

Lche_0703	1	MIKTKI	IIINKLGLHARASAKFVSTAARFQSQIDVT	SNSQTVNGKSIMGVMLAANKGSELILEI	DGPDEVQMN	EATQQLINNYFGE	G
Lpar_1390	1	MIKTKI	IIINKLGLHARASAKFVSTAARKFQSQIDVT	SNSQTVNGKSIMGVMLAANKGSELIMEI	DGPDEVQMN	EATQQLINNYFGE	G
Lste_1883	1	MIKTKI	IIINKLGLHARASAKFVSTAARFQSQIDVT	SNSQTVNGKSIMGVMLAANKGSELIMEI	DGPDEVQMN	EATLTLINNYFGE	G
Lstg_1679	1	MIKTKI	IIINNLGLHARASAKFVSTAARFQSQINVT	SNSQTVNGKSIMGVMLAANKGSELIMEI	DGPDEVQMN	EATQQLINNYFGE	G
Ltuc_2257	1	MIKTKI	IIINKLGLHARASAKFVSTAARKFQSQIDVT	SNSQTVNGKSIMGVMLAANKGSELIMEI	INGPDEVQMN	EATHLINNYFGE	G
Lgor_0052	1	MIKTKI	IIINKLGLHARASAKFVSTAARKFQSQIGVT	SNSQTVNGKSIMGVMLAANKGSELIMEI	INGPDEVQMN	EATNLINNYFGE	G
Lcin_2798	1	MIKTTI	IIINKLGLHARASAKFVSTAARFQSQIDVT	CNSQTVNGKSIMGVMLAANQGAEI	INGPDETQMN	EATHLINNFFGE	G
Lsai_2566	1	MIKTTI	IIINKLGLHARASAKFVSTAARFQSQIDVT	CNSQTVNGKSIMGVMLAANQGAEI	INGPDEVQMN	EATHLINNFFGE	G
Lgra_2781	1	MIKTKI	IIINKLGLHARASAKFVSTAARKFQSQIDVT	CNSQTVNGKSIMGVMLAANQGAEI	INGPDEIQMN	EATHLINNFFGE	G
Lsan_3711	1	MIKTKI	IIINKLGLHARASAKFVSTAARFQSQIDVT	CNSQTVNGKSIMGVMLAANQGIEI	INGPDEIQMN	EATHLINNFFGE	G
LLO_2712	1	MIKTKI	IIINKLGLHARASAKFVSTAARFQSQIDVT	CNSQTVNGKSIMGVMLAANQGAEITM	DINGPDEVQMN	EALSHLINNFFGE	G
Ldum_2026	1	MIKTNI	IIINKLGLHARASAKFVSTAARKYQSHIEFVT	SNSQTVNGKSIMGVMLAANKGSELILEI	DGPDEVQMT	EATQQLINNYFGE	G
LDG_8575	1	MIKTKI	IIINKLGLHARASAKFVSTAARYQSHIDVT	KNSQTVNGKSIMGVMLAANKGSELITLEI	GPDEERMNE	EAVQLINNYFGE	G
Lmor_2114	1	MIKTKI	IIINKLGLHARASAKFVSTAARFQSHIDVT	KDSQTVNGKSIMGVMLAANKGSELITLEI	DGPDESAMND	EAVQLINNYFGE	G
Lqua_0165	1	MIKTKI	IIINNLGLHARASAKFVSTAARFQSHIDVT	KDSQTVNGKSIMGVMLAANKGSELITLEI	DGPDESAMND	EAVQLINNYFGE	G
Lwor_1058	1	MIKTKI	IIINKLGLHARASAKFVSTAARFQSHIDVT	KDSQTVNGKSIMGVMLAANKGSELITLEI	DGPDELAMNE	EAVQLINNYFGE	G
Lsha_0051	1	MIKTKI	IIINKLGLHARASAKFVSTAARFQSHIDVT	KDQTVNGKSIMGMMLAANKGSELITLEI	DGPDEEAMND	EAVQLINNYFGE	G
Llon_0061	1	MIITKI	IIINKLGLHARASAKFVSTAARKFQSHIDVT	KDSQTVNGKSIMGVMLAANKGSELTLQI	DGPDEEAMNE	EATTELINNRFGEP	E
lpg0475	1	MIKTKI	IIINNLGLHARASAKFVSTAARKFQSHIDVT	KDQTVNGKSIMGVMLAANKGSELITLEI	DGPDEERMNE	EAVELINNRFGES	E
Lwal_2511	1	MIKTTI	IIITNLGLHARASAKFVSTAARFQSHIDVT	KDSQTVNGKSIMGVMLAANKGSELITLEI	DGPDEVEMND	EAVQLIDRFGES	E
Lery_1325	1	MIKTTV	IIINKLGLHARASAKFVSTASKFQSYIDT	TKGSQTVNGKSIMGVMLAASKGIELTLQI	DGPDEEQMEQ	EALLINNRFGEP	E
Lrub_0844	1	MIKTTV	IIINKLGLHARASAKFVSTASKFQSHIDVT	KGSQTINGKSIMGVMLAASKGIELTLQI	MGPDEEHMEQ	EAVELINNRFGEP	E
Lspi_0321	1	MIKTTI	IIINKLGLHARASAKFVSTASKFQSHIDVT	RDGQTVNGKSIMGVMLAASKGIELTLQI	DGPDEEPMEK	EAVELINNRFGEP	E
Ldro_2460	1	MIETKIKI	IIINKLGLHARASAKFVSTTARFSSHIEFVT	KDSQTVNGKSIMGVMLAANKGSELTLSI	DGPDEVEMEKA	EVALINDCFGEP	E
Lnau_0402	1	MIETKIKI	IIINKLGLHARASAKFVSTTSRFSSHIEFVT	KDSQTVNGKSIMGVMLAANKGSELTLSI	DGPDETEMEKA	VSLINDCFGEP	E
Lmic_0413	1	MIETKIKI	IIINKLGLHARASAKFVSTTSRFQSHIEFVI	KDSQTVNGKSIMGVMLAANKGCELTLRI	DGPDEVEMEKA	VDLINNCFGEP	E
Lbru_2409a	1	MIKTKV	IIINKLGLHARASAKFVSTTSRFQSHIDVT	KDSKTINGKSIMGVMLAANKGIELTITI	DGPDEIEMERA	VDLINNCFGEP	E
Lfee_1192	1	MIKTKI	IIINKLGLHARASAKFVSTTSRFQSHIDVT	KNTQTVNGKSIMGMMLAASKGIELTLQI	DGPDEVEMEKA	ATELINNRFGEP	E
Lhac_2549	1	MIKTKI	IIINKLGLHARASAKFVSTTSRFQSHIDVT	KDSKTINGKSIMGVMLAANKGSELILEI	DGPDEQEMEKA	TDLINNRFGEA	E
Ljam_2632	1	MIRTKV	IIINKLGLHARASAKFVSTTSRFQSSIDVT	KDSKTINGKSIMGVMLAANKGSELITLEI	DGPDEQEMEKA	LNLINNRFGEP	E
Llan_0639	1	MIRTKV	IIINKLGLHARASAKFVSTTSRFQSHIDTIKD	QTINGKSIMGVMLAANKGIELTLQI	DGPDEVEMERA	VNLINDRFGEP	E
Ljor_1667	1	MIRTKV	IIINKLGLHARASAKFVSTTSRFQSHIDVIKD	QTINGKSIMVMMLAHRGTTLILQI	DGPDEEMERA	LNLINDRFGEP	E
Lmac_2858	1	MRETKIKI	IIINKLGLHARASAKFVSTTSRFQSHIEFVKKD	SQTVNGKSIMGVMLAANKGCELTLCI	DGPDETEMEQA	VELINNRFGEP	E
Loak_0261a	1	MIKTKIKI	IIINKLGLHARASAKFVSTAARFQSCIDVT	KDQTINGKSIMGVMLAAHQGIELILQI	DGPDEQEMEKA	EVALINNRFGEA	E
Lisr_2665	1	MITKKIKI	IIINKLGLHARASAKFVSTAARFQSHIEFVSK	GSQTVNGKSIMGVMLAASKGSELTLQI	DGPDETAMEE	EALTSLIHNRFGEE	E
Lade_0038	1	MIKITV	PIINNLGLHARASAKFVSLAGRQFQSIAEVTK	SQTVNGKSIMGVMLAAHKGSELITLEI	DGPDEEEMA	EAVKLINNRFGDE	E
Lqui_2328	1	MIKTTV	IIINKLGLHARASAKFVALAARYQSQIDVT	FNKTFVNNGKSIMGVMLAGGVGSELELV	DGPDEVEMEKA	EVALINNRFGEP	E
Lgee_0425	1	MIQVTVTI	INVNLGLHARASAKFVATAARFQSSIEIRRG	SQCVNGKSIMGVMLAAPCGSELILLEI	DGPDEEAMEKA	EVALINNRFGEP	E
consensus	1	**	*****	*****	*****	*

Fig. S1. Sequence alignment of the NPr protein from different *Legionella* species.

The sequence of the NPr proteins from 41 *Legionella* species were aligned using MAFFT version 7 (<http://mafft.cbrc.jp/alignment/server/>). Lpg, *L. pneumophila*; LDG, *L. drancourtii*; LLO, *L. longbeachae*; the abbreviations for the rest of the species are the first three letters of the species names which appear in Fig. 2.

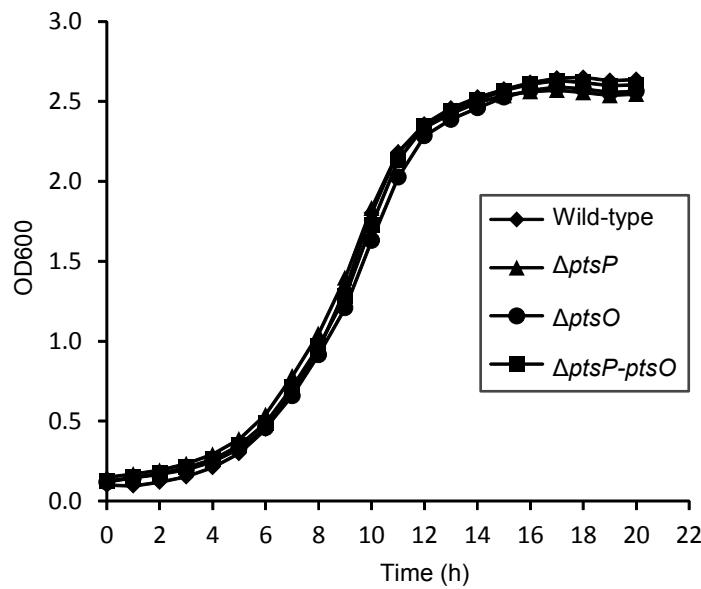


Fig. S2. In vitro growth profiles of the $\Delta ptsP$, $\Delta ptsO$ and $\Delta ptsP-ptsO$ mutants.
Growth rates of wild-type, $\Delta ptsP$, $\Delta ptsO$ and $\Delta ptsP-ptsO$ mutant strains of *L. pneumophila* in AYE broth cultures.
The optical density (OD) at 600 nm was measured every hour from triplicate samples.

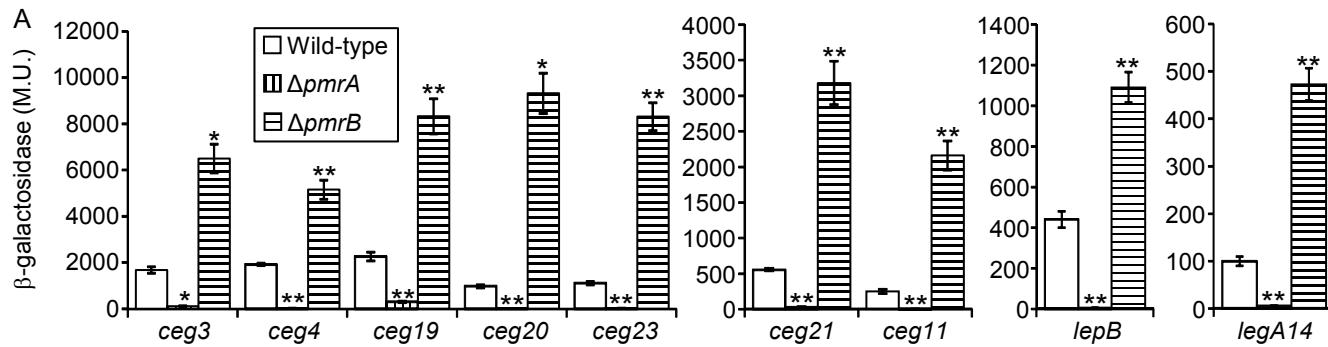


Fig. S3. The effect of the *L. pneumophila* PmrAB TCS on its target effector-encoding genes.

The expression of translational *lacZ* fusions of effector-encoding genes activated by PmrA was examined in the wild-type strain (JR32) (white bars), in the *pmrA* deletion mutant (HK-PQ1) (vertical line bars), and in the *pmrB* deletion mutant (EA-pmrB) (horizontal line bars) at the stationary phase. The levels of expression of the *lacZ* fusions were found to be significantly different (*, $P<10^{-4}$; **, $P<10^{-5}$, Student's *t* test), when comparing the expression in the wild-type strain and the *pmrA* or *pmrB* deletion mutants. The genes were grouped according to their levels of expression.

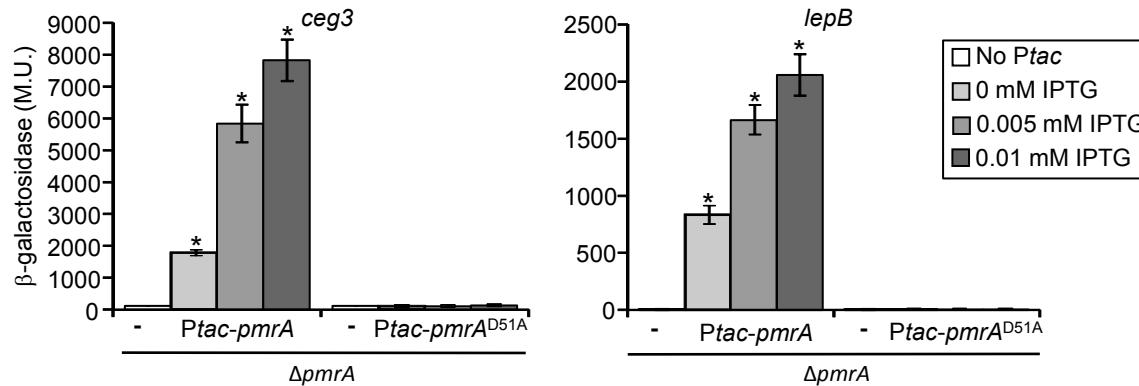


Fig. S4. PmrA must be phosphorylated in order to activate gene expression.

The levels of expression of two PmrA regulated effector-encoding genes (*ceg3* and *lepB*) were examined in the *L. pneumophila* *pmrA* deletion mutant (HK-PQ1). The bacteria contained a plasmid with the *pmrA* gene or the mutated *pmrA^{D51A}* gene cloned under the control of the IPTG inducible *Ptac* promoter. The plasmids containing the corresponding *lacZ* fusions of the examined genes without the *pmrA* gene were used as a control (white bars). The levels of expression of the *lacZ* fusions were found to be significantly different (*, P<10⁻⁵, Student's *t* test), when comparing the expression of the *lacZ* fusions containing the wild-type *pmrA* gene expressed from the *Ptac* promoter and the expression of the fusions without the *pmrA* gene.