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
MN096360.1_Myco_phg_Rita1961
MT952851.1_Myco_phg_Gervas
MG920059.1_Myco_phg_Baloo
KJ194581.1_Myco_phg_Audrey
NC_023742.1_Myco_phg_Akoma
KR080203.1_Myco_phg_OrangeOswald
KR080205.1_Myco_phg_Corofin
KJ194584.1_Myco_phg_Heathcliff
MG925338.1_Myco_phg_ChaChing
MH316565.1_Myco_phg_Mortcellus
KP027207.2_Myco_phg_Chandler
MG925353.1_Myco_phg_Nozo
NC_041965.1_Myco_phg_Athena
FJ641182.1_Myco_phg_Phlyer
MK359357.1_Myco_phg_RomaT
MG839014.1_Myco_phg_RagingRooster
MN444872.1_Myco_phg_SynergyX
MH051265.1_Myco_phg_Yahalom
MN234223.1_Myco_phg_Philly
MT310892.1_Myco_phg_Compostia
JF704095.1_Myco_phg_Daisy,
MN444873.1_Myco_phg_Abinghost
JN699018.1_Myco_phg_Kamiyu
MT310871.1_Myco_phg_Jackstina
NC_011057.1_Myco_phg_Phaedrus
NC_022983.1_Myco_phg_Bernardo
NC_023686.1_Myco_phg_Gadjet
DQ398049.1_Myco_phg_Pipefish
MH513976.1_Myco_phg_Morty007
MK061414.1_Myco_phg_Marley1013
MH576977.1_Myco_phg_Tydolla
MN096359.1_Myco_phg_Obutu