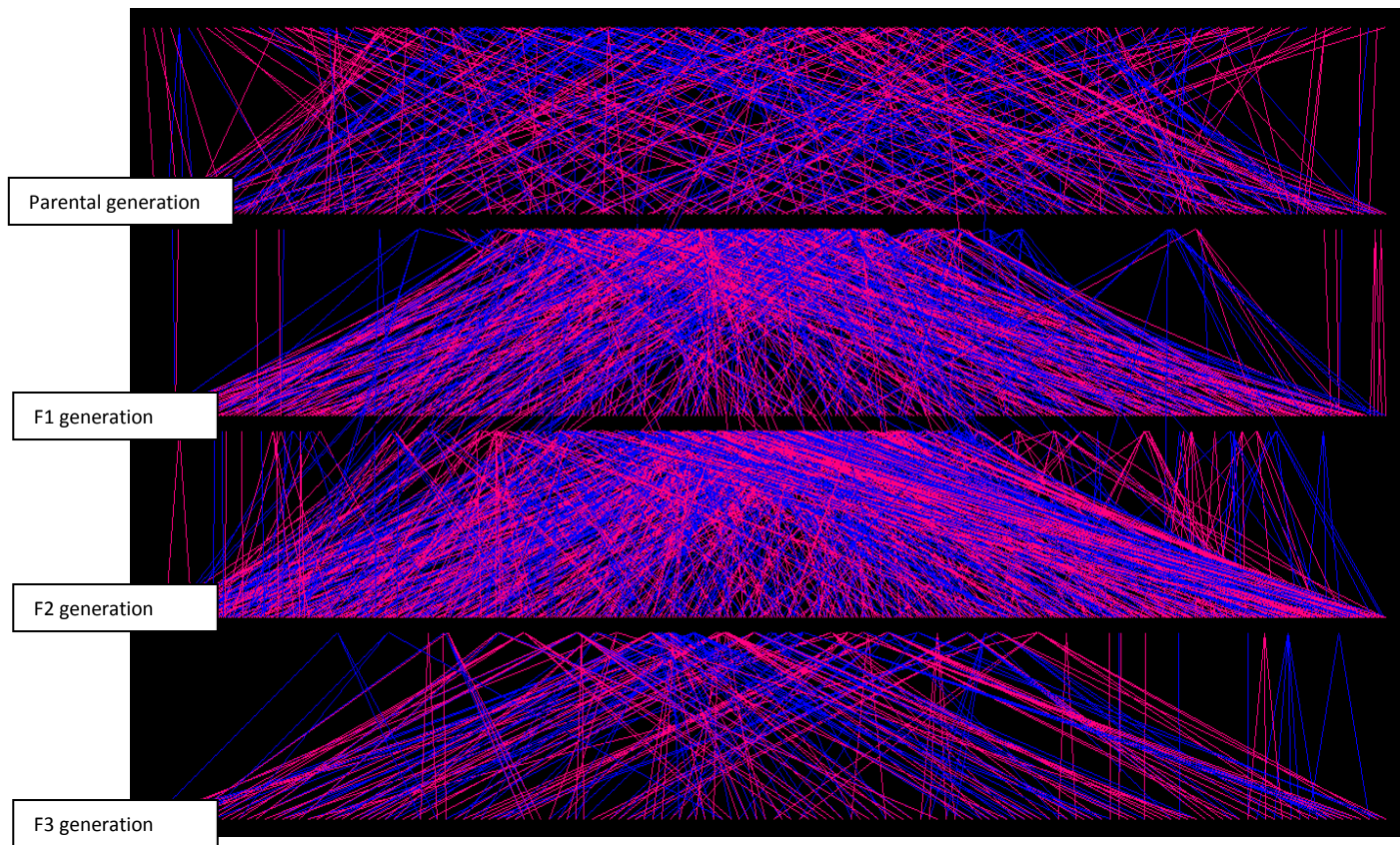
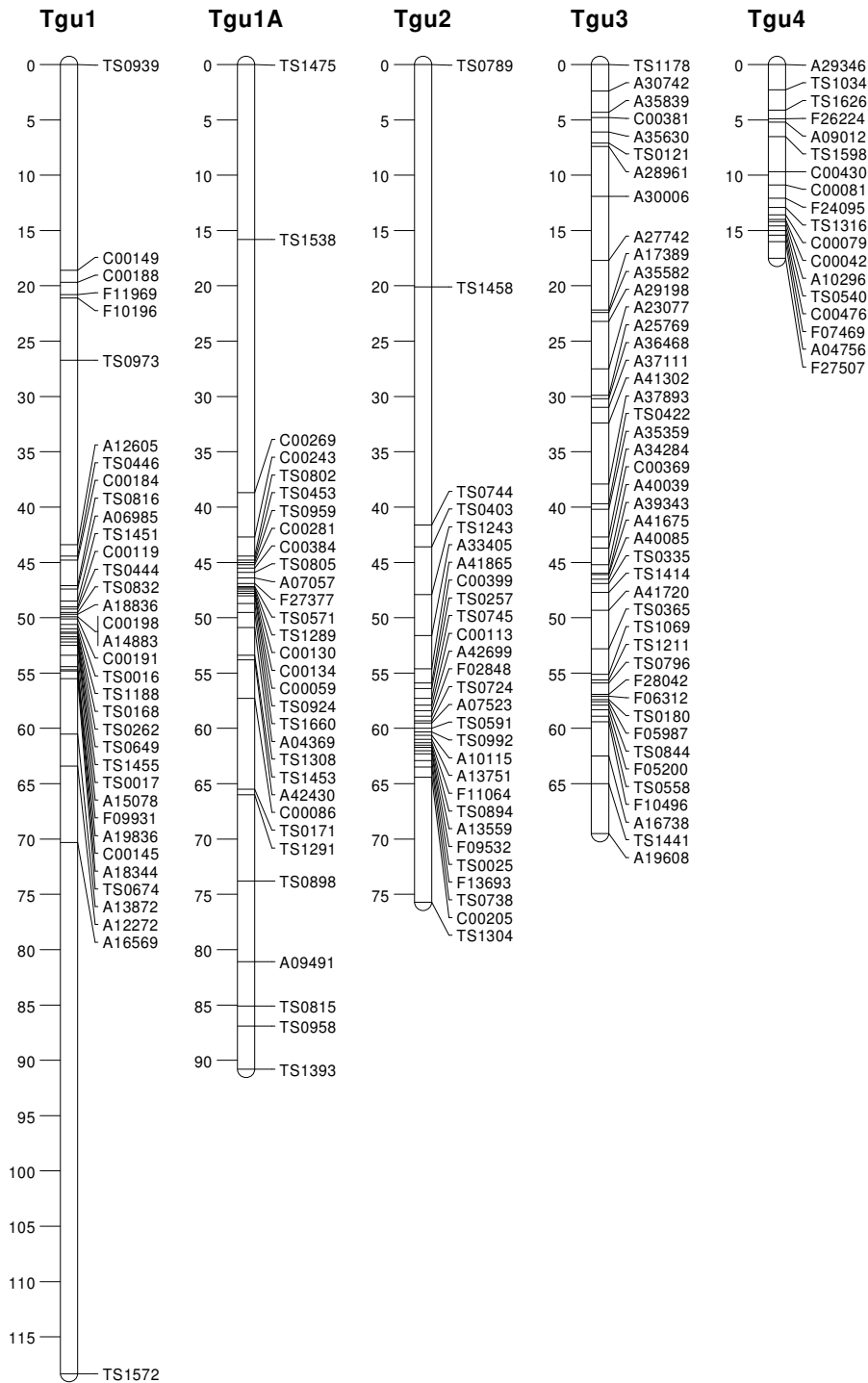
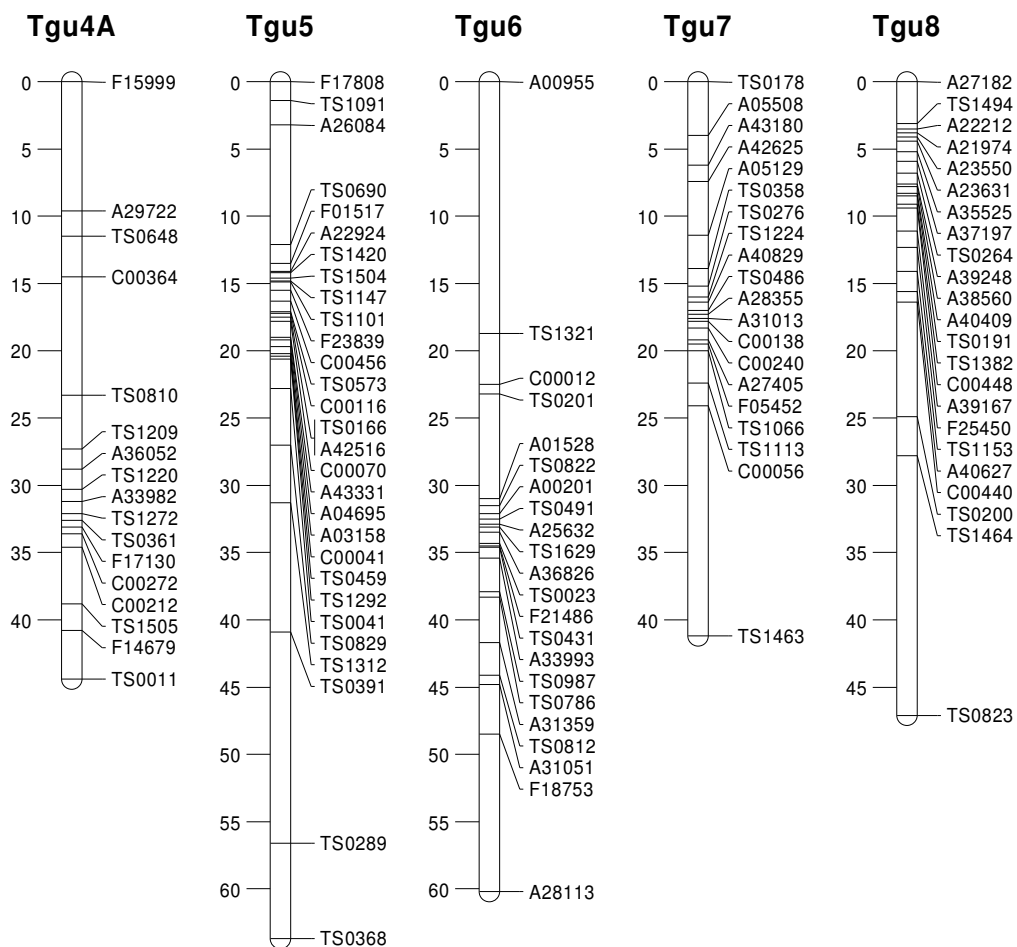




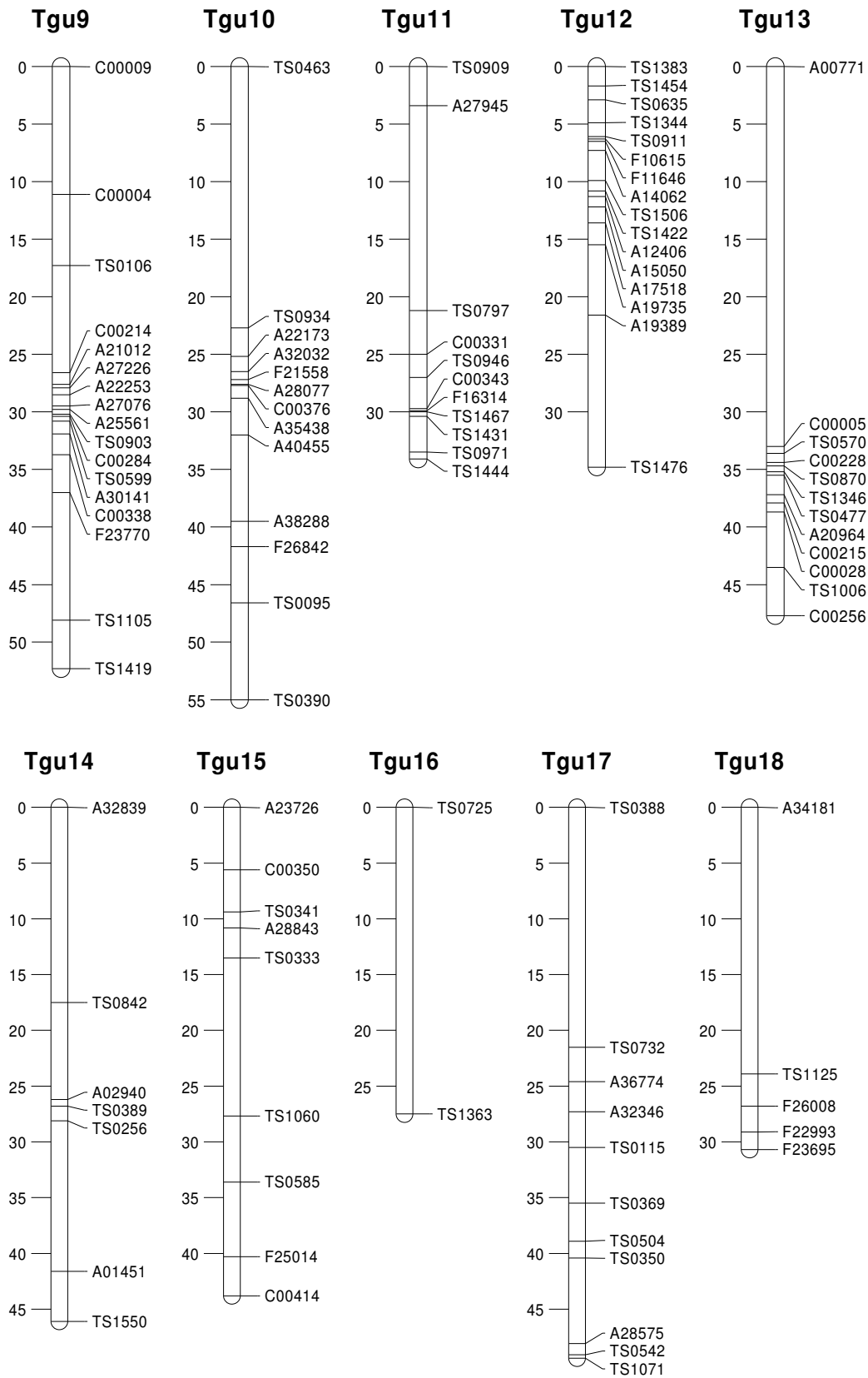
Supplementary Figure 1: Structure of the pedigree used for linkage analysis. Each horizontal black bar indicates one generation and red lines connect dams to the offspring and blue lines connect sires to the offspring.



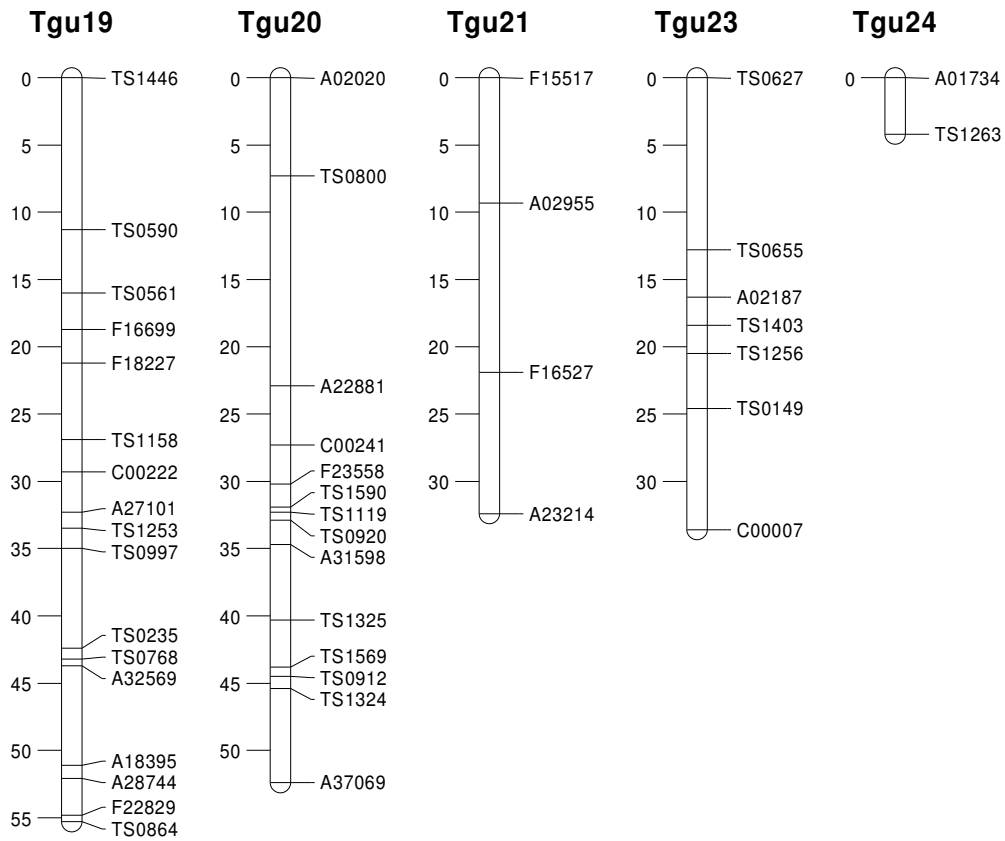
Supplementary Figure 2: Framework genetic map of the zebra finch. Marker names for individual loci are to the right of linkage groups and the genetic distances in cM are given to the left of each linkage group.



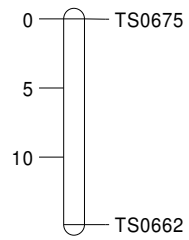
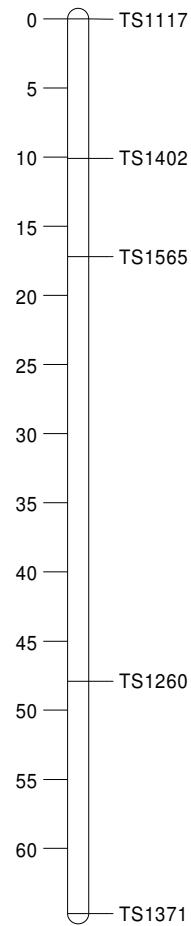
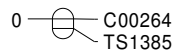
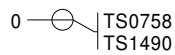
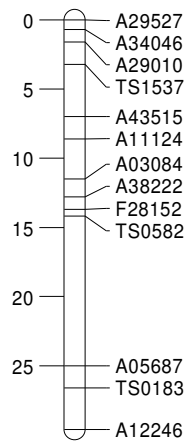
Supplementary Figure 2 continued.



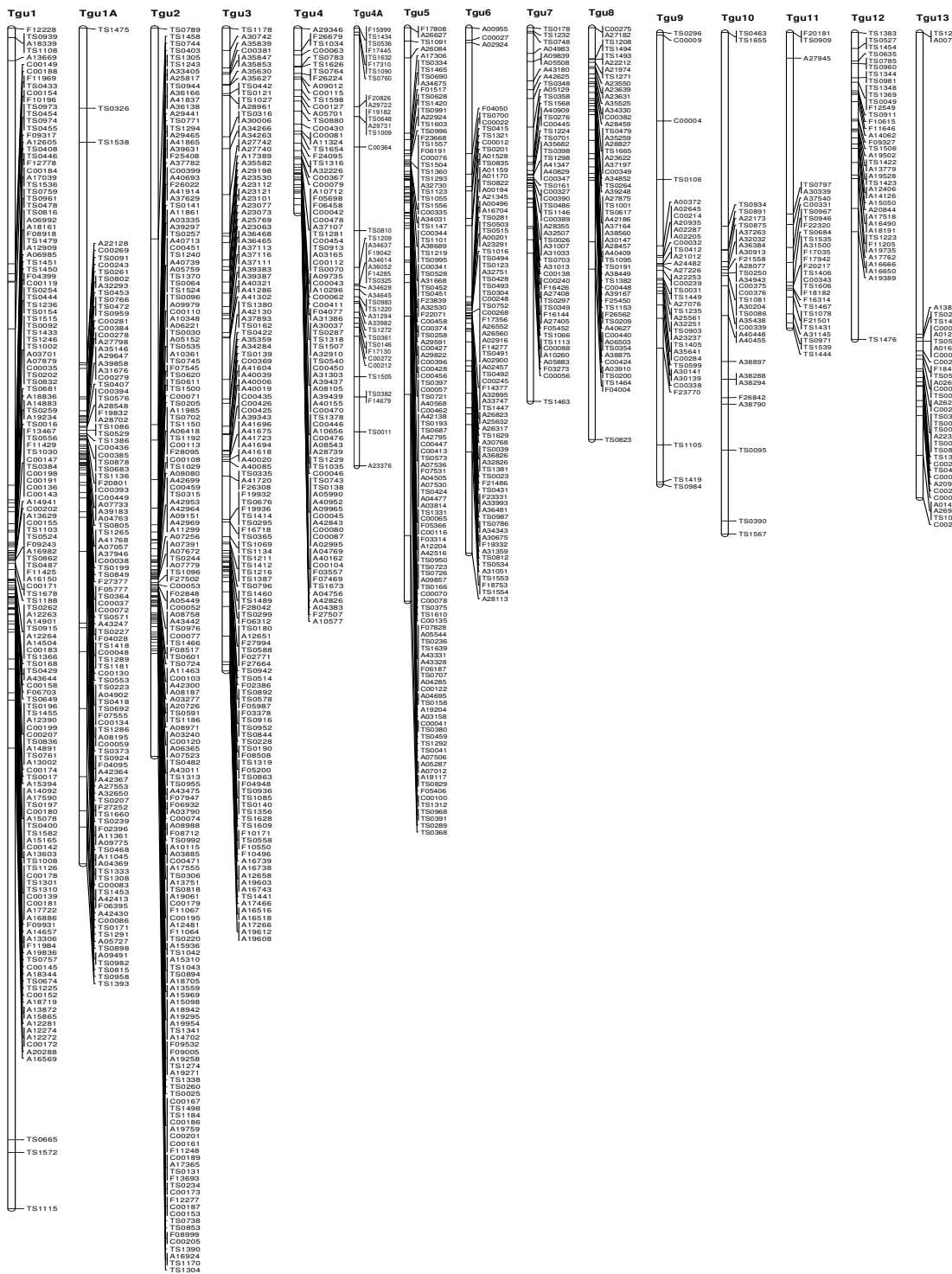
Supplementary Figure 2 continued.



Supplementary Figure 2 continued.

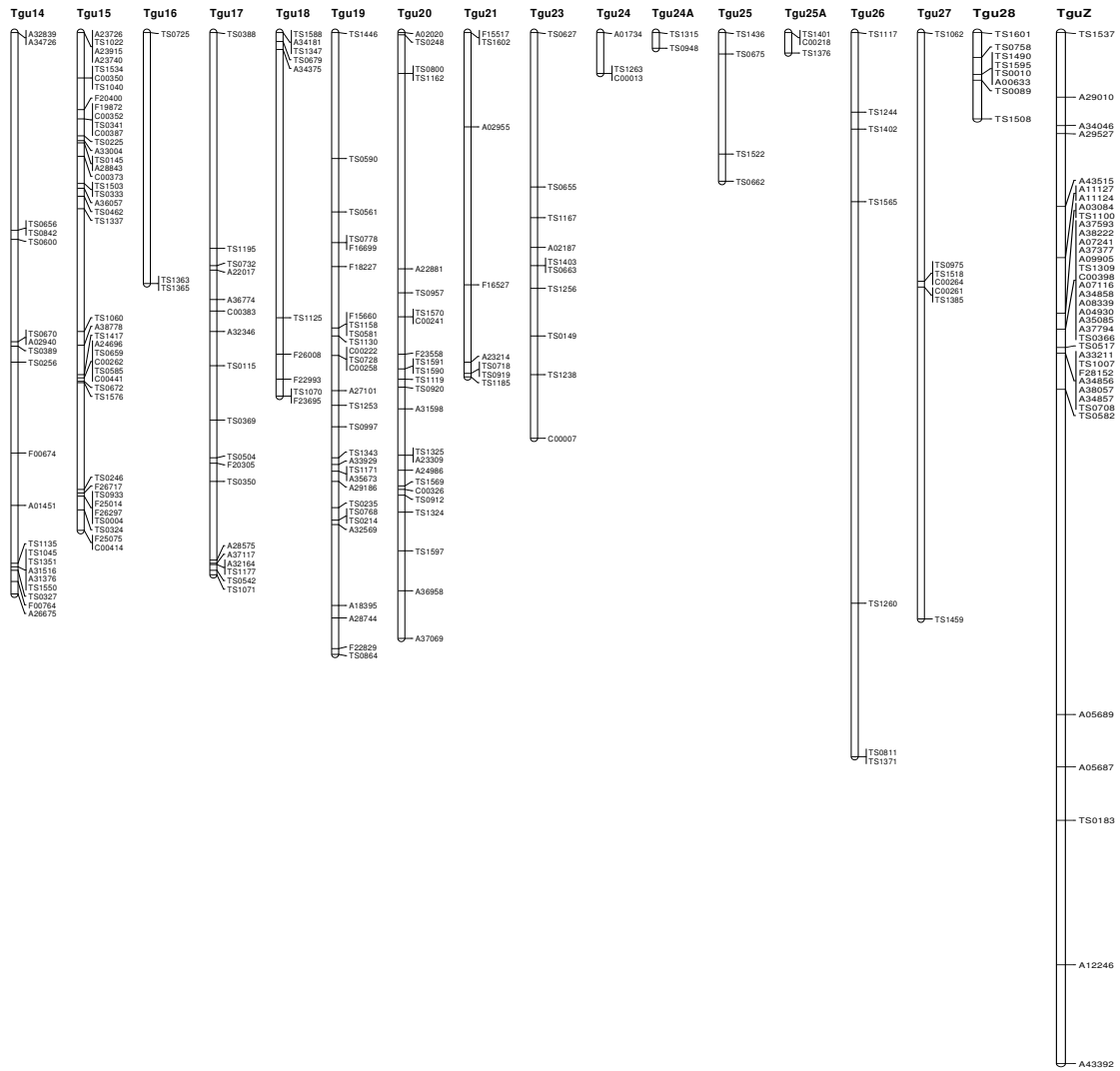
Tgu24A**Tgu25****Tgu25A****Tgu26****Tgu27****Tgu28****TguZ**

Supplementary Figure 2 continued.

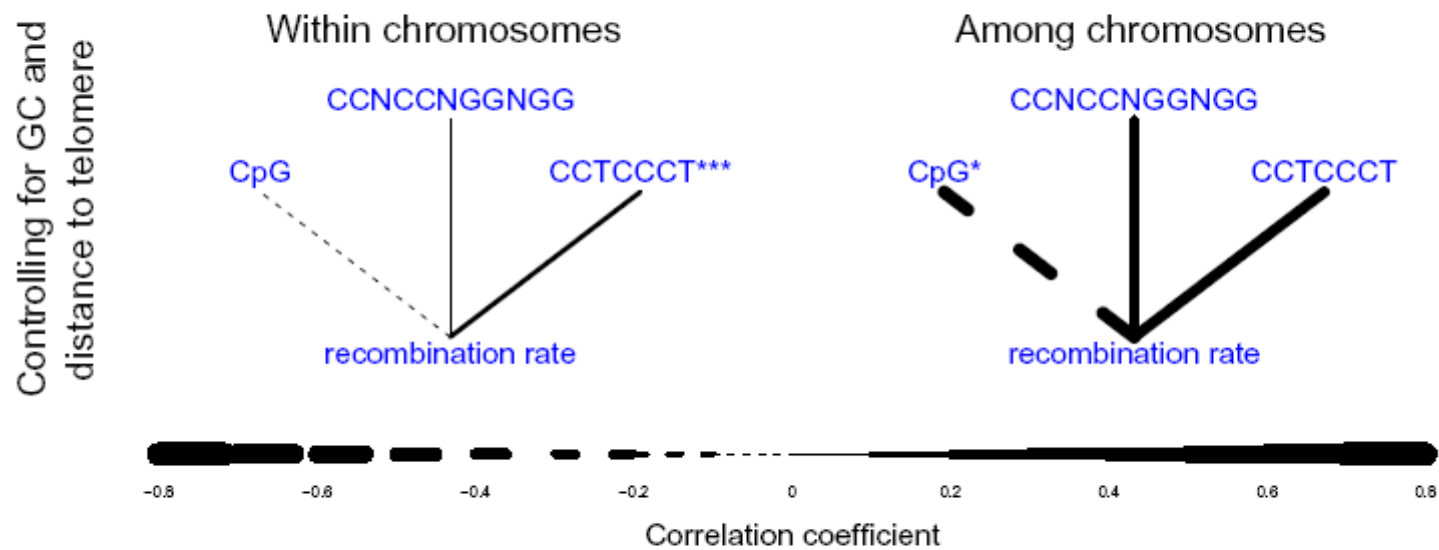


Supplementary Figure 3: Overview of the best order genetic map of the zebra finch.

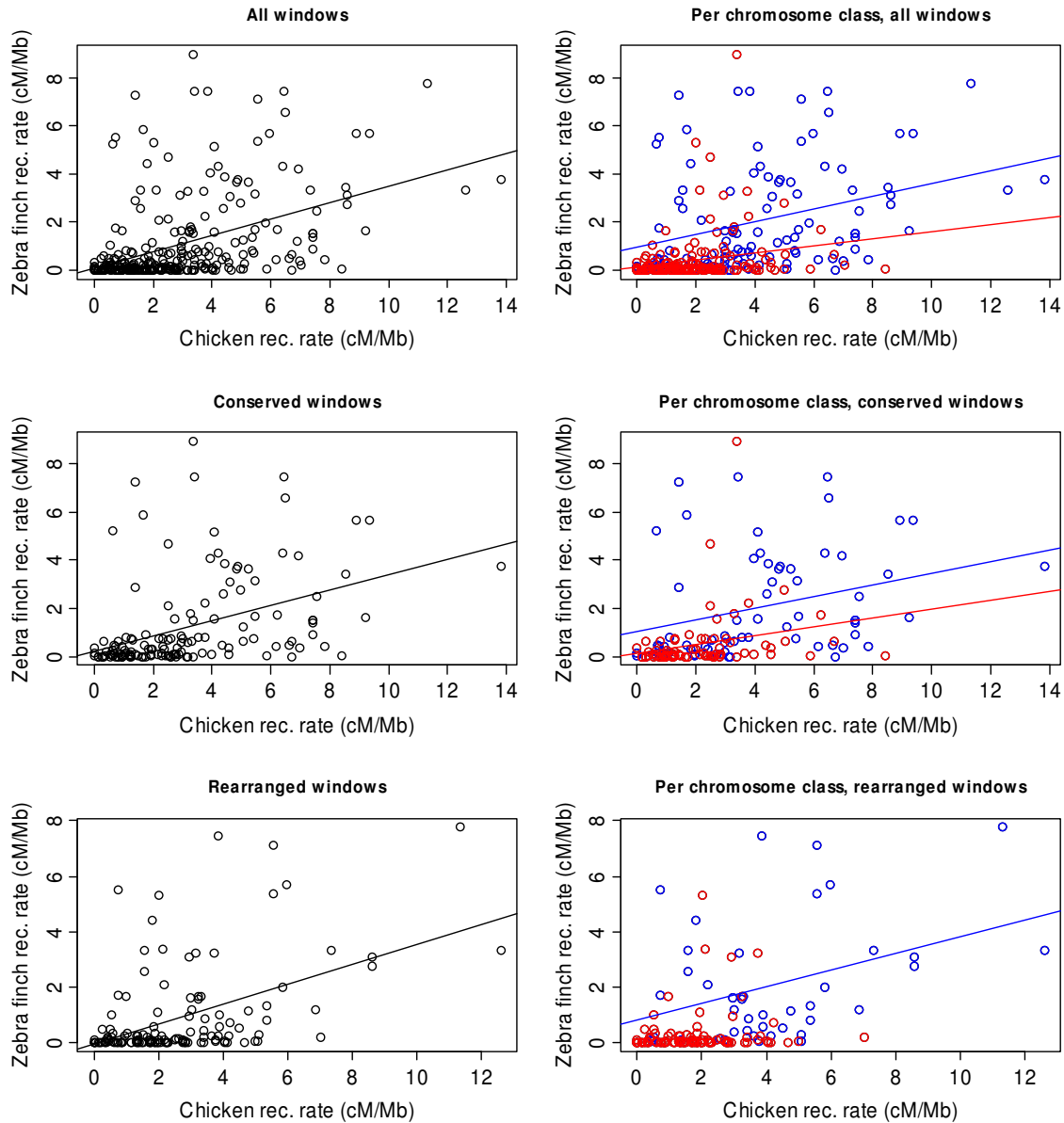
Marker names for individual loci are to the right of linkage groups and the lengths of linkage groups are scaled to reflect the genetic distance covered.



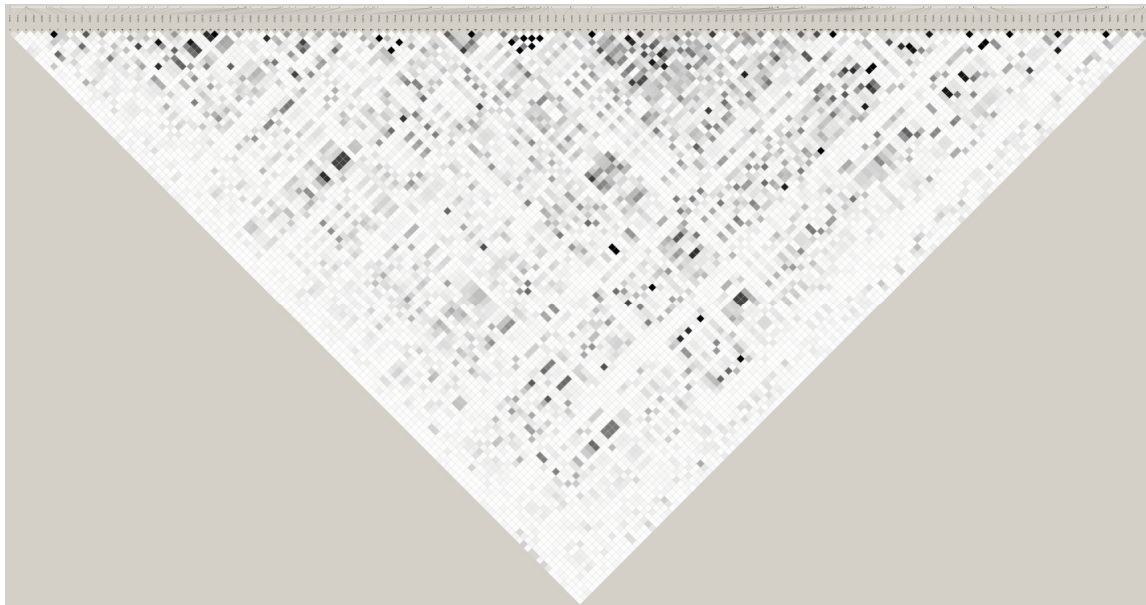
Supplementary Figure 3 continued.



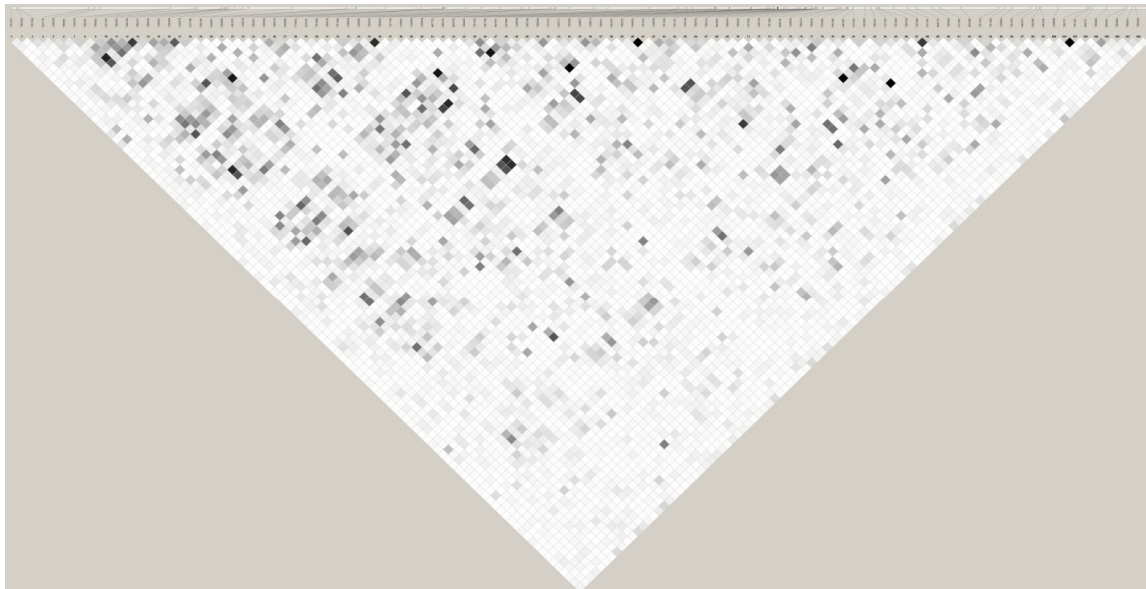
Supplementary Figure 4: Correlations between recombination rate and sequence features that are highly correlated with GC content. Plots show partial correlations controlling for GC content and distance to telomere (CpG = CG). Solid lines indicate positive and dashed lines negative correlations. Line width is proportional to the strength of the correlations. Asterisks indicate significance levels (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$).



Supplementary Figure 5. The relationship between recombination rate (cM/Mb) in orthologous 1 Mb windows in zebra finch (y-axis) and chicken (x-axis). The left column contains plots for all windows combined while the right column contains plots where large chromosomes (> 50 Mb, red) are separated from small chromosomes (< 50 Mb, blue). Upper row plots contain data from all orthologous windows, middle row plots contain data for conserved windows only and lower row plots contain data for rearranged windows only. Fitted linear regression lines are drawn for all significant correlations.

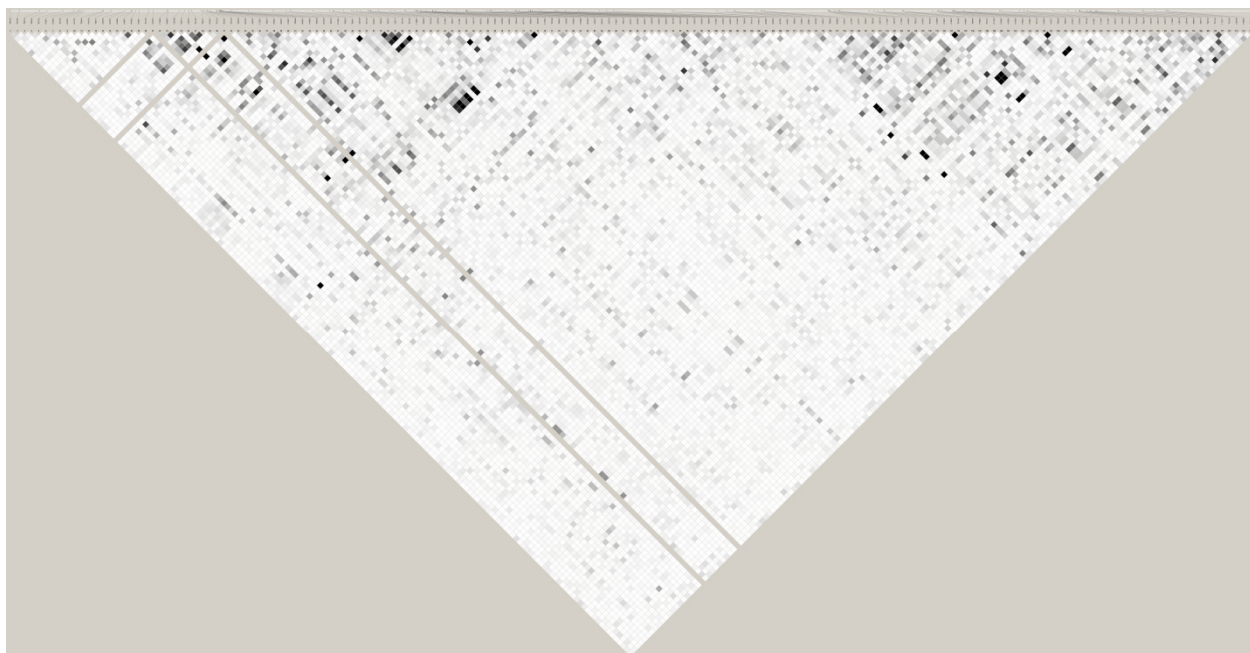


Tgu1

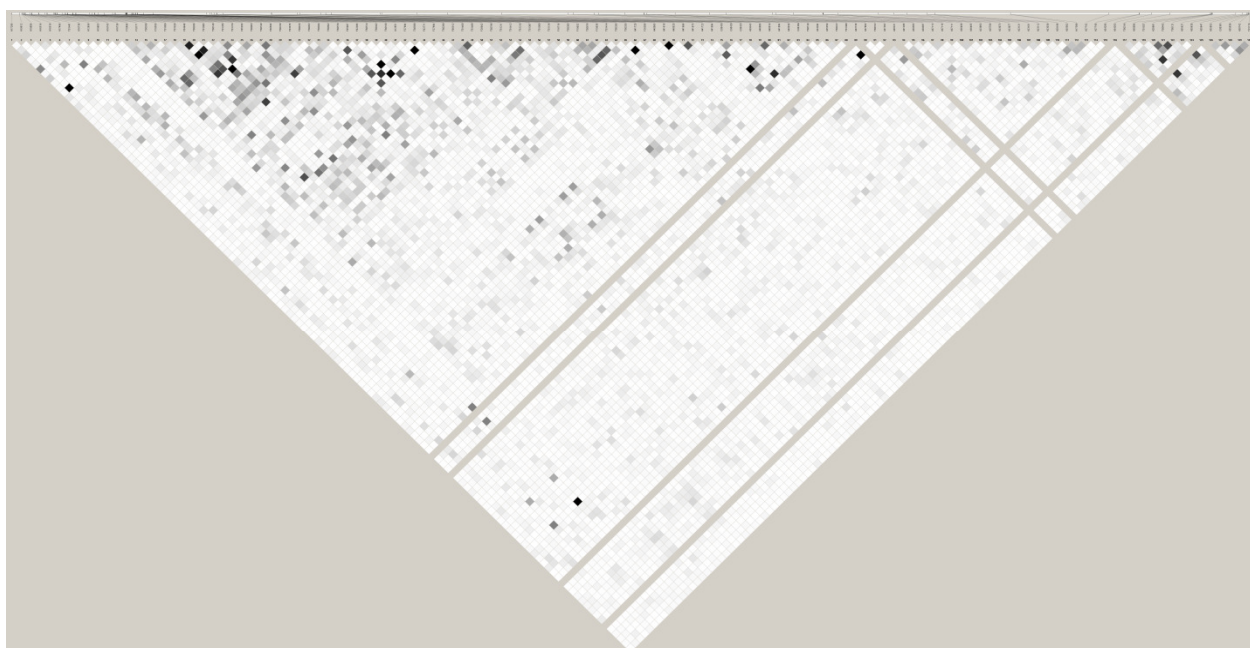


Tgu1A

Supplementary Figure 6: Pair-wise linkage disequilibrium heat-maps for all markers along zebra finch linkage groups. Marker order is the same as the physical order and level of pair-wise linkage disequilibrium (r^2) is indicated by gray-scale intensity so that white equals low LD ($r^2 = 0$), shaded squares indicate intermediate LD and black squares indicate perfect LD ($r^2 = 1$). Name of chromosome is indicated below each heat-map.

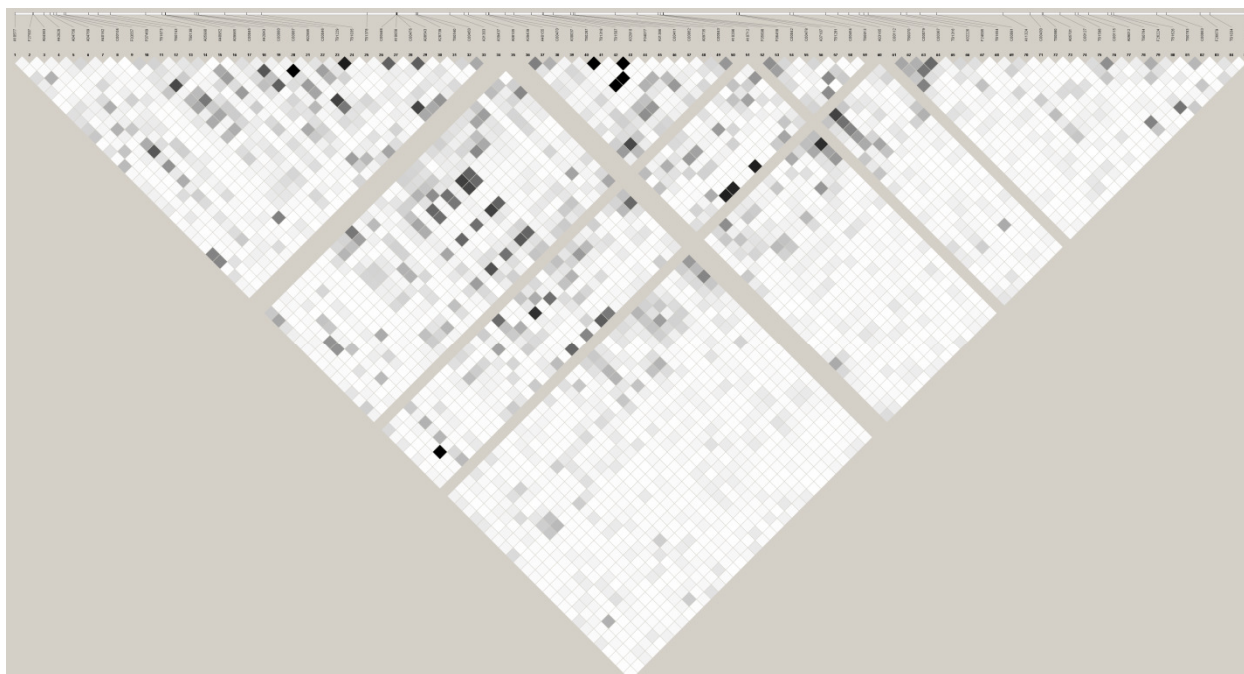


Tgu2

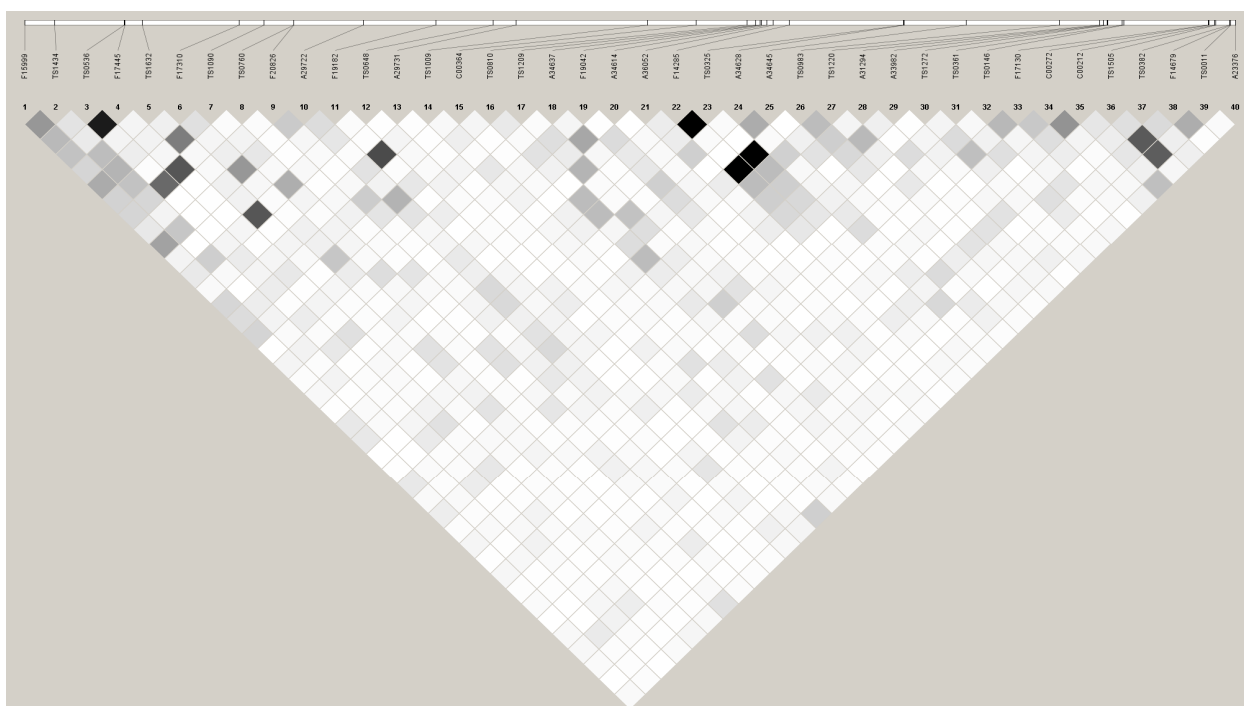


Tgu3

Supplementary Figure 6 continued.

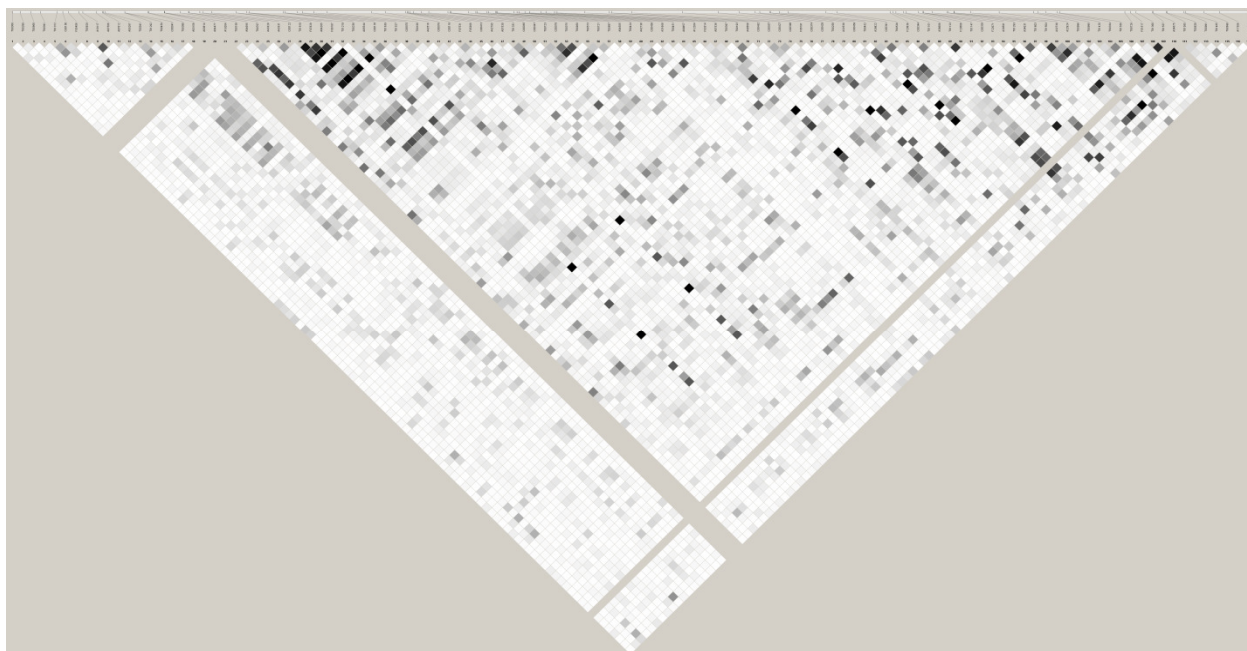


Tgu4

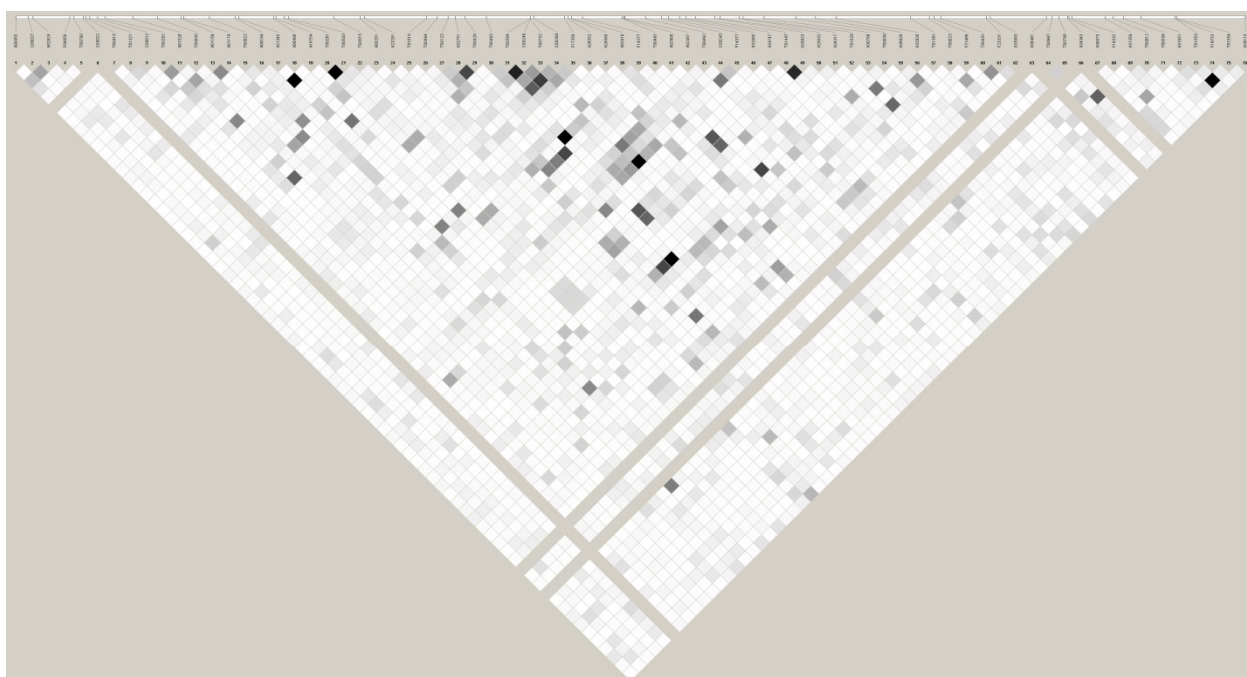


Tgu4A

Supplementary Figure 6 continued.

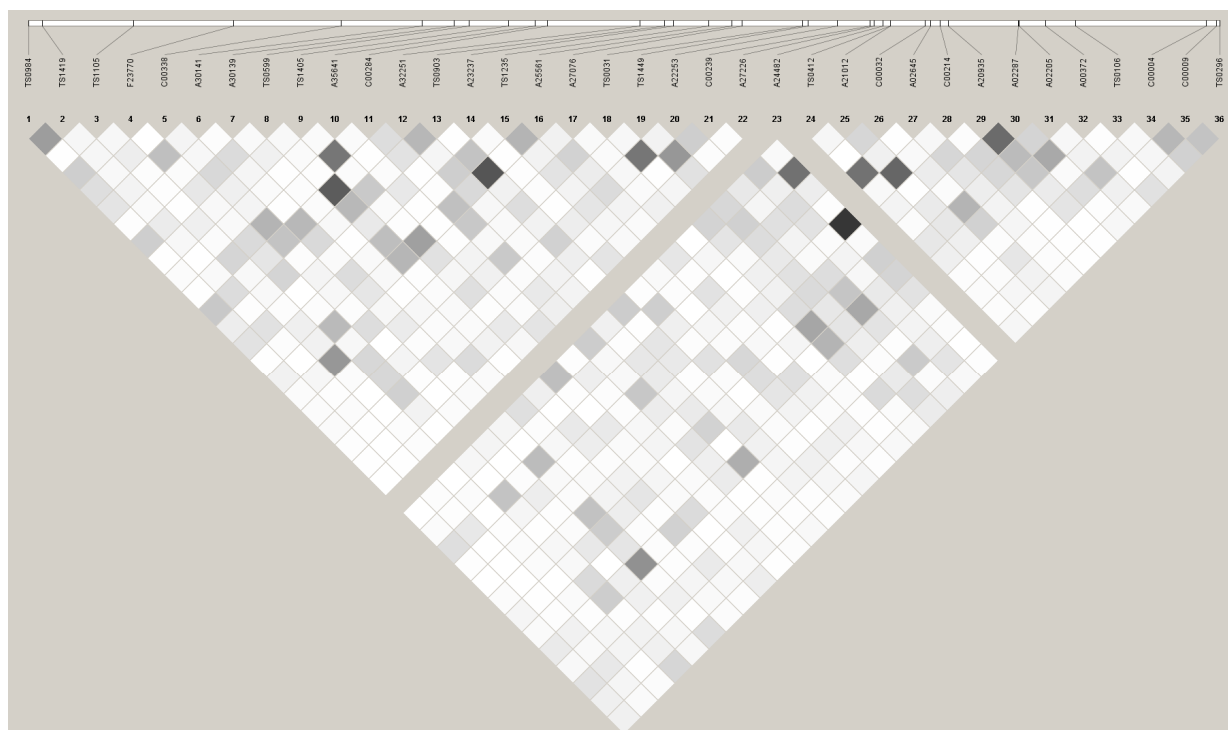


Tgu5

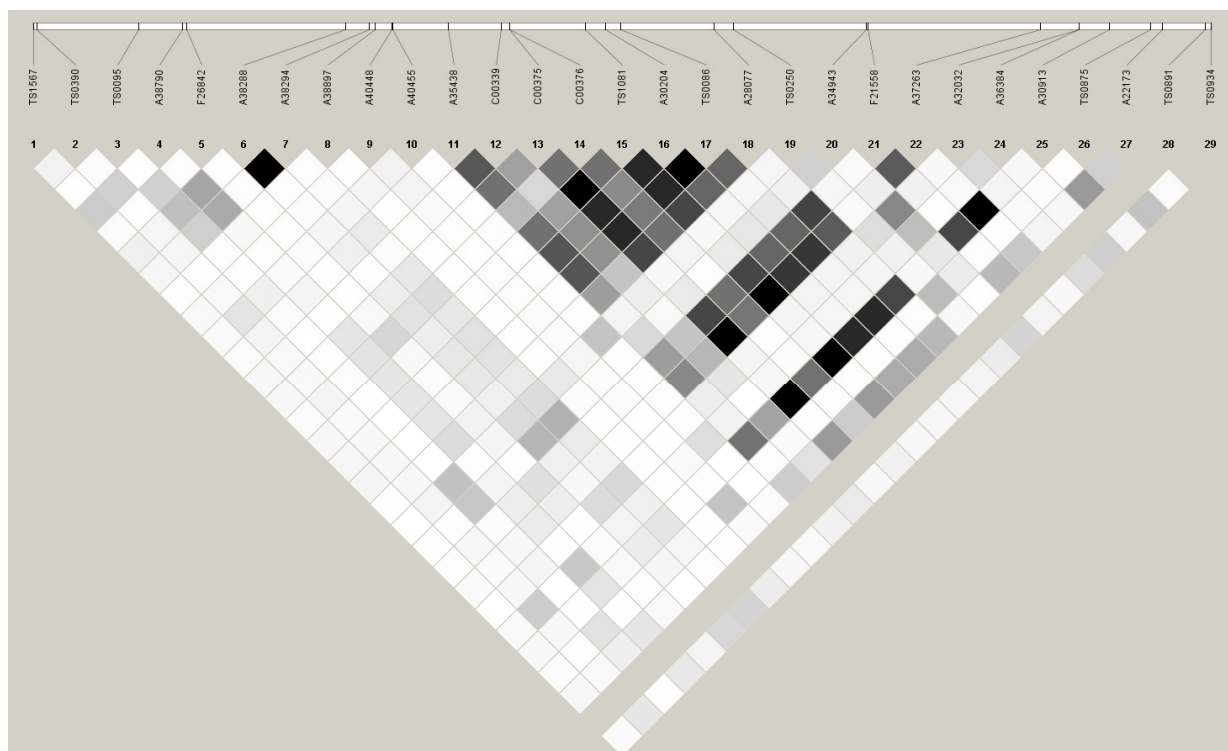


Tgu6

Supplementary Figure 6 continued.

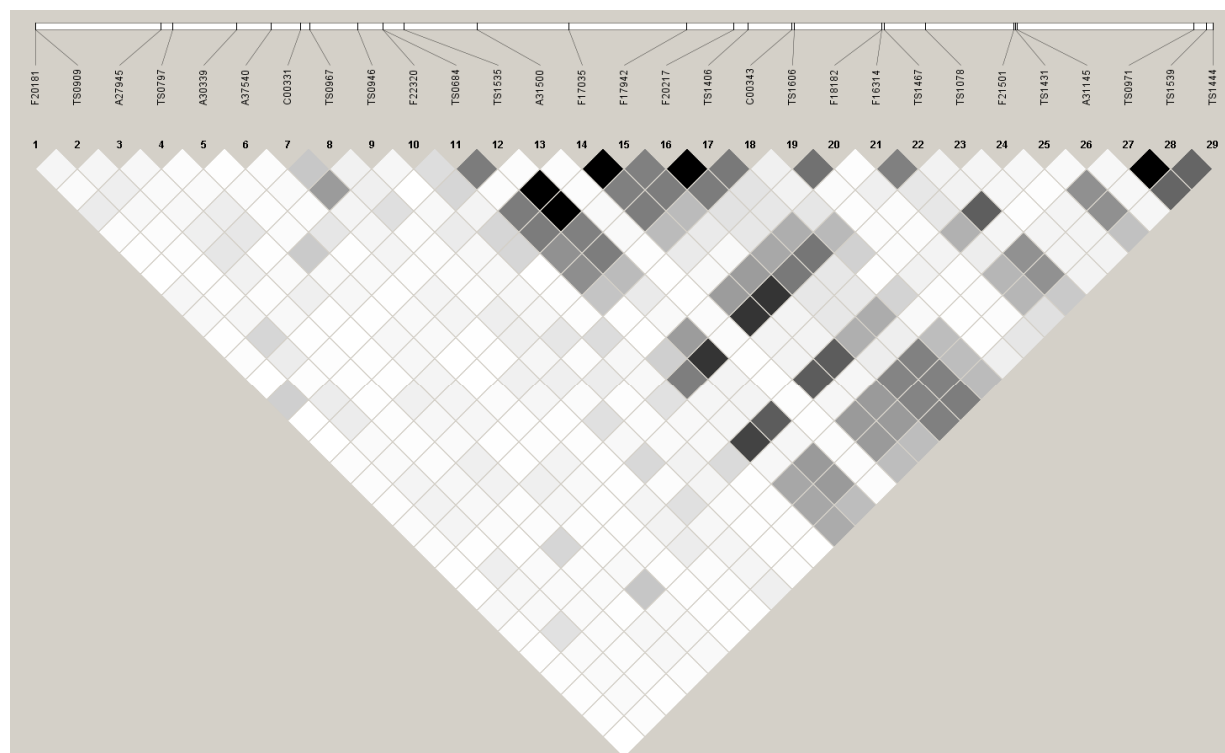


Tgu9

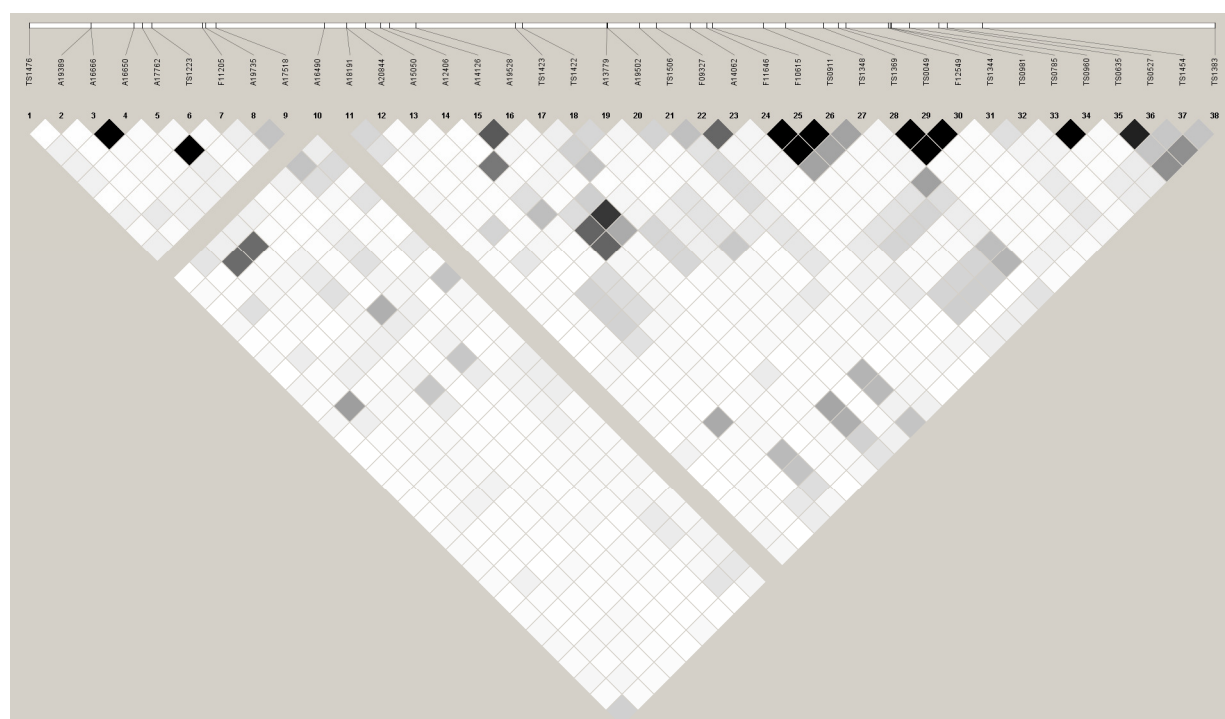


Tgu10

Supplementary Figure 6 continued.

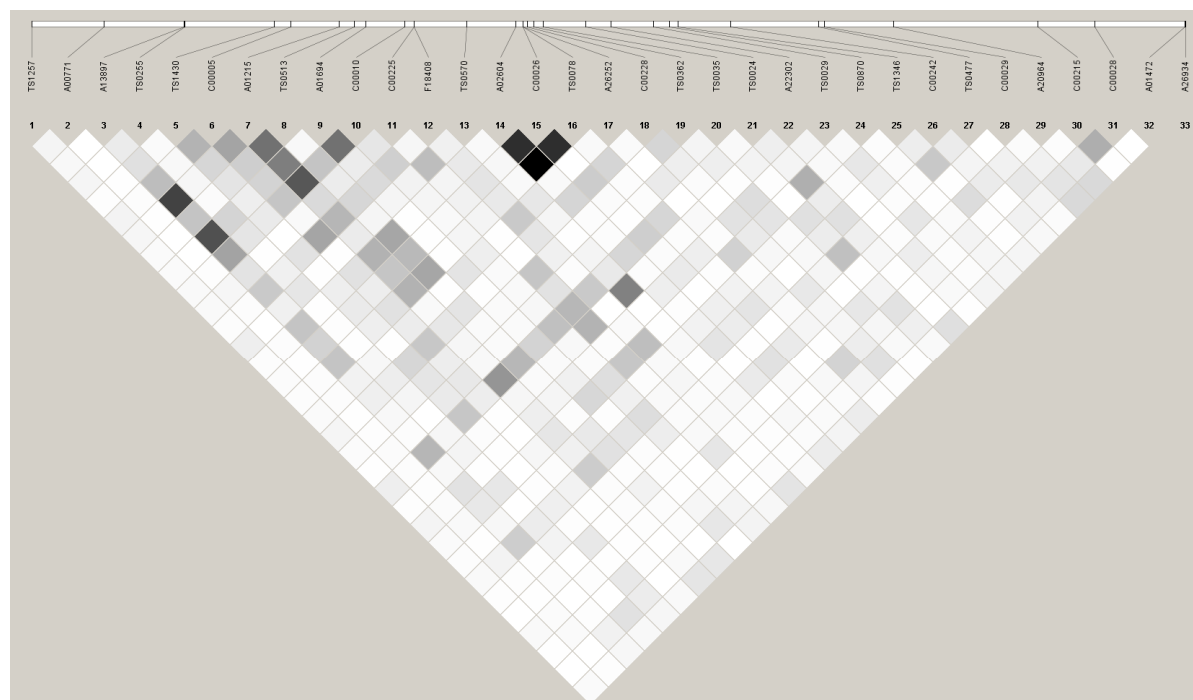


Tgu11

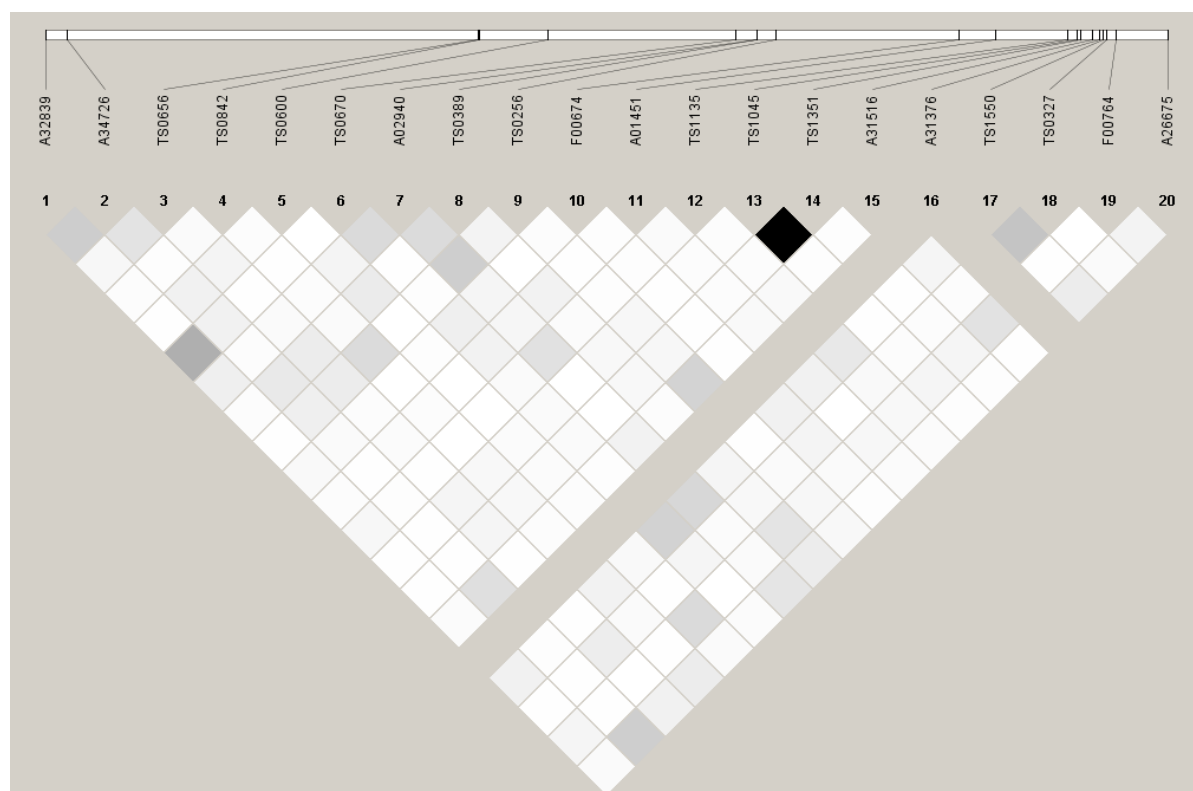


Tgu12

Supplementary Figure 6 continued.

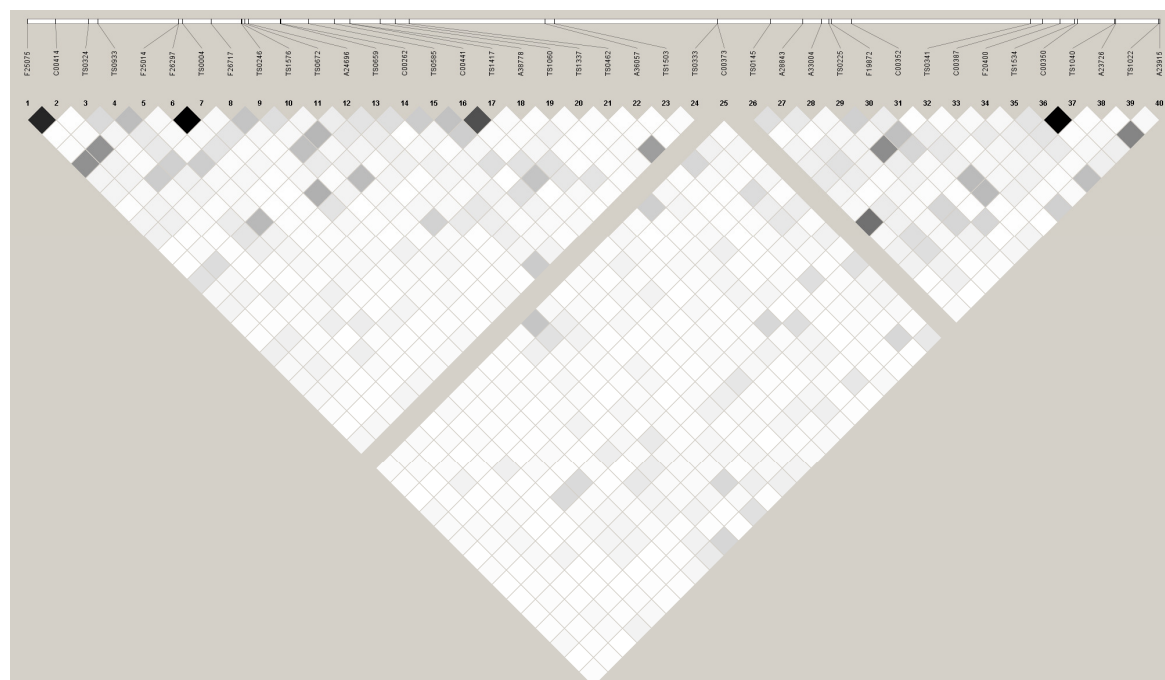


Tgu13

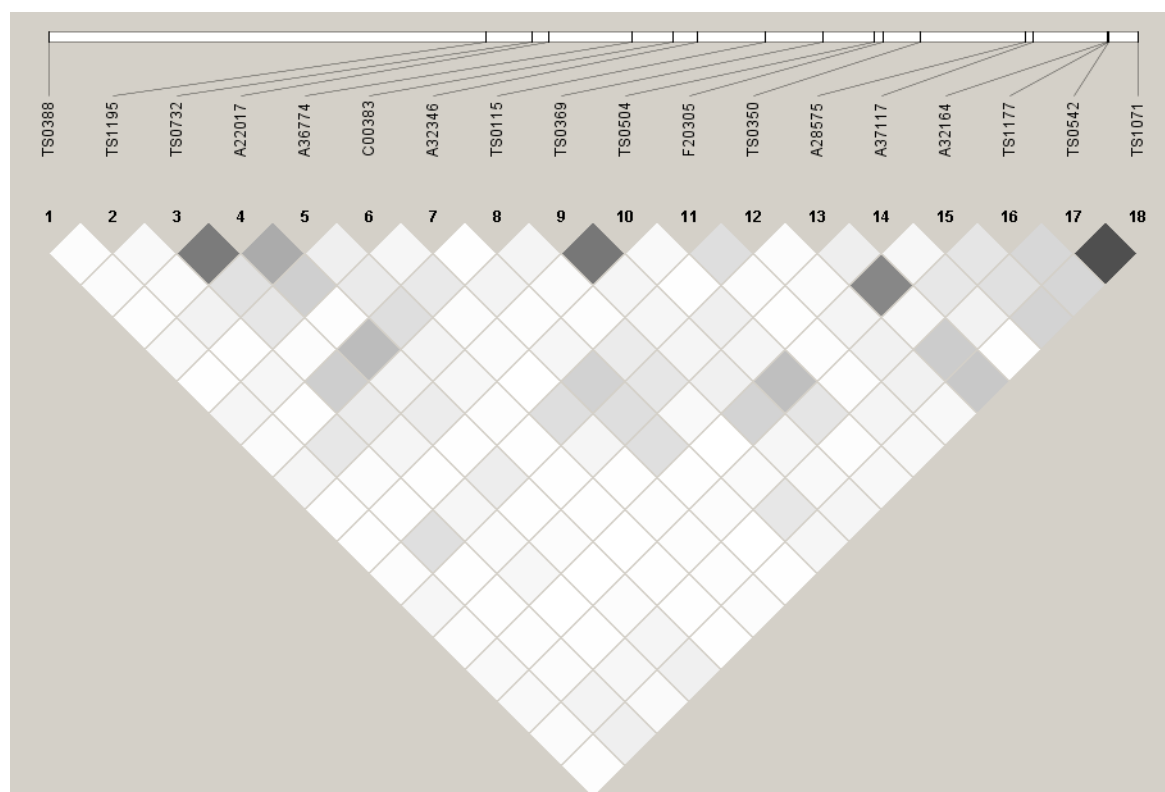


Tgu14

Supplementary Figure 6 continued.

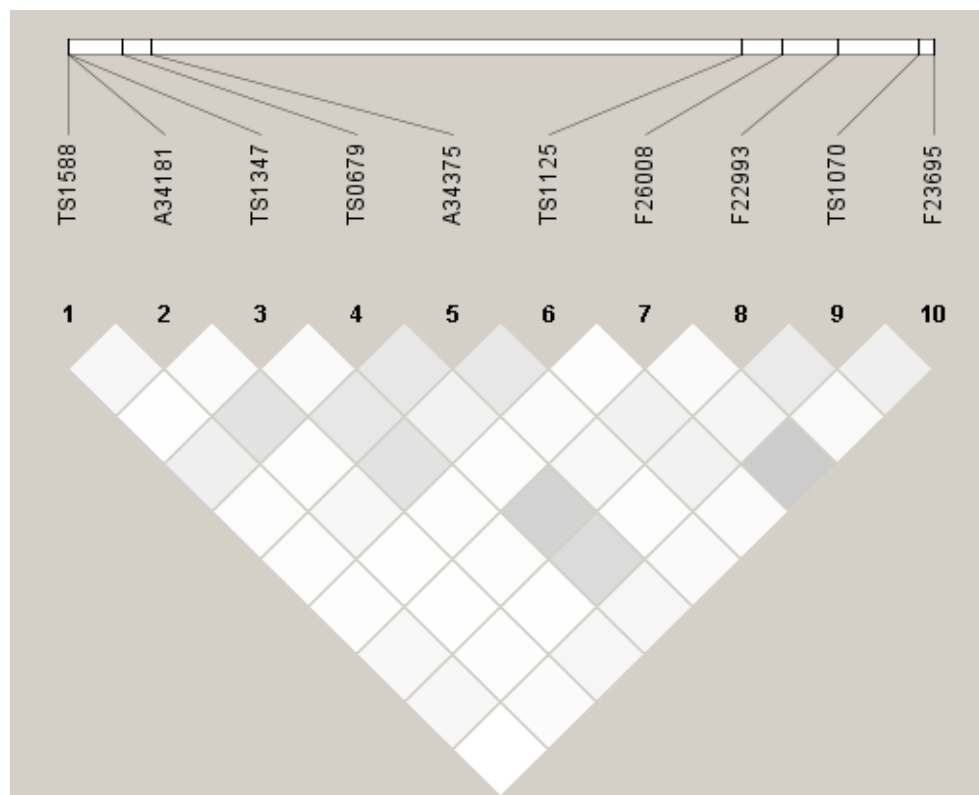


Tgu15

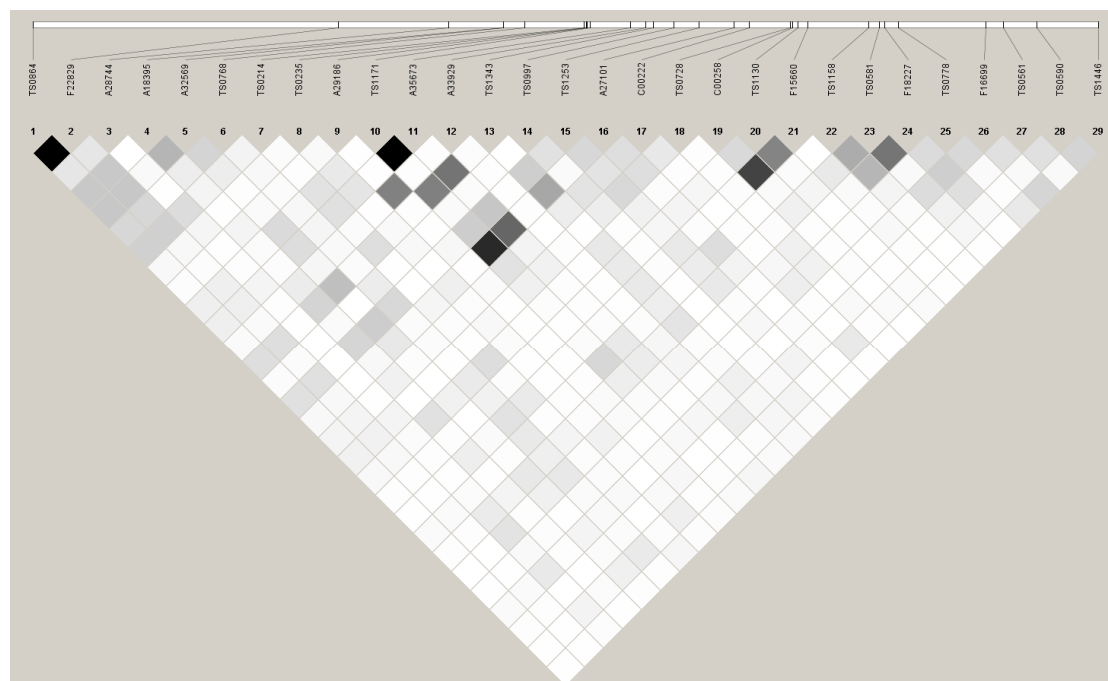


Tgu17

Supplementary Figure 6 continued.

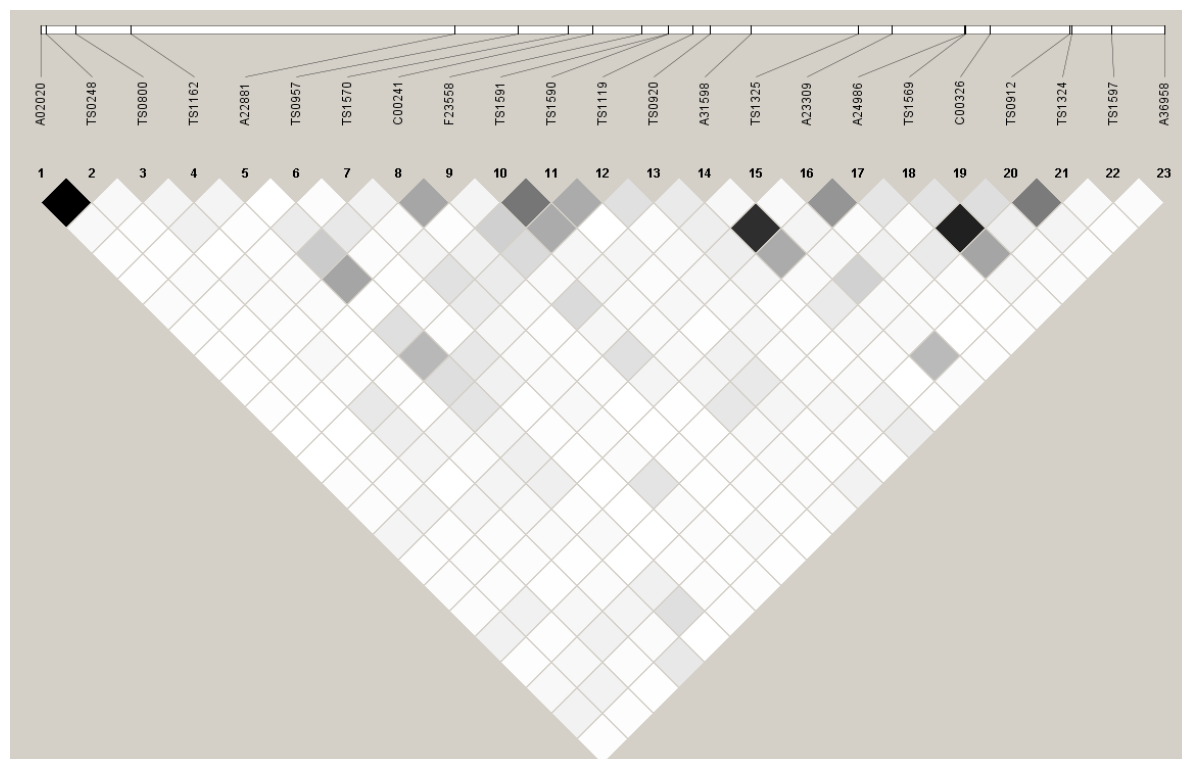


Tgu18

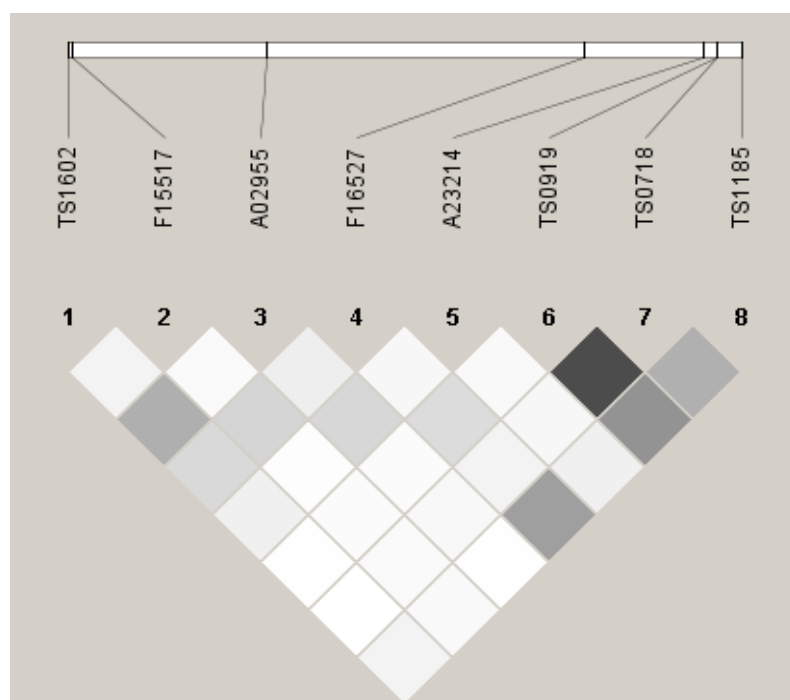


Tgu19

Supplementary Figure 6 continued.

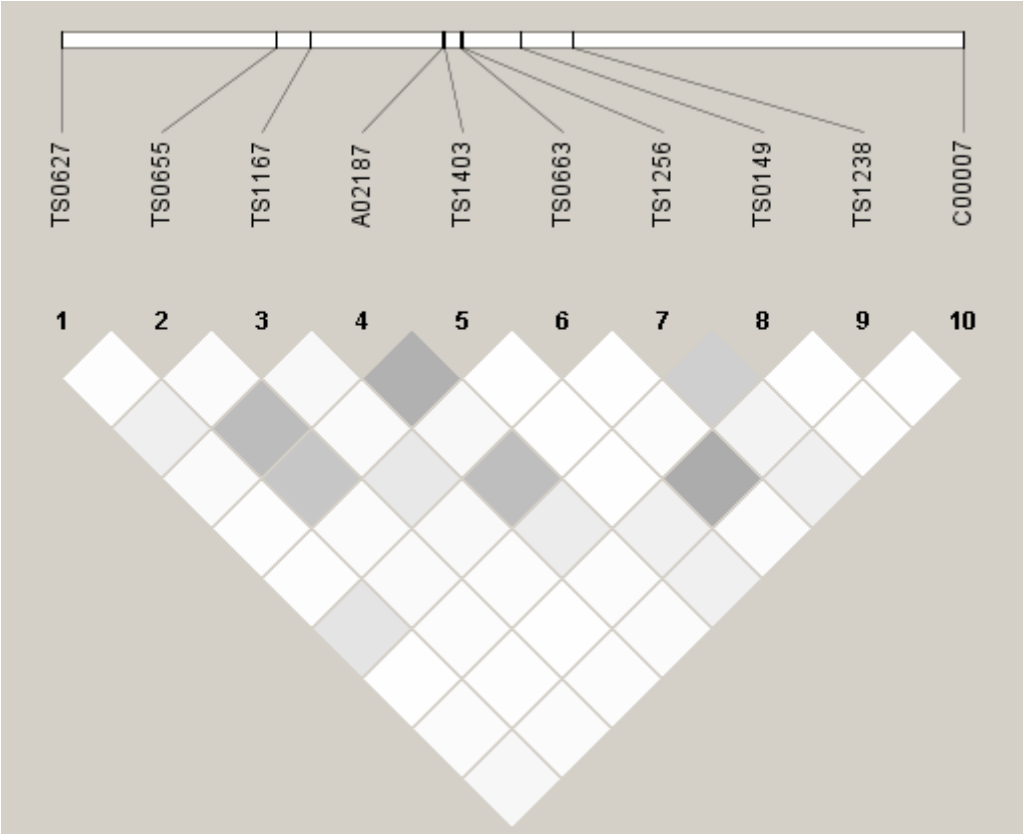


Tgu20

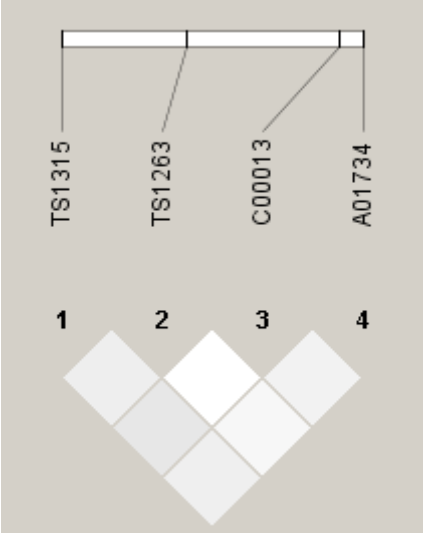


Tgu21

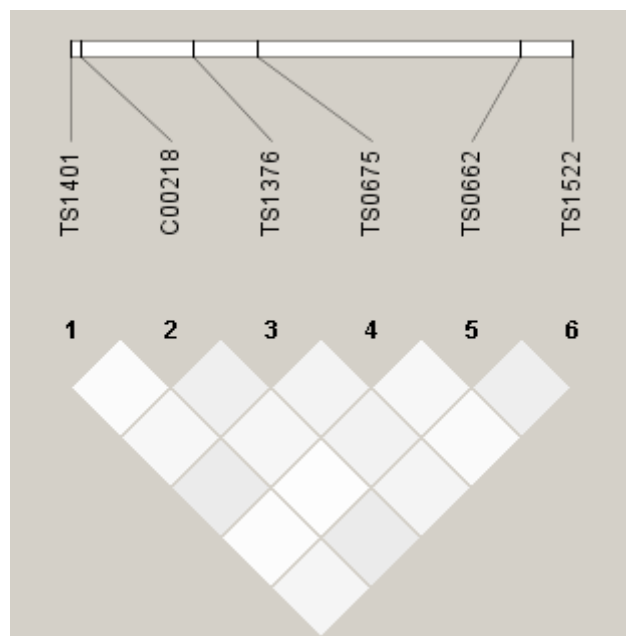
Supplementary Figure 6 continued.



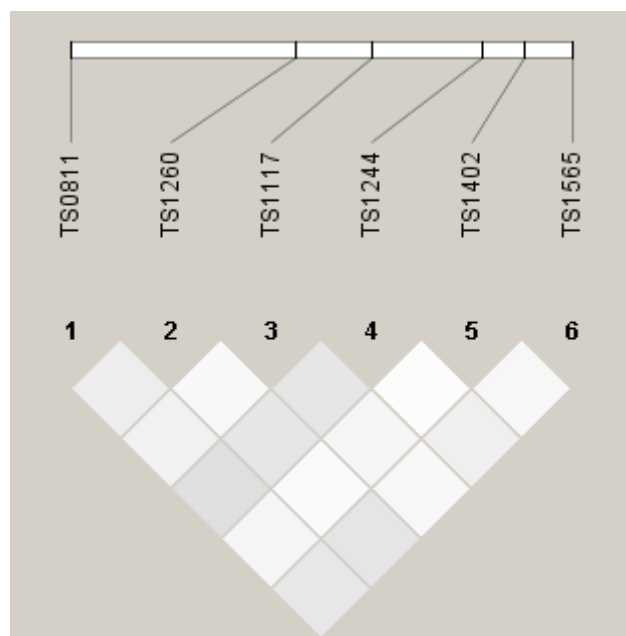
Tgu23



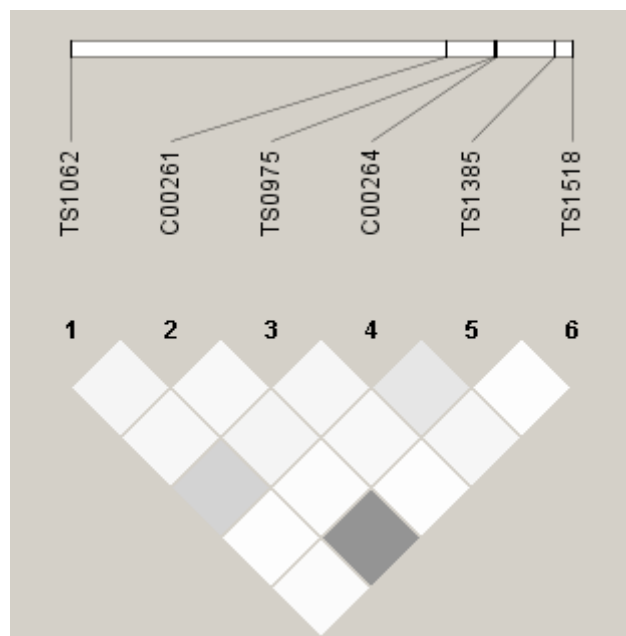
Tgu24



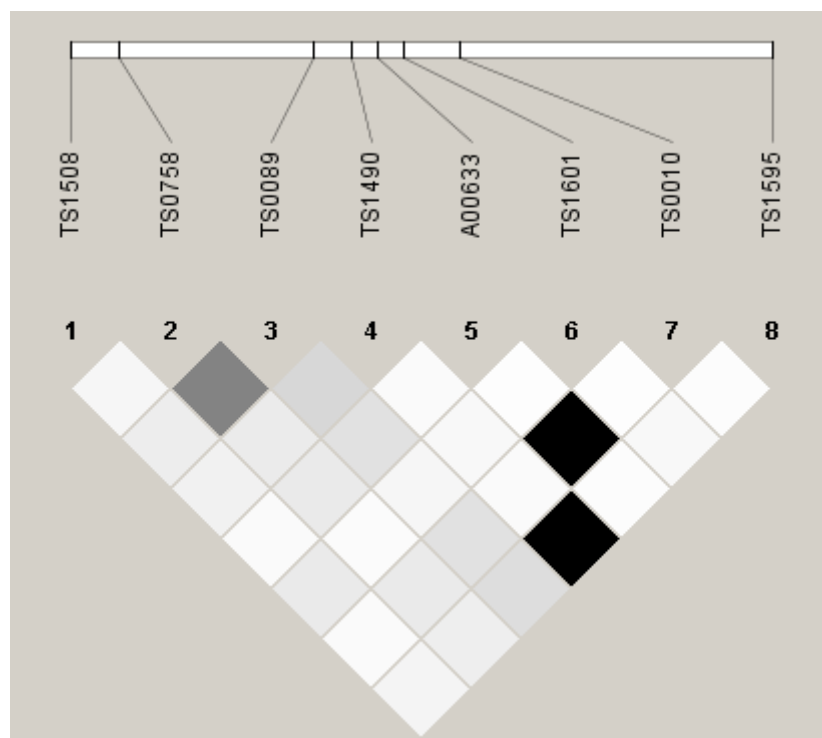
Tgu25



Tgu26

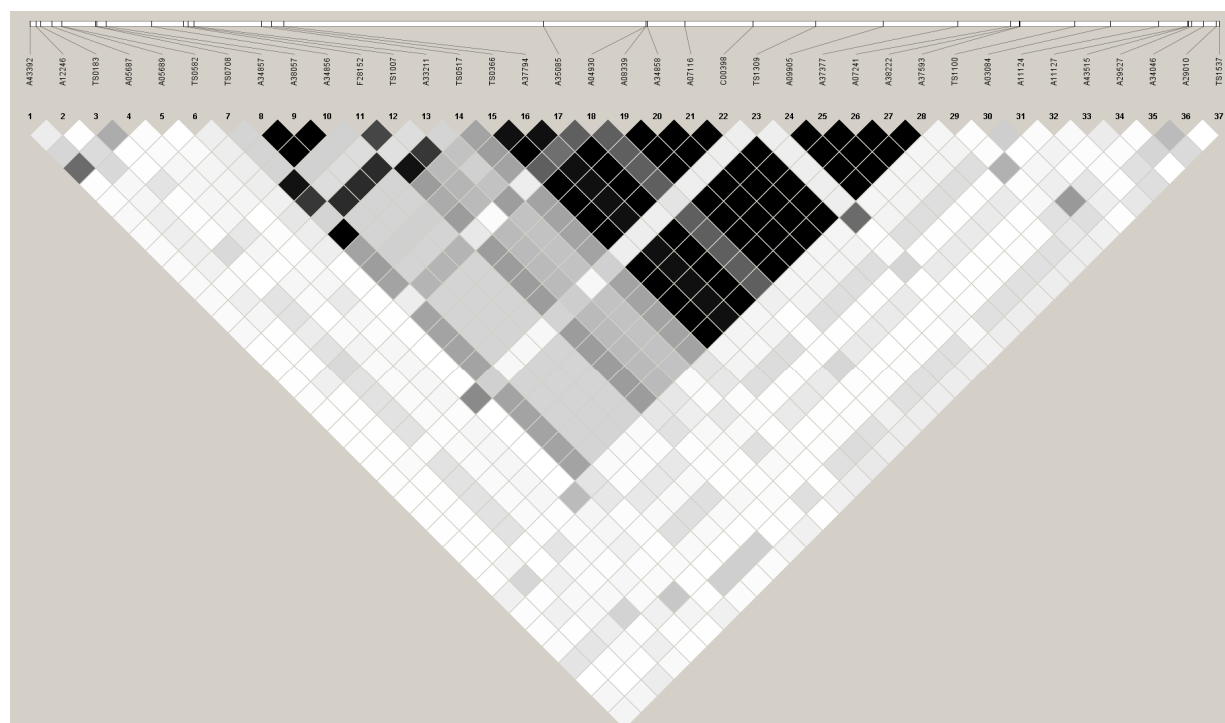


Tgu27



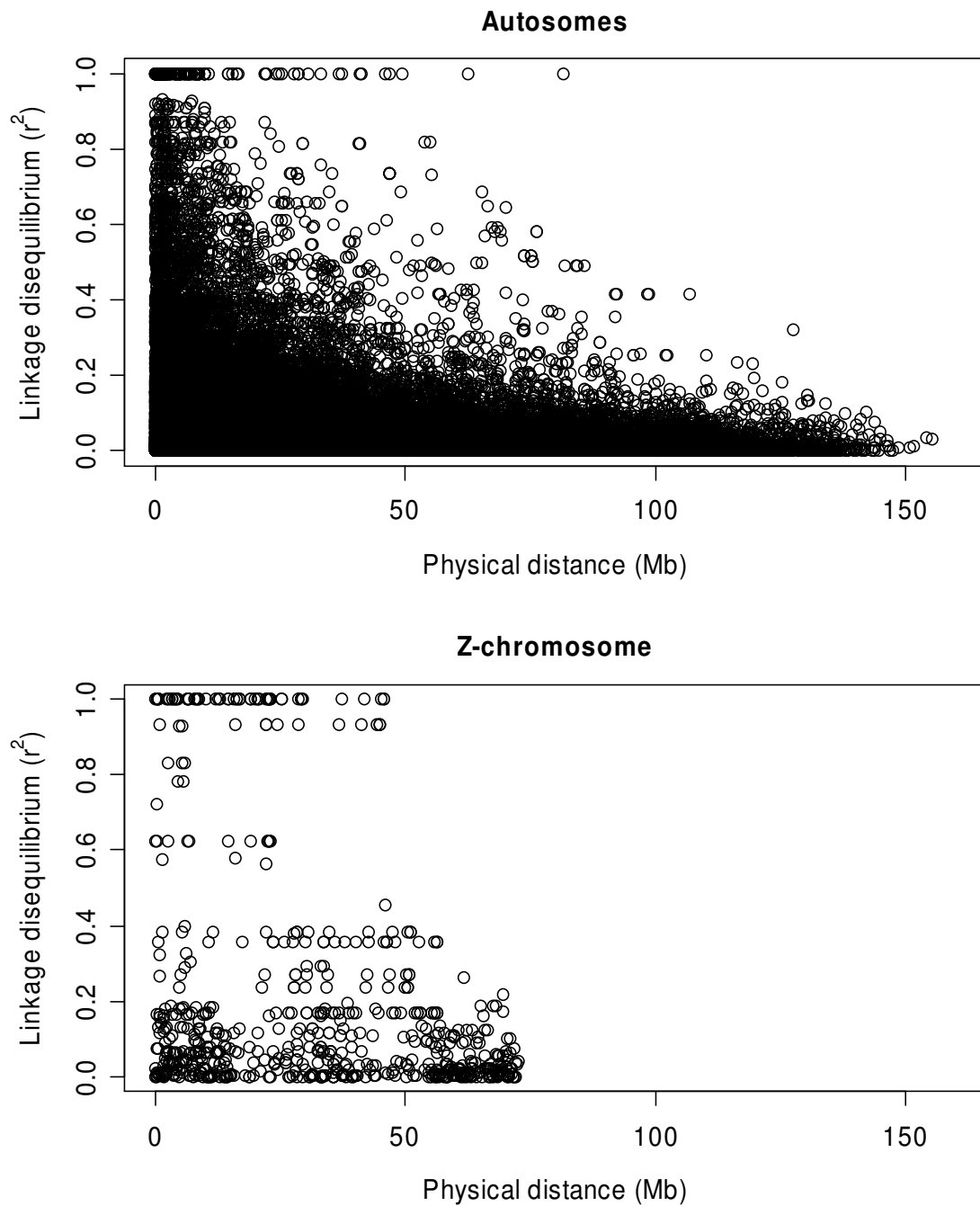
Tgu28

Supplementary Figure 6 continued.

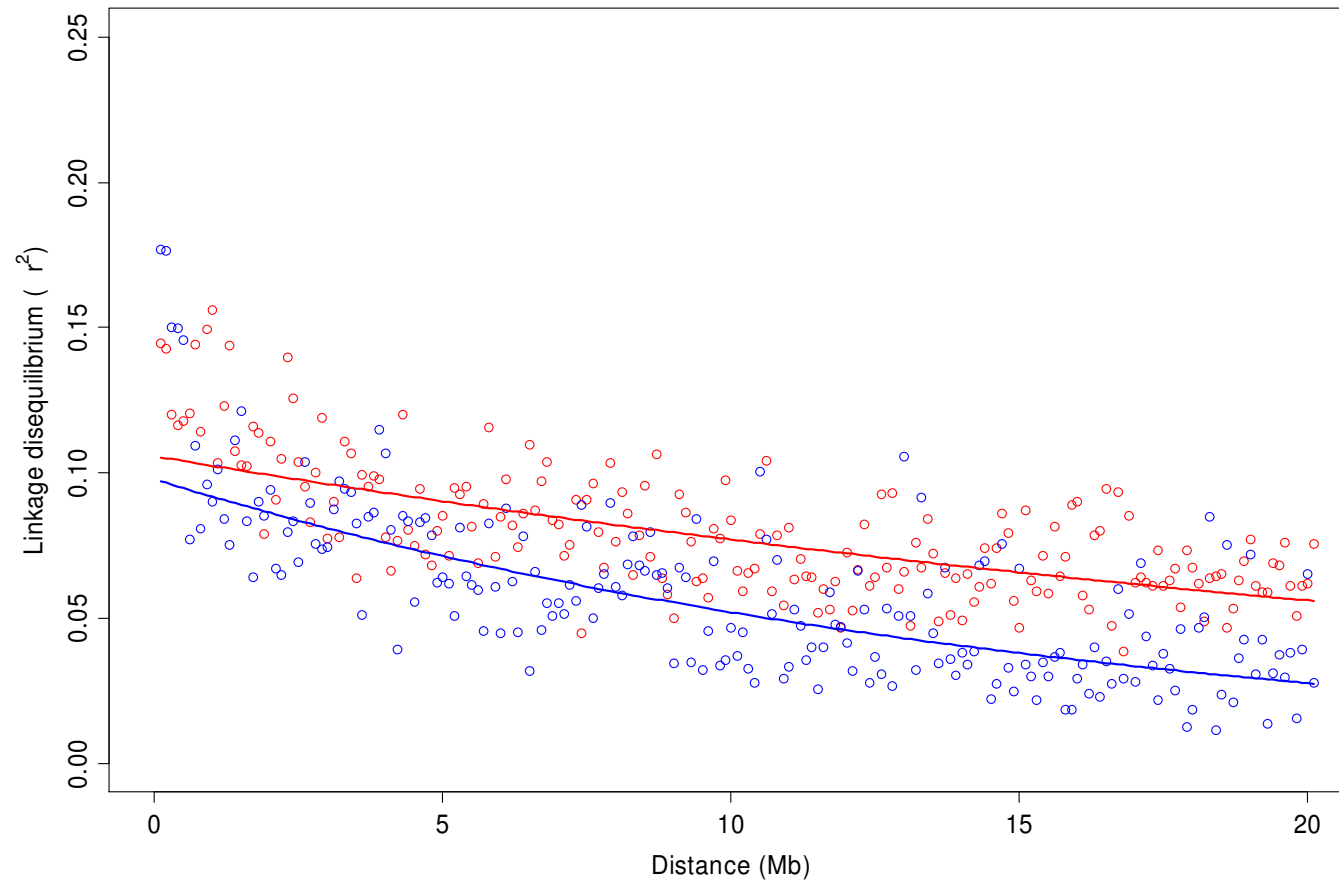


TguZ

Supplementary Figure 6 continued.



Supplementary Figure 7: The relationship between the physical distance (Mb) and the level of linkage disequilibrium (r^2) for all adjacent marker pairs within linkage groups in the zebra finch linkage map. Separate plots are given for autosomes (top) and the Z chromosome (bottom).



Supplementary Figure 8: The relationship between the physical distance (100 kb intervals) and the average level of linkage disequilibrium (mean r^2) between all marker pairs. Large chromosomes (>50 Mb) are shown in red and small chromosomes (<50 Mb) in blue. The lines indicate fitted exponential curves for each chromosomal class.