Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 22:00:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230408.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_SRR6230408 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230408.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 22:00:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230408.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,259,042
Mapped reads	3,910,296 / 91.81%
Unmapped reads	348,746 / 8.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,930 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	261,715 / 6.14%
Duplication rate	4.66%
Clipped reads	1,069,703 / 25.12%

2.2. ACGT Content

Number/percentage of A's	83,851,657 / 29.94%
Number/percentage of C's	56,922,938 / 20.32%
Number/percentage of T's	81,786,953 / 29.2%
Number/percentage of G's	57,285,864 / 20.45%
Number/percentage of N's	226,248 / 0.08%
GC Percentage	40.78%

2.3. Coverage

Mean	0.0905

Standard Deviation	1.0419

2.4. Mapping Quality

Mean Mapping Quality	47.52

2.5. Mismatches and indels

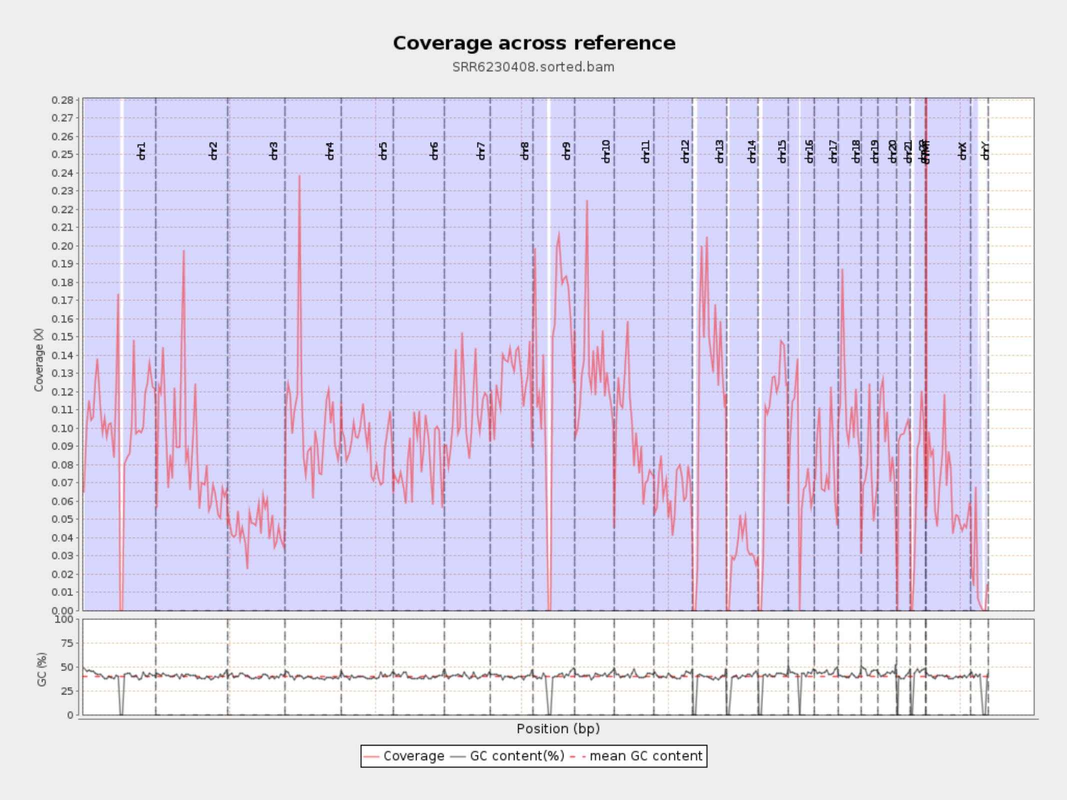
General error rate	0.96%
Mismatches	2,624,152
Insertions	27,008
Mapped reads with at least one insertion	0.69%
Deletions	73,794
Mapped reads with at least one deletion	1.86%
Homopolymer indels	46.66%

2.6. Chromosome stats

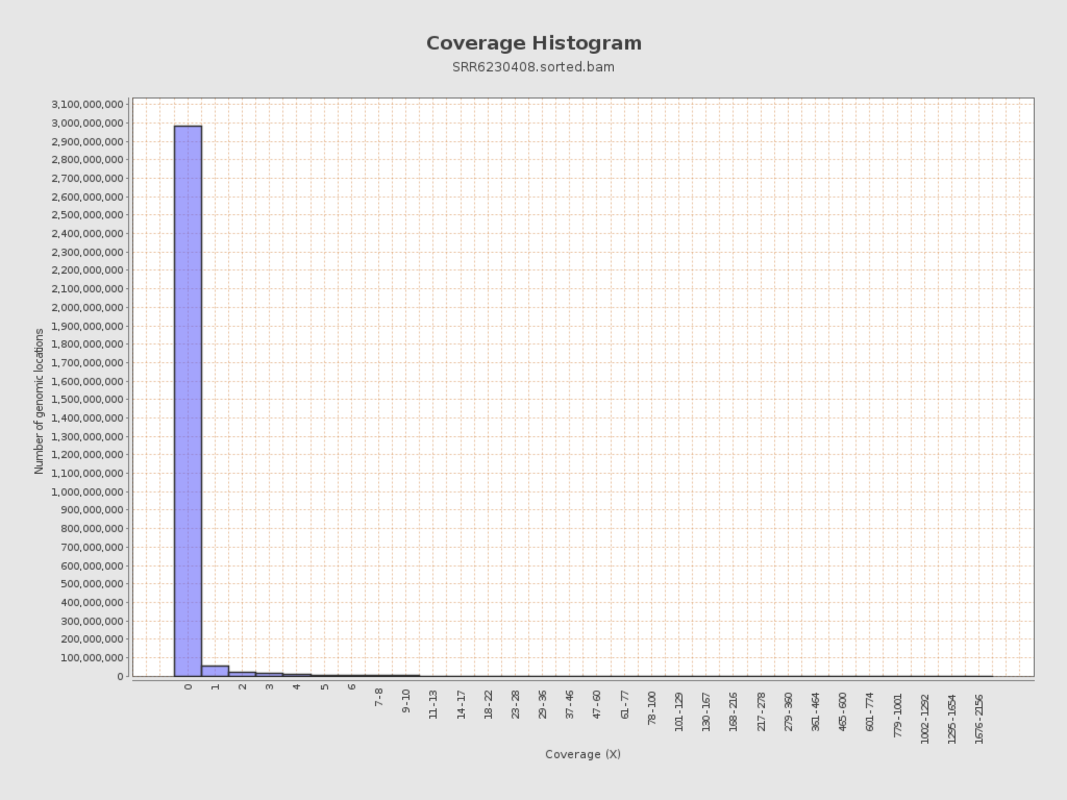
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25460463	0.1021	1.7493
chr2	243199373	21210910	0.0872	1.2773
chr3	198022430	9002319	0.0455	0.4291
chr4	191154276	19841998	0.1038	0.9249
chr5	180915260	16253399	0.0898	0.6165
chr6	171115067	14125669	0.0826	0.6318
chr7	159138663	17290099	0.1086	0.9486

chr8	146364022	18558190	0.1268	1.1935
chr9	141213431	19493549	0.138	1.1467
chr10	135534747	17534799	0.1294	1.3122
chr11	135006516	12987380	0.0962	0.9706
chr12	133851895	8676938	0.0648	0.544
chr13	115169878	14574400	0.1265	0.7298
chr14	107349540	3287312	0.0306	0.5434
chr15	102531392	10245507	0.0999	0.6427
chr16	90354753	6912369	0.0765	0.7276
chr17	81195210	6573789	0.081	0.6845
chr18	78077248	8921297	0.1143	2.385
chr19	59128983	4369372	0.0739	1.2326
chr20	63025520	5976208	0.0948	0.7147
chr21	48129895	4274589	0.0888	0.8505
chr22	51304566	3416191	0.0666	0.5083
chrMT	16571	18302	1.1045	1.6345
chrX	155270560	10257977	0.0661	0.6113
chrY	59373566	939626	0.0158	0.7187

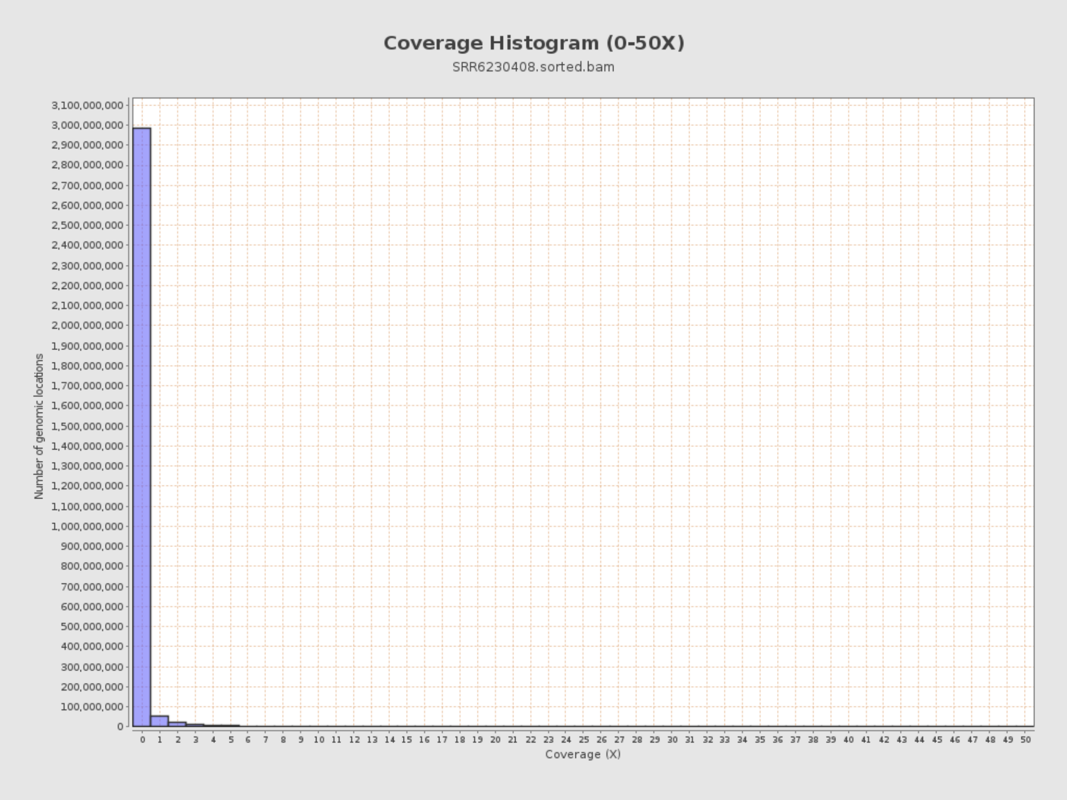
3. Results : Coverage across reference



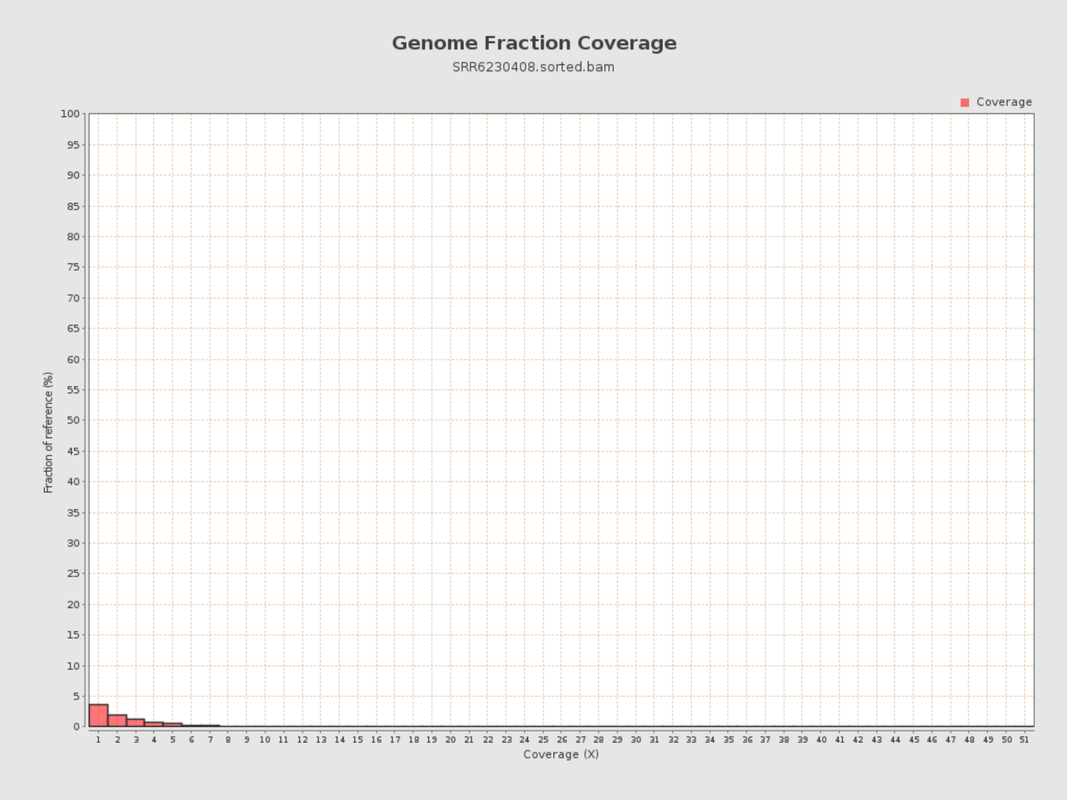
4. Results : Coverage Histogram



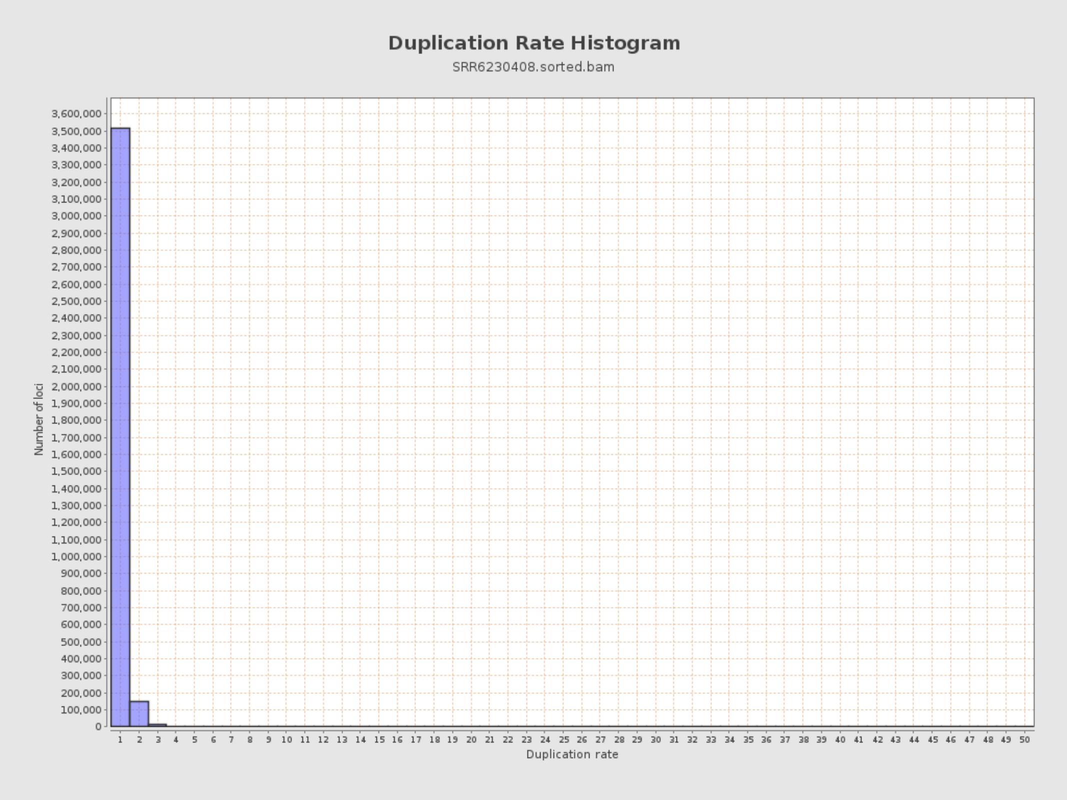
5. Results : Coverage Histogram (0-50X)



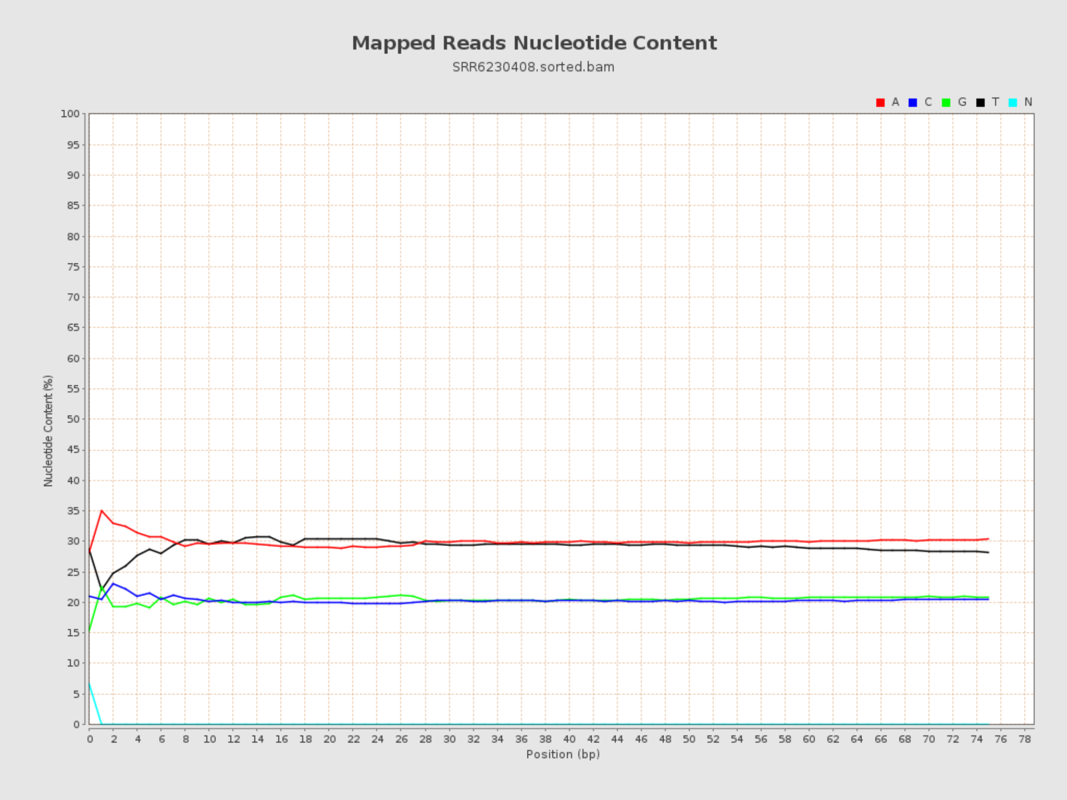
6. Results : Genome Fraction Coverage



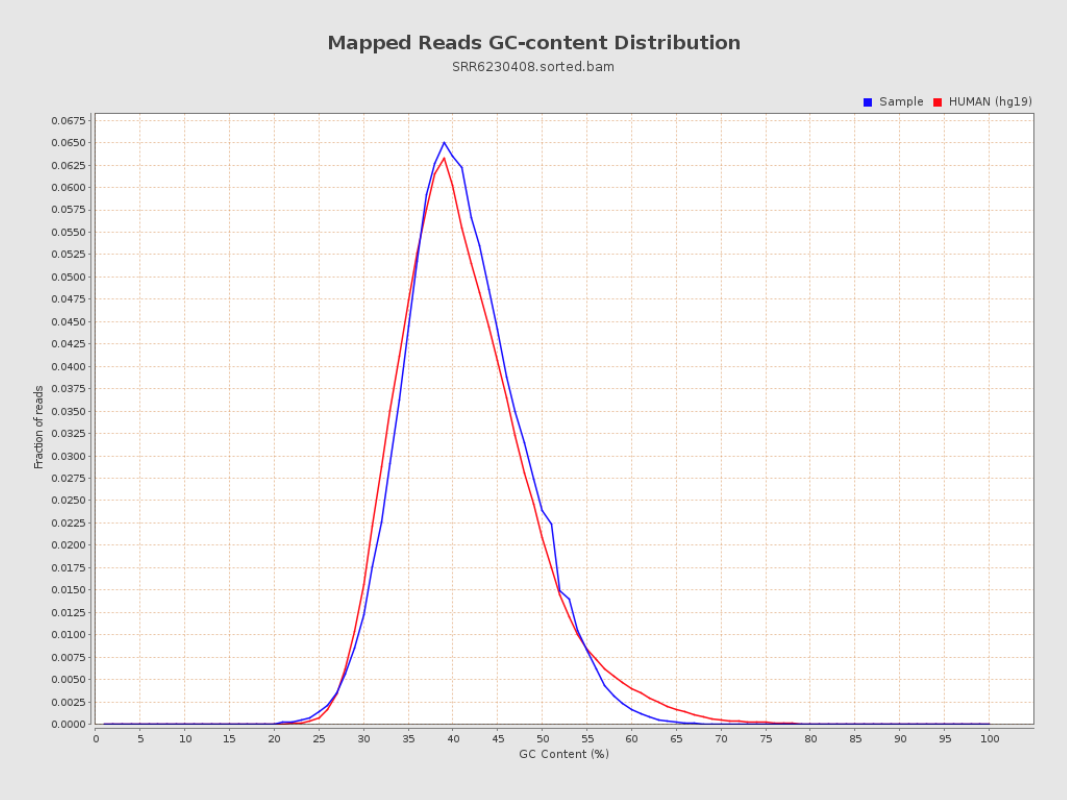
7. Results : Duplication Rate Histogram



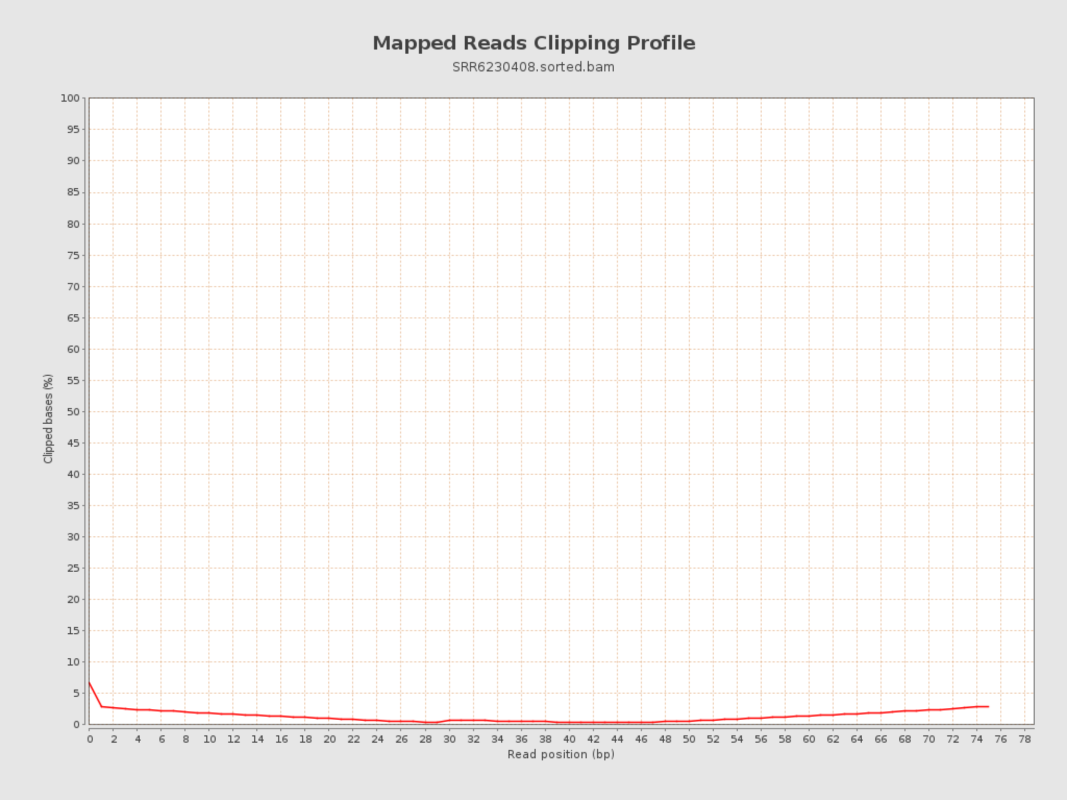
8. Results : Mapped Reads Nucleotide Content



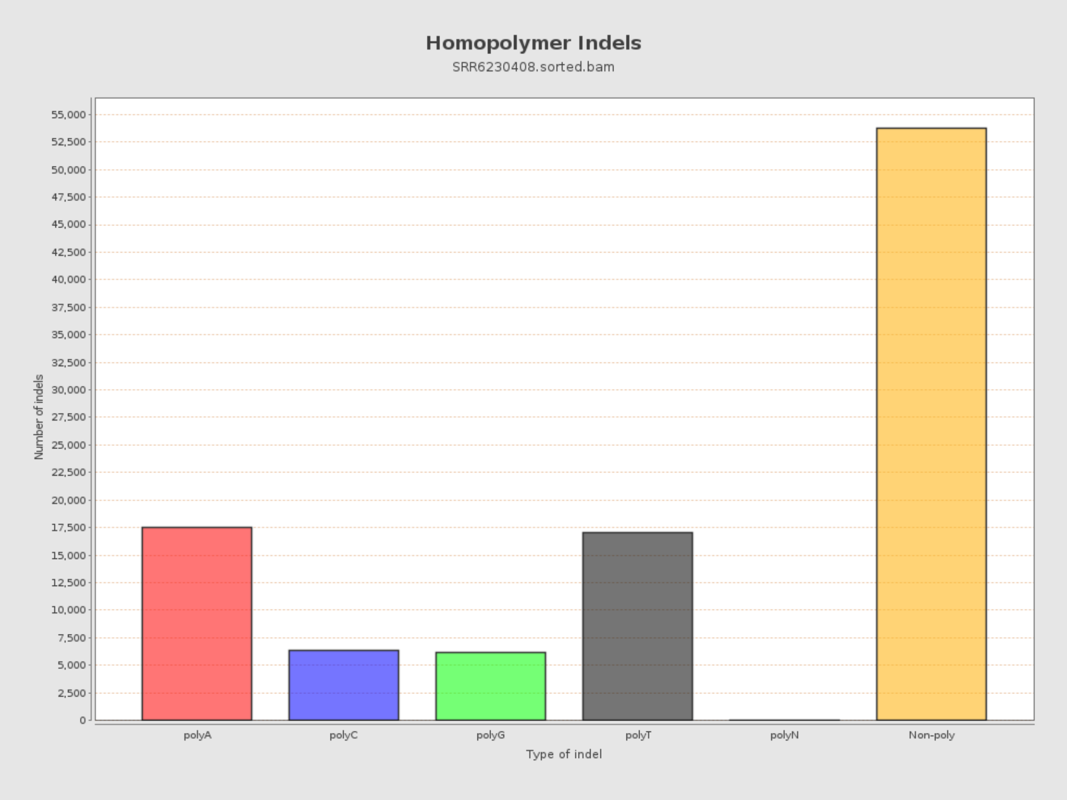
9. Results : Mapped Reads GC-content Distribution



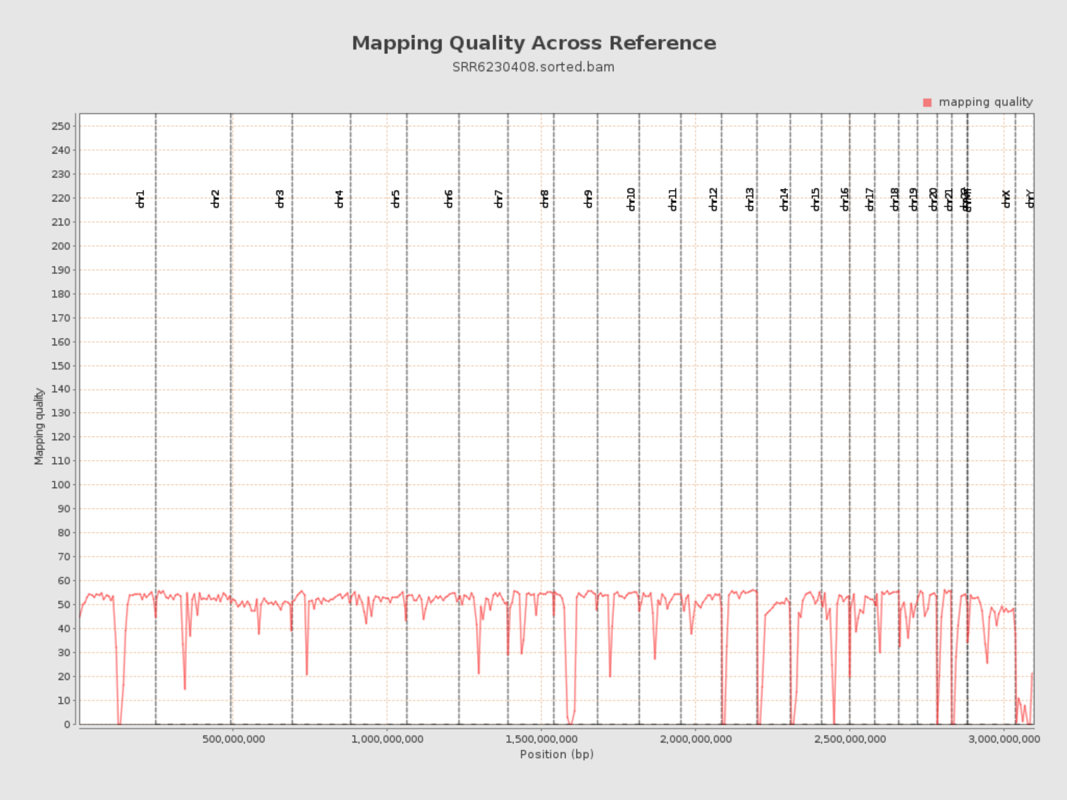
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram