













		PTK	GlyT	LRR	Ank	Cpep	SH2	L10	L22
									
PI4P-M		+	+	+					+
LED006		+	+	+	+	+	+	+	+
LED027			+	+	+			+	
LED035				+		+	+		+

GlyT – Glycosyltransferase; PTK - Protein tyrosine kinase; Cpep - Cysteine peptidase
 Ank - Ankyrin repeat; LRR - Leucine-rich repeat; SH2 - Src homology 2

FIG S1 Protein domains and LEDs found together with the predicted novel PI-binding LEDs and the PI4P-M-binding domain. Summary of known domains and LEDs which were found together in the same architecture with the PI4P-M and the novel PIs-binding LEDs.

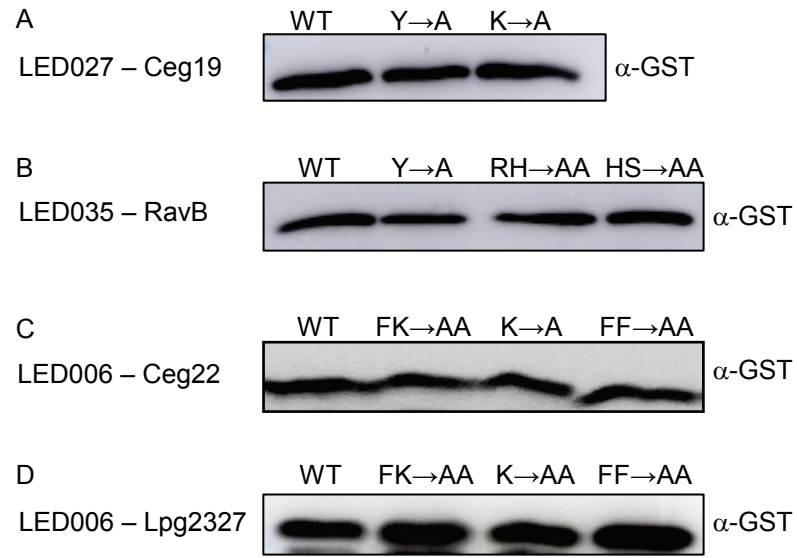


FIG S2 Western blot analysis of wild-type and mutated effectors examined on the PIs-arrays. The GST-fusion wild-type and mutated LEDs from the four effectors indicated on the left were monitored for their protein levels by western blot analysis using α -GST antibody.

Ceg22	1	SASKAANRLHQELLIASQLY---FYHKT---PEAYENFKQTCQREIERARPVLEQHR-GW
LepB	1	EASTAAKTLATKLRLEIKNY---LDNNESEKSAIINSFKINAKRHIENSKETLNQHREEW
LegK1	1	DAANAMSQLVSKLTAYTNYL---EKNPD---PFLIKFYKECCIAEIDLANLTLQNH-DA
lpg2327	1	KAHDTANTLLQSLIAARDEYERDLRANEFSQLAGRFKFLACQDAVKIAKPVLEKDI-GW
LegC6	1	KAYEAAKILLRQLQETRDQYVIDLANPQINFKEAGLKFKEASNLVIQQAKPILEKDI-GW
Lem9	1	EAKIKANDLLMSLRKNKDEA---FSNPS---LESLYDFADKSKQMIKSTISSLERES-GS
LegC5	1	PAKQRAIELLDTRLRKYKEEA---FNDPS---REKLISFAQSTKRAIQEATPILQKDI-GW
Ceg22	54	KPLLNVGAATIGLGVLYLLAASINYYKTEGRHFFHFHETDSLQKLENIINMAQSQVLR-
LepB	58	KYLLANVTLGVFLLGIGYLAAILINKATTGNYTFFSQTNSG--KKLDALEKATSSHSE
LegK1	54	LWLVAELSTAILLLGIGYLFAGFINYYNTGRLGLFSQTRSE--KLVEEMKSSVLG----
lpg2327	60	GDYLNLLKCLGN-AVIT----VFTFGYQ--QGFAYARPDSAKAVEKAEDLGLRQAA
LegC6	60	GEYLNLFKVIIVN-AIVF----CVTFGAS--QGFATTRAKSAEAVEKAESELELNQLG
Lem9	54	VVFLSDLAEQILN-TINTFLNNTLSSSTSSRSQFFGFKLSYEKVIQDLEKNIIDNELK-
LegC5	54	GDYLTNLAKQLVN-AVTFAYAVAVTFGTGTHQGFALKSSLAVSQSQNLEGAINSELS-

FIG S3 Multiple sequence alignment of *L. pneumophila* effectors harboring LED006 that bind PI3P. Multiple sequence alignment of the seven *L. pneumophila* effectors containing LED006 that were found to bind PI3P. The conserved adjacent phenylalanine-lysine and the two adjacent phenylalanine residues are marked with a red box. The conserved adjacent histidine-arginine that were found to be conserved in most of the effectors harboring LED006 and the single lysine or arginine that were found in the other effectors harboring LED006 are colored in red and boxed in blue.