



PP582757.1_Klebsiella_phage_vB_KM5a1-KLB31	100.0	93.5	93.6	71.3	71.2	71.0	70.5	69.5	69.9	69.3
AP014715.1_Edwardsiella_phage_Pei26_DNA	100.0	97.0	70.7	70.8	70.3	70.3	69.2	69.0	68.8	
NC_028683.1_Edwardsiella_phage_Pei20_DNA	100.0	100.0	70.5	70.8	70.5	70.5	69.3	69.4	69.1	<i>Kanagawavirus pei20</i>
OL355124.1_MAG:_Enterobacter_phage_ENC9	0.9	0.9	0.9	100.0	93.4	92.8	88.5	88.2	87.6	88.4
NC_048849.1_Enterobacter_phage_vB_EclM_CIP9	0.9	0.9	0.9	100.0	93.8	85.7	88.2	87.4	88.3	<i>Kanagawavirus cipnine</i>
ON630910.1_Enterobacter_phage_Entb_45	0.9	0.9	0.9	100.0	85.0	87.9	88.2	88.2	85.2	
NC_070776.1_Kosakonia_phage_305	0.9	0.9	0.9	100.0	87.0	86.7	86.8	86.8	86.8	<i>Kanagawavirus threeohfive</i>
NC_070777.1_Enterobacter_phage_vB_EhoM-IME523	0.9	0.9	0.9	100.0	89.1	88.1	88.1	88.1	88.1	<i>Kanagawavirus eclm</i>
NC_070778.1_Enterobacter_phage_vB_EclM_Q7622	0.9	0.9	0.9	100.0	92.9	92.9	92.9	92.9	92.9	<i>Kanagawavirus mime</i>
PP236086.1_Enterobacter_phage_ZX14	0.9	0.9	0.9	100.0	100.0	100.0	100.0	100.0	100.0	