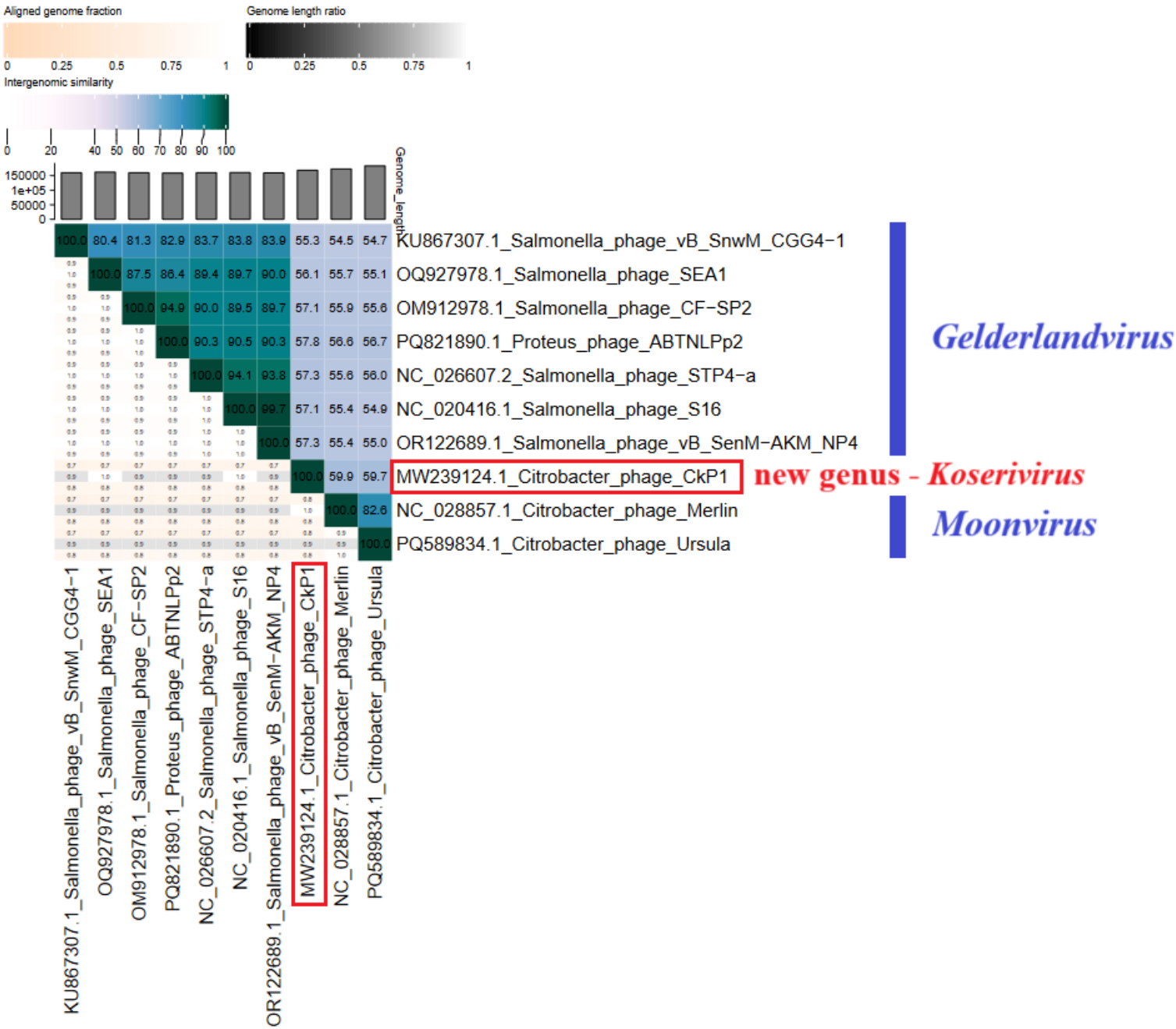
Aligned genome fraction
0 0.25 0.5 0.75 1
Genome length ratio
0 0.25 0.5 0.75 1
Intergenomic similarity
0 20 40 50 60 70 80 90 100
150000
1e+05
50000
0
Genome_length
KU867307.1_Salmonella_phage_vB_SnwM_CGG4-1
OQ927978.1_Salmonella_phage_SEA1
OM912978.1_Salmonella_phage_CF-SP2
PQ821890.1_Proteus_phage_ABTNLPp2
NC_026607.2_Salmonella_phage_STP4-a
NC_020416.1_Salmonella_phage_S16
OR122689.1_Salmonella_phage_vB_SenM-AKM_NP4
MW239124.1_Citrobacter_phage_CkP1
NC_028857.1_Citrobacter_phage_Merlin
PQ589834.1_Citrobacter_phage_Ursula
Gelderlandvirus
new genus - Koserivirus
Moonvirus