Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 08:42:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068078.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_SRR6068078 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068078.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 08:42:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068078.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,566,952
Mapped reads	2,326,519 / 90.63%
Unmapped reads	240,433 / 9.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,729 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	155,545 / 6.06%
Duplication rate	5.38%
Clipped reads	1,115,876 / 43.47%

2.2. ACGT Content

Number/percentage of A's	42,707,488 / 27.77%
Number/percentage of C's	28,566,337 / 18.57%
Number/percentage of T's	48,475,366 / 31.52%
Number/percentage of G's	34,040,876 / 22.13%
Number/percentage of N's	3,072 / 0%
GC Percentage	40.71%

2.3. Coverage

Mean	0.0497

Standard Deviation	0.4976

2.4. Mapping Quality

Mean Mapping Quality	45.04

2.5. Mismatches and indels

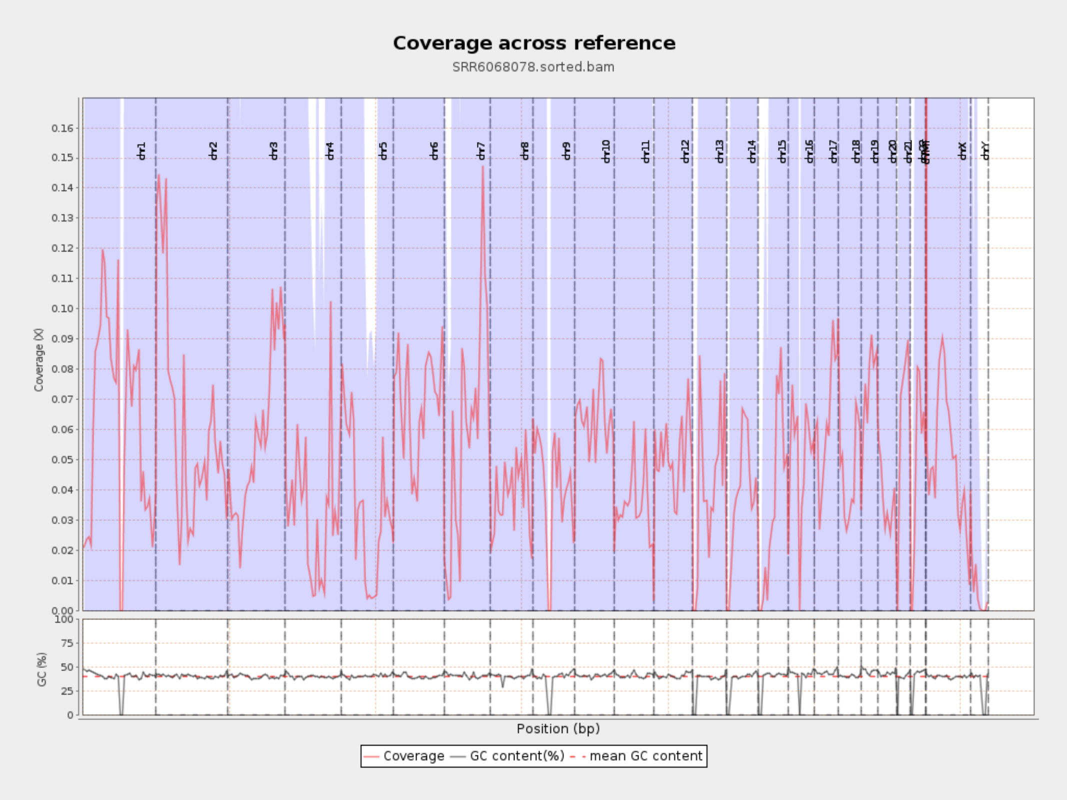
General error rate	0.78%
Mismatches	1,186,114
Insertions	12,051
Mapped reads with at least one insertion	0.51%
Deletions	41,467
Mapped reads with at least one deletion	1.76%
Homopolymer indels	46.45%

2.6. Chromosome stats

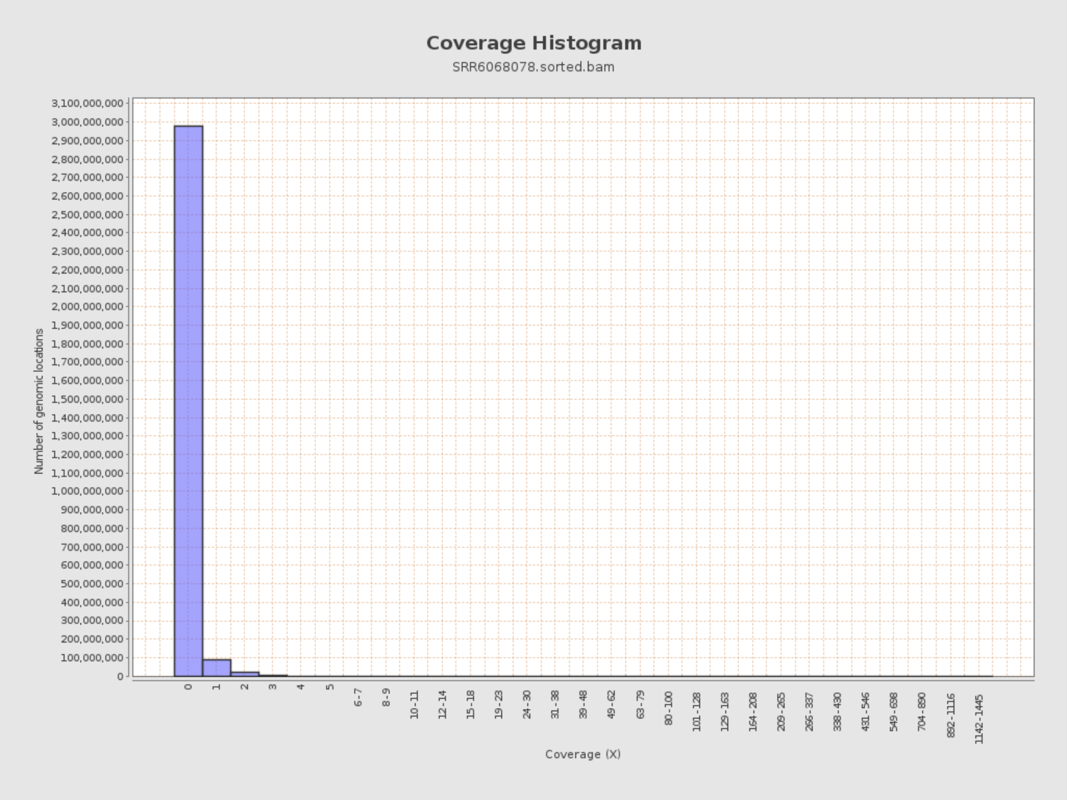
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15404176	0.0618	1.0073
chr2	243199373	15255140	0.0627	0.5499
chr3	198022430	11389593	0.0575	0.3008
chr4	191154276	6286609	0.0329	0.2479
chr5	180915260	6245135	0.0345	0.2358
chr6	171115067	11927690	0.0697	0.364
chr7	159138663	9381929	0.059	0.6292

chr8	146364022	5583068	0.0381	0.8599
chr9	141213431	5772650	0.0409	0.3832
chr10	135534747	8718955	0.0643	0.4053
chr11	135006516	4881900	0.0362	0.3109
chr12	133851895	6974677	0.0521	0.3006
chr13	115169878	4787762	0.0416	0.2572
chr14	107349540	4080011	0.038	0.2765
chr15	102531392	3533244	0.0345	0.2409
chr16	90354753	4512416	0.0499	0.302
chr17	81195210	5115339	0.063	0.3207
chr18	78077248	3683757	0.0472	0.7167
chr19	59128983	4389545	0.0742	0.6918
chr20	63025520	2305872	0.0366	0.2492
chr21	48129895	2994427	0.0622	0.3286
chr22	51304566	2460844	0.048	0.2719
chrMT	16571	16451	0.9928	1.5374
chrX	155270560	7826725	0.0504	0.3298
chrY	59373566	332410	0.0056	0.1331

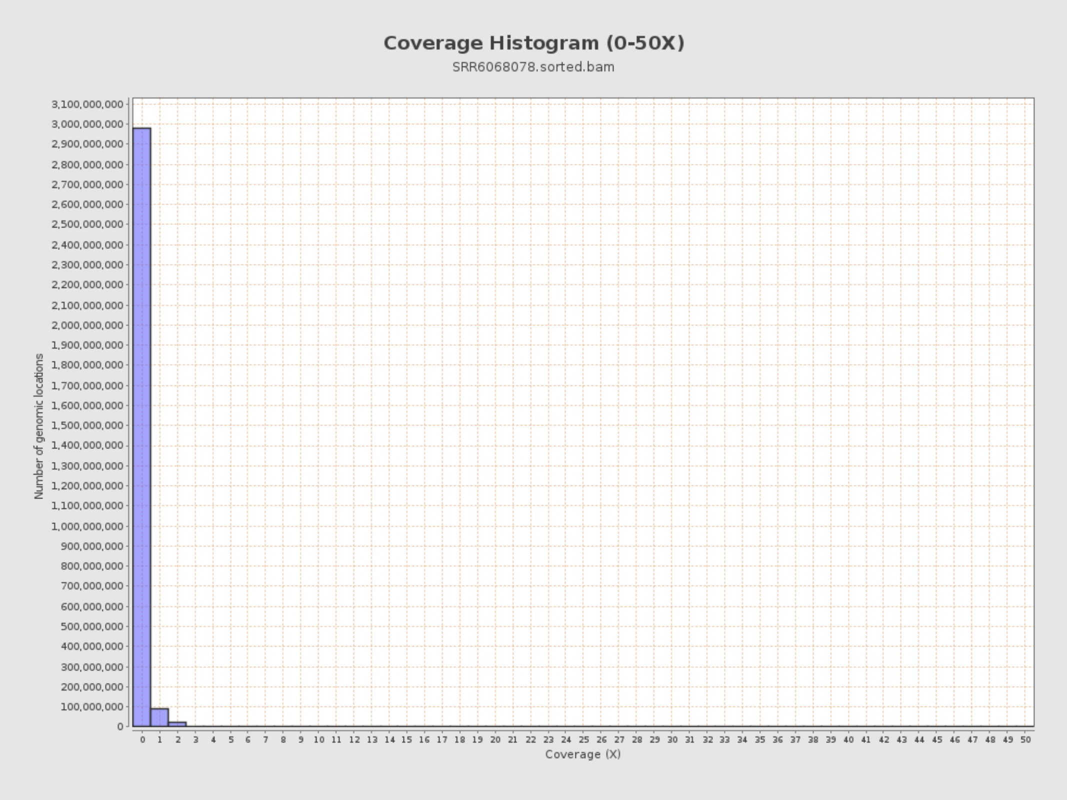
3. Results : Coverage across reference



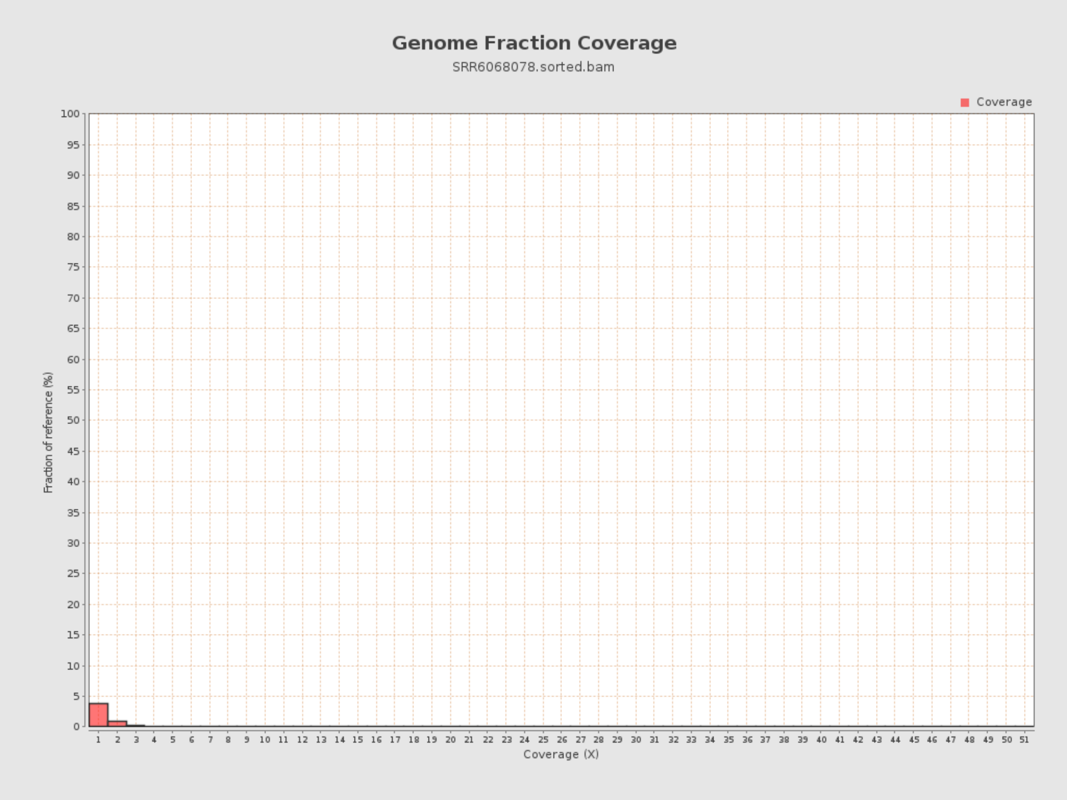
4. Results : Coverage Histogram



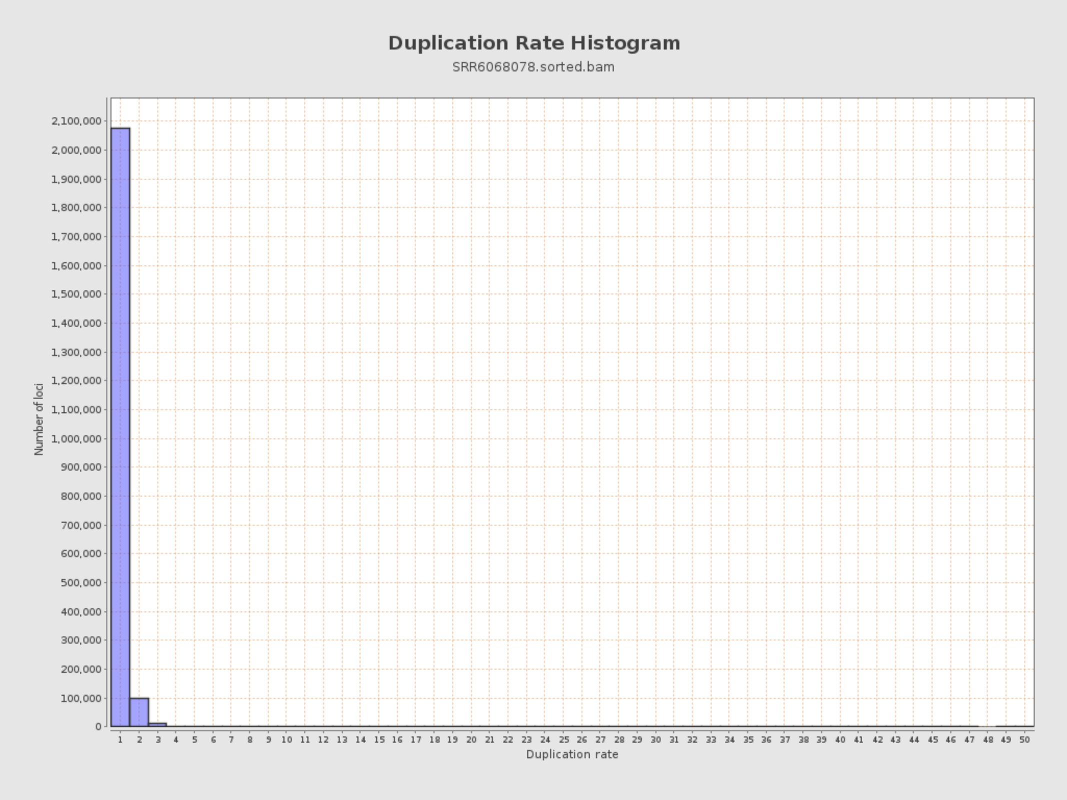
5. Results : Coverage Histogram (0-50X)



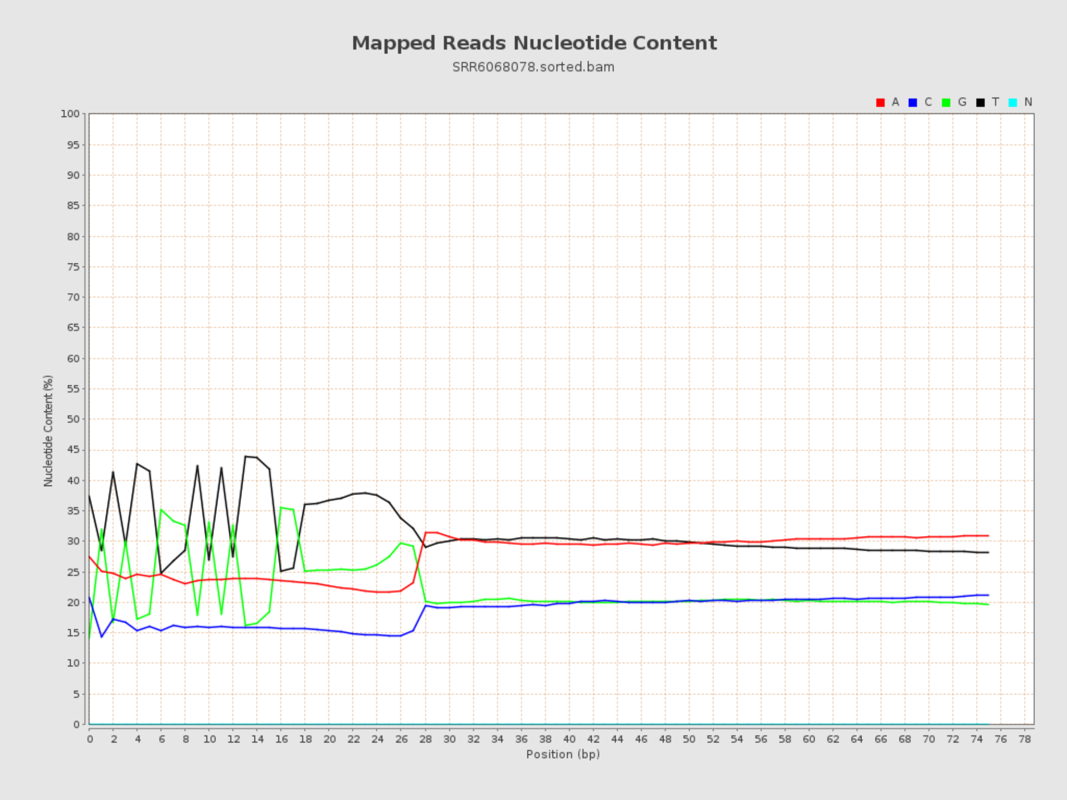
6. Results : Genome Fraction Coverage



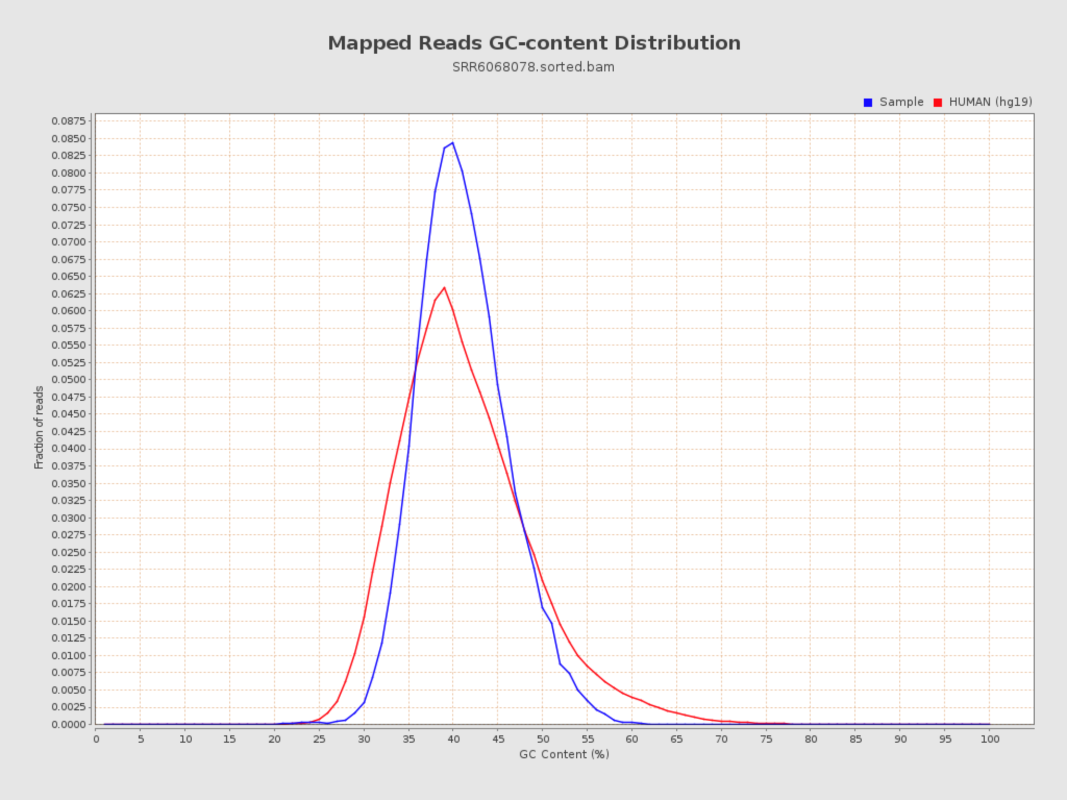
7. Results : Duplication Rate Histogram



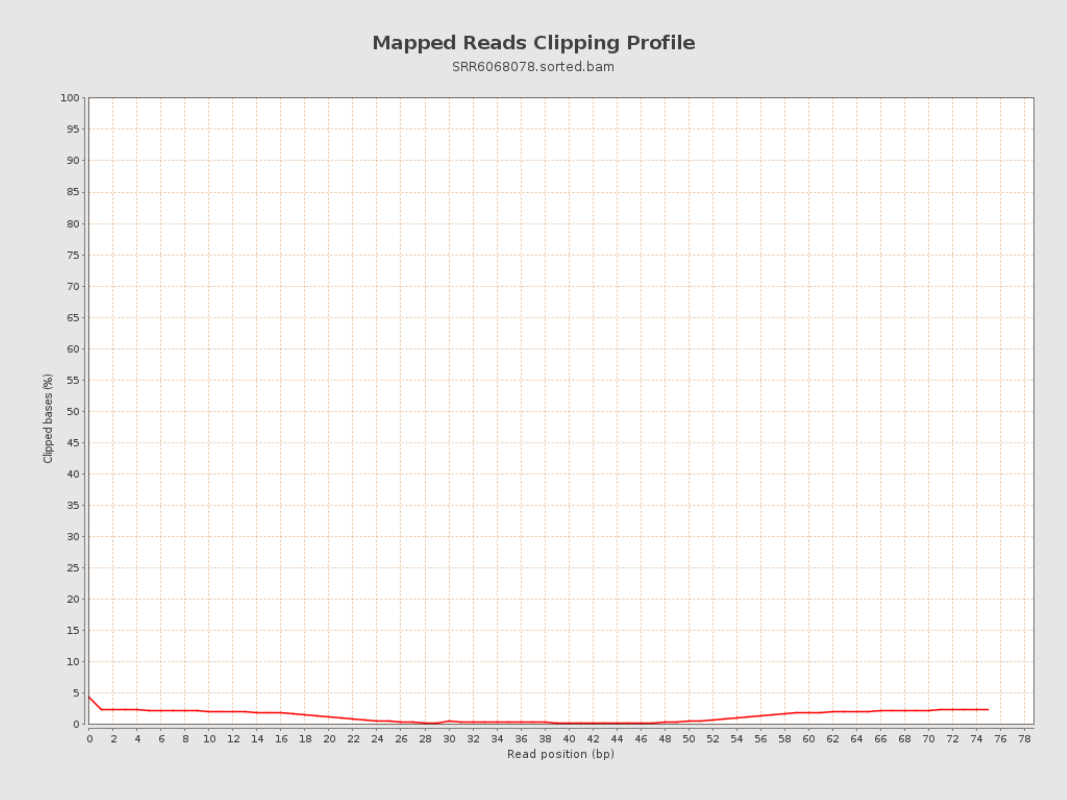
8. Results : Mapped Reads Nucleotide Content



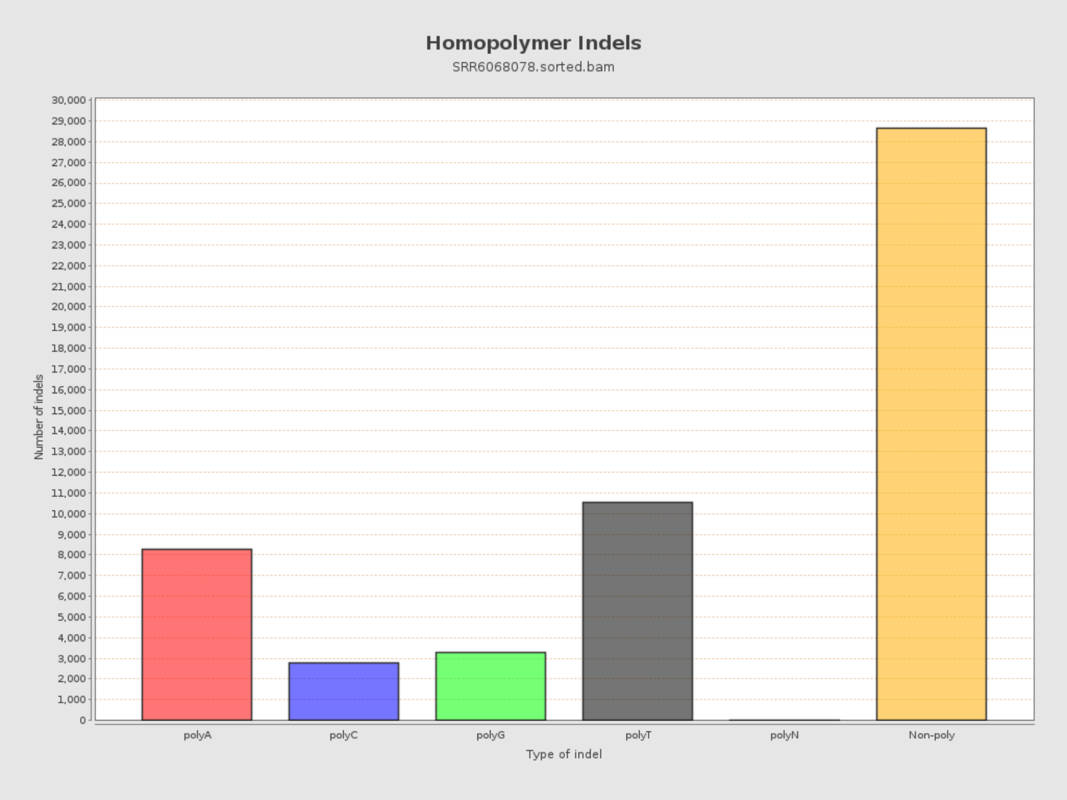
9. Results : Mapped Reads GC-content Distribution



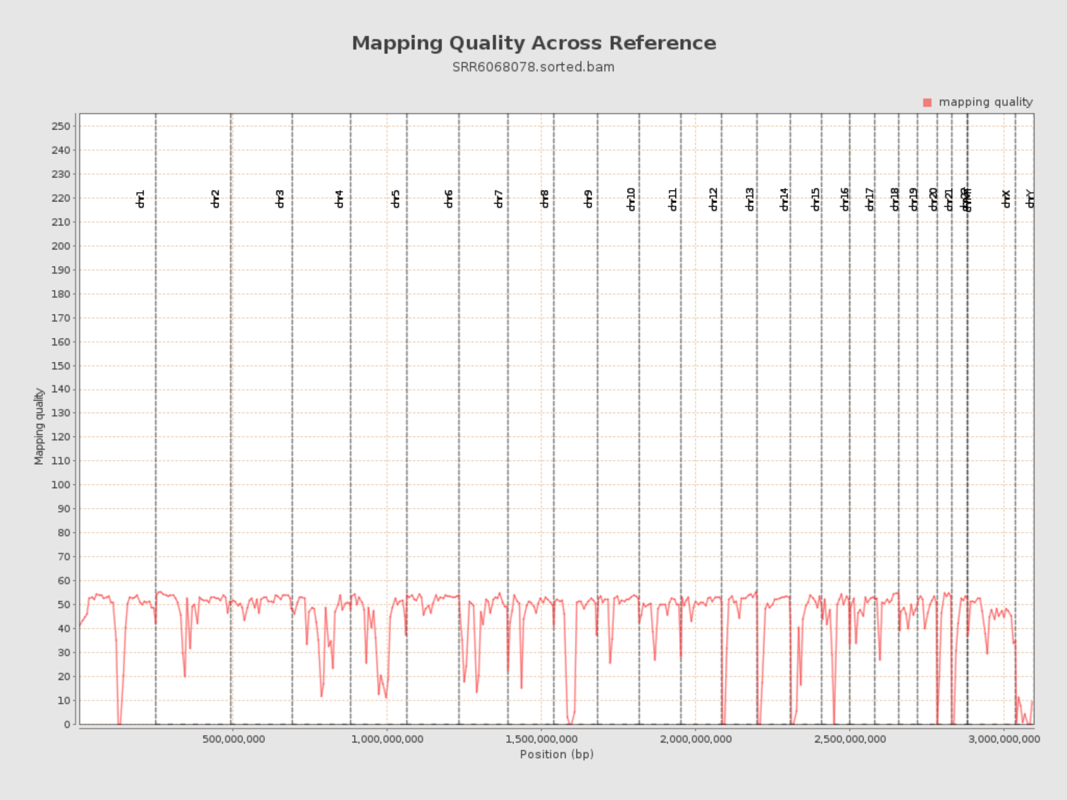
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram