CLC bio

Generated by: sr320
Date: Mon Jul 22 18:36:50 PDT 2013

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1. Selected input sequences

1.1 Sequence reads

Name	Number of reads	Longest read	paired
s_1.GTGTCTAC_1 (paired) -1 trimmed (paired)	49,463,220	50	yes

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

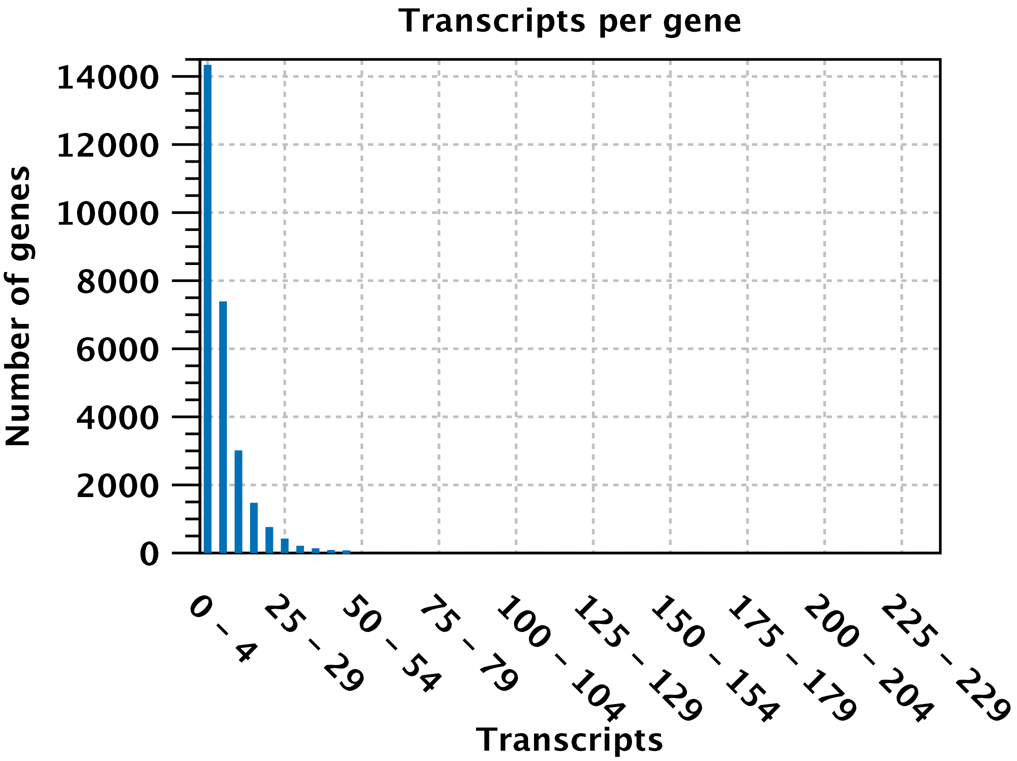
1.2 Reference Sequences

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

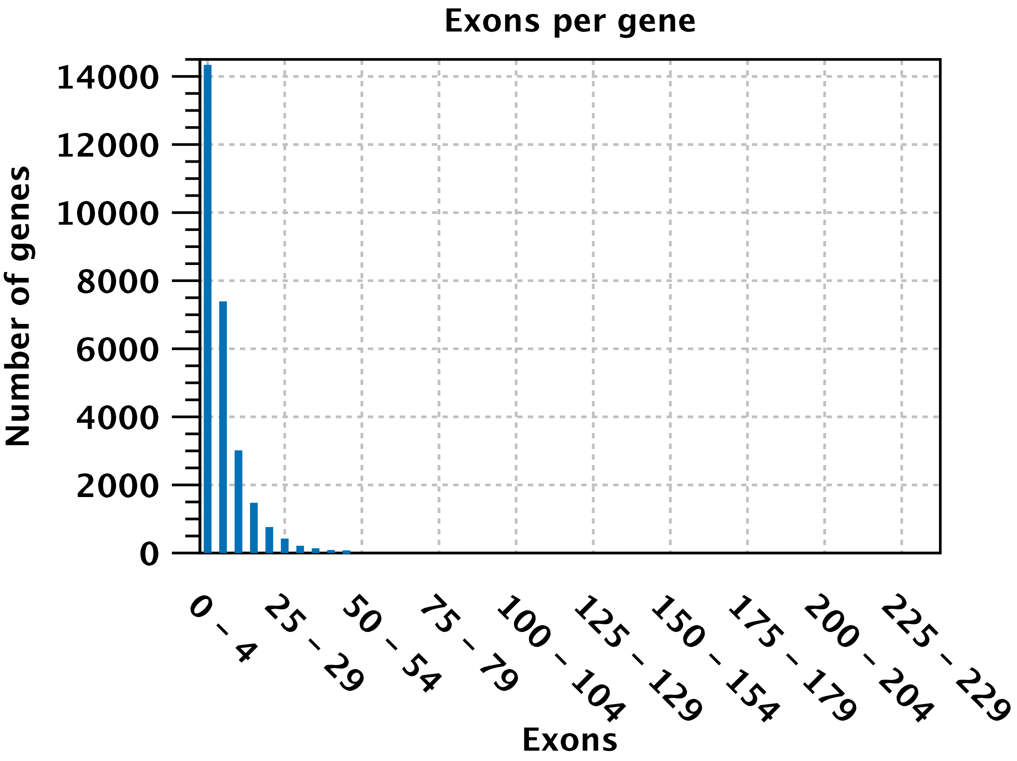
2. References

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

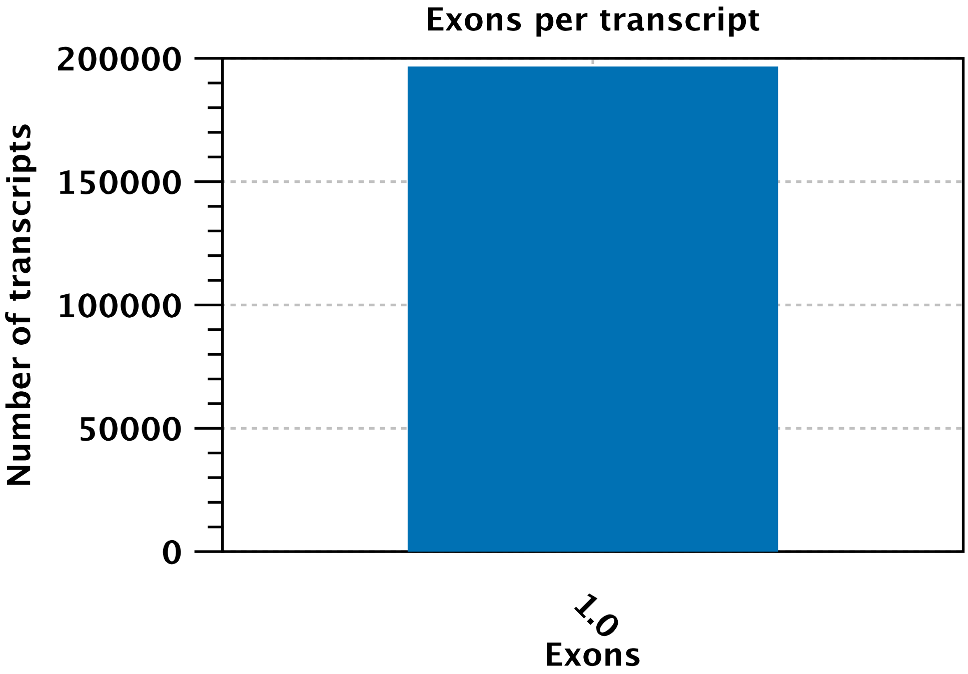
2.1 Transcripts per gene



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	1,081,914	100.00
- uniquely	0	0.00	940,217	100.00
- non-specifically	0	0.00	141,697	100.00
Uncounted fragments	0	0.00	23,649,696	100.00
Total fragments	0	0.00	24,731,610	100.00

Total	% of Total Fragments
1,081,914	4.37
940,217	3.80
141,697	0.57
23,649,696	95.63

Total	% of Total Fragments
24,731,610	100.00

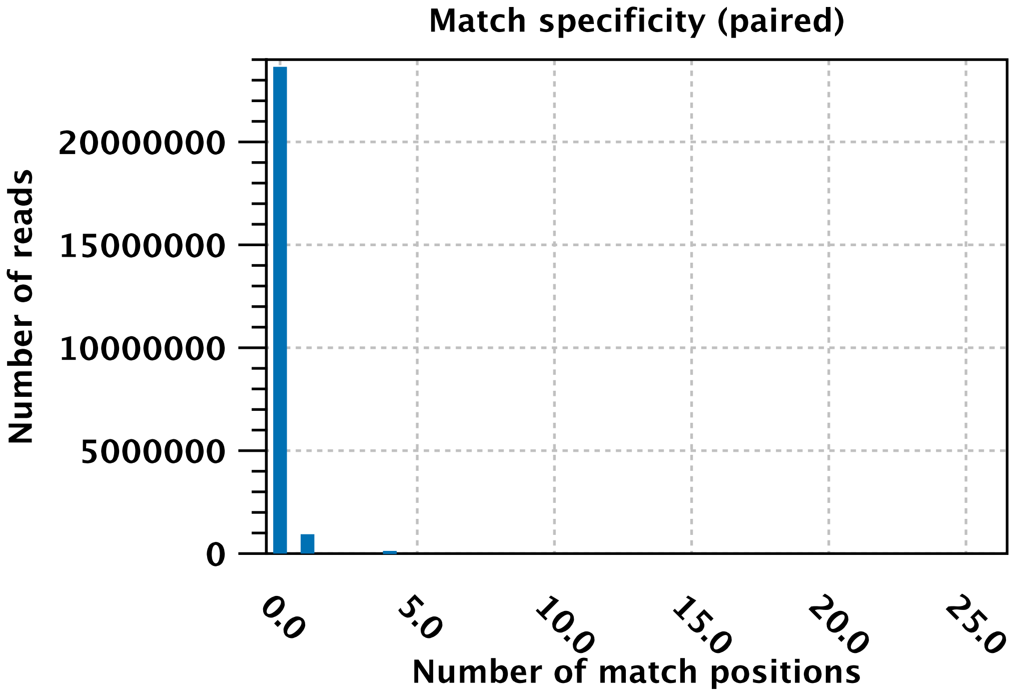
Default counting scheme ('Fragment counts'): A intact pair is counted as one, broken pairs are ignored

3.2 Paired reads

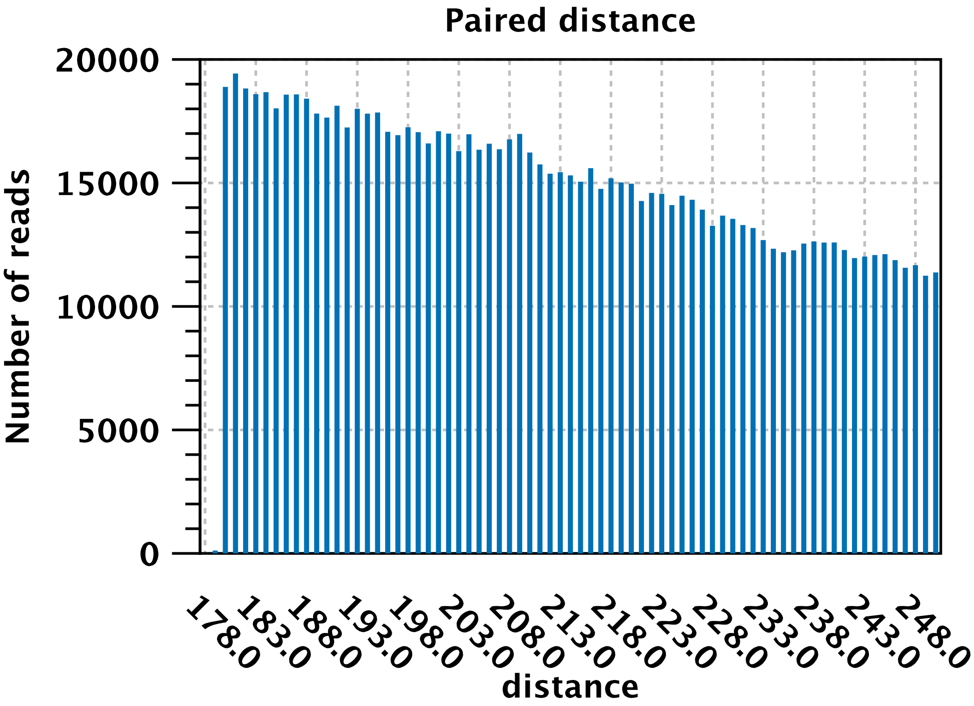
	Number of sequences	%
Reads mapped in pairs	2,163,828	4.37
Reads mapped in broken pairs	15,397,316	31.13
Reads not mapped	31,902,076	64.50
Total	49,463,220	100.00

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	67,541	0.87	10,252	0.13
Total exon	638,709	0.84	122,764	0.16
Total intron	301,508	0.94	18,933	0.06
Total gene	940,217	0.87	141,697	0.13

Mapped	% of total mapped
0	0.00
77,793	7.19
761,473	70.38
320,441	29.62
1,081,914	100.00

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