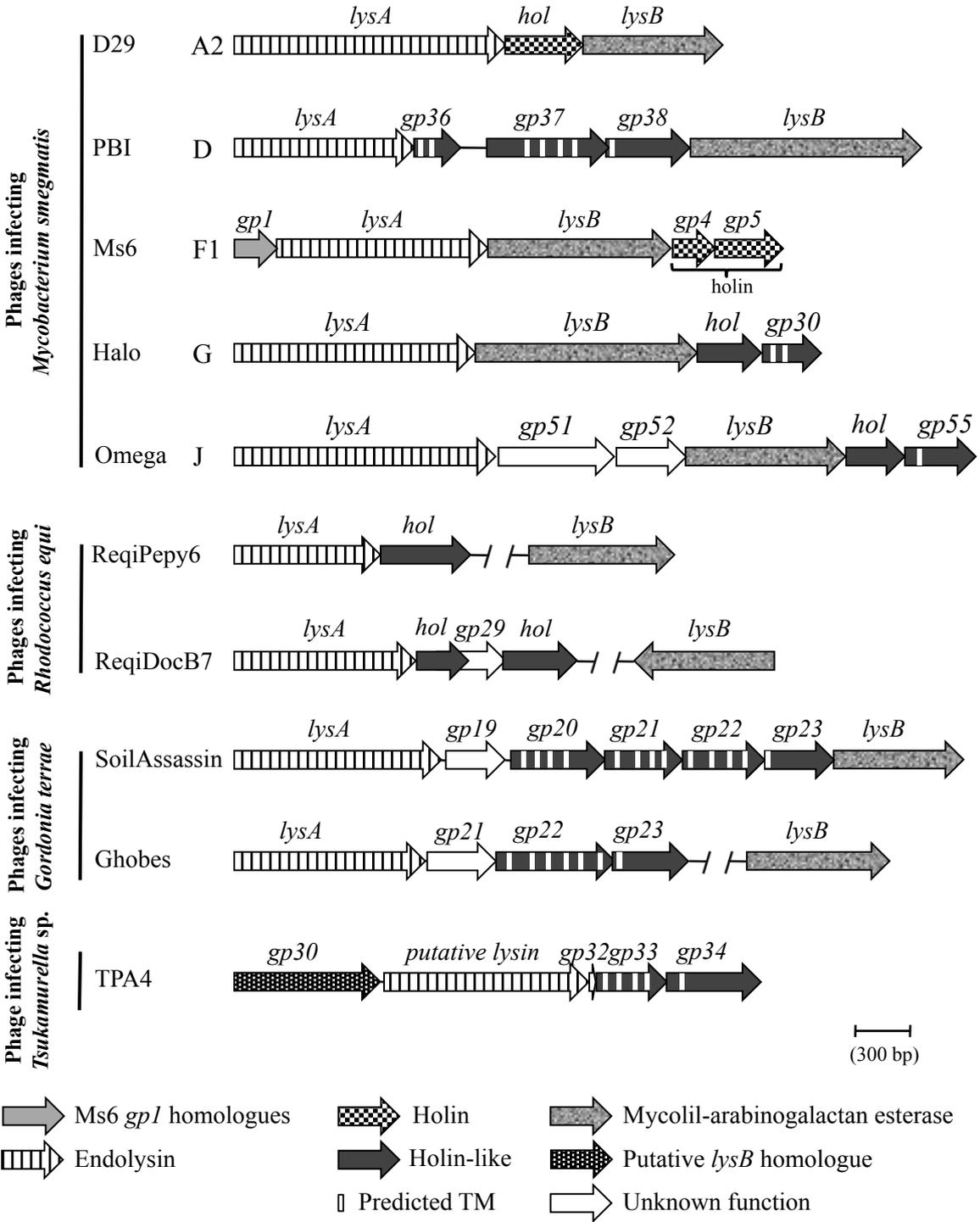


Figure S1

A

Phage Cluster/
Subcluster

Lysis Genes Organization



B

D29	70	...ADPYADFAMAGYSQGAIVVGQVLKH...	95
PBI1	168	...KDPDVEFWFSGYSQKADGLEDALEI...	193
Ms6	156	...RIETHGTALAGYSQGAVVLSELWMN...	181
Halo	175	...VNPKIRVVIGGYSAGAIAAAMF-RA...	199
Omega	85	...RTTPGKIVLSAYSQSAVAFAFAYVWRD...	110
ReqiPepy6	76	...SNPGKQFILLAYSGGNRVIHEW-ME...	100
ReqiDocB7	53	...-FTRQAI FVAGYSQGGTVVTKAIKH...	77
SoilAssassin	71	...ERSQFDVVVAGYSQGA AVAVHY-AL...	95
Ghobes	77	...AHPDDR FVVLGYS LGALVGTKF-LE...	101
TPA4	73	...AAARGRFVGLGYSQGG SLLTEWLN...	98

Figure S1 Comparison of *lysB* genes from phages infecting members of the Mycolata group. **(A)** Illustrated are representatives of mycobacteriophages and phages infecting *Rhodococcus equi*, *Gordoniae terrae* and *Tsukamurella* spp.. The genes marked with a white segment indicate genes not previously assigned as holins, but having predicted transmembrane segments. **(B)**. Alignment of Ms6 LysB and putative LysB protein homologues. The conserved pentapeptide (G/A-X-S-X-G) is highlighted on a grey background. Numbers refer to the amino acid positions.