

Qualimap Analysis Results

RNA Seq QC analysis

Generated by Qualimap v.2.2.2-dev

2024/01/22 18:19:36

1. Input data & parameters

1.1. Input

Analysis date:	Mon Jan 22 18:19:33 EST 2024
BAM file:	YZ_15T_hRGC_sorted.chr21.bam
Counting algorithm:	uniquely-mapped-reads
GTF file:	/dcs04/hicks/data/sparthib/references /genome/GENCODE/gencode.v44.ch r_patch_hapl_scaff.annotation.gtf
Paired-end sequencing:	no
Protocol:	non-strand-specific
Sorting performed:	no

2. Summary

2.1. Reads alignment

Number of mapped reads:	3,246,563
Total number of alignments:	3,246,563
Number of secondary alignments:	0
Number of non-unique alignments:	0
Aligned to genes:	142,712
Ambiguous alignments:	1,255
No feature assigned:	3,102,596
Not aligned:	0
Strand specificity estimation (fwd/rev):	0.39 / 0.61

2.2. Reads genomic origin

Exonic:	142,712 / 4.4%
Intronic:	2,892,068 / 89.12%
Intergenic:	210,528 / 6.49%
Intronic/intergenic overlapping exon:	535,806 / 16.51%
Exonic inside rRNA:	0 / 0%

2.3. Transcript coverage profile

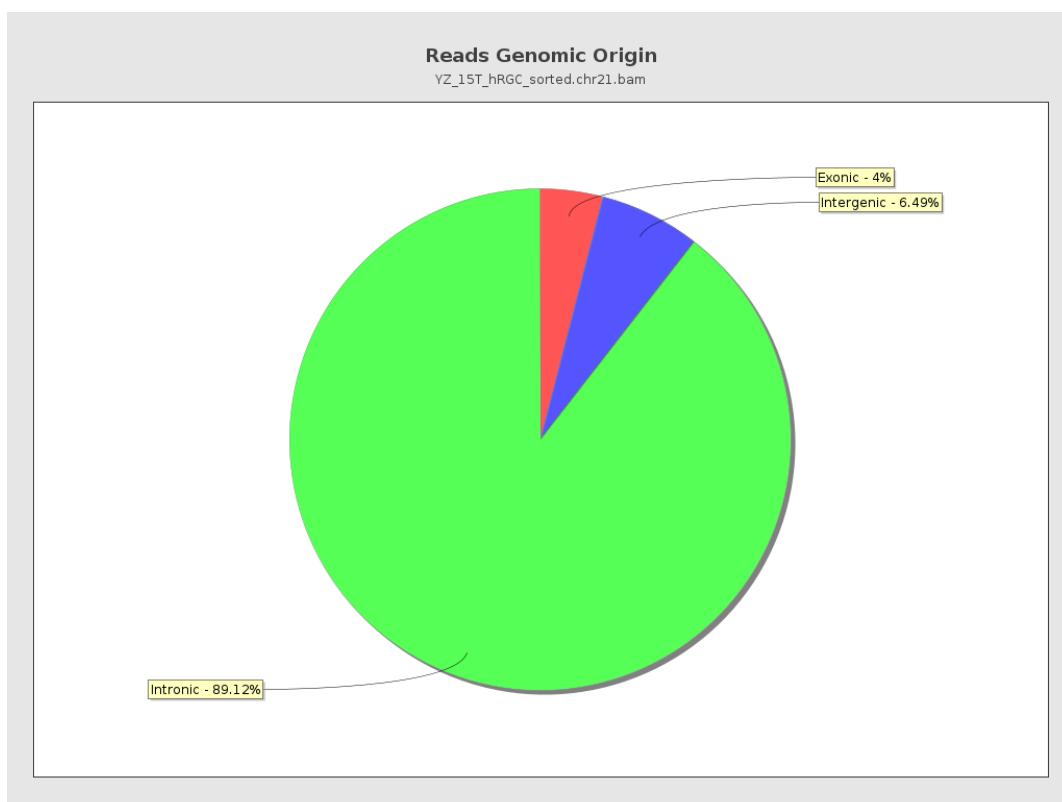
5' bias:	0.56
3' bias:	0.42
5'-3' bias:	1.55

2.4. Junction analysis

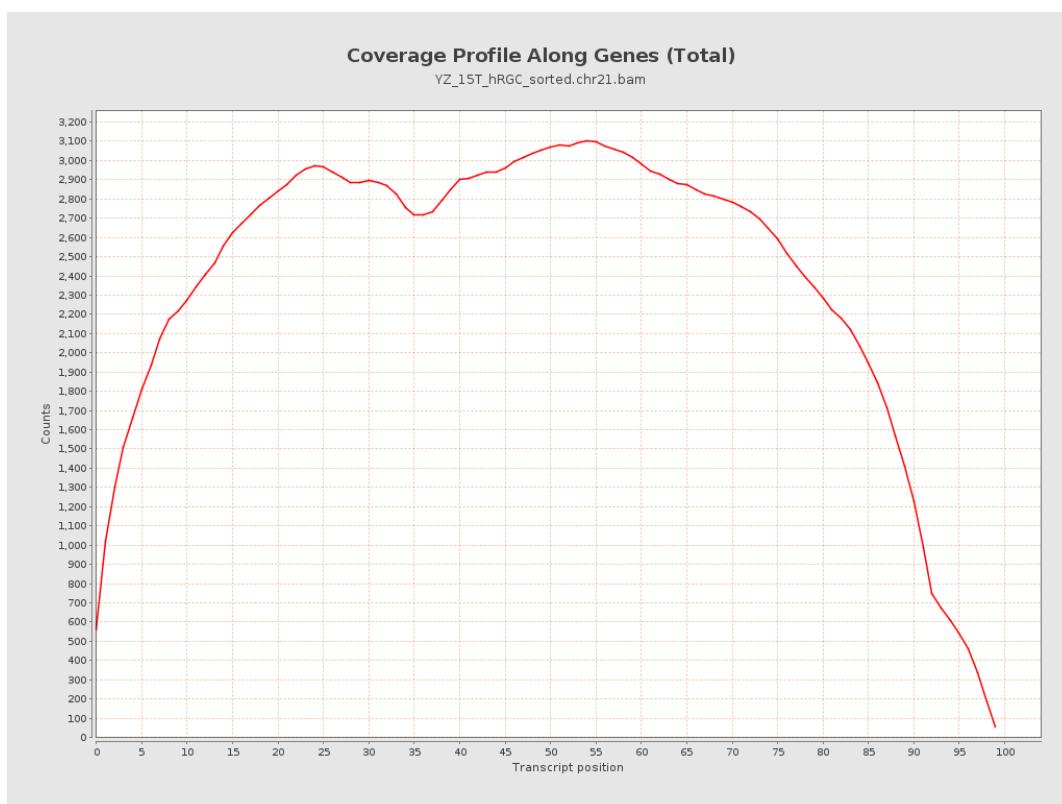
Reads at junctions:

0

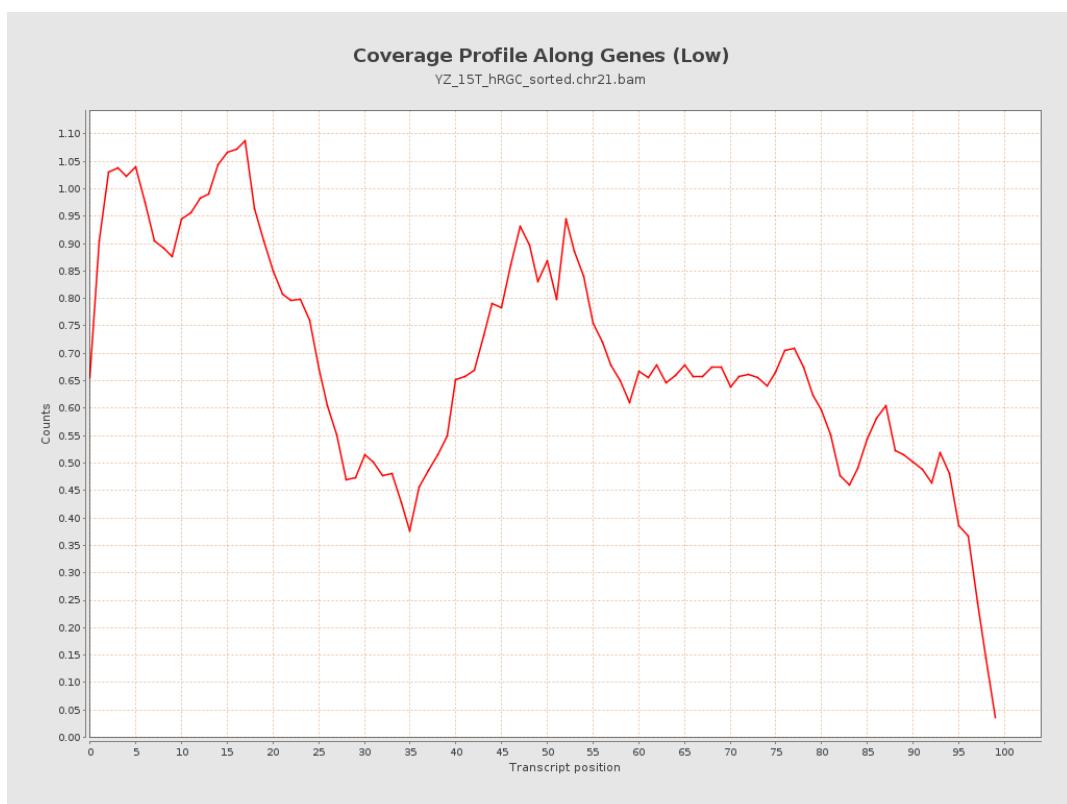
3. Results : Reads Genomic Origin



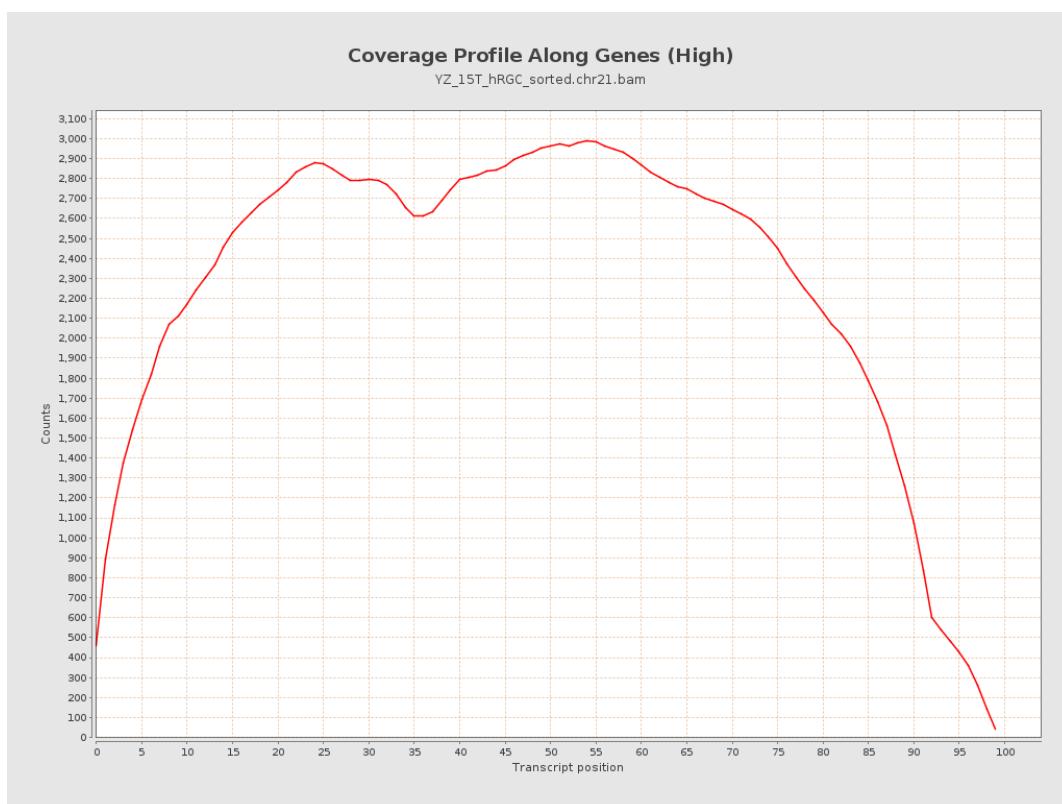
4. Results : Coverage Profile Along Genes (Total)



5. Results : Coverage Profile Along Genes (Low)



6. Results : Coverage Profile Along Genes (High)



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

