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1. Selected input sequences

1.1 Sequence reads

Name	Number of reads	Longest read	paired
Mgo_1 (paired)	54,739,722	90	yes

For 'paired' data, there are two 'reads' in a pair.

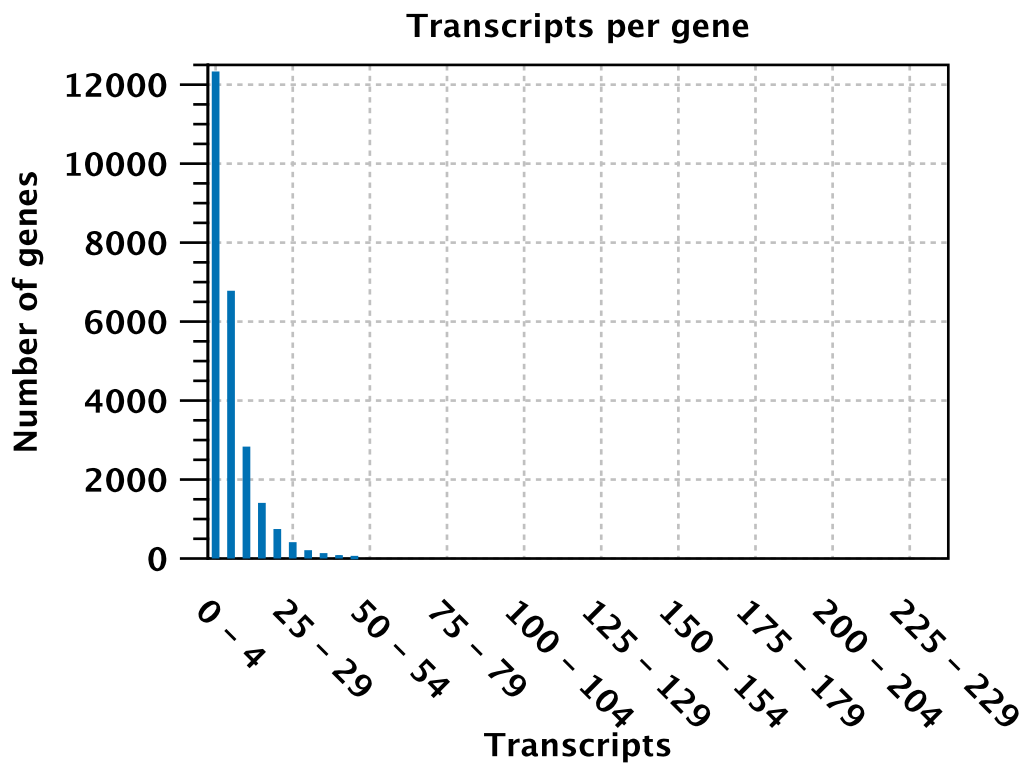
1.2 Reference Sequences

Name	Number of sequences	Longest sequence
oyster.v9_90-7	1,670	1,964,558

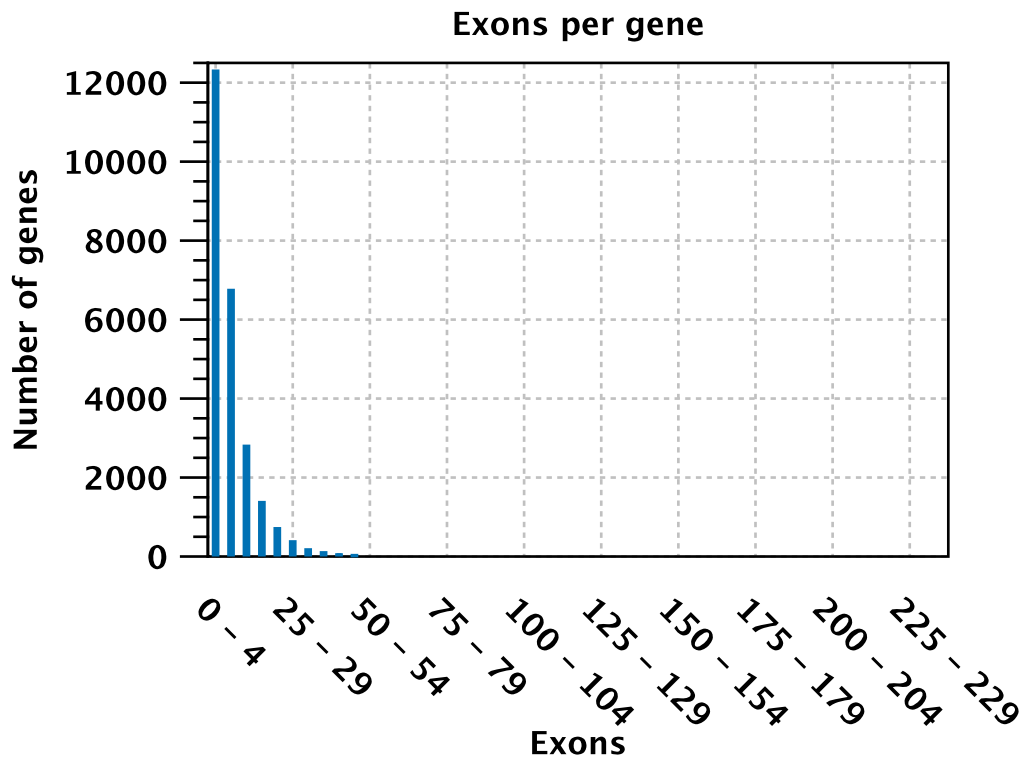
2. References

Input contained 25,123 genes and 184,046 transcripts.

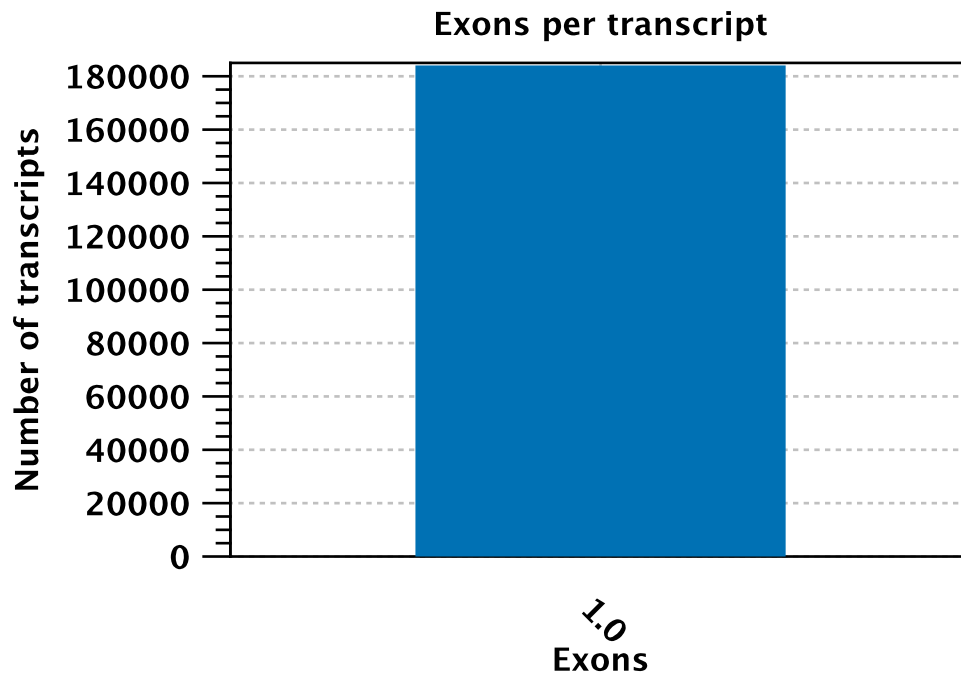
2.1 Transcripts per gene



2.2 Exons per gene



2.3 Exons per transcript



3. Mapping statistics

3.1 Fragment counting

	Single	% of Total	Paired	% of Total
Counted fragments	0	0.00	5,057,011	100.00
- uniquely	0	0.00	4,706,404	100.00
- non-specifically	0	0.00	350,607	100.00
Uncounted fragments	0	0.00	22,312,850	100.00
Total fragments	0	0.00	27,369,861	100.00

Total	% of Total Fragments
5,057,011	18.48
4,706,404	17.20
350,607	1.28
22,312,850	81.52

Total	% of Total Fragments
27,369,861	100.00

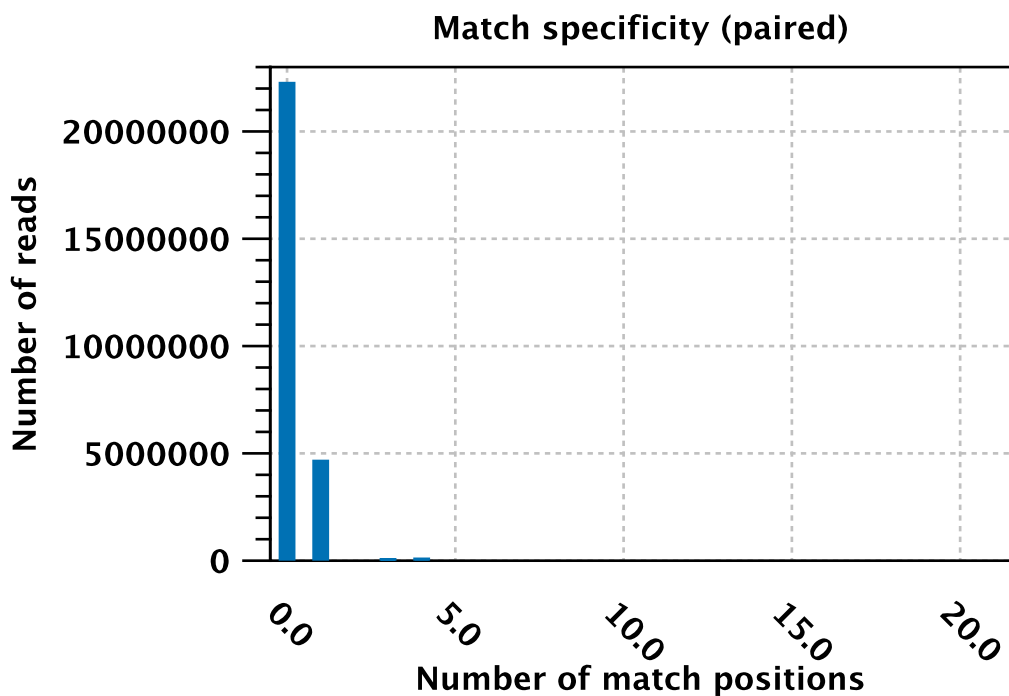
Default counting scheme ('Fragment counts'): A intact pair is counted as one, broken pairs are ignored

3.2 Paired reads

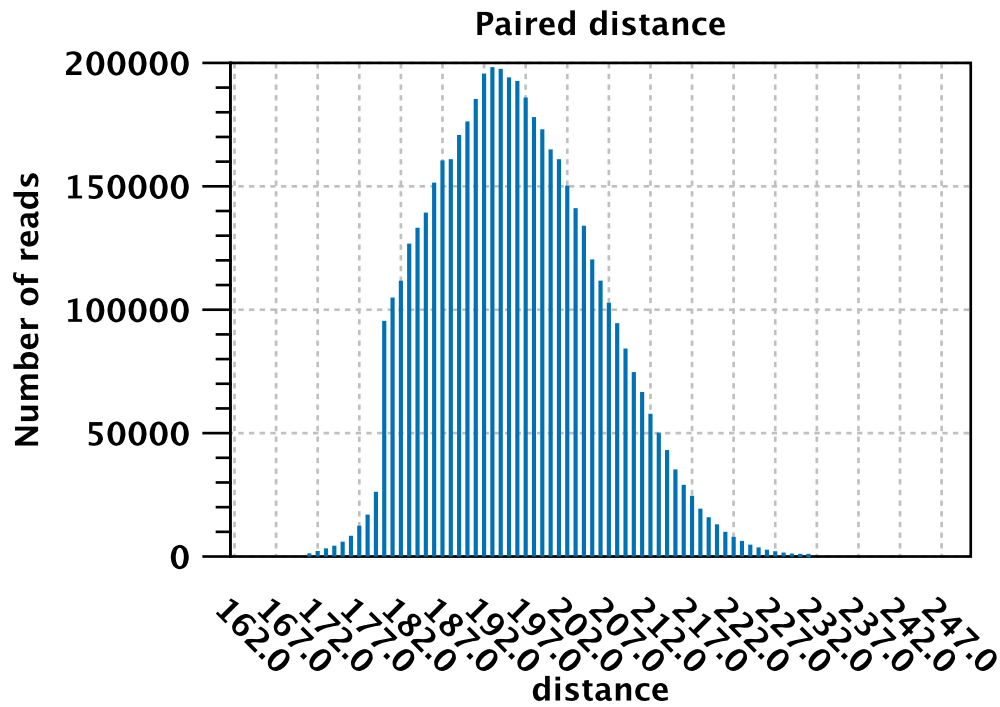
	Number of sequences	%
Reads mapped in pairs	10,114,022	18.48
Reads mapped in broken pairs	15,571,791	28.45
Reads not mapped	29,053,909	53.08
Total	54,739,722	100.00

For 'paired' data, there are two 'reads' in a pair.

3.3 Match specificity (paired)



3.4 Paired distance



4. Detailed mapping statistics

	Uniquely mapped	Fraction	Non-specifically mapped	Fraction
Exon-exon	0	0.00	0	0.00
Exon-intron	469,208	0.96	20,218	0.04
Total exon	3,658,117	0.94	223,466	0.06
Total intron	1,048,287	0.89	127,141	0.11
Total gene	4,706,404	0.93	350,607	0.07

Mapped	% of total mapped
0	0.00
489,426	9.68
3,881,583	76.76
1,175,428	23.24
5,057,011	100.00

Default counting scheme ('Fragment counts'): A intact pair is counted as one, broken pairs are ignored