	0.1	4	<b>1.6</b>	0.4	2	<b>0.7</b>	0.1	3
OE7064R	hypothetical protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.0	2	<b>0.9</b>	0.1	3
OE7070R	conserved hypothetical protein	<b>0.4</b>	0.2	4	<b>0.8</b>	0.1	2	<b>1.2</b>	0.2	3
OE7071F	conserved hypothetical protein	<b>0.4</b>	0.1	3	<b>1.1</b>	0.1	3	<b>1.1</b>	0.1	3
OE7075F	conserved hypothetical protein	<b>0.5</b>	0.2	4	<b>1.1</b>	0.1	2	<b>1.5</b>		1
OE7077F	conserved hypothetical protein	<b>0.4</b>	0.1	3	<b>0.8</b>	0.1	2	<b>1.8</b>	0.1	3
OE7089R	conserved hypothetical protein	<b>0.5</b>	0.2	4	<b>1.0</b>	0.2	2	<b>1.7</b>	0.6	2
OE7091F	hypothetical protein	<b>0.5</b>	0.2	4	<b>1.0</b>	0.3	2			0
OE7092F	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.7</b>	0.3	2	<b>1.6</b>		1
OE7099R	conserved hypothetical protein	<b>0.4</b>	0.2	4	<b>1.1</b>	0.2	2			0
OE7100R	ParA domain protein	<b>0.5</b>	0.1	2	<b>0.9</b>	0.2	3	<b>1.0</b>	0.0	2
OE7104R	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.2</b>	0.3	2	<b>0.9</b>	0.1	3
OE7106F	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.9</b>	0.3	2	<b>1.4</b>	0.4	3
OE7108R	conserved hypothetical protein	<b>0.5</b>	0.2	4	<b>0.9</b>	0.2	2	<b>1.2</b>	0.2	3
	(nonfunctional, C-terminal part, interrupted by ISH2)									
OE7111F	conserved hypothetical protein	<b>0.4</b>	0.2	4	<b>1.2</b>	0.1	2	<b>1.8</b>		1
OE7124R	hypothetical protein	<b>0.5</b>	0.2	4	<b>1.1</b>	0.1	2			0
OE7131R	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.3</b>	0.4	2			0
OE7135R	hypothetical protein	<b>0.3</b>	0.1	3	<b>1.1</b>	0.2	2			0
OE7139R	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.3</b>	0.3	2			0
OE7141R	multidrug resistance transport protein homolog	<b>0.4</b>	0.2	4	<b>1.0</b>	0.0	2	<b>1.1</b>	0.2	3
OE7145R	hypothetical protein	<b>0.4</b>	0.2	4	<b>1.0</b>	0.1	3	<b>0.9</b>	0.1	3
OE7148F	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.1</b>	0.1	2			0
	(nonfunctional, C-terminal part, interrupted by ISH8)									
OE7150R	conserved hypothetical protein	<b>0.5</b>	0.1	4	<b>0.9</b>	0.1	2	<b>1.5</b>		1
OE7152R	hypothetical protein	<b>0.5</b>	0.1	4	<b>1.1</b>	0.1	2	<b>1.2</b>	0.2	3
OE7154R	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.1</b>	0.0	2	<b>0.9</b>	0.0	3
OE7161R	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.4</b>	0.4	2	<b>1.2</b>	0.3	3
OE7164R	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.1</b>	0.2	2			0
OE7165R	hypothetical protein	<b>0.5</b>	0.3	4	<b>0.9</b>	0.1	3	<b>1.6</b>	0.3	3
OE7166F	conserved hypothetical protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.0	3	<b>1.0</b>	0.1	3
OE7167F	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.0</b>	0.0	3	<b>1.1</b>	0.1	3
OE7172F	hypothetical protein	<b>0.5</b>	0.1	4	<b>0.9</b>	0.1	2	<b>1.3</b>	0.0	3
OE7176R	helicase homolog	<b>0.4</b>	0.2	4	<b>1.2</b>	0.2	2	<b>1.7</b>	0.5	3
OE7177F	conserved hypothetical protein	<b>0.5</b>	0.2	4	<b>1.3</b>	0.2	2	<b>1.1</b>	0.2	3
OE7189F	conserved hypothetical protein	<b>0.3</b>	0.1	4	<b>0.9</b>	0.1	2	<b>0.8</b>	0.1	3
OE7190R	hypothetical protein	<b>0.5</b>	0.2	4	<b>0.9</b>	0.0	2	<b>1.6</b>	0.2	3
OE7191F	predicted orf	<b>0.4</b>	0.1	4	<b>1.0</b>	0.3	2	<b>0.7</b>	0.1	3
OE7192F	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.1</b>	0.1	2			0
OE7195R	predicted orf	<b>0.4</b>	0.2	4	<b>1.0</b>	0.1	3	<b>0.9</b>	0.1	3
OE7196F	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.2</b>	0.1	2			0
OE7209F	conserved hypothetical protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.2	2	<b>0.7</b>	0.1	3
OE7212R	hypothetical protein	<b>0.4</b>	0.1	4	<b>1.0</b>	0.1	2			0
OE7215F	conserved hypothetical protein	<b>0.4</b>	0.1	4	<b>1.3</b>	0.5	2			0
OE7216F	conserved hypothetical protein	<b>0.4</b>	0.2	4	<b>1.0</b>	0.1	2	<b>0.9</b>	0.1	3
OE7220F	hypothetical protein	<b>0.3</b>	0.2	2	<b>0.9</b>	0.1	2	<b>0.9</b>	0.1	3
OE7223F	conserved hypothetical protein	<b>0.3</b>	0.1	4	<b>1.1</b>	0.2	2	<b>0.6</b>	0.1	3
	(nonfunctional, N-terminal part, interrupted by ISH2)									
OE8007F	hypothetical protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.1	3	<b>1.3</b>	0.2	3
OE8047F	conserved hypothetical protein	<b>0.5</b>	0.2	4	<b>1.1</b>	0.1	2	<b>0.6</b>	0.1	3
OE8048F	conserved hypothetical protein	<b>0.4</b>	0.2	4	<b>0.9</b>	0.0	2	<b>1.2</b>	0.4	3
orf19a		<b>0.4</b>	0.2	3	<b>0.8</b>	0.1	3			0

1 <sup>\*1</sup>All genes are tabulated which have a “translational repression factor” of  $\leq 0.5$  differentially in  
2 exponential phase (lower part) or in stationary phase (one gene on top of the list). The translational  
3 repression factor is the quotient of free RNA to polysome-bound RNA (normalized to the average of all  
4 genes). If available, also the relative transcript levels of these genes are listed (Quotient stationary  
5 phase / exponential phase). ORF numbers and gene products were taken from the genome website  
6 [www.halolex.mpg.de](http://www.halolex.mpg.de). The columns  $\bar{x}$ , SD and n list average value, standard deviation and number of  
7 repetitions.