Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:13:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008670.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_SRR6008670 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008670.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:13:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008670.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,562,713
Mapped reads	1,406,689 / 90.02%
Unmapped reads	156,024 / 9.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,418 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	46,120 / 2.95%
Duplication rate	2.52%
Clipped reads	584,855 / 37.43%

2.2. ACGT Content

Number/percentage of A's	27,307,820 / 28.96%
Number/percentage of C's	17,376,639 / 18.43%
Number/percentage of T's	29,444,363 / 31.23%
Number/percentage of G's	20,150,277 / 21.37%
Number/percentage of N's	16,905 / 0.02%
GC Percentage	39.8%

2.3. Coverage

Mean	0.0305

Standard Deviation	0.2867

2.4. Mapping Quality

Mean Mapping Quality	44.67

2.5. Mismatches and indels

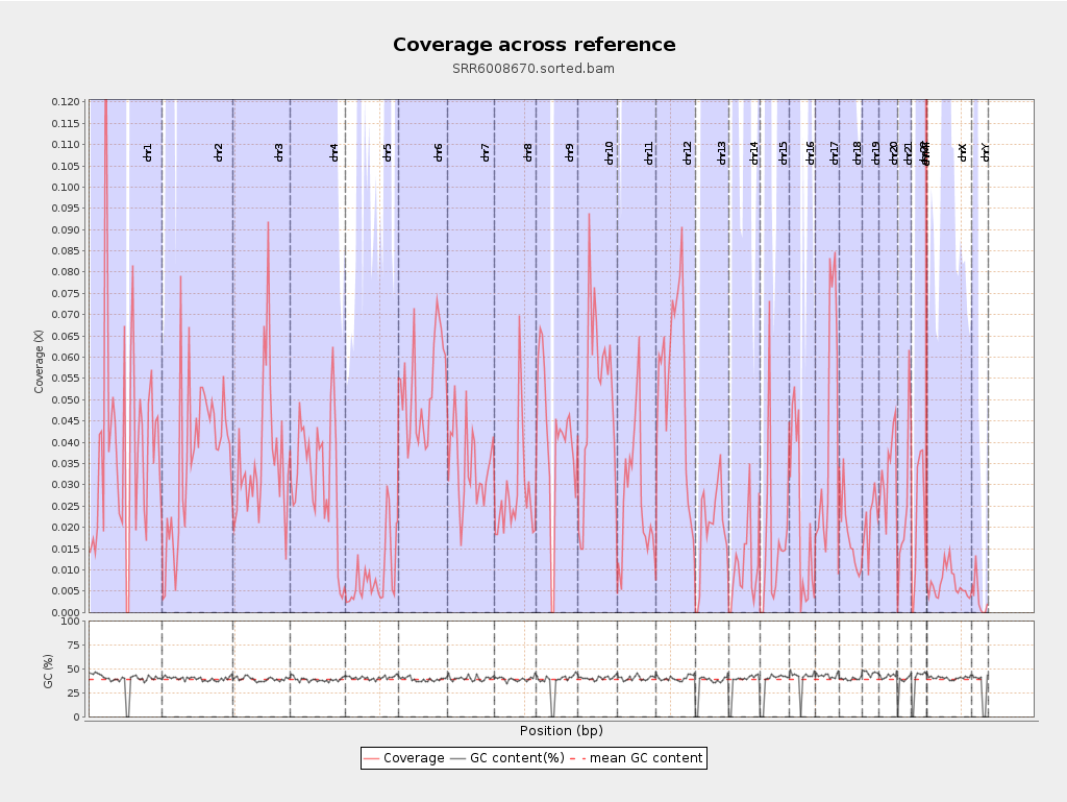
General error rate	0.75%
Mismatches	694,181
Insertions	8,097
Mapped reads with at least one insertion	0.57%
Deletions	30,301
Mapped reads with at least one deletion	2.13%
Homopolymer indels	46.76%

2.6. Chromosome stats

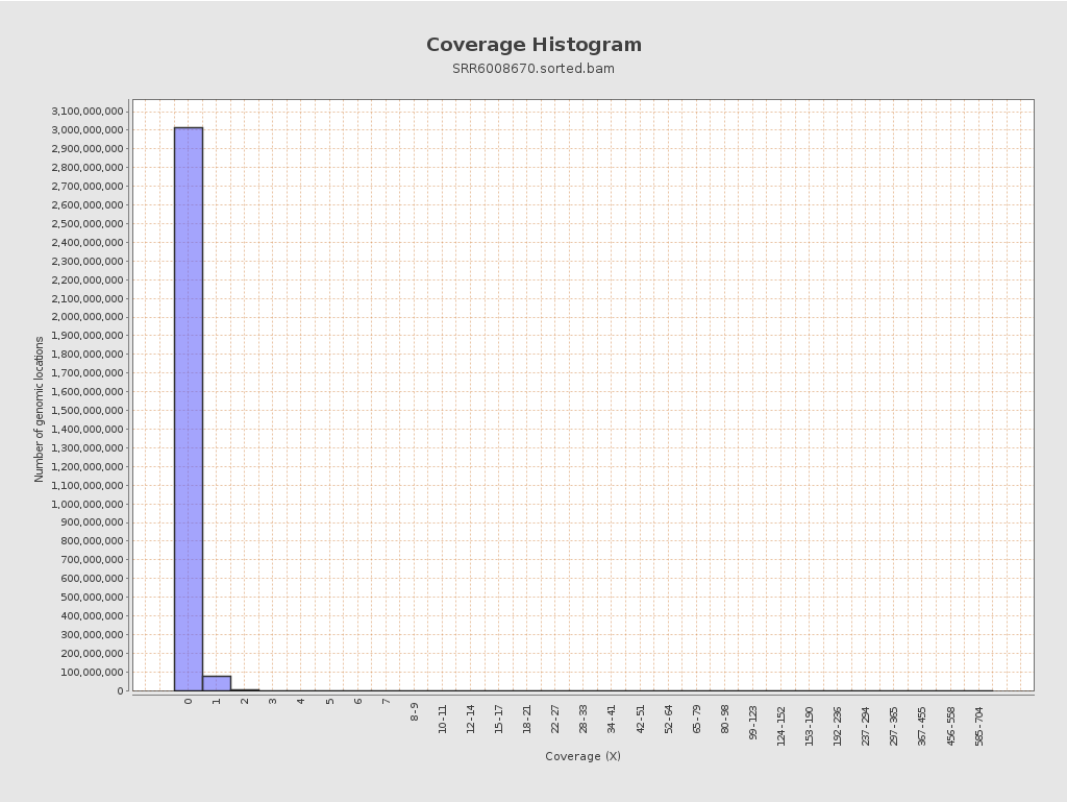
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9624330	0.0386	0.4352
chr2	243199373	8950960	0.0368	0.3034
chr3	198022430	7172862	0.0362	0.2158
chr4	191154276	5948463	0.0311	0.2003
chr5	180915260	1580723	0.0087	0.1058
chr6	171115067	9047923	0.0529	0.3046
chr7	159138663	5557750	0.0349	0.3537

chr8	146364022	4025450	0.0275	0.4448
chr9	141213431	5766763	0.0408	0.2947
chr10	135534747	6822286	0.0503	0.4873
chr11	135006516	3671155	0.0272	0.22
chr12	133851895	7253566	0.0542	0.2543
chr13	115169878	2263840	0.0197	0.1499
chr14	107349540	1095053	0.0102	0.126
chr15	102531392	1735306	0.0169	0.1415
chr16	90354753	1978936	0.0219	0.1883
chr17	81195210	3371541	0.0415	0.2295
chr18	78077248	1402387	0.018	0.4049
chr19	59128983	1275456	0.0216	0.302
chr20	63025520	2127294	0.0338	0.2011
chr21	48129895	1251739	0.026	0.1869
chr22	51304566	1110971	0.0217	0.1575
chrMT	16571	69185	4.1751	3.1426
chrX	155270560	1044521	0.0067	0.1156
chrY	59373566	197940	0.0033	0.1236

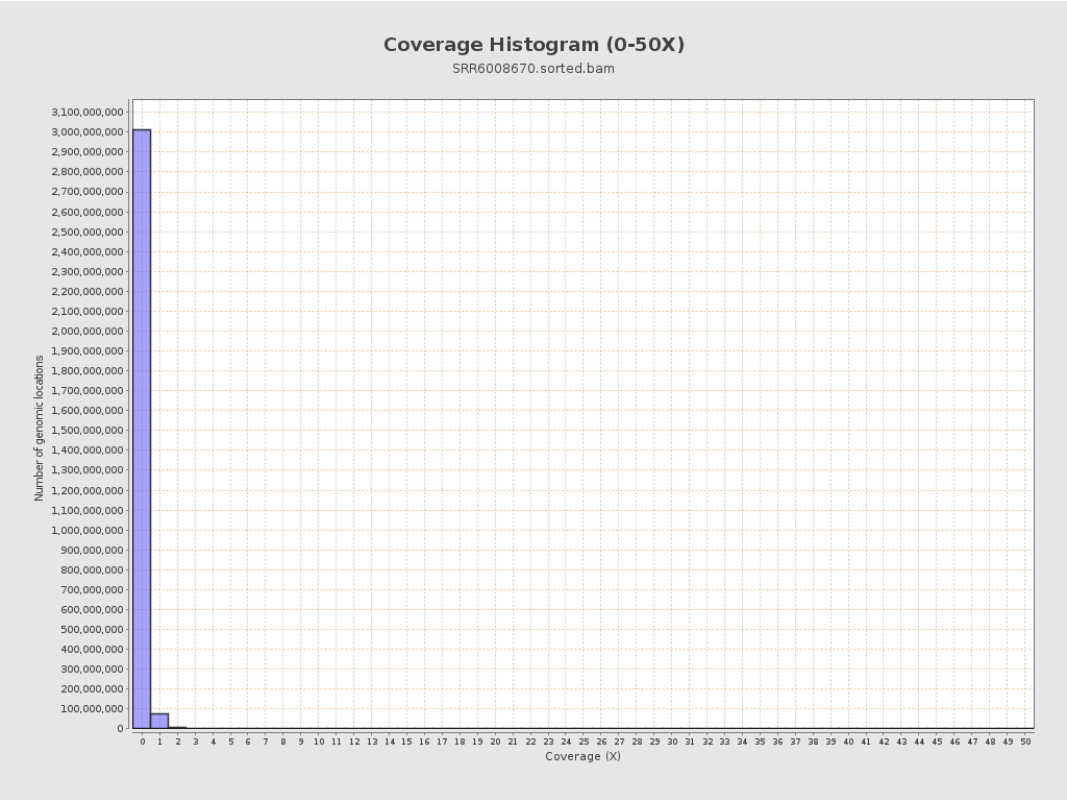
3. Results : Coverage across reference



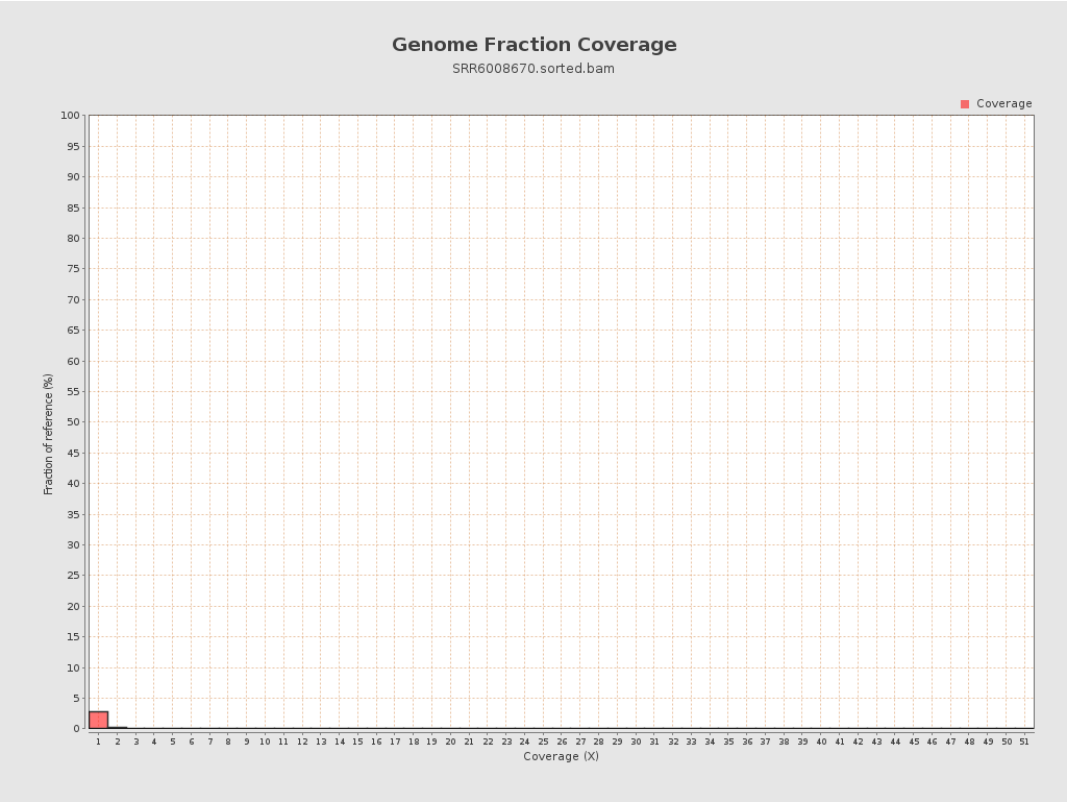
4. Results : Coverage Histogram



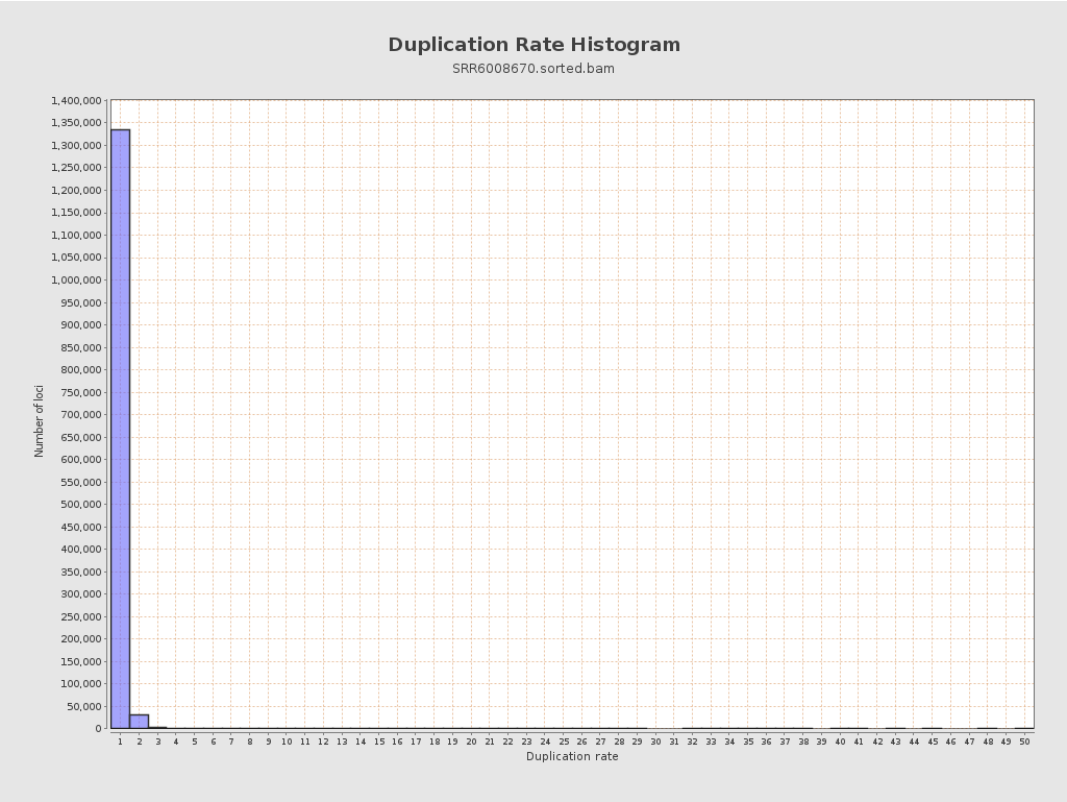
5. Results : Coverage Histogram (0-50X)



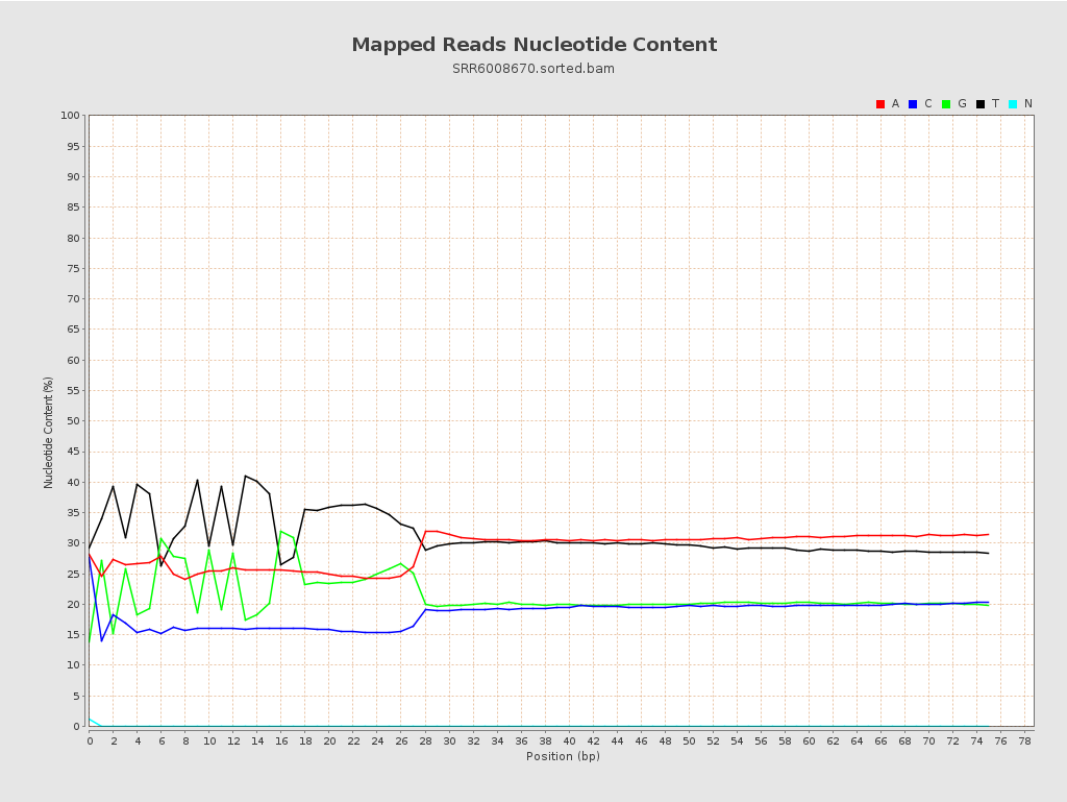
6. Results : Genome Fraction Coverage



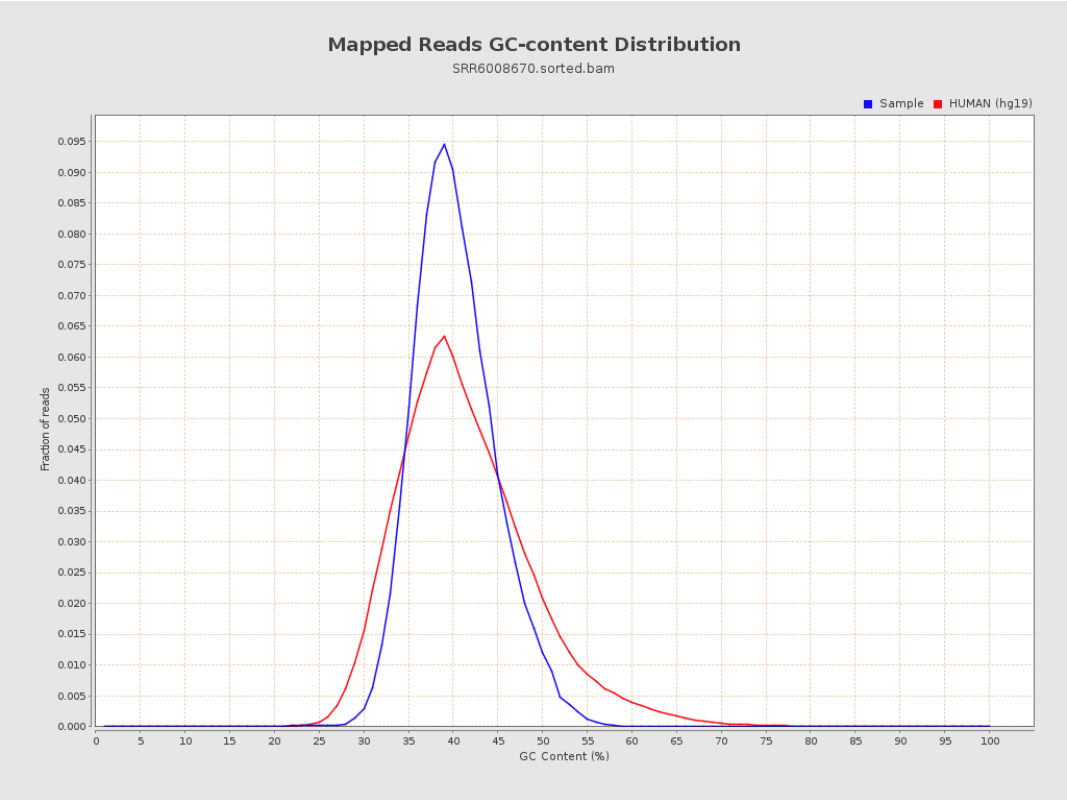
7. Results : Duplication Rate Histogram



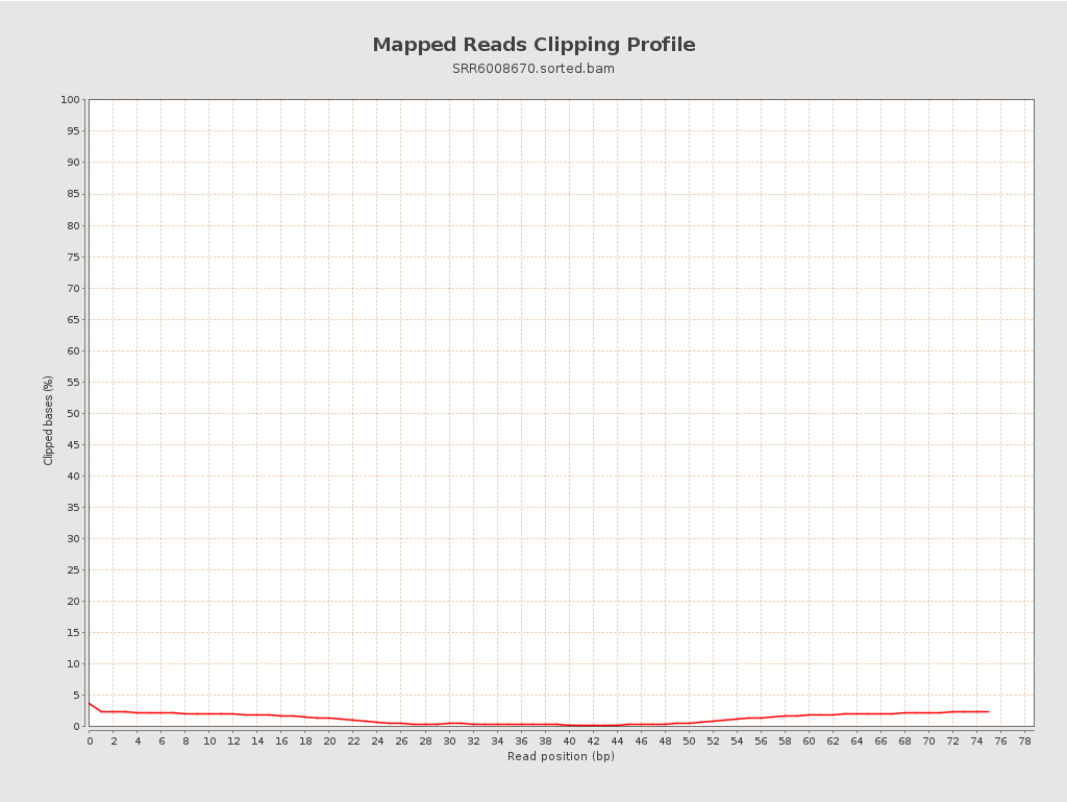
8. Results : Mapped Reads Nucleotide Content



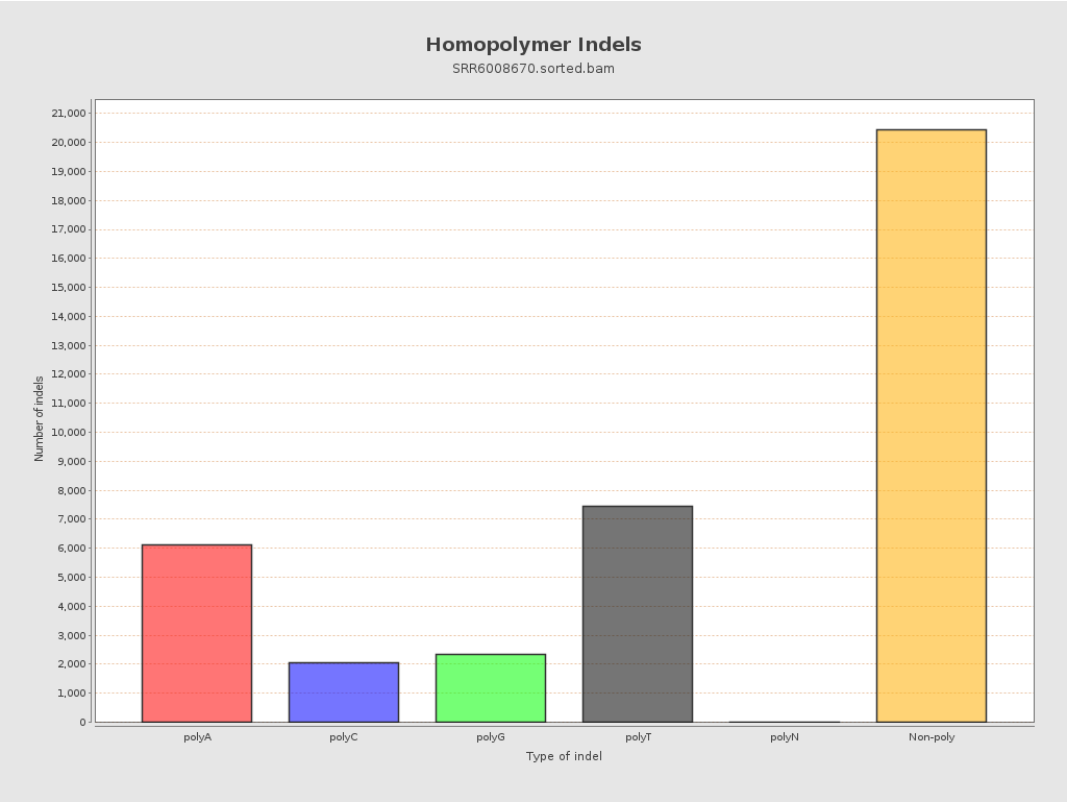
9. Results : Mapped Reads GC-content Distribution



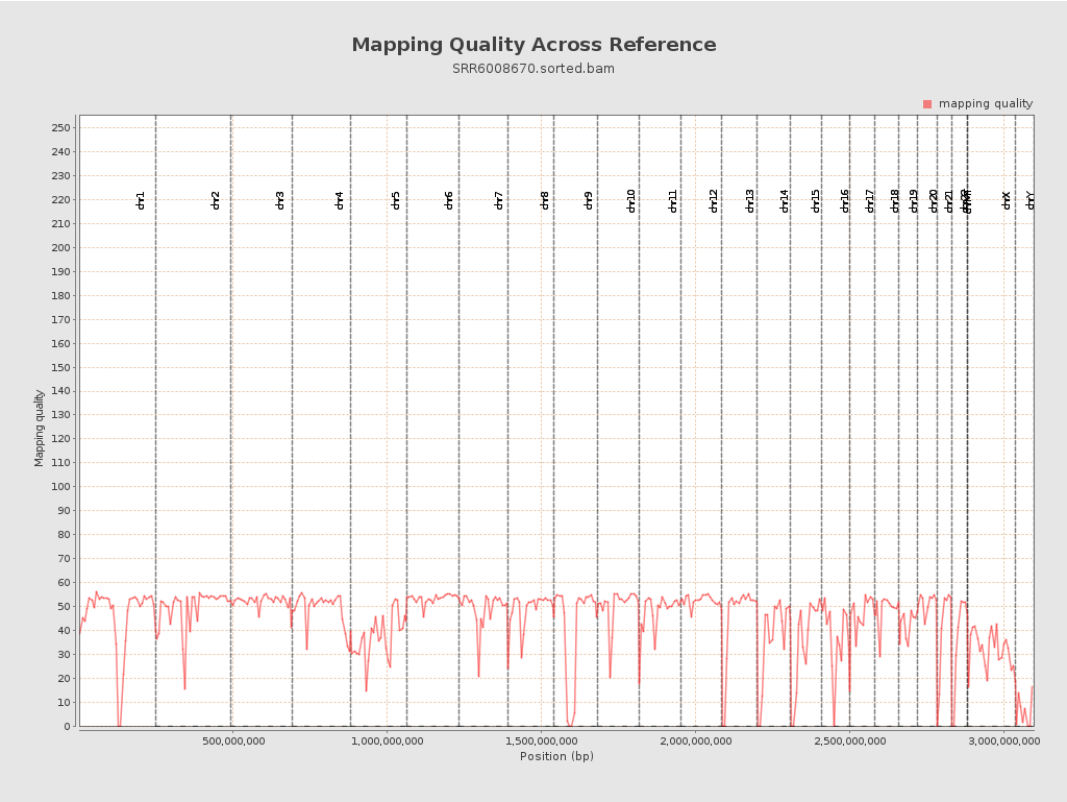
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram