

Reference: pacbio.prim.assembly.FINAL.longscaf.fasta

Number of sequences: 30

Total sequence length: 320.58 Mbp

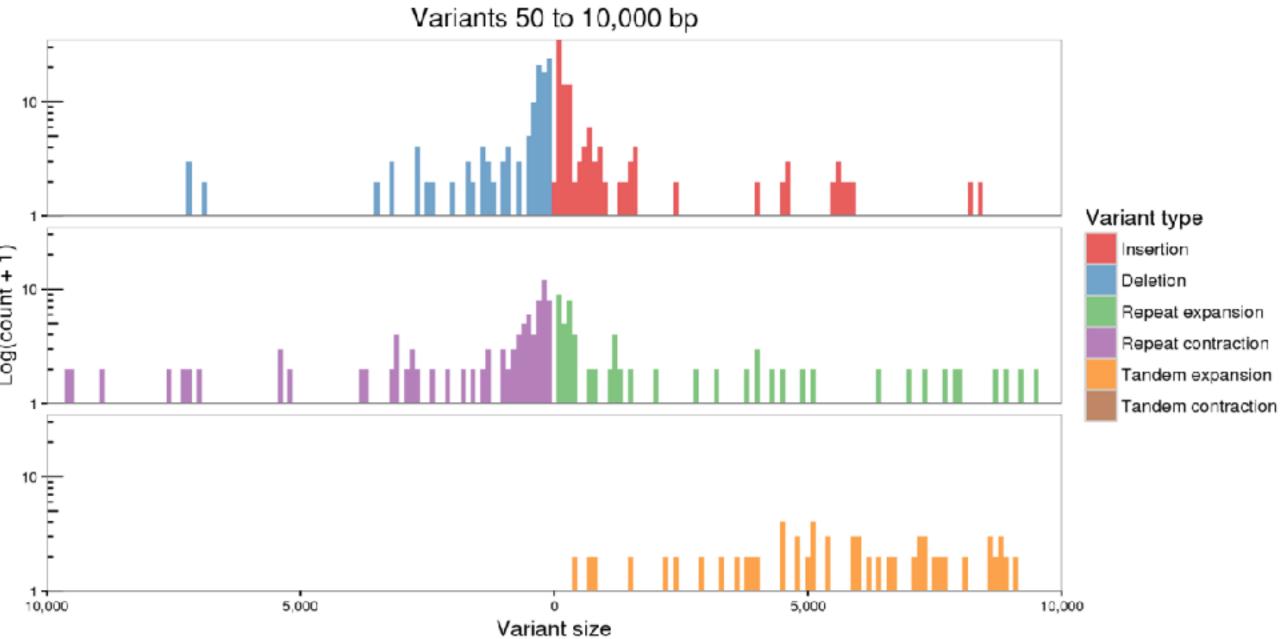
Mean: 10.69 Mbp N50: 11.49 Mbp

Query: pacbio.prim.assembly.fasta

Number of sequences: 196

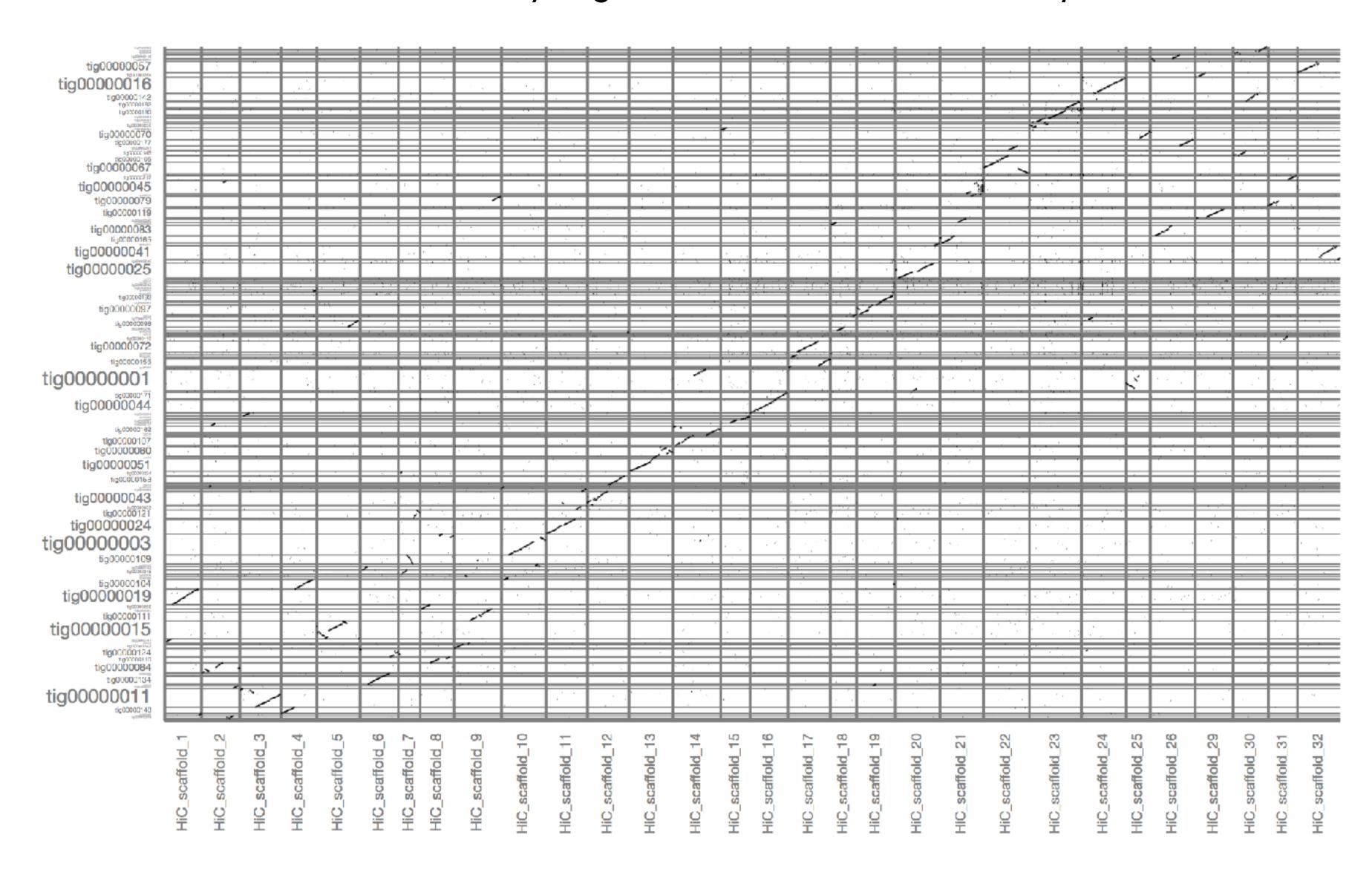
Total sequence length: 430.53 Mbp

Mean: 2.2 Mbp N50: 5.6 Mbp



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Selected scaffolds from PacBio assembly aligned to PacBio + HiC assembly



Selected scaffolds from PacBio assembly aligned to PacBio + HiC assembly: close up

