Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 00:23:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004080.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_SRR6004080 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004080.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 00:23:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004080.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,526,377
Mapped reads	4,960,104 / 89.75%
Unmapped reads	566,273 / 10.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,442 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	297,123 / 5.38%
Duplication rate	4.36%
Clipped reads	2,001,388 / 36.22%

2.2. ACGT Content

Number/percentage of A's	95,536,800 / 28.29%
Number/percentage of C's	63,673,056 / 18.86%
Number/percentage of T's	106,985,516 / 31.68%
Number/percentage of G's	71,449,592 / 21.16%
Number/percentage of N's	46,393 / 0.01%
GC Percentage	40.01%

2.3. Coverage

Mean	0.1091

Standard Deviation	0.922

2.4. Mapping Quality

Mean Mapping Quality	46.49

2.5. Mismatches and indels

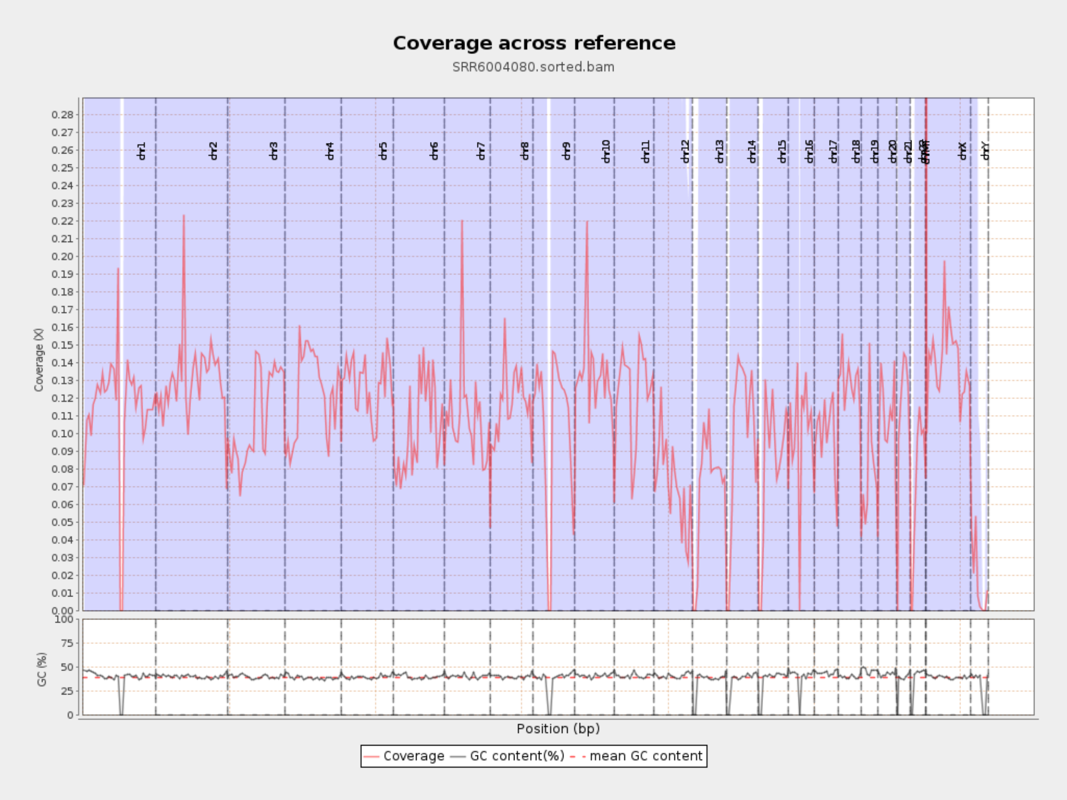
General error rate	0.98%
Mismatches	3,264,995
Insertions	29,079
Mapped reads with at least one insertion	0.58%
Deletions	85,705
Mapped reads with at least one deletion	1.71%
Homopolymer indels	47.23%

2.6. Chromosome stats

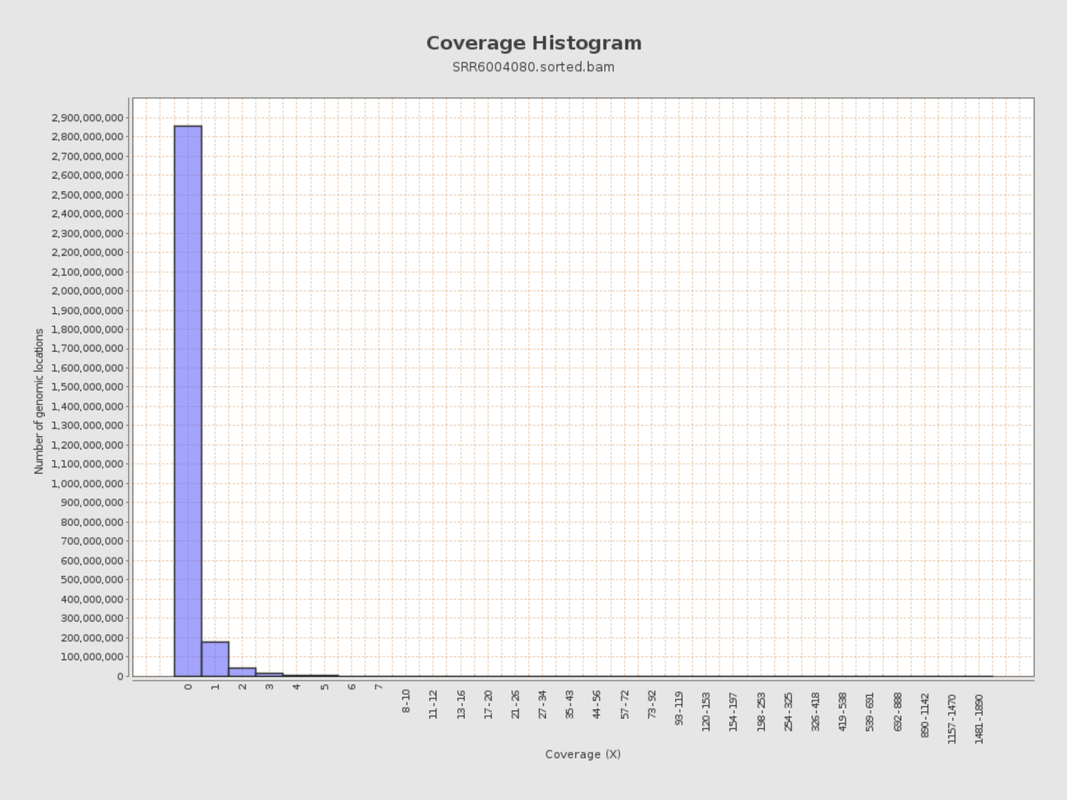
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28393793	0.1139	1.6761
chr2	243199373	31875534	0.1311	1.074
chr3	198022430	21425970	0.1082	0.4474
chr4	191154276	23472623	0.1228	0.5627
chr5	180915260	23042317	0.1274	0.4866
chr6	171115067	17751420	0.1037	0.5564
chr7	159138663	17446270	0.1096	1.4236

chr8	146364022	17077780	0.1167	0.9911
chr9	141213431	14793262	0.1048	0.9784
chr10	135534747	18163746	0.134	0.9187
chr11	135006516	16765327	0.1242	0.8593
chr12	133851895	9423171	0.0704	0.3887
chr13	115169878	8053272	0.0699	0.3432
chr14	107349540	10844931	0.101	0.534
chr15	102531392	8438791	0.0823	0.3804
chr16	90354753	8886855	0.0984	0.6105
chr17	81195210	8144723	0.1003	0.5329
chr18	78077248	10167702	0.1302	2.0486
chr19	59128983	4655698	0.0787	1.0702
chr20	63025520	7123129	0.113	0.483
chr21	48129895	5293494	0.11	0.5696
chr22	51304566	3705351	0.0722	0.3482
chrMT	16571	78169	4.7172	3.8218
chrX	155270560	21828964	0.1406	0.621
chrY	59373566	980947	0.0165	0.3926

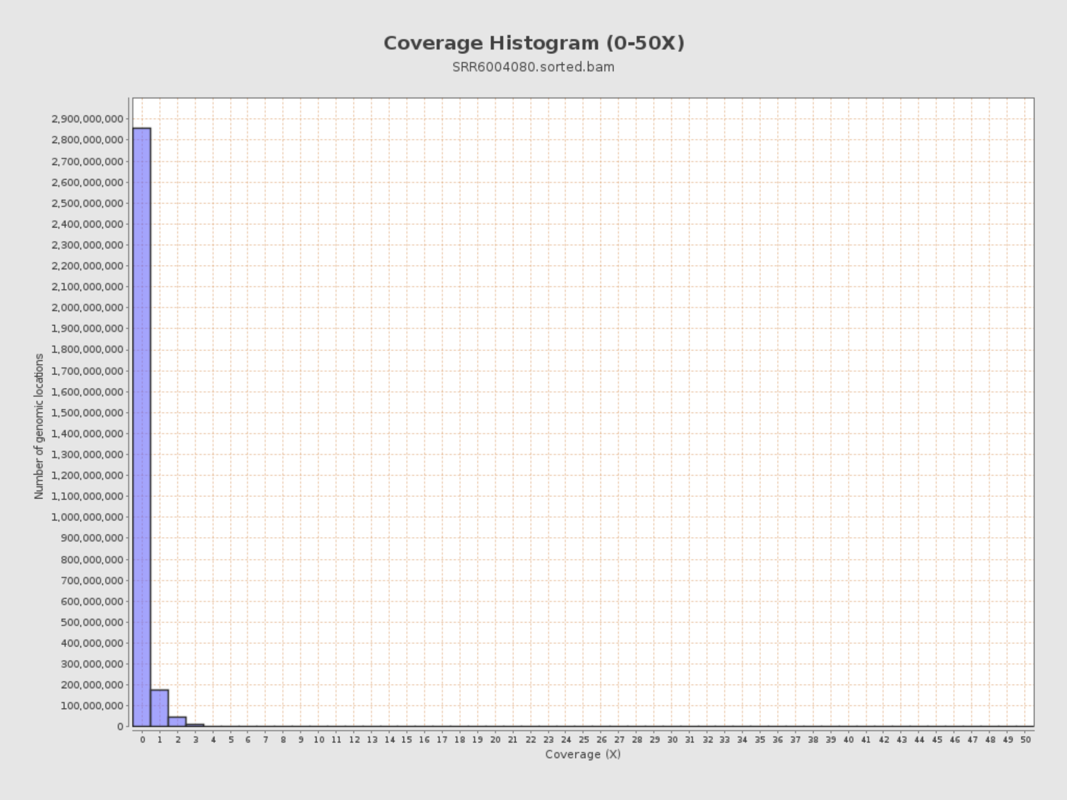
3. Results : Coverage across reference



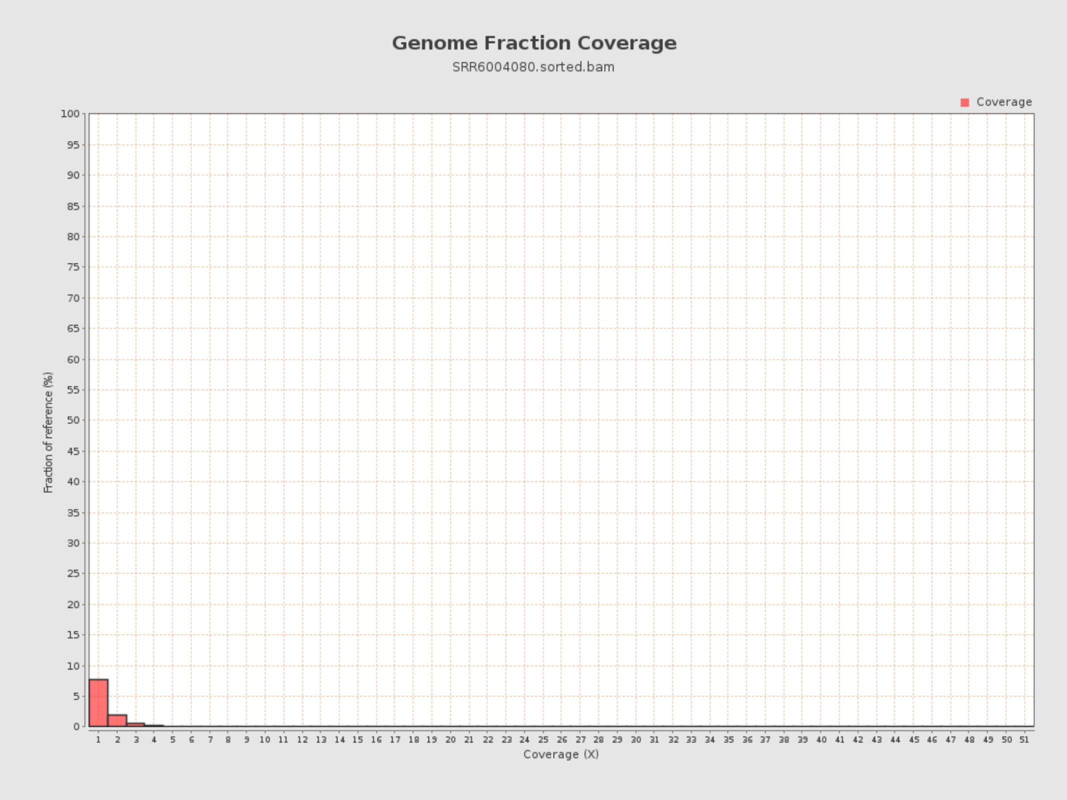
4. Results : Coverage Histogram



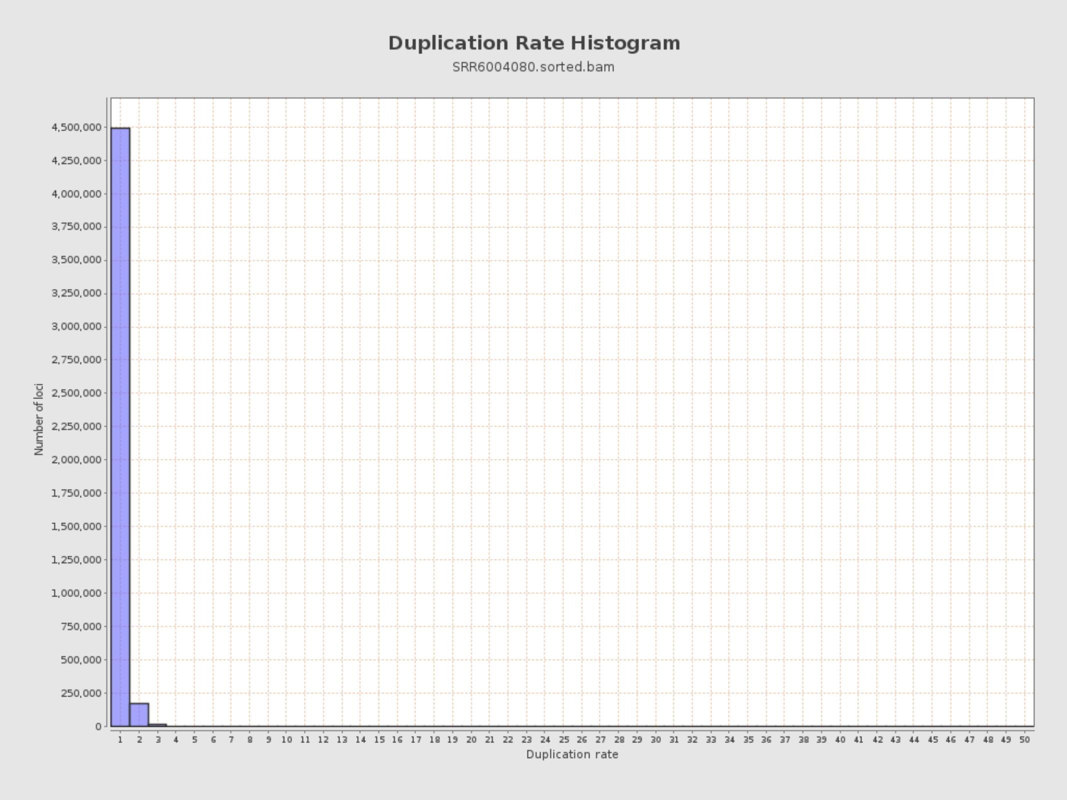
5. Results : Coverage Histogram (0-50X)



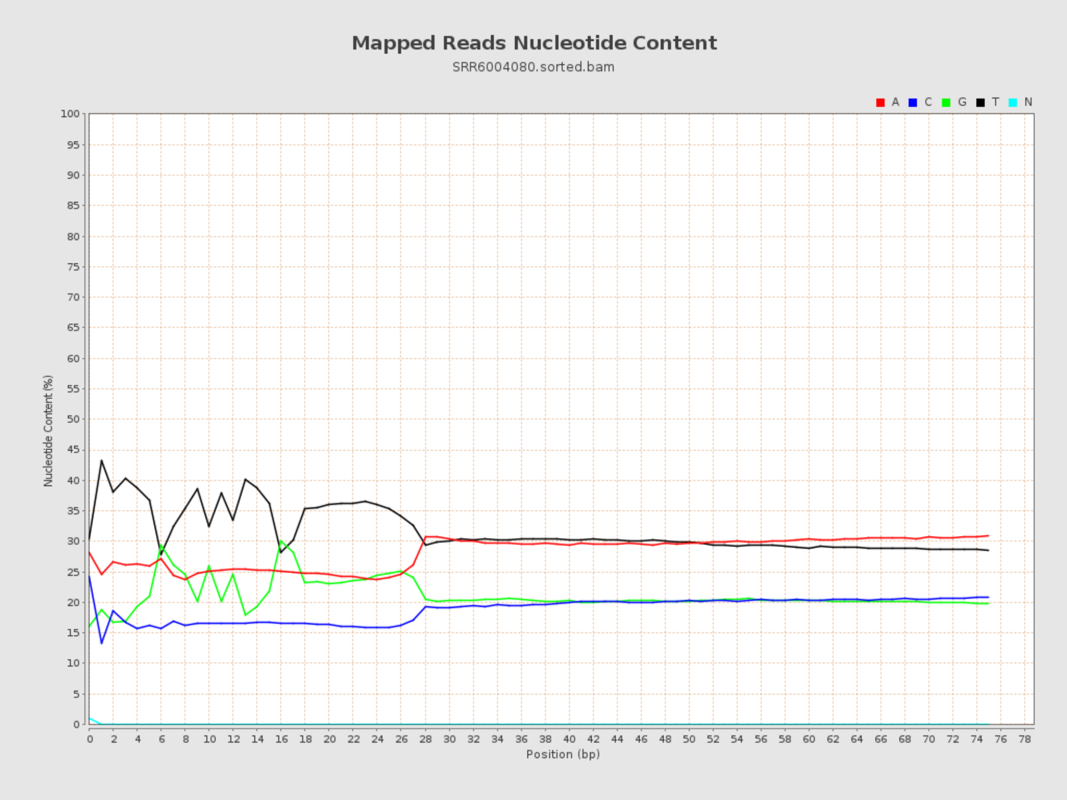
6. Results : Genome Fraction Coverage



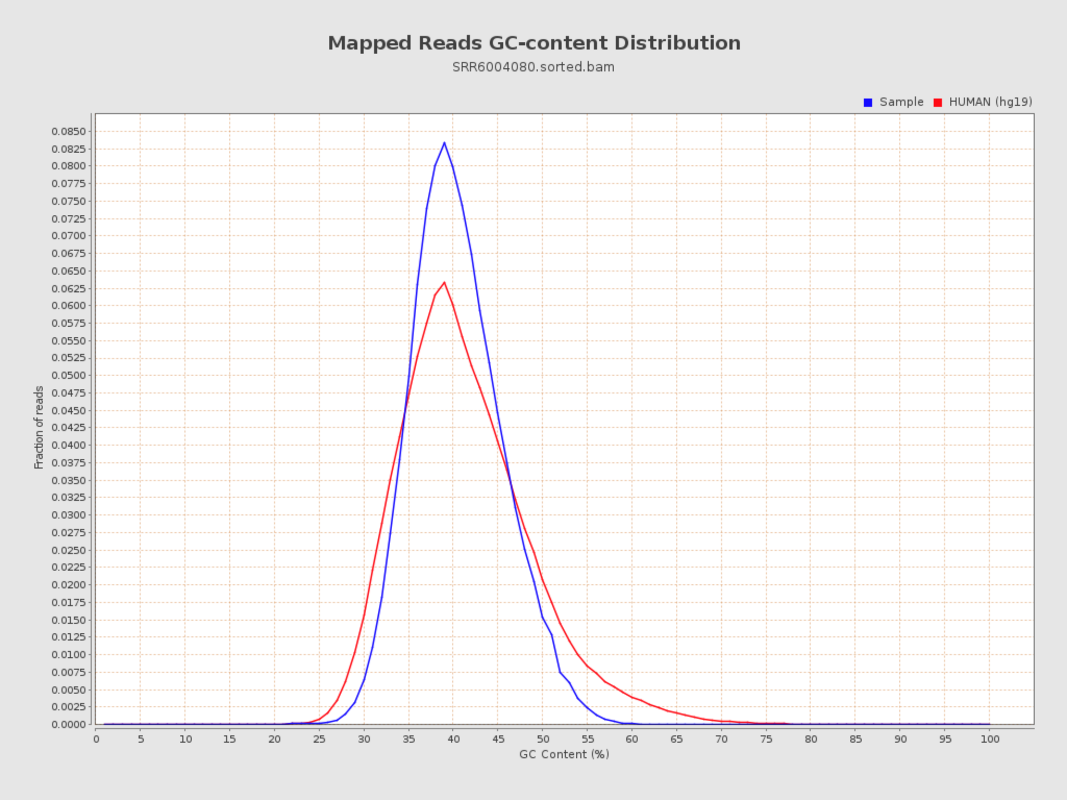
7. Results : Duplication Rate Histogram



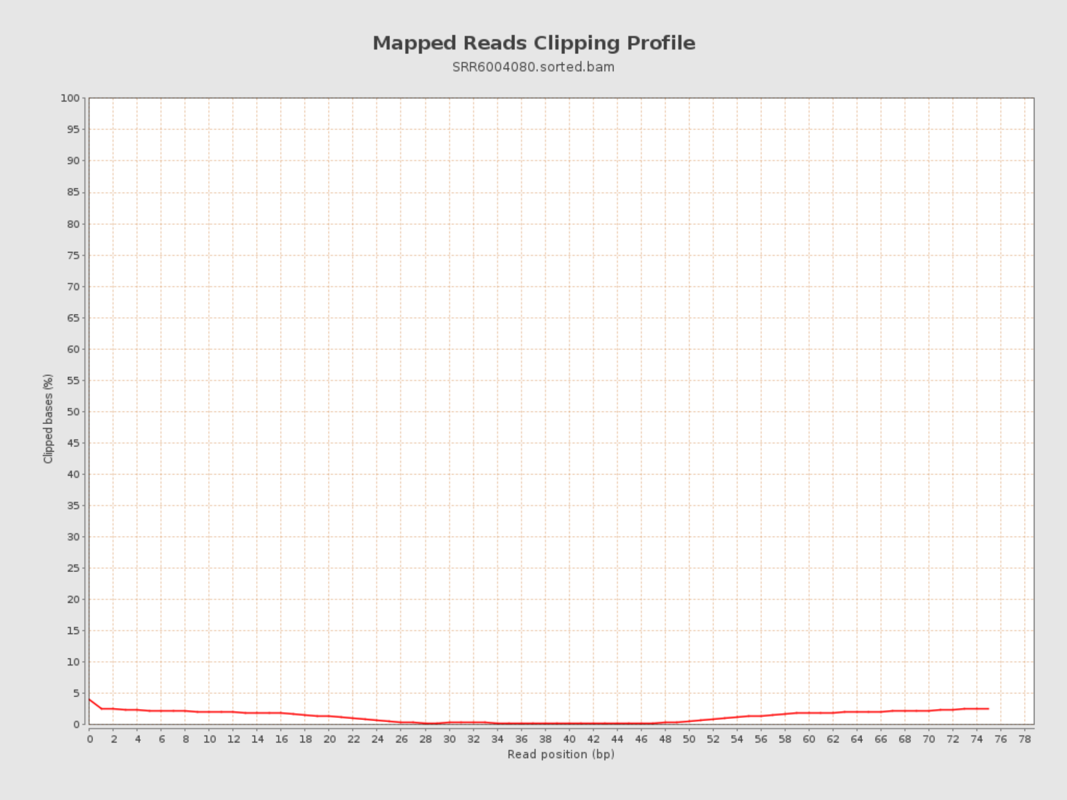
8. Results : Mapped Reads Nucleotide Content



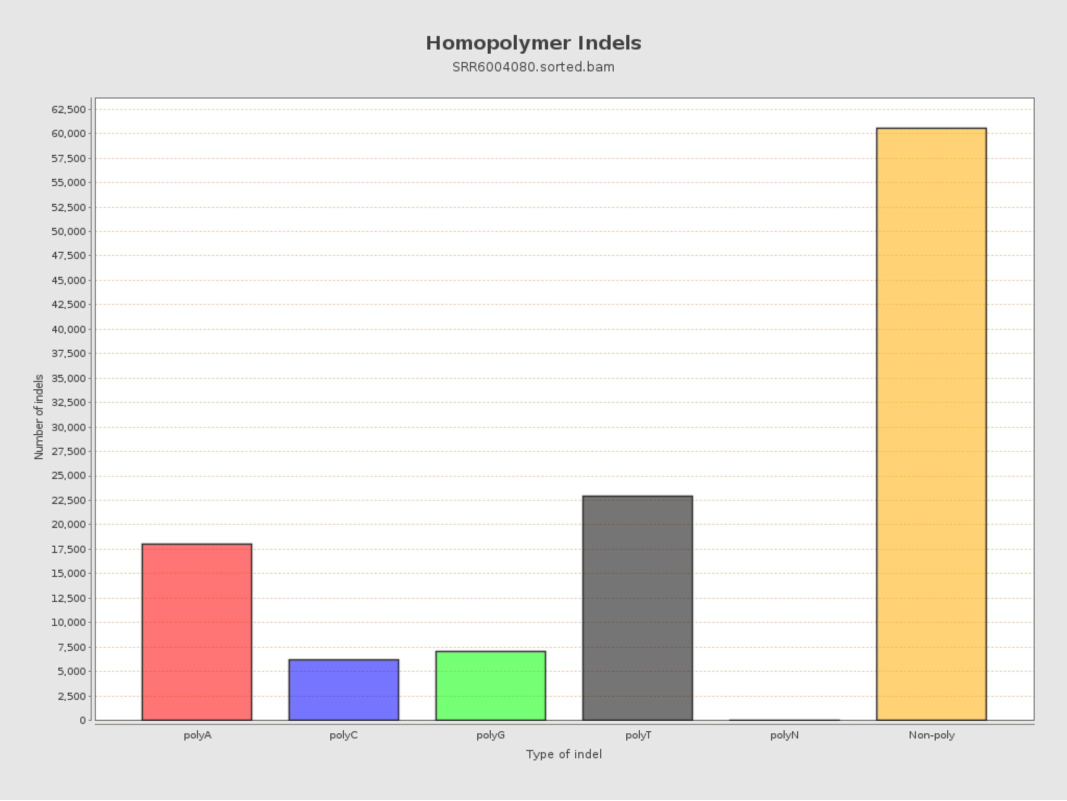
9. Results : Mapped Reads GC-content Distribution



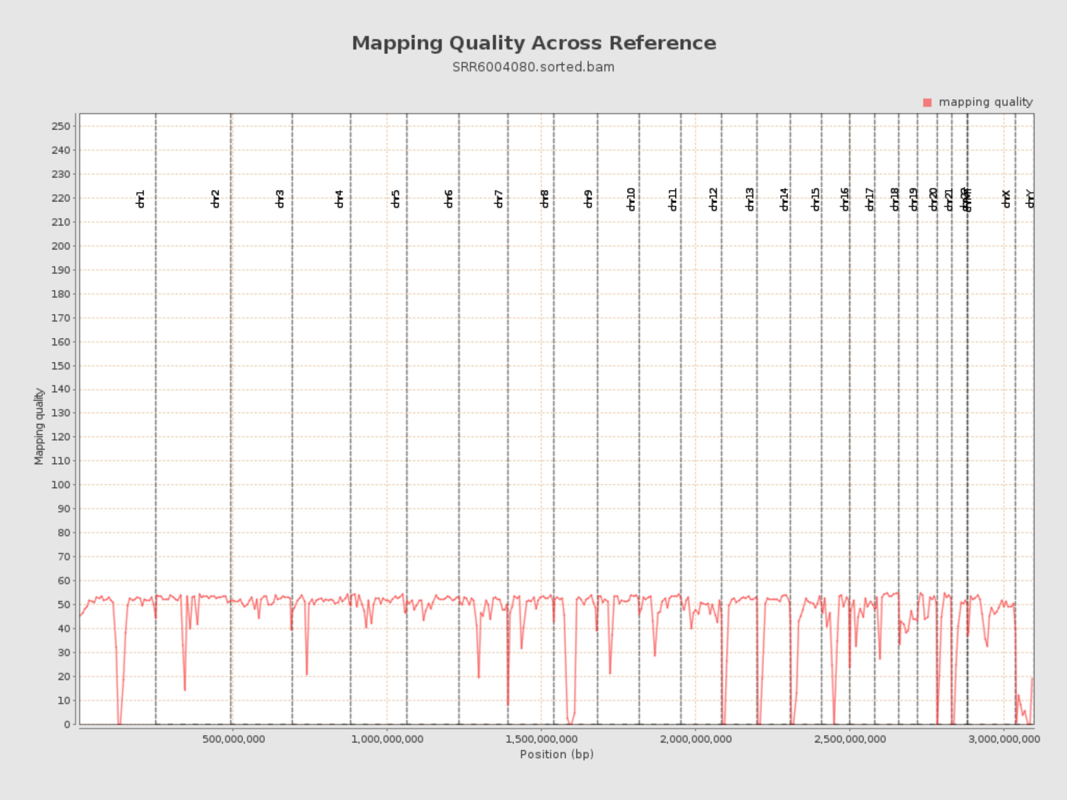
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram