Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 15:47:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068927.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_SRR6068927 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068927.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 15:47:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068927.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,861,119
Mapped reads	1,170,954 / 62.92%
Unmapped reads	690,165 / 37.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,878 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	127,865 / 6.87%
Duplication rate	9.05%
Clipped reads	721,323 / 38.76%

2.2. ACGT Content

Number/percentage of A's	19,052,196 / 26.07%
Number/percentage of C's	12,144,247 / 16.62%
Number/percentage of T's	24,940,690 / 34.13%
Number/percentage of G's	16,788,689 / 22.97%
Number/percentage of N's	158,533 / 0.22%
GC Percentage	39.59%

2.3. Coverage

Mean	0.0236

Standard Deviation	0.2633

2.4. Mapping Quality

Mean Mapping Quality	45.98

2.5. Mismatches and indels

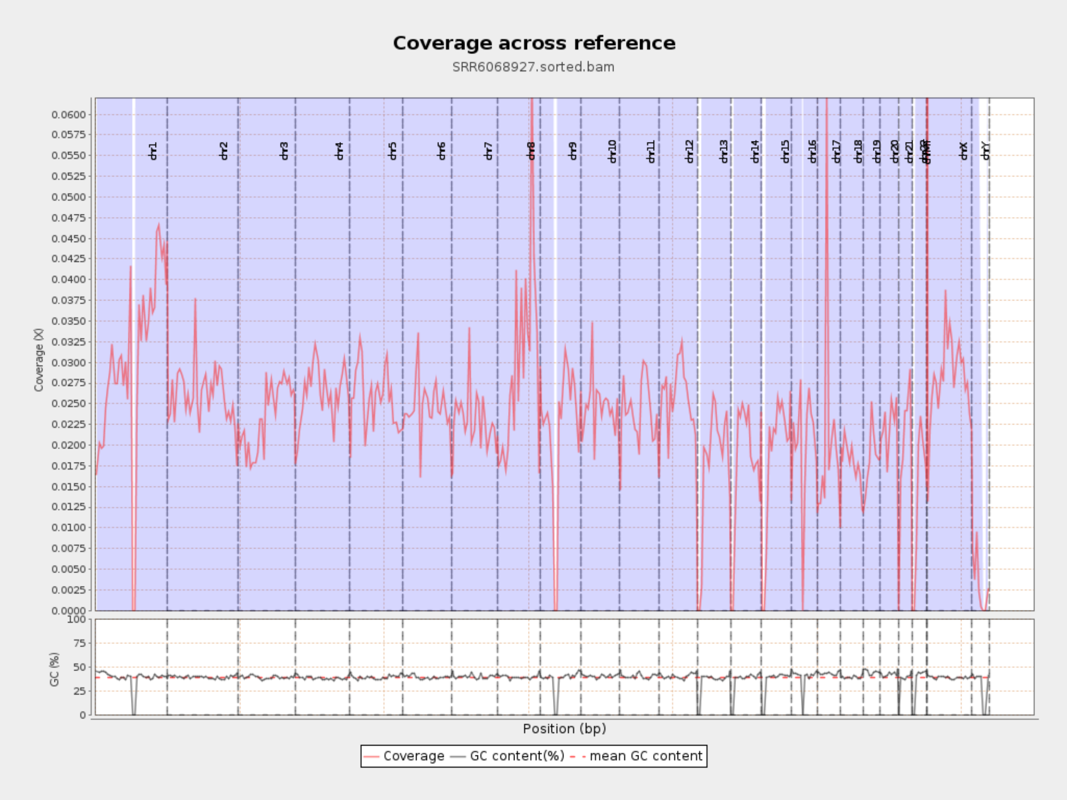
General error rate	1.12%
Mismatches	810,988
Insertions	6,374
Mapped reads with at least one insertion	0.54%
Deletions	26,442
Mapped reads with at least one deletion	2.23%
Homopolymer indels	48.84%

2.6. Chromosome stats

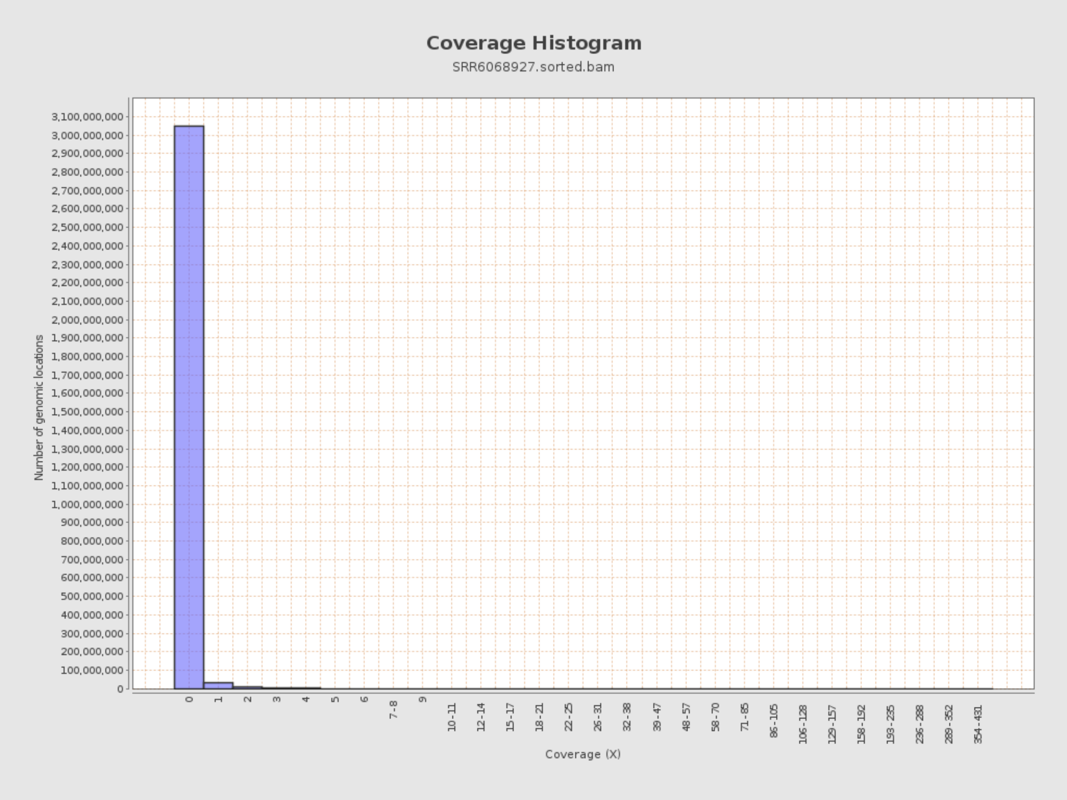
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7497886	0.0301	0.3965
chr2	243199373	6357094	0.0261	0.2762
chr3	198022430	4656180	0.0235	0.2187
chr4	191154276	5032566	0.0263	0.2403
chr5	180915260	4695300	0.026	0.2333
chr6	171115067	4205143	0.0246	0.2521
chr7	159138663	3681785	0.0231	0.294

chr8	146364022	4366897	0.0298	0.3501
chr9	141213431	3091065	0.0219	0.2509
chr10	135534747	3317329	0.0245	0.2537
chr11	135006516	3256809	0.0241	0.2515
chr12	133851895	3461516	0.0259	0.235
chr13	115169878	2018449	0.0175	0.1901
chr14	107349540	1877324	0.0175	0.1939
chr15	102531392	1866697	0.0182	0.1968
chr16	90354753	1780270	0.0197	0.2053
chr17	81195210	1719065	0.0212	0.2182
chr18	78077248	1404011	0.018	0.344
chr19	59128983	1089814	0.0184	0.2596
chr20	63025520	1387286	0.022	0.2143
chr21	48129895	962031	0.02	0.2089
chr22	51304566	725345	0.0141	0.1676
chrMT	16571	88747	5.3556	4.7127
chrX	155270560	4402798	0.0284	0.2493
chrY	59373566	184273	0.0031	0.0842

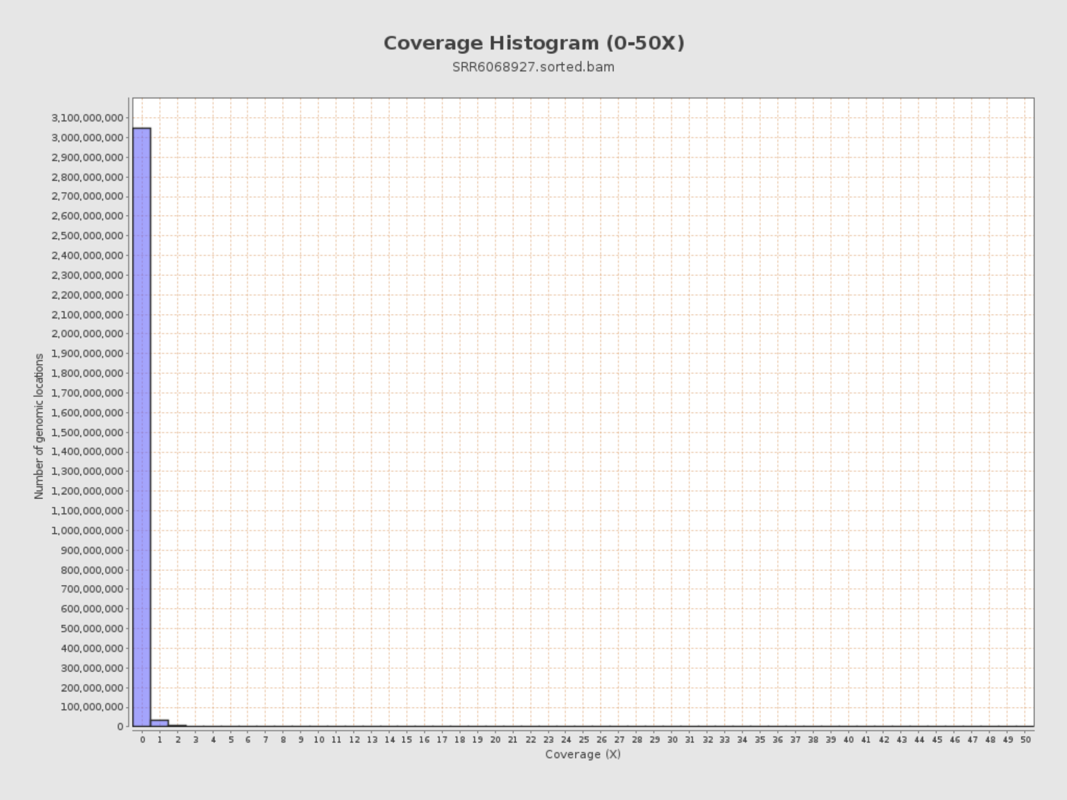
3. Results : Coverage across reference



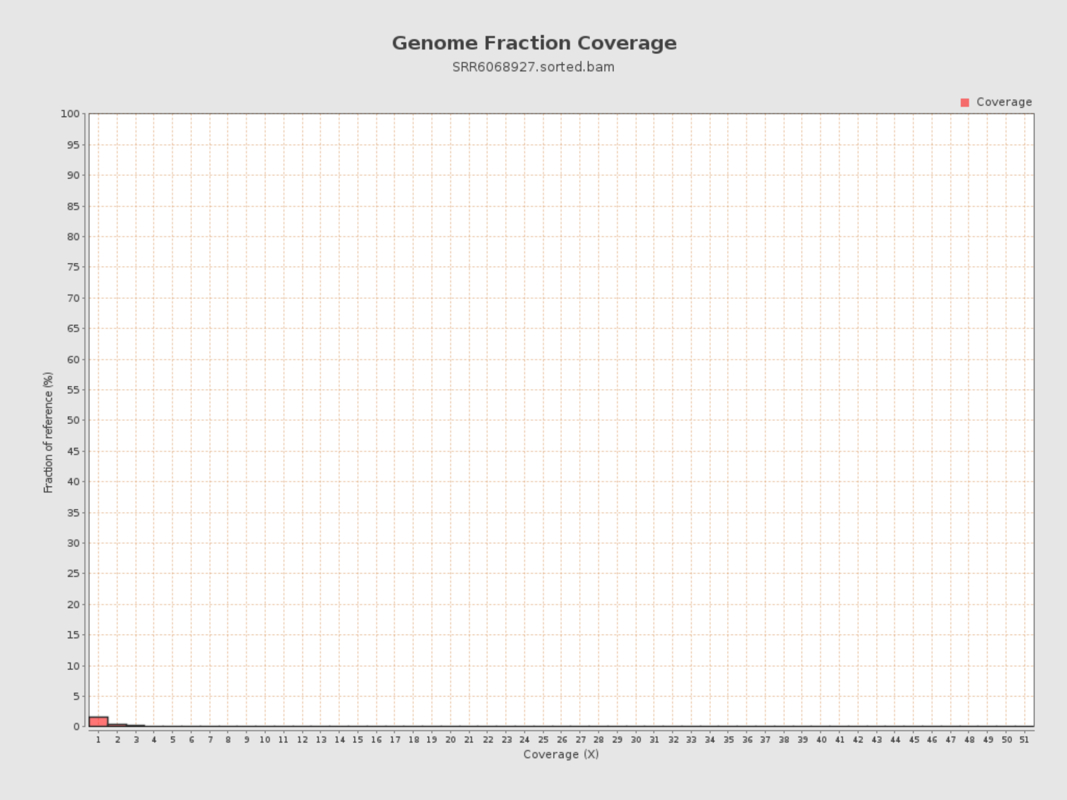
4. Results : Coverage Histogram



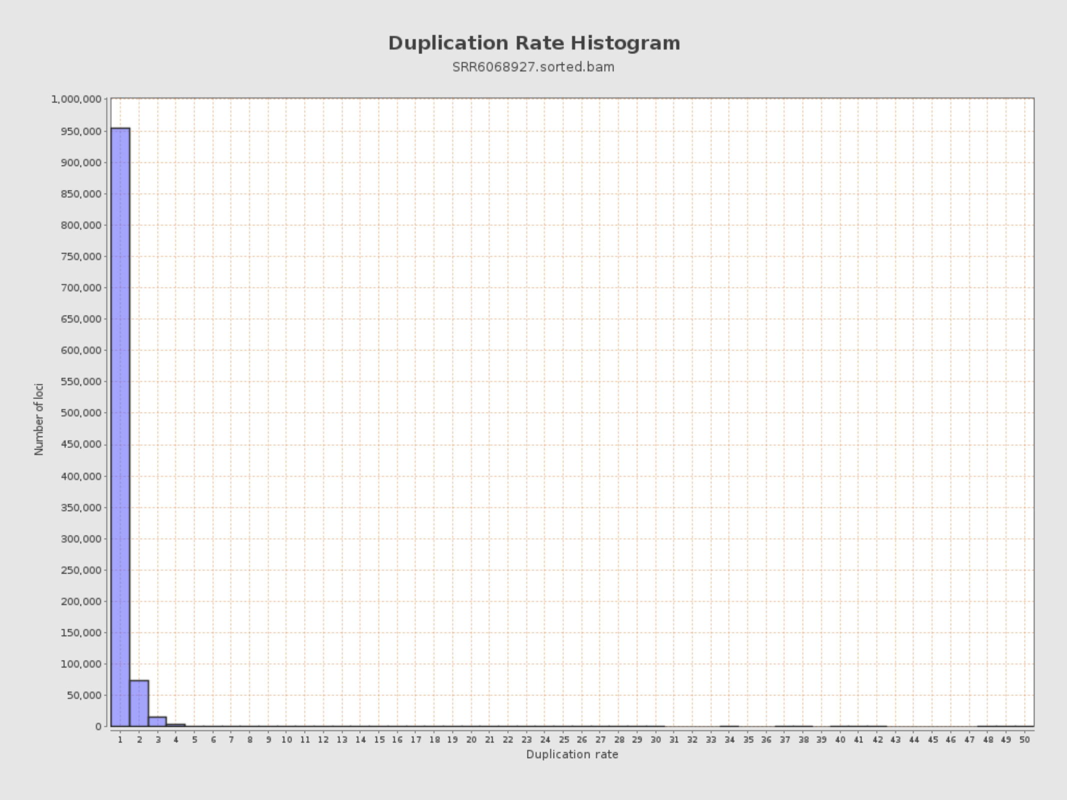
5. Results : Coverage Histogram (0-50X)



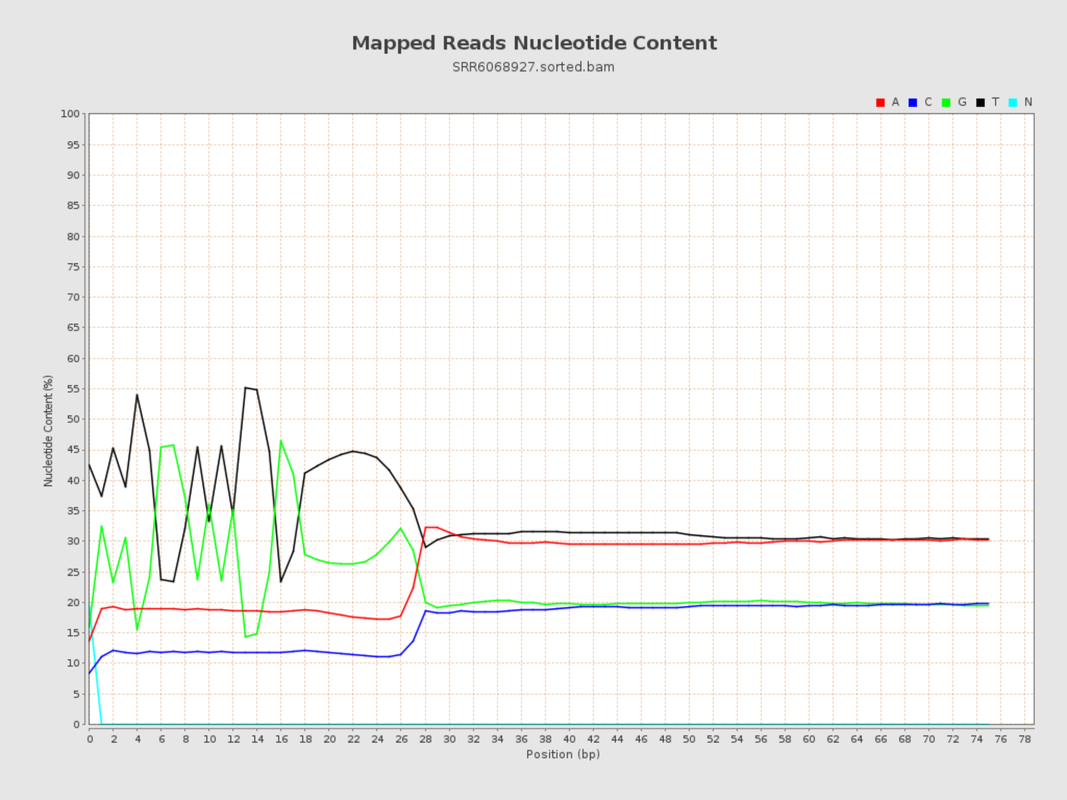
6. Results : Genome Fraction Coverage



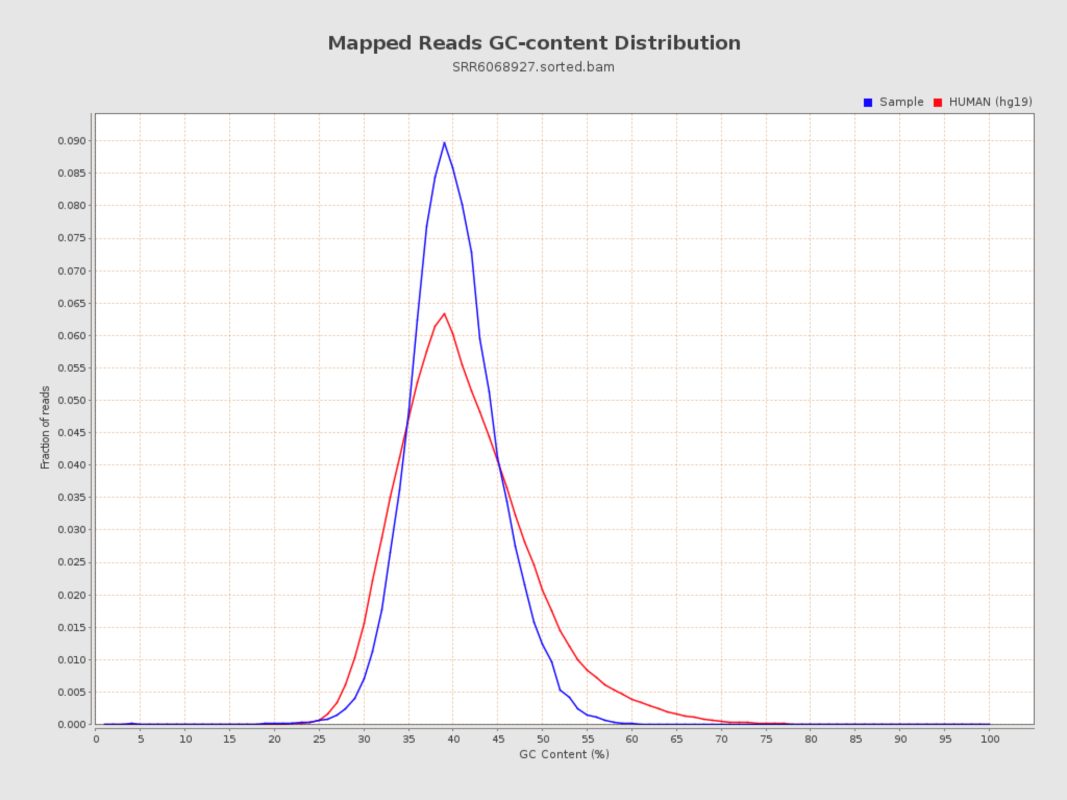
7. Results : Duplication Rate Histogram



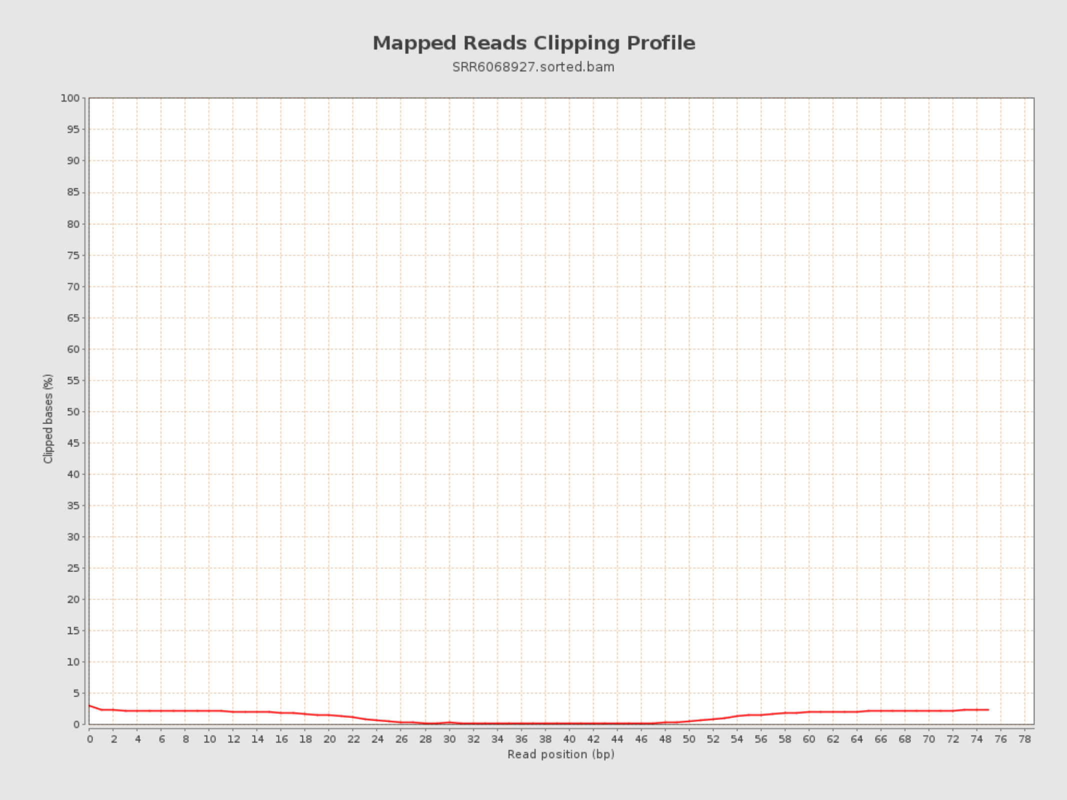
8. Results : Mapped Reads Nucleotide Content



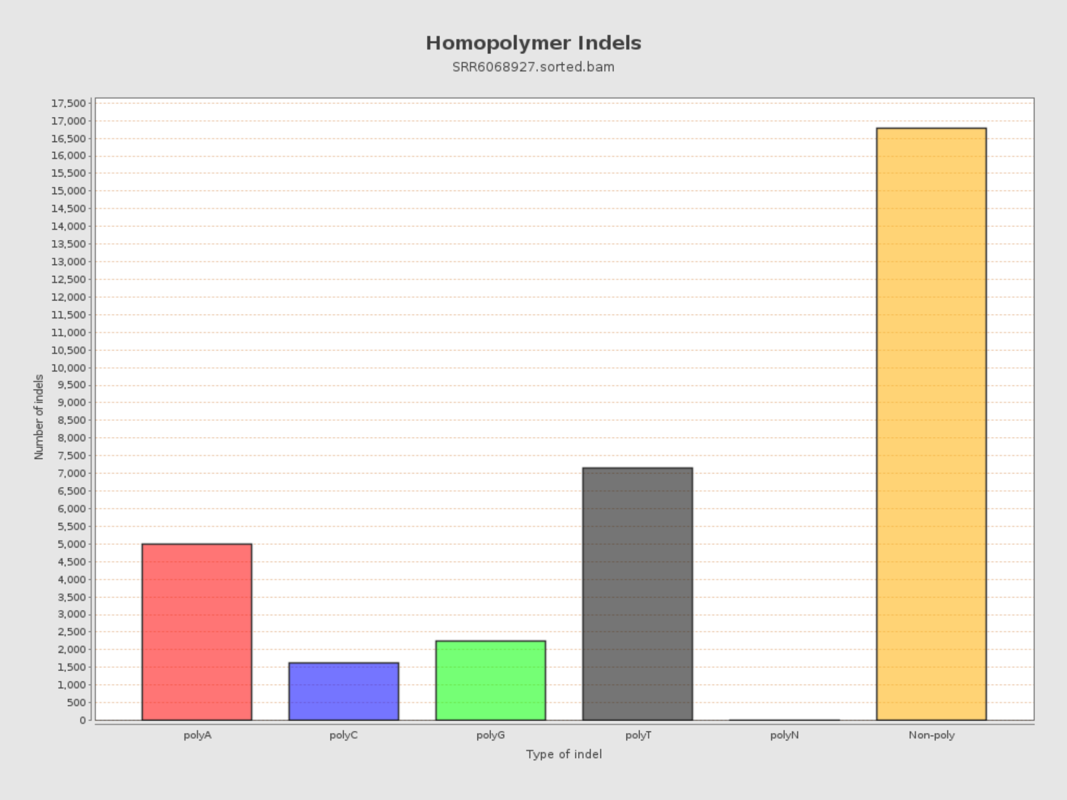
9. Results : Mapped Reads GC-content Distribution



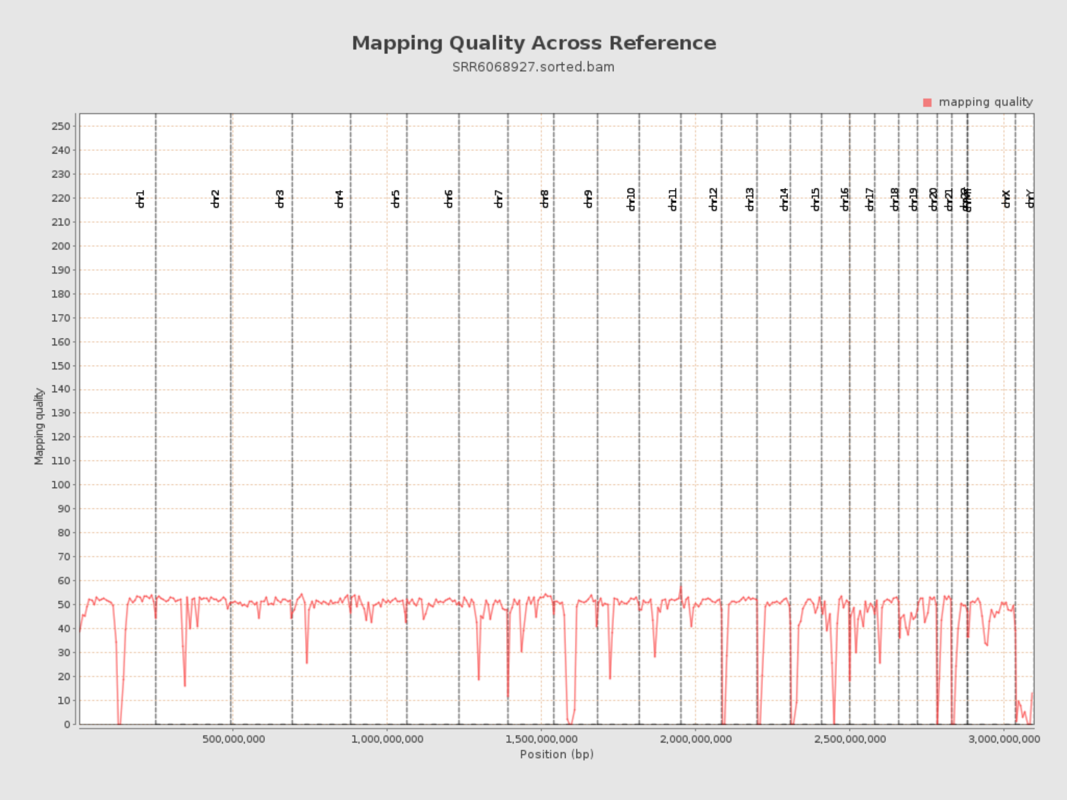
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram