Generated by: ethan
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1. Selected input sequences

1.1 Sequence reads

Name	Number of reads	Longest read	Paired
SRR10571752_1 (paired, trimmed pairs)	118,123,778	51	yes

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

1.2 Reference Sequences

References	Length	Genes
164,291	597,293,918	164,291

2. References

3. Read quality control

3.1 Strand specificity

Strand specific setting	Both
Forward % of reads mapped	0.64
Reverse % of reads mapped	99.36
Reads with known strand	90,373,578
Ignored reads (wrong strand)	0
Ignored reads % (wrong strand)	0.00

Strand specificity refers to whether a read is generated by sequencing an RNA fragment in the Forward (5' to 3') or Reverse (3' to 5') orientation. In a strand-specific protocol almost all reads are generated from a specific orientation. In other protocols a mix of both orientations is expected.

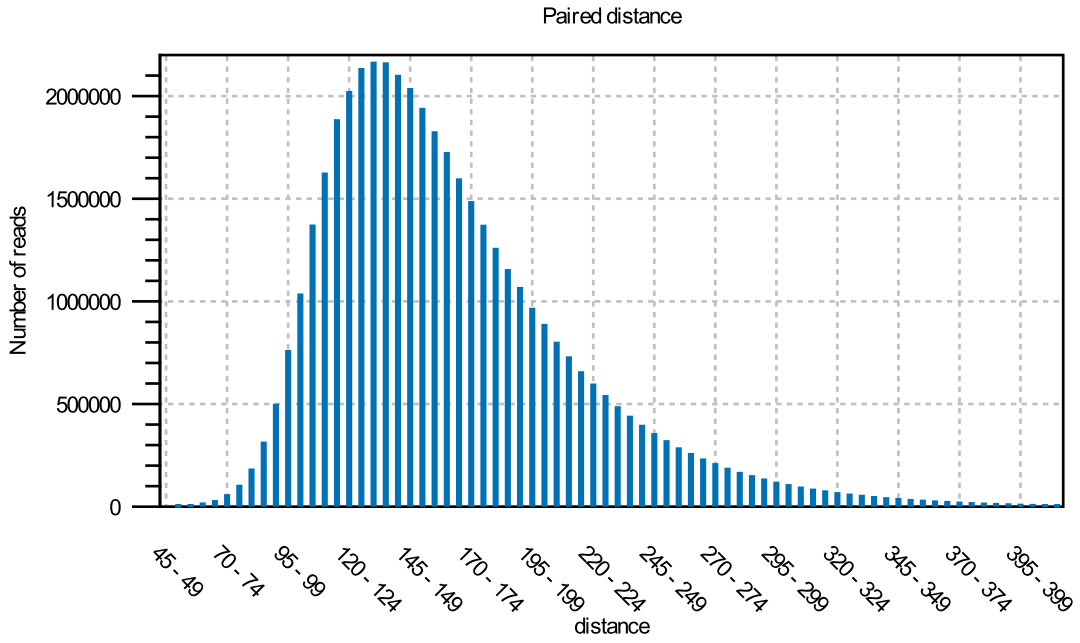
Strand specific setting: >90% of reads were mapped in the same orientation. Consider re-running the tool with a strand specific setting ("Forward"/"Reverse").

3.2 Adapter read-through

Estimated % containing read-through adapters	0.00

This value is estimated from the number of mapped paired-end reads where one read is longer than the sequenced RNA fragment.
A small percentage of read-through adapters is unlikely to affect the quantification of expression, but their presence may lead to false positive variant calls. To remove a read-through adapter, run the "Trim Reads" tool on the input reads, using either Automatic read-through adapter trimming or a Trim Adapter List configured to remove the adapter sequence from the 3' end.

3.3 Paired distance



The graph shows the distribution of paired-end distances, which is equivalent to the distribution of sequenced RNA fragment sizes. There should be a single broad peak at the target fragment size. An asymmetric peak may indicate problems in size selection.

Reads	Paired distance estimates	Messages
SRR10571752_1 (paired, trimmed pairs)	45 to 413 bp	OK

4. Mapping statistics

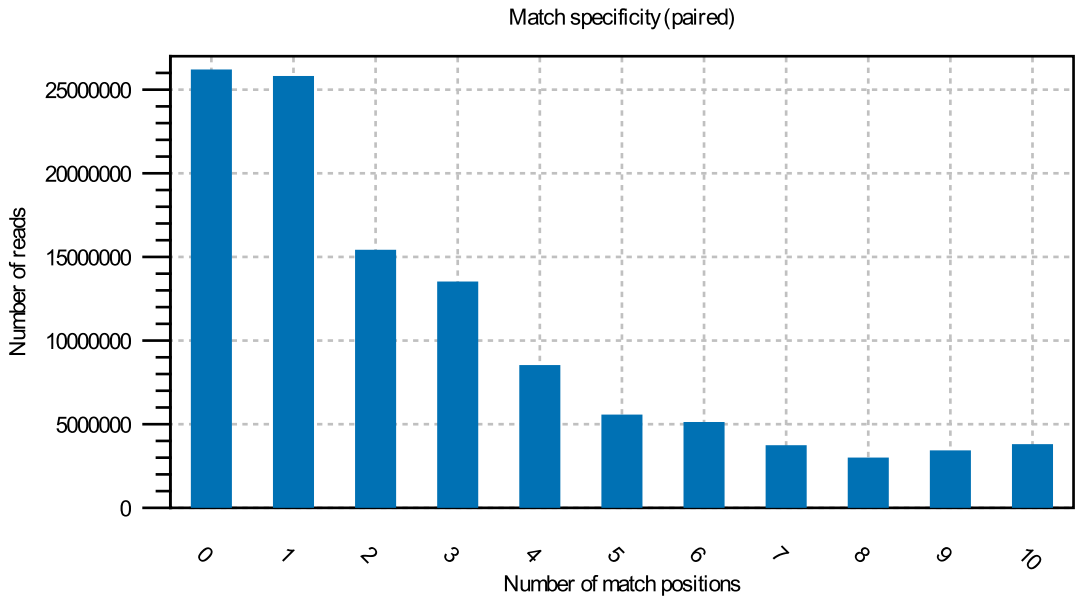
4.1 Paired reads

	Number of sequences	%
Reads mapped in pairs	88,011,112	74.51
Reads mapped in broken pairs	2,362,466	2.00
Reads not mapped	27,750,200	23.49
Total	118,123,778	100.00

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

If a strand specific setting was used, 'Reads not mapped' will include those reads that were ignored because they mapped to the wrong strand.

4.2 Match specificity (paired)



5. Fragment statistics

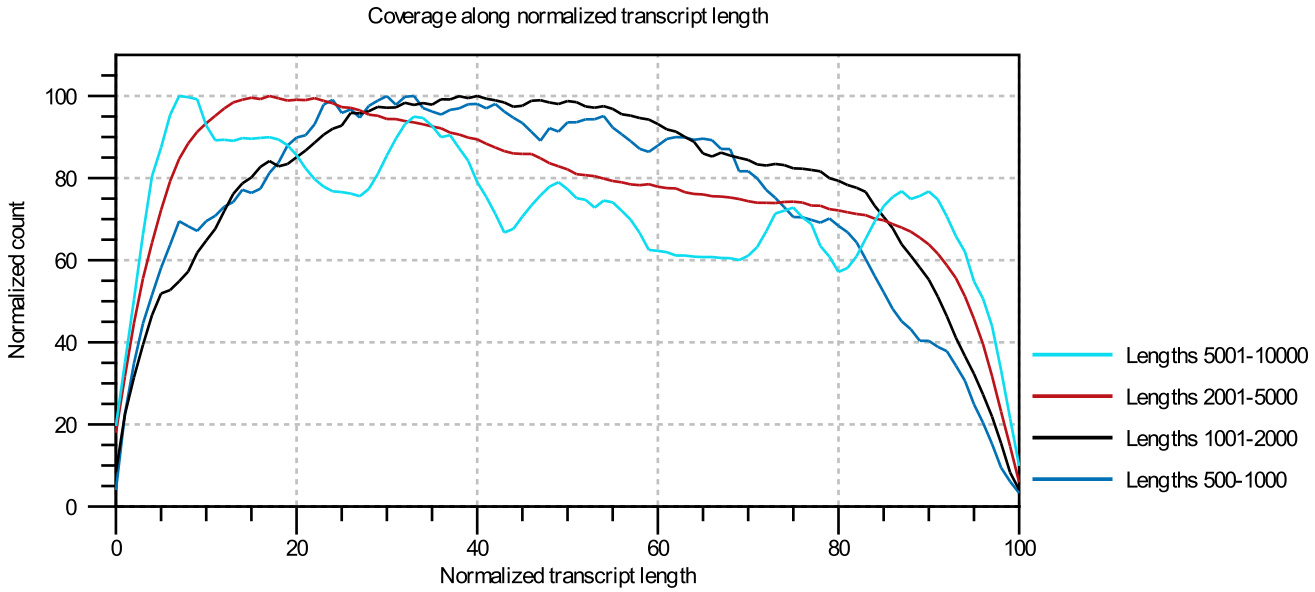
5.1 Fragment counting (total)

	Fragments	% of total
Counted fragments	44,005,556	74.51
- unique fragments	12,908,860	21.86
- non-specifically	31,096,696	52.65
Uncounted fragments	15,056,333	25.49

	Fragments	% of total
Total fragments	59,061,889	100.00

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

6. Transcript length coverage



Expected coverage bias	Unbiased
Difference between average 3’ and 5’ normalized counts	-16.25
% reads mapping to transcripts > 10000 bp	3.03
% reads mapping to transcripts 5001 - 10000 bp	17.41
% reads mapping to transcripts 2001 - 5000 bp	42.44
% reads mapping to transcripts 1001 - 2000 bp	26.64
% reads mapping to transcripts 500 - 1000 bp	9.74
% reads mapping to transcripts < 500 bp	0.74

The plot shows the normalized coverage across a transcript body for four different groupings of transcript length. The lines should be flat in the center of the plot, and the plot should be approximately symmetric. An erratic line may indicate that there are few transcripts in the given length range.