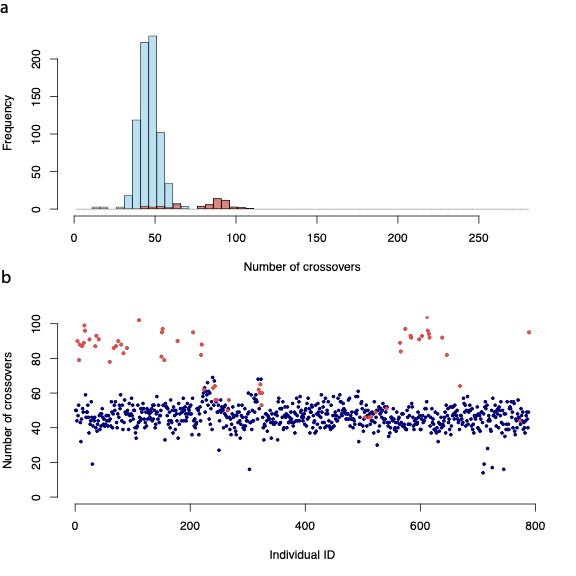
**Additional information for:**  
Genotyping by low-coverage whole-genome sequencing in intercross pedigrees from outbred founders: a cost efficient approach

Yanjun Zan, Thibaut Payen, Mette Lillie, Christa F. Honaker, Paul B. Siegeland Örjan Carlborg

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***Figure S1. Visualization of the number of crossover in all F2 individuals****. A) Histogram of number of imputed crossover events for the 803 genotyped F2 individuals; B) Number of imputed crossover events in each individual, sorted by the 73 full-sib families. Individuals with low call rate (call Rate <0.9) are coloured into red.*