Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 23:59:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231750.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_SRR6231750 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231750.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 23:59:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231750.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,232,223
Mapped reads	5,899,015 / 94.65%
Unmapped reads	333,208 / 5.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,447 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	500,910 / 8.04%
Duplication rate	3.73%
Clipped reads	2,341,202 / 37.57%

2.2. ACGT Content

Number/percentage of A's	103,331,759 / 25.83%
Number/percentage of C's	77,005,980 / 19.25%
Number/percentage of T's	113,566,604 / 28.39%
Number/percentage of G's	106,000,860 / 26.5%
Number/percentage of N's	89,388 / 0.02%
GC Percentage	45.75%

2.3. Coverage

Mean	0.1293

Standard Deviation	29.8719

2.4. Mapping Quality

Mean Mapping Quality	42.68

2.5. Mismatches and indels

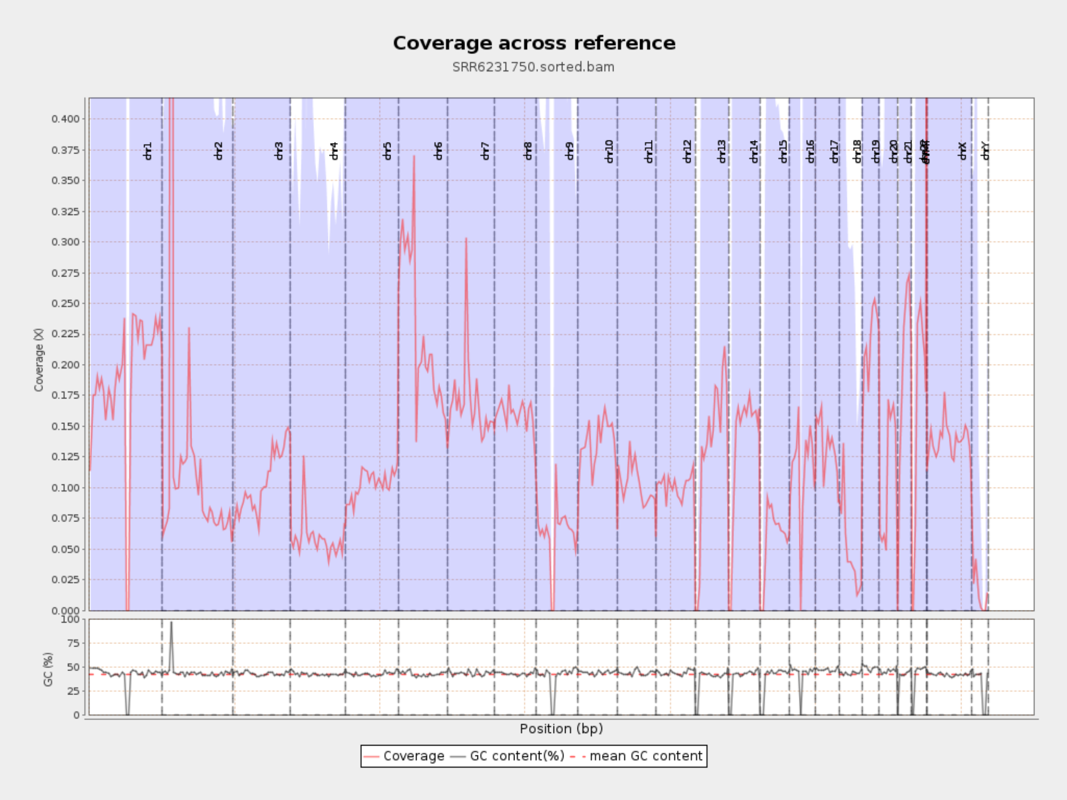
General error rate	0.67%
Mismatches	2,630,572
Insertions	28,554
Mapped reads with at least one insertion	0.48%
Deletions	86,501
Mapped reads with at least one deletion	1.45%
Homopolymer indels	46.34%

2.6. Chromosome stats

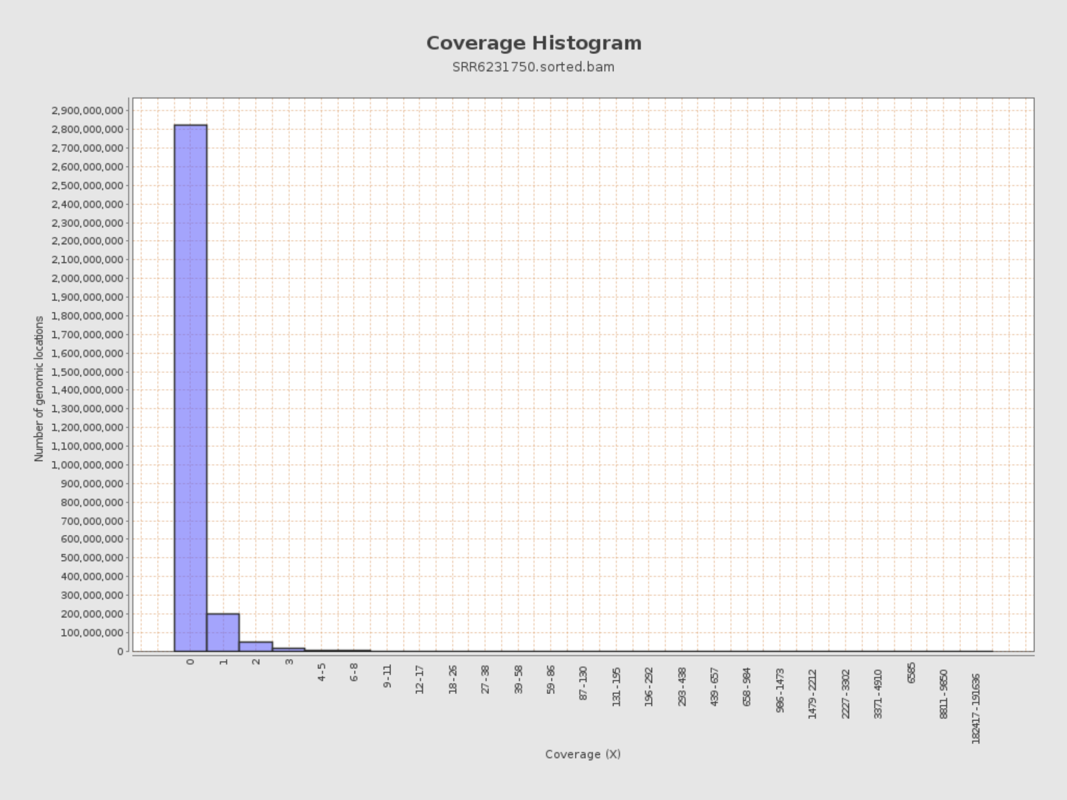
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	46779812	0.1877	1.4969
chr2	243199373	38373585	0.1578	106.5199
chr3	198022430	20506931	0.1036	0.4236
chr4	191154276	11126819	0.0582	0.4158
chr5	180915260	18692268	0.1033	0.437
chr6	171115067	38675620	0.226	1.1299
chr7	159138663	27051999	0.17	2.4413

chr8	146364022	23476890	0.1604	0.7979
chr9	141213431	8748765	0.062	0.7826
chr10	135534747	18657171	0.1377	0.7178
chr11	135006516	13736364	0.1017	1.0685
chr12	133851895	13520823	0.101	0.4232
chr13	115169878	15379270	0.1335	0.4918
chr14	107349540	14370354	0.1339	0.7321
chr15	102531392	6091505	0.0594	0.3392
chr16	90354753	10436340	0.1155	0.5829
chr17	81195210	10822645	0.1333	0.6609
chr18	78077248	3917944	0.0502	1.9315
chr19	59128983	12948576	0.219	1.1183
chr20	63025520	6949447	0.1103	0.4879
chr21	48129895	9293521	0.1931	0.6837
chr22	51304566	8007140	0.1561	0.5713
chrMT	16571	16459	0.9932	1.4416
chrX	155270560	21556578	0.1388	0.6954
chrY	59373566	999753	0.0168	0.2608

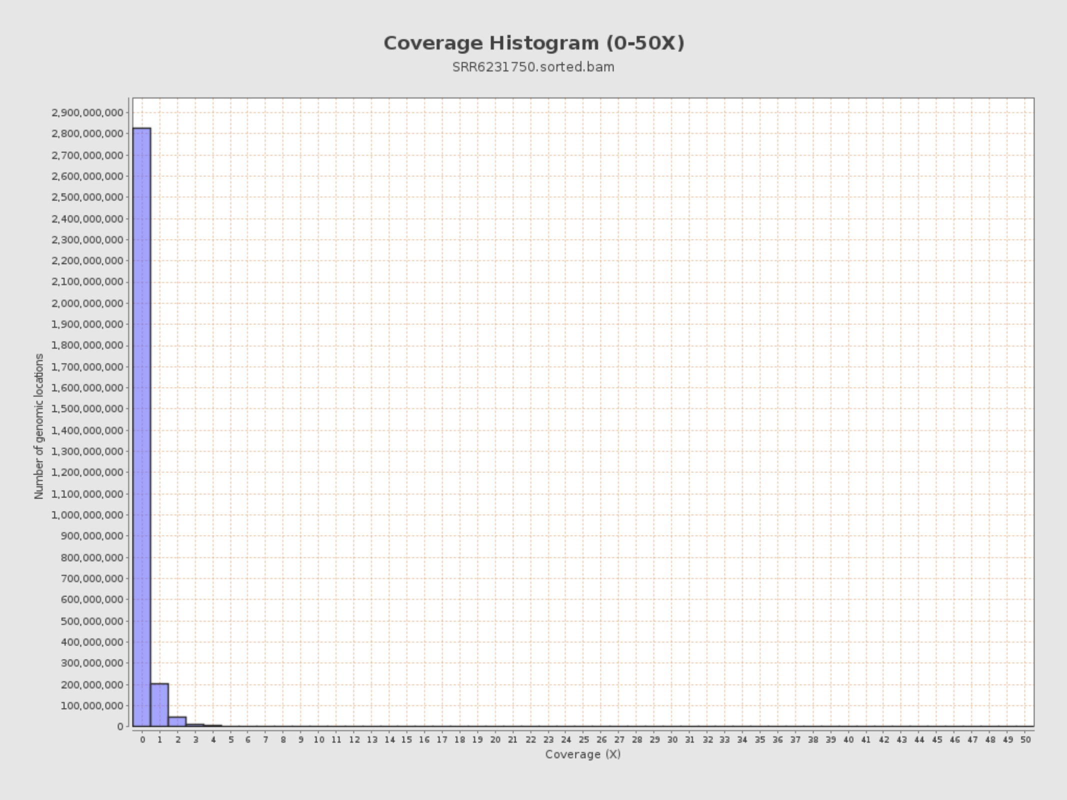
3. Results : Coverage across reference



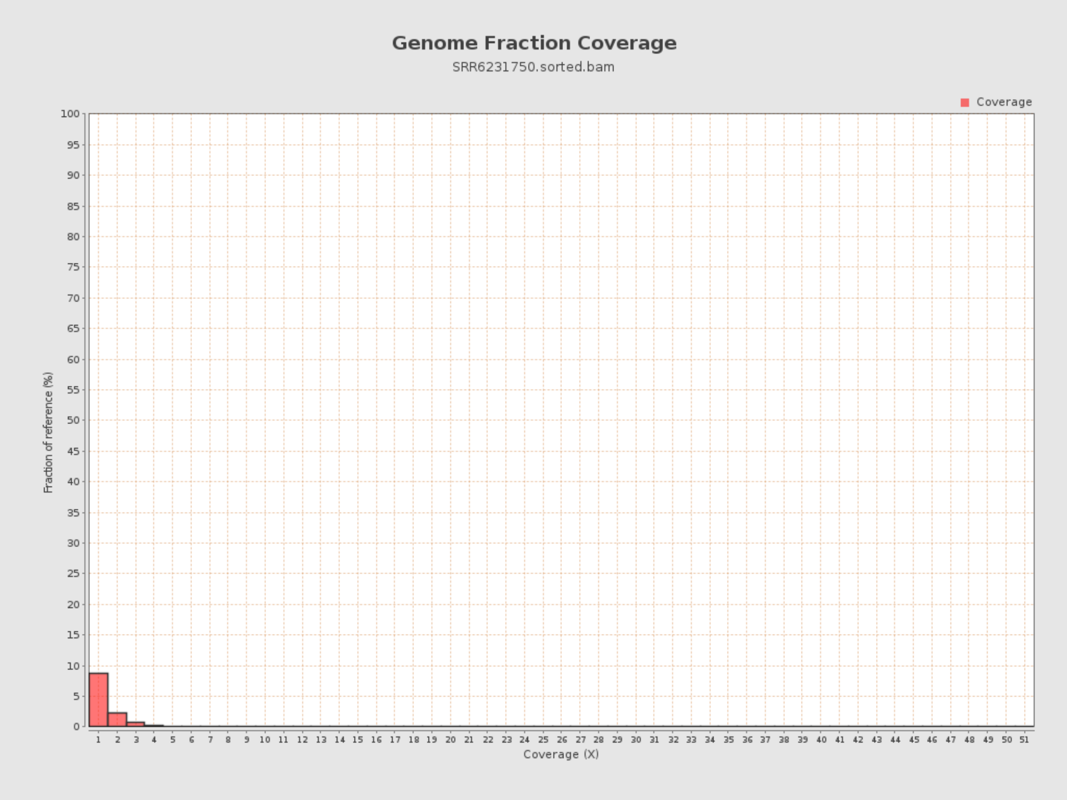
4. Results : Coverage Histogram



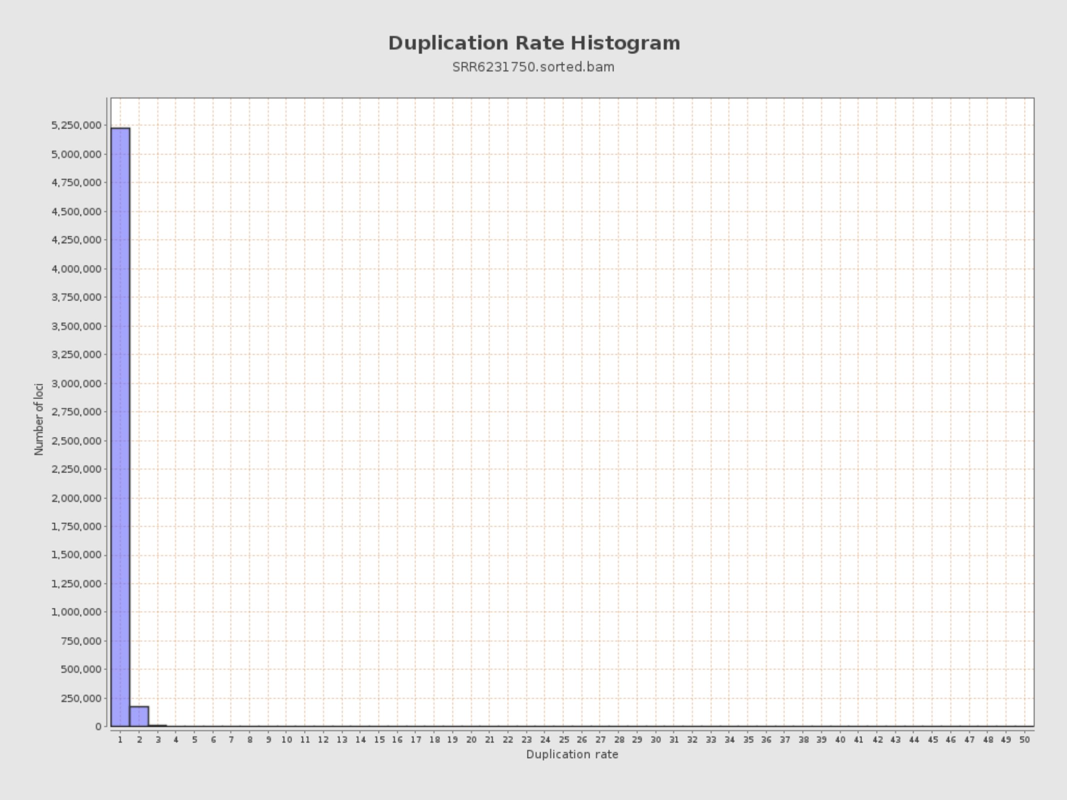
5. Results : Coverage Histogram (0-50X)



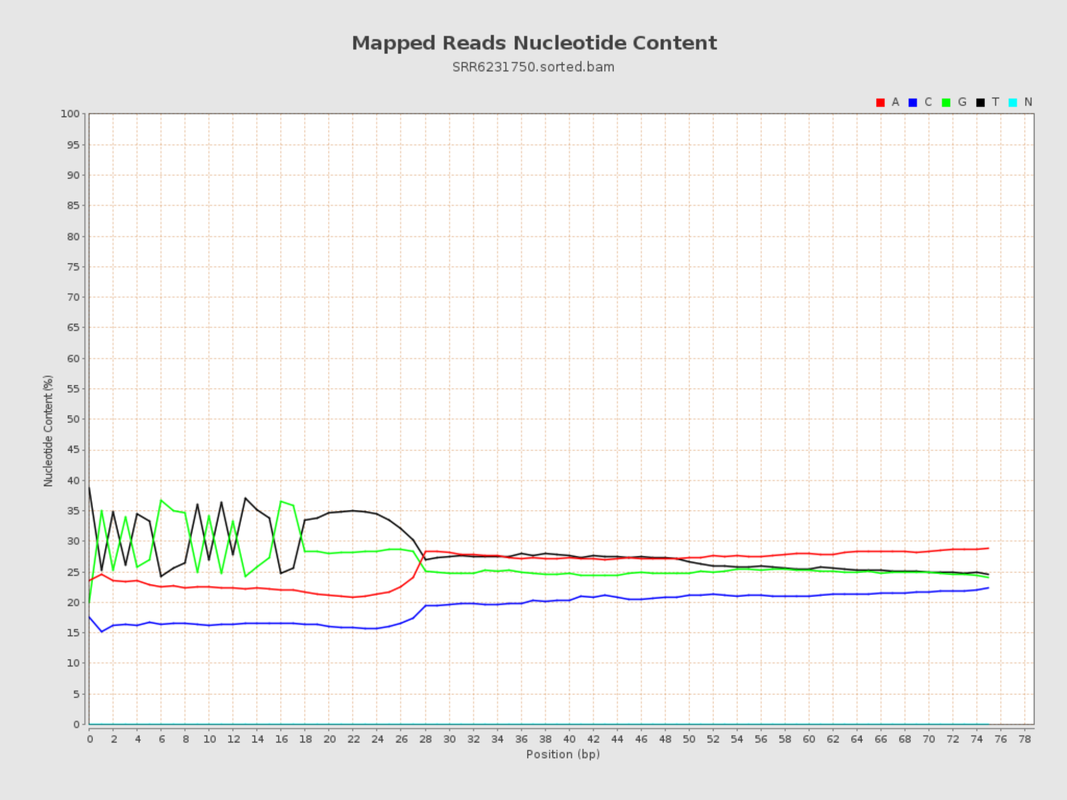
6. Results : Genome Fraction Coverage



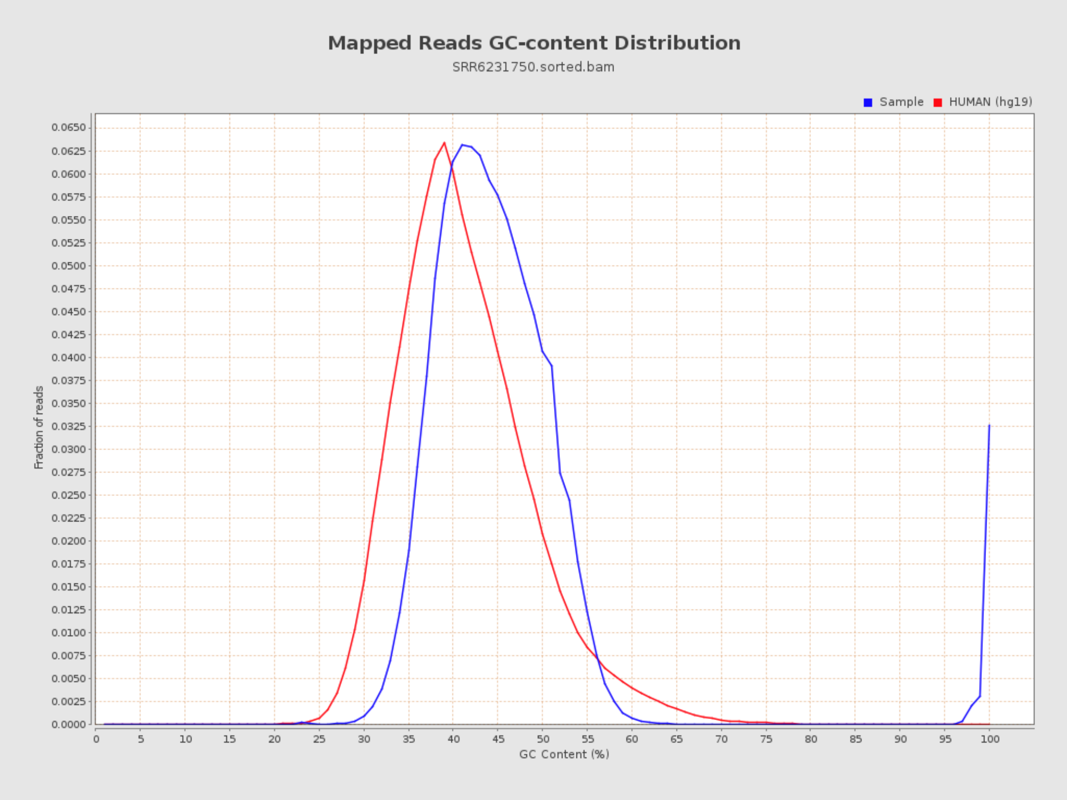
7. Results : Duplication Rate Histogram



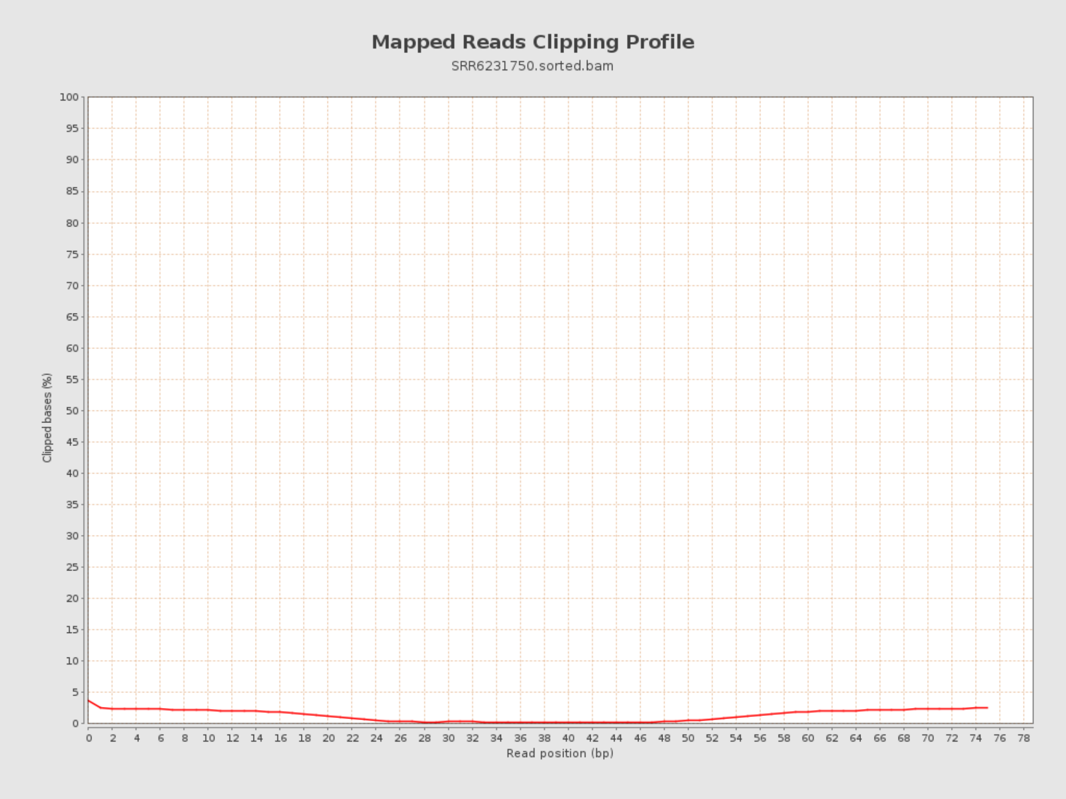
8. Results : Mapped Reads Nucleotide Content



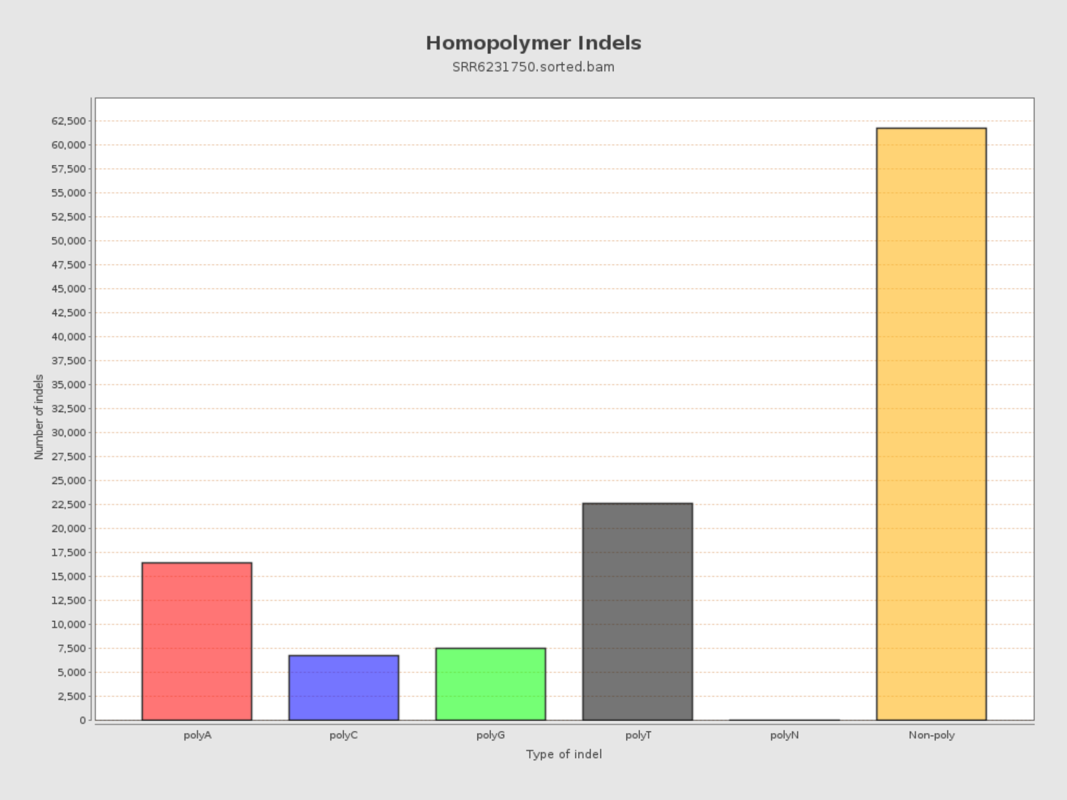
9. Results : Mapped Reads GC-content Distribution



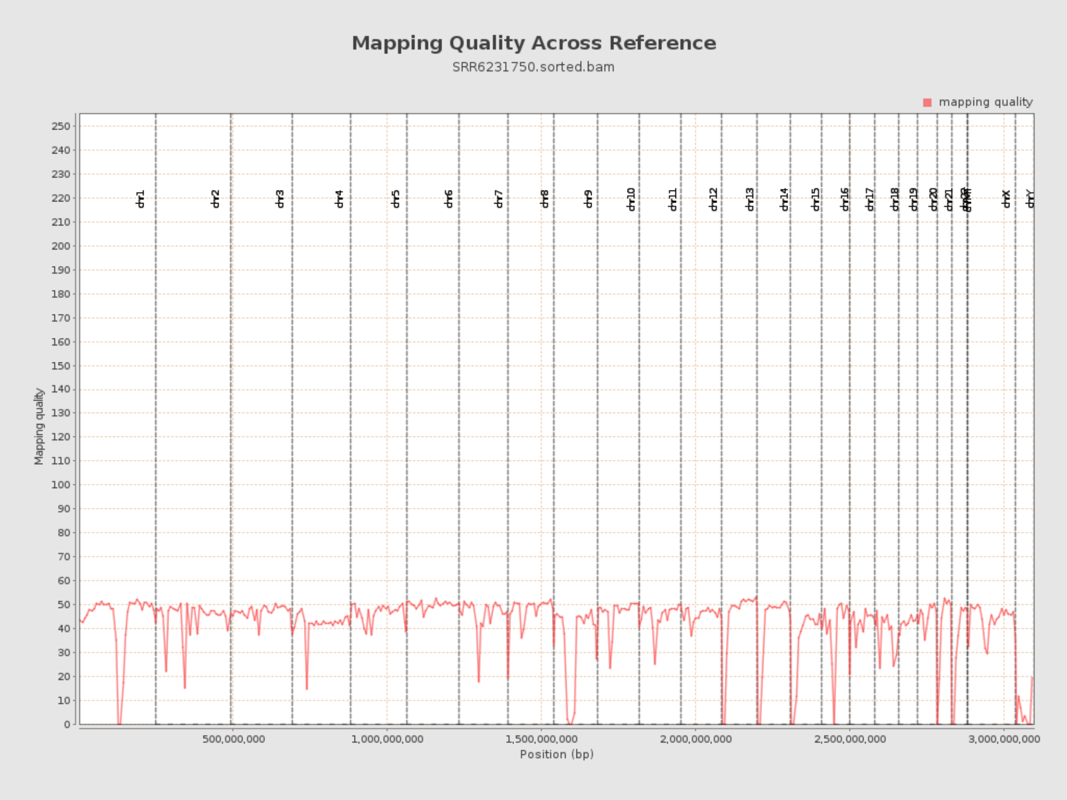
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram