

Description of Additional Supplementary File

File name: Supplementary Data 1

Description: Statistics summary for the haplotype-resolved mapping and duplicate removal using mammalian data.

The number of read pairs is provided for each replicate from Ke *et al.*²⁶ and Du *et al.*²⁵ datasets.

Total raw read pairs ('Total') include unmapped read pairs with multiple or low score alignments comprising also reads without SNVs ('Total_unmapped'), and read pairs where only single side ('Total_ss_mapped') or both sides are mapped ('Total_mapped'). Total mapped read pairs contain non-duplicates and discarded PCR duplicates. Non-duplicates are subdivided into *cis* and *trans* read pairs.