Supplementary Figure S3. Clustering recombinants based on their genotype. The number of differences in genotype was calculated between every pair of recombinants for the set of window-based markers on the five major chromosome arms (X, 2L, 2R, 3L, 3R). This dissimilarity, or mismatch matrix was then subjected to hierarchical clustering using the 'hclust' function in R [GenoTree <- hclust(as.dist(MismatchMatrix),method="average")]. The plot below depicts the resulting dendrogram, with recombinants highlighted based on genotyping data collection method (black, MSG; red, WGS). There is no clear clustering of animals genotyped with the same method.

181 Recombinants Clustered by Genomewide Genotypes