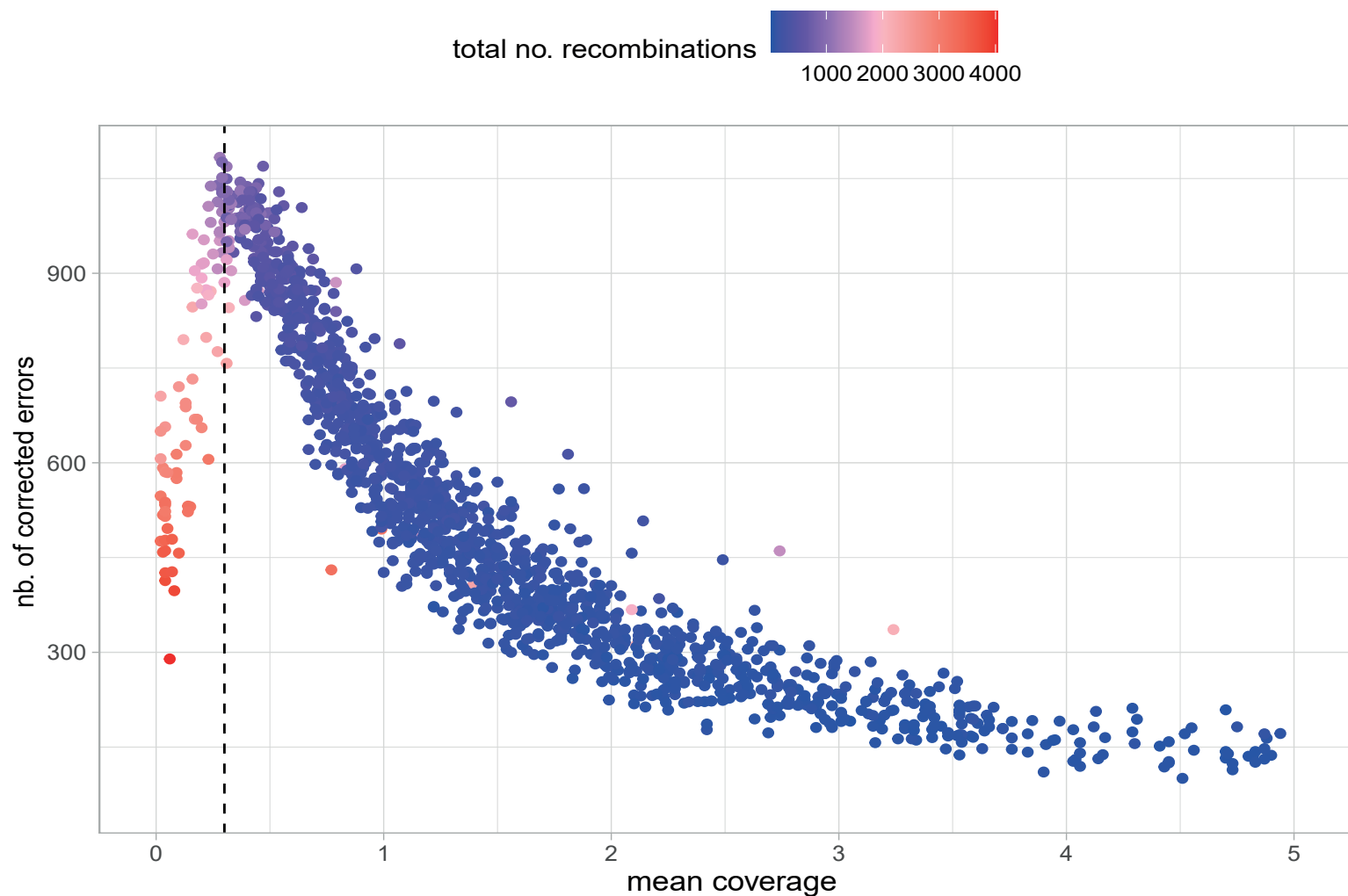




**Suppl. Fig. 3:** Relationship between mean haploid genome coverage and the number of genotyping errors corrected by Smooth Descent. The level of genotypic noise indicated by the total number of predicted recombination events is displayed with a pseudo-color ranging from low noise in blue to high noise in red. The minimal haploid genome coverage necessary for effective error correction by Smooth Descent is indicated by the vertical dash line.