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
Genome_length
80000
60000
40000
20000
0
KX898400.1_Pseudomonas_phage_JG054
NC_041953.1_Pseudomonas_phage_PaMx25
MN504636.1_Pseudomonas_phage_Quinobequin−P09
KX129925.1_Pseudomonas_phage_NP1
KX898399.1_Pseudomonas_phage_JG012
MK892759.1_Prokaryotic_dsDNA_virus_sp._isolate_Tp1_38_OMZ_0−0d2_C1907826_1
AY576273.1_Alphaproteobacteria_phage_PhiJL001
NC_047877.1_Bordetella_phage_CN2
NC_047878.1_Bordetella_phage_FP1
NC_047879.1_Bordetella_phage_MW2
KX961385.2_
NC_047876.1_Bordetella_phage_CN1
AM749441.1_Pseudomonas_phage_YuA
JX131330.1_Pseudomonas_phage_MP1412
KT734862.1_Pseudomonas_phage_PAE1
MT118302.1_Pseudomonas_phage_Epa38
MF490239.1_Pseudomonas_phage_vB_PaeS_S218
NC_041934.1_Pseudomonas_phage_LKO4
DQ163916.1_Bacteriophage_M6
KX198613.1_Pseudomonas_phage_AN14
MN862068.1_Brevundimonas_phage_vB_BsubS−Delta
KX241618.1_Xanthomonas_phage_Xoo−sp2
LR743532.1_Xanthomonas_phage_Bosa
MG018224.1_Stenotrophomonas_phage_DLP4
JQ067093.2_Pseudomonas_phage_PaMx74,
JQ067089.2_Pseudomonas_phage_PaMx28,
KU204984.2_Pseudomonas_phage_AAT−1
JQ067087.2_Pseudomonas_phage_PaMx11
LN610584.1_Pseudomonas_phage_vB_PaeS_PAO1_Ab19
KU356689.1_Pseudomonas_phage_ZC01
LN610577.1_Pseudomonas_phage_vB_PaeS_PAO1_Ab18
LN610585.1_Pseudomonas_phage_vB_PaeS_PAO1_Ab20
MT118296.1_Pseudomonas_phage_Epa19
MT108725.1_Pseudomonas_phage_Epa5
MT108731.1_Pseudomonas_phage_Epa43