Supplementary Material: Evolved distal tail protein of skunaviruses facilitates adsorption to exopolysaccharide-encoding lactococci

Supplementary Table 1. Amino acid identity among evolved Dits in this study.

	Typical								EpsM Variant			
	Amino Acid Identity (%)											
	D4839	D6869	D6875	D6887	D6888	D970	D1113	D6067	D753	D4006	D4842	D5604
D6869	99.8											
D6875	97.9	97.6										
D6887	98.5	98.3	97.6									
D6888	97.9	97.6	100	97.6								
D970	91.2	91.4	93.3	91.8	93.3							
D1113	92.3	92.1	94.4	92.5	94.4	98.9						
D6067	91.8	91.6	94.0	92.5	94.0	98.9	99.6					
D753	61.4	61.4	61.6	61.6	61.6	58.2	58.3	58.3				
D4006	61.4	61.4	61.6	61.6	61.6	58.2	58.3	58.3	99.8			
D4842	61.4	61.4	61.6	61.6	61.6	58.2	58.3	58.3	99.7	99.8		
D5604	61.4	61.4	61.6	61.6	61.6	58.2	58.3	58.3	99.7	99.8	100	
D2929	58.0	58.0	58.8	58.2	58.8	61.4	61.3	61.3	88.0	87.8	87.8	87.8

(Row labels D6869–D6067 grouped as "Typical"; D753–D2929 grouped as "EpsM Variant")
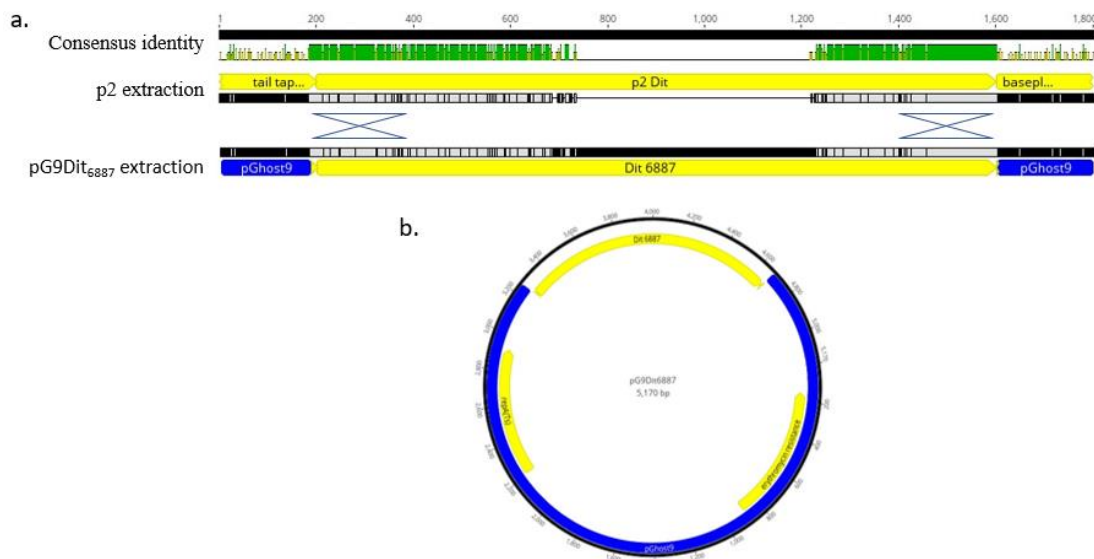
Percent pairwise identity of the deduced amino acid sequences of the evolved Dits is shown. Phages that infect strains encoding the typical 6073-like EPS vs. EpsM variant are indicated. Blue box highlights the comparison of Dits belonging to phages infecting strains encoding the typical vs EpsM variant EPS.

Supplementary Figure 1. Dit exchange by homologous recombination. **a. DNA sequence alignment of representative classical *dit* encoded by phage p2 and *dit*$_{6887}$ cloned onto pGhost9, including flanking regions. b. pG9Dit$_{6887}$ vector map.** Blue bars indicate pGhost9 sequence. Yellow arrows indicate CDS. In the consensus identity bar, green indicates identity, yellow indicates polymorphism, and red indicates low identity. The sequence homology found at the 5' and 3' ends of the *dits* served as regions for homologous recombination.