Generated by: sr320
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1. Selected input sequences

1.1 Sequence reads

Name	Number of reads	Longest read	paired
s_1.GACTAAGA_1 (paired) trimmed (paired)	104,137,372	50	yes

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

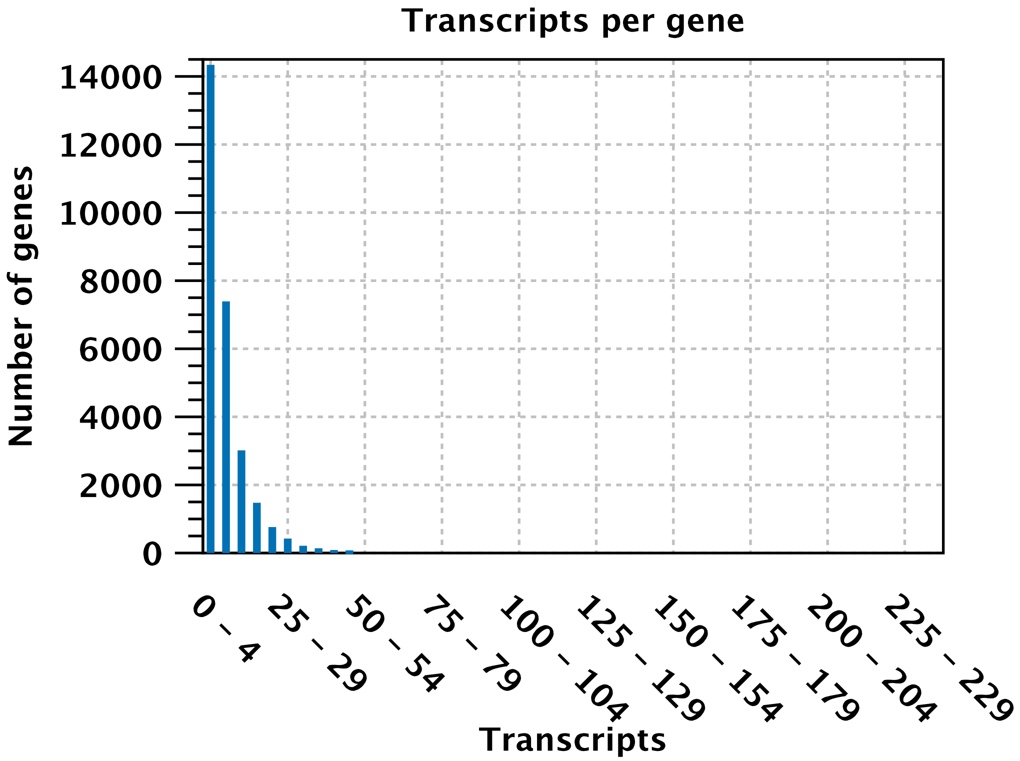
1.2 Reference Sequences

Name	Number of sequences	Longest sequence
oyster.v9	11,969	1,964,558

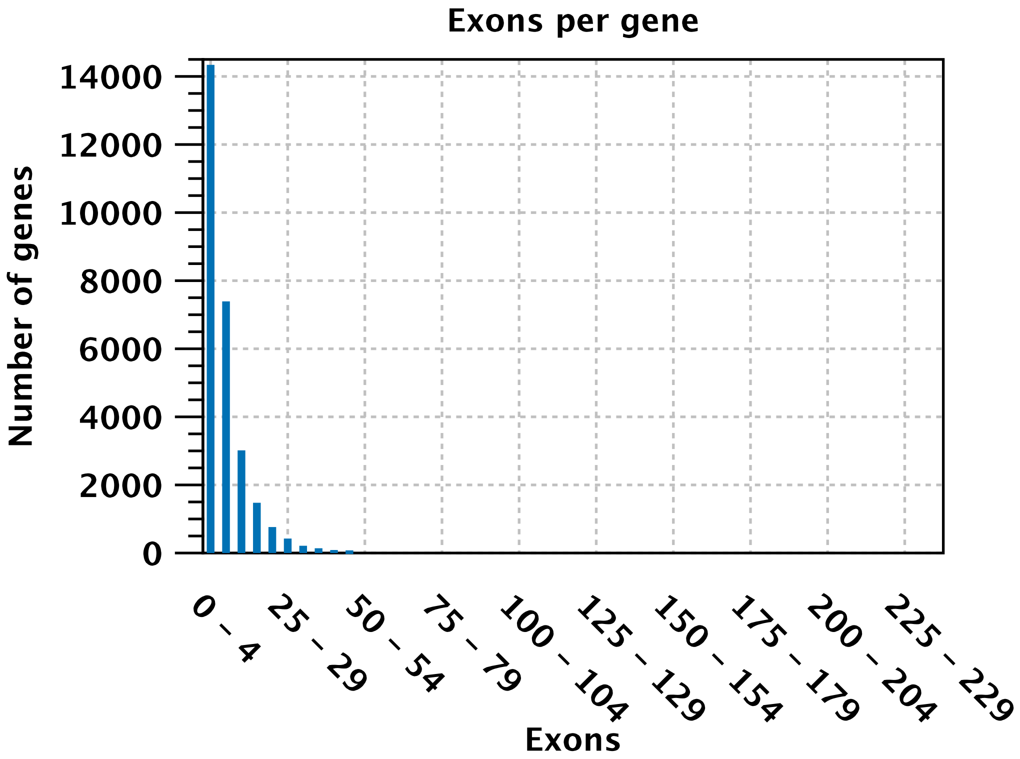
2. References

Input contained 28,027 genes and 196,691 transcripts.

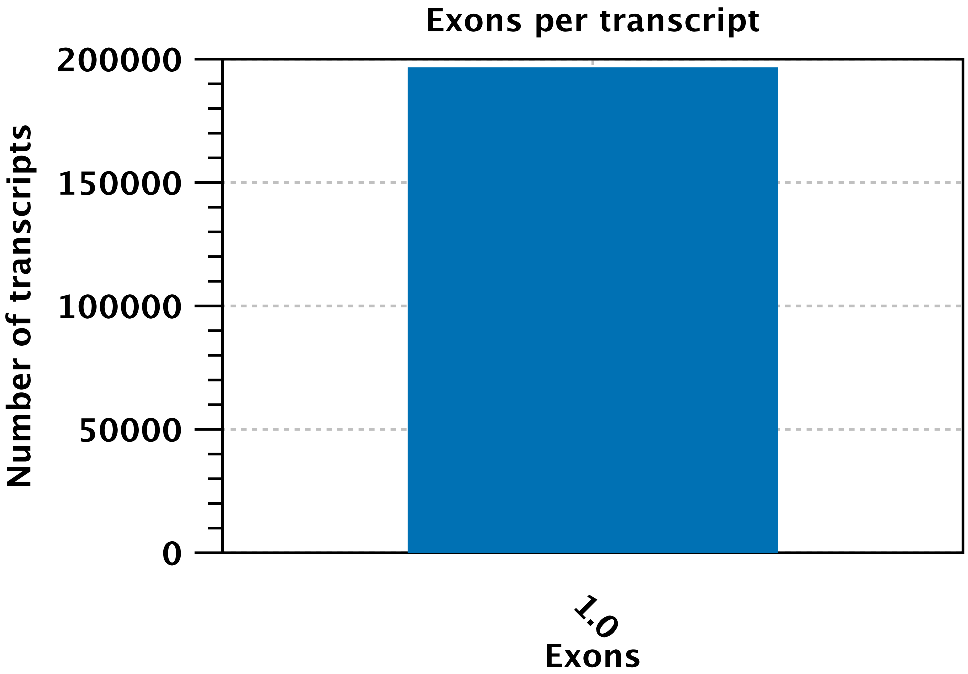
2.1 Transcripts per gene



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	6,762,801	100.00
- uniquely	0	0.00	5,911,398	100.00
- non-specifically	0	0.00	851,403	100.00
Uncounted fragments	0	0.00	45,305,885	100.00
Total fragments	0	0.00	52,068,686	100.00

Total	% of Total Fragments
6,762,801	12.99
5,911,398	11.35
851,403	1.64
45,305,885	87.01

Total	% of Total Fragments
52,068,686	100.00

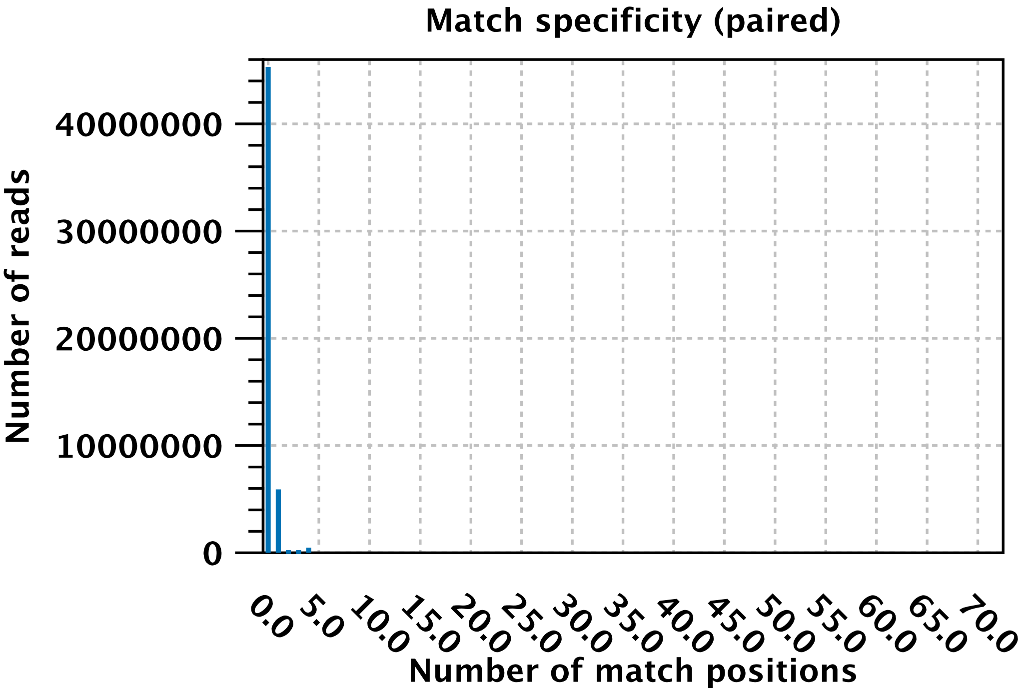
Default counting scheme ('Fragment counts'): A intact pair is counted as one, broken pairs are ignored

3.2 Paired reads

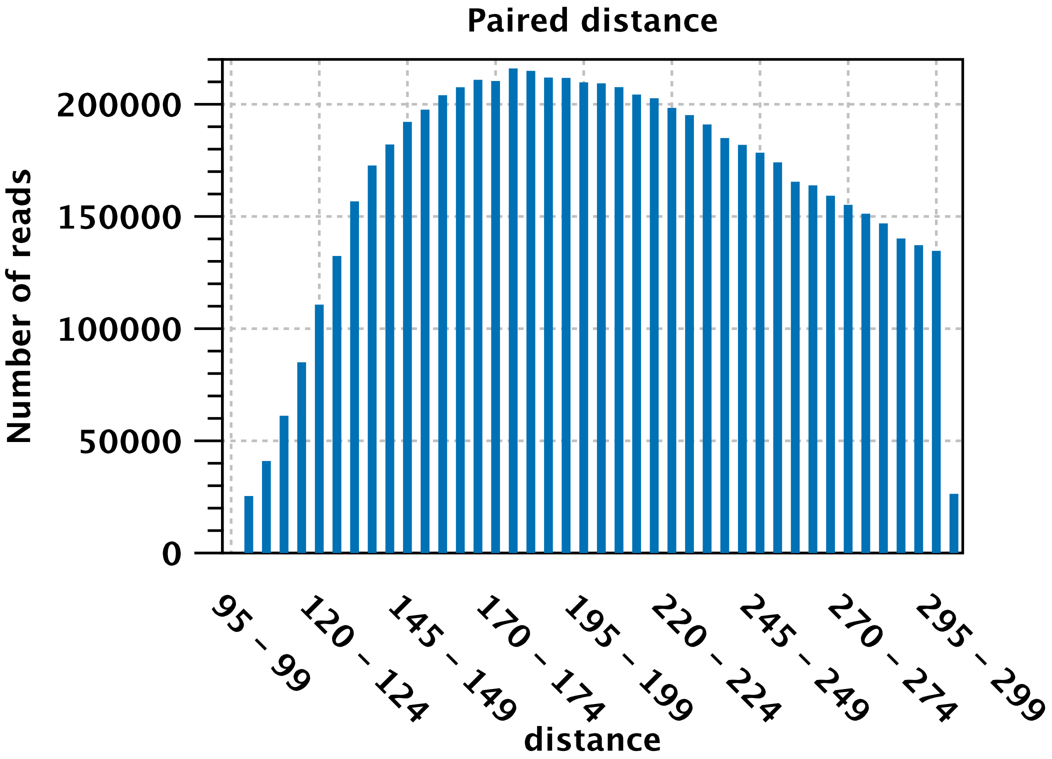
	Number of sequences	%
Reads mapped in pairs	13,525,602	12.99
Reads mapped in broken pairs	32,225,972	30.95
Reads not mapped	58,385,798	56.07
Total	104,137,372	100.00

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	556,583	0.86	88,863	0.14
Total exon	3,947,801	0.86	644,113	0.14
Total intron	1,963,597	0.90	207,290	0.10
Total gene	5,911,398	0.87	851,403	0.13

Mapped	% of total mapped
0	0.00
645,446	9.54
4,591,914	67.90
2,170,887	32.10

Mapped	% of total mapped
6,762,801	100.00

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