Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 09:45:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080648.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_SRR3080648 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080648.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 09:45:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080648.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,402,434
Mapped reads	1,258,943 / 89.77%
Unmapped reads	143,491 / 10.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,539 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	47,561 / 3.39%
Duplication rate	3.26%
Clipped reads	598,445 / 42.67%

2.2. ACGT Content

Number/percentage of A's	22,247,777 / 26.84%
Number/percentage of C's	15,351,493 / 18.52%
Number/percentage of T's	26,186,643 / 31.59%
Number/percentage of G's	19,104,238 / 23.05%
Number/percentage of N's	3,660 / 0%
GC Percentage	41.57%

2.3. Coverage

Mean	0.0268

Standard Deviation	0.2266

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

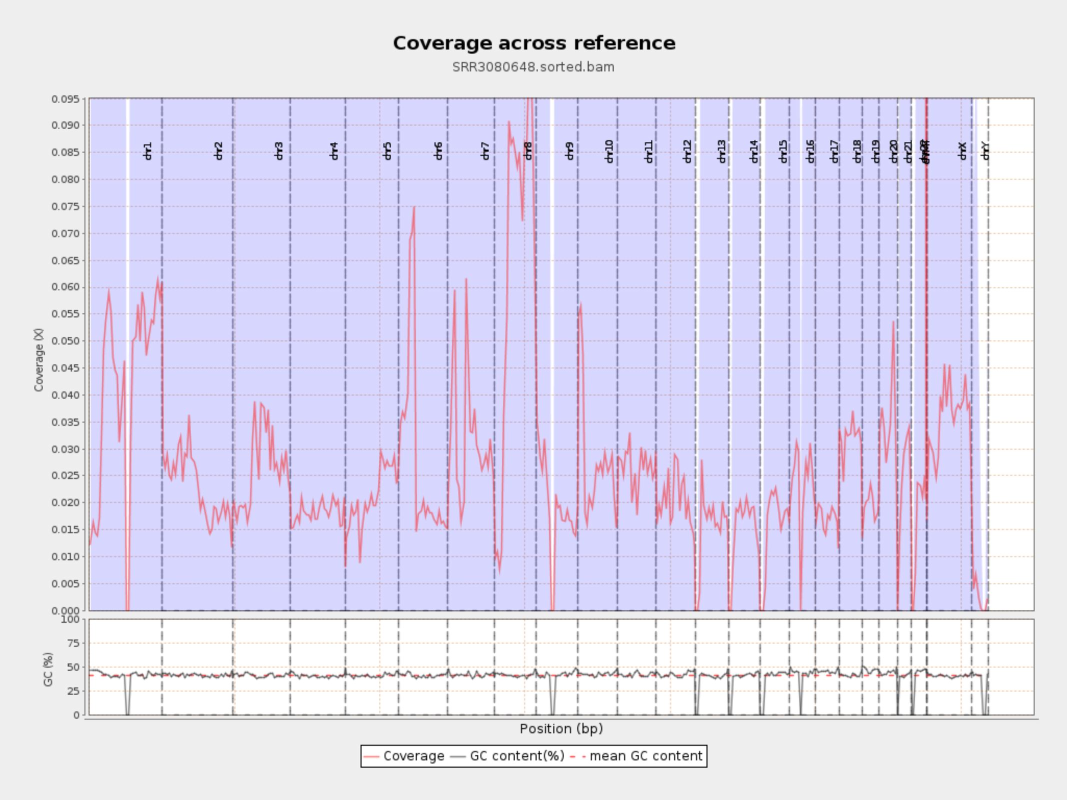
General error rate	0.7%
Mismatches	566,632
Insertions	6,026
Mapped reads with at least one insertion	0.48%
Deletions	19,161
Mapped reads with at least one deletion	1.51%
Homopolymer indels	48.22%

2.6. Chromosome stats

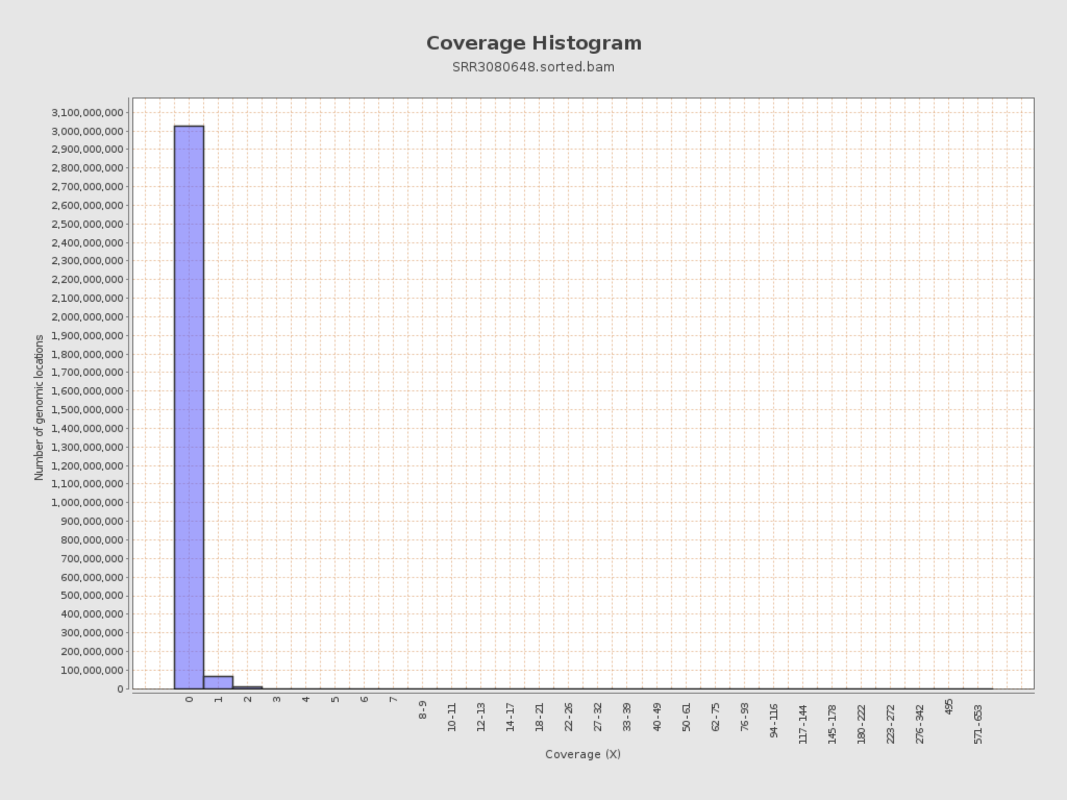
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10261049	0.0412	0.2611
chr2	243199373	5610789	0.0231	0.33
chr3	198022430	5269805	0.0266	0.187
chr4	191154276	3482709	0.0182	0.1529
chr5	180915260	3835588	0.0212	0.162
chr6	171115067	4881275	0.0285	0.2264
chr7	159138663	5218826	0.0328	0.4155

chr8	146364022	9573585	0.0654	0.3143
chr9	141213431	2652994	0.0188	0.1705
chr10	135534747	3839926	0.0283	0.1951
chr11	135006516	3570419	0.0264	0.1954
chr12	133851895	2712785	0.0203	0.1647
chr13	115169878	1767273	0.0153	0.1418
chr14	107349540	1600898	0.0149	0.1387
chr15	102531392	1570296	0.0153	0.1455
chr16	90354753	2126005	0.0235	0.177
chr17	81195210	1379758	0.017	0.1519
chr18	78077248	2520349	0.0323	0.2321
chr19	59128983	1160523	0.0196	0.1702
chr20	63025520	2209174	0.0351	0.2134
chr21	48129895	1119090	0.0233	0.1722
chr22	51304566	815784	0.0159	0.1394
chrMT	16571	20004	1.2072	1.3677
chrX	155270560	5549597	0.0357	0.2172
chrY	59373566	176025	0.003	0.0625

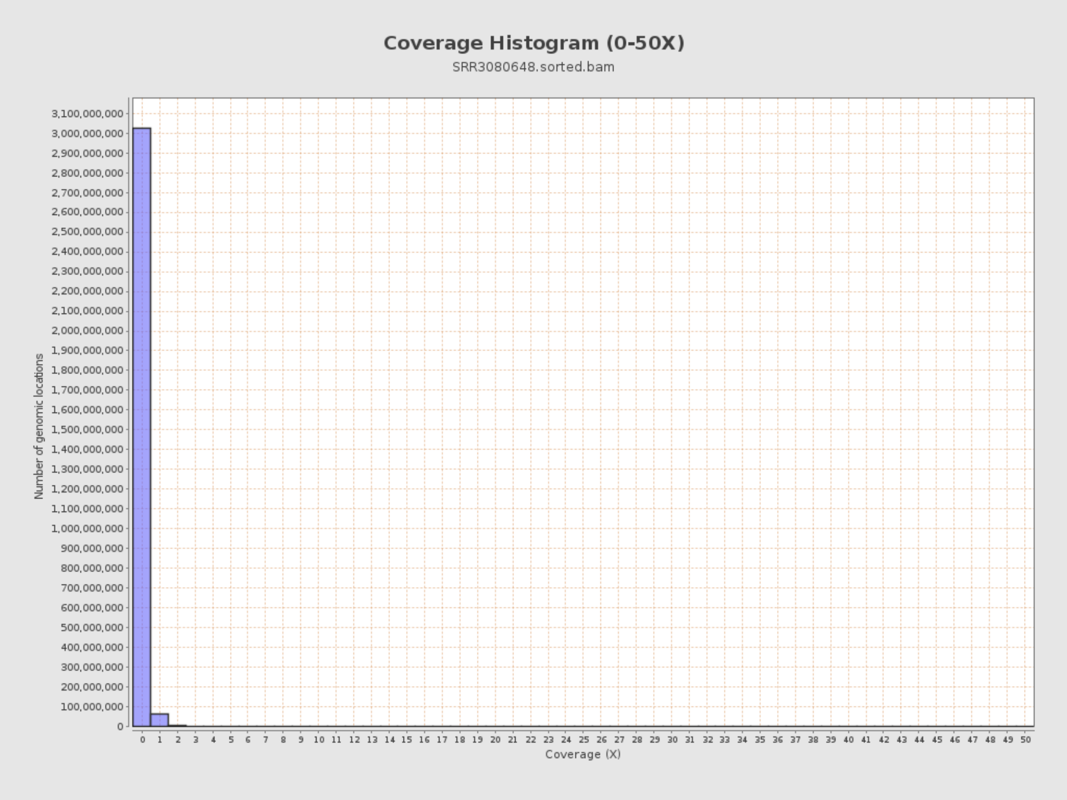
3. Results : Coverage across reference



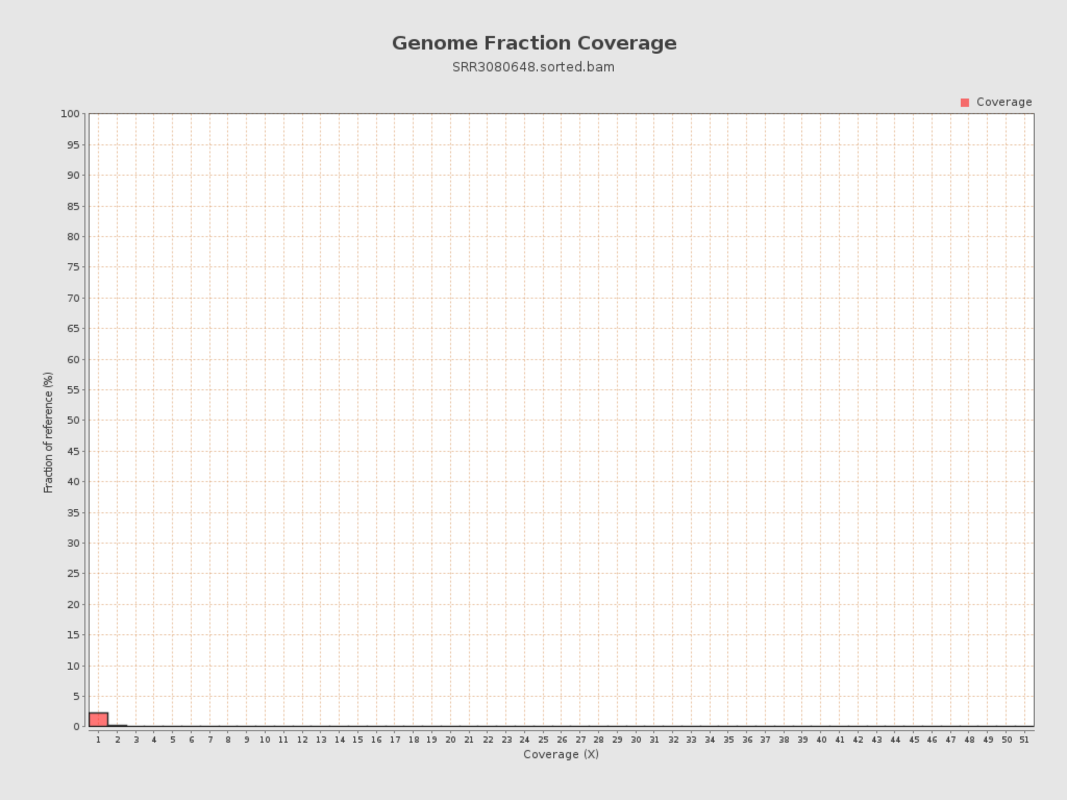
4. Results : Coverage Histogram



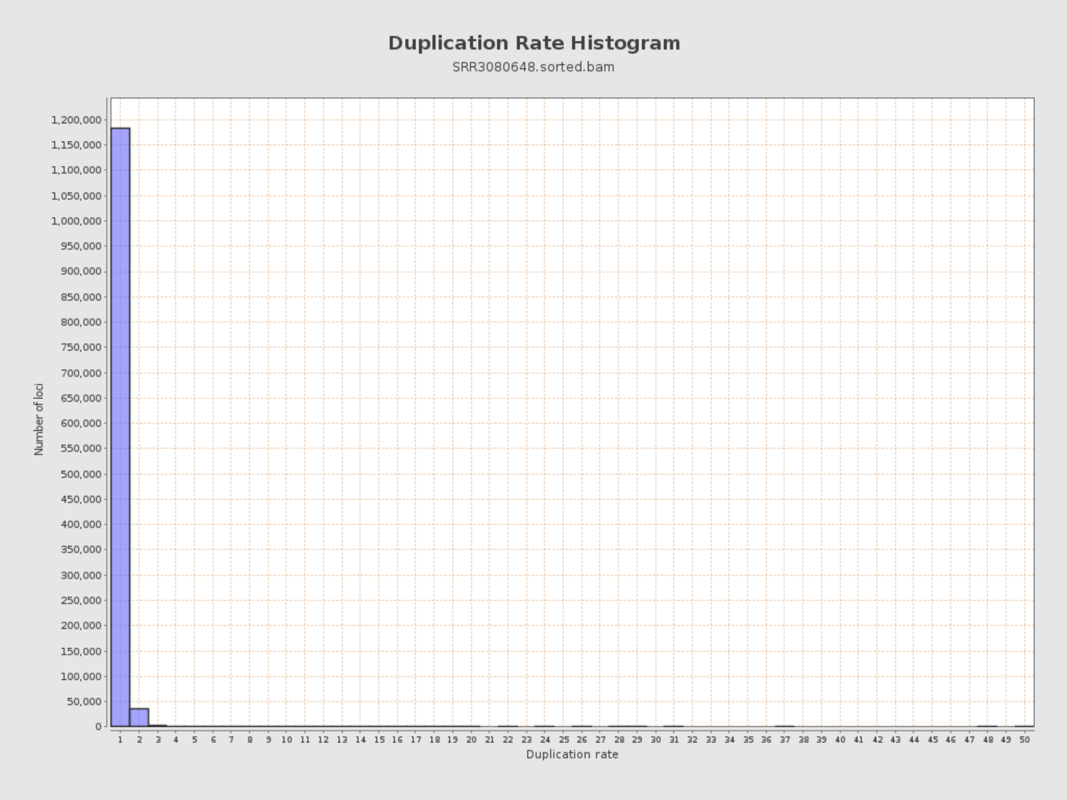
5. Results : Coverage Histogram (0-50X)



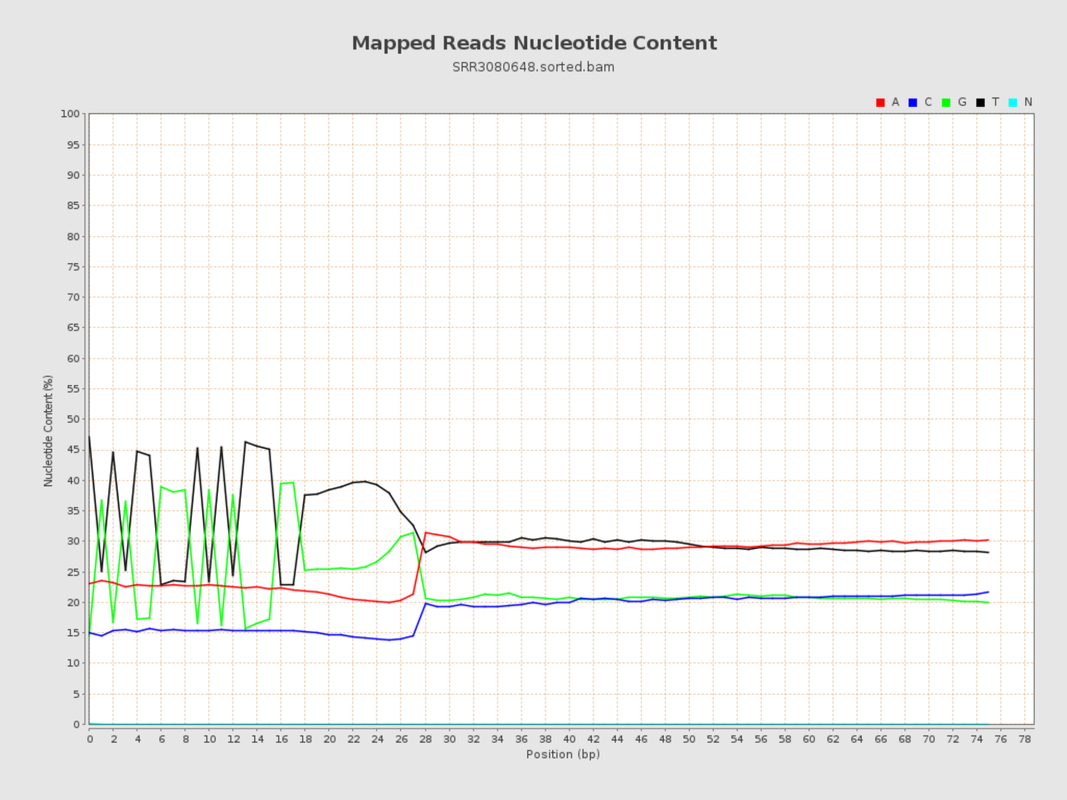
6. Results : Genome Fraction Coverage



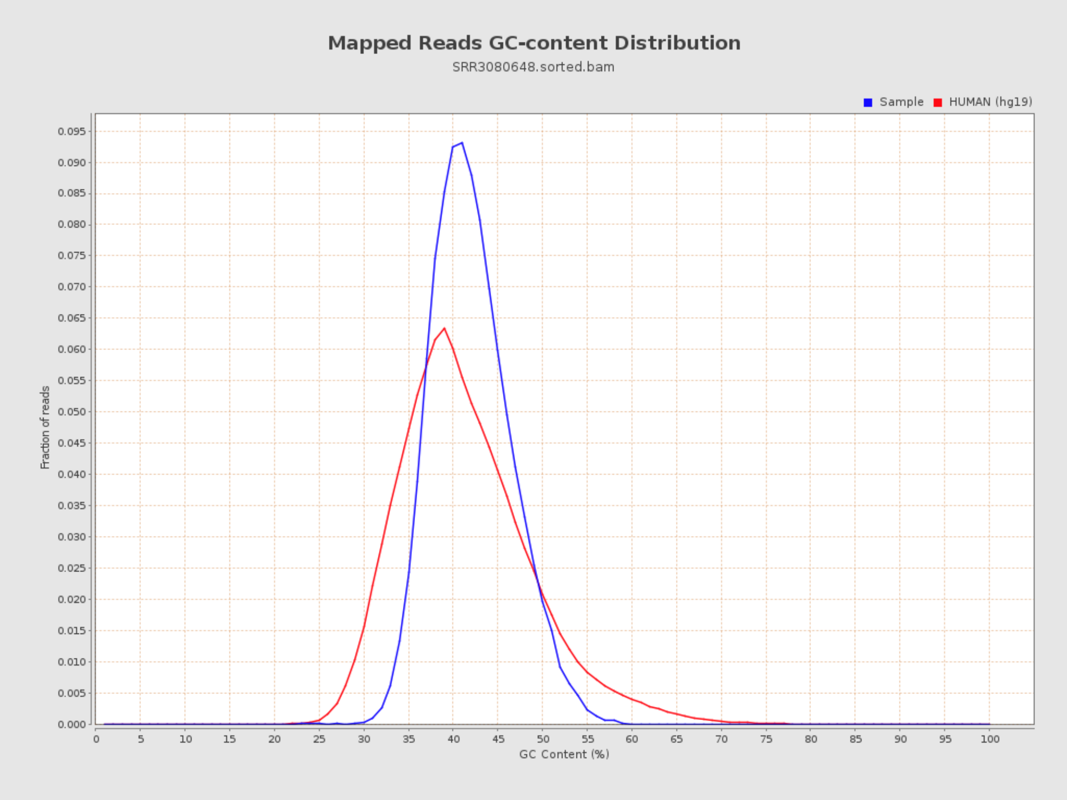
7. Results : Duplication Rate Histogram



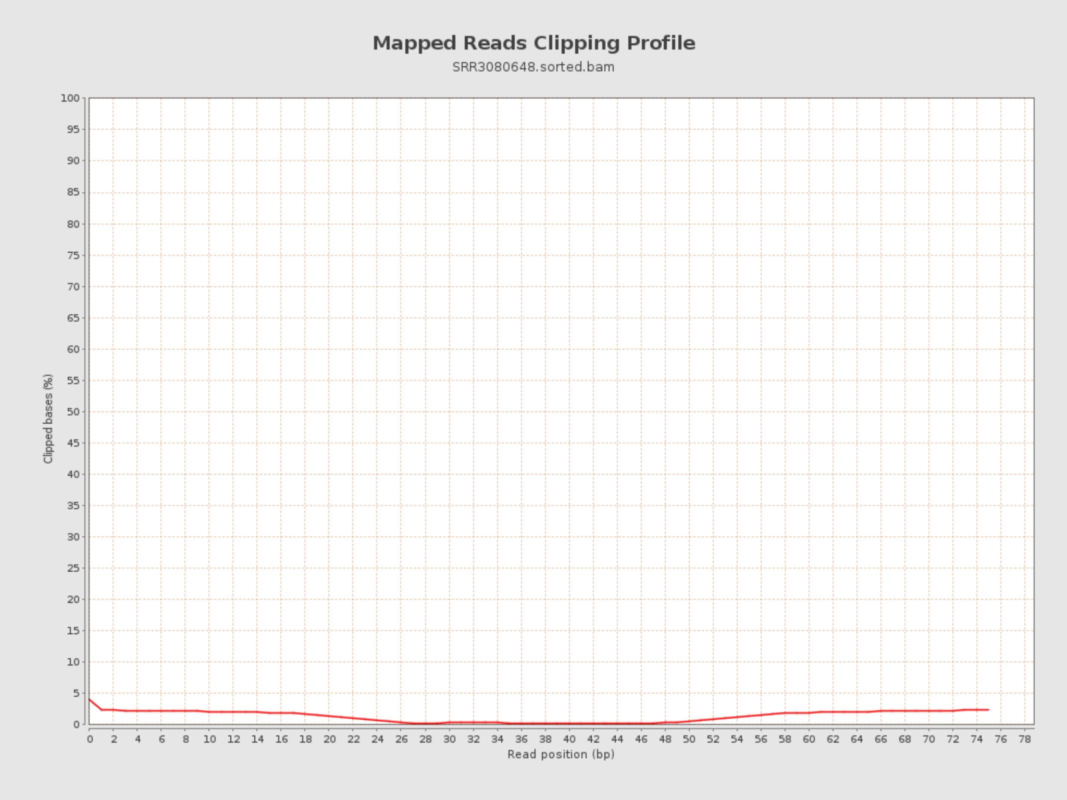
8. Results : Mapped Reads Nucleotide Content



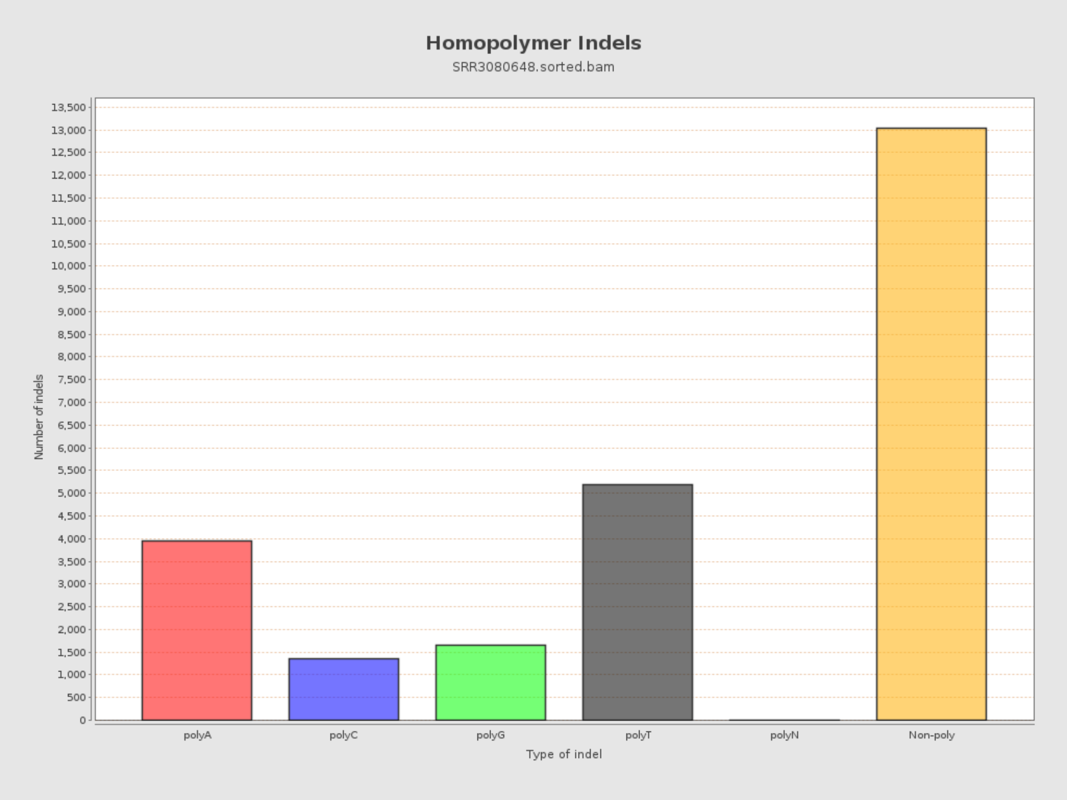
9. Results : Mapped Reads GC-content Distribution



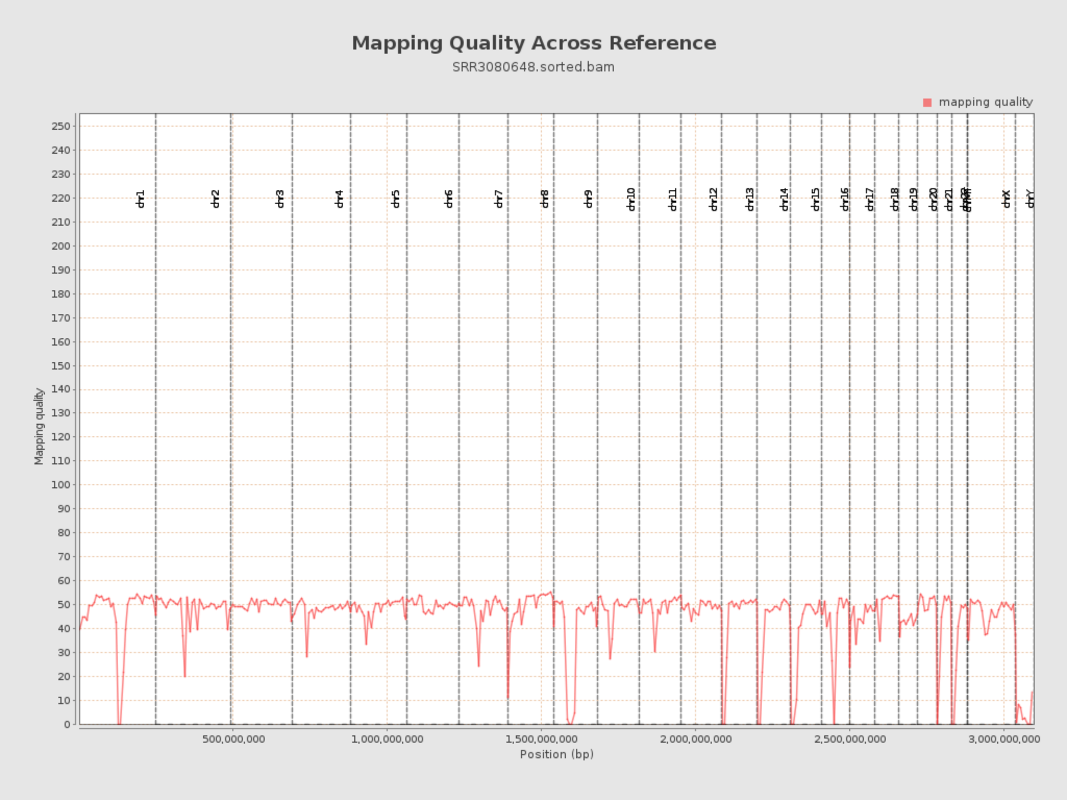
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram