**TABLE S3**

**Optical mapping - Reference assemblies**

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| For each Sample, optical maps were obtained for two labelling enzymes. These optical maps were then aligned to optical map references of both the mm10 and the PWK/PHJ genomes. Optical map references are computed, based on the in-silico presence of enzyme recognition site in the reference genome. For each assembly, the total number of contigs, genome N50 and total assembled genome length, in Mb is summarized. |