

Qualimap Analysis Results

RNA Seq QC analysis

Generated by Qualimap v.2.3

2025/02/15 08:04:11

1. Input data & parameters

1.1. Input

Analysis date:	Sat Feb 15 08:04:09 GMT 2025
BAM file:	2.sorted.bam
Counting algorithm:	uniquely-mapped-reads
GTF file:	/rds-d7/user/cx264/rds-scrna_spatial-6qULnBz5AIM/Chongjing_Xia/01.SpatialTranscriptomics/00.ref/M.truncatula_genome_v4/Mtruncatula_285_Mt4.0v1.gene.gtf
Number of bases for 5'-3' bias computation:	100
Number of transcripts for 5'-3' bias computation:	1,000
Paired-end sequencing:	no
Protocol:	non-strand-specific
Sorting performed:	no

2. Summary

2.1. Reads alignment

Number of mapped reads:	46,538,950
Total number of alignments:	46,538,950
Number of secondary alignments:	0
Number of non-unique alignments:	1,208,019
Aligned to genes:	31,814,265
Ambiguous alignments:	0
No feature assigned:	13,293,464
Missing chromosome in annotation:	223,202
Not aligned:	2,673,862
Strand specificity estimation (fwd/rev):	0.53 / 0.47

2.2. Reads genomic origin

Exonic:	31,814,265 / 70.53%
Intronic:	7,699,741 / 17.07%
Intergenic:	5,593,723 / 12.4%
Intronic/intergenic overlapping exon:	6,780,028 / 15.03%

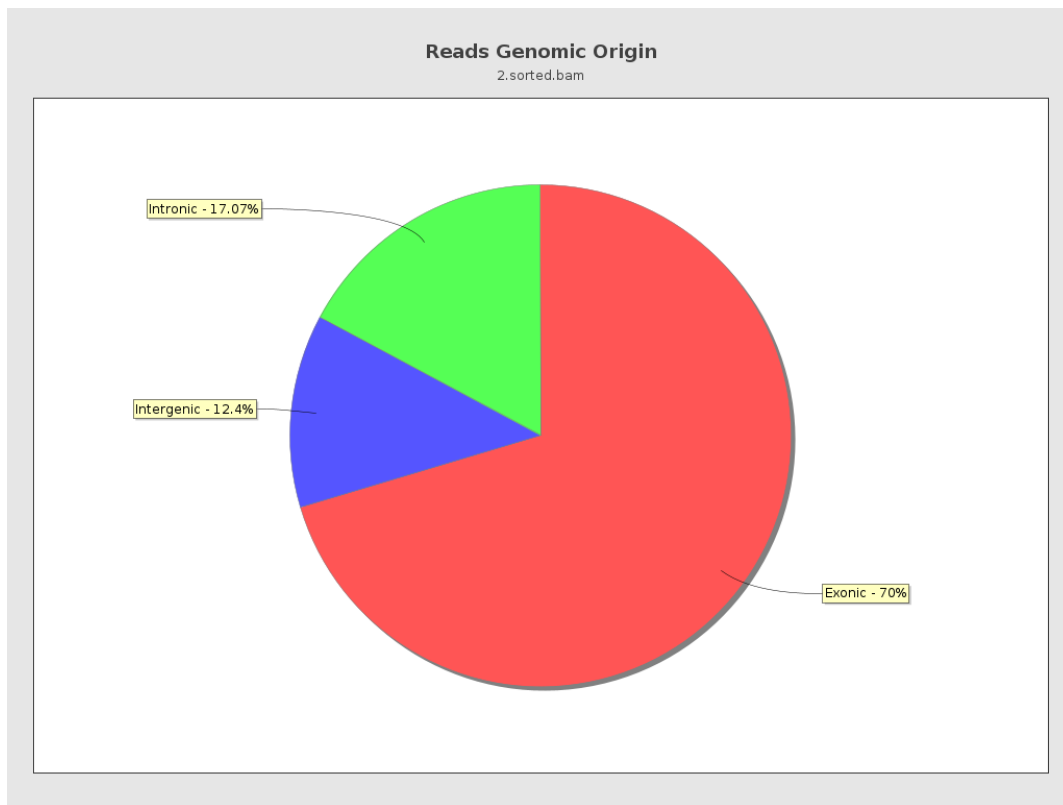
2.3. Transcript coverage profile

5' bias:	0.11
3' bias:	0.07
5'-3' bias:	2

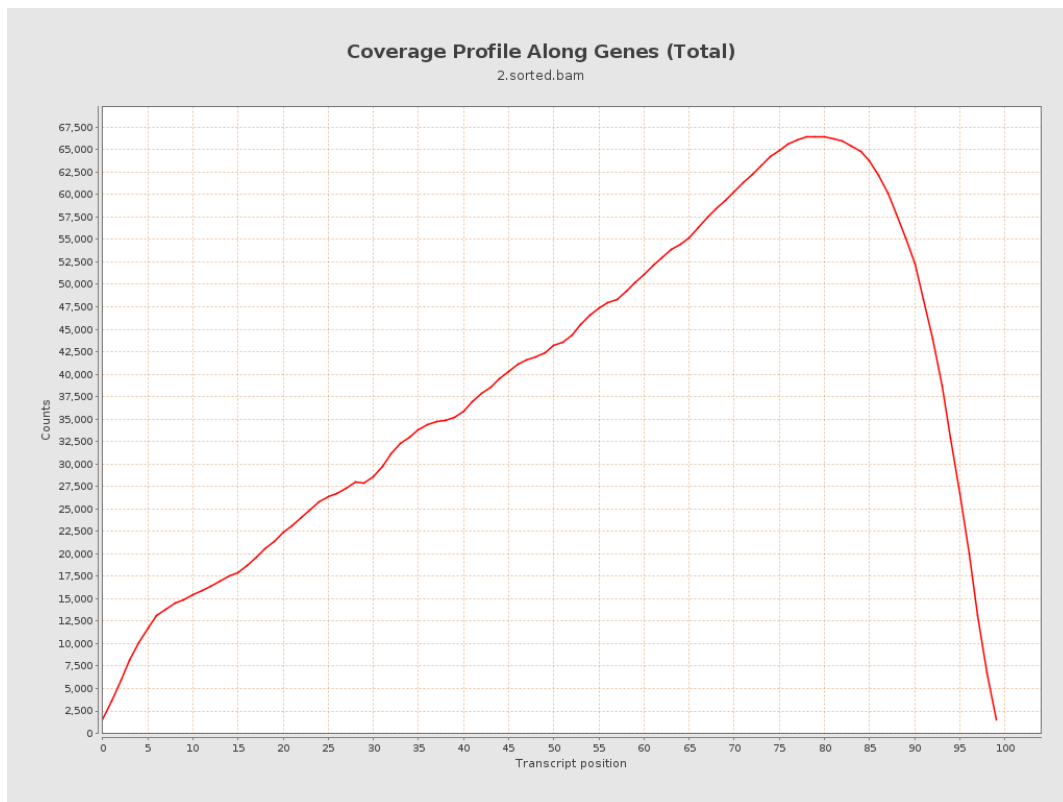
2.4. Junction analysis

Reads at junctions:	0
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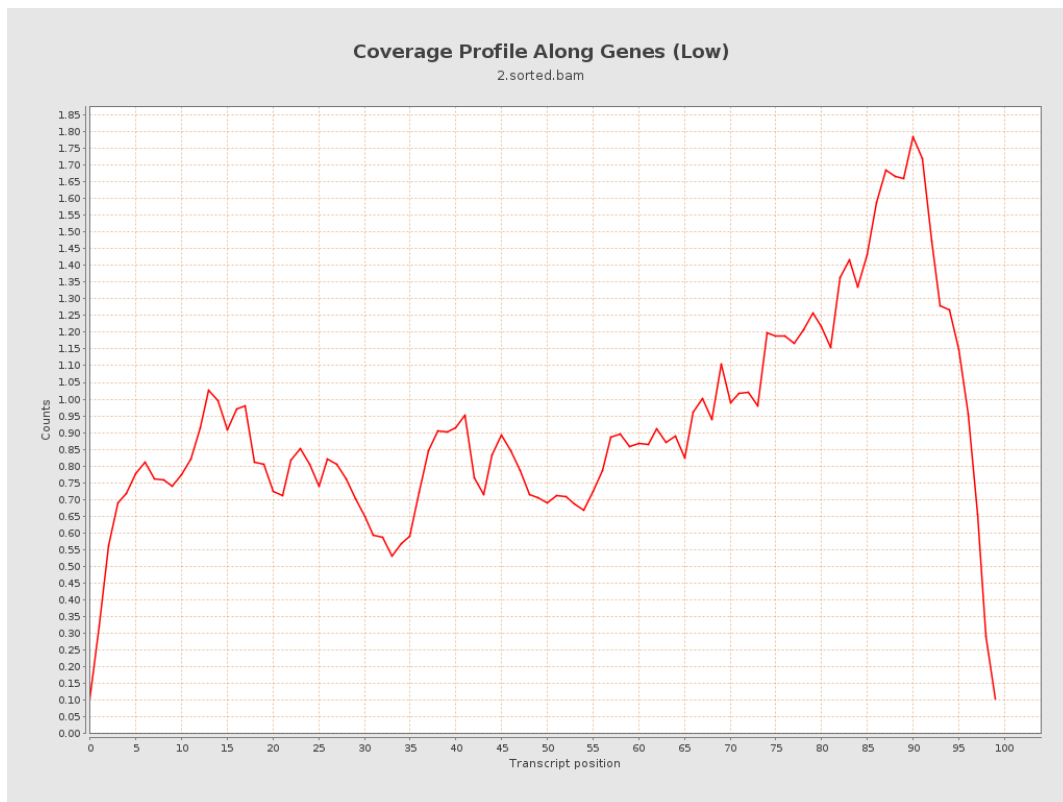
3. Results : Reads Genomic Origin



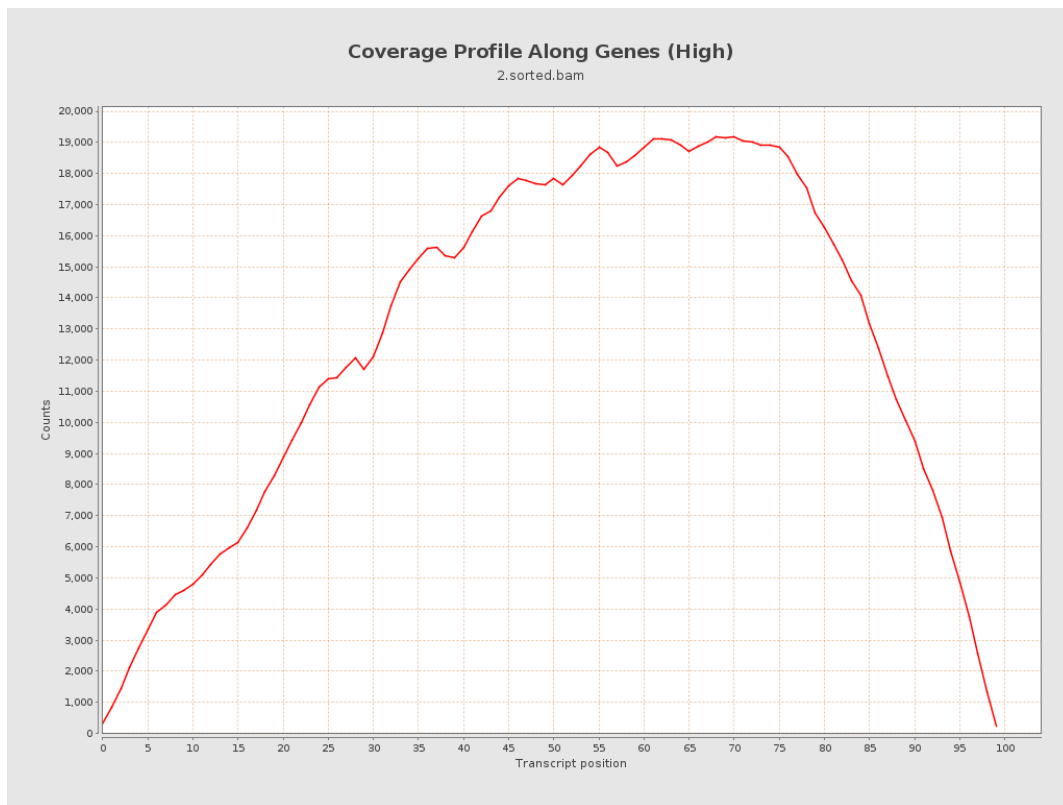
4. Results : Coverage Profile Along Genes (Total)



5. Results : Coverage Profile Along Genes (Low)



6. Results : Coverage Profile Along Genes (High)



7. Results : Coverage Histogram (0-50X)

