Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 09:49:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068096.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_SRR6068096 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068096.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 09:49:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068096.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,011,262
Mapped reads	852,362 / 84.29%
Unmapped reads	158,900 / 15.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,233 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	19,237 / 1.9%
Duplication rate	1.64%
Clipped reads	352,716 / 34.88%

2.2. ACGT Content

Number/percentage of A's	17,147,286 / 29.68%
Number/percentage of C's	10,449,540 / 18.09%
Number/percentage of T's	17,688,801 / 30.62%
Number/percentage of G's	12,477,598 / 21.6%
Number/percentage of N's	1,141 / 0%
GC Percentage	39.69%

2.3. Coverage

Mean	0.0187

Standard Deviation	0.2285

2.4. Mapping Quality

Mean Mapping Quality	44.95

2.5. Mismatches and indels

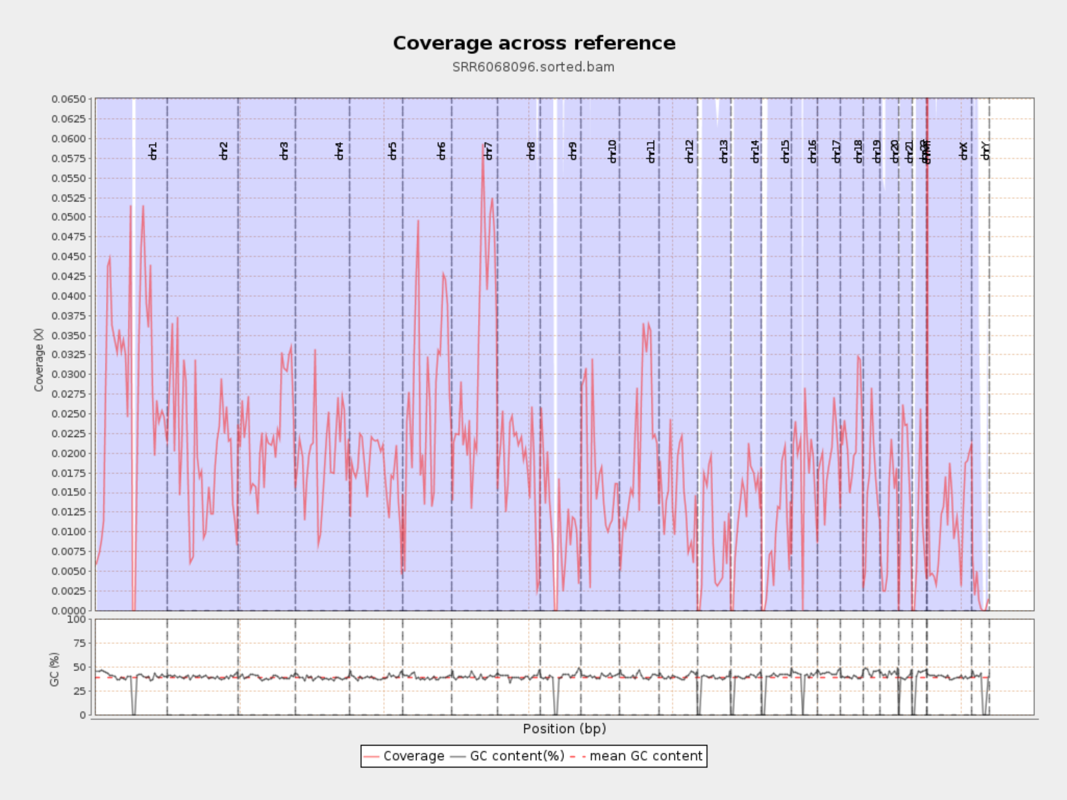
General error rate	1.05%
Mismatches	597,521
Insertions	4,866
Mapped reads with at least one insertion	0.57%
Deletions	16,799
Mapped reads with at least one deletion	1.95%
Homopolymer indels	45.41%

2.6. Chromosome stats

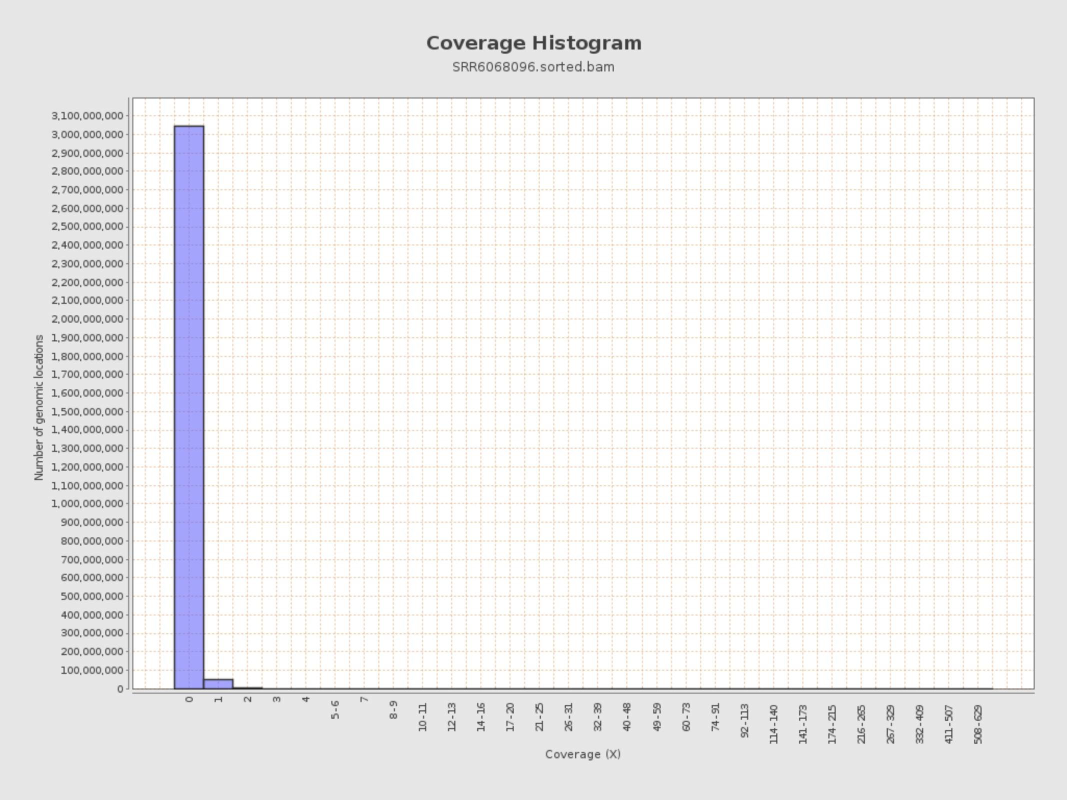
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7041023	0.0282	0.5106
chr2	243199373	4886213	0.0201	0.203
chr3	198022430	4559337	0.023	0.1597
chr4	191154276	3774364	0.0197	0.1485
chr5	180915260	3244550	0.0179	0.1404
chr6	171115067	4665883	0.0273	0.2012
chr7	159138663	5139510	0.0323	0.2245

chr8	146364022	2739217	0.0187	0.3569
chr9	141213431	1533428	0.0109	0.1531
chr10	135534747	2310831	0.017	0.1974
chr11	135006516	2878289	0.0213	0.1787
chr12	133851895	1935298	0.0145	0.1303
chr13	115169878	1006270	0.0087	0.0978
chr14	107349540	1396956	0.013	0.1257
chr15	102531392	902717	0.0088	0.0992
chr16	90354753	1644284	0.0182	0.1515
chr17	81195210	1550781	0.0191	0.1533
chr18	78077248	1759698	0.0225	0.2754
chr19	59128983	927852	0.0157	0.3258
chr20	63025520	697225	0.0111	0.1178
chr21	48129895	786544	0.0163	0.1367
chr22	51304566	474601	0.0093	0.1009
chrMT	16571	15499	0.9353	1.1607
chrX	155270560	1812001	0.0117	0.1243
chrY	59373566	109678	0.0018	0.0502

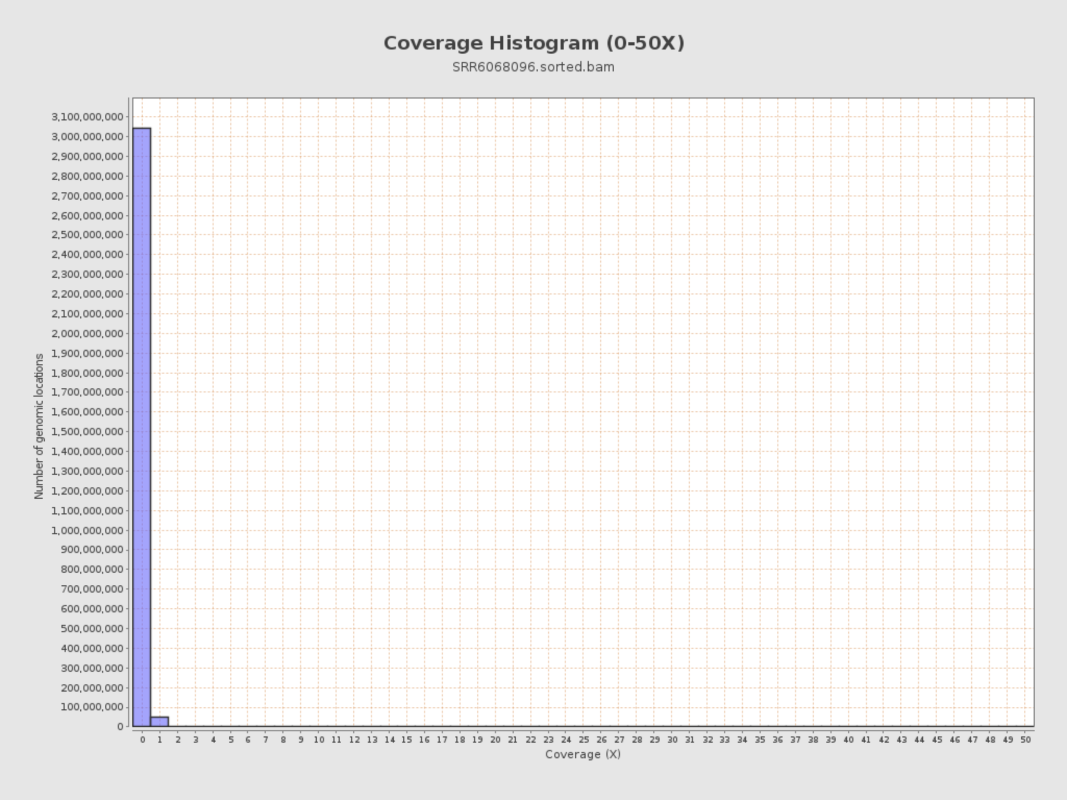
3. Results : Coverage across reference



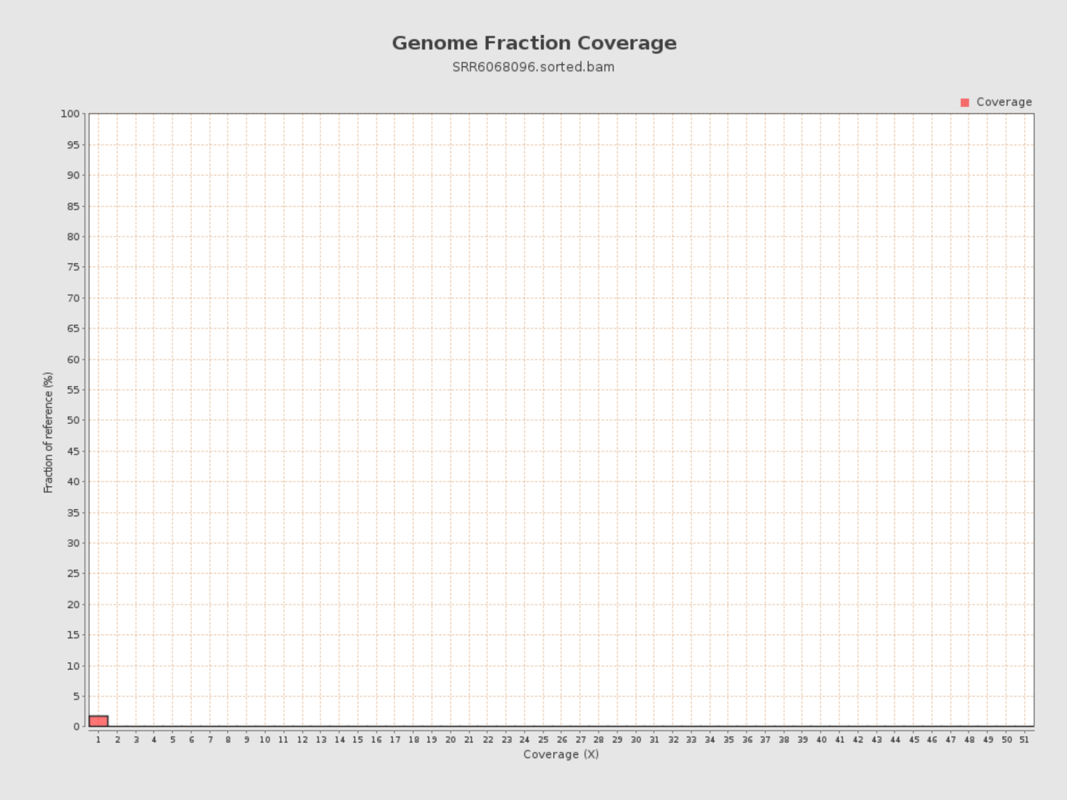
4. Results : Coverage Histogram



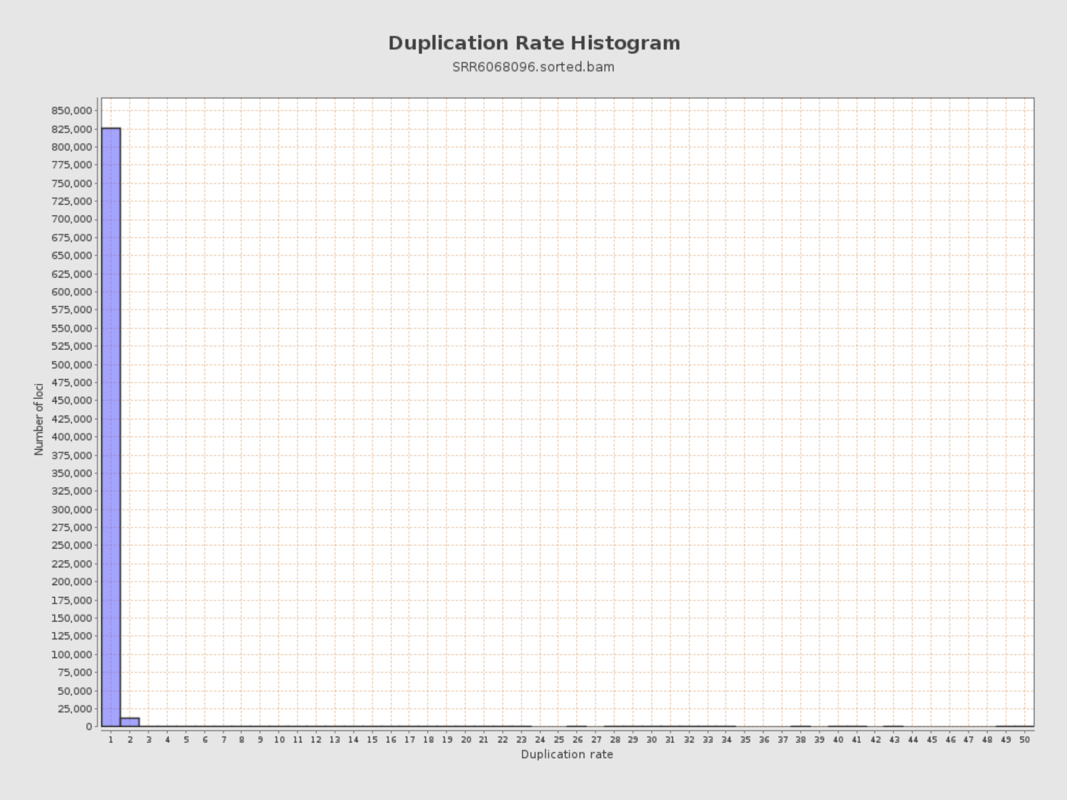
5. Results : Coverage Histogram (0-50X)



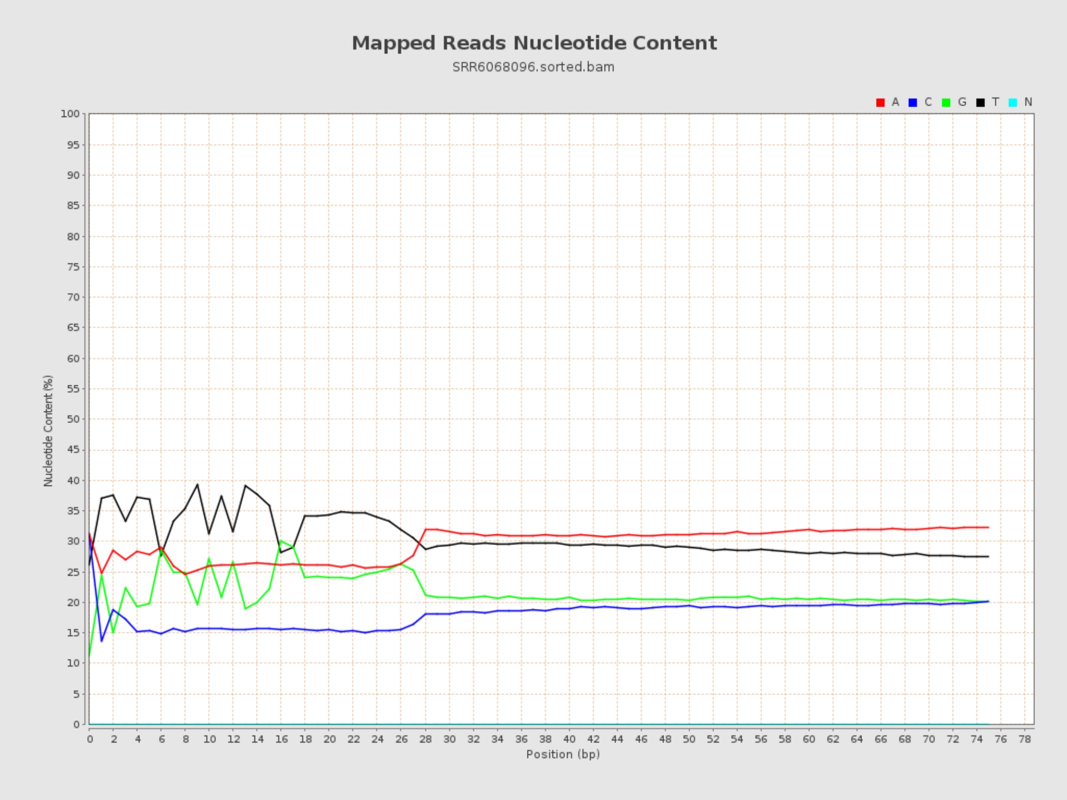
6. Results : Genome Fraction Coverage



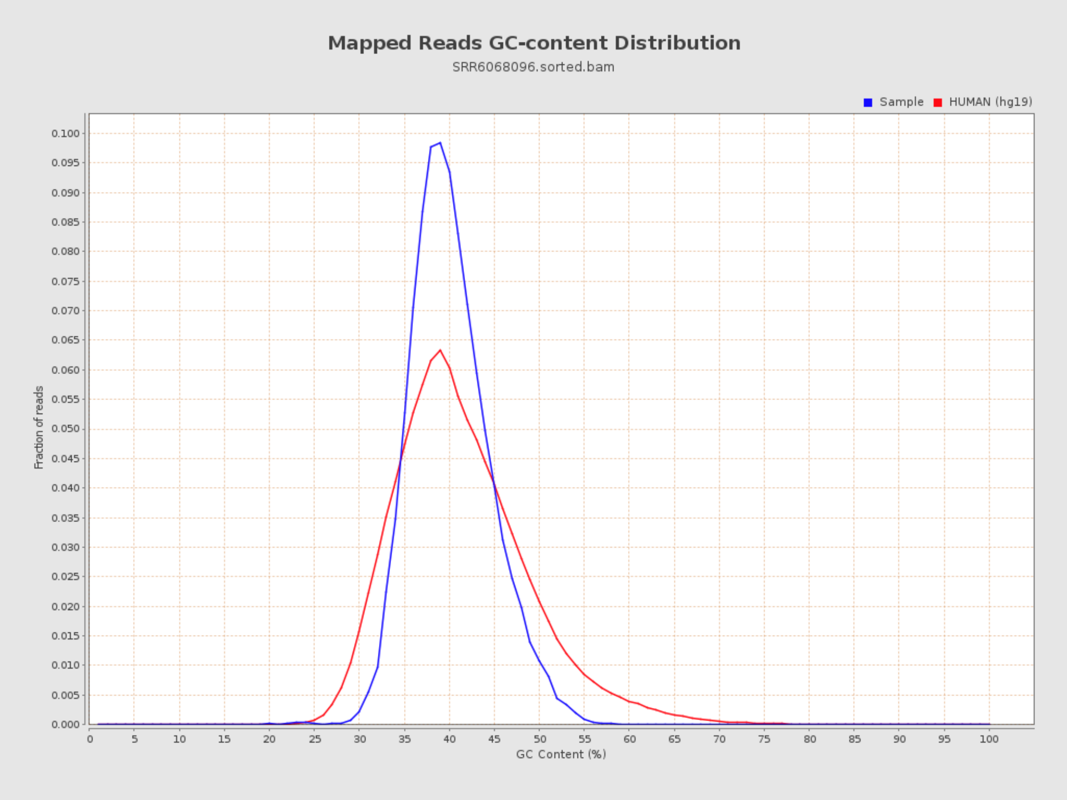
7. Results : Duplication Rate Histogram



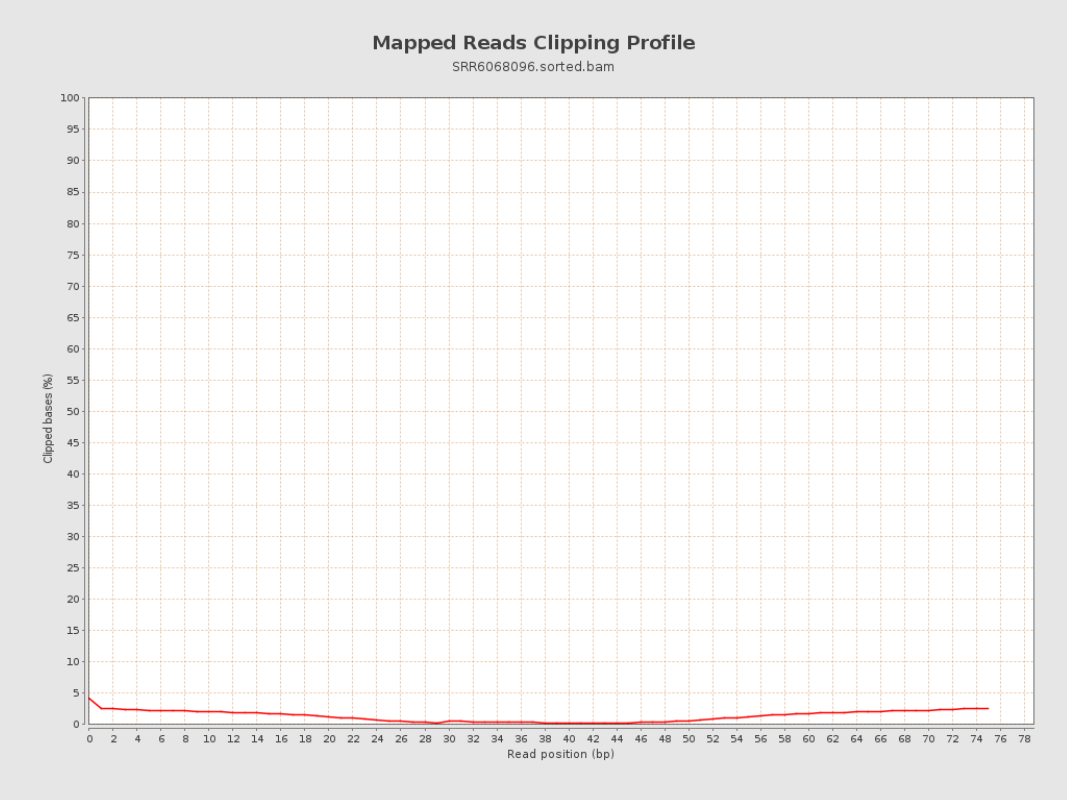
8. Results : Mapped Reads Nucleotide Content



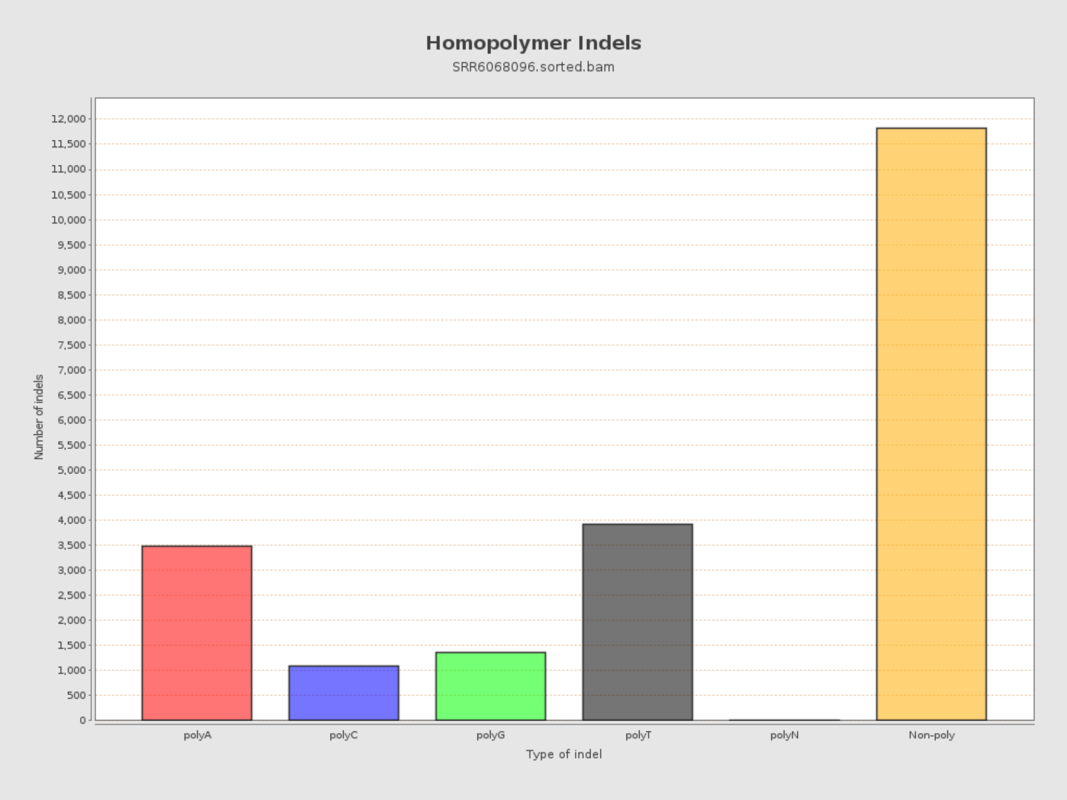
9. Results : Mapped Reads GC-content Distribution



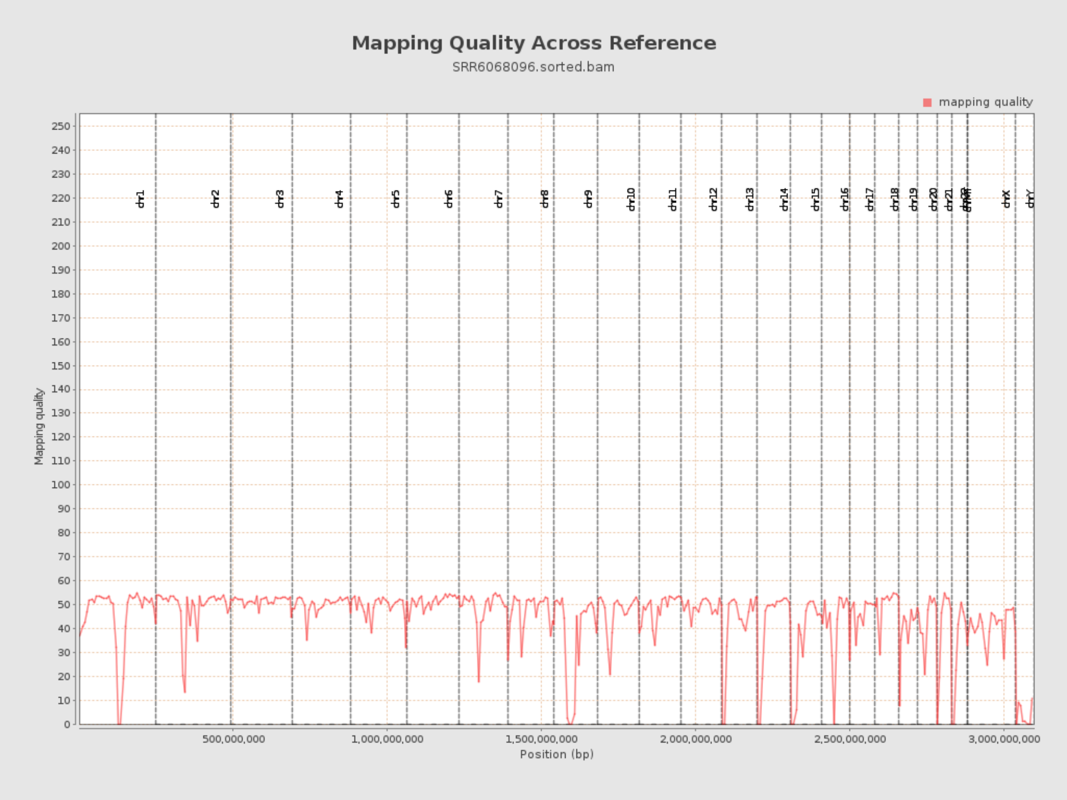
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram