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
60000
40000
20000
0
Genome_length
FJ168659.1_Myco_phage_Brujita
HM152765.1_Myco_phage_Island3
MN428052.1_Myco_phage_Smooch
AY129335.1_Myco_virus_Corndog
KJ829260.1_Myco_phage_YungJamal
NC_023712.1_Myco_phage_Firecracker
KT281796.1_Myco_phage_Zakhe101
NC_022325.1_Myco_phage_Dylan
MH590592.1_Myco_phage_Ryadel
MT818418.1_Myco_phage_Shida
MH926062.1_Myco_phage_Vorrps
MN428058.1_Myco_phage_Krili
MT818425.1_Myco_phage_NiebruSaylor
MG872838.1_Myco_phage_JangDynasty
MN585964.1_Myco_phage_Blessica
NC_022057.1_Myco_phage_Catdawg
MW314845.1_Myco_phage_TelAviv
MG099943.1_Myco_phage_Familton
MH020246.1_Myco_phage_SchoolBus