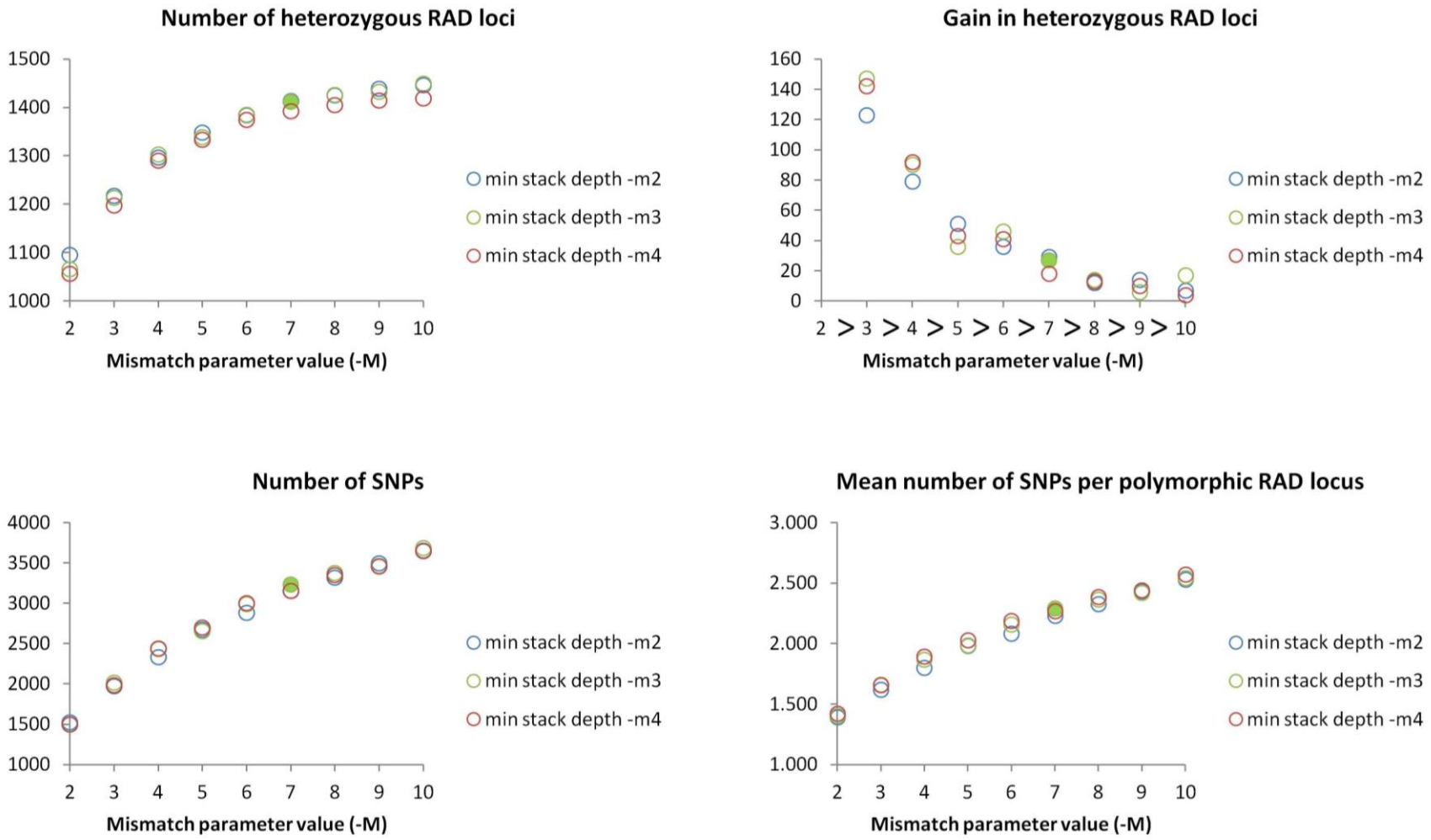
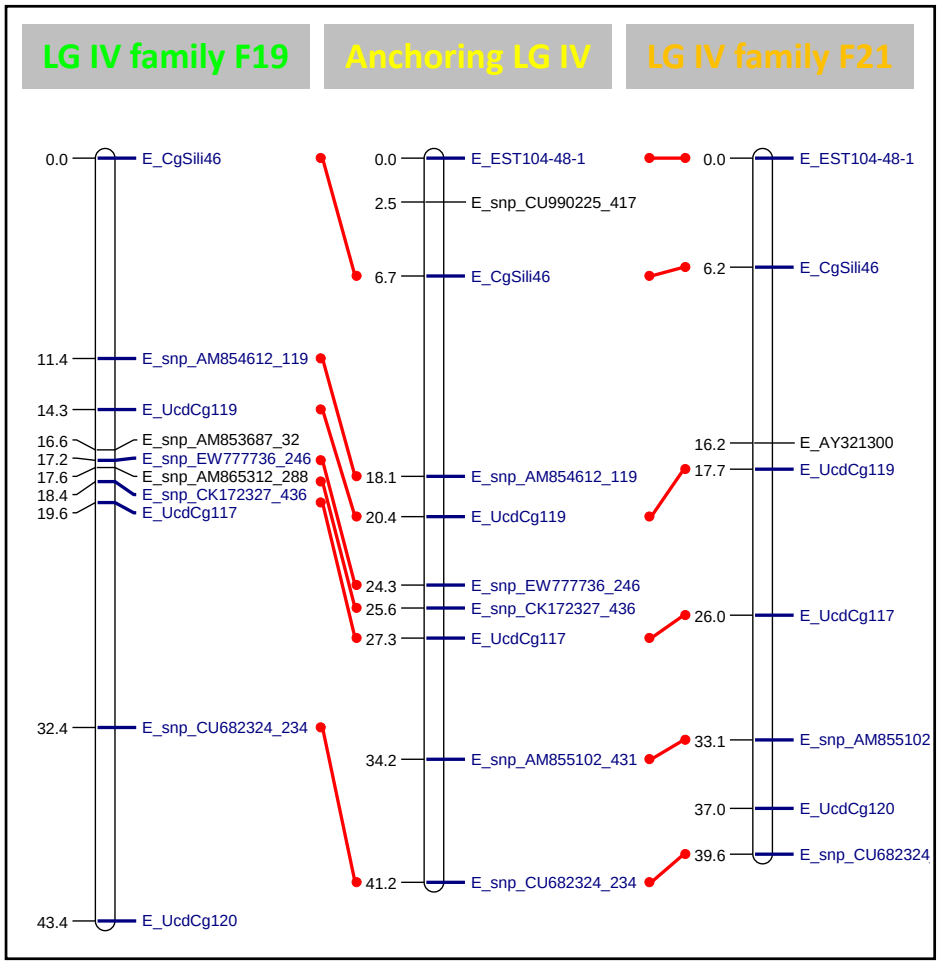


Figure S1: Optimization of *Ustacks* parameters for *de novo* stack assembly in Parent F1_029. The retained combination of parameters based on empirical distributions of the number of polymorphic markers is –m 3 –M 7 (green circle).

low-density map (136 SNPs)
F2-19: 293 F2; F2-21: 282 F2



high-density map (1516 SNPs)
F2-19: 106 F2; F2-21: 106 F2

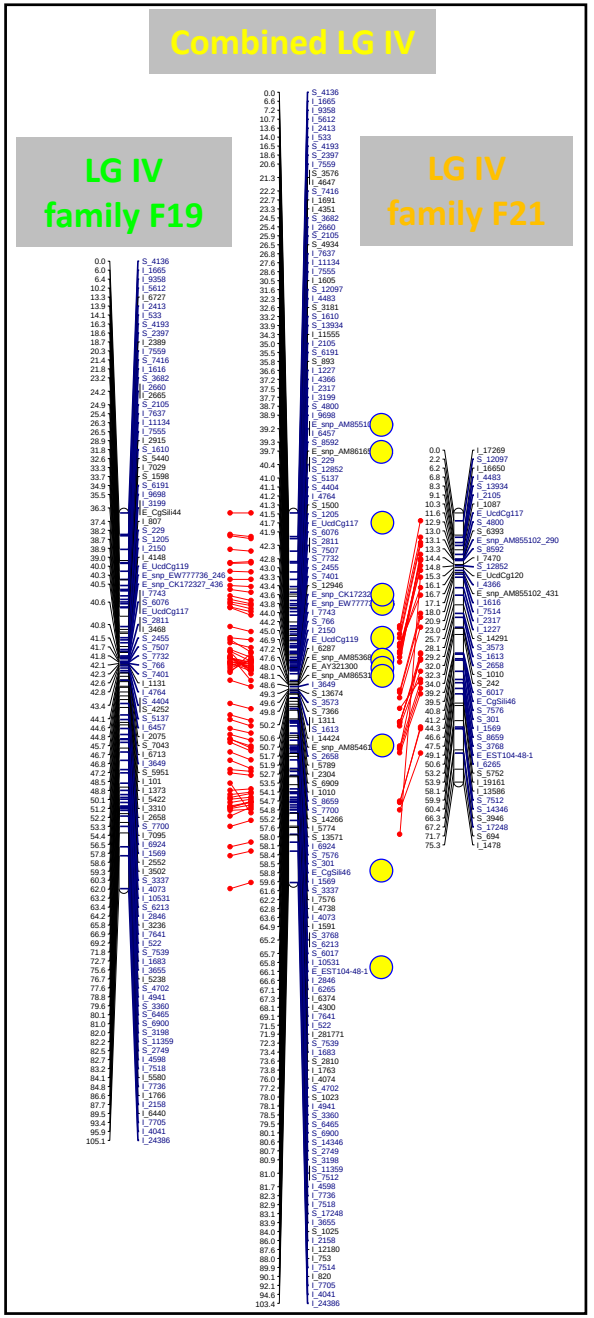


Figure S2: The low-density consensus linkage map (left, LG IV) was used as an anchoring map to set fixed orders (yellow points) to support the construction of the combined RAD linkage map (right, LG IV).

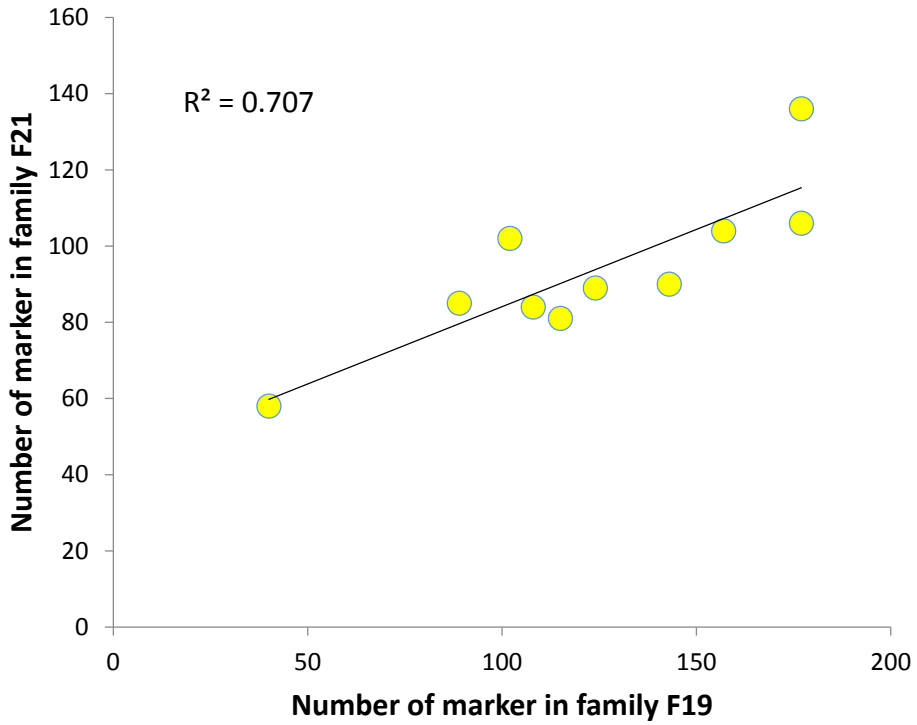


Figure S3: Correlation between the number of retained RAD markers per LG between family F19 and family F21

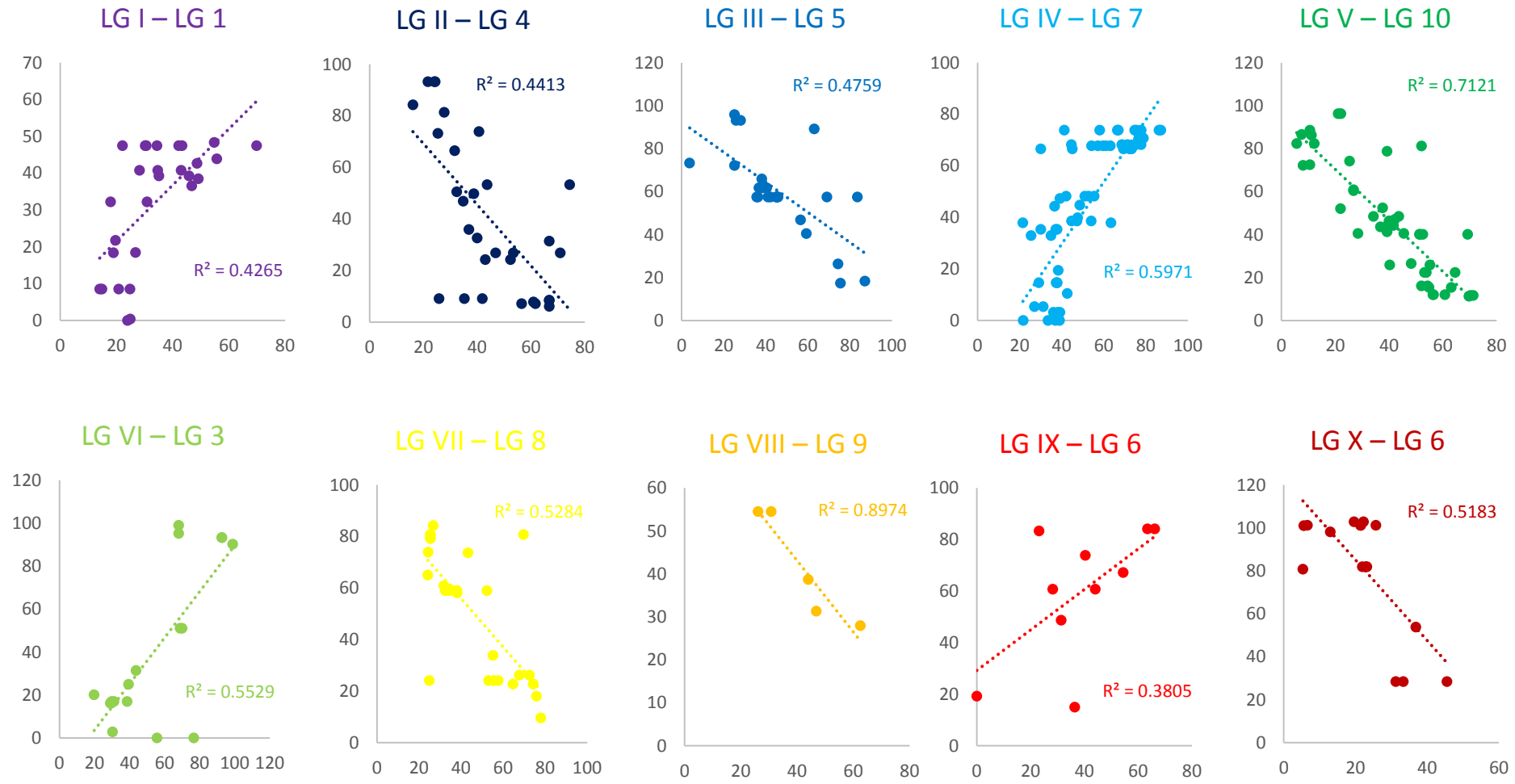


Figure S4: Correlations between the marker positions from the new consensus linkage map (LG I to X, x axis) and the positions from Hedgecock et al. 2015 (LG 1 to 10, y axis). A total of 278 pairs of markers colocalized to the same scaffolds were used to identify homologous regions between the two genetic maps.

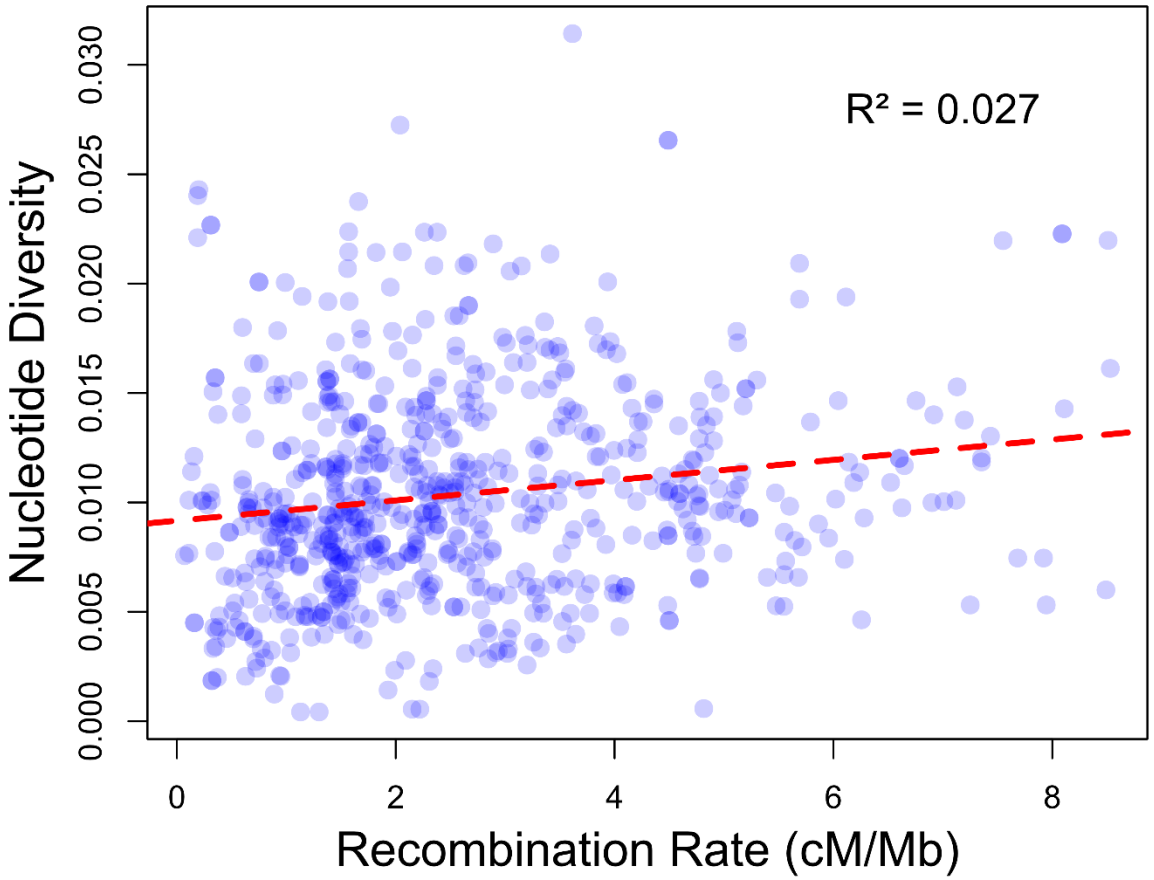


Figure S5: Correlation between nucleotide diversity and the local recombination rate assessed with *MareyMap*. Each point represents an estimate of π and recombination rate averaged in a 500 kb window. The red dashed line is the linear regression line ($P = 1.1 \times 10^{-5}$).