Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 10:44:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008770.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_SRR6008770 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008770.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 10:44:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008770.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,680,662
Mapped reads	4,266,321 / 75.1%
Unmapped reads	1,414,341 / 24.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,525 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	973,199 / 17.13%
Duplication rate	15.21%
Clipped reads	2,136,291 / 37.61%

2.2. ACGT Content

Number/percentage of A's	75,638,836 / 27.34%
Number/percentage of C's	48,636,934 / 17.58%
Number/percentage of T's	90,422,769 / 32.68%
Number/percentage of G's	61,905,290 / 22.37%
Number/percentage of N's	88,728 / 0.03%
GC Percentage	39.95%

2.3. Coverage

Mean	0.0894

Standard Deviation	0.892

2.4. Mapping Quality

Mean Mapping Quality	41.09

2.5. Mismatches and indels

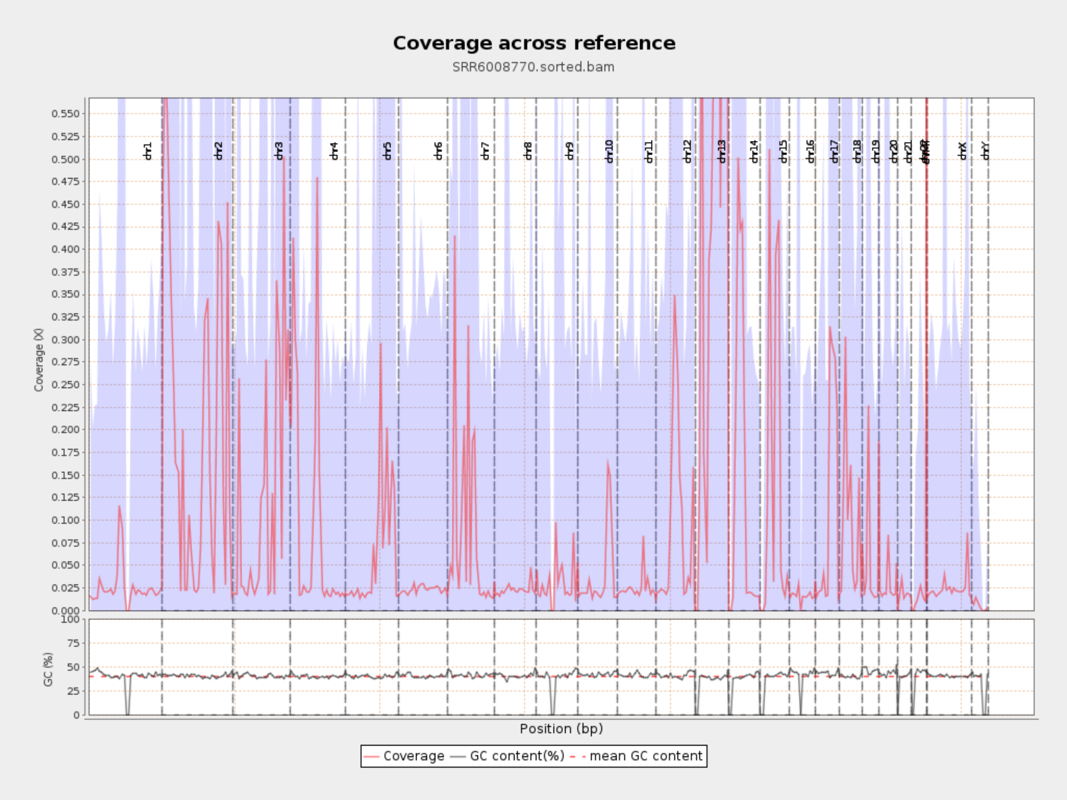
General error rate	0.77%
Mismatches	2,093,847
Insertions	19,662
Mapped reads with at least one insertion	0.46%
Deletions	66,110
Mapped reads with at least one deletion	1.54%
Homopolymer indels	48.73%

2.6. Chromosome stats

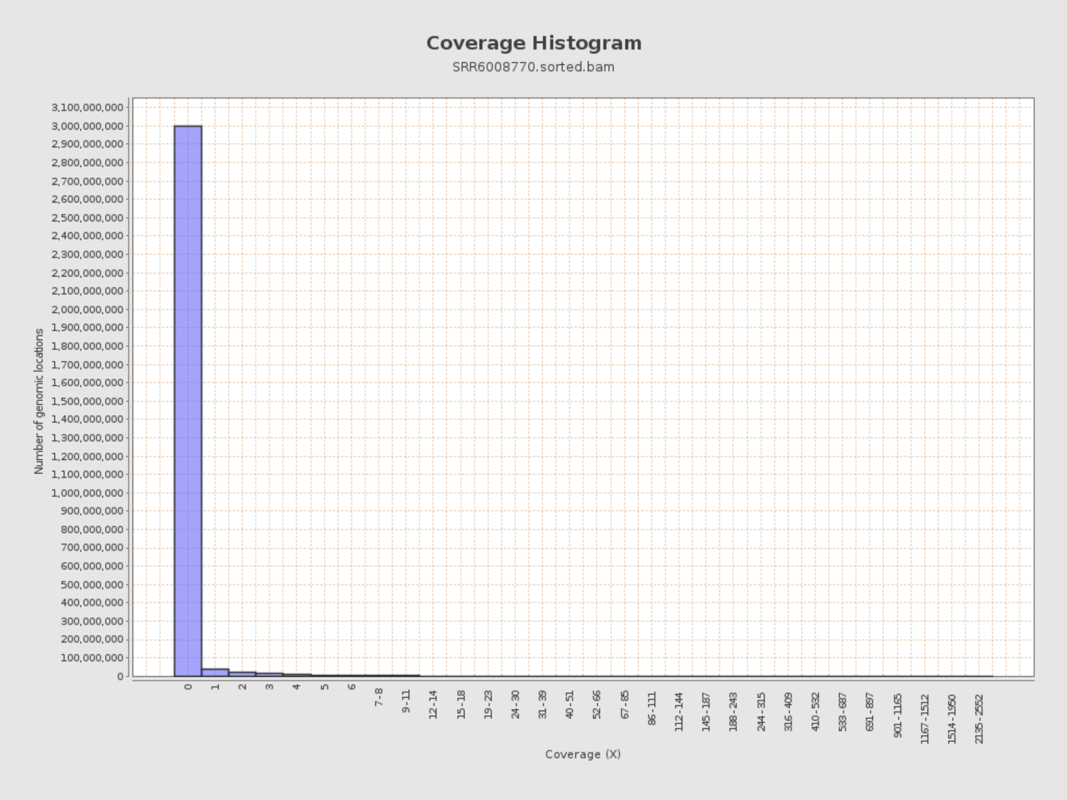
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6297700	0.0253	0.3942
chr2	243199373	48867556	0.2009	1.19
chr3	198022430	23793689	0.1202	0.8039
chr4	191154276	18452833	0.0965	0.6971
chr5	180915260	11787161	0.0652	0.5804
chr6	171115067	4002128	0.0234	0.3586
chr7	159138663	14187356	0.0892	0.7178

chr8	146364022	3395233	0.0232	0.4227
chr9	141213431	4184154	0.0296	0.4623
chr10	135534747	5225384	0.0386	0.4416
chr11	135006516	3440776	0.0255	0.3464
chr12	133851895	12364319	0.0924	0.6869
chr13	115169878	62021874	0.5385	1.7415
chr14	107349540	15080728	0.1405	1.1158
chr15	102531392	14138377	0.1379	0.8565
chr16	90354753	1471452	0.0163	0.4448
chr17	81195210	9690940	0.1194	0.7943
chr18	78077248	7615874	0.0975	3.1232
chr19	59128983	3299009	0.0558	0.6633
chr20	63025520	1798822	0.0285	0.7462
chr21	48129895	876487	0.0182	0.2794
chr22	51304566	602398	0.0117	0.212
chrMT	16571	25370	1.531	2.8421
chrX	155270560	3878940	0.025	0.5161
chrY	59373566	299651	0.005	0.1254

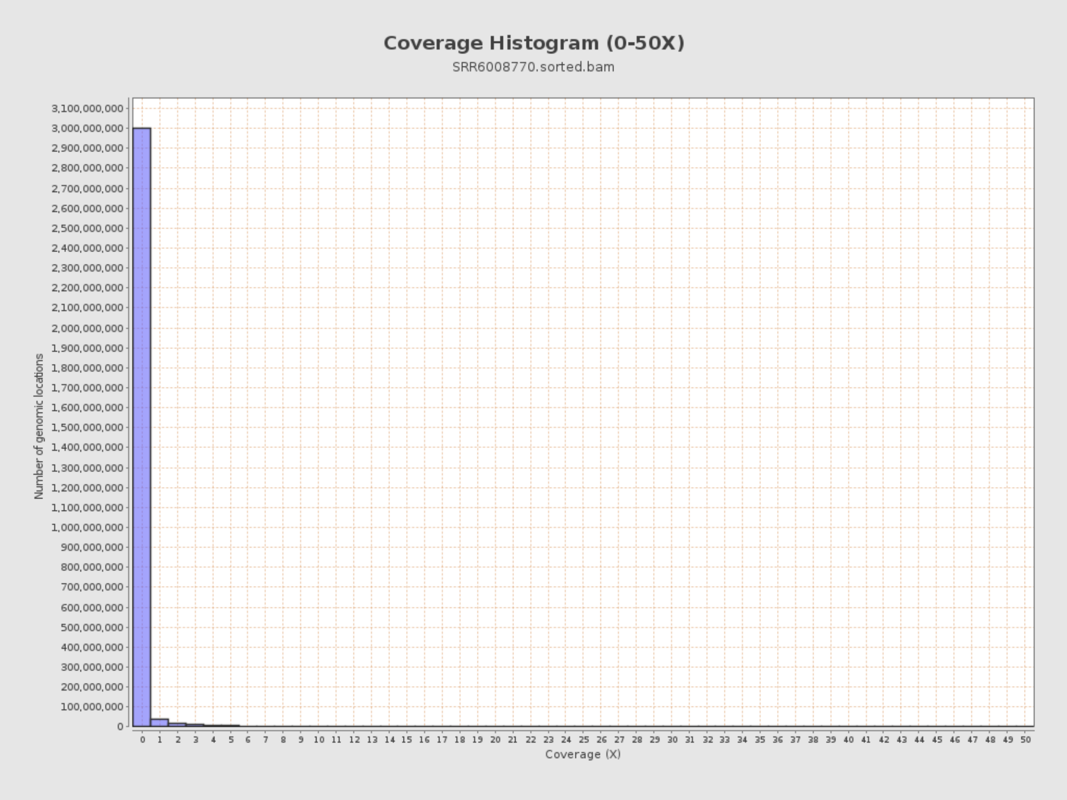
3. Results : Coverage across reference



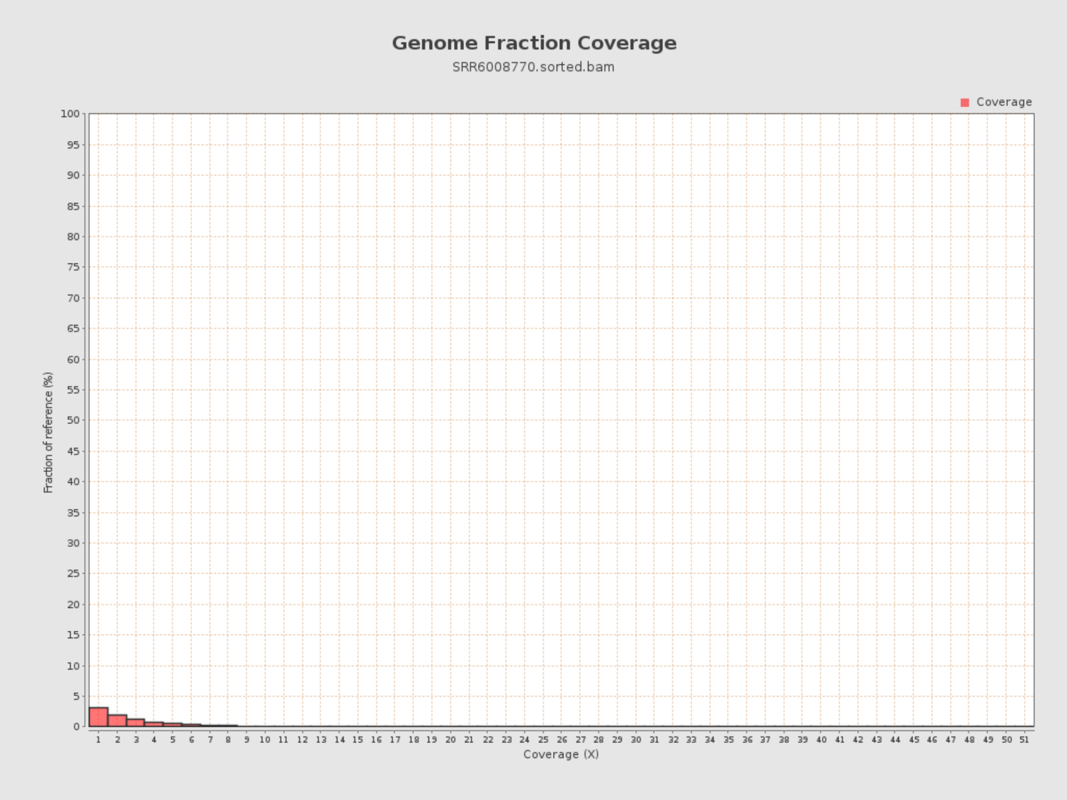
4. Results : Coverage Histogram



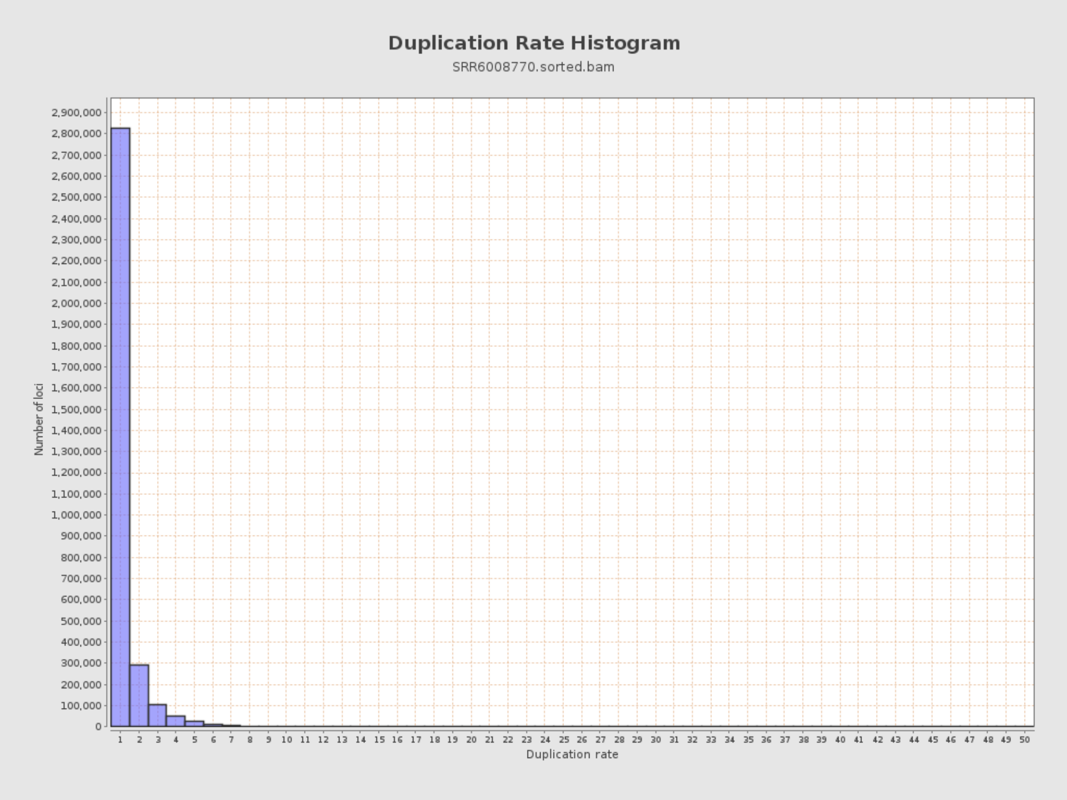
5. Results : Coverage Histogram (0-50X)



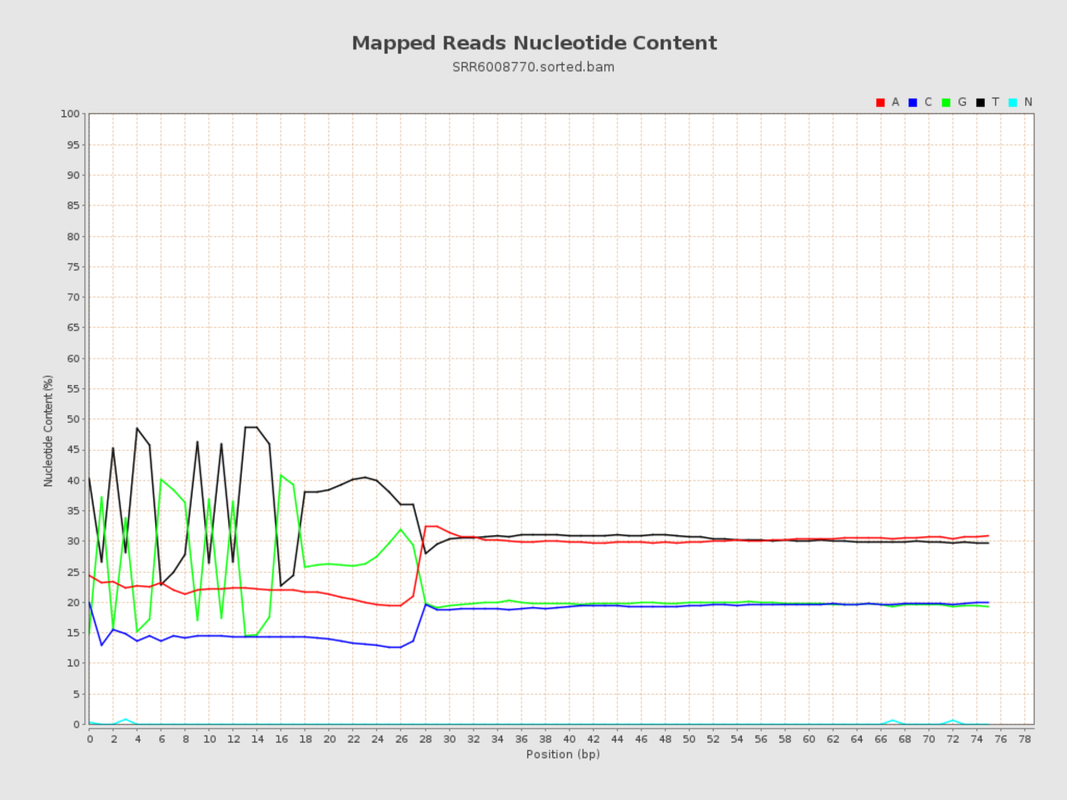
6. Results : Genome Fraction Coverage



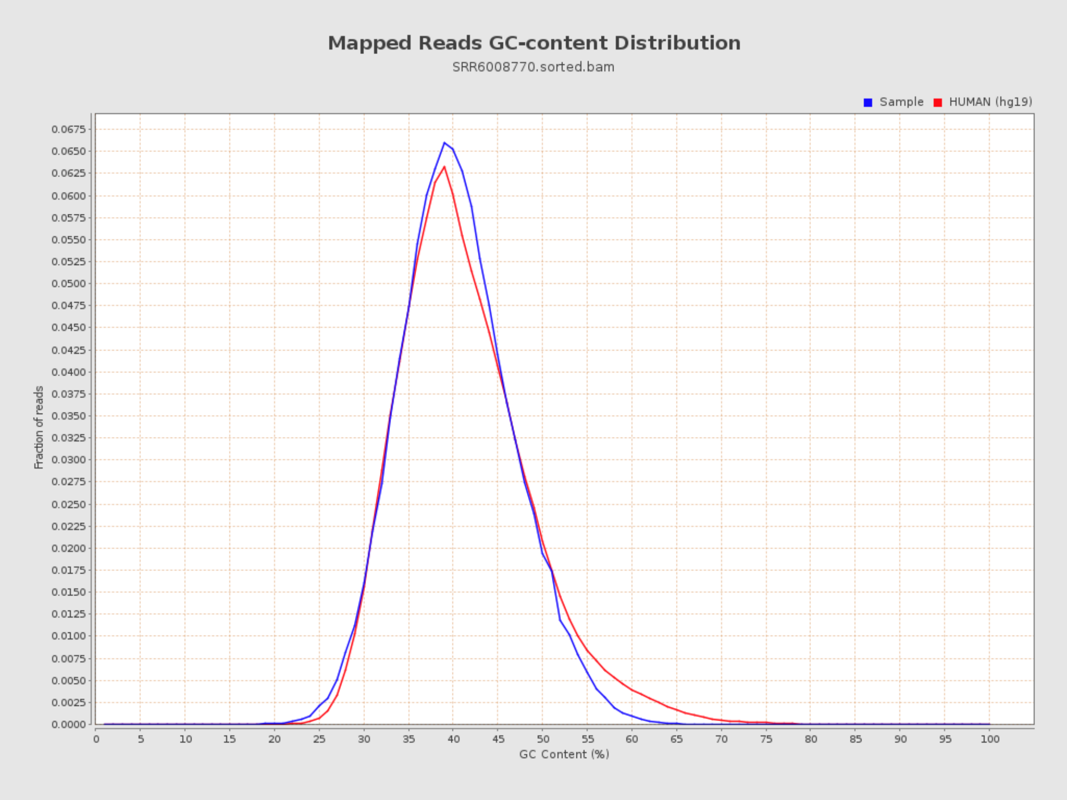
7. Results : Duplication Rate Histogram



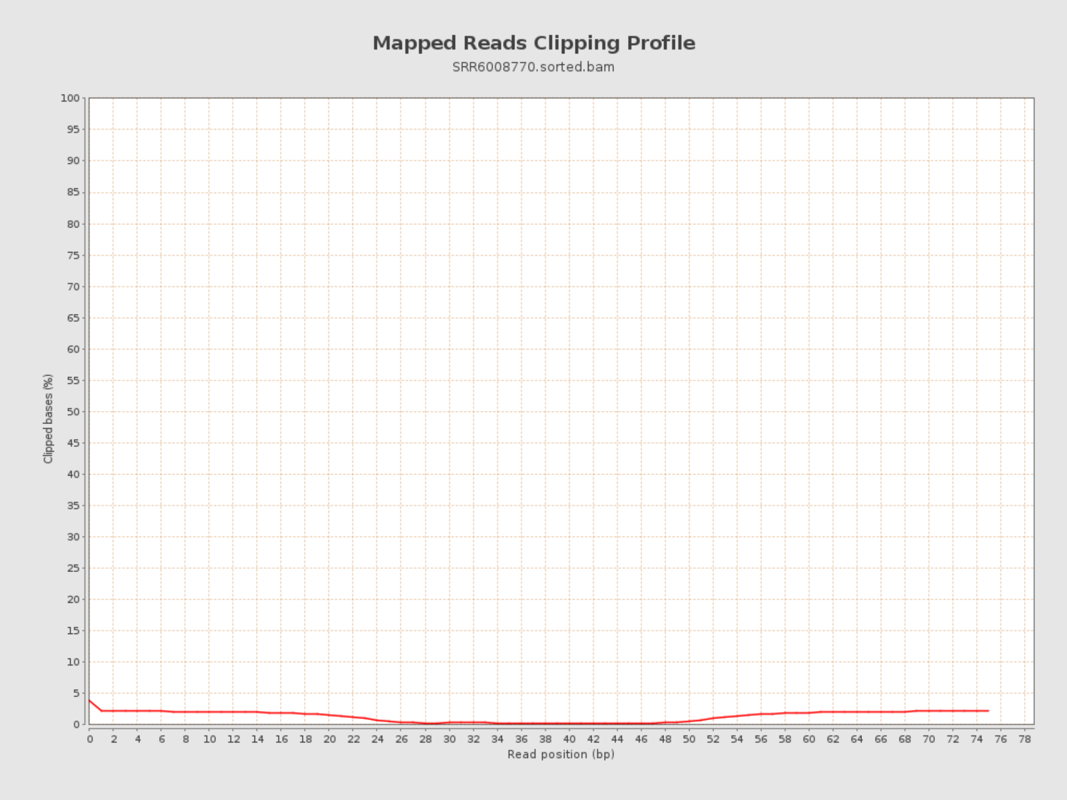
8. Results : Mapped Reads Nucleotide Content



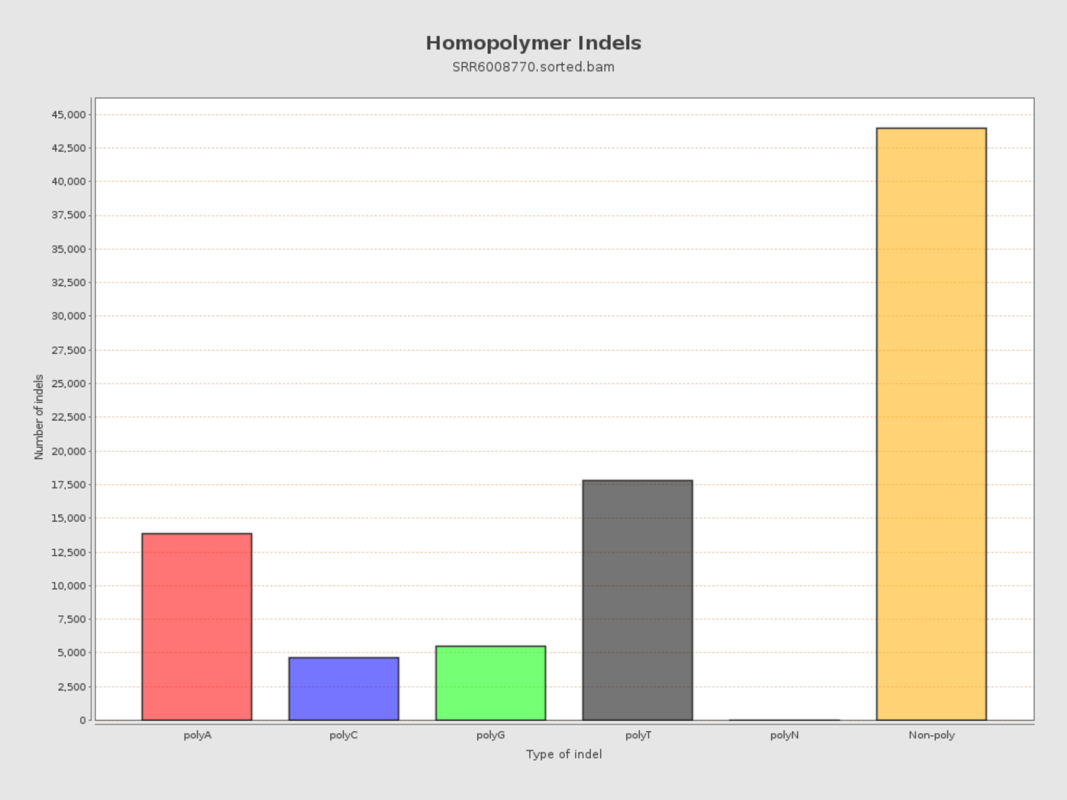
9. Results : Mapped Reads GC-content Distribution



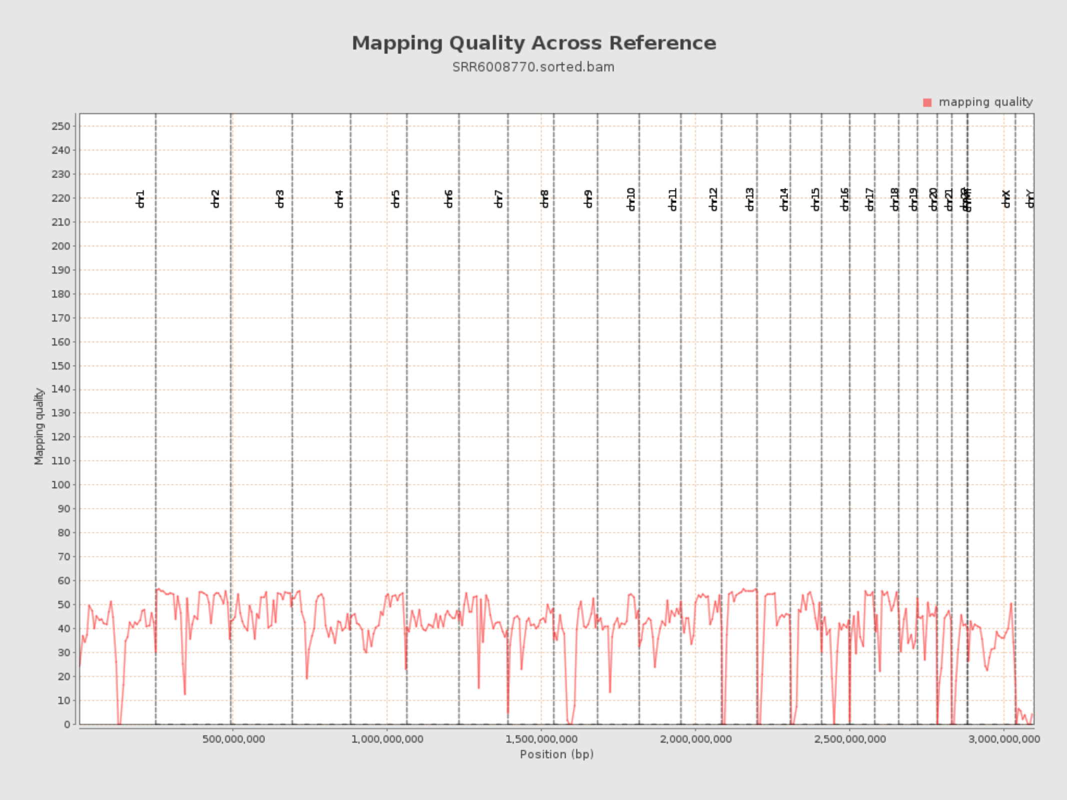
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram