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
KR080200.1_Myco_phg_AlanGrant
NC_028934.1_Myco_phg_Vincenzo
MT639648.1_Myco_phg_Heath
MT818419.1_Myco_phg_Lolalove
MW435857.1_Myco_phg_Hydro
NC_042035.1_Myco_phg_Zemanar,
MH513970.1_Myco_phg_Hangman
MK524486.1_Myco_phg_Waleliano
NC_028968.1_Myco_phg_BrownCNA
MN369759.1_Myco_phg_Mithril
MN234171.1_Myco_phg_Magpie
MT897910.1_Myco_phg_VioletZ
MN428050.1_Myco_phg_Apex
KF279412.2_Myco_phg_Bane1
KF279413.1_Myco_phg_Bane2
KX589269.1_Myco_phg_Fortunato
MT310870.1_Myco_phg_RawrgerThat
NC_023554.1_Myco_phg_JAMaL
NC_042034.1_Myco_phg_ChrisnMich,
EU770221.1_Myco_phg_Nigel
NC_023741.1_Myco_phg_Stinger
DQ398044.1_Myco_phg_Cooper
KF279411.1_Myco_phg_Adawi