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
40000
20000
0
NC_051730.1_Myco_phage_Jung
MN096356.1_Myco_phage_Bunnies
MF281061.1_Myco_phage_Ksquared
NC_051732.1_Myco_phage_Ksquared
MF373843.1_Myco_phage_StevieRay
MG198785.1_Myco_phage_Thespis
NC_028747.1_Myco_phage_Brusacoram
MF140399.1_Myco_phage_Bartholomew
MK814758.1_Myco_phage_FirstPlacePfu
NC_051735.1_Myco_phage_FirstPlacePfu
NC_041969.1_Myco_phage_Jebeks
MK937604.1_Myco_phage_Necropolis
MN010757.1_Myco_phage_HUHilltop
NC_023552.1_Myco_phage_Donovan
MK919480.1_Myco_phage_Techage
NC_021302.1_Myco_phage_Fishburne
MF919492.1_Myco_phage_Arib1
MK524508.1_Myco_phage_Zilizebeth
MF472894.1_Myco_phage_Majeke
MK016499.1_Myco_phage_Mangethe
FJ168659.1_Myco_phage_Brujita
HM152765.1_Myco_phage_Island3
MN234195.1_Myco_phage_Xula
MN234236.1_Myco_phage_QueenHazel
AP018487.1_Myco_phage_HC
NC_023697.1_Myco_phage_Babsiella
AY129333.1 Myco_virus_Che9c
NC_026589.1_Myco_phage_Sbash