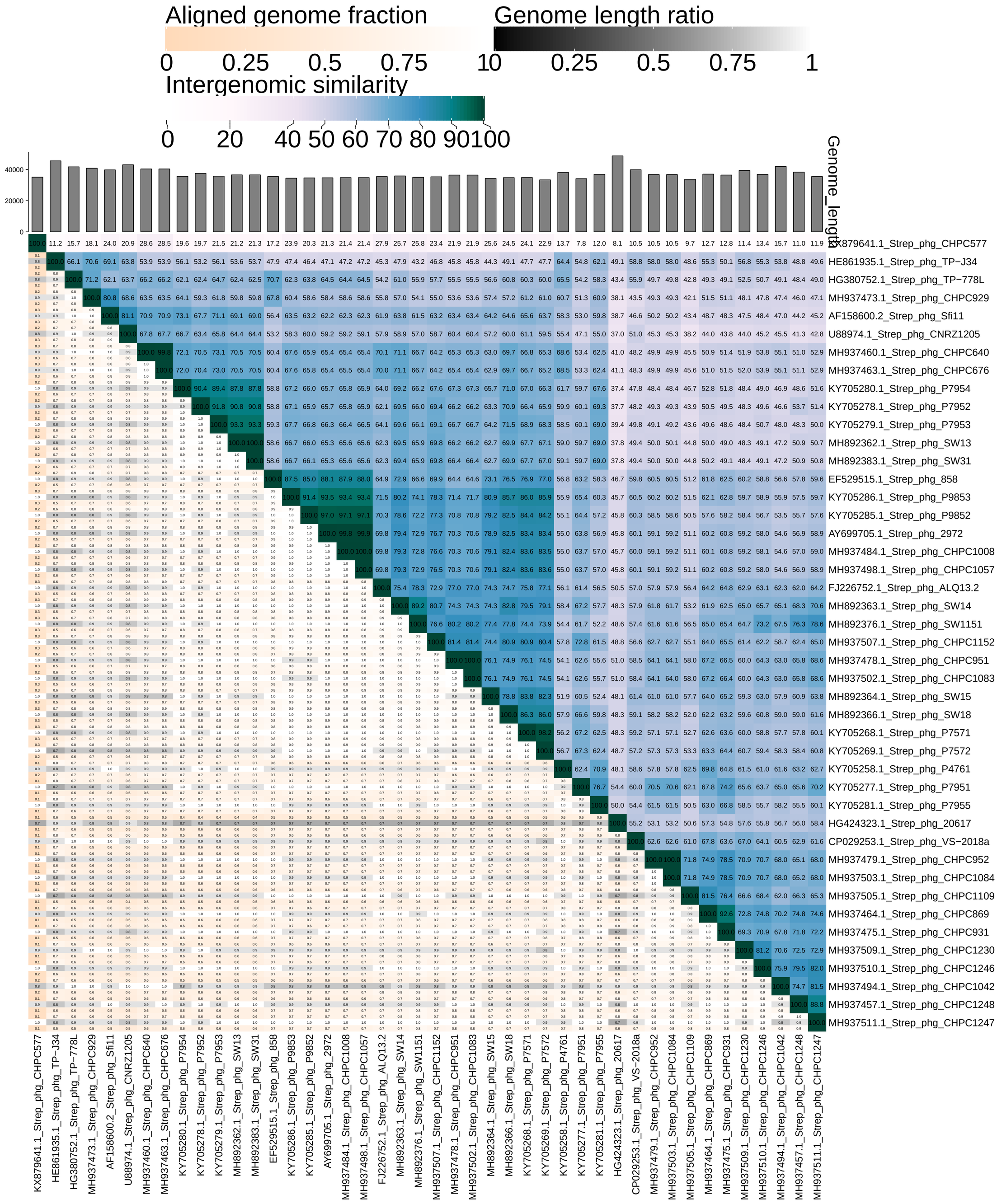
Aligned genome fraction
0
0.25
0.5
0.75
1
Genome length ratio
0
0.25
0.5
0.75
1
Intergenomic similarity
0
20
40
50
60
70
80
90
100
Genome_length
40000
20000
0
KX879641.1_Strep_phg_CHPC577
HE861935.1_Strep_phg_TP−J34
HG380752.1_Strep_phg_TP−778L
MH937473.1_Strep_phg_CHPC929
AF158600.2_Strep_phg_Sfi11
U88974.1_Strep_phg_CNRZ1205
MH937460.1_Strep_phg_CHPC640
MH937463.1_Strep_phg_CHPC676
KY705280.1_Strep_phg_P7954
KY705278.1_Strep_phg_P7952
KY705279.1_Strep_phg_P7953
MH892362.1_Strep_phg_SW13
MH892383.1_Strep_phg_SW31
EF529515.1_Strep_phg_858
KY705286.1_Strep_phg_P9853
KY705285.1_Strep_phg_P9852
AY699705.1_Strep_phg_2972
MH937484.1_Strep_phg_CHPC1008
MH937498.1_Strep_phg_CHPC1057
FJ226752.1_Strep_phg_ALQ13.2
MH892363.1_Strep_phg_SW14
MH892376.1_Strep_phg_SW1151
MH937507.1_Strep_phg_CHPC1152
MH937478.1_Strep_phg_CHPC951
MH937502.1_Strep_phg_CHPC1083
MH892364.1_Strep_phg_SW15
MH892366.1_Strep_phg_SW18
KY705268.1_Strep_phg_P7571
KY705269.1_Strep_phg_P7572
KY705258.1_Strep_phg_P4761
KY705277.1_Strep_phg_P7951
KY705281.1_Strep_phg_P7955
HG424323.1_Strep_phg_20617
CP029253.1_Strep_phg_VS−2018a
MH937479.1_Strep_phg_CHPC952
MH937503.1_Strep_phg_CHPC1084
MH937505.1_Strep_phg_CHPC1109
MH937464.1_Strep_phg_CHPC869
MH937475.1_Strep_phg_CHPC931
MH937509.1_Strep_phg_CHPC1230
MH937510.1_Strep_phg_CHPC1246
MH937494.1_Strep_phg_CHPC1042
MH937457.1_Strep_phg_CHPC1248
MH937511.1_Strep_phg_CHPC1247