Supplementary Figures and Tables

Supplementary Table 1. Proteins co-immunoprecipitated with the FLAG protein. Proteins which were identified in three independent co-immunoprecipitations with only the FLAG peptide are listed. The accession numbers (www.halolex.mpg.de) and the peptide scores are listed.

Supplementary Table 2. Proteins co-immunoprecipitated with the FLAG-Lsm protein (without crosslinking). Proteins which were identified in three independent co-immunoprecipitations are listed. Proteins which were found in the control reaction (Supplementary Table 1) were subtracted. Protein 1 is the FLAG-tagged Lsm protein and protein 2 is the Lsm protein. The accession numbers (www.halolex.mpg.de) and the peptide scores are listed.

Supplementary Table 3. Proteins co-immunoprecipitated with the FLAG-Lsm protein. Proteins which were identified in three independent co-immunoprecipitation with the crosslinked FLAG-Lsm protein are listed.

Supplementary Figure S1. Alignment of Lsm protein sequences. A. The *Haloferax* Lsm protein was aligned with 31 homologous archaeal Lsm1 proteins. **B.** The archaeal Lsm proteins show a high sequence similarity to each other and some similarity to the eukaryotic Lsm proteins. Only slight similarities are present in the *E. coli* and *M. jannaschii* Hfq proteins. E.co: *Escherichia coli* Hfq protein, M.ja: *M. jannaschii* Hfq-like protein, S.ce-Lsm3: Lsm3 protein from *S. cerevisiae*, S.ce-Lsm7: Lsm7 protein from *S. cerevisiae*, P.fu: Lsm protein from *Pyrococcus furiosus*, M.ma: *Methanosarcina mazei* Lsm protein, H.vo: Lsm protein from *H. volcanii*.

Supplementary Figure S2. Determination of the intracellular copy number of the Lsm protein. A. Western blot analysis with an Lsm-specific antiserum. S1, S2 and S3 are cytoplasmic extracts from three independent cultures; the remaining lanes contain the indicated amounts of purified Lsm protein. **B.** Standard curve generated from the signals of the purified Lsm protein.

Supplementary Figure S3. Expression of the *lsm* gene in *E. coli.* The *lsm* gene was expressed in *E. coli* as described in Materials and methods as an S-tag fusion protein (lane Lsm-S). The S-tag was successfully removed from the recombinant protein (lane Lsm). The Lsm protein from *Haloferax* has a calculated molecular weight of 8.3 kDa, but it runs comparatively slower on the SDS-PAGE, which might be because of the acidic pI of 3.9. The Lsm-S-tag fusion protein is slightly larger, thereby it runs a little bit slower on the SDS-PAGE.

Supplementary Figure S4. Determination of the dissociation constant. EMSA were performed with different concentrations of recombinant Lsm protein as described in Materials and methods.

Supplementary Figure S5. A. The genomic localisation of the *lsm* gene is shown schematically. The whole reading frame of the Lsm protein was removed (except for the last four nucleotides, which overlap with the L37e frame). The promoter of the dicistronic RNA was retained. Relevant restriction sites are indicated by arrows. The location of the probe used in the southern analyses is shown in bold below. **B.** Southern blot analysis shows that the deletion of the Lsm frame was successful. Lanes 1 and 2: DNA from two *lsm* deletion strains, lane wt: DNA from the wildtype strain, lane m: DNA size marker in kb.

Supplementary Figure S6. A. The FLAG-Lsm fusion protein is expressed in *Haloferax*. The FLAG-fusion Lsm plasmid was transformed into the *lsm* deletion strain to analyse its expression. Proteins were extracted and analysed using a western blot. Both fusion proteins are expressed efficiently in *Haloferax.* **B. Protein interaction partners of Lsm.** Proteins co-purifying with the FLAG-Lsm protein were separated on an SDS-PAGE und subjected to mass spectrometry. **C. Co-immunoprecipitation reveals several RNAs associated with Lsm.** Cells were treated with formaldehyde to crosslink proteins and RNA to the Lsm protein. Subsequently an S100 extract was isolated, which was purified using a FLAG column. Fractions eluted from the column were analysed for their protein and RNA content. RNAs were isolated from the eluted FLAG-Lsm fraction and 3´ labelled using pCp. RNAs were analysed on denaturing PAGE. Lane I: RNA isolated from the precipitated fraction. Lane m: DNA size marker in nt.

Supplementary Table 1. FLAG only

no.	acc. number	score	protein
1	HVO_0812	258	phosphoenolpyruvate synthase
2	HVO_1829	115	aminopeptidase homolog
3	HVO_2452	88	ribonucleoside-diphosphate reductase, adenosylcobalamin-dependent
4	HVO_2916	80	2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase
5	HVO_A0475	57	superoxide dismutase
6	HVO_1590	41	chaperone protein DnaK

Supplementary Table 2. FLAG-Lsm without crosslink

no.	acc. number	score	protein
1	LSM_3Flag	751	3xFLAG-Lsm-fusion protein
2	HVO_2723	516	Lsm protein
3	HVO_1571	28	DNA topoisomerase VI, B subunit

Protein Name	Accession Number	Sample 1 # of MSMS spectra	Sample 2 # of MSMS spectra	Sample 3 # of MSMS spectra
translation elongation factor aEF-2 [Haloferax volcanii DS2]	gi|291370268	47	43	34
phosphoenolpyruvate synthase [Haloferax volcanii DS2]	gi|291371817	37	35	23
translation elongation factor aEF-1 alpha subunit [Haloferax volcanii DS2]	gi|291371442	29	26	29
heat shock protein Cct2 [Haloferax volcanii]	gi|2459984	31	32	25
heat shock protein Cct1 [Haloferax volcanii]	gi|2459986	30	17	20
chaperone protein DnaK [Haloferax volcanii DS2]	gi|291372194	18	14	16
DNA-directed RNA polymerase subunit A [Haloferax volcanii DS2]	gi|291371230	12	15	10
CBS domain pair, putative [Haloferax volcanii DS2]	gi|291371699	16	13	8
ribonucleoside-diphosphate reductase, adenosylcobalamin-dependent [Haloferax volcanii DS2]	gi|291372162	12	12	12
mRNA 3-end processing factor homolog [Haloferax volcanii DS2]	gi|291372149	13	11	10
cell division control protein 48 [Haloferax volcanii DS2]	gi|291371302	11	12	11
Betaine aldehyde dehydrogenase [Haloferax volcanii DS2]	gi|291370978	12	16	7
snRNP homolog [Haloferax volcanii DS2]	gi|291371013	13	5	7
cell division control protein 48 [Haloferax volcanii DS2]	gi|291371169	15	12	5
coiled-coil protein [Haloferax volcanii DS2]	gi|291372672	6	8	9
pyruvate--ferredoxin oxidoreductase alpha subunit [Haloferax volcanii DS2]	gi|291370401	10	9	8
predicted hydrolase [Haloferax volcanii DS2]	gi|291370676	7	10	7
chlorite dismutase family protein [Haloferax volcanii DS2]	gi|291371600	8	12	5
SMC-like protein Sph2 [Haloferax volcanii DS2]	gi|291369325	7	8	10
glutamate synthase [NADPH] large chain [Haloferax volcanii DS2]	gi|291370629	16	10	0
ribosomal protein S3 [Haloferax volcanii DS2]	gi|291370935	10	4	7
phosphopyruvate hydratase [Haloferax volcanii DS2]	gi|291370999	5	6	7
thermosome subunit 3 [Haloferax volcanii DS2]	gi|291371446	8	10	6
threonyl-tRNA synthetase [Haloferax volcanii DS2]	gi|291370664	9	6	5
aconitate hydratase, putative [Haloferax volcanii DS2]	gi|291370588	10	4	8
RecName: Full=Proteasome subunit alpha 1; AltName: Full=Multicatalytic endopeptidase complex subunit alpha 1	gi|12229946	7	8	6
short-chain family oxidoreductase [Haloferax volcanii DS2]	gi|291370228	6	7	6
ribosomal protein S3a.eR [Haloferax volcanii DS2]	gi|291372949	8	6	6
acetyl-CoA synthetase [Haloferax volcanii DS2]	gi|291372641	3	10	4
Fumarate hydratase class II [Haloferax volcanii DS2]	gi|291371792	9	6	6
anthranilate phosphoribosyltransferase [Haloferax volcanii DS2]	gi|291370820	6	7	3
DNA double-strand break repair ATPase Rad50 [Haloferax volcanii DS2]	gi|291371675	9	6	3
aspartyl-tRNA synthetase [Haloferax volcanii DS2]	gi|291371103	10	7	3
glucoamylase [Haloferax volcanii DS2]	gi|291370181	6	8	2
valyl-tRNA synthetase [Haloferax volcanii DS2]	gi|291372246	4	7	7
alanyl-tRNA synthetase [Haloferax volcanii DS2]	gi|291372225	5	4	2
putative nuclease [Haloferax volcanii DS2]	gi|291370734	6	5	5
uspA domain protein [Haloferax volcanii DS2]	gi|291370215	7	6	4
cobyrinic acid ac-diamide synthase [Haloferax volcanii DS2]	gi|291370671	5	6	3
aspartate carbamoyltransferase [Haloferax volcanii DS2]	gi|291370997	7	4	6
aconitate hydratase 1 [Haloferax volcanii DS2]	gi|291370327	6	8	0
putative orotatephosphoribosyl transferase [Haloferax volcanii]	gi|21698806	4	8	4
isoleucyl-tRNA synthetase [Haloferax volcanii DS2]	gi|291371634	3	6	5
conserved hypothetical protein [Haloferax volcanii DS2]	gi|291372332	11	3	3
Formyltetrahydrofolate deformylase [Haloferax volcanii DS2]	gi|291372601	8	2	6
probable oxidoreductase (aldo-keto reductase family protein) [Haloferax volcanii DS2]	gi|291372540	6	2	7
CTP synthase [Haloferax volcanii DS2]	gi|291372881	5	5	3
inosine-5-monophosphate dehydrogenase [Haloferax volcanii DS2]	gi|291371697	4	6	6
DNA topoisomerase VI subunit B [Haloferax volcanii DS2]	gi|291371984	6	2	2
replication factor C small subunit [Haloferax volcanii DS2]	gi|291370302	4	4	4
cell division protein FtsZ [Haloferax volcanii DS2]	gi|291372351	3	4	3
conserved hypothetical protein [Haloferax volcanii DS2]	gi|291372275	7	3	3
methionyl-tRNA synthetase [Haloferax volcanii DS2]	gi|291371457	5	3	3
DNA-directed RNA polymerase subunit B [Haloferax volcanii DS2]	gi|291372796	5	4	4
cell division protein FtsZ [Haloferax volcanii DS2]	gi|291370430	0	4	2

Predicted RNA-binding protein [Haloferax volcanii DS2]	gi|291370661	3	5	4
GMP synthase (glutamine-hydrolyzing) subunit B [Haloferax volcanii DS2]	gi|291371351	3	5	4
phosphoenolpyruvate carboxylase [Haloferax volcanii DS2]	gi|291371035	7	4	3
excinuclease ABC subunit A [Haloferax volcanii DS2]	gi|187455580	3	3	4
sugar-specific transcriptional regulator TrmB [Haloferax volcanii DS2]	gi|291370598	4	6	4
conserved hypothetical protein [Haloferax volcanii DS2]	gi|291371577	2	4	4
RNA polymerase subunit B' [Haloferax volcanii]	gi|242392244	0	5	2
D-3-phosphoglycerate dehydrogenase [Haloferax volcanii DS2]	gi|291370333	4	3	3
conserved protein [Haloferax volcanii DS2]	gi|291372364	4	4	0
isocitrate dehydrogenase (NADP+) [Haloferax volcanii DS2]	gi|291370583	0	5	0
conserved protein [Haloferax volcanii DS2]	gi|291370317	3	4	0
L-lactate dehydrogenase [Haloferax volcanii DS2]	gi|291370848	5	3	2
ribosomal protein S5 [Haloferax volcanii DS2]	gi|291372147	5	4	2
pyruvate--ferredoxin oxidoreductase beta subunit [Haloferax volcanii DS2]	gi|291371065	4	4	0
ATPase:SUBUNIT=alpha	gi|1098057	5	4	0
transcription initiation factor TFB [Haloferax volcanii DS2]	gi|291370098	3	3	3
uspA domain protein [Haloferax volcanii DS2]	gi|291371021	2	3	3
oxoglutarate--ferredoxin oxidoreductase alpha subunit [Haloferax volcanii DS2]	gi|291371502	3	5	2
uspA domain protein [Haloferax volcanii DS2]	gi|291371482	2	5	3
glyceraldehyde-3-phosphate dehydrogenase, type II [Haloferax volcanii DS2]	gi|291372664	0	2	4
cobalamin biosynthesis protein [Haloferax volcanii DS2]	gi|291369173	0	3	3
ribosomal protein L19.eR [Haloferax volcanii DS2]	gi|291372121	0	3	3
DNA binding domain protein [Haloferax volcanii DS2]	gi|291372232	4	5	0
branched-chain amino acid aminotransferase [Haloferax volcanii DS2]	gi|291371760	0	5	0
pyridoxine biosynthesis protein [Haloferax volcanii DS2]	gi|291372428	3	2	3
glycine hydroxymethyltransferase [Haloferax volcanii DS2]	gi|291370984	3	3	2
HD domain protein [Haloferax volcanii DS2]	gi|291372437	0	2	4
FeS assembly protein SufB [Haloferax volcanii DS2]	gi|291372896	0	2	4
FeS assembly protein SufD [Haloferax volcanii DS2]	gi|291371934	2	4	0
hypothetical protein (TBD) [Haloferax volcanii DS2]	gi|291372701	0	3	3
co-chaperone GrpE [Haloferax volcanii DS2]	gi|291372562	0	3	3
acyl-CoA synthetase [Haloferax volcanii DS2]	gi|291369860	3	5	0
uspA domain protein [Haloferax volcanii DS2]	gi|291372669	3	2	0
NADH dehydrogenase-like complex subunit CD [Haloferax volcanii DS2]	gi|291371958	0	4	2
ArcR family transcription regulator [Haloferax volcanii DS2]	gi|291369661	4	3	0
nadh-dependent flavin oxidoreductase [Haloferax volcanii DS2]	gi|291370075	2	0	2
orotatephosphoribosyl transferase [Haloferax volcanii]	gi|21698808	4	0	3
Uncharacterized protein family (UPF0148) family [Haloferax volcanii DS2]	gi|291370425	5	0	3
oxidoreductase [Haloferax volcanii DS2]	gi|2459734	3	3	0
dihydrolipoamide S-acyltransferase [Haloferax volcanii DS2]	gi|291370375	0	3	3
succinyl-CoA synthase, beta subunit [Haloferax volcanii DS2]	gi|291371580	3	3	0
transcription regulator (homolog to phosphate uptake regulator) [Haloferax volcanii DS2]	gi|291371250	3	0	2
seryl-tRNA synthetase [Haloferax volcanii DS2]	gi|291371684	0	3	3
uracil phosphoribosyltransferase [Haloferax volcanii DS2]	gi|291372087	0	2	2
conserved hypothetical protein TIGR01213 [Haloferax volcanii DS2]	gi|291370136	0	3	0
ribosomal protein S2 [Haloferax volcanii DS2]	gi|291370311	0	3	0
FeS assembly ATPase SufC [Haloferax volcanii DS2]	gi|291371877	0	0	4
translation initiation factor aIF-5A [Haloferax volcanii DS2]	gi|291371355	0	0	2
Circ1 [Haloferax volcanii]	gi|251829611	0	2	3
conserved hypothetical protein [Haloferax volcanii DS2]	gi|291372104	2	0	0
nonhistone chromosomal protein [Haloferax volcanii DS2]	gi|291370853	3	0	0
glycyl-tRNA synthetase [Haloferax volcanii DS2]	gi|291372518	4	0	0
stomatin-prohibitin homolog, transmembrane [Haloferax volcanii DS2]	gi|291370466	3	0	0
homoserine dehydrogenase [Haloferax volcanii DS2]	gi|291371903	3	0	0
3-hydroxyacyl-CoA dehydrogenase [Haloferax volcanii DS2]	gi|291370353	2	0	0
nadp-dependent malic enzyme [Haloferax volcanii DS2]	gi|291371778	0	0	2
Domain of unknown function DUF147 family [Haloferax volcanii DS2]	gi|291372090	0	0	2

glyceraldehyde-3-phosphate dehydrogenase, type I [Haloferax volcanii DS2]	gi|291370936	0	2	0
dihydroxyacetone kinase, L subunit [Haloferax volcanii DS2]	gi|291371659	0	3	2
ribosomal protein S8.eR [Haloferax volcanii DS2]	gi|291370413	0	0	2
RadA [Haloferax volcanii]	gi|1378032	0	3	0
23,4,5-tetrahydropyridine-2-carboxylateN-succinyl transferase [Haloferax volcanii DS2]	gi|291372945	3	0	0
conserved hypothetical protein [Haloferax volcanii DS2]	gi|291372886	0	2	0
6,7-dimethyl-8-ribityllumazine synthase [Haloferax volcanii DS2]	gi|291371740	4	0	0
succinate dehydrogenase subunit A (flavoprotein) [Haloferax volcanii DS2]	gi|291371633	0	5	0
aspartyl-tRNA(Asn) amidotransferase subunit B [Haloferax volcanii DS2]	gi|291372481	0	0	3
Orc1-type DNA replication protein [Haloferax volcanii DS2]	gi|291372465	0	2	0
putative PRC-barrel domain protein [Haloferax volcanii DS2]	gi|291371598	0	2	0
DNA topoisomerase I [Haloferax volcanii DS2]	gi|291370931	0	2	0
Chain A, Crystal Structure Of The Haloferax Volcanii Proliferating Cell Nuclear Antigen	gi|257097713	3	0	0
TATA-binding transcription initiation factor [Haloferax volcanii DS2]	gi|291372685	3	0	0
proteasome-activating nucleotidase A [Haloferax volcanii DS2]	gi|291372419	0	3	0
ornithine carbamoyltransferase [Haloferax volcanii DS2]	gi|291371507	2	0	0
folylpolyglutamate synthase / 7,8-dihydropteroate reductase / dihydropteroate synthase [Haloferax volcanii DS2]	gi|291370736	0	2	0
ribosomal protein L14 [Haloferax volcanii DS2]	gi|291371299	2	0	2
conserved hypothetical protein TIGR00294 [Haloferax volcanii DS2]	gi|291372807	0	0	3
sulfatase arylsulfatase A-like protein [Haloferax volcanii DS2]	gi|291372722	0	2	0
ribulose bisphosphate carboxylase, type III [Haloferax volcanii DS2]	gi|291371926	0	3	0
translation initiation factor aIF-2 beta subunit / probable RNA-binding protein homolog [Haloferax volcanii DS2]	gi|291372914	0	2	0
ATP phosphoribosyltransferase [Haloferax volcanii DS2]	gi|291372544	0	2	0
FtsZ [Haloferax volcanii]	gi|1017833	0	2	0
Adenylate kinase [Haloferax volcanii DS2]	gi|291372675	3	0	0
dihydrodipicolinate synthase [Haloferax volcanii DS2]	gi|291371202	2	0	0
IS200-type transposase [Haloferax volcanii DS2]	gi|291370781	0	0	2
aspartokinase [Haloferax volcanii DS2]	gi|291370134	0	2	0
hydroxymethylglutaryl-CoA synthase [Haloferax volcanii DS2]	gi|291371901	0	3	0
glutamyl-tRNA(Gln) amidotransferase subunit E [Haloferax volcanii DS2]	gi|291370152	0	3	0
ABC-type transport system ATP-binding protein (probable substrate dipeptides/oligopeptides) [Haloferax volcanii DS2]	gi|291370617	2	0	0
leucyl-tRNA synthetase [Haloferax volcanii DS2]	gi|291372251	0	3	0
UDP-glucose 4-epimerase [Haloferax volcanii DS2]	gi|291371641	0	0	3
glycerol kinase [Haloferax volcanii DS2]	gi|291372173	0	2	0
coenzyme PQQ synthesis protein E homolog [Haloferax volcanii DS2]	gi|291371422	0	2	0
DNA mismatch repair protein mutS [Haloferax volcanii DS2]	gi|291372283	0	2	0
conserved hypothetical protein TIGR00291 [Haloferax volcanii DS2]	gi|291371002	2	0	0

Supplementary Figure S1A: Alignment of archaeal Lsm proteins

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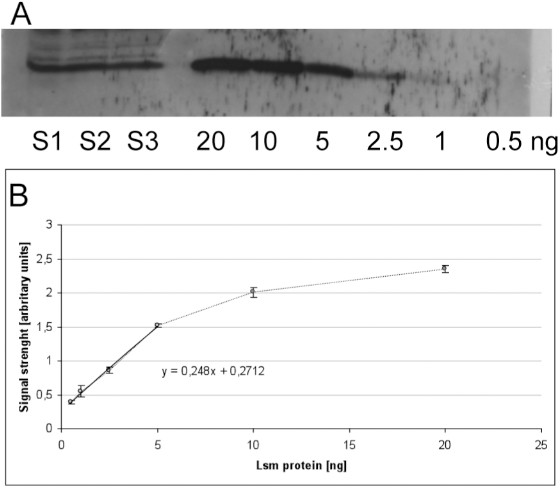
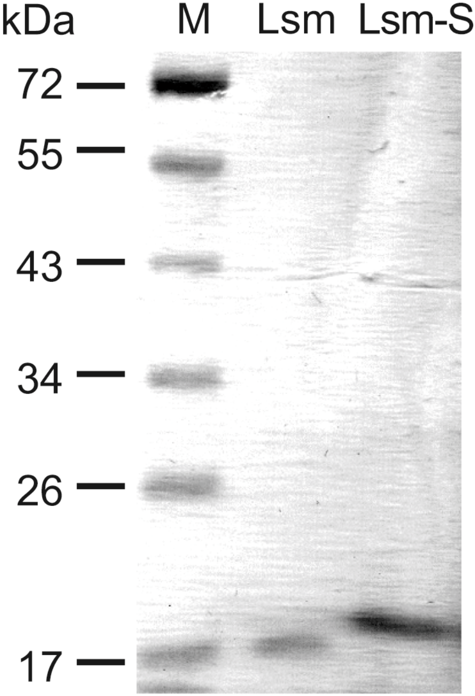
Hf. volcanii      --------MS--GRPLDVLEASLD-EPVTVLLKDGNAYFGVLAGYDQHMNVVLEEALD-- 47
Hr. lacispofundi  --------MS--GRPLDVLEASLE-EPVTVHLKDGTTYYGILAGYDQHMNIVIEPETDVD 49
Hb. salinarum     --------MS--GRPLDVLEESLE-ETVTVRLKDGDEFTGVLTGYDQHMNVVIE------ 43
Hq. walsbyi       --------MS--GRPLDVLEAALD-DTVTITLKDGSAYHGTLAGYDQHMNAVLDPAMAS- 48
Ha. Marismotrue   --------MS--GRPLDVLEASLG-ETVTVQLKGGELFEGELTGYDQHMNLVVED----- 44
Nm. pharaonis     --------MS--NRPLDVLEETLG-AEVHVTLKGGETYEGTLSGYDQHMNLVLEE----- 44
Tc. kodakaraensis --------MA--ERPLDVIHKSLD-KDVLVLLKRGNEFRGKLIGYDIHLNVVLADAELI- 48
Tc. gammatolerans --------MA--ERPLDVIHRSLD-KDVLVLLKRGGEFRGKLIGYDIHLNVVLAGADYI- 48
Pc. horikoshii    --------MA--ERPLDVIHRSLD-KDVLVILKKGFEFRGRLIGYDIHLNVVLADAEMV- 48
Pc. abyssii       --------MA--ERPLDVIHRSLD-KDVLVILKKGFEFRGRLIGYDIHLNVVLADAEMI- 48
Pc. furiosus      --------MA--ERPLDVIHKSLD-KDVLVILKKGFEFRGKLIGYDIHLNVVLANAELL- 48
Tc. onnurineus    --------MA--ERPLDVIHRSLD-KDVLVILKKGFEFRGKLIGYDIHLNIVLAGAEMI- 48
Tc. Sibiricus     --------MA--ERPLDVIHKSLD-KEVLVILKRGAEYRGKLIGYDIHLNVVLADAQLI- 48
Mc. maripaludis   --------MMDTQRPLDALGKSIN-TNVTVFLKDGKVVKGRLKAYDLHMNVALENAKIE- 50
Mc. vannielii     --------MMDTQRPLDALGKSIN-TNVTVYLKDGKLVKGRLKAYDLHMNVALENAKIE- 50
Mc. aeolicus      --------MIDNQRPLDALGKSIN-TNVLVKLKDGQTVKGRLKAYDLHLNVALENAKFD- 50
Mb. smithii       MSGQ----NV--QRPLDALGKSVN-SPVLIKLKGDREFRGILKSFDLHMNLVLNDAEEL- 52
Ms. stadtmanae    MNDQKNNNNT--SRPLDALGQALN-SQVLIKLKGGKEFRGALQSFDMHMNLVLNDAEEI- 56
Ms. thermopnila   --------MA--QRPLDILNESLN-SPVIVRLKDGRAFRGELQGYDIHMNLVLENTEEI- 48
Uncultured meth.  --------MS--QRPLDVLNEALN-SPVIVRLKGGREFRGELQGYDMHMNLVLDNAEEL- 48
Ms. mazei         --------MA--NRPLDILNNALD-TPVIVRLKGAREFRGELKGYDIHMNLVLDNAEEL- 48
Ms. azetivorans   --------MA--NRPLDILNNALD-TPVIVRLKGAREFRGELKGYDIHMNLVLDNAEEL- 48
Ms. barkeri       --------MA--NRPLDILNNALD-TPVIVRLKGAREFRGELKGYDIHMNLVLDNAEEL- 48
Mc. burtonii      --------MG--NRPLDILNDALN-TSVIVRLKGAREFRGVLQGYDVHMNLVLDEAEEL- 48
Ag. fulgidus      --------MP--PRPLDVLNRSLK-SPVIVRLKGGREFRGTLDGYDIHMNLVLLDAEEI- 48
Mc. labreanum     --------MT--KRPLEILDQVLNRQPVIISLKGGREIRGVLQGYDVHMNLVLDKAEEE- 49
Mc. marisnigri    --------MT--PRPLDILDQVLNRQPVIISLKGGREIRGILQGYDVHMNLVLDKAEEE- 49
Ms. hungatei      ---MQGIDMT--KRPMDILDQVLNRQPVLISLKGGREIKGVLQGYDVHMNLVLDKAEEI- 54
Mr. boonei        --------MT--KRPLDILDLVLNRQPVIVSLKGGREIRGVLQGYDVHMNLVLDKAEET- 49
Tp. acidophilum   ----MP-KTPANVKPMDVLKSALS-RNVLIDVKGNREYSGILEGYDVYMNIVLQNASEI- 53
Tp. volcanium     ----MP-KTVANTKPMDVLKNALS-RNVLIDVKGNREYSGILEGYDVYMNVVLQNASEI- 53
Pp. torridus      ----MANKTAYVSKPMDVLKNSLE-KNIMVDVKGNRTYSGTLEGYDIYMNVVLSNVSET- 54
                               :*:: :   :    : : :*      * * .:* ::* .:

Hf. volcanii      ---EDTVPGDIELEQVQDTTIIRGDNVVTIKA------ 76
Hr. lacispofundi  DRVDDDLDGEFAVA-IEDTTIIRGDNVVTIKA------ 80
Hb. salinarum     --------GE-------DTTIIRGDNVVTIKP------ 60
Hq. walsbyi       ---ETVDPGTLDVTEVEDTTIIRGDNIVTINV------ 77
Ha. Marismotrue   ----------------EDTTIIRGDNVVSITP------ 60
Nm. pharaonis     --------G-------DNVTIIRGDNVVSIEP------ 61
Tc. kodakaraensis --------QDGEVVKKYGKIVIRGDNVLALSPVELE-- 76
Tc. gammatolerans --------QDGEVVKSYGKIVVRGDNVLAISPVDIE-- 76
Pc. horikoshii    --------QDGEVVKKYGKIVIRGDNVLAISPTEE--- 75
Pc. abyssii       --------QDGEVVKRYGKIVIRGDNVLAISPTEE--- 75
Pc. furiosus      --------QDGEVVKKYGKIVIRGDNVLAISPTEEG-- 76
Tc. onnurineus    --------QDGEVVKKYGKIVIRGDNVLAISPVDVGVE 78
Tc. Sibiricus     --------ENGEPKKSYGKIVIRGDNVLAISPVEIE-- 76
Mc. maripaludis   --------NDEE--KEFPMLVVRGDNVLYVSL------ 72
Mc. vannielii     --------SDEE--KEFPMLVVRGDNVLYVSL------ 72
Mc. aeolicus      --------G-EE--KEYPLIVVRGDNVLFISL------ 71
Mb. smithii       --------QDGEVTRRLGVVLIRGDNIVYISP------ 76
Ms. stadtmanae    --------KDGESICRLGVVLVRGDNIVYISPG----- 81
Ms. thermopnila   --------AEG-TARKIGAVIVRGDNVVYISP------ 71
Uncultured meth.  --------KENEASRKLGTIIVRGDTVVYVSP------ 72
Ms. mazei         --------REGEVVSKFSSVVIRGDNVVYVSP------ 72
Ms. azetivorans   --------RDGEVVSKFSSVVIRGDNVVYVSP------ 72
Ms. barkeri       --------REGEVVSKFGSVVIRGDNVVYVSP------ 72
Mc. burtonii      --------KDGEIVRKIGGVVIRGDNVVYVSP------ 72
Ag. fulgidus      --------QNGEVVRKVGSVVIRGDTVVFVSPAPGGE- 77
Mc. labreanum     --------GEN-GTVSLGTLIVRGDNVIYISPSVE--- 75
Mc. marisnigri    --------VDG-AAQKLGTLIVRGDNVIYITPSVE--- 75
Ms. hungatei      --------VQG-QAQSIGTLIIRGDNVIYISPNPQ--- 80
Mr. boonei        --------ENG-QVVKVGTLIVRGDNVIYISPSLES-- 76
Tp. acidophilum   --------INGENKGVYDRVLVRGDNVIFVSPSKGDGS 83
Tp. volcanium     --------INGENKGVFDRILVRGDNVIFVSPSKGDNE 83
Pp. torridus      --------INGENKGVFEKMLVRGDNIIFVSPSRSD-- 82
                                      ::***.:: :
```

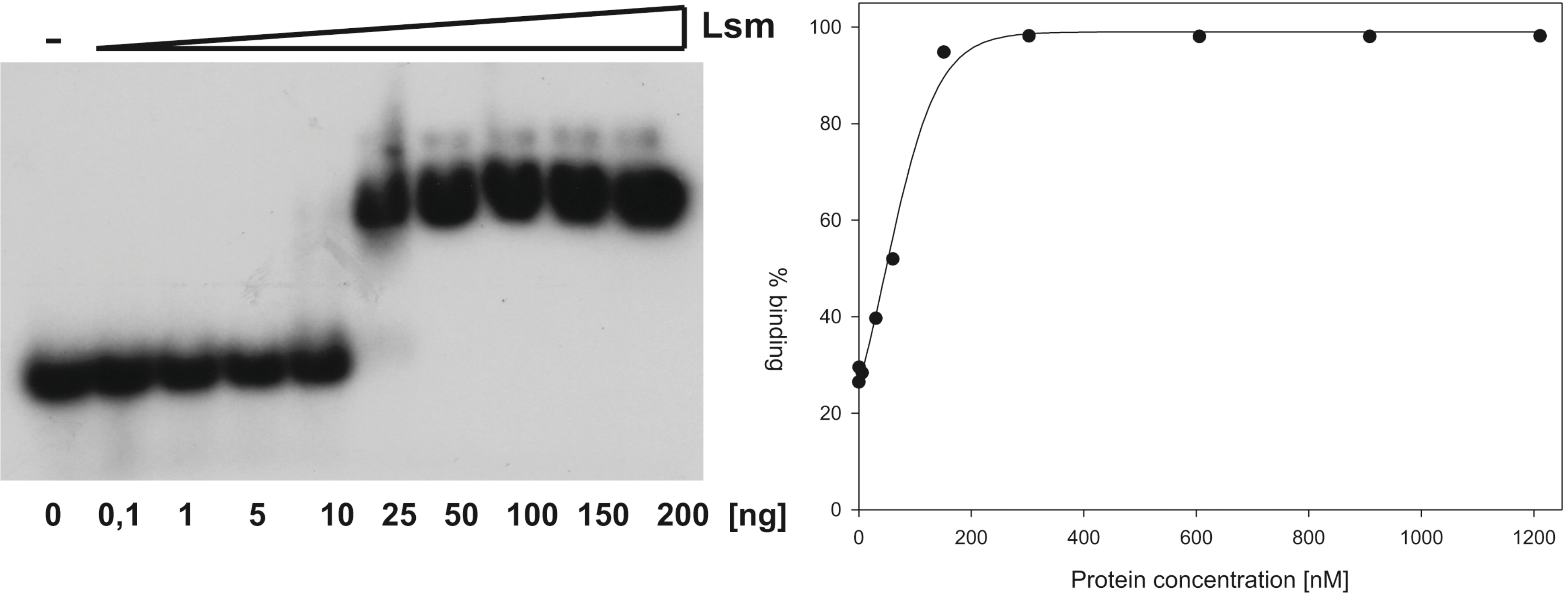
Supplementary Figure 1B



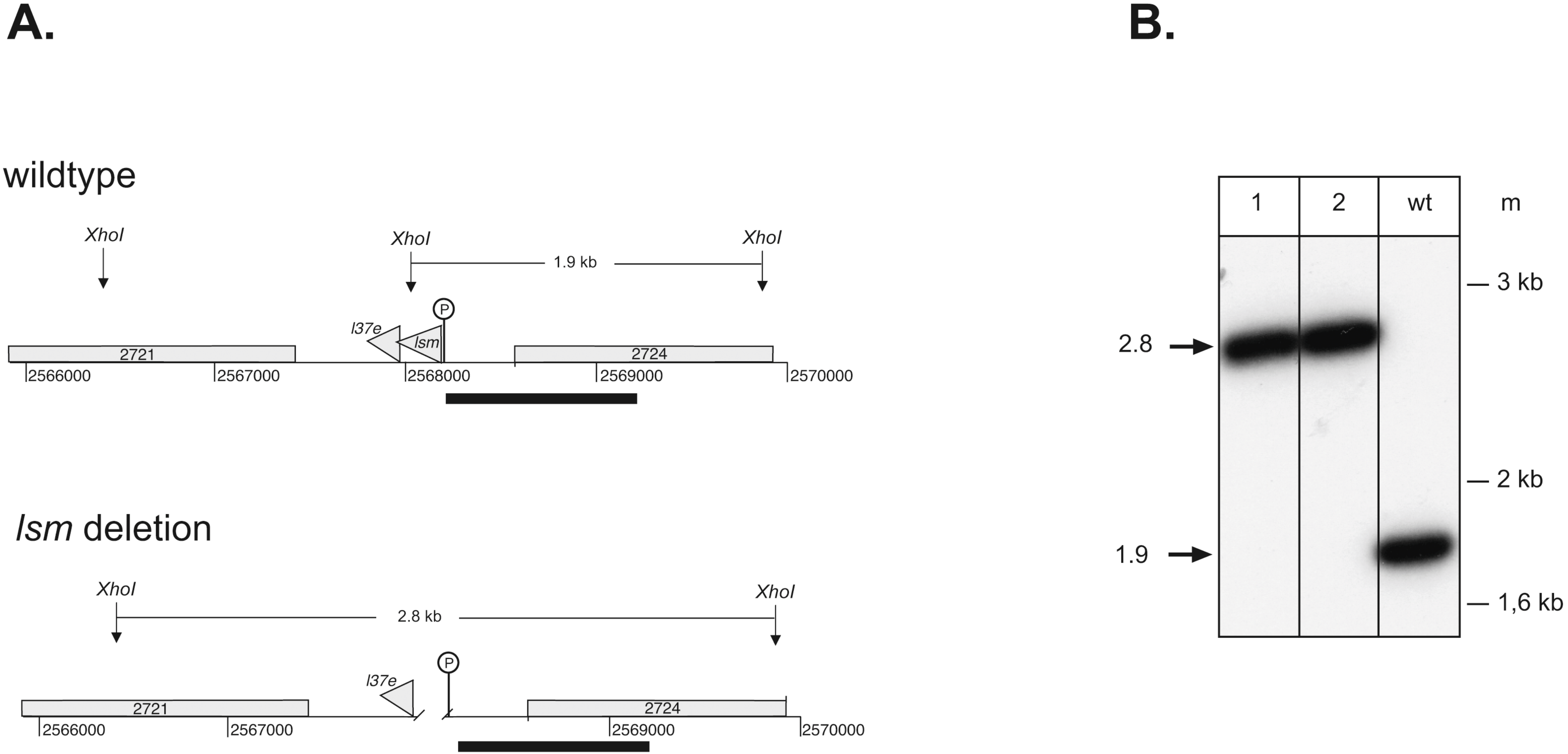
Supplementary Figure S2



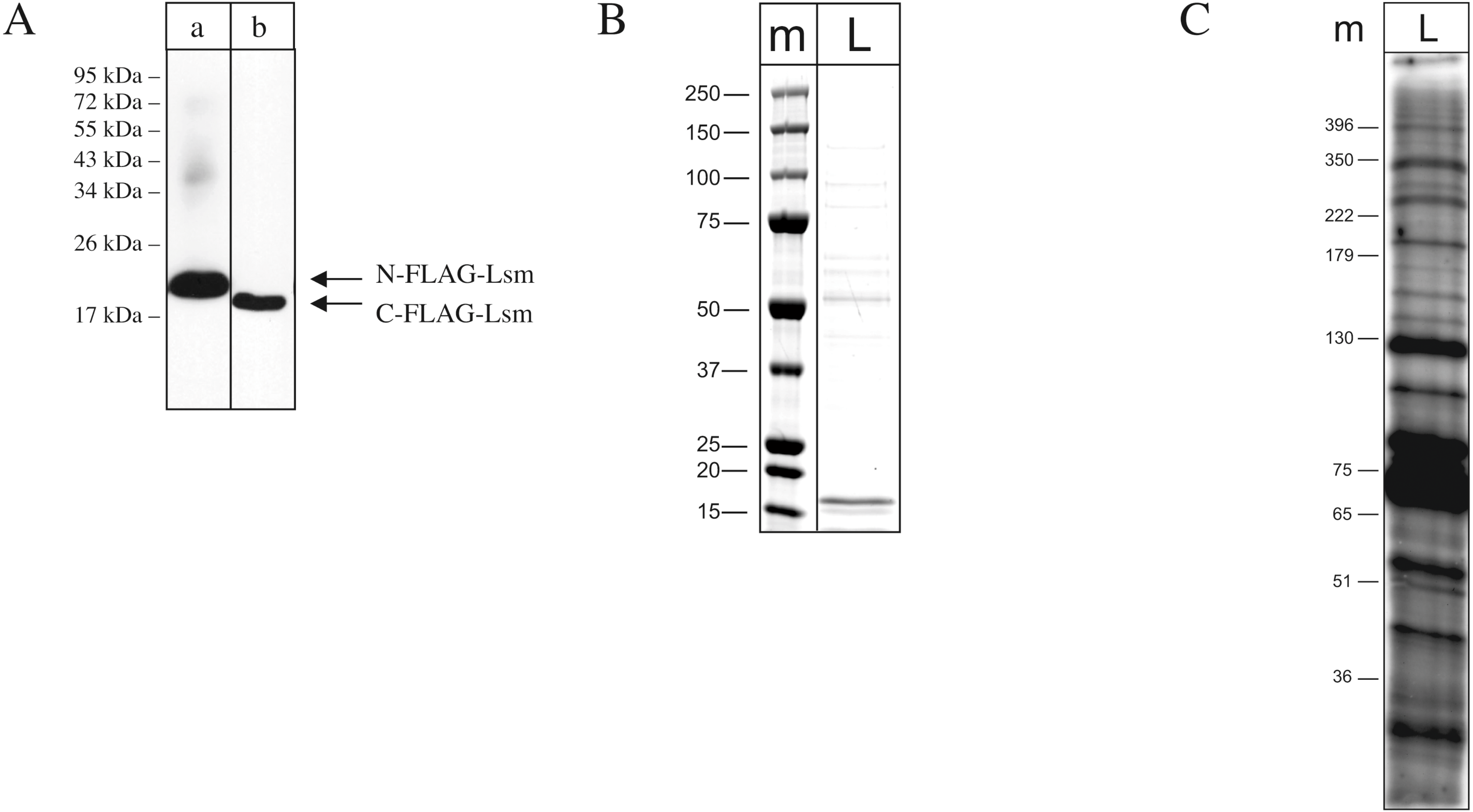
Supplementary Figure S3



Supplementary Figure S4



Supplementary Figure 5



Supplementary Figure 6