Qualimap Report: RNA Seq QC

QualiMap

Input data and parameters

Input

Analysis date:	Fri Oct 03 15:19:59 IST 2025
BAM file:	./aligned_reads2/LNCAP_Hypoxia_S1.bam
Counting algorithm:	uniquely-mapped-reads
GTF file:	Homo_sapiens.GRCh38.114.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

Summary

Reads alignment

Number of mapped reads:	47,045,908
Total number of alignments:	53,992,740
Number of secondary alignments:	6,946,832
Number of non-unique alignments:	10,582,779
Aligned to genes:	36,189,018
Ambiguous alignments:	2,633,842
No feature assigned:	4,569,705
Missing chromosome in annotation:	17,396
Not aligned:	3,318,590
Strand specificity estimation (fwd/rev):	0.04 / 0.96

Reads genomic origin

Exonic:	36,189,018 / 88.79%
Intronic:	3,986,643 / 9.78%
Intergenic:	583,062 / 1.43%
Intronic/intergenic overlapping exon:	1,707,244 / 4.19%

Transcript coverage profile

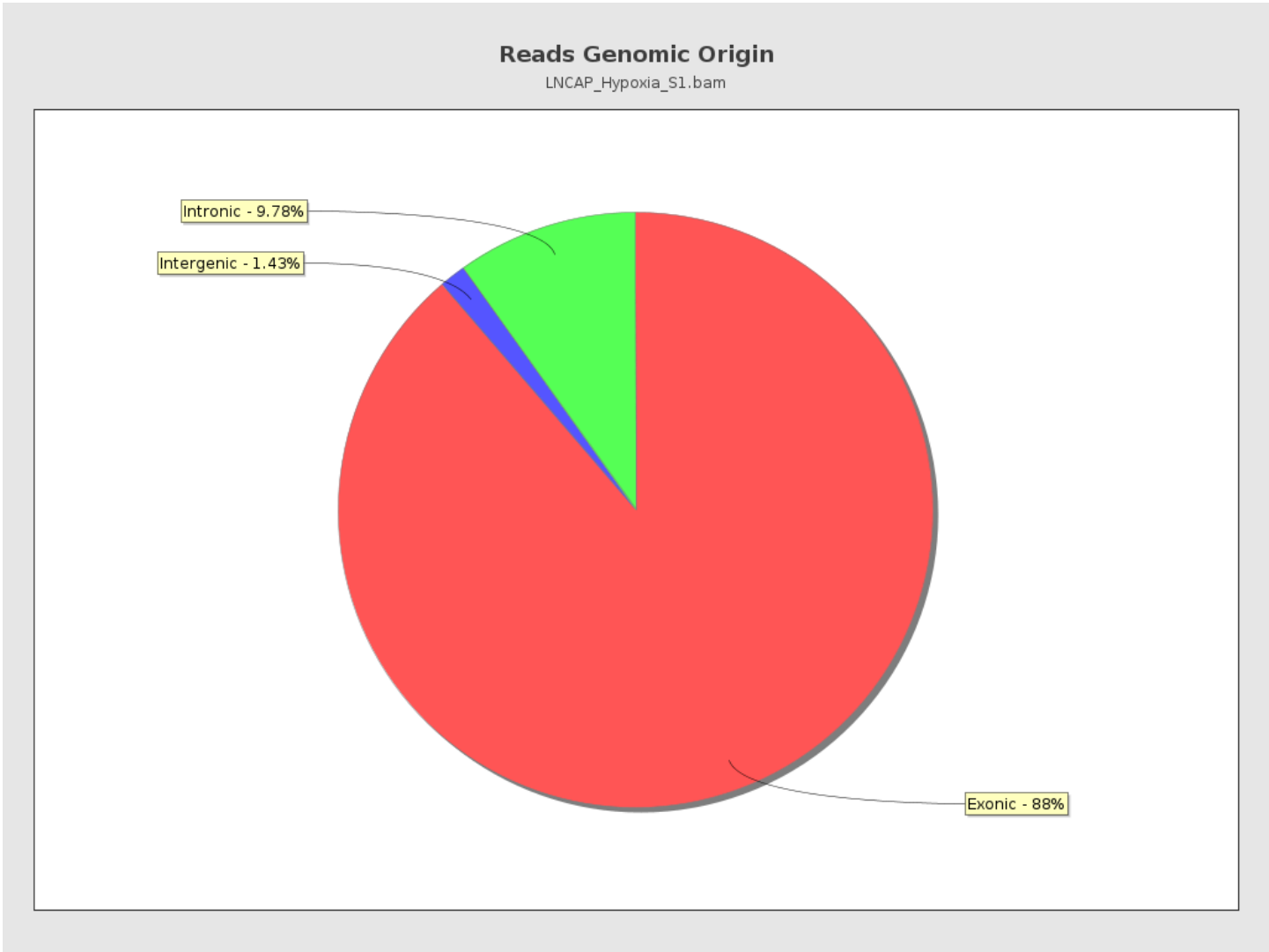|	
5' bias:	0.37
3' bias:	0.32
5'-3' bias:	1.1

Junction analysis

Reads at junctions:	10,657,430

CONTENTS

ACCT	5.02%
AGGT	4.7%
AGGA	4.02%
TCCT	3.72%
ATCT	3.33%
AGCT	2.73%
GCCT	2.48%
AGGC	2.46%
AGAT	2.43%
AGGG	2.4%
TTCT	2.13%

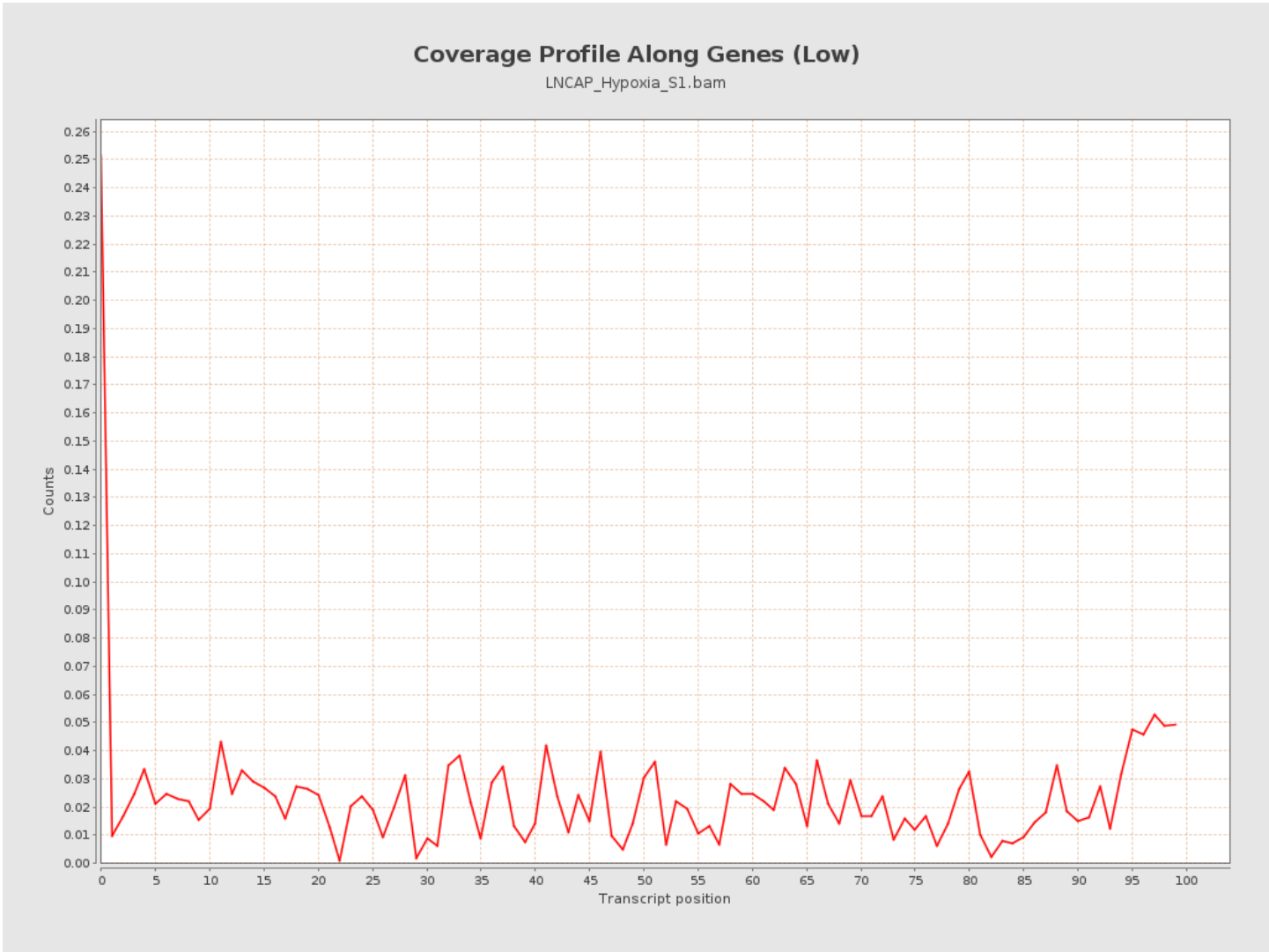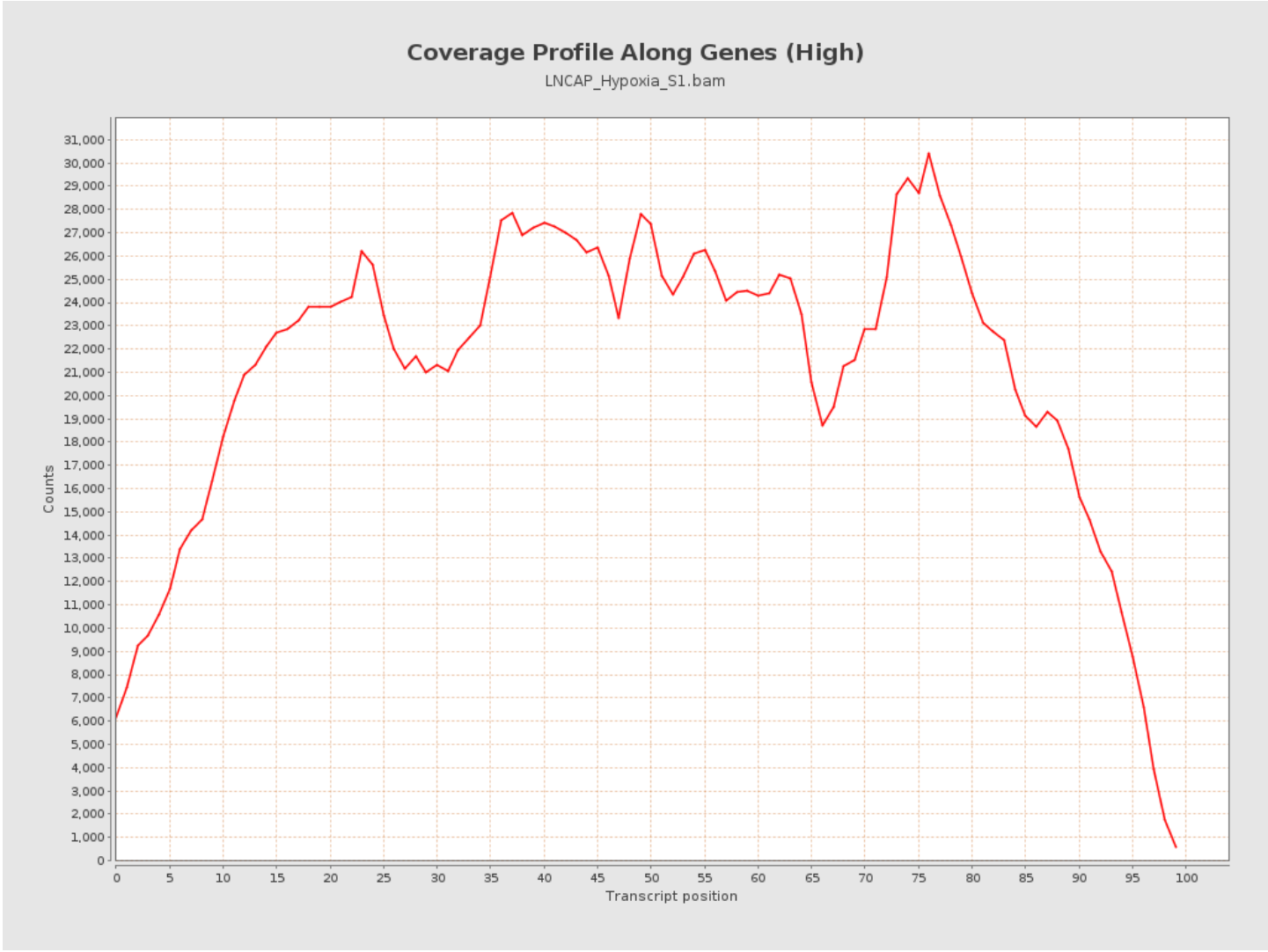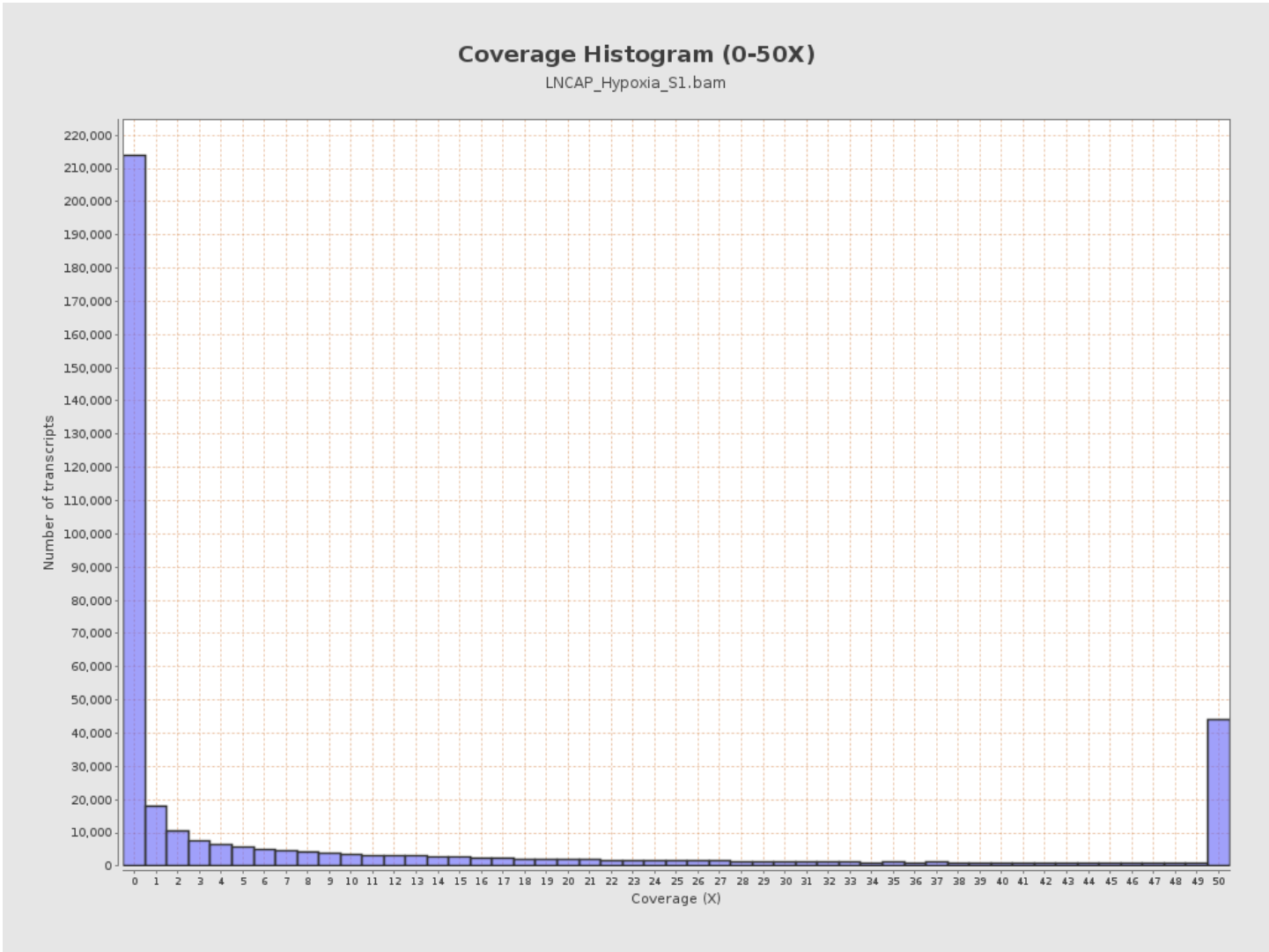## Reads Genomic Origin

Reads Genomic Origin
LNCAP_Hypoxia_S1.bam

Intronic - 9.78%
Intergenic - 1.43%
Exonic - 88%

Coverage Profile Along Genes (Total)
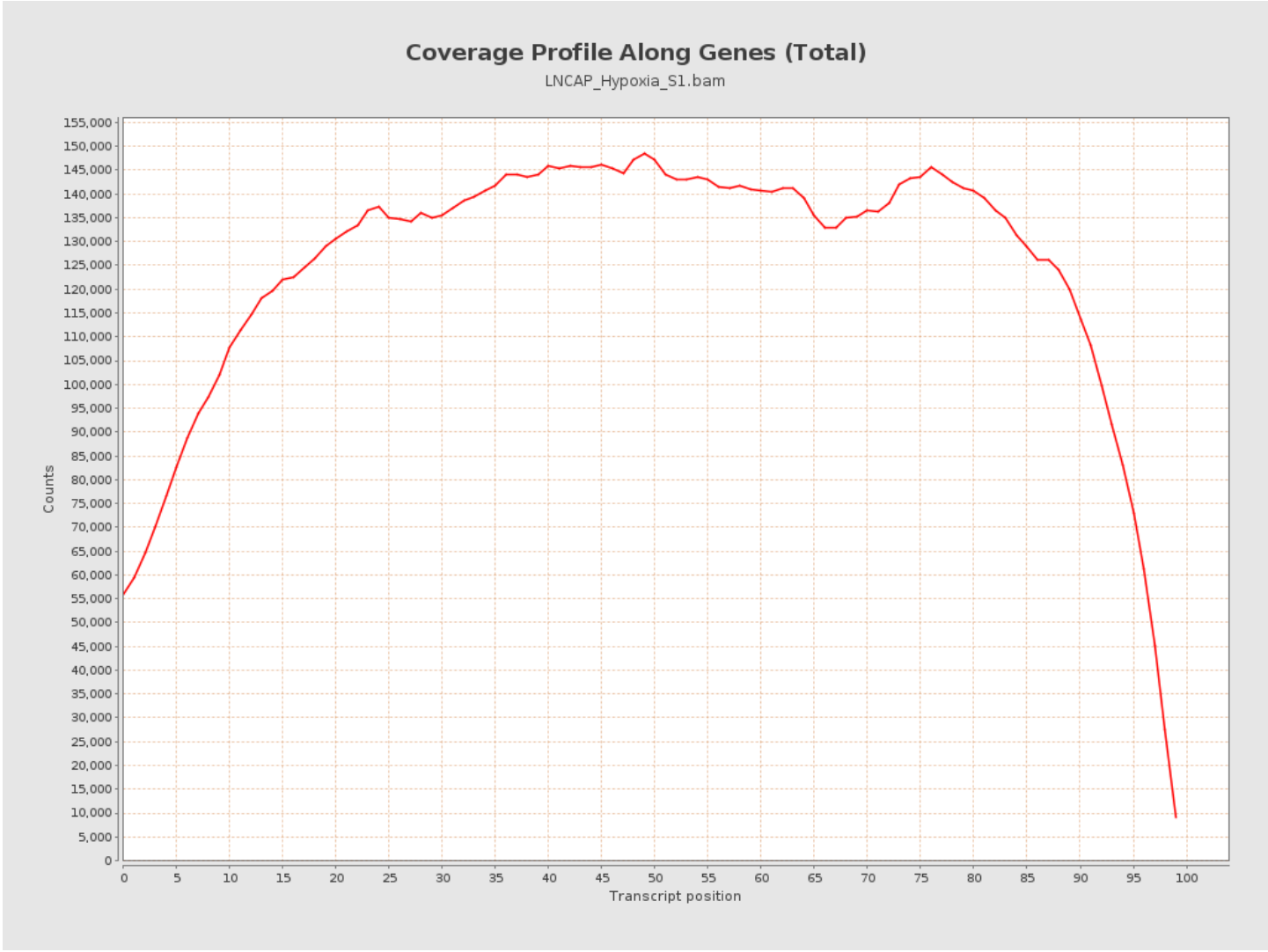
Coverage Profile Along Genes (Low)

Coverage Profile Along Genes (High)

file://wsl.localhost/Ubuntu/home/vaibhav/portfolio/RNA-seq/7_Aligned_reads_quality/LNCAP_Hypoxia_S1_qc/qualimapReport.html

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Coverage Profile Along Genes (High)
LNCAP_Hypoxia_S1.bam

Coverage Histogram (0-50X)

Coverage Histogram (0-50X)
LNCAP_Hypoxia_S1.bam

Junction Analysis

Junction Analysis

LNCAP_Hypoxia_S1.bam

2025/10/03 15:20:02
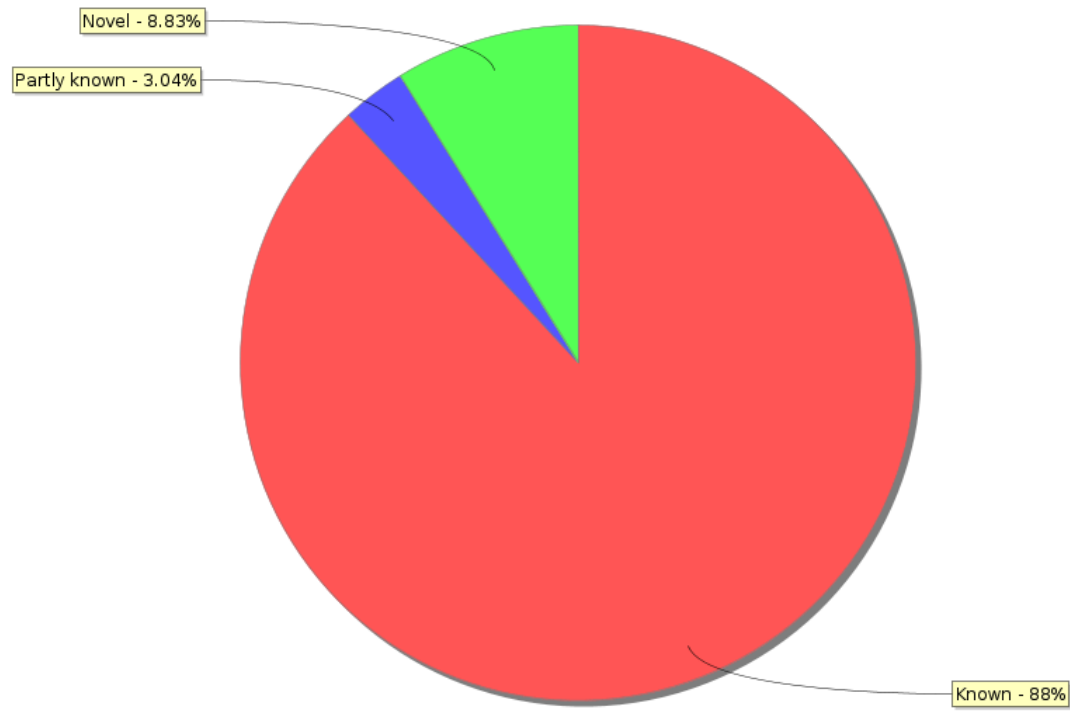
Generated by QualiMap v.2.3