Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:36:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008678.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_SRR6008678 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008678.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:36:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008678.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,102,839
Mapped reads	969,623 / 87.92%
Unmapped reads	133,216 / 12.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,376 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	29,300 / 2.66%
Duplication rate	2.31%
Clipped reads	498,257 / 45.18%

2.2. ACGT Content

Number/percentage of A's	17,588,953 / 28%
Number/percentage of C's	11,352,169 / 18.07%
Number/percentage of T's	19,779,354 / 31.49%
Number/percentage of G's	14,082,920 / 22.42%
Number/percentage of N's	10,994 / 0.02%
GC Percentage	40.49%

2.3. Coverage

Mean	0.0203

Standard Deviation	0.2221

2.4. Mapping Quality

Mean Mapping Quality	45.52

2.5. Mismatches and indels

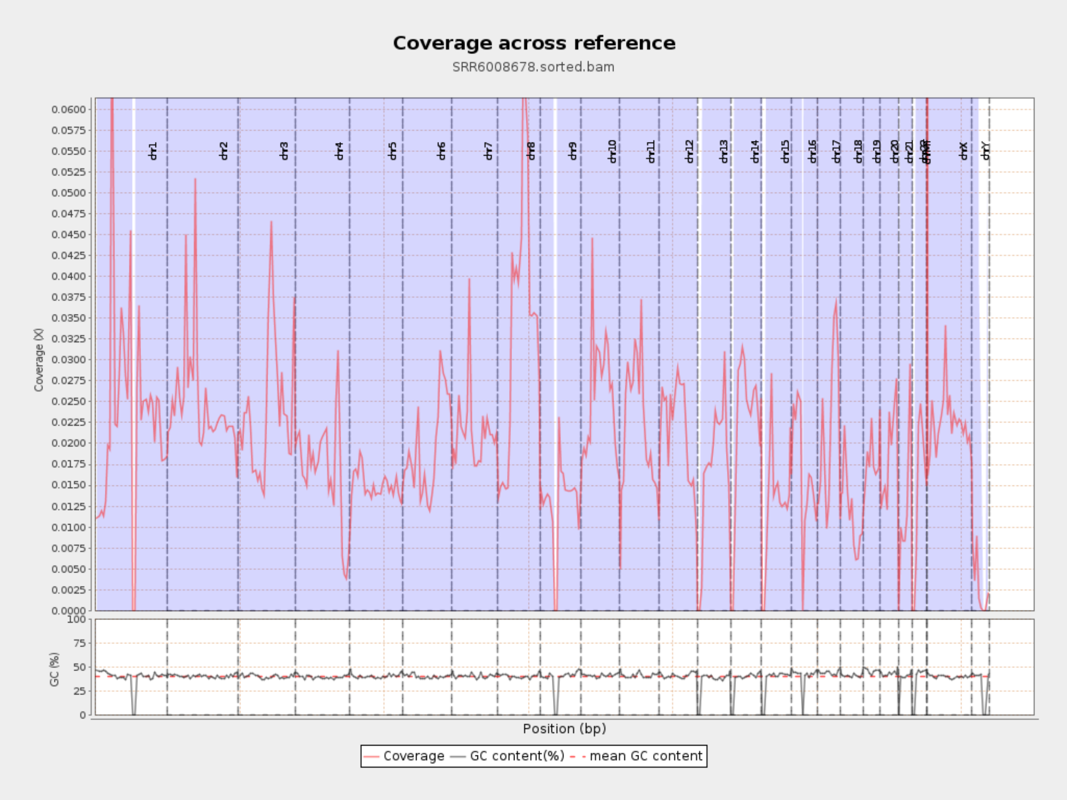
General error rate	0.76%
Mismatches	466,935
Insertions	5,307
Mapped reads with at least one insertion	0.54%
Deletions	18,125
Mapped reads with at least one deletion	1.85%
Homopolymer indels	46.99%

2.6. Chromosome stats

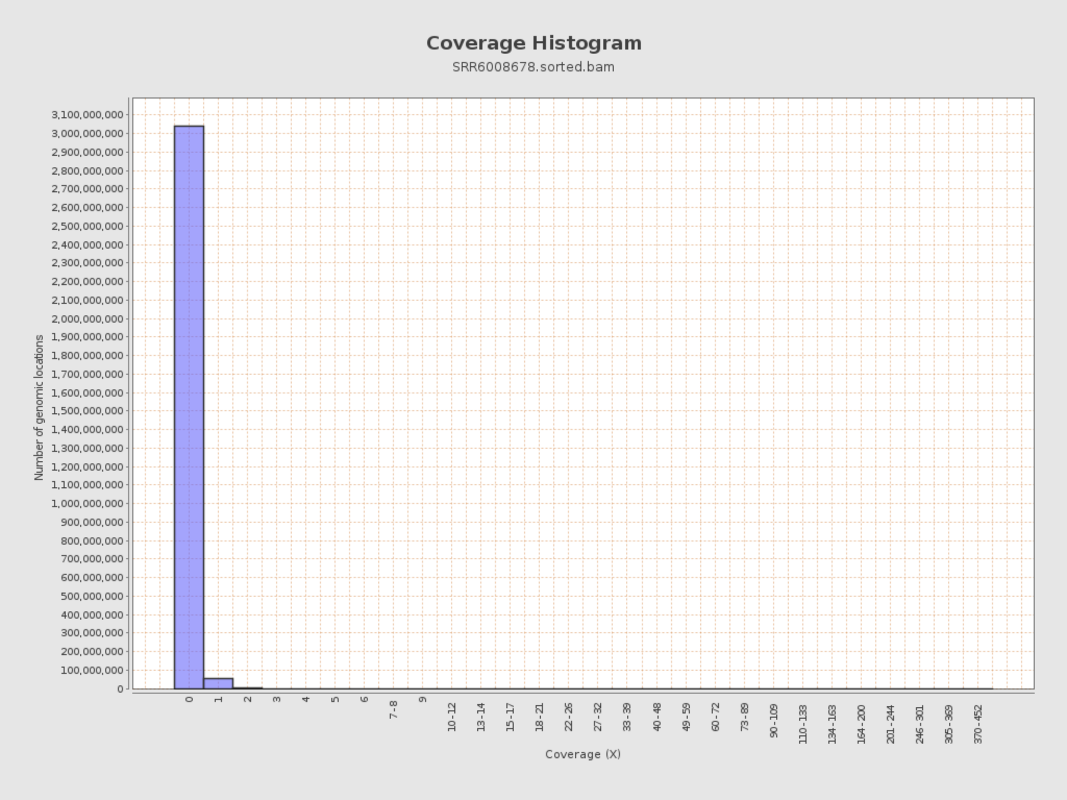
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5835846	0.0234	0.4067
chr2	243199373	6089473	0.025	0.243
chr3	198022430	4766456	0.0241	0.1659
chr4	191154276	3241824	0.017	0.142
chr5	180915260	2720281	0.015	0.1303
chr6	171115067	3321287	0.0194	0.1617
chr7	159138663	3419254	0.0215	0.2731

chr8	146364022	5093086	0.0348	0.3042
chr9	141213431	1813053	0.0128	0.1806
chr10	135534747	3487288	0.0257	0.238
chr11	135006516	3044377	0.0225	0.2444
chr12	133851895	2946750	0.022	0.1579
chr13	115169878	1937322	0.0168	0.1364
chr14	107349540	2354373	0.0219	0.1602
chr15	102531392	1310098	0.0128	0.1196
chr16	90354753	1473659	0.0163	0.1473
chr17	81195210	1784653	0.022	0.1863
chr18	78077248	896915	0.0115	0.3121
chr19	59128983	1052172	0.0178	0.2568
chr20	63025520	1183046	0.0188	0.1481
chr21	48129895	615706	0.0128	0.1248
chr22	51304566	738311	0.0144	0.1259
chrMT	16571	51919	3.1331	2.4056
chrX	155270560	3498028	0.0225	0.1759
chrY	59373566	168584	0.0028	0.0839

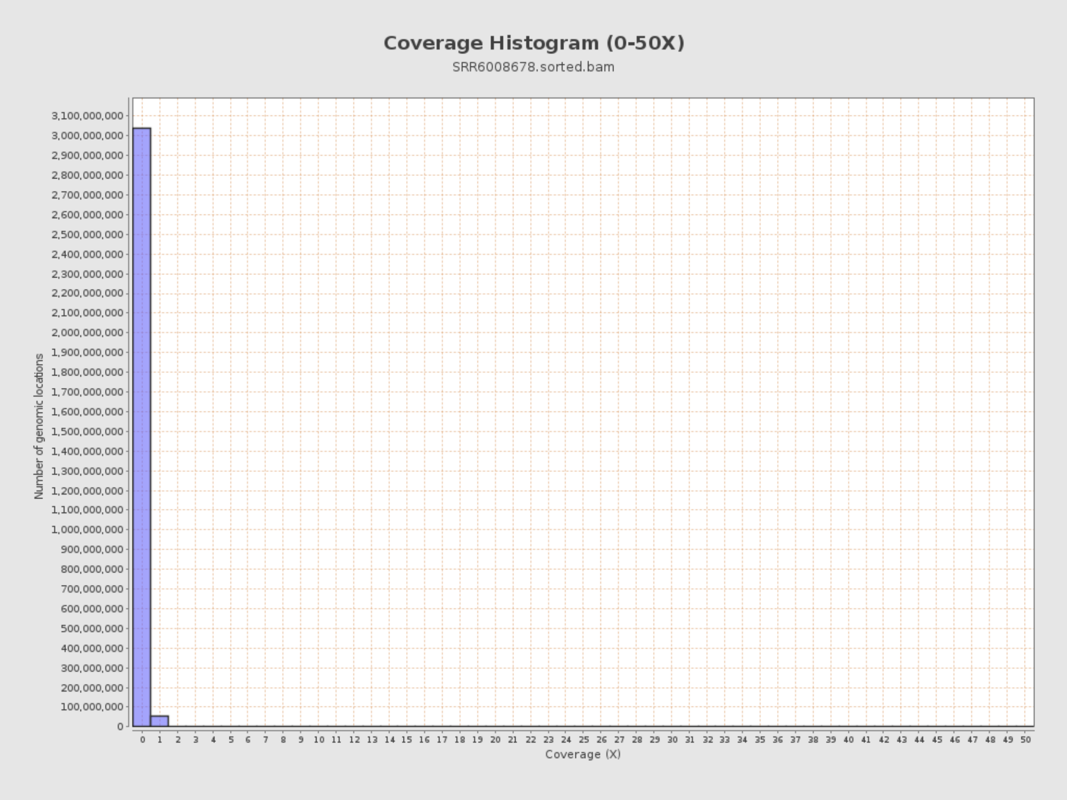
3. Results : Coverage across reference



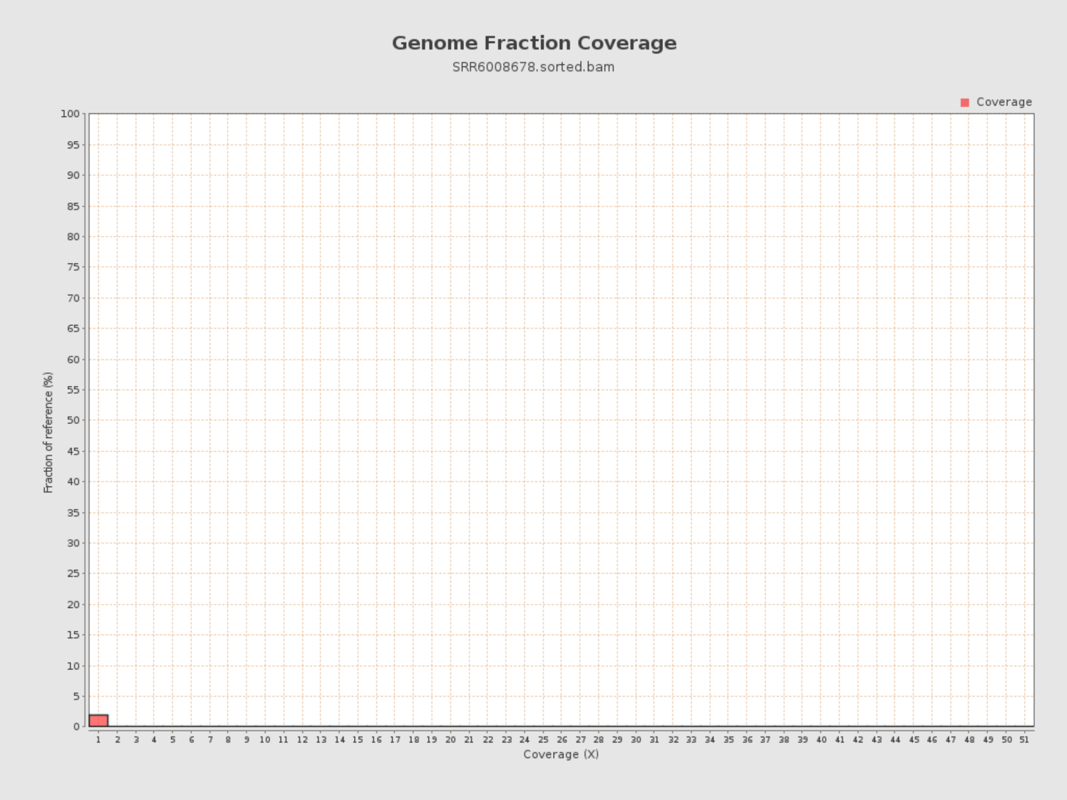
4. Results : Coverage Histogram



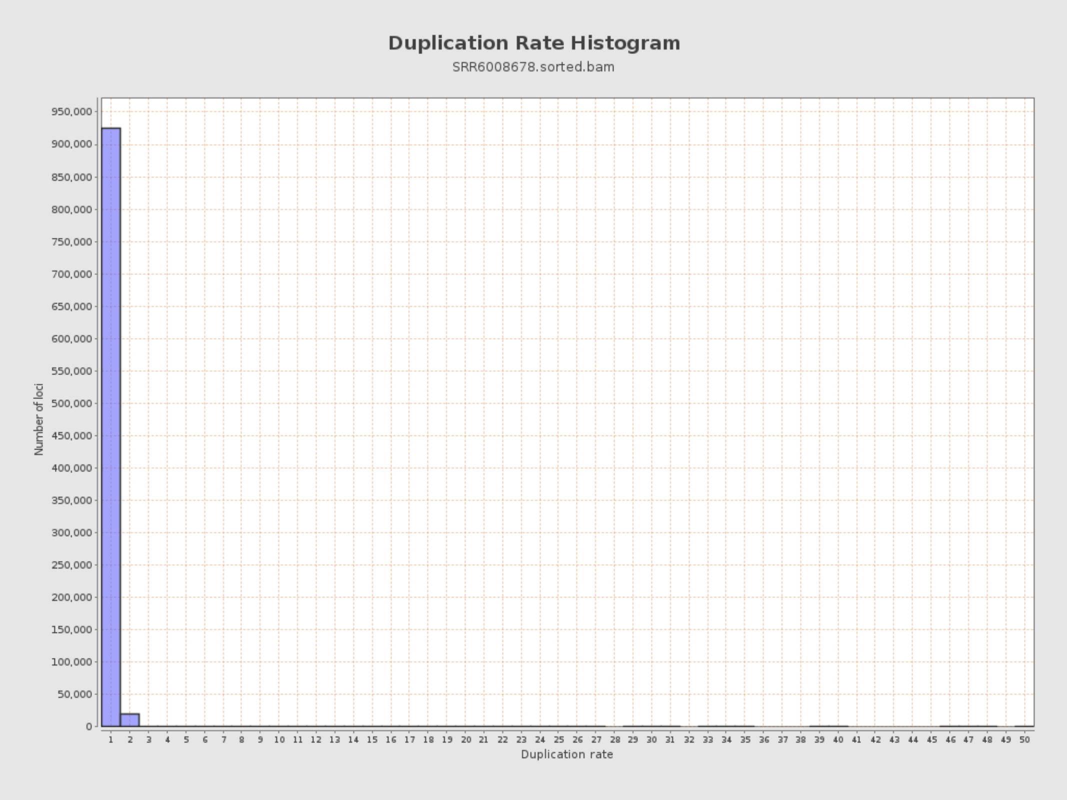
5. Results : Coverage Histogram (0-50X)



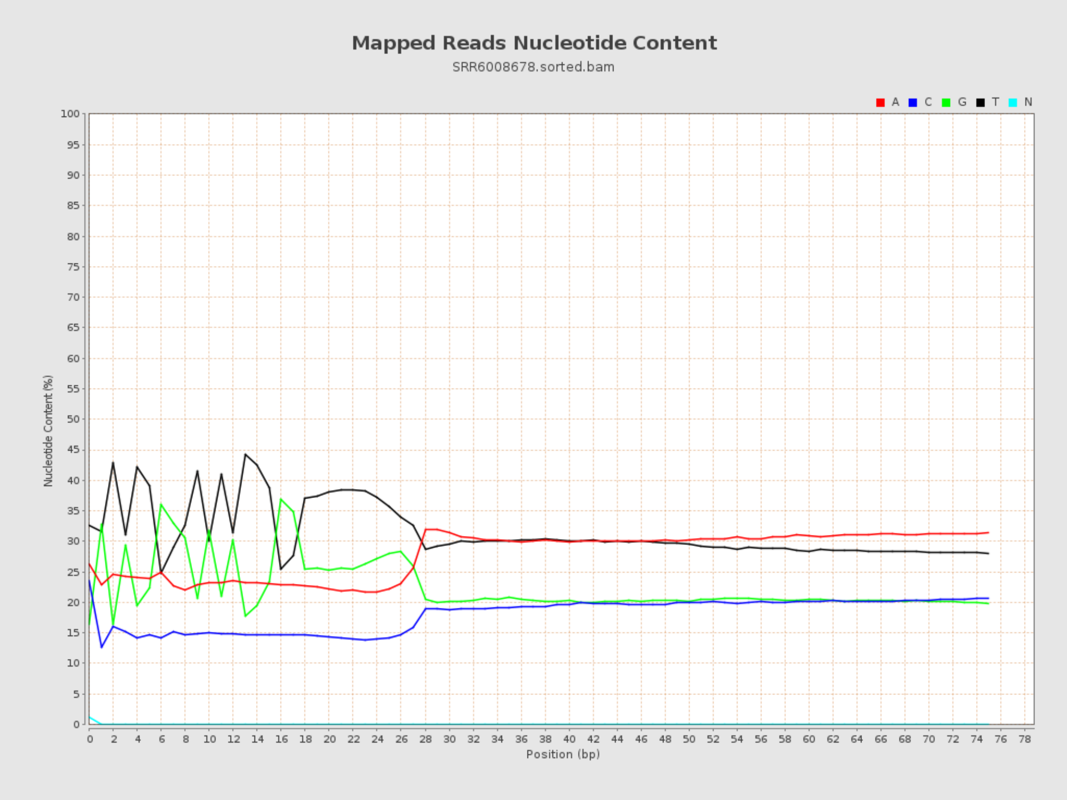
6. Results : Genome Fraction Coverage



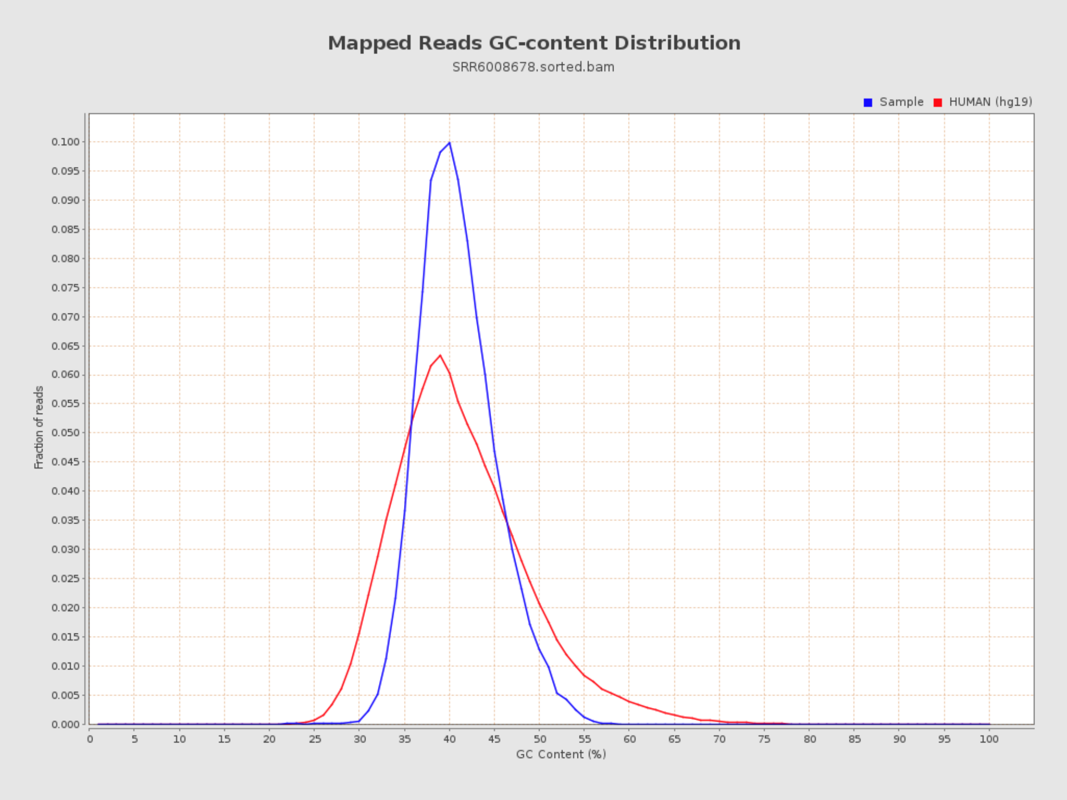
7. Results : Duplication Rate Histogram



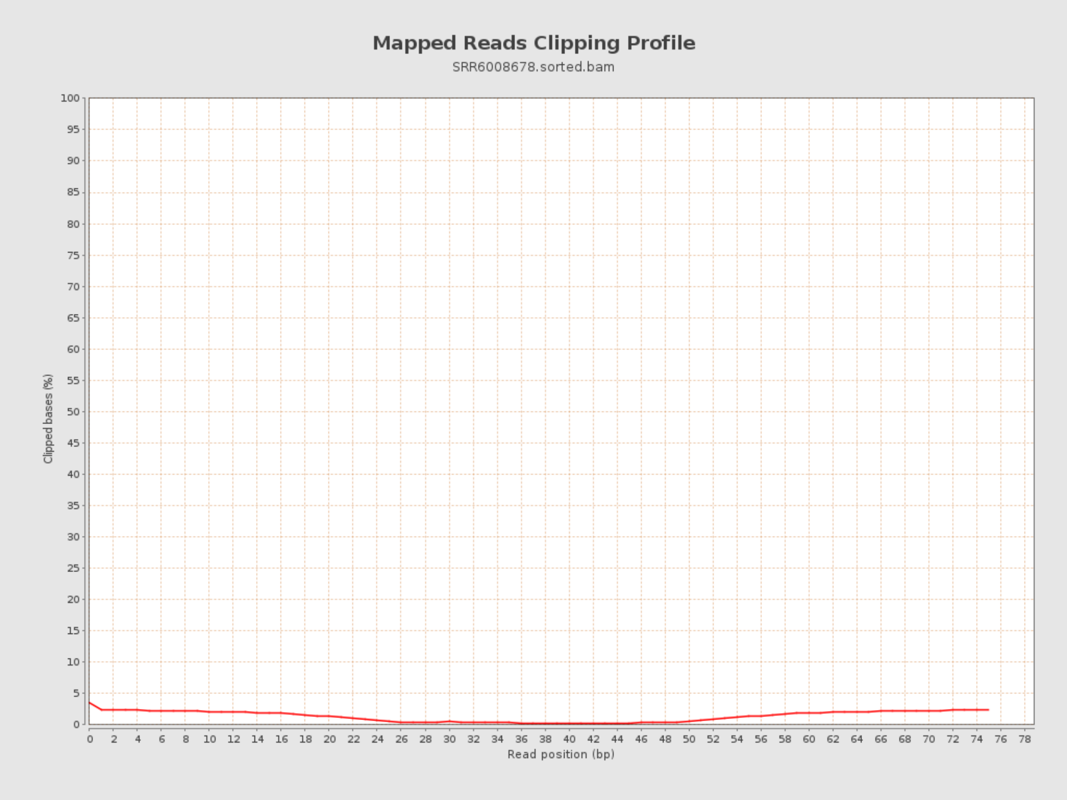
8. Results : Mapped Reads Nucleotide Content



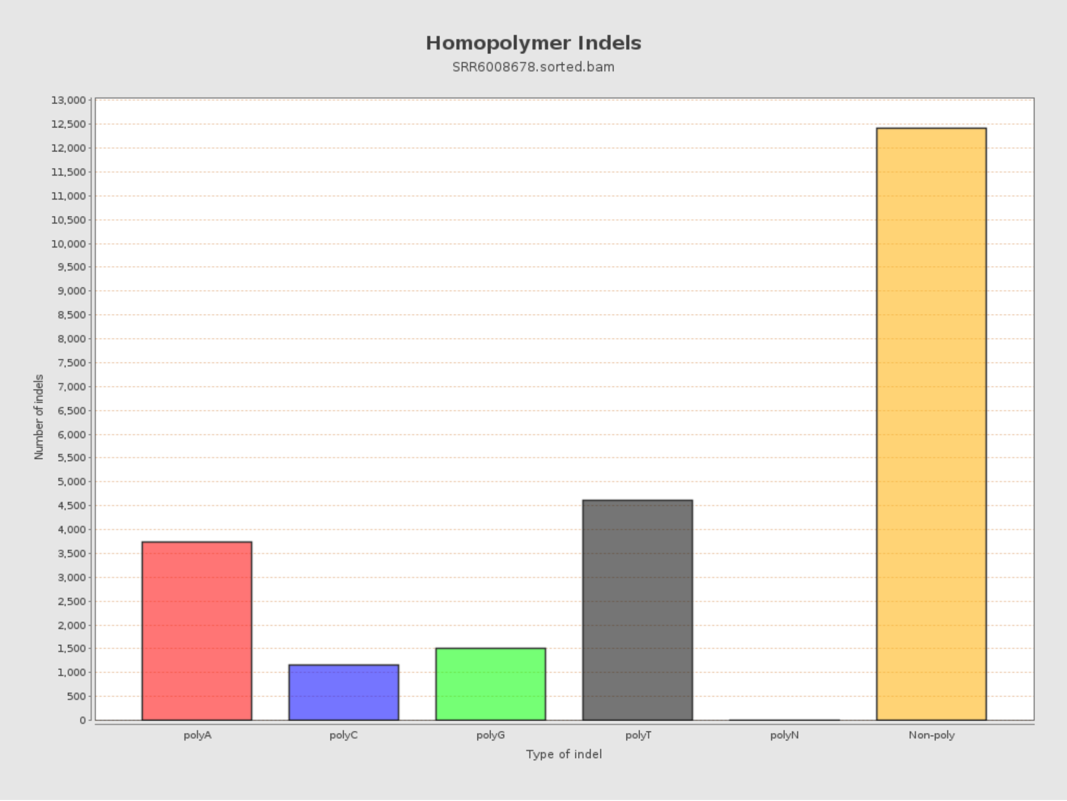
9. Results : Mapped Reads GC-content Distribution



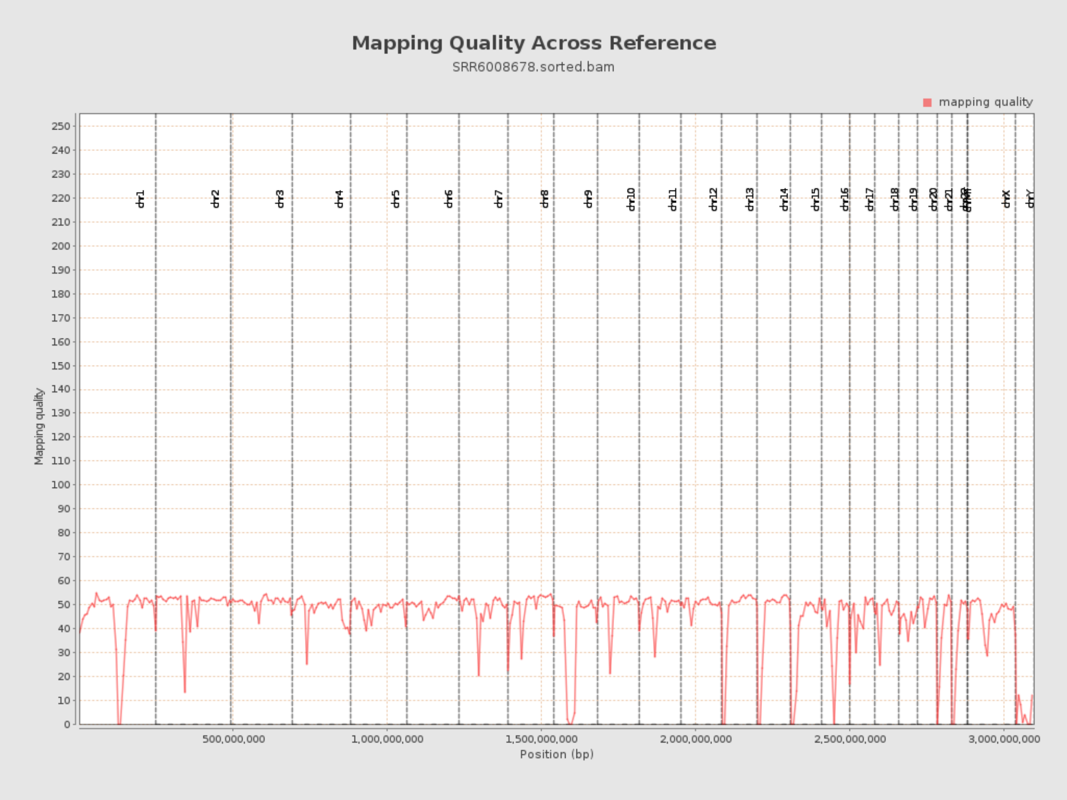
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram