Qualimap Analysis Results

RNA Seq QC analysis
Generated by Qualimap v.2.3
2025/06/23 22:31:50

1. Input data & parameters

1.1. Input

Analysis date:	Mon Jun 23 22:31:48 BST 2025
BAM file:	D4W1Aligned.sortedByCoord.out.bam
Counting algorithm:	uniquely-mapped-reads
GTF file:	/data/pathology/cxia/projects/0.ref/1.HeteroderaSchachtii/heterodera_schachtii.PRJNA522950.WBPS19/heterodera_schachtii.PRJNA522950.WBPS19.annotations.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:	229,778,823
Total number of alignments:	229,778,823
Number of secondary alignments:	0
Number of non-unique alignments:	0
Aligned to genes:	200,694,046
Ambiguous alignments:	383,442
No feature assigned:	28,700,693
Missing chromosome in annotation:	642
Not aligned:	0
Strand specificity estimation (fwd/rev):	0.52 / 0.48

2.2. Reads genomic origin

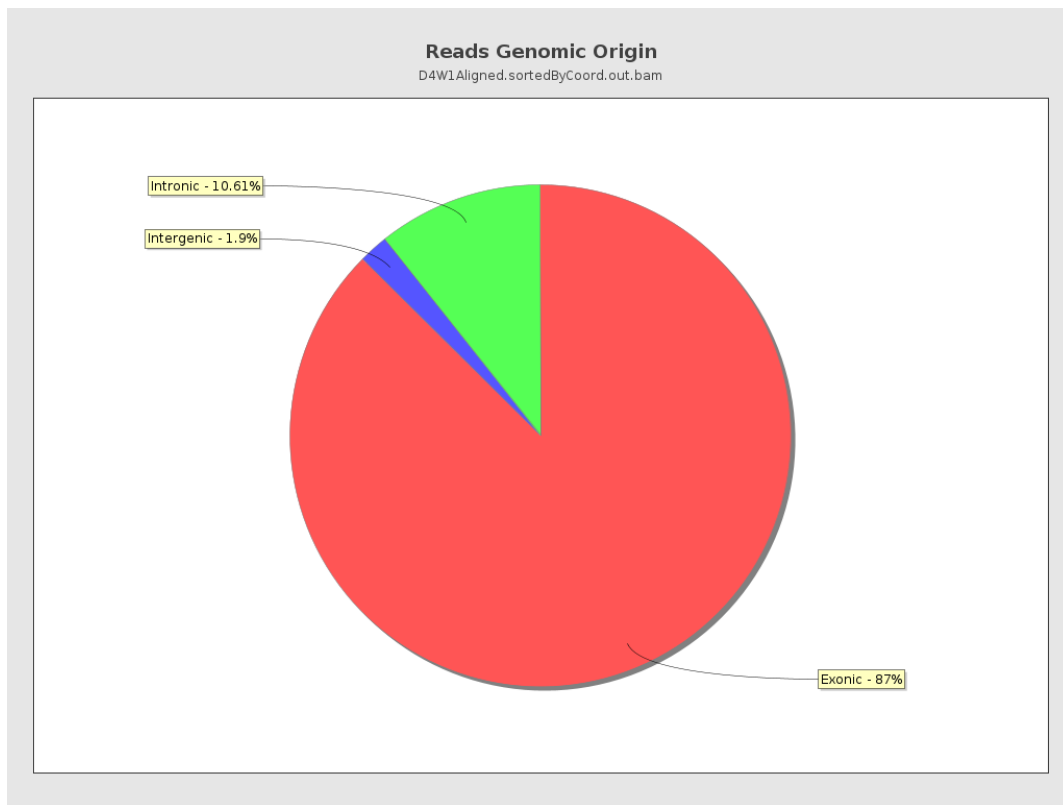|	
Exonic:	200,694,046 / 87.49%
Intronic:	24,342,903 / 10.61%
Intergenic:	4,357,790 / 1.9%
Intronic/intergenic overlapping exon:	24,103,643 / 10.51%

2.3. Transcript coverage profile

5' bias:	0.49
3' bias:	0.27
5'-3' bias:	1.29

2.4. Junction analysis

Reads at junctions:	183,582,757
AGGT	2.9%
ACCT	2.84%
TCCT	2.64%
AGGC	2.36%
AGGA	2.19%
AGAT	2.03%
ATCT	1.98%
GCCT	1.94%
AGCT	1.59%
TTCT	1.44%
AGAA	1.41%

3. Results : Reads Genomic Origin
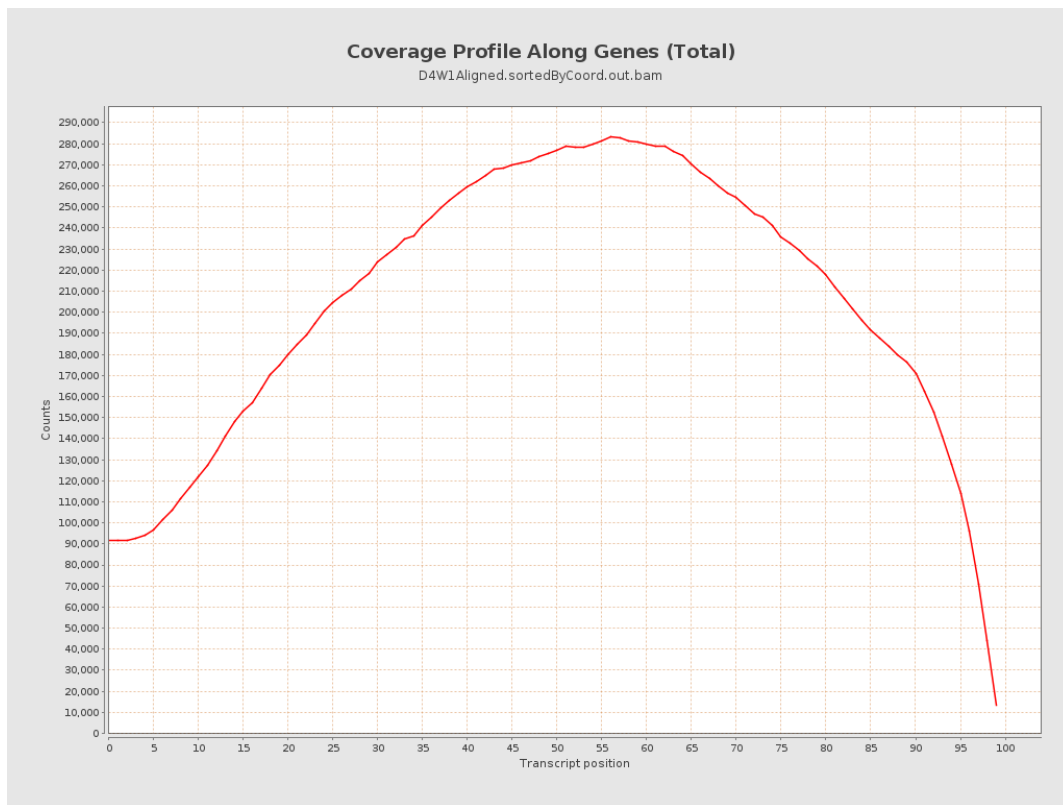
Reads Genomic Origin
D4W1Aligned.sortedByCoord.out.bam

Intronic - 10.61%

Intergenic - 1.9%

Exonic - 87%

4. Results : Coverage Profile Along Genes (Total)

Coverage Profile Along Genes (Total)
D4W1Aligned.sortedByCoord.out.bam

5. Results : Coverage Profile Along Genes (Low)

Coverage Profile Along Genes (Low)
D4W1Aligned.sortedByCoord.out.bam

6. Results : Coverage Profile Along Genes (High)

Coverage Profile Along Genes (High)
D4W1Aligned.sortedByCoord.out.bam
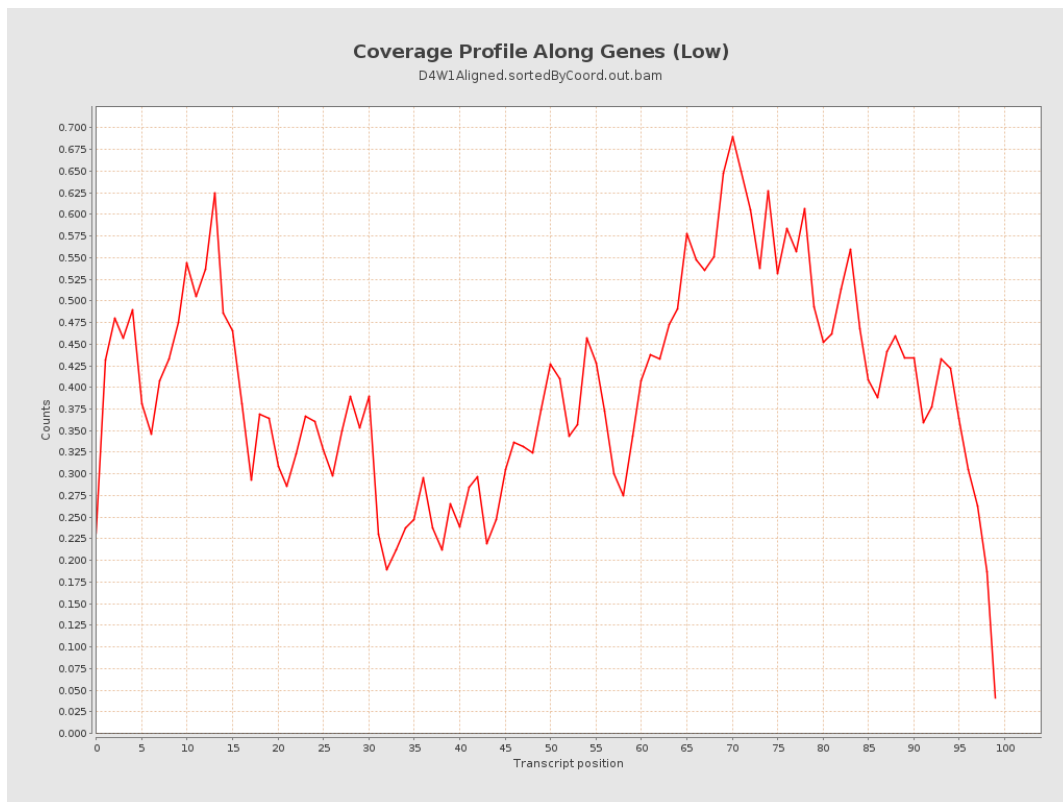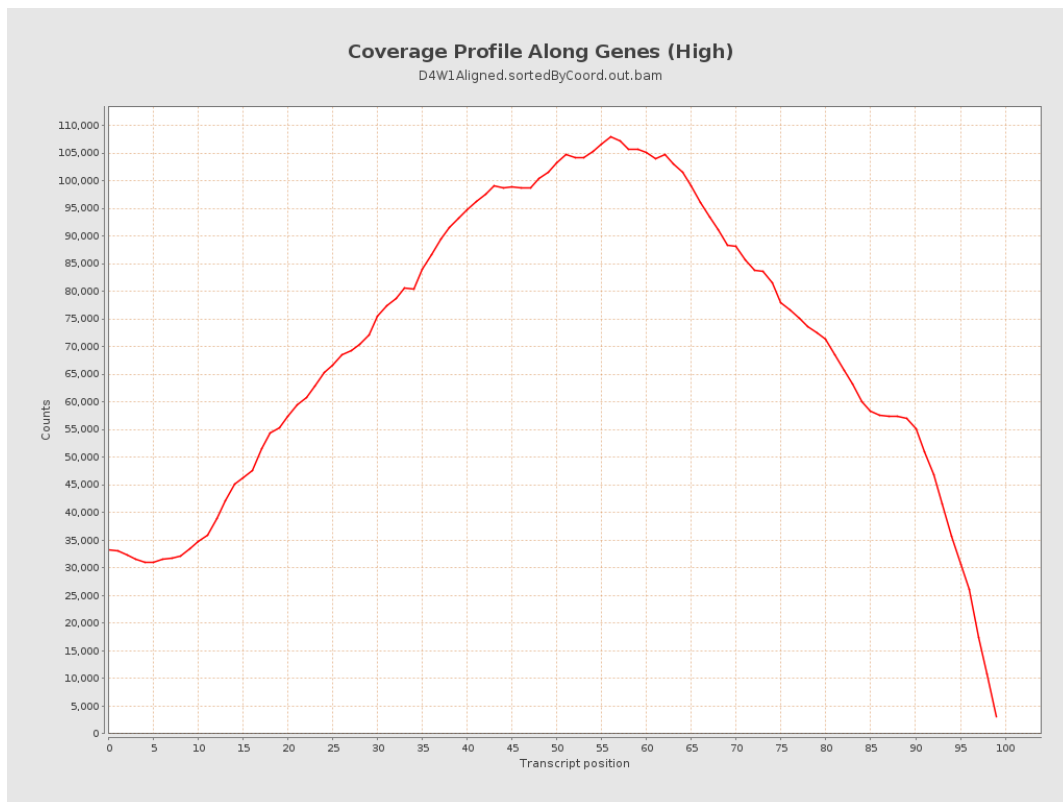
7. Results : Coverage Histogram (0-50X)

Coverage Histogram (0-50X)
D4W1Aligned.sortedByCoord.out.bam
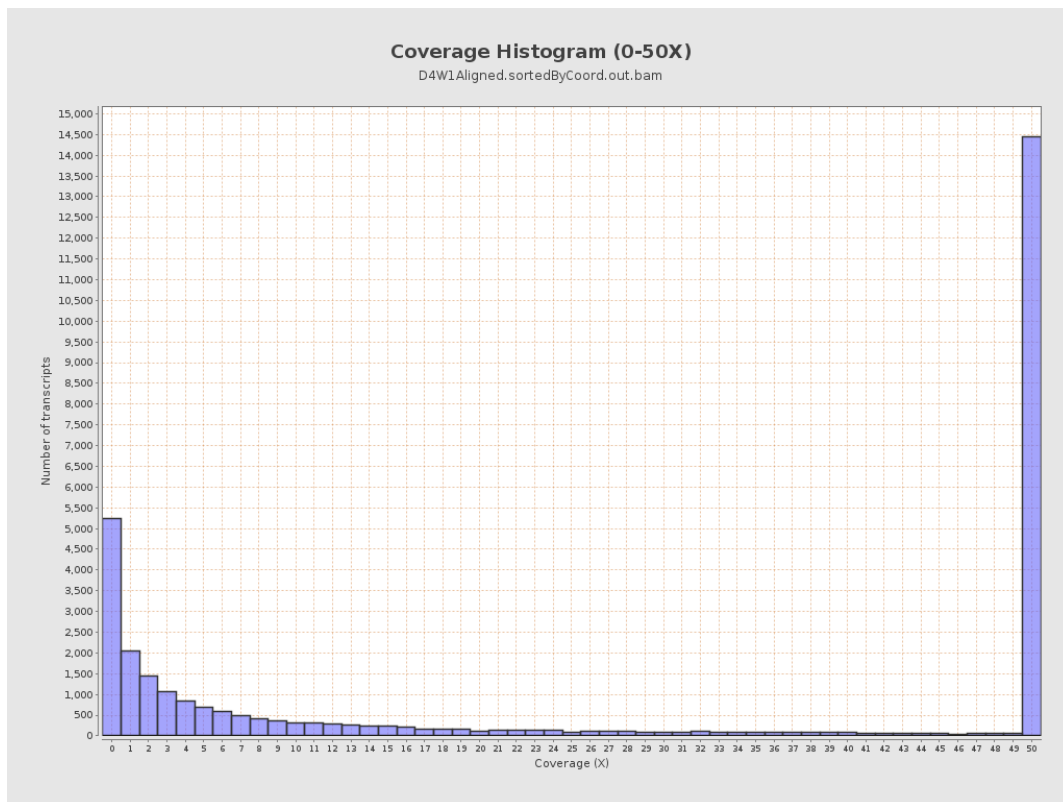
8. Results : Junction Analysis