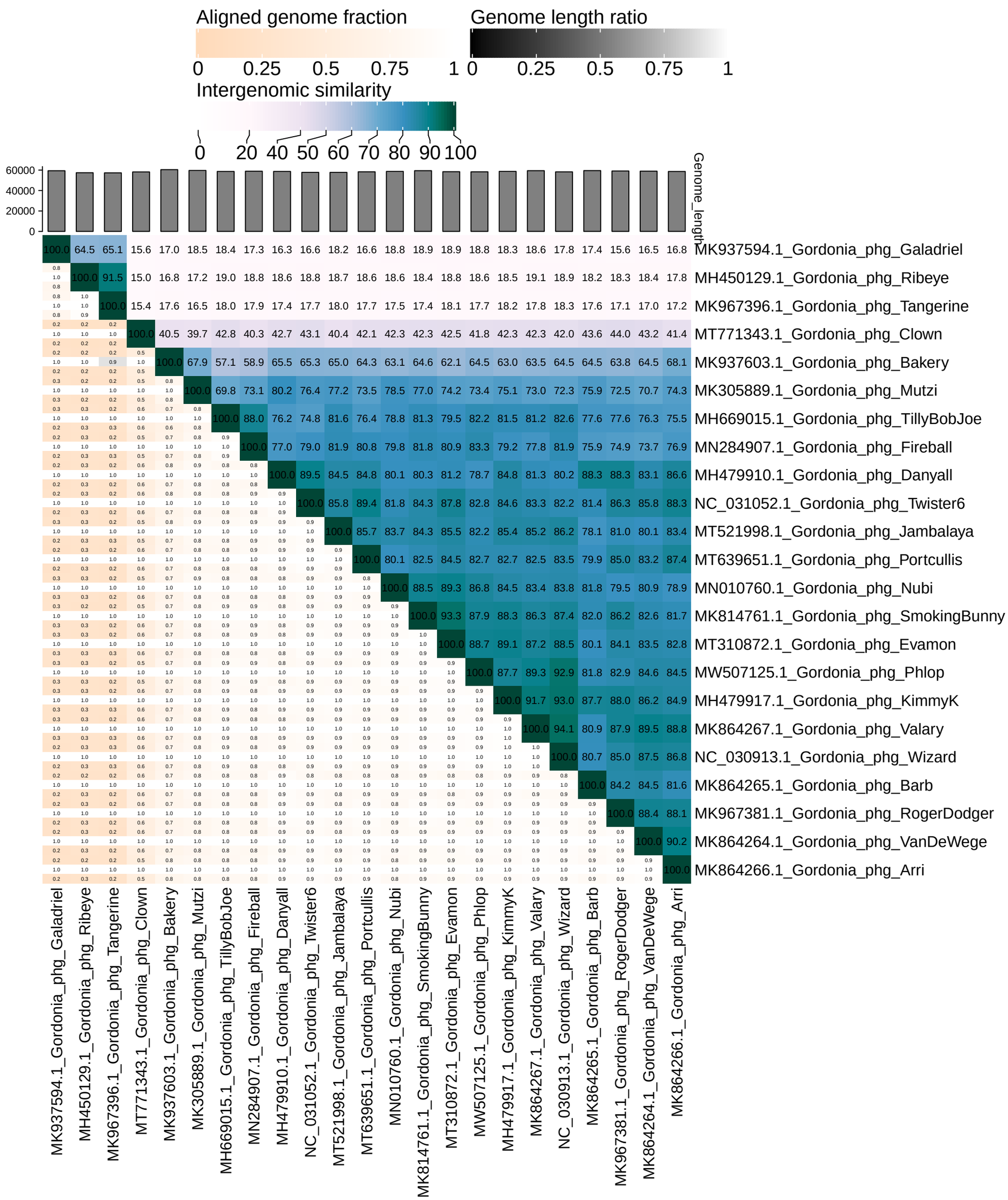
Aligned genome fraction
0 0.25 0.5 0.75 1
Genome length ratio
0 0.25 0.5 0.75 1
Intergenomic similarity
0 20 40 50 60 70 80 90 100
Genome_length
60000
40000
20000
0
MK937594.1_Gordonia_phg_Galadriel
MH450129.1_Gordonia_phg_Ribeye
MK967396.1_Gordonia_phg_Tangerine
MT771343.1_Gordonia_phg_Clown
MK937603.1_Gordonia_phg_Bakery
MK305889.1_Gordonia_phg_Mutzi
MH669015.1_Gordonia_phg_TillyBobJoe
MN284907.1_Gordonia_phg_Fireball
MH479910.1_Gordonia_phg_Danyall
NC_031052.1_Gordonia_phg_Twister6
MT521998.1_Gordonia_phg_Jambalaya
MT639651.1_Gordonia_phg_Portcullis
MN010760.1_Gordonia_phg_Nubi
MK814761.1_Gordonia_phg_SmokingBunny
MT310872.1_Gordonia_phg_Evamon
MW507125.1_Gordonia_phg_Phlop
MH479917.1_Gordonia_phg_KimmyK
MK864267.1_Gordonia_phg_Valary
NC_030913.1_Gordonia_phg_Wizard
MK864265.1_Gordonia_phg_Barb
MK967381.1_Gordonia_phg_RogerDodger
MK864264.1_Gordonia_phg_VanDeWege
MK864266.1_Gordonia_phg_Arri