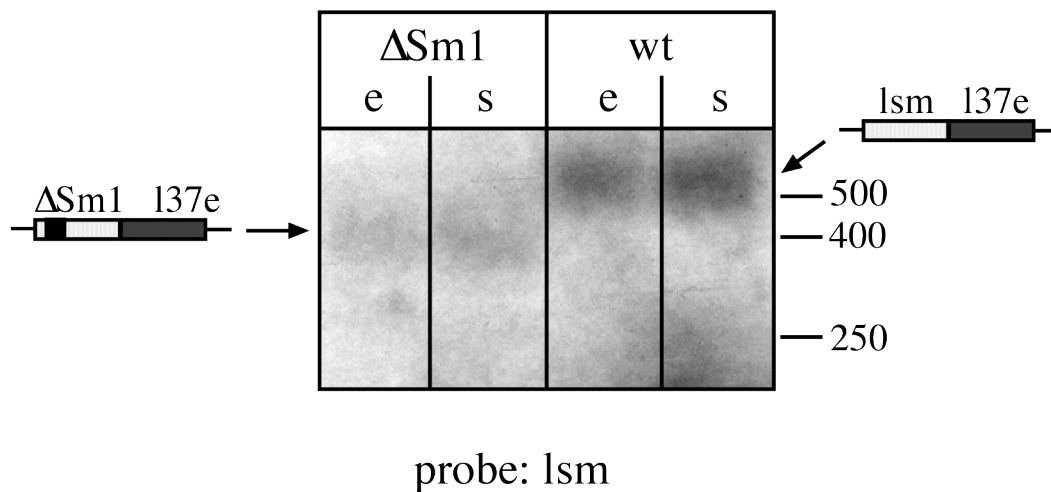


Supplemental Data



Supplementary Figure 1. Expression of the *lsm* and *rpI37R* genes. A Northern blot hybridised with a probe against the *lsm* mRNA shows that the *lsm* and *rpI37R* genes are expressed together as a dicistronic mRNA in exponential as well as stationary phase (lanes wt, RNA of about 500 nts) (see also Figure 2). The deletion strain Δ Sm1 generates a slightly shorter mRNA due to the deletion of the Sm1 domain. Lanes wt: RNA isolated from wild type *Haloferax* cells, lanes Δ Sm1: RNA isolated from the deletion strain; lanes e and s: RNA isolated from cells grown to exponential and stationary phase, respectively. The mRNAs are shown schematically at the sides, a size marker is shown at the right in nucleotides.

Supplementary Table 1. Overlap of *lsm* and *rpI37R* genes in archaeal genomes.

Column "organism": Archaeal organisms investigated for overlapping genes, column "overlap": if an overlap with the downstream *rpI37R* gene is present, this is indicated with "YES"; if not, it is indicated with "NO".

Organism	Overlap
<i>Haloferax_mediterranei</i> .ATCC_33500	YES
<i>Halogeometricum_borinquense</i> .DSM_11551	YES
<i>Haloquadratum_walsbyi</i> .DSM_16854	YES
<i>Haloquadratum_walsbyi</i> C23	YES
<i>Halorubrum_lacusprofundi</i> .ATCC_49239	YES
<i>Halopiger_xanaduensis</i> .SH-6	YES
<i>Natronobacterium_gregoryi</i> .SP2 DRAFT	YES
<i>Haloterrigena_turkmenica</i> .DSM_5511	YES
<i>Halobacterium_sp.</i> NRC-1	YES
<i>Halobacterium_salinarum</i> .R1	YES
<i>Natrialba_magadii</i> .ATCC_43099	YES
<i>Natrinema sp.</i> J7-2	YES
<i>Halomicrobium_mukohataei</i> .DSM_12286	YES
<i>Haladaptatus_paucihalophilus</i> .DX253	YES
<i>Haloarcula_hispanica</i> .ATCC_33960	YES
<i>Haloarcula_marismortui</i> .ATCC_43049 MPIB	YES
<i>Halalkalicoccus_jeotgali</i> .B3	YES
<i>Natronomonas_pharaonis</i> .DSM_2160	YES
<i>Methanosaeta_thermophila</i> .PT	NO
<i>Aciduliprofundum_boonei</i> .T469	NO
<i>Halorhabdus_utahensis</i> .DSM_12940	YES

Thermococcus_kodakaraensis.KOD1	NO
Archaeoglobus_profundus.DSM_5631	NO
Thermococcus_sibiricus.MM_739	NO
Methanocella_paludicola.SANAE	NO
Methanosarcina_mazei.Goe1	NO
Methanosarcina_acetivorans.C2A	NO
Methanospirillum_hungatei.JF-1	NO
Pyrococcus_horikoshii.OT3	NO
Pyrococcus_abyssi.GE5	NO
Methanosarcina_barkeri.fusaro	NO
Pyrococcus_furiosus.DSM_3638	NO
Halorhabdus_tiamatea.SARL4B	YES
Thermococcus_gammatolerans.EJ3	NO
Methanoculleus_marisnigri.JR1	NO
Thermococcus_onnurineus.NA1	NO
Methanococcoides_burtonii.DSM_6242	NO
Archaeoglobus_fulgidus.DSM4304	YES
Ferroglobus_placidus.DSM_10642	NO
Methanococcus_maripaludis.C6	NO
Thermoplasma_acidophilum.DSM_1728	YES
Methanobrevibacter_ruminantium.M1	NO
Methanococcus_vannielii.SB	NO
Methanobrevibacter_smithii.ATCC_35061	NO
Thermoplasma_volcanium.GSS1	YES

Supplementary Table 2. Transcripts down regulated in Δ Sm1
 Genes for ABC-type transport system proteins are highlighted in brown.

gene name	LOG ₂ (M)	protein
down regulated		
tsgC4 HVO_A0147	4,95	ABC-type transport system permease protein (probable substrate sugar)
tsgD4 HVO_A0148	4,89	ABC-type transport system periplasmic substrate-binding protein (probable substrate sugar)
tsgB4 HVO_A0146	4,47	ABC-type transport system permease protein (probable substrate sugar)
snp HVO_2723	3,81	snRNP homolog: Lsm
carB HVO_2361	3,71	carbamoyl-phosphate synthase, large subunit
tsgA4 HVO_A0145	3,47	ABC-type transport system ATP-binding protein (probable substrate sugar)
HVO_1116	3,47	hypothetical protein
cga2 HVO_A0149	3,30	glucan 14-alpha-glucosidase
HVO_1747	3,15	hypothetical protein
HVO_0489	3,14	hypothetical protein
carA HVO_2508	3,07	carbamoyl-phosphate synthase, small subunit
boa2 HVO_1117	3,05	bacterio-opsin activator-like protein
HVO_0488	2,77	hypothetical protein
HVO_2021	2,57	hypothetical protein
HVO_1115	2,54	hypothetical protein
trh7 HVO_2507	2,38	transcription regulator
HVO_A0534	2,37	hypothetical protein
HVO_0493	2,36	hypothetical protein
HVO_0799	2,31	hypothetical protein
HVO_A0192	2,30	Polysaccharide deacetylase domain protein
HVO_C0025	2,22	hypothetical protein
HVO_1860	2,15	hypothetical protein
HVO_A0366	2,15	hypothetical protein
HVO_2401	2,04	Glycine cleavage system P-protein
HVO_2395	1,97	ATP:cob(I)alamin adenosyltransferase, putative
znuC1 HVO_2398	1,95	ABC-type transport system ATP-binding protein (probable substrate zinc)
HVO_3031	1,89	tRNA-Gly; K14225 tRNA Gly
HVO_2608	1,86	Uvs037
znuA1 HVO_2397	1,83	ABC-type transport system periplasmic substrate-binding protein (probable substrate zinc)
qcrA HVO_2655	1,79	Rieske iron-sulfur protein

Supplementary Table 3. Transcripts up regulated in Δ Sm1

Motility related genes are highlighted in orange.

gene name	LOG ₂ (M)	protein
acd3 HVO_1199	-1,90	acyl-CoA dehydrogenase
HVO_B0346	-1,90	mandelate racemase
acd4 HVO_1373	-1,91	acyl-CoA dehydrogenase
flaD1 HVO_1203	-1,91	fla cluster protein FlaD1
gabT6 HVO_A=306	-1,92	4-aminobutyrate aminotransferase
HVO_2104	-1,92	presumptive arabinol PTS enzyme IIB
HVO_0404	-1,92	hypothetical protein
HVO_A0094	-1,93	transporter gate domain protein
HVO_B0094	-1,93	hypothetical protein
arcR21 HVO_B0320	-1,93	ArcR family transcription regulator
cheB HVO_1224	-1,93	protein-glutamate methyltransferase CheB
hbd2 HVO_A0097	-1,93	3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase
HVO_1426	-1,94	hypothetical protein
HVO_B0240	-1,95	hypothetical protein
HVO_A0222	-1,95	hypothetical protein
HVO_A0570	-1,95	D-hydantoinase, authentic frameshift; K01464 dihydropyrimidinase [EC:3.5.2.2]
arcR14 HVO_B0040	-1,96	ArcR family transcription regulator
HVO_0927	-1,96	hypothetical protein
HVO_B0086	-1,96	choline-sulfatase; K01133 choline-sulfatase [EC:3.1.6.6]
xloA HVO_2088	-1,97	xylosidase/arabinosidase
livH1 HVO_0900	-1,97	ABC-type transport system permease protein (probable substrate branched-chain amino acids)
HVO_2935	-1,97	hypothetical protein
HVO_0834	-1,97	hypothetical protein; K07068
tsgD8 HVO_B0109	-1,98	ABC-type transport system ATP-binding protein (probable substrate sugar)
HVO_A0203	-1,98	hypothetical protein
acs3 HVO_1236	-1,99	acyl-CoA synthetase
HVO_2323	-2,01	hypothetical protein
HVO_0746	-2,01	hypothetical protein
HVO_A0566	-2,01	3-isopropylmalate dehydratase small subunit 2
HVO_A0099	-2,01	probable transposase (homolog to transposon ISSod10 OrfB)
HVO_2277	-2,01	hypothetical protein
aroD HVO_0603	-2,01	3-dehydroquinate dehydratase
HVO_0898	-2,01	hypothetical protein
HVO_A0078	-2,01	helicase, SNF2/RAD54 family, putative
HVO_1644	-2,01	hypothetical protein

HVO_1321	-2,01	hypothetical protein
tsgD13 HVO_B0316	-2,01	ABC-type transport system ATP-binding protein (probable substrate glucose)
HVO_0376	-2,01	hypothetical protein
dppD15 HVO_B0331	-2,01	dppD15; peptide ABC transporter ATP-binding protein; K02031 peptide/nickel transport system ATP-binding protein
HVO_0613	-2,01	metallo-beta-lactamase superfamily, putative
HVO_2940	-2,03	hypothetical protein
HVO_A0289	-2,04	endoribonuclease L-PSP, putative
HVO_B0347	-2,04	glucose-fructose oxidoreductase, putative
HVO_B0300	-2,04	Uricase
HVO_A0095	-2,05	amidohydrolase
HVO_B0113	-2,06	Luciferase-like monooxygenase superfamily
HVO_A0323	-2,07	ABC-type transport system ATP-binding protein
dppC12 HVO_B0091	-2,07	ABC-type transport system permease protein (probable substrate dipeptides/oligopeptides)
HVO_B0215	-2,08	probable secreted glycosyl hydrolase
tsgB2 HVO_2116	-2,10	ABC-type transport system permease protein (probable substrate sugar)
orf5 HVO_A0539	-2,10	CopG family ribbon-helix-helix transcription regulator
HVO_B0038 A	-2,11	D-xylonate dehydratase
dppB12 HVO_B0092	-2,12	ABC-type transport system permease protein (probable substrate dipeptides/oligopeptides)
tsgC8 HVO_B0108	-2,12	ABC-type transport system permease protein (probable substrate sugar)
HVO_B0308	-2,12	dehydrogenase; K03518 carbon-monoxide dehydrogenase small subunit [EC:1.2.99.2]
HVO_C0010	-2,12	hypothetical protein
HVO_A0430 A	-2,14	hypothetical protein
HVO_1619	-2,15	hypothetical protein
tsgA5 HVO_A0283	-2,15	ABC-type transport system periplasmic substrate-binding protein (probable substrate sugar)
HVO_B0213	-2,15	myo-inositol-1-phosphate synthase
flaF HVO_1214	-2,16	fla cluster protein FlaF
HVO_0241	-2,16	hypothetical protein
arsB2b HVO_0411	-2,16	arsenite transport protein C-terminal domain protein
HVO_A0286	-2,16	hypothetical protein
pilB1 HVO_620	-2,19	type IV pilus biogenesis complex ATPase subunit
HVO_B0209	-2,20	hypothetical protein
HVO_A0414	-2,20	hypothetical protein
HVO_1775	-2,23	oxygen-insensitive NAD(P)H nitroreductase/dihydropteridine reductase
HVO_1001	-2,23	hypothetical protein
HVO_0851	-2,23	hypothetical protein (TBD)
HVO_B0348	-2,23	dihydrodipicolinate synthase, putative
HVO_1776	-2,23	probable hydantoin racemase
HVO_B0325	-2,23	exo-poly-alpha-D-galacturonosidase precursor

HVO_1220	-2,23	hypothetical protein
thiE HVO_2668	-2,23	thiamine-phosphate pyrophosphorylase
HVO_0271	-2,23	hypothetical protein
HVO_A0403	-2,23	probable transposase (homolog to transposon ISSod10 OrfA)
flgA1 HVO_1210	-2,24	flagellin A1
HVO_A0276	-2,25	sugar kinase, FGGY family, putative
pacF HVO_A0508	-2,27	PacF protein
HVO_1902	-2,28	hypothetical protein
HVO_A0275	-2,28	hypothetical protein
HVO_2000	-2,28	hypothetical protein
tsgB8 HVO_B0107	-2,29	ABC-type transport system permease protein (probable substrate sugar)
HVO_A0287	-2,32	mandelate racemase/muconate lactonizing enzyme family protein, putative
HVO_A0068	-2,33	hypothetical protein
cheR HVO_1222	-2,33	protein-glutamate O-methyltransferase CheR
HVO_A0058	-2,33	hypothetical protein
HVO_0917	-2,33	hypothetical protein
dppA15 HVO_B0328	-2,34	ABC-type transport system periplasmic substrate-binding protein (probable substrate dipeptides/oligopeptides)
tsgD5 HVO_A0281	-2,35	ABC-type transport system ATP-binding protein (probable substrate sugar)
HVO_2140	-2,36	hypothetical protein
arcR18 HVO_B0201	-2,37	ArcR family transcription regulator
tfb9 HVO_A0026	-2,38	transcription initiation factor TFB
ureX HVO_A0429	-2,39	N-acyl-D-amino acid deacylase family protein
HVO_A0018	-2,39	IS1341-type transposase
flgA2 HVO_1211	-2,40	flagellin A2
gabD HVO_B0069	-2,41	succinate-semialdehyde dehydrogenase
dppC16 HVO_C0072	-2,41	ABC-type transport system permease protein (probable substrate dipeptides/oligopeptides)
HVO_A0239 A	-2,42	hypothetical protein
HVO_3015	-2,42	hypothetical protein
dppBC15 HVO_B0329	-2,42	ABC-type transport system permease protein (probable substrate dipeptides/oligopeptides)
HVO_B0299	-2,42	Hypothetical transthyretin-like protein
livH6 HVO_B0218	-2,42	ABC-type transport system permease protein (probable substrate branched-chain amino acids)
HVO_B0330	-2,42	hypothetical protein
HVO_1363	-2,42	predicted transporter component
tfb12 HVO_A0098	-2,42	transcription initiation factor TFB
mobA1	-2,42	molybdopterin-guanine dinucleotide biosynthesis protein

HVO_B0245		A
tsgB5 HVO_A0284	-2,44	ABC-type transport system permease protein (probable substrate sugar)
HVO_B0216	-2,45	hypothetical protein
livF6 HVO_B0221	-2,45	ABC-type transport system ATP-binding protein (probable substrate branched-chain amino acids)
livG6 HVO_B0220	-2,45	ABC-type transport system ATP-binding protein (probable substrate branched-chain amino acids)
pelZ HVO_B0322	-2,45	pectate lyase
HVO_2107	-2,47	conserved hypothetical protein TIGR00149
tsgC2 HVO_2117	-2,48	ABC-type transport system permease protein (probable substrate sugar)
HVO_A0085	-2,50	hypothetical protein
dppA16 HVO_C0075	-2,50	ABC-type transport system periplasmic substrate-binding protein (probable substrate dipeptides/oligopeptides)
HVO_3042	-2,50	tRNA-Cys; K14222 tRNA Cys
livM6 HVO_B0219	-2,50	ABC-type transport system permease protein (probable substrate branched-chain amino acids)
HVO_A0282	-2,51	creatininase
HVO_2243	-2,51	hypothetical protein
HVO_1292	-2,51	Protein of unknown function (DUF1648) family
HVO_A0041	-2,51	hypothetical protein
graD4 HVO_A0595	-2,51	sugar nucleotidyltransferase
dppA8 HVO_A0380	-2,53	ABC-type transport system periplasmic substrate-binding protein (probable substrate dipeptides/oligopeptides)
HVO_0611	-2,53	tricarboxylate transport membrane protein RctA
tsgA9 HVO_B0228	-2,56	ABC-type transport system periplasmic substrate-binding protein (probable substrate sugar)
idi HVO_B0214	-2,57	probable isopentenyl-diphosphate delta isomerase
HVO_2570	-2,59	small CPxCG-related zinc finger protein
HVO_A0446	-2,59	hypothetical protein
HVO_1643	-2,59	hypothetical protein
HVO_A0404	-2,59	probable transposase (homolog to transposon ISSod10 OrfB)
HVO_A0034	-2,59	hypothetical protein
yoaN HVO_B0224	-2,59	putative cupin
HVO_B0203	-2,60	FAD-linked oxidase domain protein
HVO_2786	-2,63	thioredoxin
HVO_2103	-2,64	PTS system, galactitol-specific enzyme II, C component
HVO_0833	-2,65	hypothetical protein
HVO_0610	-2,68	hypothetical protein
dppC8 HVO_A0382	-2,69	ABC-type transport system permease protein (probable substrate dipeptides/oligopeptides)
HVO_B0237	-2,70	hypothetical protein
HVO_1311	-2,71	short-chain family oxidoreductase
livJ6 HVO_B0217	-2,72	ABC-type transport system periplasmic substrate-binding protein (probable substrate branched-chain amino acids)
HVO_B0068	-2,75	hypothetical protein
ltrC3 HVO_A0141	-2,75	LtrC-like protein

ilvA3 HVO_B0262	-2,75	threonine ammonia-lyase
tsgA7 HVO_B0034	-2,75	ABC-type transport system periplasmic substrate-binding protein (probable substrate sugar)
HVO_A0325	-2,75	cellulase
tsgC5 HVO_A0285	-2,81	ABC-type transport system permease protein (probable substrate sugar)
HVO_3025	-2,82	tRNA-Asn; K14220 tRNA Asn
HVO_0607	-2,86	hypothetical protein
tsgA8 HVO_B0106	-2,87	ABC-type transport system periplasmic substrate-binding protein (probable substrate sugar)
tsgD2 HVO_2118	-2,91	ABC-type transport system ATP-binding protein (probable substrate sugar)
HVO_B0211	-2,93	hypothetical protein
HVO_2120	-2,94	BNR/Asp-box repeat domain protein
HVO_A0571	-2,95	hydrolase, isochorismatase family
tsgC9 HVO_B0230	-2,97	ABC-type transport system permease protein (probable substrate sugar)
cheD HVO_1205	-2,97	taxis cluster protein CheD
dppD8 HVO_A0383	-2,99	ABC-type transport system ATP-binding protein (probable substrate dipeptides/oligopeptides)
flaG HVO_1215	-3,01	fla cluster protein FlaG
HVO_B0150	-3,01	iron ABC transporter substrate-binding protein
HVO_2112	-3,07	ygbK domain protein
dppF5 HVO_2444	-3,12	ABC-type transport system ATP-binding protein (probable substrate dipeptides/oligopeptides)
HVO_A0173	-3,12	hypothetical protein
gpdB2 HVO_A0270	-3,18	glycerol-3-phosphate dehydrogenase subunit B
HVO_2136	-3,23	hypothetical protein
HVO_A0089	-3,25	hypothetical protein
HVO_1843	-3,38	hypothetical protein
gabT1 HVO_B0070	-3,41	aminotransferase class III (probable 4-aminobutyrate aminotransferase)
cheW2 HVO_A0607	-3,42	purine-binding chemotaxis protein CheW
HVO_B0103	-3,42	glucose fructose oxidoreductase, putative
gpdC2 HVO_A0271	-3,48	glycerol-3-phosphate dehydrogenase subunit C
HVO_1844	-3,51	hypothetical protein
HVO_B0028	-3,67	xylose dehydrogenase (NAD/NADP)
HVO_3058	-3,88	tRNAGlu
HVO_B0210	-4,09	putative isomerase

Supplementary Table 4. Primers, plasmids and strains used in this study

A. Primers

Primer	Sequence (5' – 3')
Lsm37.u1	TAATAGGTACCCATGTTCGATGGGGTCTTCGAGGACCG
Lsm37.u2	TAATAGGATCCCGGCTCGTCGAGTGACGCTTCGAGGAC
Lsm37.d1	TAATAGGATCCGACGAAGACACCGTGCCCGGGGATATC
L3sm7.d2	TAATAGCGGCCGCCGAACGGCTGGGCGCACGACTTC
Smwt1	TAATATGGGCCCGTTTCTGGTACTGAGTTCTACTCAGC
Smwt2	TAATATACTAGTCCGAAGCCGCAAGACGAGCAGAC
Lsm#11	GCATGAGCGGCCGACCCCTCGAC
Lsm#12	GGCACGGTGTCTTCGTCCAGCG
L37#11	CATGACGGGTGCAGGAACCCCCAG
L37#12	GTCGCCGGACTTCGACTGCCAGG
bgah#1	GGCCGAGGCTGGAATCGAATAC
bgah#2	GTCGTA CTGCTGGCTCCAAAAC
ABC#1	GCTTCGTGCTAGCCACCACGAC
ABC#2	CGACCACTTGGACGCTTCGGGC
Glucan#1	GGGATTCGGCGGCATCGTGTCTCCTCAGC
Glucan#2	GCGACTCTCCTCGTACTCTTCGGACG
bgaNde2	CACCACATCGATCATTGCATATGACAGTTGG, <i>Clal</i> and <i>NdeI</i> sites underlined
bgaR	GTTGACTAGTGGTCCCGTGCCGAC, <i>SpeI</i> site underlined
ProL37P#2	TATACATATGTCCTGCACCCGTCATGCTTTGATGGTGAC
ProL37P#3	TATAGGGCCCGCGTACTTCGGCGTCTCCTCGCTG

B. Plasmids and strains

Strains	Genotype	Source/Reference
DH5α	F- ϕ 80 <i>lacZ</i> ΔM15 Δ(<i>lacZYA-argF</i>) U169 <i>recA1 endA1 hsdR17</i> (rk-, mk+) <i>gal- phoA supE44 λ- thi-1 gyrA96 relA1</i>	(invitrogen)
GM121	F- <i>dam-3 dcm-6 ara-14 fhuA31 galk2 galT22 hdsR3 lacY1 leu-6 thi-1 thr-1 tsx-78</i>	[1]
H119	Δ <i>pyrE2</i> Δ <i>trpA</i> Δ <i>leuB</i>	[2]
H555	Δ <i>pyrE2</i> , Δ <i>bgaH</i>	this study
Δ <i>Sm1</i>	Δ <i>pyrE2</i> , Δ <i>leuB</i> , Δ <i>trpA</i> , Δ <i>Sm1</i>	this study
Plasmids	Relevant properties	Source/Reference
pTA128	integrative vector with <i>bgaHa</i> gene	[3]
pTA131	integrative vector with <i>pyrE2</i> marker	[2]
pTA230	Shuttle vector with <i>pyrE2</i> marker and pHV2 replication origin	[2]
pTA425	contains fragment encoding L11 terminator	[4]
pTA506	integrative vector containing <i>bgaH</i> gene with up- and down-stream regions	this study
pTA617	integrative vector with up- and down-stream regions of <i>bgaH</i> gene (but without <i>bgaH</i> gene)	this study
pTA919	Shuttle vector with <i>pyrE2</i> marker and pHV1 replication origin	[5], this study
pTA131-Lsm37up	contains 1 kb fragment upstream region of SM1 encoding DNA	this study
pTA131-	contains 1 kb fragment upstream region of SM1 encoding	this study

Lsm37up+down	DNA and 1 kb fragment downstream region of SM1 encoding DNA	
pTA919-psyn	contains the psyn promotor	
pTA919-L37#2	contains the promotor for the <i>rpl37R</i> gene	this study

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