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
NC_043767.1_Myco_vir_TA17a
MK814751.1_Myco_phg_Bananafish
MH001452.1_Myco_phg_Kheth
MT639652.1_Myco_phg_MasterPo
MH727546.1_Myco_phg_Eaglehorse
MH590591.1_Myco_phg_Sabella
KT365402.1_Myco_phg_Tres
MG757162.1_Myco_phg_Opia
MN813678.1_Myco_phg_Lephleur
KM101117.1_Myco_phg_LizLemon
KT880194.1_Myco_phg_Glass
MH697584.1_Myco_phg_FrenchFry
MN234225.1_Myco_phg_Rhinoforte
MK061411.1_Myco_phg_Faze9
MK620898.1_Myco_phg_Coffee
MN428049.1_Myco_phg_West99
MH051249.1_Myco_phg_Boyle
JN698991.1_Myco_phg_Hedgerow
AY129334.1_Myco_phg_Rosebush
MN586045.1_Myco_phg_Brownie5
MN586046.1_Myco_phg_Tinciduntsolum
MG812491.1_Myco_phg_ItsyBitsy1
JN618996.1_Myco_phg_Arbiter
MG812490.1_Myco_phg_Holeinone
NC_053503.1_Myco_phg_Laurie
NC_042050.1_Myco_phg_Godines
DQ398048.1_Myco_phg_Qyrzula
JN699004.1_Myco_phg_Ares