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
60000
40000
20000
0
MW269554.1_Achromobacter_phg_vB_AchrS_AchV4
MF476925.1_Klebsiella_phg_YMC16/01/N133_KPN_BP
KY971609.1_Pseudomonas_phg_PspYZU01
MN478374.1_Pseudomonas_phg_Phobos
HQ632859.1_Loktanella_phg_pCB2051−A
KY249644.1_Synechococcus_virus_S−ESS1
MN062188.1_Proteus_phg_Saba
MW145139.1_Providencia_phg_Kokobel1
MG030346.1_Proteus_phg_PM87
KP063118.1_Proteus_phg_pPM_01
MN604053.1_Escherichia_phg_E21
MT330372.1_Cronobacter_phg_JC01
MG835858.1_Klebsiella_phg_KPN
MH817999.1_Klebsiella_phg_Seifer
MN106244.1_Klebsiella_phg_Soft
JQ340774.2_Enterobacter_phg_Enc34
MN871450.1_Serratia_phg_KpYy_1_41
KR296689.1_Salmonella_phg_35
KY620117.1_Salmonella_phg_BSPM4
MH791395.1_Salmonella_phg_SeWh−1
MH631453.1_Salmonella_phg_Siskin
KX765862.1_Salmonella_phg_ST−101
KR296691.1_Salmonella_phg_37
MW355479.1_Salmonella_phg_ER24
KM366098.1_Salmonella_phg_BP12C
KM458633.1_Salmonella_phg_Chi
MG280946.1_Salmonella_phg_KFS−SE1
KU927500.1_Salmonella_phg_118970_sal1
LR026998.1_Salmonella_phg_YSD1
LC553736.1_Salmonella_phg_SAP012
JX296113.1_Providencia_phg_Redjac
MT675124.1_Providencia_phg_PibeRecoleta
MT675125.1_Providencia_phg_Stilesk
MN317029.1_Aeromonas_phg_vB_AhyS−A18P4
MK838113.1_Aeromonas_phg_LAh_7
MT952005.1_Aeromonas_phg_BUCT551
MN184886.1_Erwinia_phg_pEp_SNUABM_08
MN505213.1_Serratia_phg_JS26
KF626665.1_Xylella_phg_Sano
KF626668.1_Xylella_phg_Salvo
LR743524.1_Xylella_phg_Bacata
AY357582.2_Burkholderia_phg_BcepNazgul
JN564907.1_Burkholderia_phg_AH2
KT321316.2_Achromobacter_phg_phiAxp−2
MN536026.1_Pseudomonas_phg_vB_Pae−SS2019XI
MN692199.1_Pectobacterium_phg_MA12