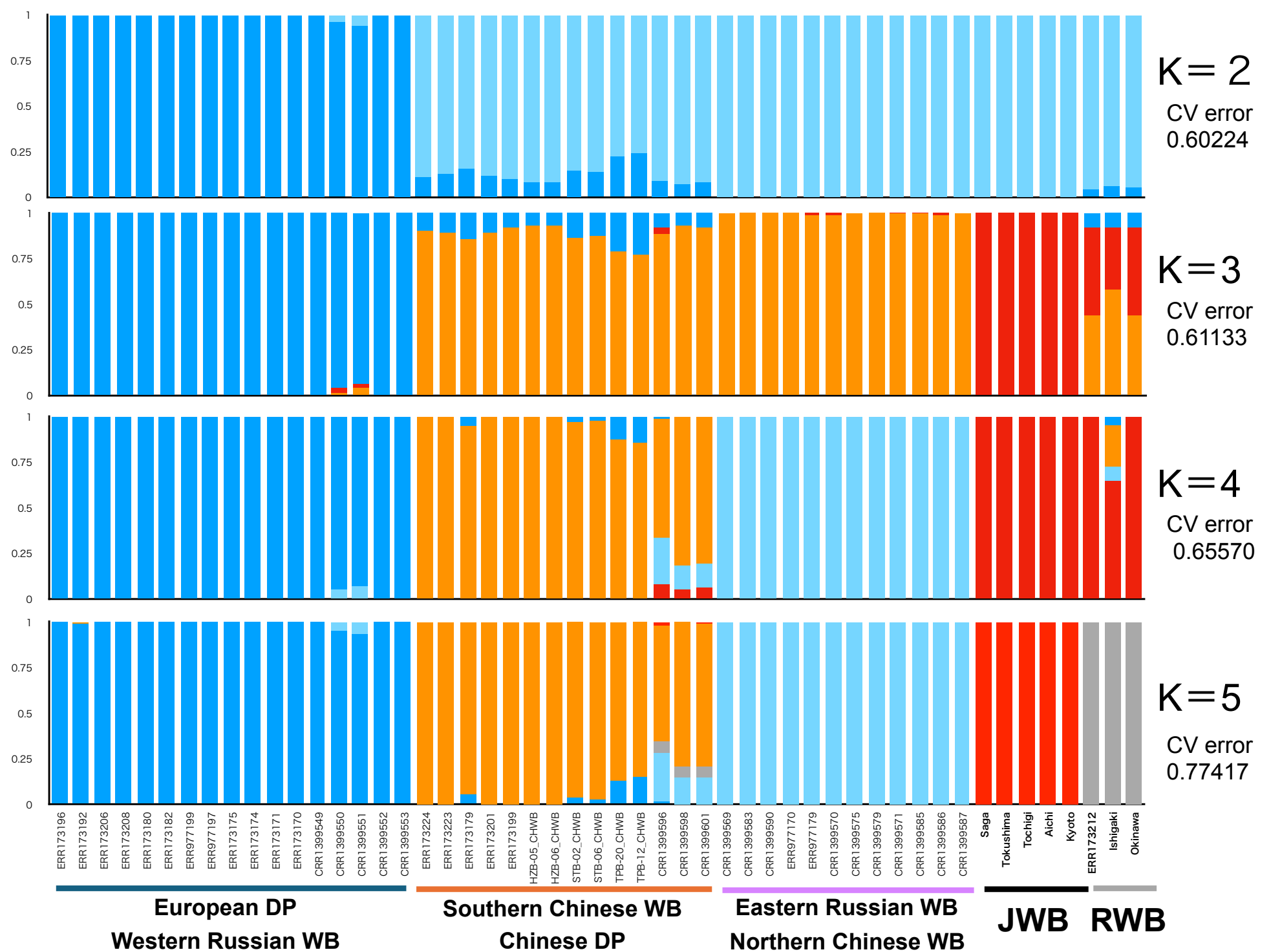


Supplement Figure

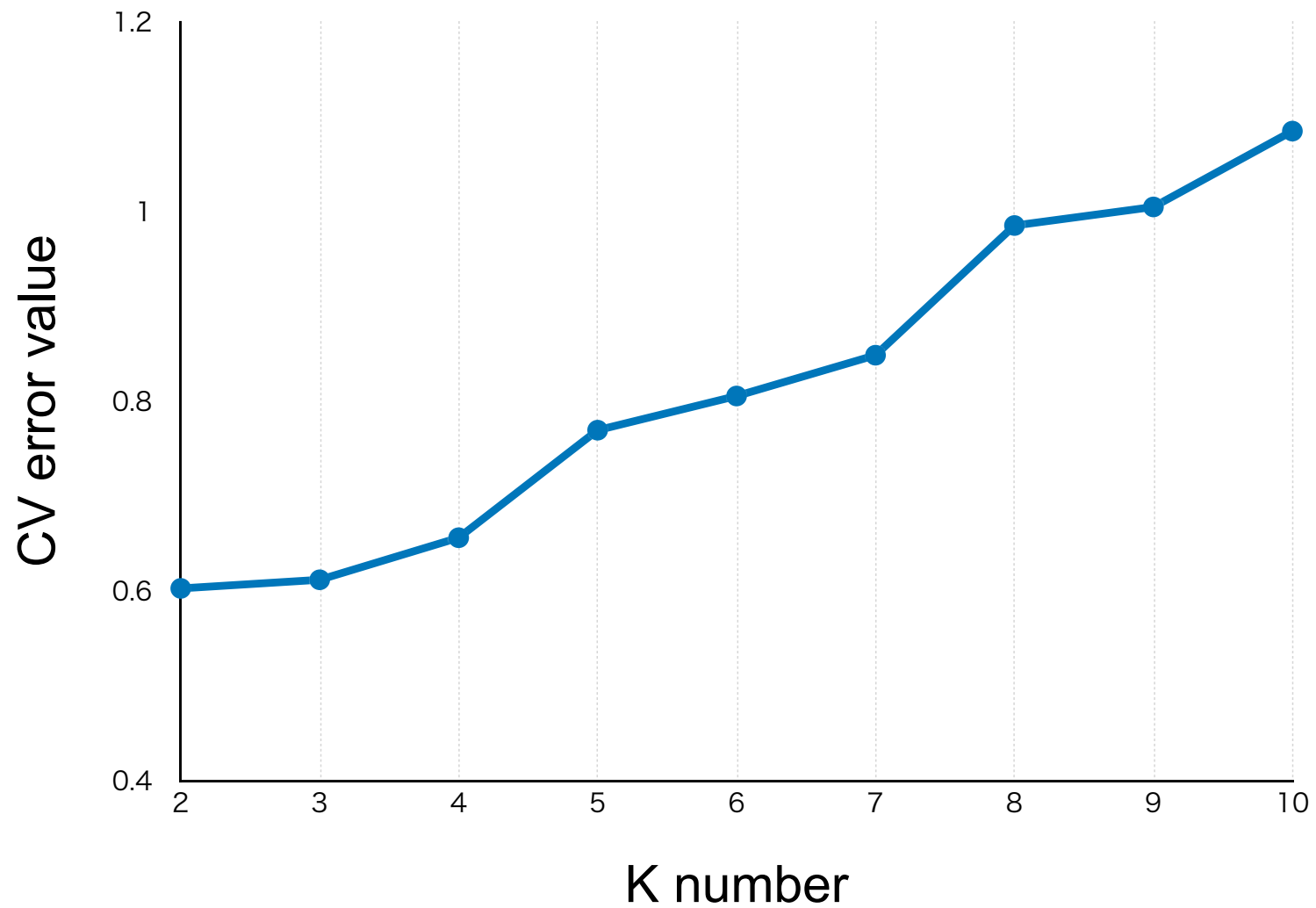
Whole-genome analyses reveal the phylogeny and gene flow of Japanese and Ryukyu wild boars

Rikako Itoi, David Gammarra, Yohey Terai, Jun Gojobori and Masaaki Taniguchi

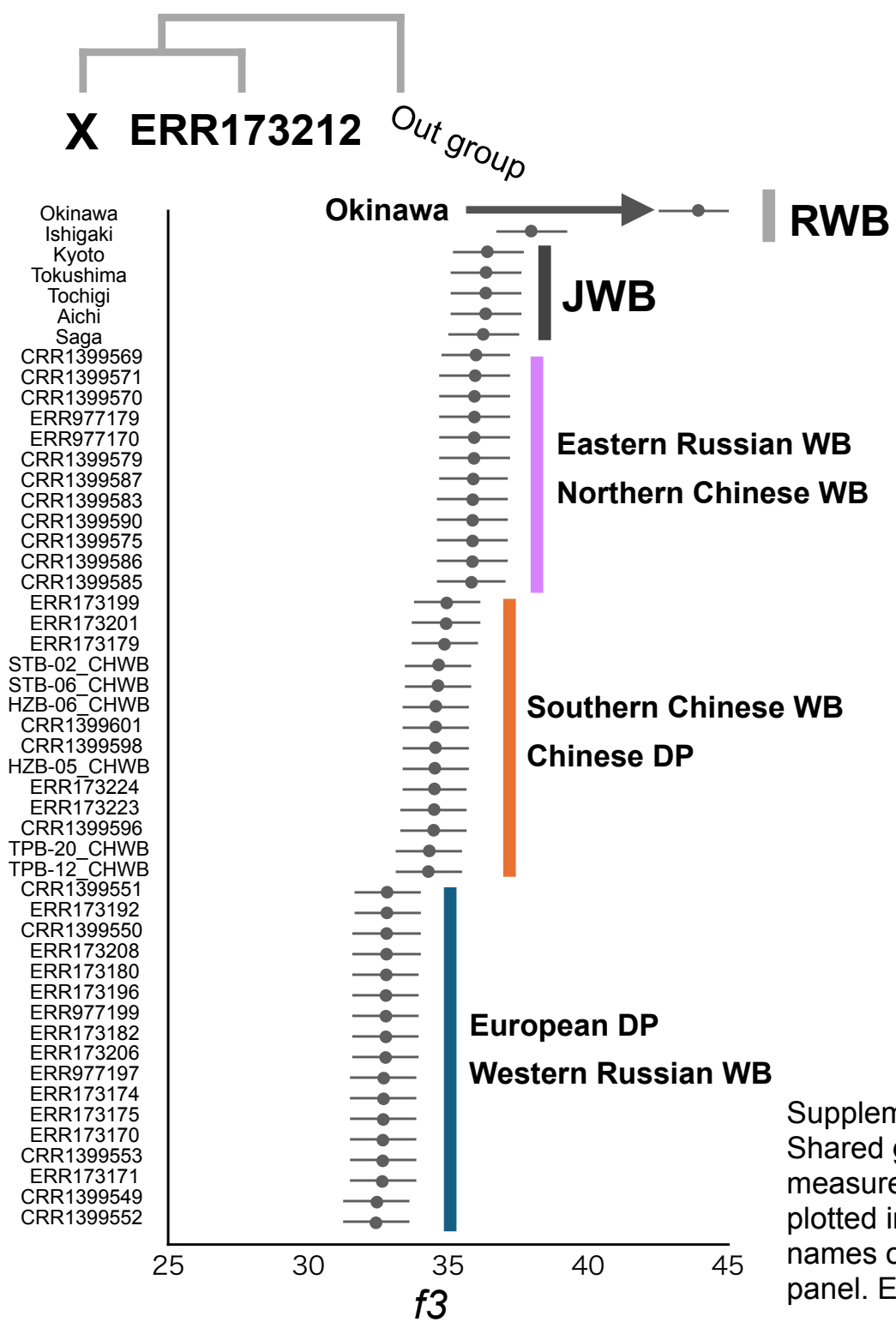


Supplement Figure 1

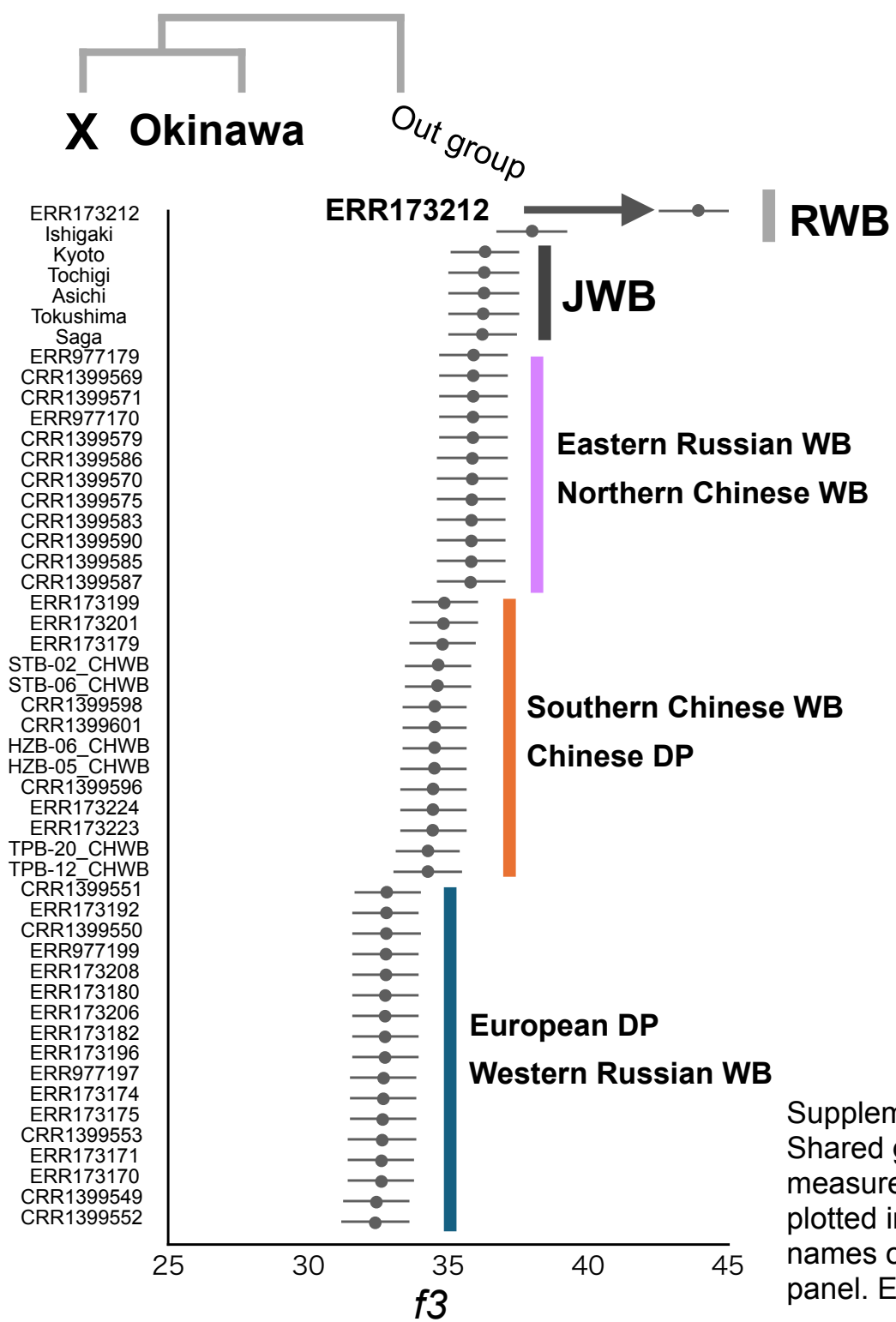
ADMIXTURE results for K = 2 to 5. The names of the WB/DP populations are shown at the bottom.



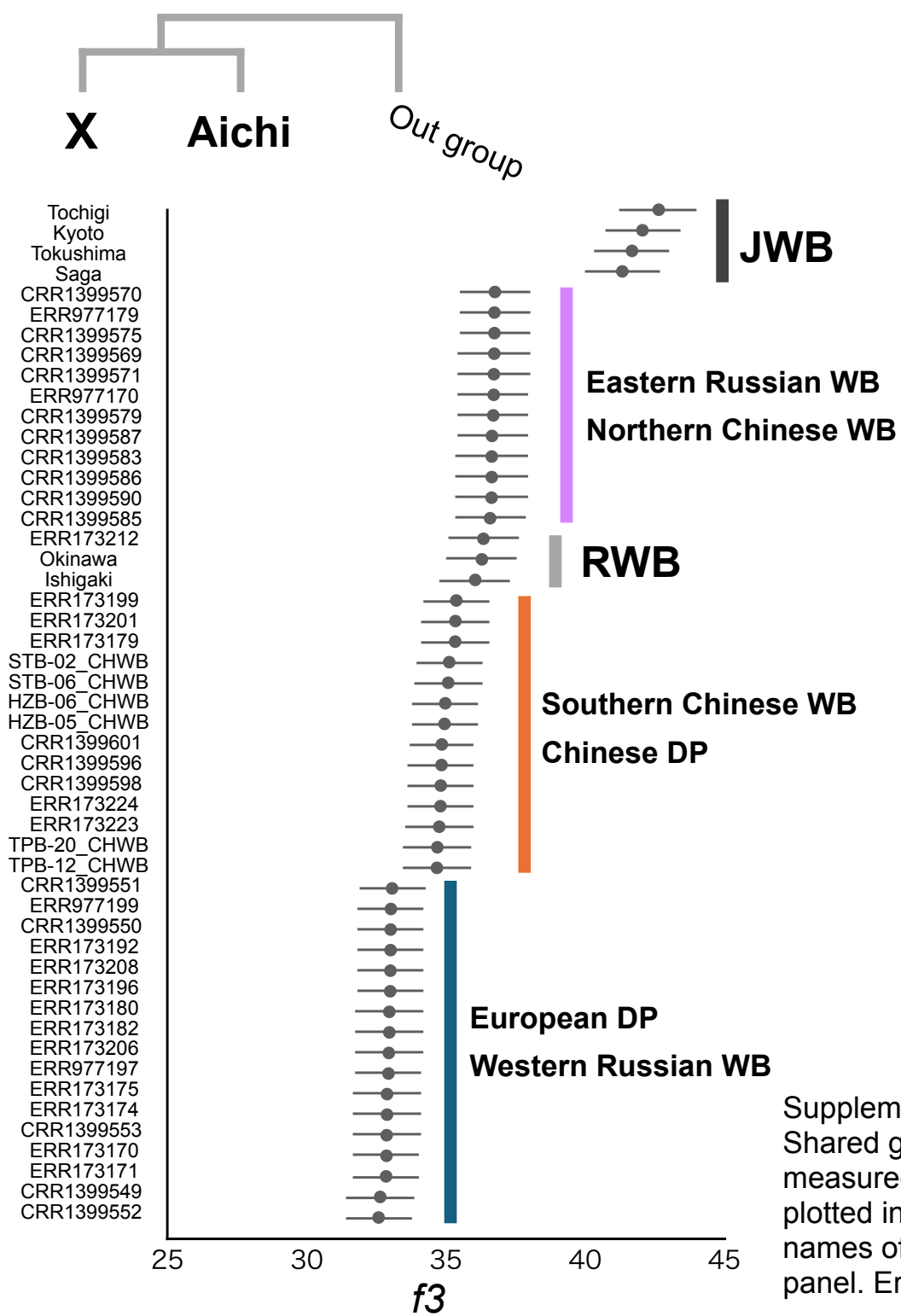
Supplement Figure 2
Cross validation (CV) values for ADMIXTURE analysis (Supplementary Figure.1)



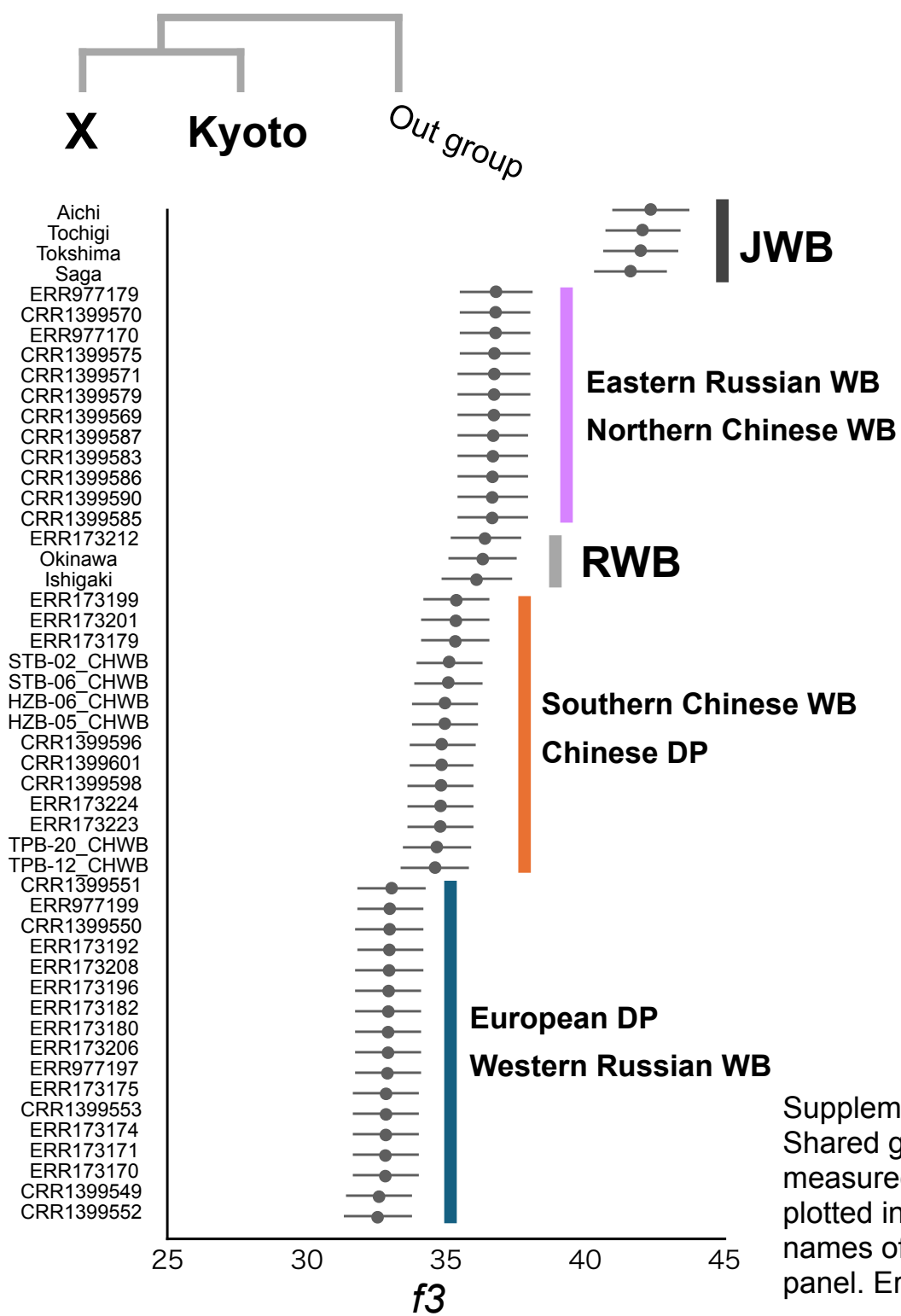
Supplement Figure 3
 Shared genetic drift between ERR173212 and all other WB/DP measured by outgroup f_3 statistics. Each f_3 statistical value is plotted in order of highest to lowest value from the top. The names of the WB/DP individuals are shown on the left side of the panel. Error bars represent standard errors.



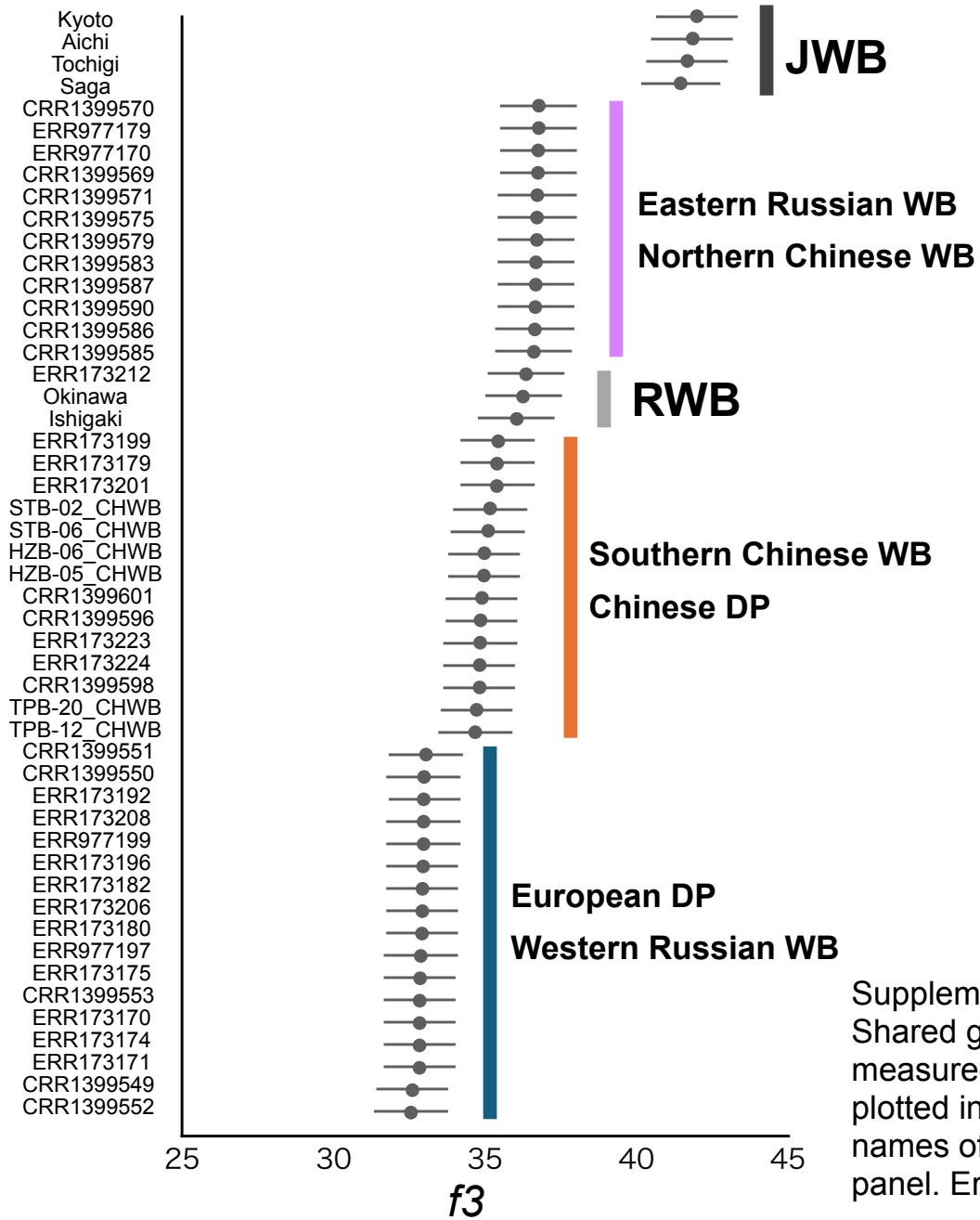
Supplement Figure 4
 Shared genetic drift between Okinawa and all other WB/DP measured by outgroup f_3 statistics. Each f_3 statistical value is plotted in order of highest to lowest value from the top. The names of the WB/DP individuals are shown on the left side of the panel. Error bars represent standard errors.



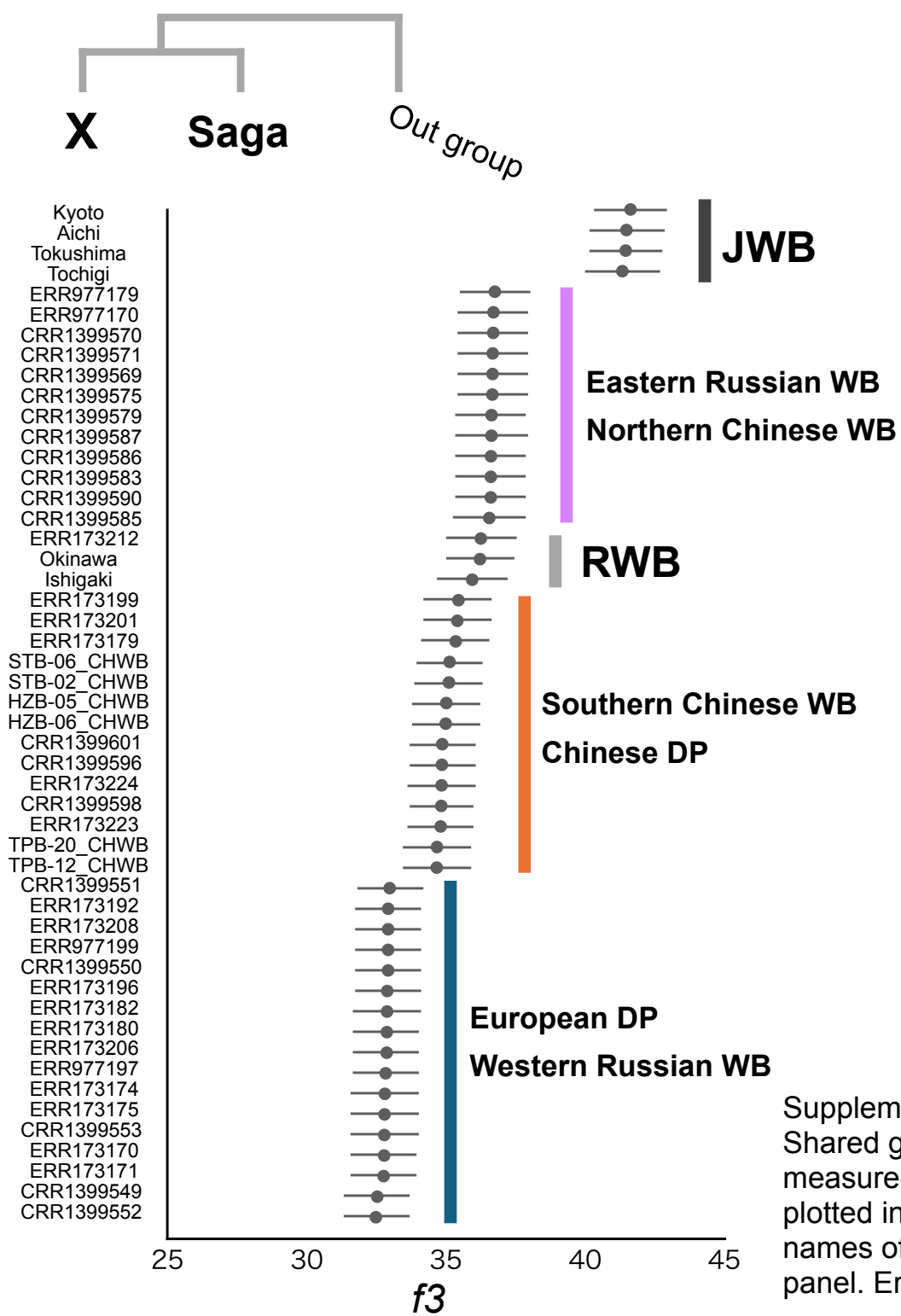
Supplement Figure 5
 Shared genetic drift between Aichi and all other WB/DP measured by outgroup f_3 statistics. Each f_3 statistical value is plotted in order of highest to lowest value from the top. The names of the WB/DP individuals are shown on the left side of the panel. Error bars represent standard errors.



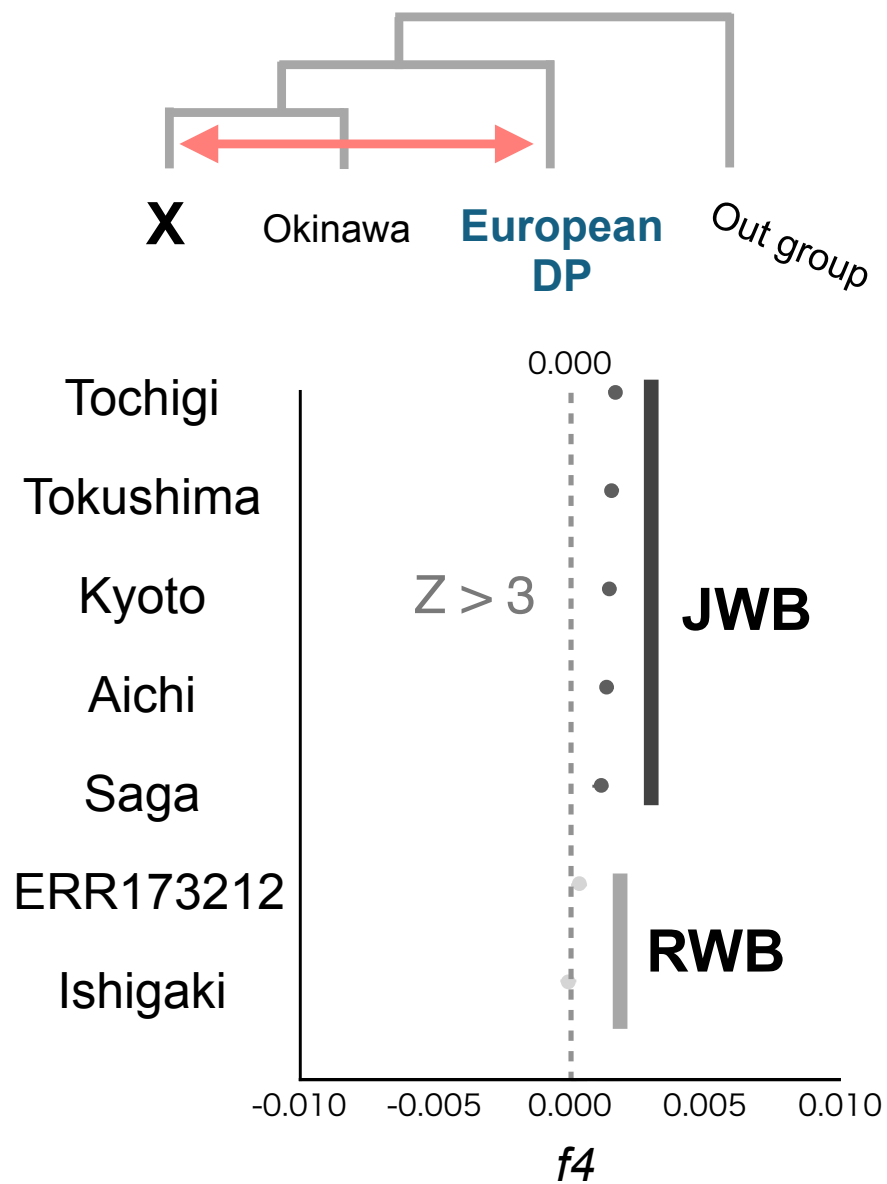
Supplement Figure 6
 Shared genetic drift between Kyoto and all other WB/DP measured by outgroup f_3 statistics. Each f_3 statistical value is plotted in order of highest to lowest value from the top. The names of the WB/DP individuals are shown on the left side of the panel. Error bars represent standard errors.



Supplement Figure 7
 Shared genetic drift between Tokushima and all other WB/DP measured by outgroup f_3 statistics. Each f_3 statistical value is plotted in order of highest to lowest value from the top. The names of the WB/DP individuals are shown on the left side of the panel. Error bars represent standard errors.



Supplement Figure 8
 Shared genetic drift between Saga and all other WB/DP measured by outgroup f_3 statistics. Each f_3 statistical value is plotted in order of highest to lowest value from the top. The names of the WB/DP individuals are shown on the left side of the panel. Error bars represent standard errors.



Supplement Figure 9

f4 statistics testing the genetic affinity of the JWB with EuropeanDP(ERR173170). f4 values for each combination are plotted. Each f4 value is listed in order of highest to lowest value from the top, and the names of the boars are shown on the left side of the panel. f4 values with Z score over 3 are shown in dark gray. Error bars represent standard errors.