Figure S1: *Saccharomyces* **phylogenomics**, *S. cerevisiae* strains with clean lineages highlighted in grey, with colour indicating source (name) and geographic origin (dots). Figure extracted from figure 1 of (Liti et al. 2009)

Figure S2: Frequency of fluorescence extinction for each marker locus in the 22 hybrids between SK1 and different strains of the collection, including YIIc17_E5 (red dots) and UWOPS83_787_3 (green dots) which show particularly high levels of extinction.
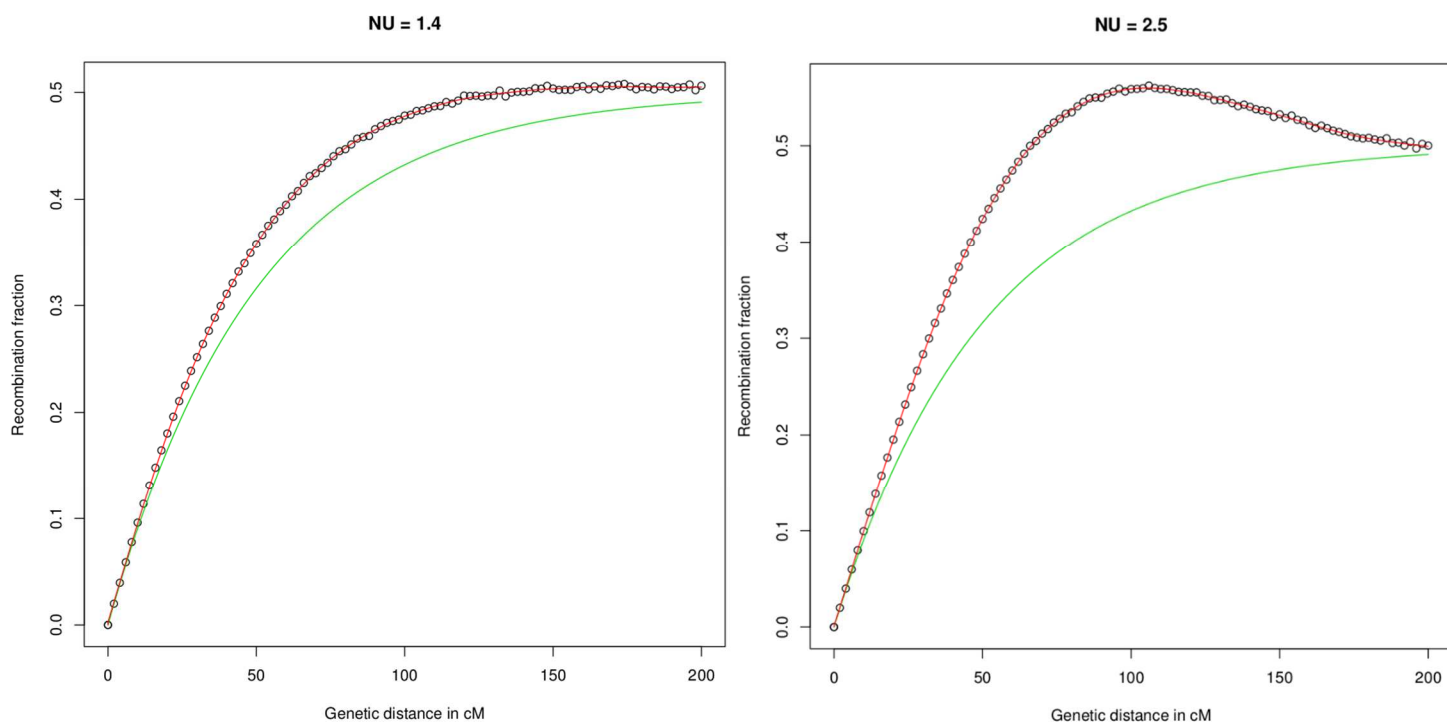
Figure S3: Examples of relationship between genetic distance (mean number of crossovers per meiosis in the considered interval multiplied by 100, expressed in centiMorgans) and recombination fraction between two markers for moderate (v = 1.4; left panel) or strong (v = 2.5; right panel) positive interference (see Supp Methods). Dots and interpolating red curve: simulated values. Green curve: theoretical expectation in the absence of interference (Haldane mapping function)
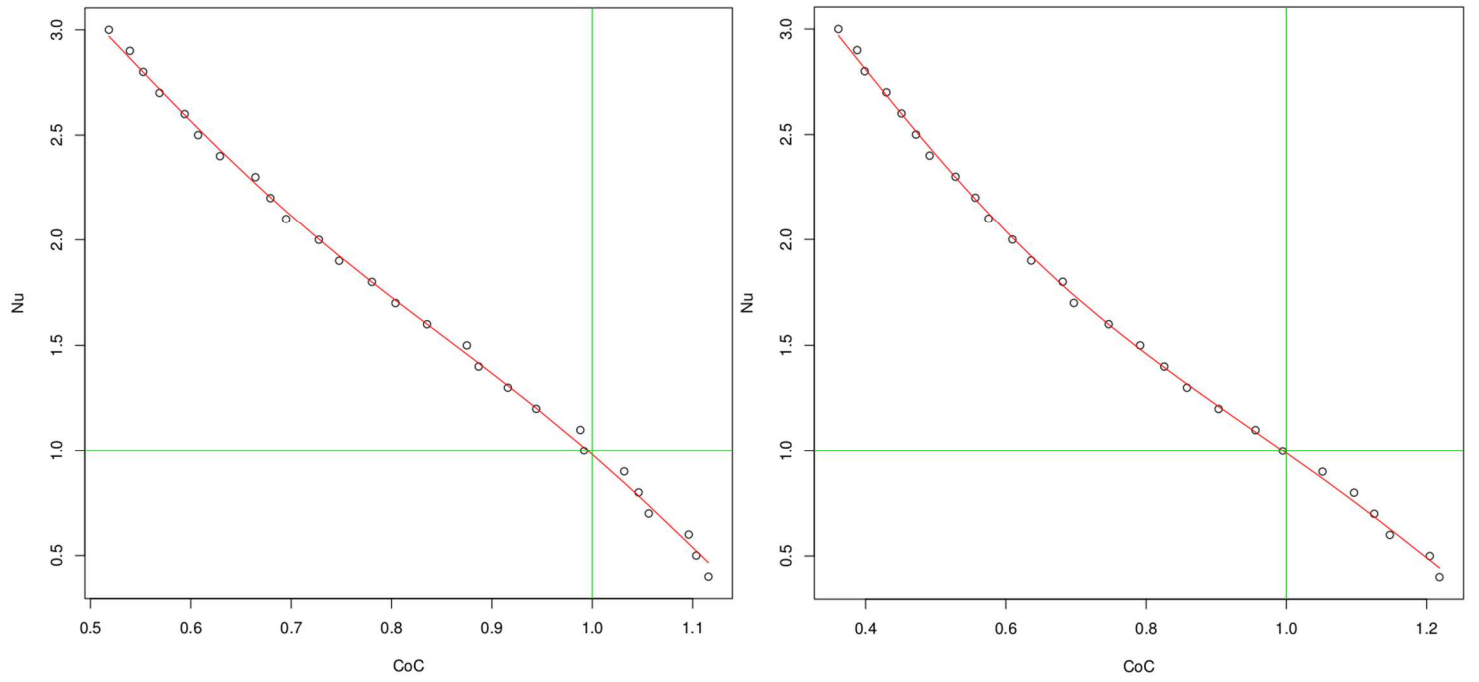
Figure S4: Examples of the relationship between Coefficient of Coincidence (CoC) and interference strength measured by the parameter ν of the gamma model (Nu) in the case of SK1 strain and tester VI-C1Y2R3 (left panel), or YPS128 strain and tester XI-R8Y9C10 (right panel). Dots and interpolating red curve: simulated values. Scatter of dots is due statistical errors in the simulations. Green lines indicate the case without interference, where CoC and ν are equal to one.

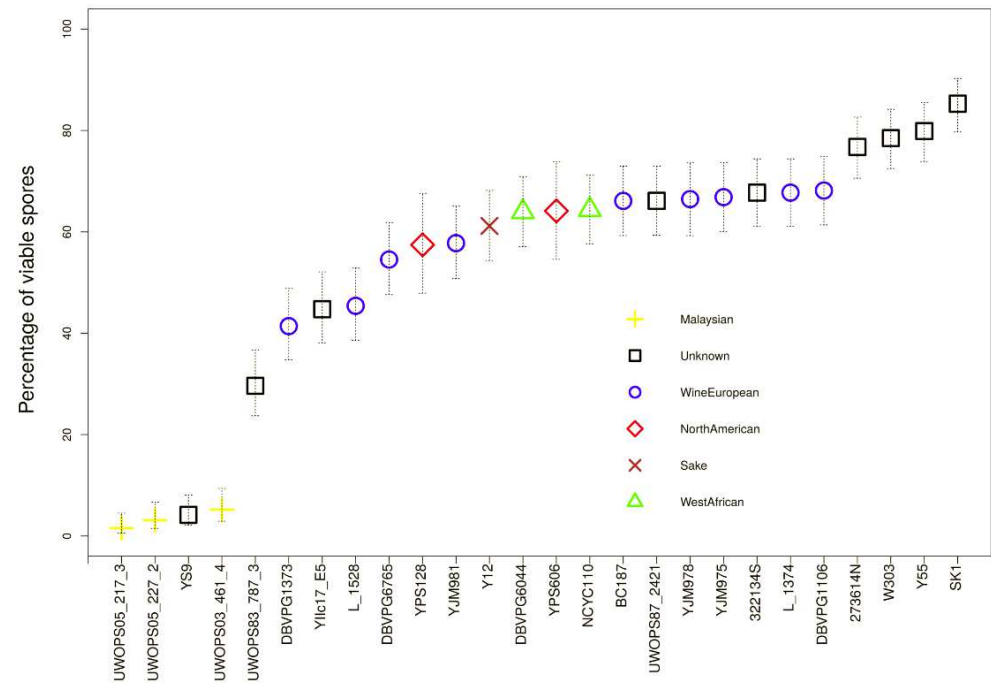**Figure S5**: see separate file Figure_S5.pdf

A
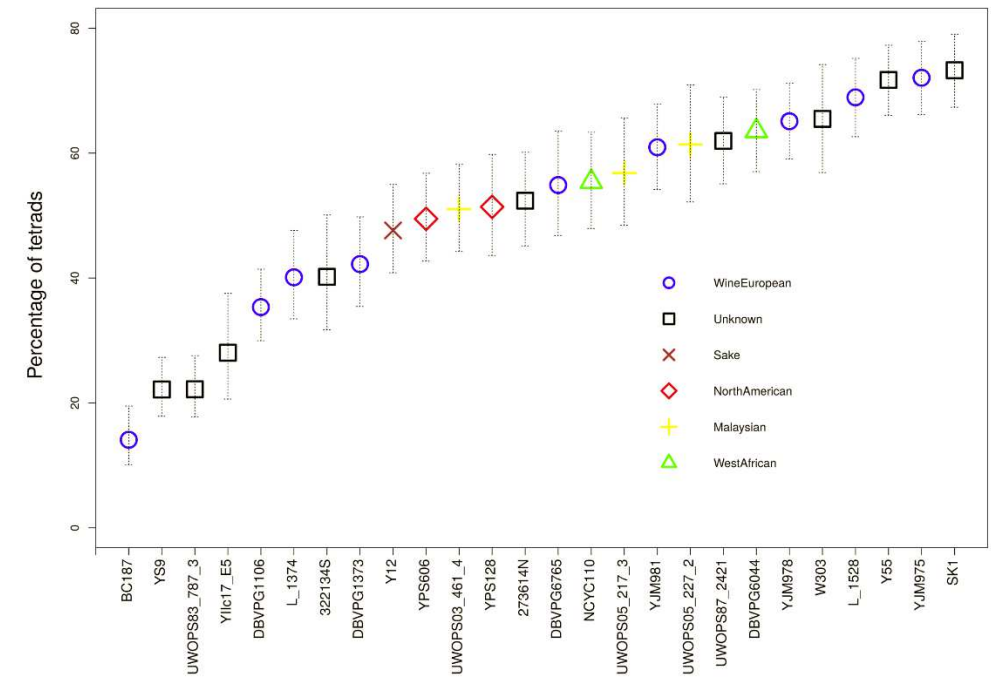
B

Figure S6: Sporulation and spore viability rates. X-axis: Names of the strains crossed with tester SK1-XI-R1C2Y3 to obtain the hybrid. Bars indicate 95% confidence intervals based on binomial law. Panel A: Percentage of tetrads after 10 days for the 26 hybrids. Panel B: Percentage of viable spores. Colors refer to the phylogenetic groups of the parental strains
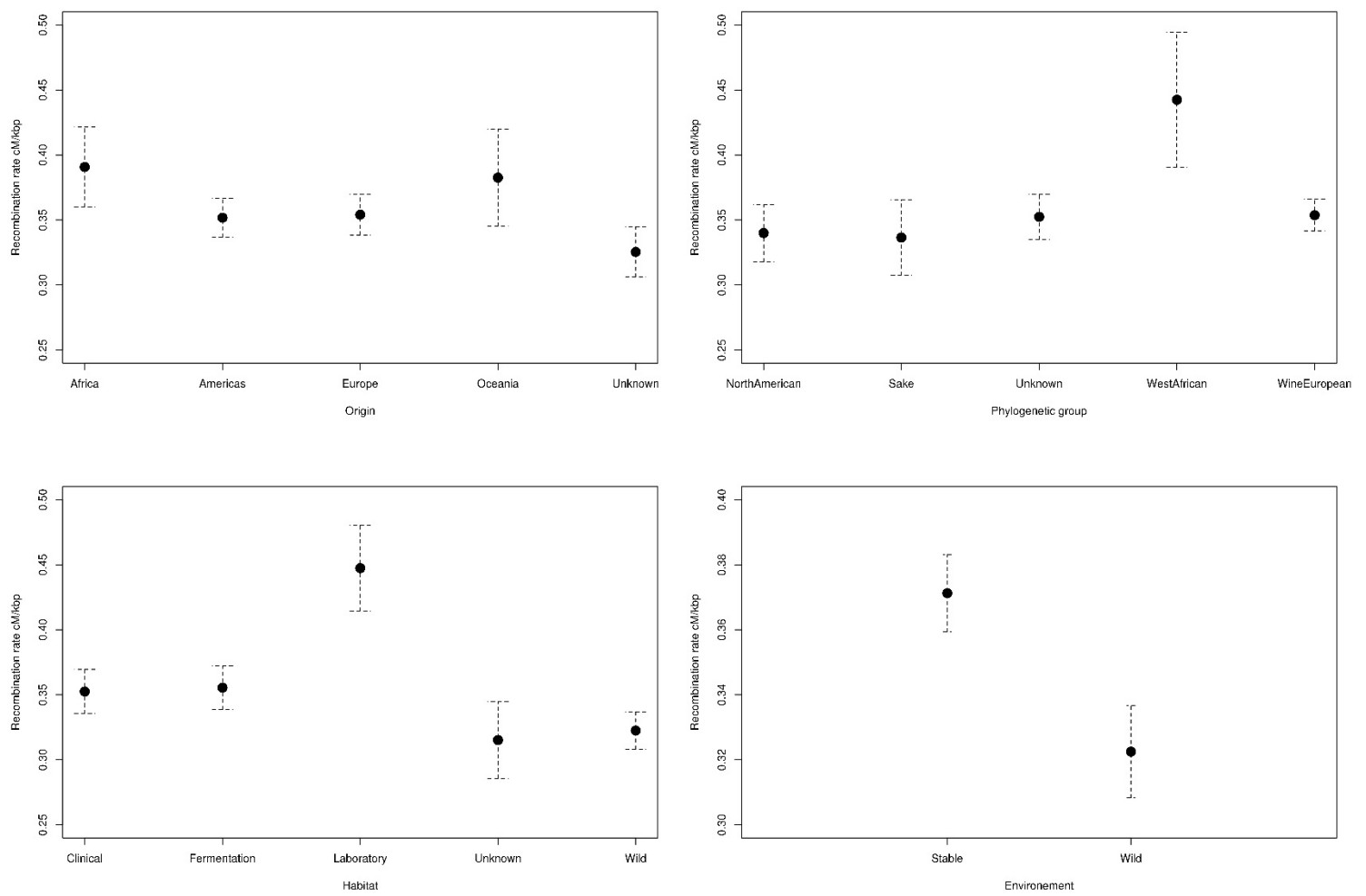
Figure S7: see separate file Figure_S7.pdf

Figure S8: Recombination rates when pooling strains based on their geographic origin, phylogenetic group (Liti et al. 2009), habitat, or stable environment (including laboratory, fermentation, and clinical strains) *vs* wild environment. Error bars indicate 95% confidence interval.

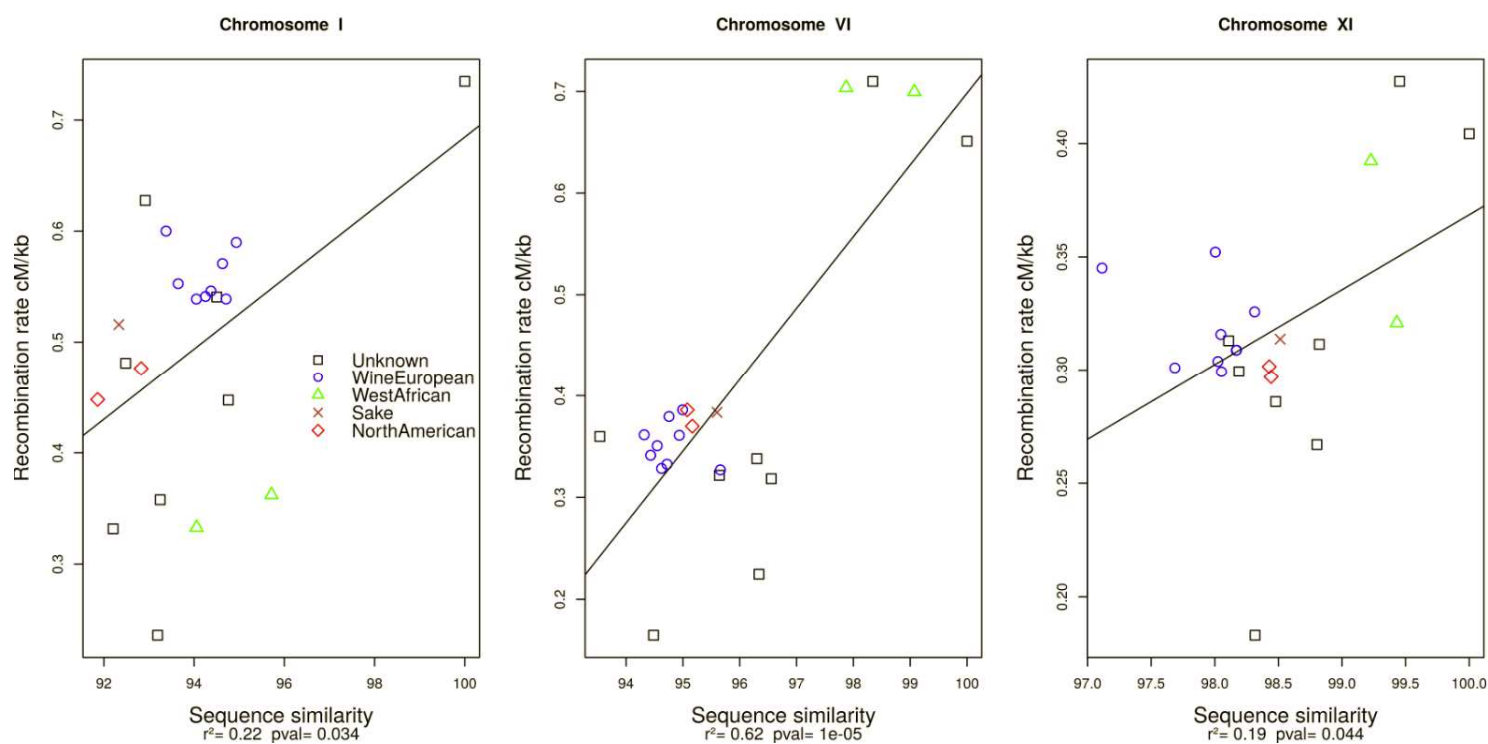**Figure S9**: see separate file Figure_S9.pdf

Figure S10: Correlation between sequence similarity (across intervals of one given chromosome), and the mean recombination rate of hybrids. X-axis: percentage of sequence similarity (see Materials & Methods), Y-axis: for each strain of the collection, average of the recombination rates of the hybrids obtained by crossing the strain with the tester(s) corresponding to the chromosome considered. Colors refer to the phylogenetic groups of the parental strains.
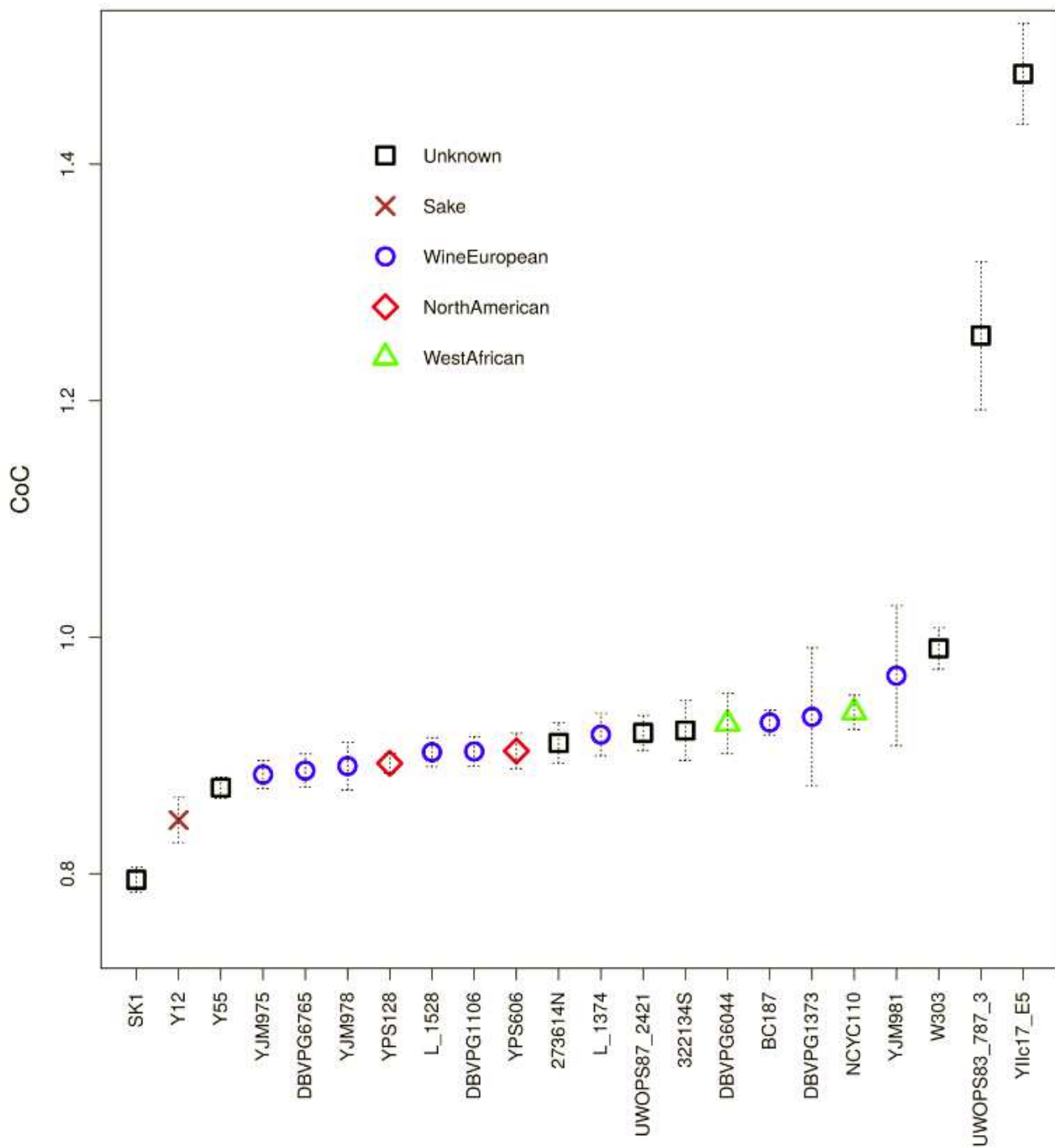
Figure S11: Values of the coefficient of coincidence (CoC) across hybrids. X-axis: name of the parent crossed with SK1 tester to produce the hybrids. Y-axis: average CoC value over all seven testers. Error bars indicate 95% confidence interval based on four biological replicates. Colors refer to the phylogenetic group of the strains.
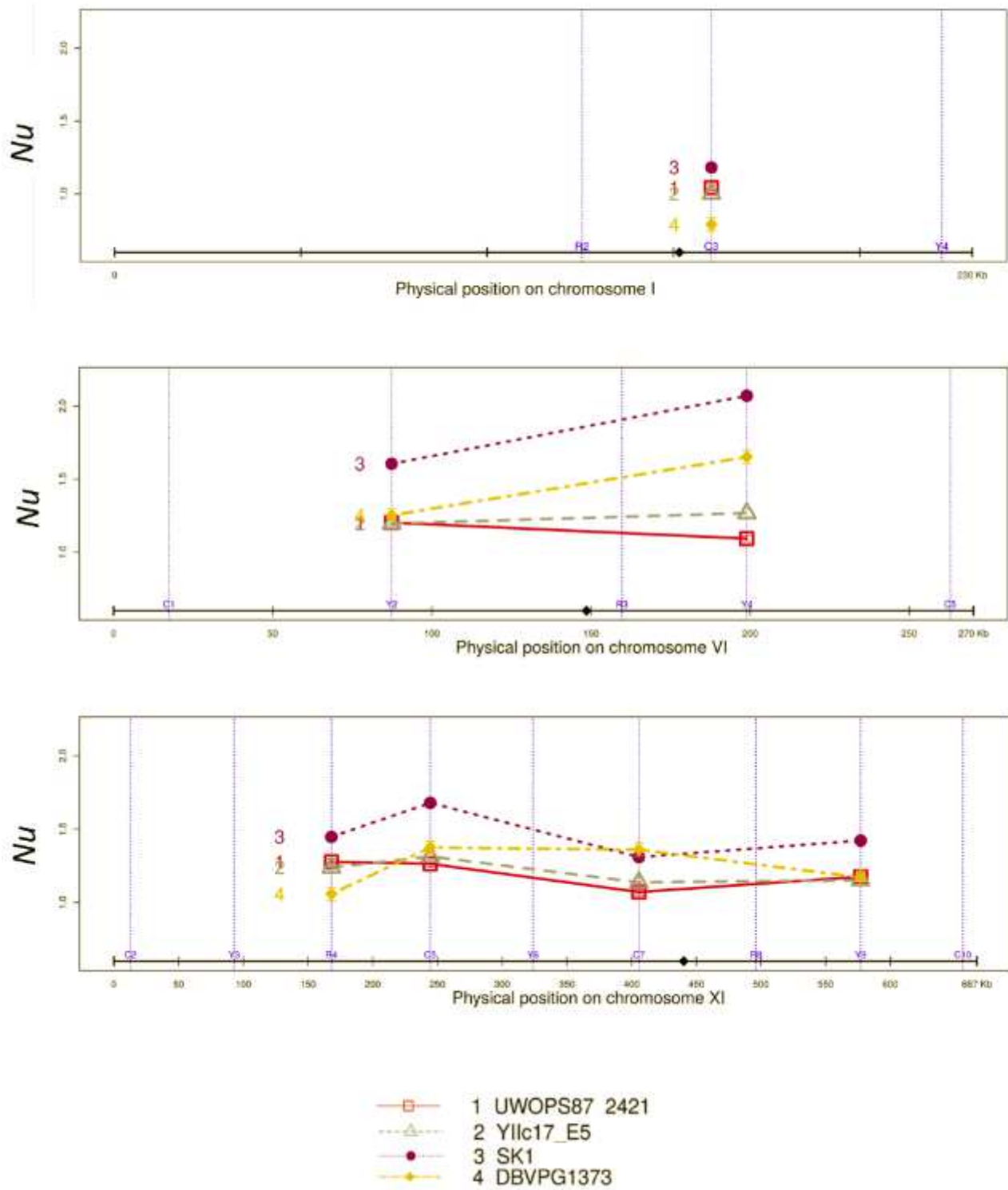
Figure S12: Interference strength profiles along chromosomes for three strains that illustrate different patterns. X-axis: physical position along chromosome I (upper panel), VI (middle panel) or XI (lower panel). Error bars indicate 95% confidence interval based on four biological replicates. Vertical blue dashed lines indicate the positions of fluorescent markers. Diamonds at the bottom show centromere positions.

Model Y = Mu + aDivSeq + INB + AGC1 + AGC2 + ASC + ε

1 SK1xY12
2 YPS128xDBVPG6765
3 SK1xDBVPG6765
4 SK1xYPS128
5 SK1xSK1
6 Y12xYPS128
7 YPS128xDBVPG6044
8 DBVPG6765xDBVPG6044
9 YPS128xYPS128
10 SK1xDBVPG6044

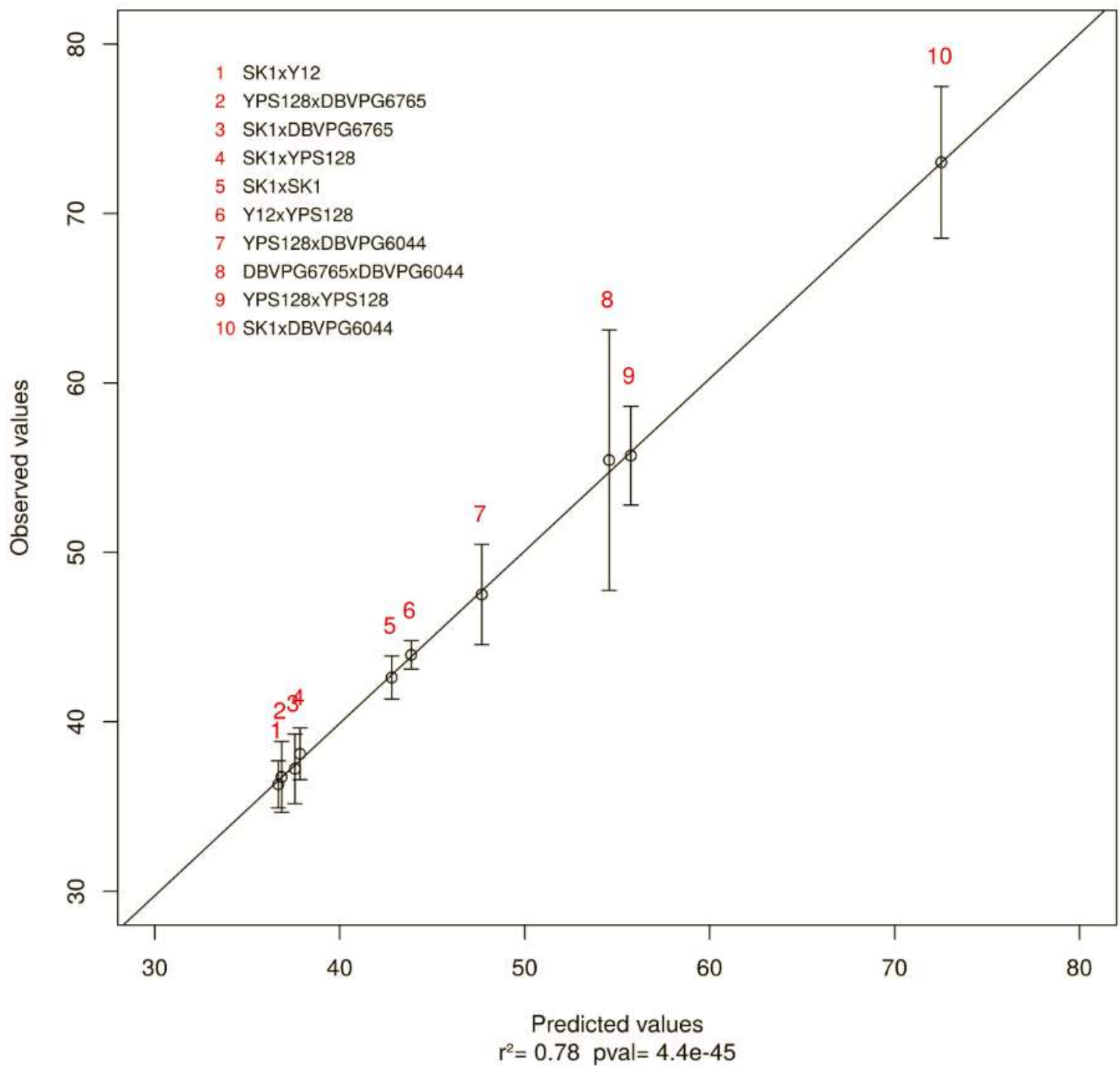Predicted values
r² = 0.78 pval= 4.4e-45

Figure S13: correlation between observed and predicted values of recombination after fitting the model (see Results) with the diallel data.
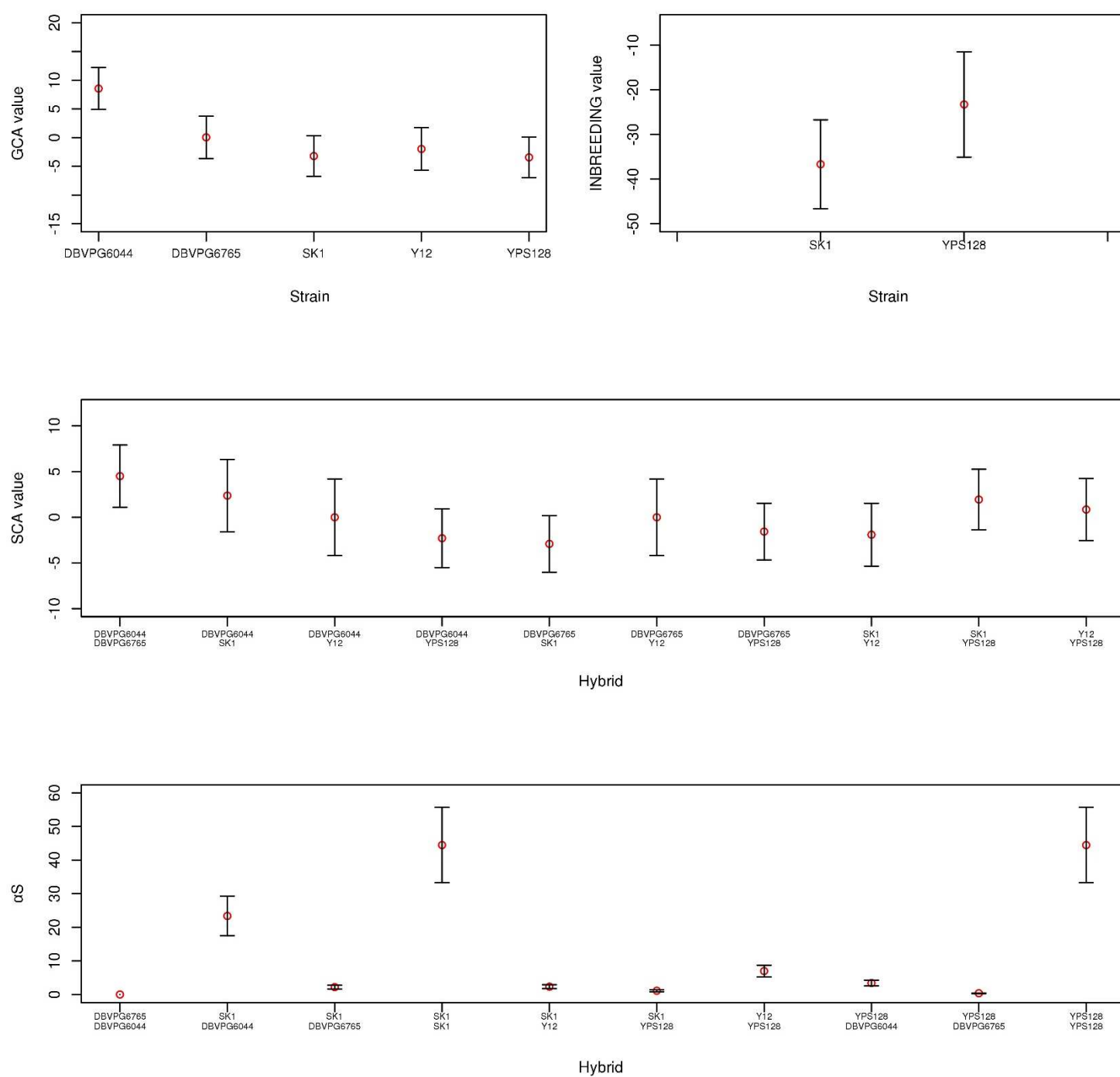
Figure S14: Estimated values of the parameters of the diallel model. GCA: general combining ability (in centiMorgans). SCA: specific combining ability (in centiMorgans). αS: predicted effect of sequence divergence (in centiMorgans) .