

Figure S1. Morphology of lysis plaques and electron microscopy of wide host range and narrow host range phages. Morphology of lysis plaques and electron microscopy of transmission in (A) wide host range phage (B) narrow host range phage.

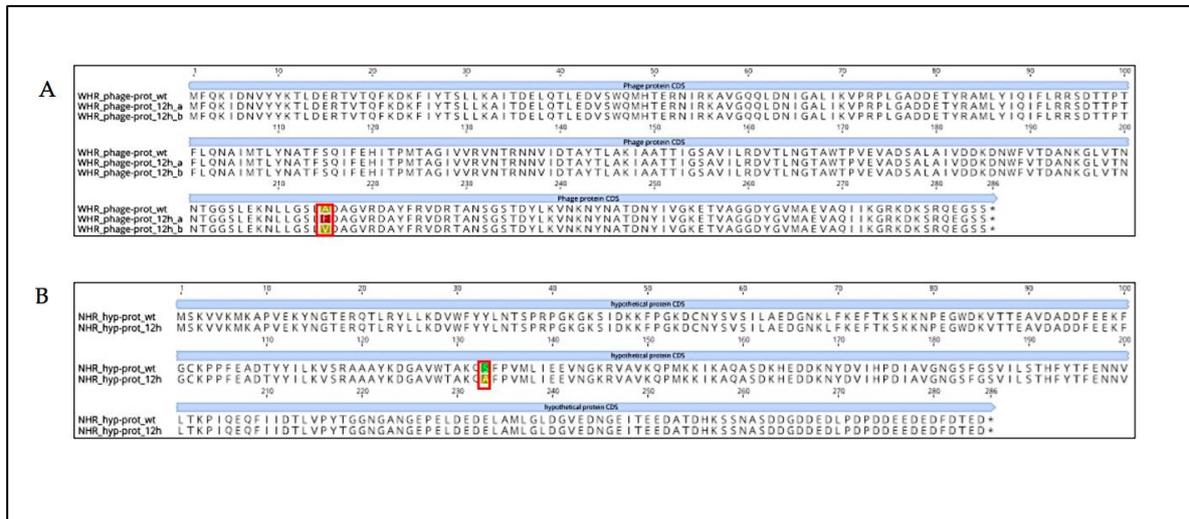


Figure S2. Amino acid alignment of phage protein and hypothetical protein in wild-type phage compared to WHR or NHR phage exposed to *S. Infantis* for 12-h. (A) Amino acid alignment of phage protein in wild-type WHR phage and WHR phage exposed to *S. Infantis* for 12-h. Sequences a and b represent two different mutations observed at the same position. (B) Amino acid alignment of hypothetical protein in wild-type NHR phage and NHR phage exposed to *S. Infantis* for 12-h. The nucleotide sequence of the gene from the wild type genome was extracted and modified to reflect the mutation, then the wild type and mutation-containing nucleotide sequences were translated and aligned with ClustalW[75] in Geneious Prime[76]. Amino acids labeled with different colors represent differences among sequences of wild-type phages and the 12-h exposed phages. Amino acid changes caused by SNPs are marked in red frames.

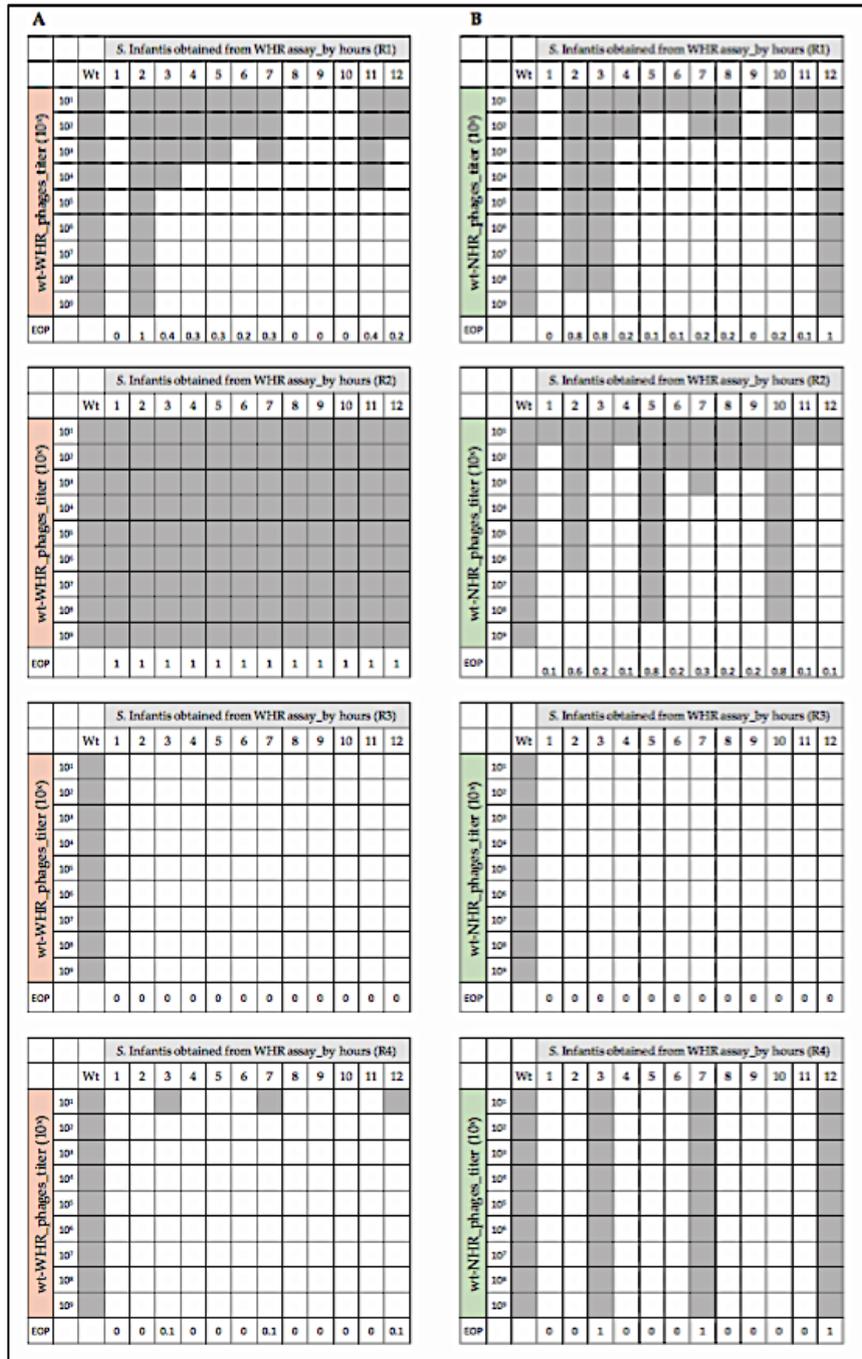


Figure S3. Evaluation of phage sensitivity by efficiency of plating (EOP) on isolated *S. Infantis* SI survivors to WHR phage and cross-resistance assays. It shows the titer of the wild type phage on *S. Infantis* obtained from challenge assay. Lysis is marked in grey and no lysis in white. A. Evaluation of phage sensitivity of EOP in *S. Infantis* obtained every hours of wide assay, exposed to wild type (wt)-WHR phage. B. Cross-resistance assay of EOP in *S. Infantis* obtained every hour of wide assay, exposed to wild type (wt)-NHR phage.

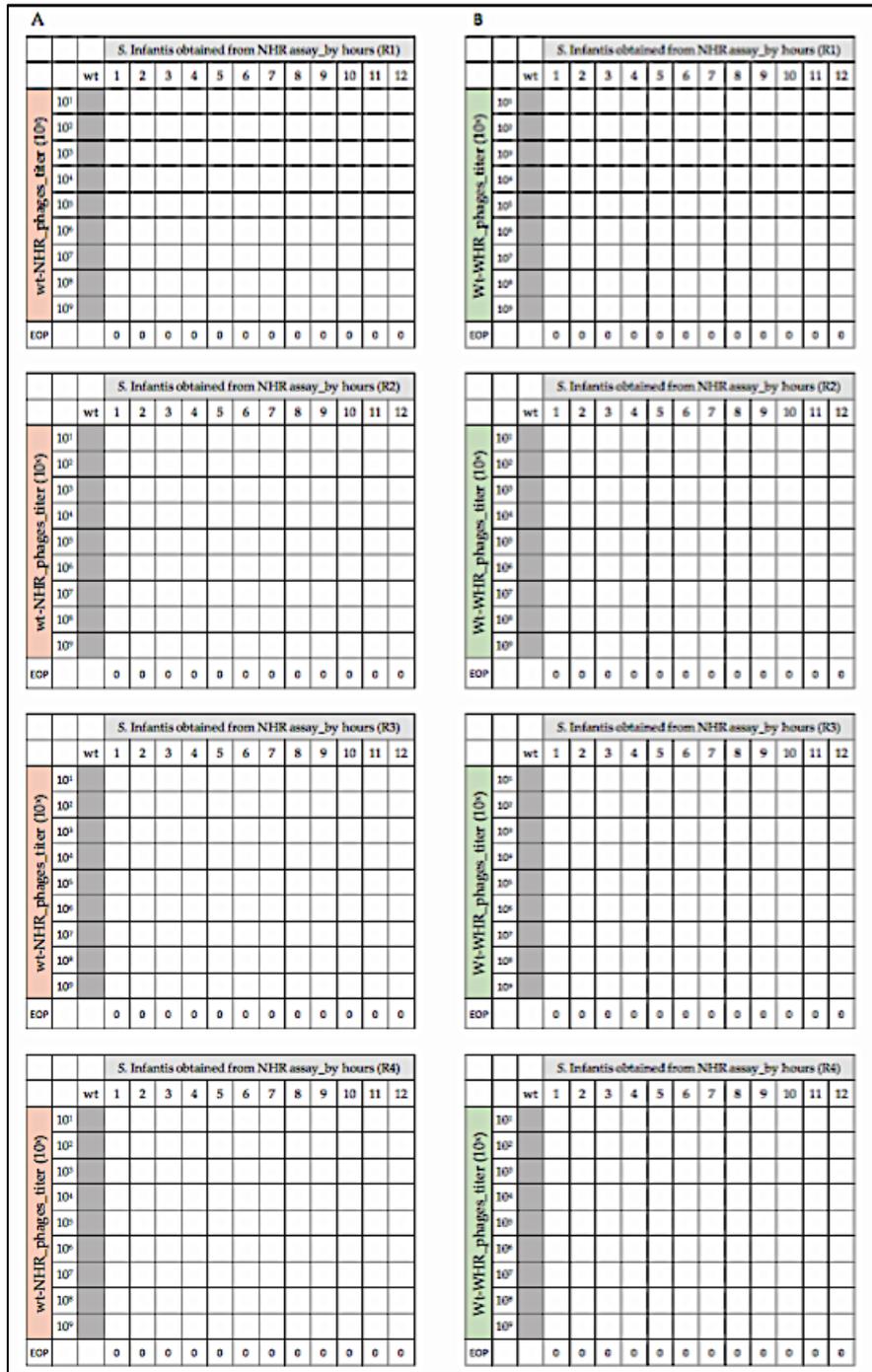


Figure S4. Evaluation of phage sensitivity by efficiency of plating (EOP) on isolated SI survivors to NHR phage and cross-resistance assays. It shows the titer of the wild type phage on *S. Infantis* obtained from challenge assay. Lysis is marked in grey and no lysis in white. **A.** EOP in *S. Infantis* obtained every hour of narrow assay, exposed to (wt) wild type-NHR phage. **B.** Cross-resistance assay of EOP in *S. Infantis* obtained every hours of narrow assay, exposed to wild type (wt)-WHR phage.

Table S1. Antigenic somatic formulae (O) and presence of *rfaB* and *rfaK* gene in serovars of *Salmonella enterica* susceptible to wide and narrow host range phages obtained from challenge assays.

Characteristics of susceptible serovars of both wide and narrow host range phages			
Serovars (Serogroup)	Somatic antigenic (O) formulae	Presence <i>rfaB</i> ¹ (ID) ²	Presence <i>rfaK</i> ³ (ID) ²
Typhimurium (Group O:4 [B])	1,4,[5],12	TMV96147.1	ASF66624.1
Virchow (Group O:7 [C ₁])	6,7,14	AZH72471.1	AZH72476.1
Oranienburg (Group O:7 [C ₁])	6,7,14	THC06534.1	SUH68841.1
Braenderup (Group O:7 [C ₁])	6,7,14	Not found ⁴	SUH55395.1
Infantis (Group O:7 [C ₁])	6,7,14	TMV47934.1	SQI71138.1
Newport (Group O:8 [C ₂])	6,8,20	TMM69866.1	AGS27141.1
Corvallis (Group O:8 [C ₃])	8,20	TLC03182.1	Not found ⁴
Kentucky (Group O:8 [C ₃])	8,20	TMW25308.1	KUD18860.1
Javiana (Group O:9 [D ₁])	1,9,12	Not found ⁴	KUD61483.1
Dublin (Group O:9 [D ₁])	1,9,12	TKX13464.1	SUI05380.1
Panama (Group O:9 [D ₁])	1,9,12	Not found ⁴	SUH76918.1
Characteristics of susceptible serovars of only wide host range phage			
Muenster (Group O:3,10 [E ₁])	3,{10}{15}{15,34}	Not found⁴	KTW46212.1
Agona (Group O:4 [B])	1,4,[5],12	TLA84965.1	RKD15901.1
Saintpaul (Group O:4 [B])	1,4,[5],12	QCW59584.1	KUD72187.1
Heidelberg (Group O:4[B])	1,4,[5],12	TMV96713.1	RFN36928.1
I 4,5,12:i:- (monophasic variant of Typhimurium) (Group O:4 [B])	4,5,12	BBH80090.1	BBH80095.1
Stanley (Group O:4 [B])	1,4,[5],12,[27]	TLC20503.1	SQH42842.1
Choleraesuis (Group O:7 [C ₁])	6,7	Not found⁴	Not found⁴
Mbandaka (Group O:7 [C ₁])	6,7,14	RJJ85429.1	RAN13577.1
Montevideo (Group O:7 [C ₁] or O:54 ⁵)	6,7,14 or {6,7,14}{54} ⁵	TMM93554.1	AJQ76118.1
Enteritidis (Group O:9 [D ₁])	1,9,12	TLC90283.1	SUI12981.1

¹(*rfaB*) gene encoding for the enzyme waaB engaged in the polymerization of core LPS adding UDP-D-galactose lipopolysaccharide

1,6 glucosyltransferase or Lipopolysaccharide 1,6-galactosyltransferase.

²GenBank ID: Accession number.

³(*rfaK*) gene encoding for the enzyme waaK engaged in the polymerization of core LPS adding UDP-D-glucose:lipopolysaccharide α -1,2 glucosyltransferase or lipopolysaccharide 1,2-N acetylglucosaminetransferase.

⁴Not Found: These genes were not found in the mentioned serovars but have been described for *Salmonella enterica*.

⁵Factor O:54 is plasmid-controlled. In serovar Montevideo, factors O:6,7,14 are expressed in the absence of O:54.

Reference of Somatic antigenic (O) formulae: Grimont et al,[82].