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
KM101124.1_Myco_phg_Squirty
MH020235.1_Myco_phg_Batiatus
MH155865.1_Myco_phg_BobaPhett
MH651169.1_Myco_phg_Burwell21
KY348865.1_Myco_phg_Bubbles123
MN586012.1_Myco_phg_Blexus
KM347889.1_Myco_phg_BuzzLyseyear
AY129330.1_Myco_virus_Che8
MH744415.1_Myco_phg_ArcusAngelus
MN945900.1_Myco_phg_BodEinwohner17
MH001449.1_Myco_phg_MooMoo
JF704115.1_Myco_phg_Yoshi
MF919502.1_Myco_phg_Demsculpinboyz
MT522000.1_Myco_phg_Soul22
JQ809702.1_Myco_phg_Avani
KF017003.1_Myco_phg_Jabbawokkie
KJ567041.1_Myco_phg_Zapner
MN908688.1_Myco_phg_Cornie
MH651187.1_Myco_phg_Renaud18
MH077585.1_Myco_phg_TChen
MK977709.1_Myco_phg_ThetaBob