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Table 2. Host integration sites of P2 related phages.

Phage	Host	Integration site (kb from ori)	Gene (s) or orf (s)	AttB sequence **	Reference / accession number
P2	<i>E. coli</i> K-12	2 165.2	Between <i>yegQ</i> – <i>b2083</i>	AAAAA <u>TAAGCCCGTGT</u> <u>AAGGGAGATT</u>	Yu et al., 1989
”	<i>E. coli</i> O157:E7	2 842.6	Between <i>Ec2889</i> – <i>Ec2890</i>	”	Hayashi et al., 2001
”	<i>E. coli</i> O157:E7 EDL933	2 912.8	Between <i>Z3250</i> (<i>yegQ</i>) – <i>Z3251</i>	”	Perna et al., 2001
WΦ	<i>E. coli</i> K-12	4 103.9	Between <i>cpxR</i> – <i>pfkA</i>	GACACCATCCCTGTCTT <u>CCCCACATGCTGTGGGGGTTTTTTTTATC</u>	Liu and Haggård-Ljungquist, 1999
186	”	2 783.8 and 3 213.3	Within <i>ileY</i> and <i>ileX</i> tRNA ^{ile}	TGCTGGACTTGAACCAGCGACCAAGCGATTATGAGT	U32222, NC_001317
HP1	<i>Haemophilus influenzae</i>	91.8 and 139.6	Within tRNA ^{leu}	<u>AGGGA</u> ↓ <u>TTTTAAA</u> ↓ <u>TCCCTT</u>	Hauser and Scocca, 1992a , Hauser and Scocca, 1992b
ΦCTX	<i>Pseudomonas aeruginosa</i>	2 947.6	Within tRNA ^{ser}	ATATGGCGGAGGCGGTGAGATTCGAACTC	Hayashi et al., 1993
K139	<i>Vibrio cholerae</i>	2 334.4 (chromosome I)	Between <i>FlaC</i> – Flagellin core protein A	<u>CAGAAAAGGGGCTTTTCTTTTTTC*</u>	Nesper et al., 1999

* Not verified experimentally

** The cleavage sites in HP1 are indicated by arrows. Inverted repeats are underlined with a single line, direct repeats are underlined with a double line.