Dovetail Caenorhabditis sp. Genome Assembly

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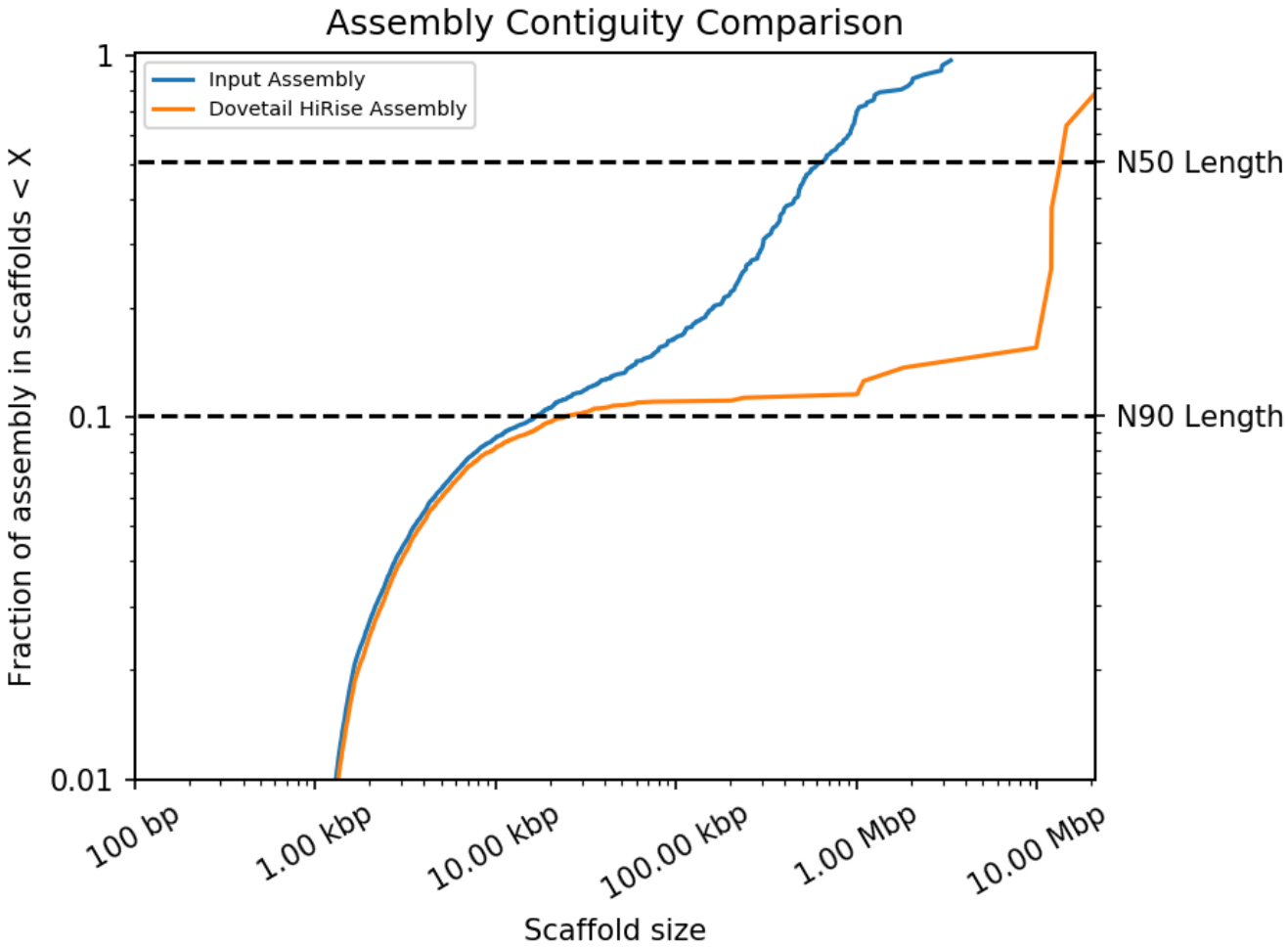
Caenorhabditis sp.

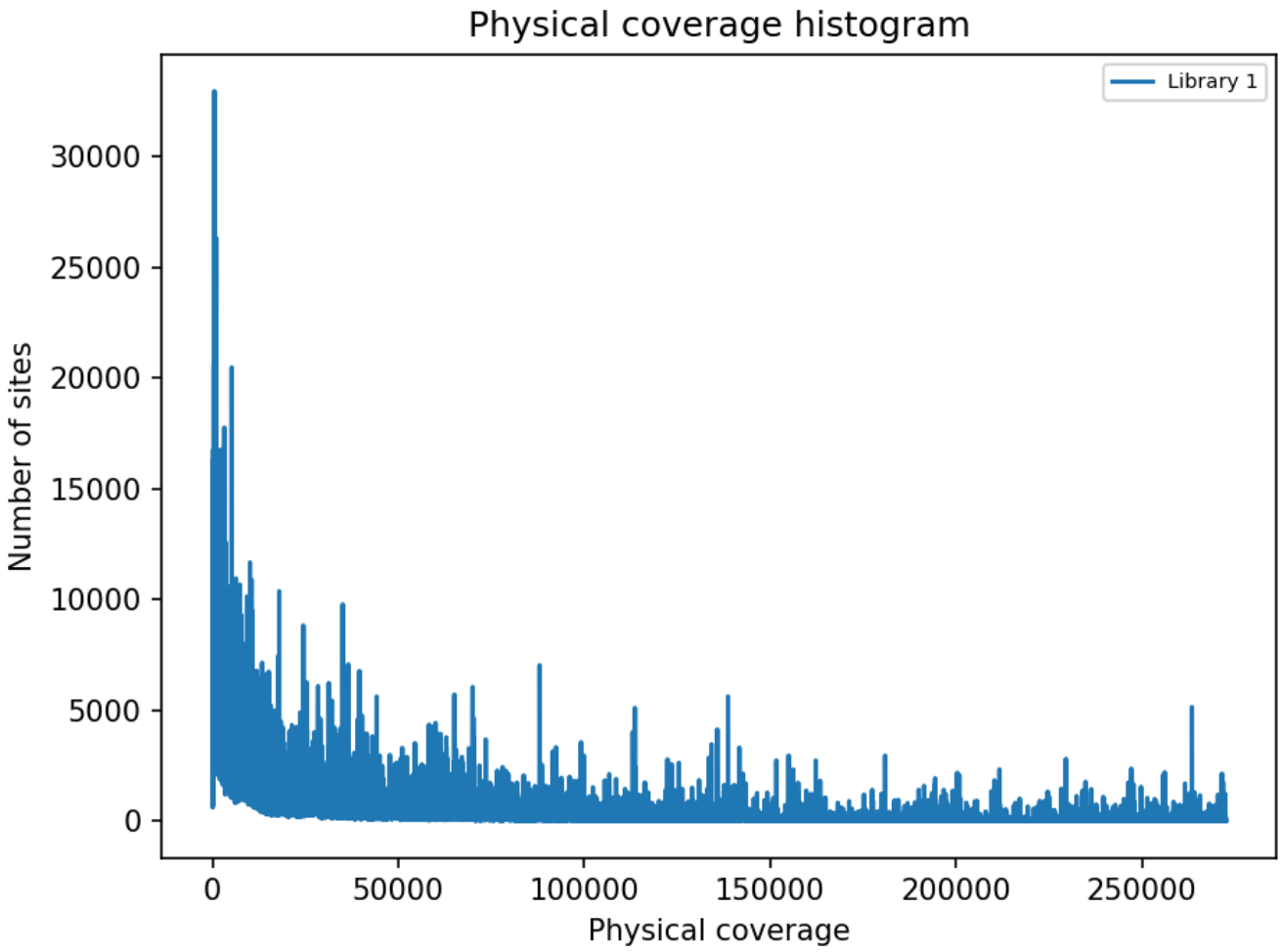
Dovetail Assembly

Estimated physical coverage (10-10,000 kb pairs): 31,321.98X

	Input Assembly	Dovetail HiRise Assembly
Total Length	104.65 Mb	104.70 Mb
L50/N50	47 scaffolds; 0.525 Mb	4 scaffolds; 12.021 Mb
L90/N90	1,464 scaffolds; 0.003 Mb	1,079 scaffolds; 0.003 Mb



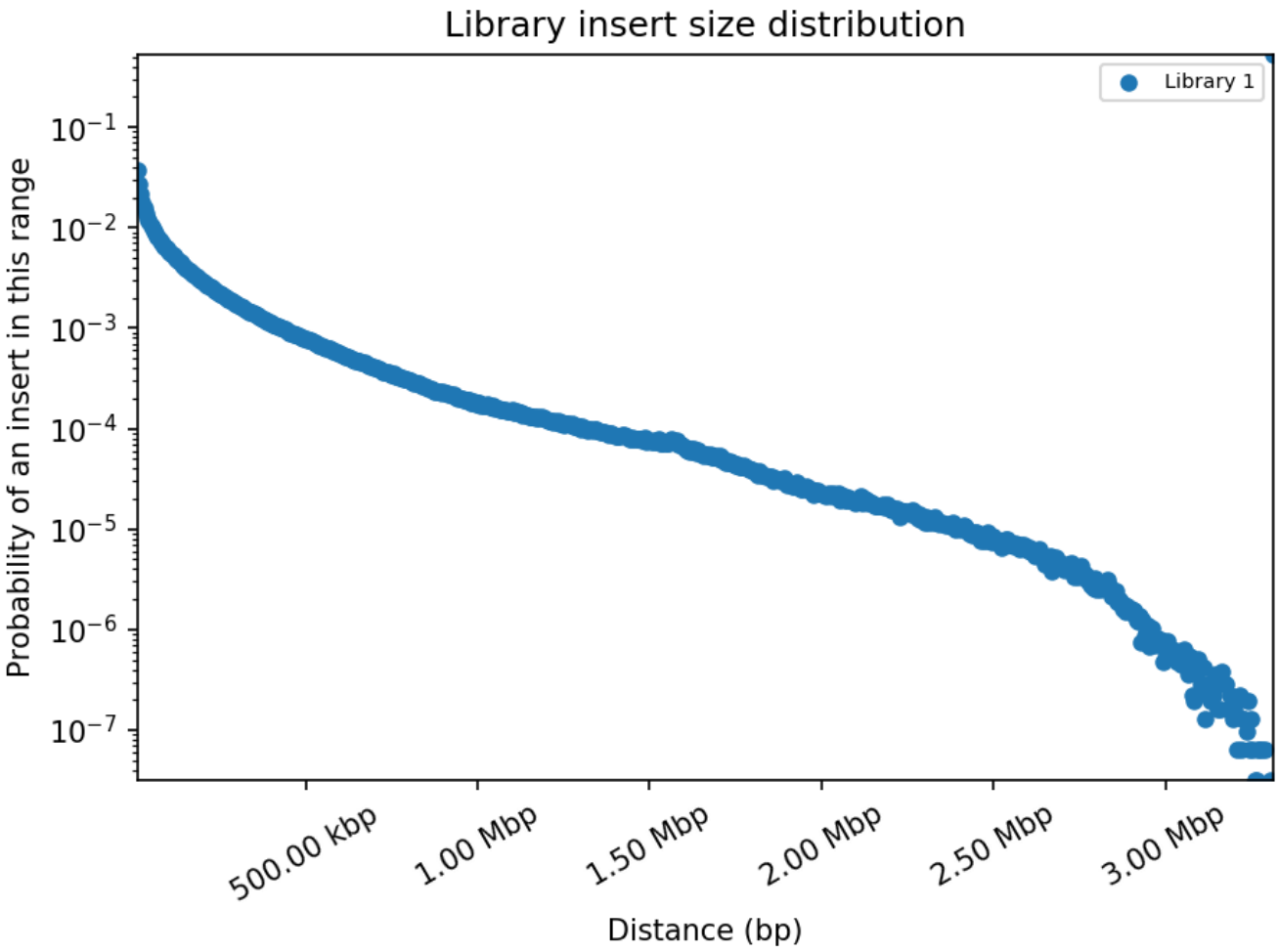
A comparison of the contiguity of the input assembly and the final HiRise scaffolds. Each curve shows the fraction of the total length of the assembly present in scaffolds of a given length or smaller. The fraction of the assembly is indicated on the Y-axis and the scaffold length in basepairs is given on the X-axis. The two dashed lines mark the N50 and N90 lengths of each assembly. Scaffolds less than 1 kb are excluded.



Histogram of physical coverage over input assembly. Coverage values are calculated as the number of read pairs with inserts between 10 and 10,000 kb spanning each position in the input assembly.

BUSCO Stats					
	Single copy	**Duplicated**	**Fragmented**	**Missing**	**Total**
Input Assembly	278	11	2	12	303
Dovetail HiRise Assembly	280	9	2	12	303

Number of BUSCO (Benchmarking Universal Single-Copy Ortholog) genes found in the assembly before and after HiRise using the eukaryota odb9 dataset. Genes are split into four categories: complete and single-copy, complete and duplicated, fragmented, and missing.

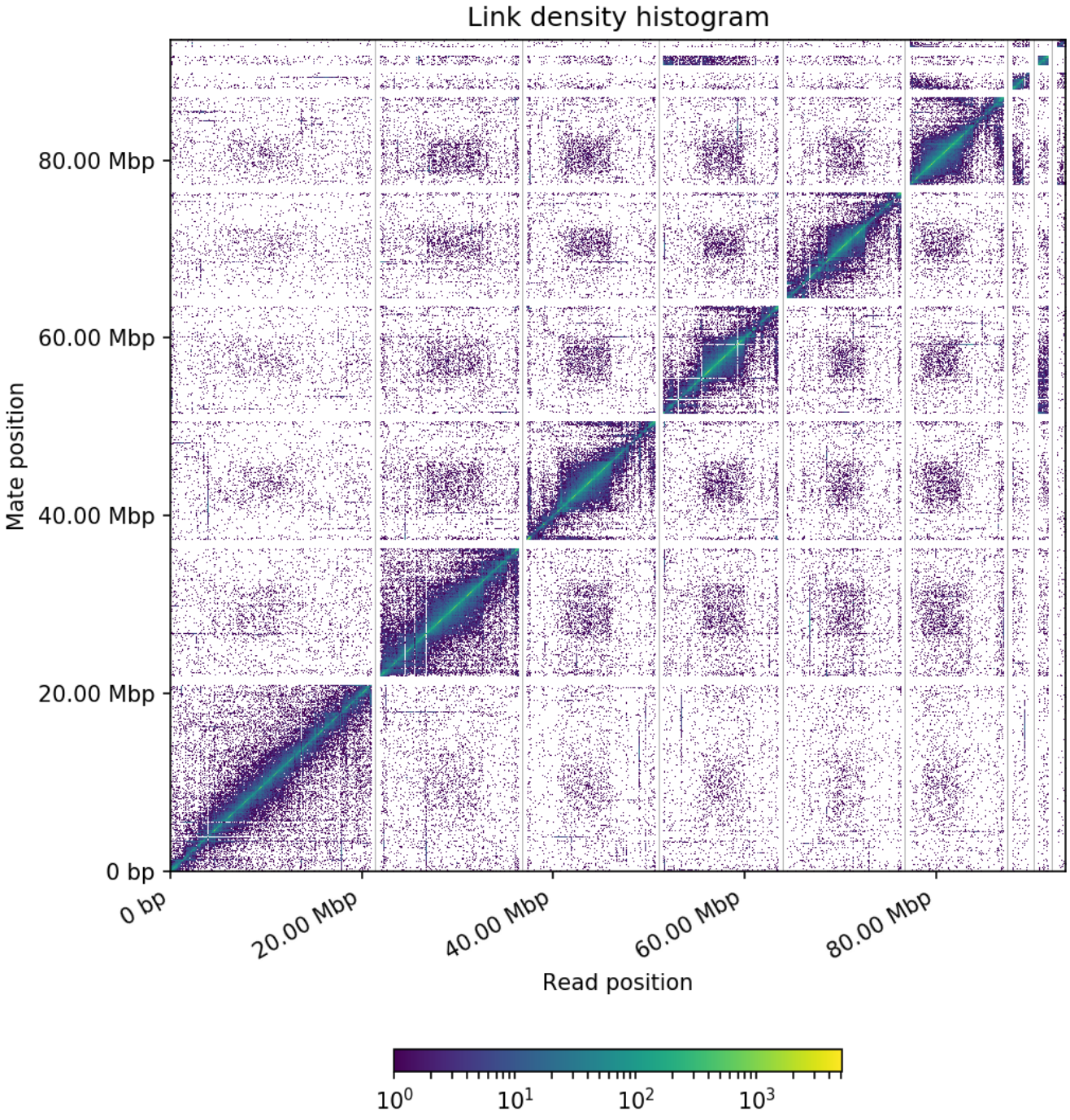


This figure shows the distribution of insert sizes in the Dovetail library. The distance between the forward and reverse reads is given on the X-axis in basepairs, and the probability of observing a read pair with a given insert size is shown on the Y-axis.

Comparative Assembly Statistics		
	Input Assembly	**Dovetail HiRise Assembly**
Longest Scaffold	3,317,958 bp	20,987,453 bp
Number of scaffolds	40,220	39,766
Number of scaffolds > 1kb	3,835	3,381
Contig N50	57.45 kb	57.41 kb
Number of gaps	12,300	12,769
Percent of genome in gaps	2.35%	2.40%

* Note: Every join made by HiRise creates a gap.

Other Statistics	
Number of breaks made to input assembly by HiRise	12
Number of joins made by HiRise	463
Number of gaps closed after HiRise	0
Library 1 stats	108M read pairs; 2x150 bp



In this figure, the x and y axes give the mapping positions of the first and second read in the read pair respectively, grouped into bins. The color of each square gives the number of read pairs within that bin. White vertical and black horizontal lines have been added to show the borders between scaffolds. Scaffolds less than 1 Mb are excluded.

Glossary

Sequence Coverage - For a given position in the genome, the sequence coverage is the number of times this basepair is directly observed in the sequencing data. Typically given as an average over the whole genome, or estimated by the total length of reads divided by the genome size.

Physical Coverage - For a given position in the genome, the physical coverage is the number of read pairs that span this position. Typically given as an average over the whole genome, or estimated by the area under the insert distribution divided by the genome size.

Contig - A contiguous genomic sequence without any gaps in an assembly.

Scaffold - A genomic sequence consisting of contigs that have been ordered and oriented relative to each other. Contigs within scaffolds are separated by gaps (indicated by stretches of Ns).

N50 - The scaffold length such that the sum of the lengths of all scaffolds of this size or larger is equal to 50% of the total assembly length.

N90 - The scaffold length such that the sum of the lengths of all scaffolds of this size or larger is equal to 90% of the total assembly length.

L50 - The smallest number of scaffolds that make up 50% of the total assembly length.

L90 - The smallest number of scaffolds that make up 90% of the total assembly length.