Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 23:14:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231737.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6231737 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231737.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 23:14:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231737.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,670,389
Mapped reads	526,106 / 31.5%
Unmapped reads	1,144,283 / 68.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,702 / 0.22%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	52,495 / 3.14%
Duplication rate	7.5%
Clipped reads	310,594 / 18.59%

2.2. ACGT Content

Number/percentage of A's	8,982,845 / 27.6%
Number/percentage of C's	5,392,501 / 16.57%
Number/percentage of T's	10,993,700 / 33.78%
Number/percentage of G's	7,178,338 / 22.05%
Number/percentage of N's	835 / 0%
GC Percentage	38.62%

2.3. Coverage

Mean	0.0105

Standard Deviation	0.236

2.4. Mapping Quality

Mean Mapping Quality	43.79

2.5. Mismatches and indels

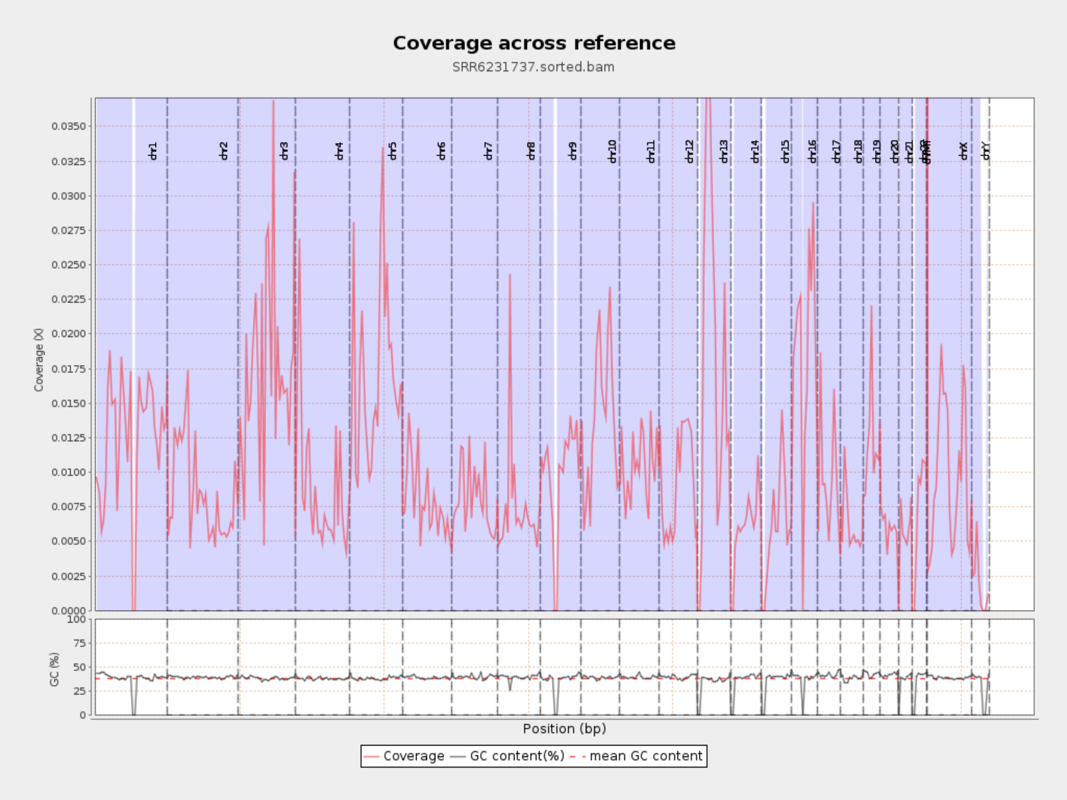
General error rate	1.03%
Mismatches	328,067
Insertions	3,545
Mapped reads with at least one insertion	0.66%
Deletions	11,675
Mapped reads with at least one deletion	2.18%
Homopolymer indels	43.12%

2.6. Chromosome stats

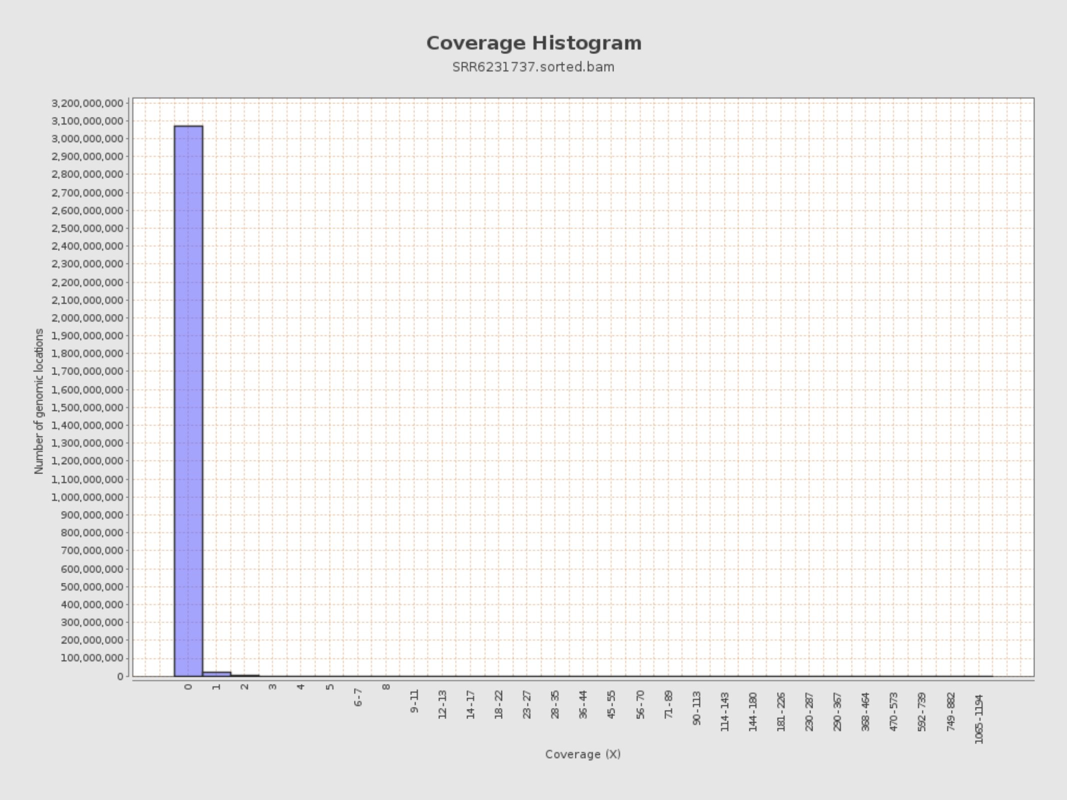
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3114373	0.0125	0.2145
chr2	243199373	2065052	0.0085	0.1671
chr3	198022430	3386068	0.0171	0.1746
chr4	191154276	1646075	0.0086	0.131
chr5	180915260	3103428	0.0172	0.1738
chr6	171115067	1341138	0.0078	0.1277
chr7	159138663	1281332	0.0081	0.1453

chr8	146364022	1092757	0.0075	0.7961
chr9	141213431	1393213	0.0099	0.1451
chr10	135534747	1863487	0.0137	0.1686
chr11	135006516	1421812	0.0105	0.145
chr12	133851895	1239785	0.0093	0.1382
chr13	115169878	2088398	0.0181	0.1876
chr14	107349540	651486	0.0061	0.1034
chr15	102531392	616178	0.006	0.1271
chr16	90354753	1636604	0.0181	0.1785
chr17	81195210	775038	0.0095	0.1267
chr18	78077248	474187	0.0061	0.3537
chr19	59128983	729975	0.0123	0.18
chr20	63025520	373992	0.0059	0.106
chr21	48129895	273788	0.0057	0.1045
chr22	51304566	365398	0.0071	0.1044
chrMT	16571	10390	0.627	1.0517
chrX	155270560	1512345	0.0097	0.1478
chrY	59373566	112338	0.0019	0.0566

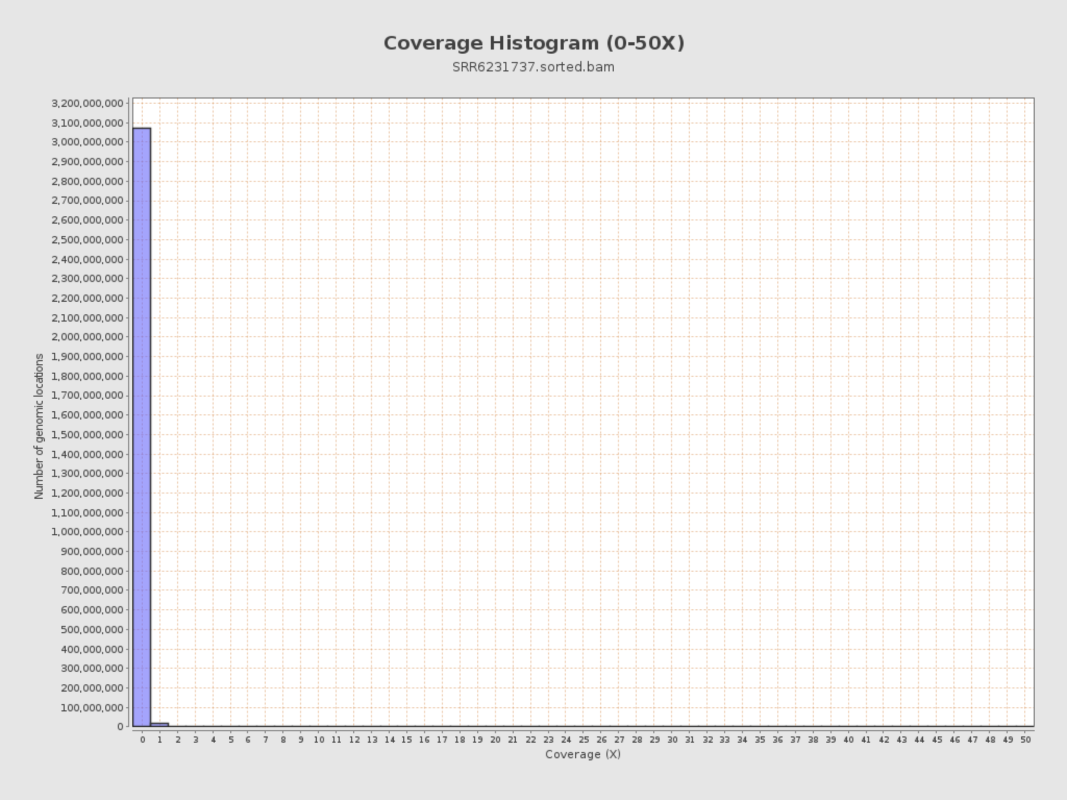
3. Results : Coverage across reference



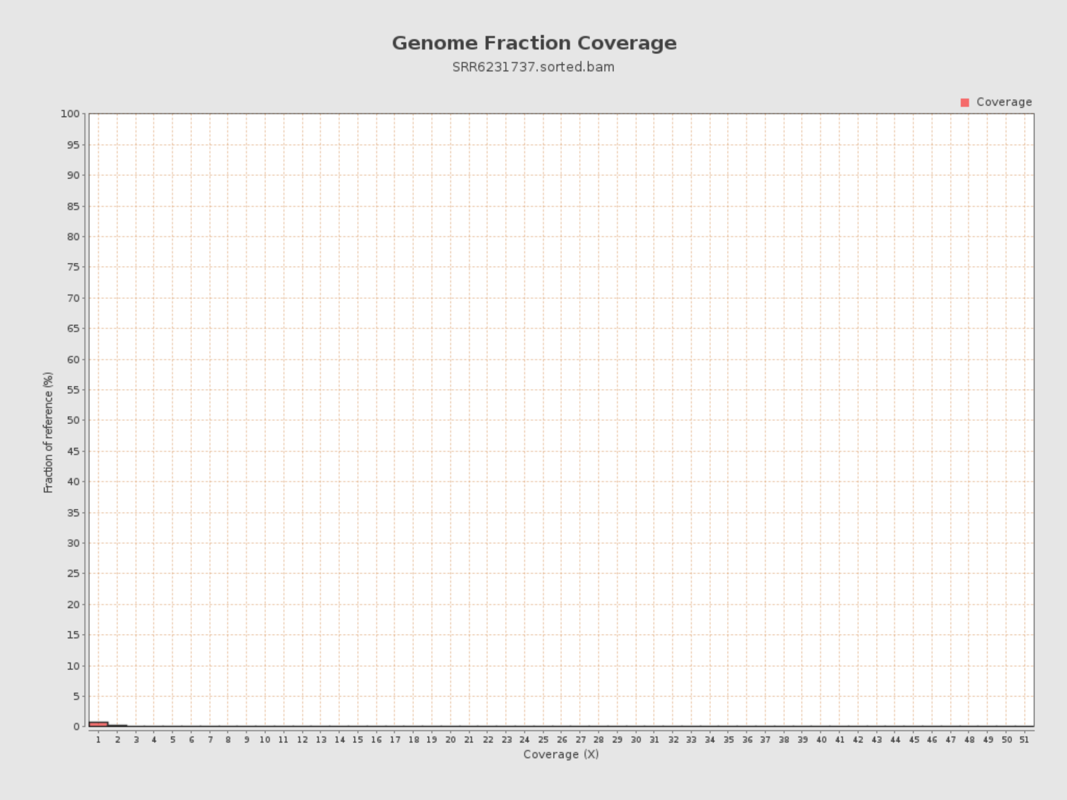
4. Results : Coverage Histogram



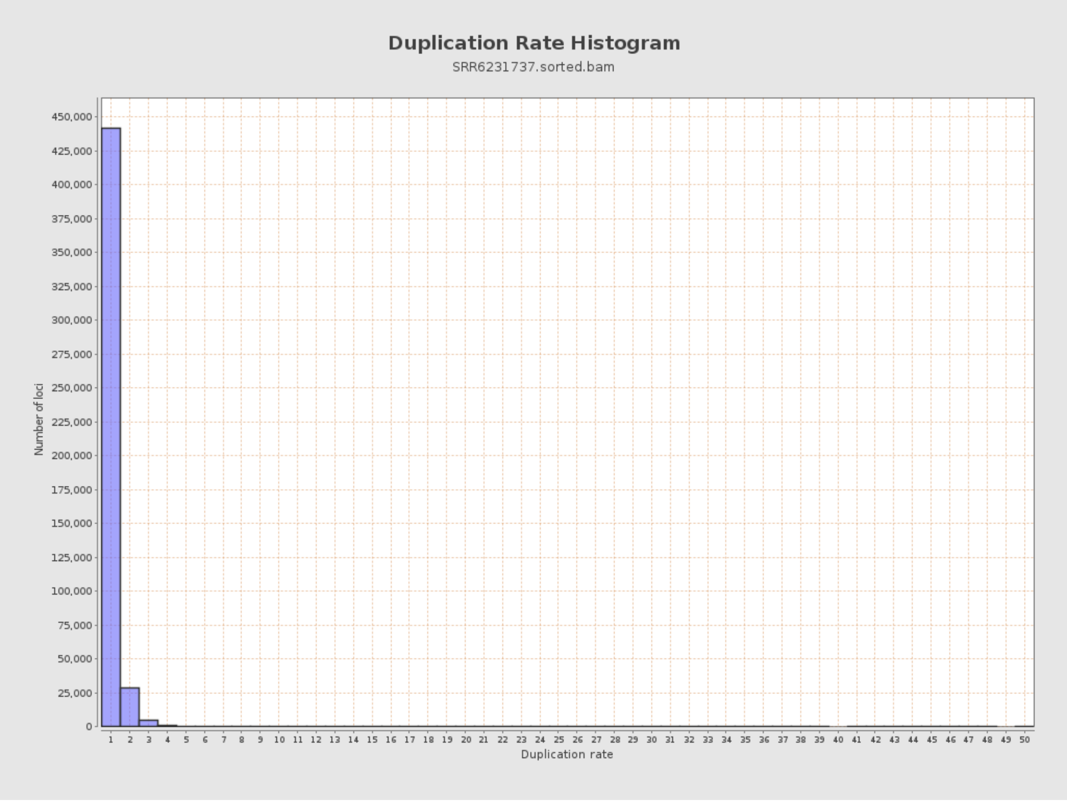
5. Results : Coverage Histogram (0-50X)



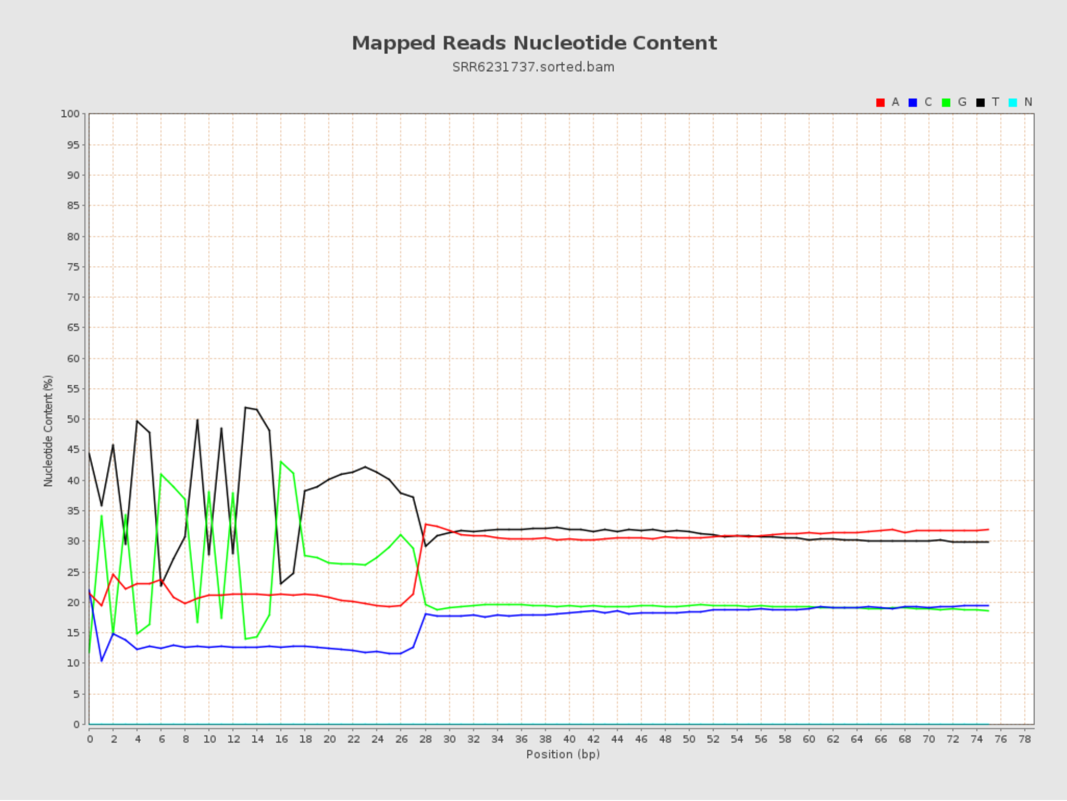
6. Results : Genome Fraction Coverage



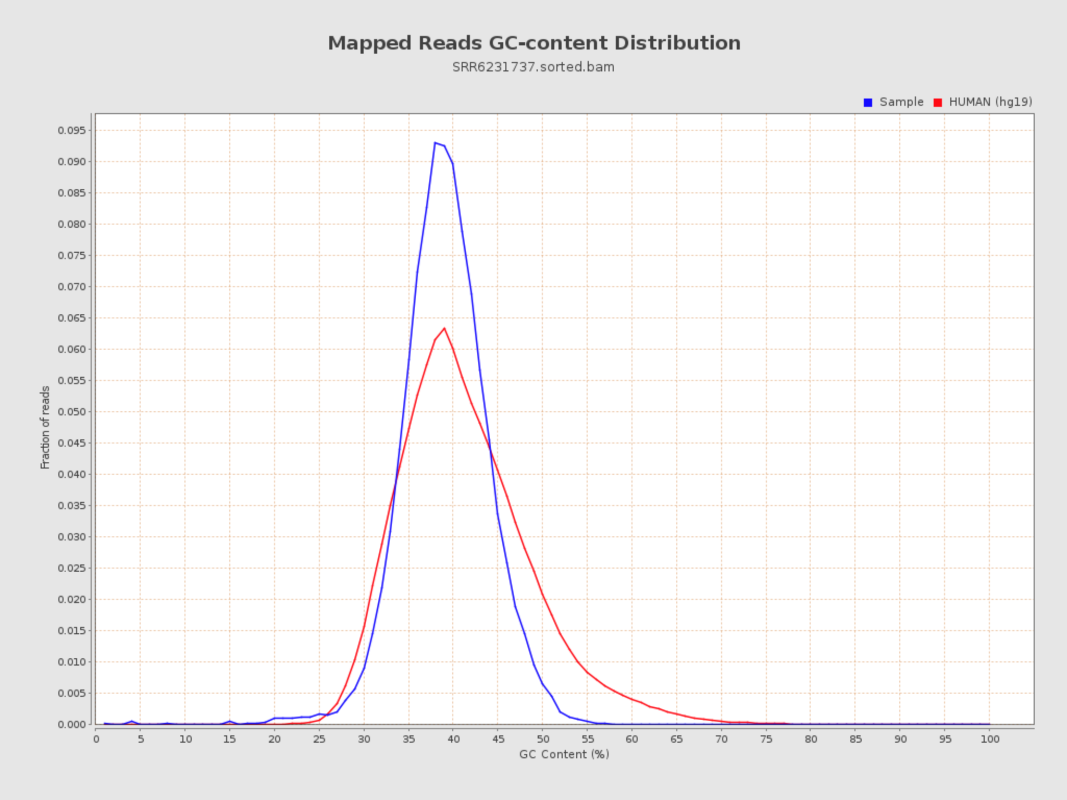
7. Results : Duplication Rate Histogram



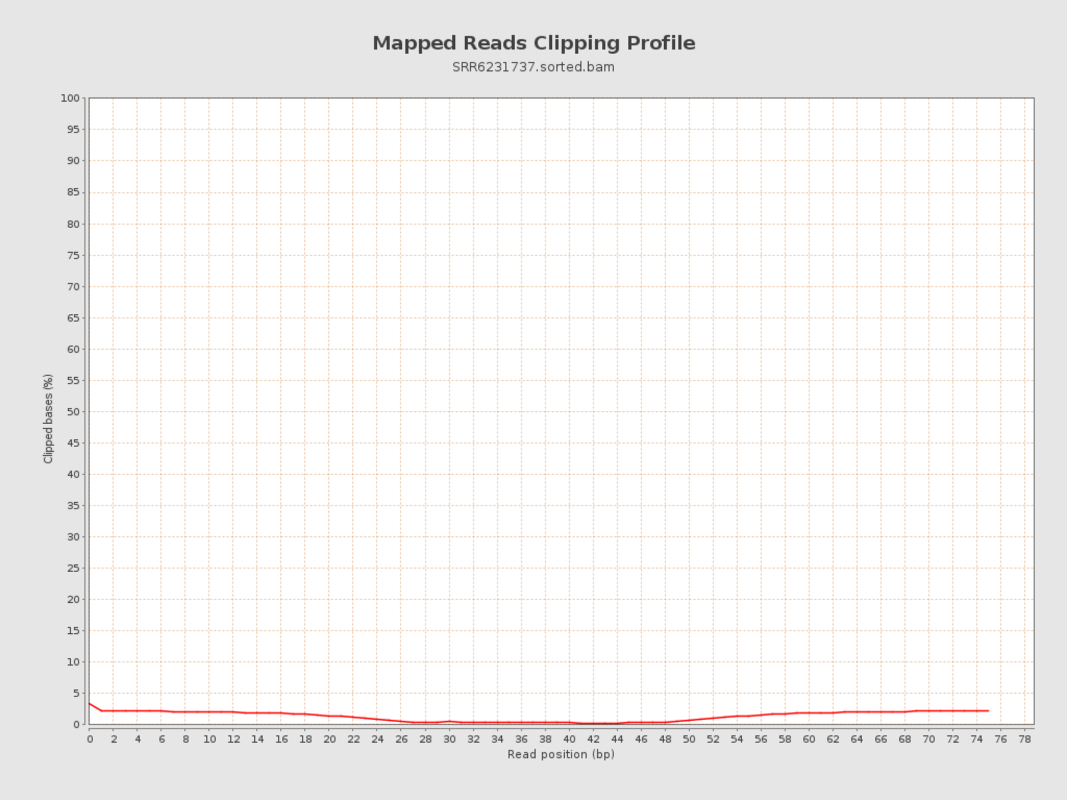
8. Results : Mapped Reads Nucleotide Content



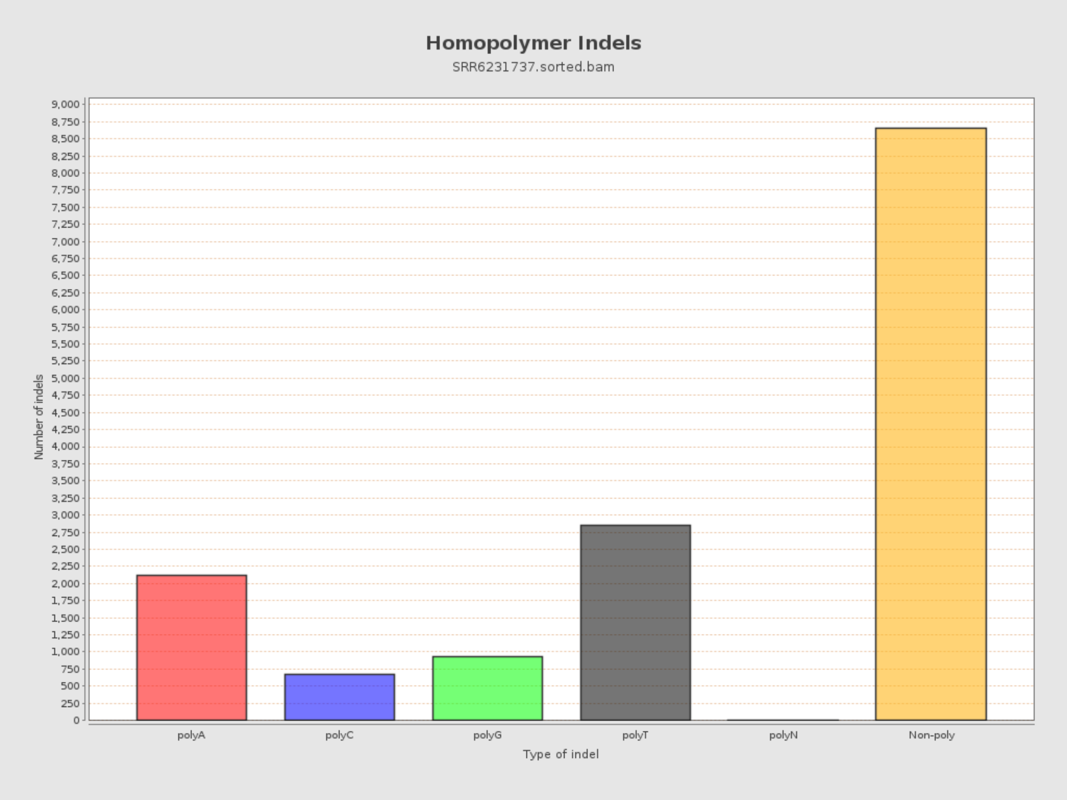
9. Results : Mapped Reads GC-content Distribution



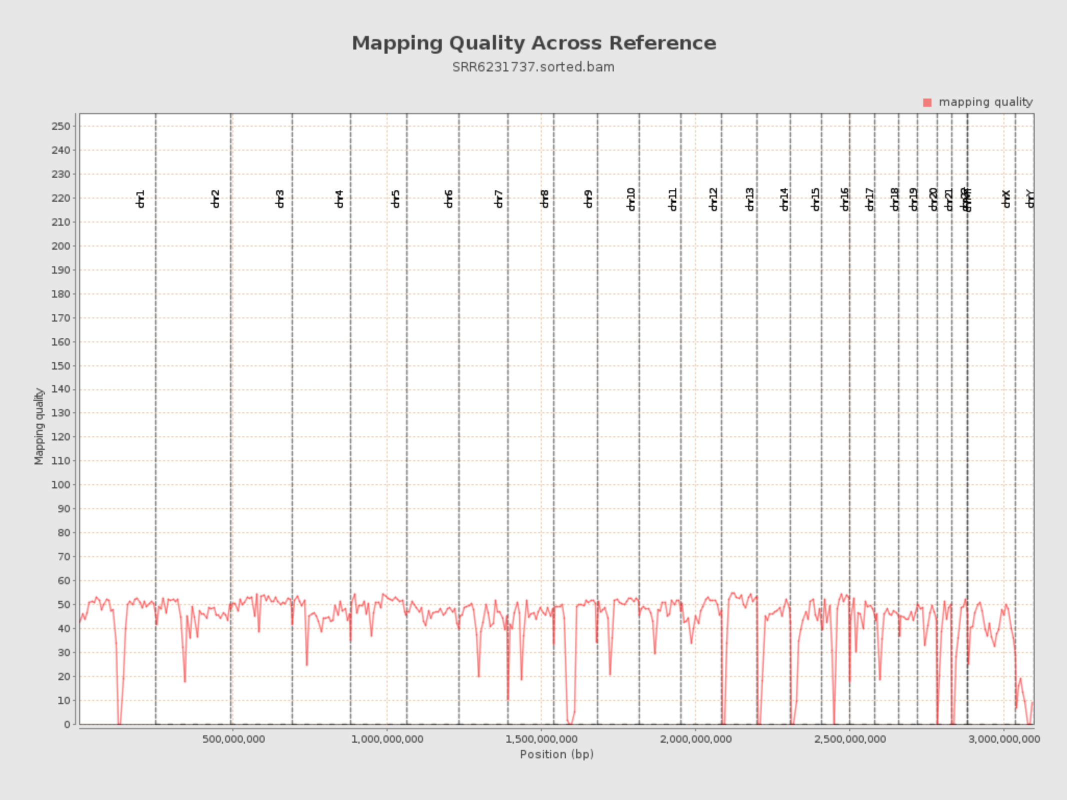
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram