Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:24:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081208.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_SRR3081208 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081208.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:24:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081208.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,020,345
Mapped reads	4,857,421 / 80.68%
Unmapped reads	1,162,924 / 19.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	54,683 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	596,848 / 9.91%
Duplication rate	8.85%
Clipped reads	2,098,869 / 34.86%

2.2. ACGT Content

Number/percentage of A's	89,029,544 / 27.23%
Number/percentage of C's	64,799,459 / 19.82%
Number/percentage of T's	99,395,099 / 30.41%
Number/percentage of G's	73,498,076 / 22.48%
Number/percentage of N's	175,873 / 0.05%
GC Percentage	42.31%

2.3. Coverage

Mean	0.1056

Standard Deviation	0.9485

2.4. Mapping Quality

Mean Mapping Quality	46.35

2.5. Mismatches and indels

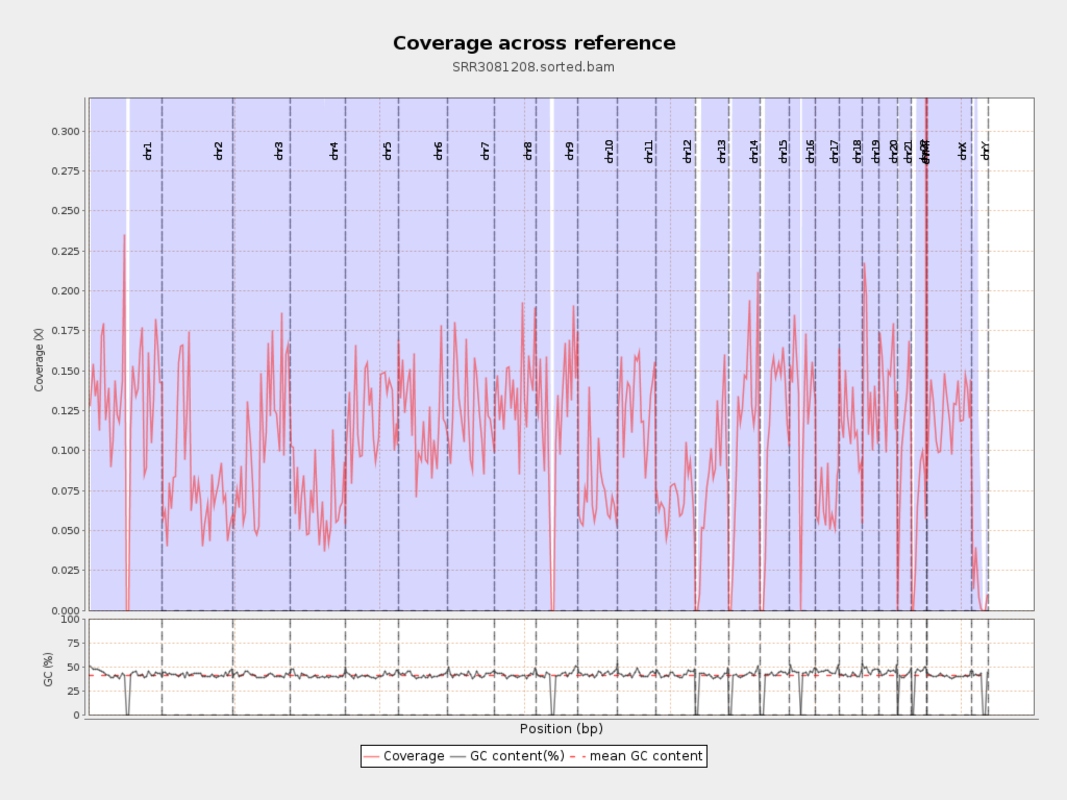
General error rate	1.01%
Mismatches	3,272,371
Insertions	23,234
Mapped reads with at least one insertion	0.47%
Deletions	71,637
Mapped reads with at least one deletion	1.46%
Homopolymer indels	46.35%

2.6. Chromosome stats

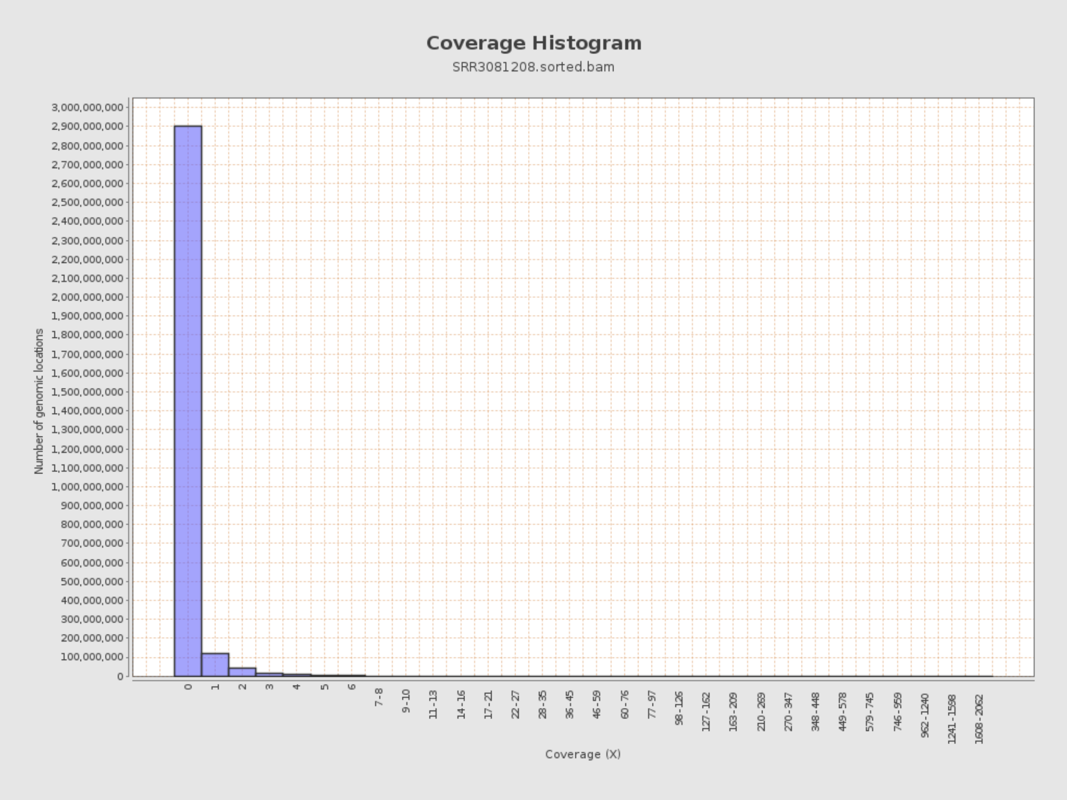
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	32603849	0.1308	1.77
chr2	243199373	19934972	0.082	0.787
chr3	198022430	20812672	0.1051	0.4987
chr4	191154276	12987951	0.0679	0.4223
chr5	180915260	22482707	0.1243	0.5452
chr6	171115067	20526542	0.12	0.6637
chr7	159138663	19786897	0.1243	1.191

chr8	146364022	20255269	0.1384	1.3985
chr9	141213431	16513512	0.1169	0.7375
chr10	135534747	9843376	0.0726	0.8276
chr11	135006516	17534799	0.1299	0.7788
chr12	133851895	9414998	0.0703	0.4223
chr13	115169878	9086381	0.0789	0.4261
chr14	107349540	12153165	0.1132	2.0001
chr15	102531392	11379724	0.111	0.5102
chr16	90354753	11895219	0.1317	0.6014
chr17	81195210	5447330	0.0671	0.4424
chr18	78077248	9166886	0.1174	1.2216
chr19	59128983	8195575	0.1386	1.3305
chr20	63025520	9023398	0.1432	0.6197
chr21	48129895	5062234	0.1052	0.5338
chr22	51304566	2965823	0.0578	0.3667
chrMT	16571	51087	3.0829	2.7151
chrX	155270560	19135702	0.1232	0.601
chrY	59373566	753696	0.0127	0.2401

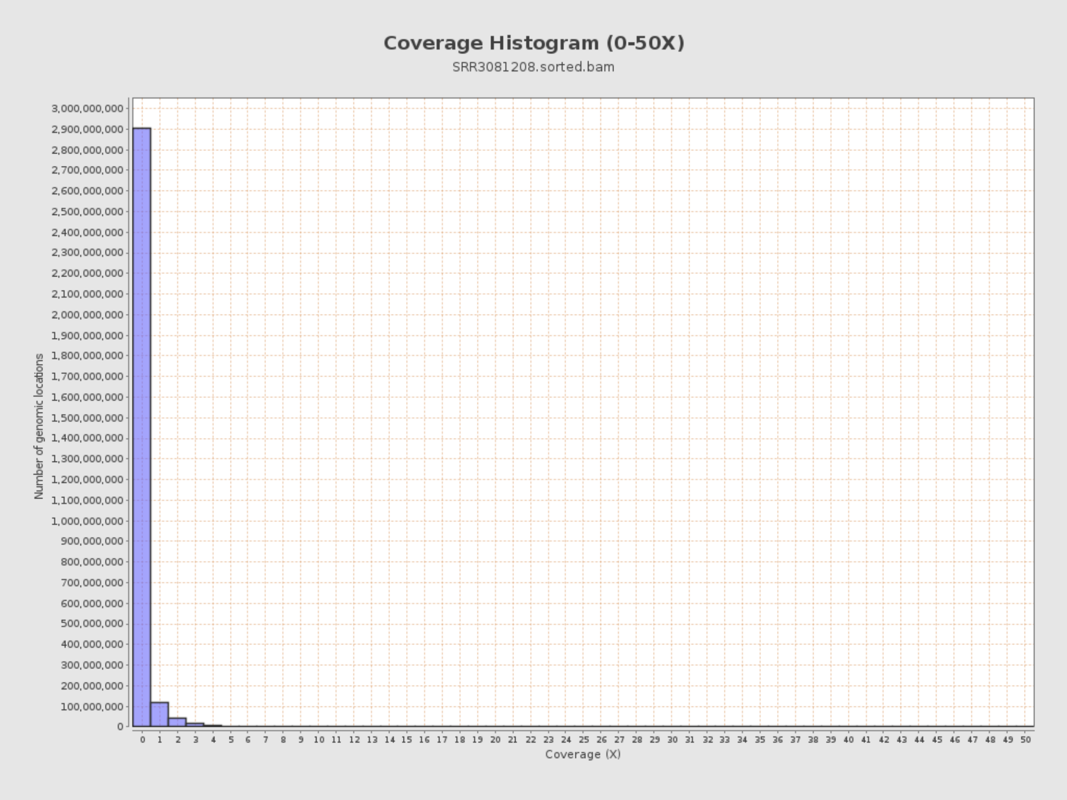
3. Results : Coverage across reference



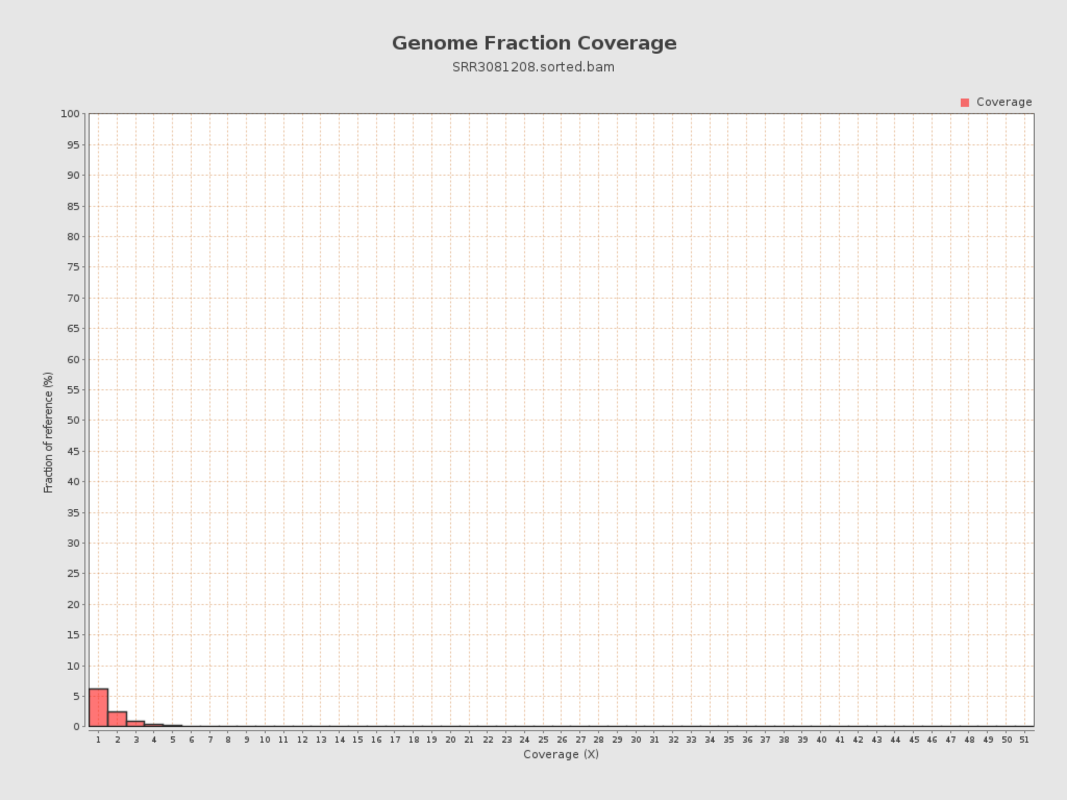
4. Results : Coverage Histogram



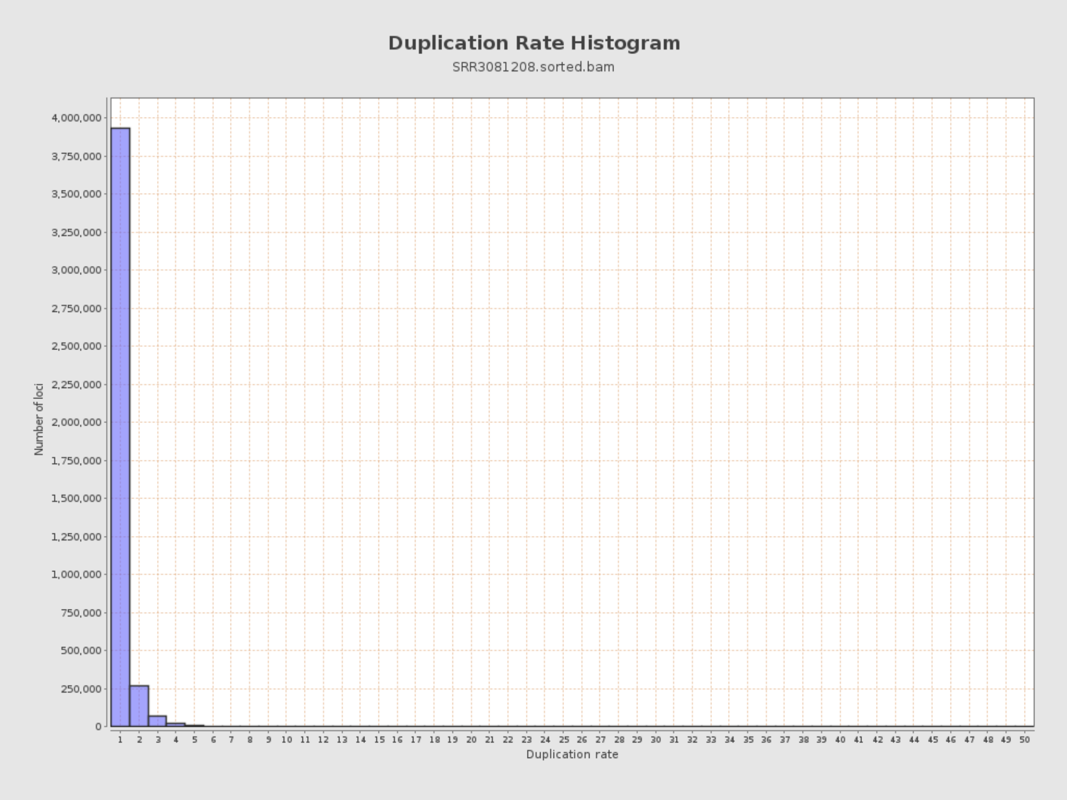
5. Results : Coverage Histogram (0-50X)



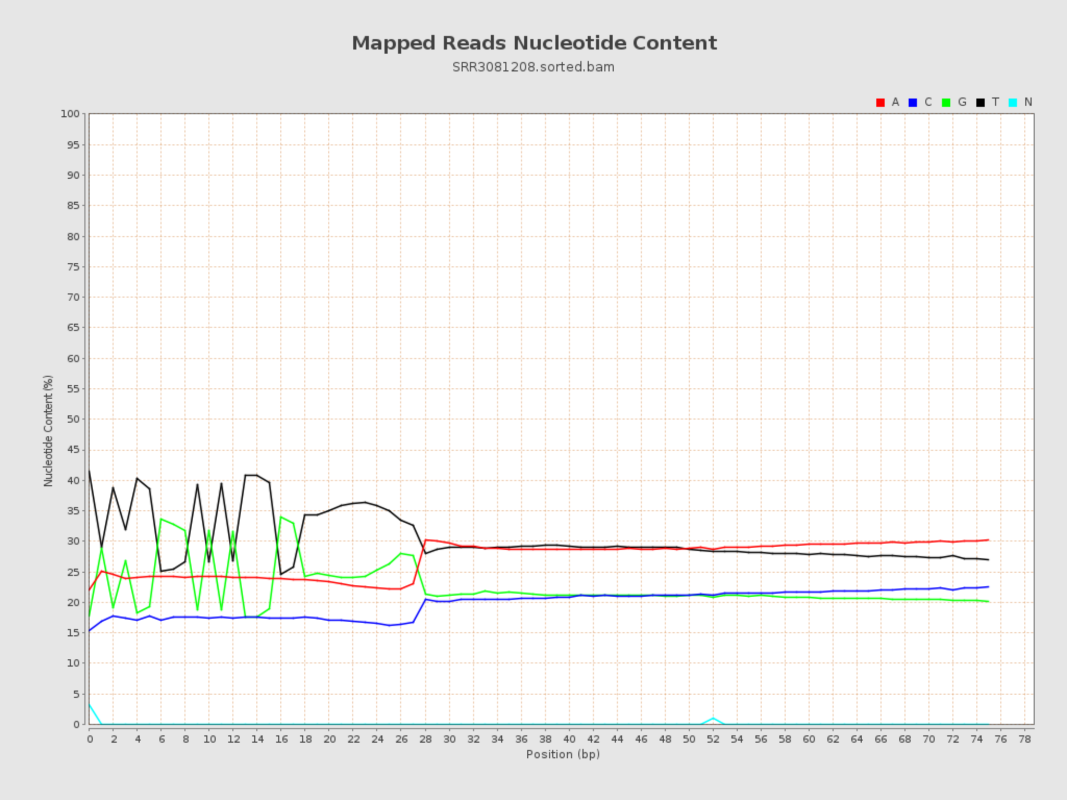
6. Results : Genome Fraction Coverage



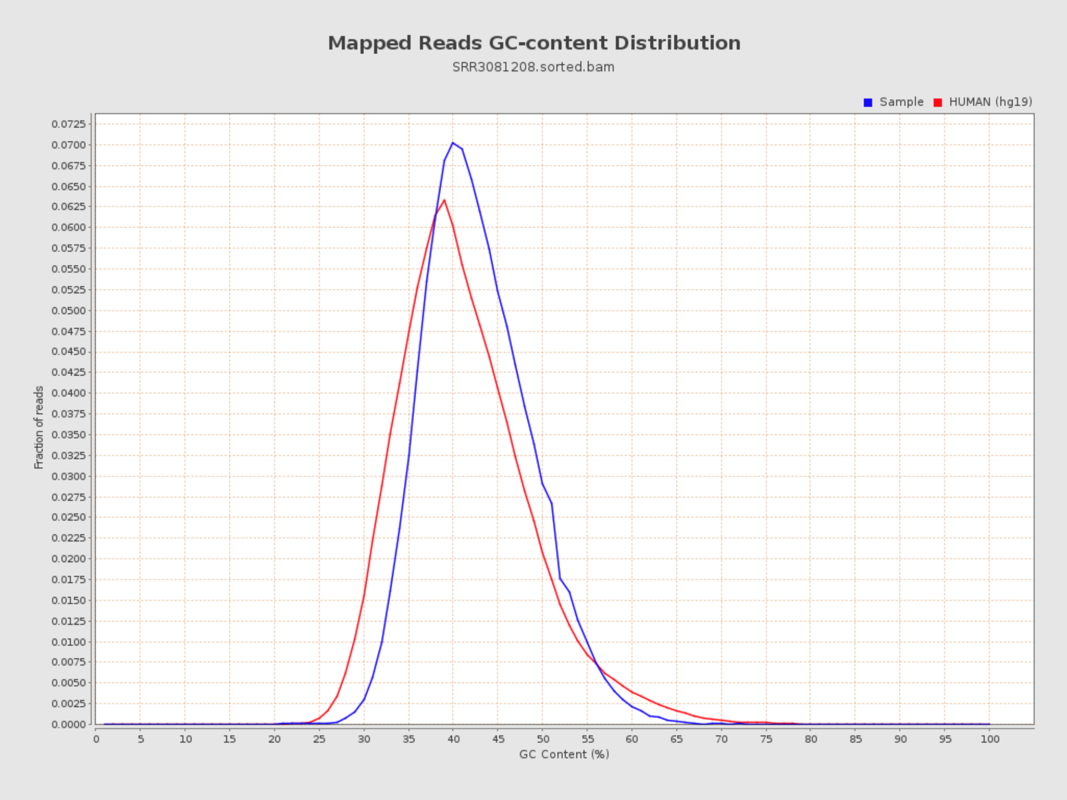
7. Results : Duplication Rate Histogram



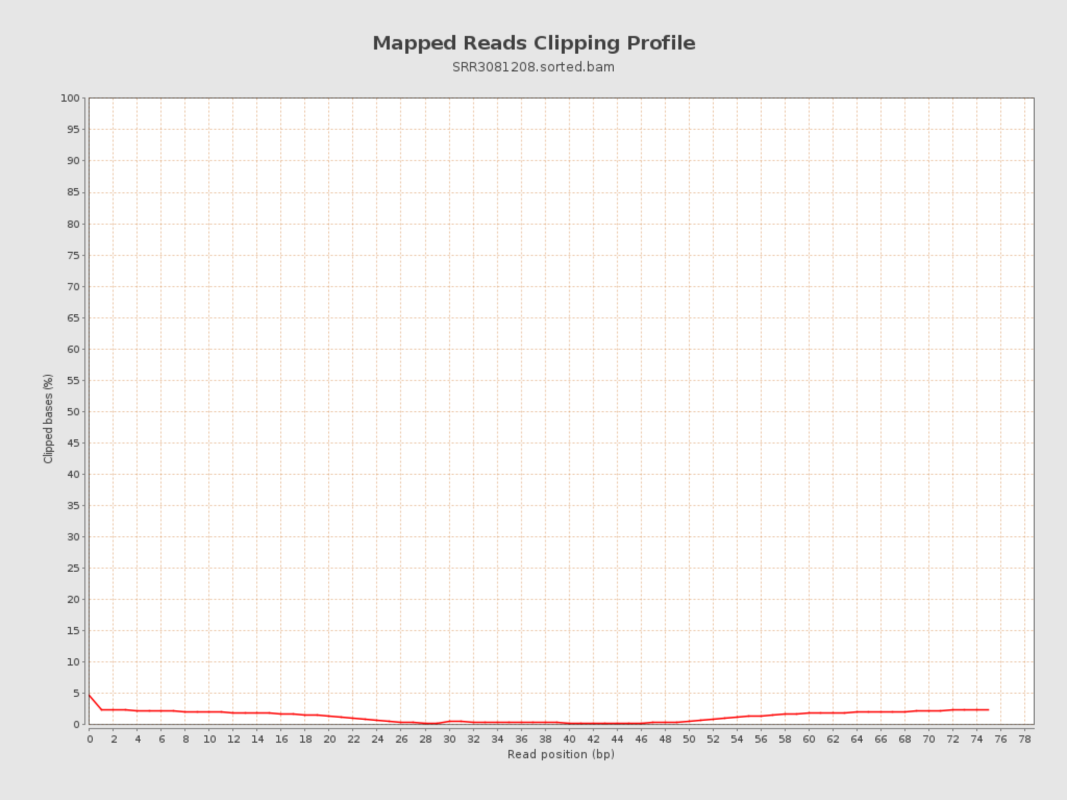
8. Results : Mapped Reads Nucleotide Content



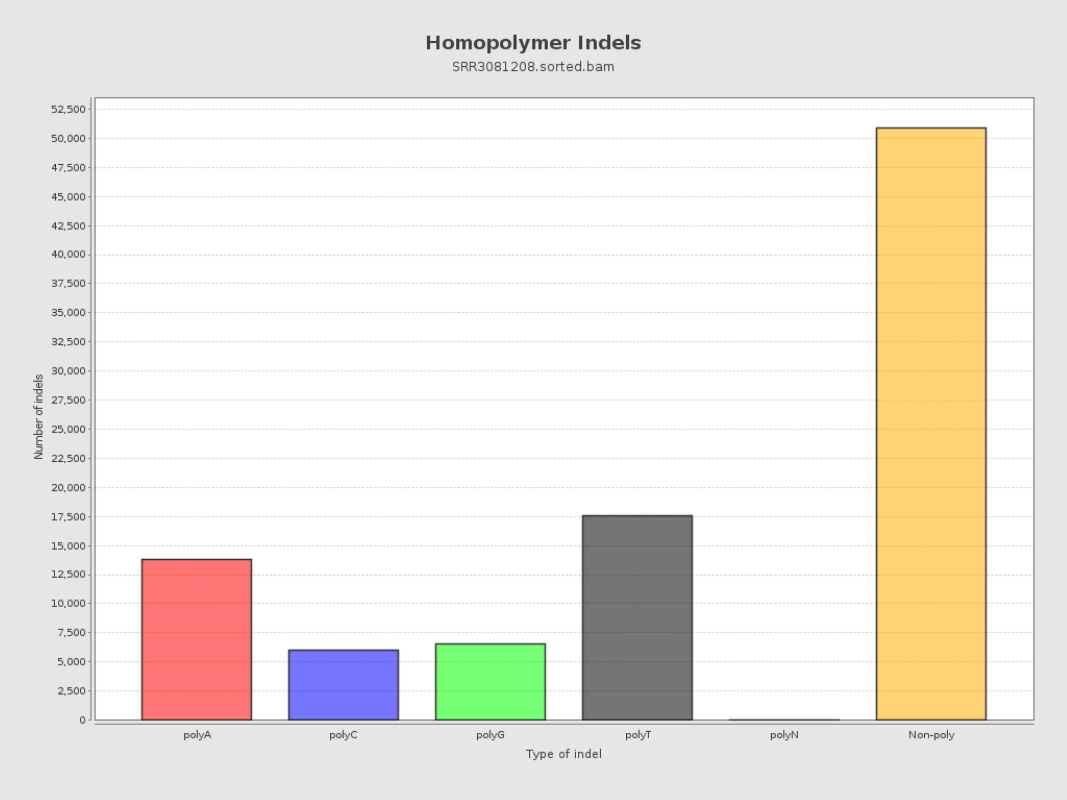
9. Results : Mapped Reads GC-content Distribution



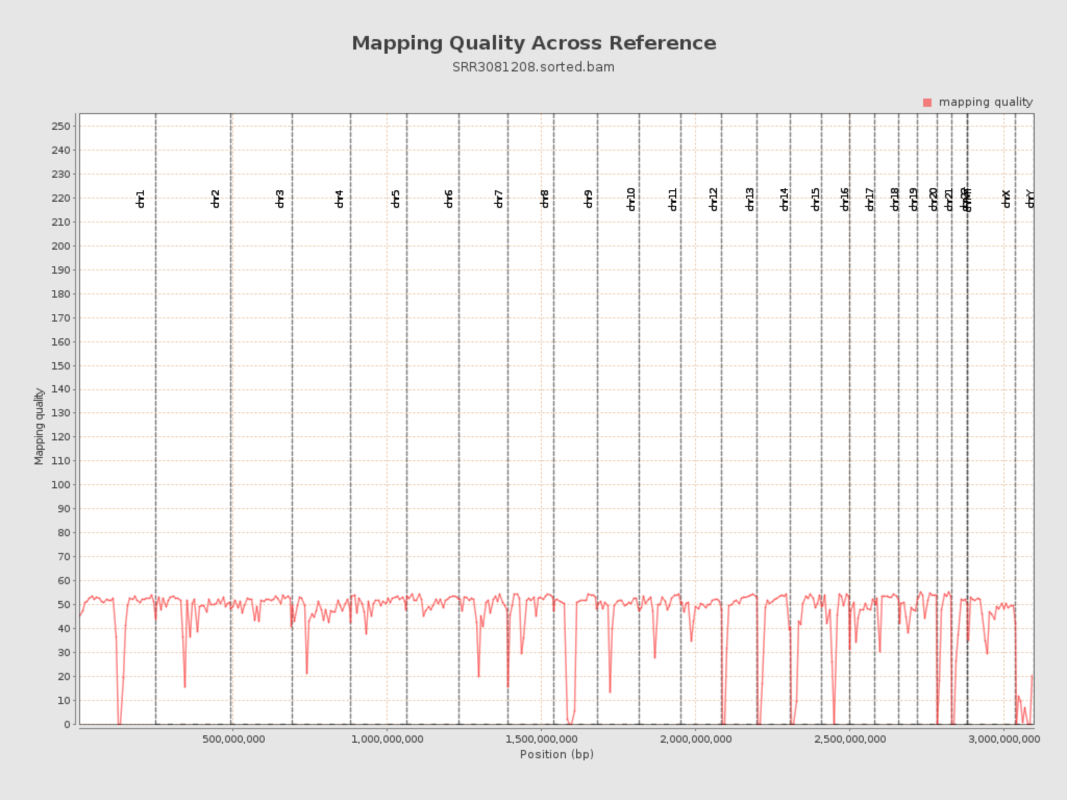
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram