Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 17:33:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068961.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_SRR6068961 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068961.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 17:33:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068961.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,977,447
Mapped reads	1,458,150 / 73.74%
Unmapped reads	519,297 / 26.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,582 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	79,313 / 4.01%
Duplication rate	3.82%
Clipped reads	957,161 / 48.4%

2.2. ACGT Content

Number/percentage of A's	23,036,095 / 25.45%
Number/percentage of C's	15,015,314 / 16.59%
Number/percentage of T's	30,379,545 / 33.57%
Number/percentage of G's	21,874,068 / 24.17%
Number/percentage of N's	201,258 / 0.22%
GC Percentage	40.76%

2.3. Coverage

Mean	0.0293

Standard Deviation	0.3641

2.4. Mapping Quality

Mean Mapping Quality	42.09

2.5. Mismatches and indels

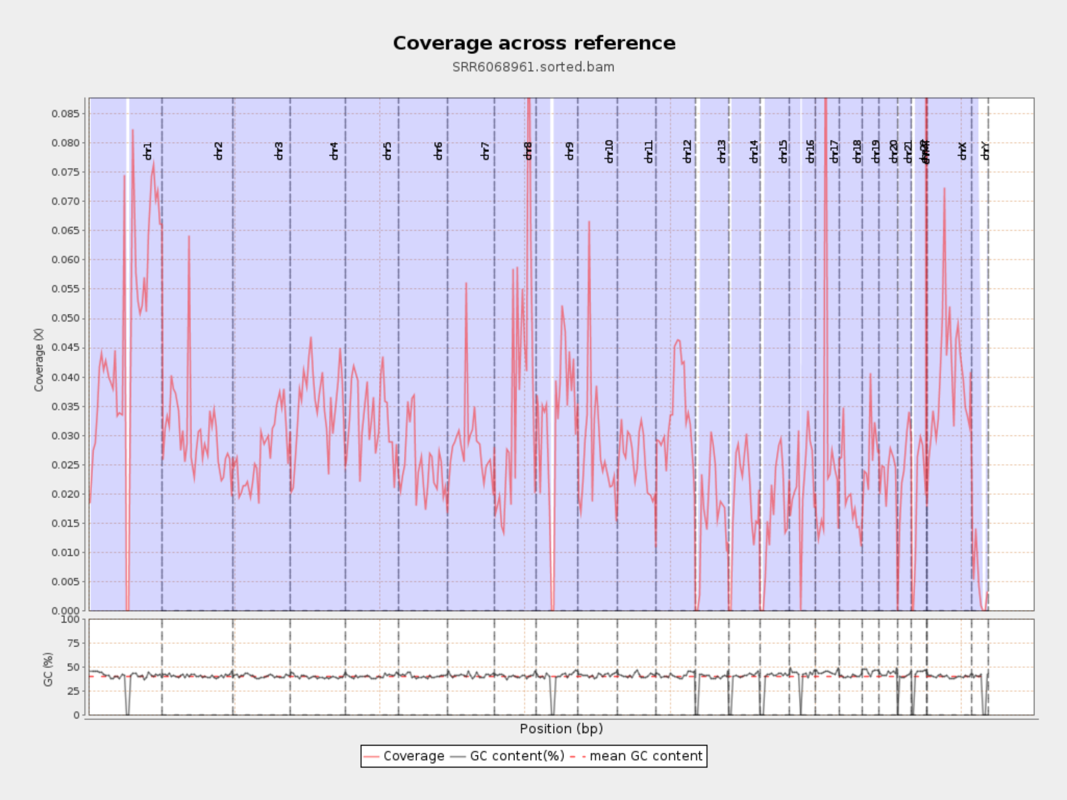
General error rate	1.03%
Mismatches	914,709
Insertions	8,568
Mapped reads with at least one insertion	0.58%
Deletions	31,745
Mapped reads with at least one deletion	2.15%
Homopolymer indels	49%

2.6. Chromosome stats

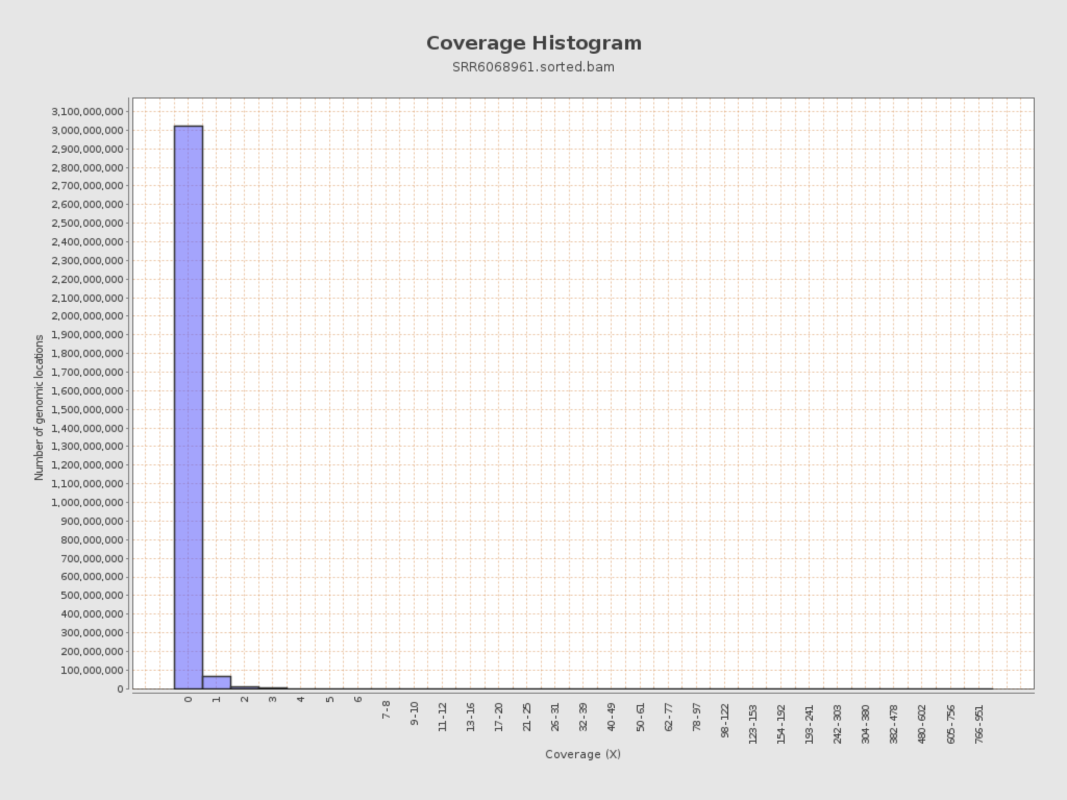
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11595004	0.0465	0.7242
chr2	243199373	7392262	0.0304	0.3713
chr3	198022430	5344256	0.027	0.1988
chr4	191154276	6715814	0.0351	0.2391
chr5	180915260	5996190	0.0331	0.212
chr6	171115067	4256542	0.0249	0.2453
chr7	159138663	4557295	0.0286	0.4843

chr8	146364022	5457937	0.0373	0.3857
chr9	141213431	4542980	0.0322	0.4334
chr10	135534747	3726009	0.0275	0.4172
chr11	135006516	3473794	0.0257	0.2924
chr12	133851895	4544448	0.034	0.2251
chr13	115169878	1905528	0.0165	0.149
chr14	107349540	1995252	0.0186	0.2367
chr15	102531392	1643129	0.016	0.1592
chr16	90354753	1984994	0.022	0.2009
chr17	81195210	2311812	0.0285	0.2334
chr18	78077248	1540444	0.0197	0.5471
chr19	59128983	1601409	0.0271	0.5294
chr20	63025520	1480344	0.0235	0.1985
chr21	48129895	1115189	0.0232	0.1957
chr22	51304566	936302	0.0182	0.1514
chrMT	16571	60694	3.6627	3.8651
chrX	155270560	6113269	0.0394	0.3116
chrY	59373566	266487	0.0045	0.1211

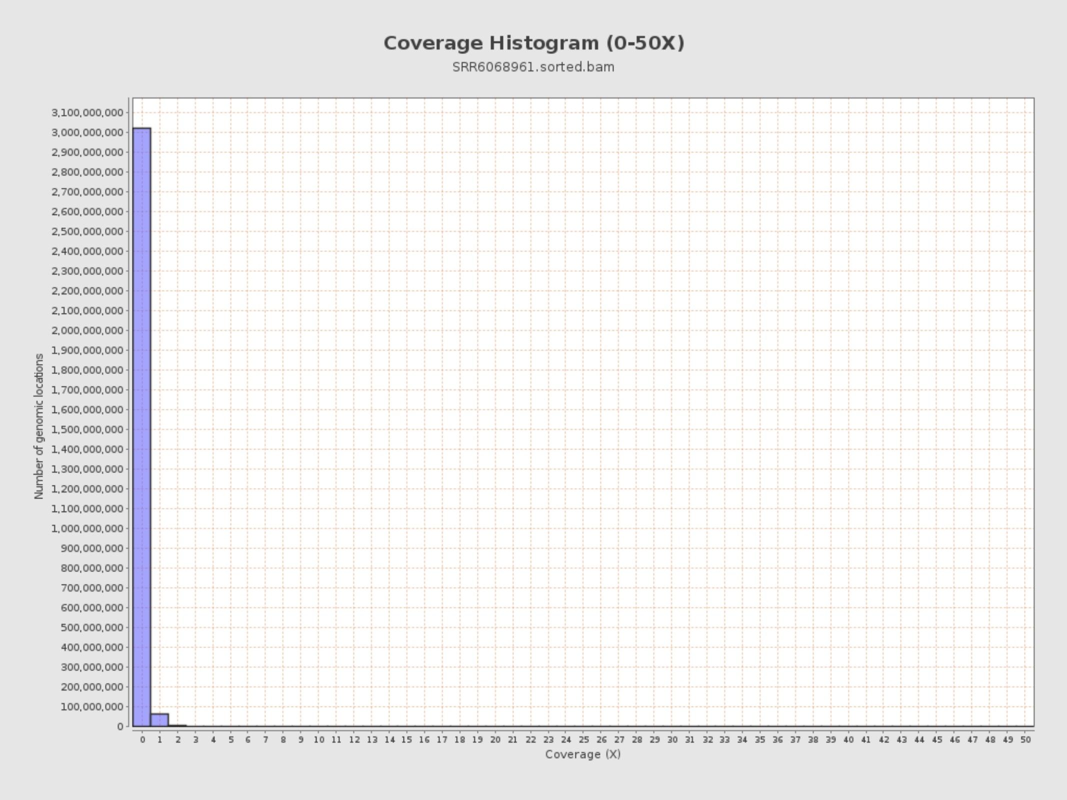
3. Results : Coverage across reference



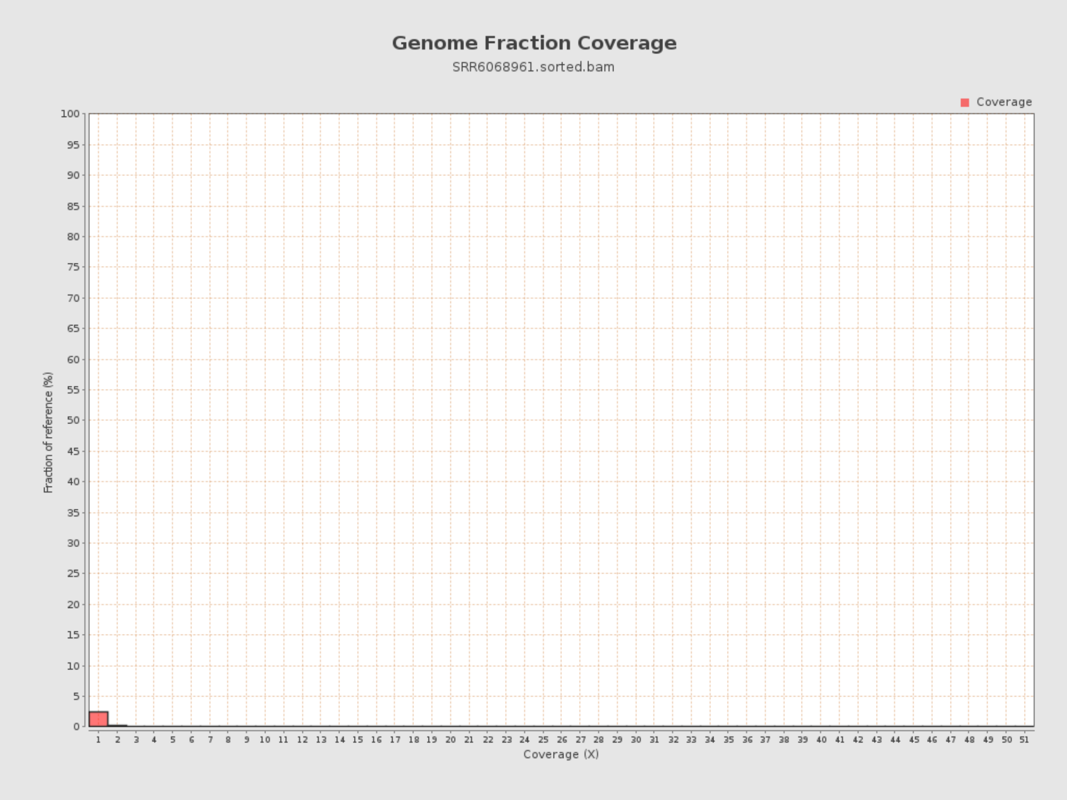
4. Results : Coverage Histogram



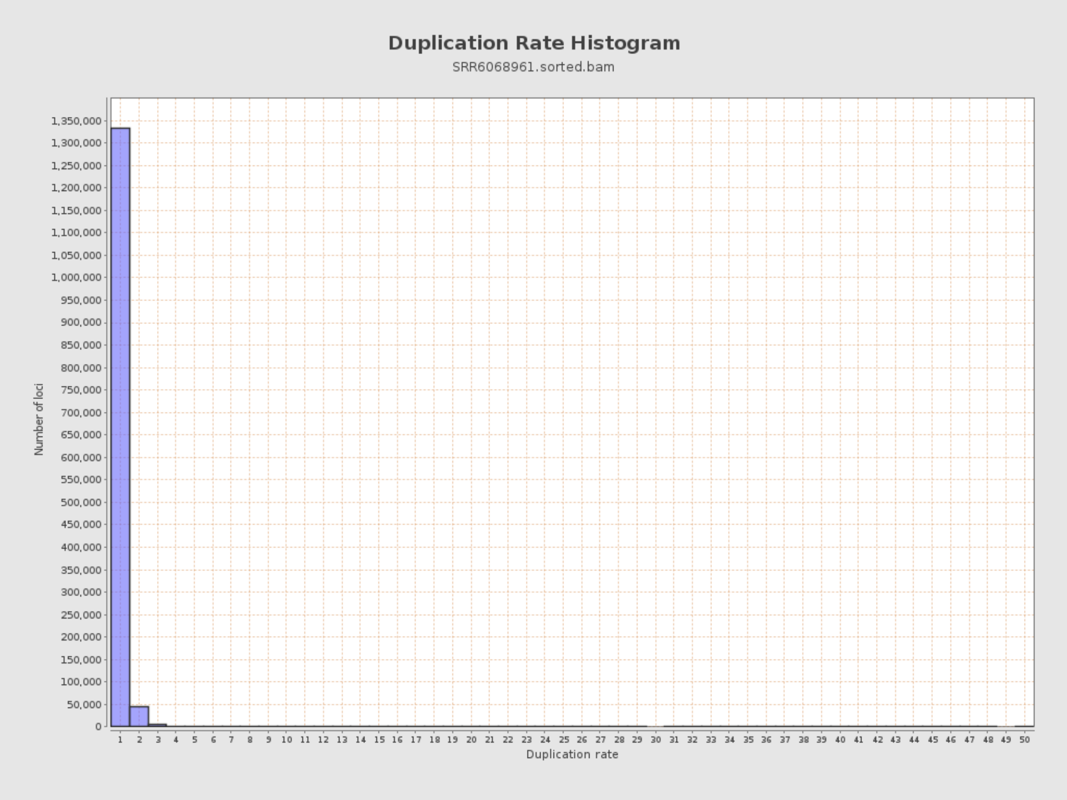
5. Results : Coverage Histogram (0-50X)



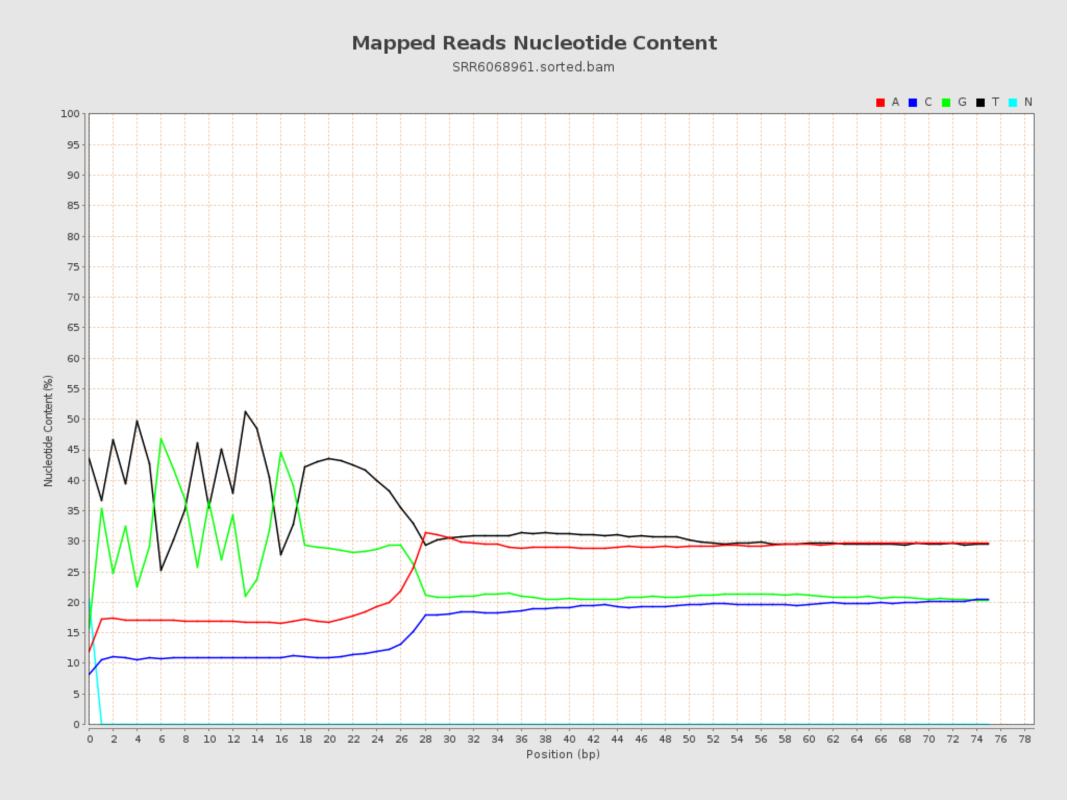
6. Results : Genome Fraction Coverage



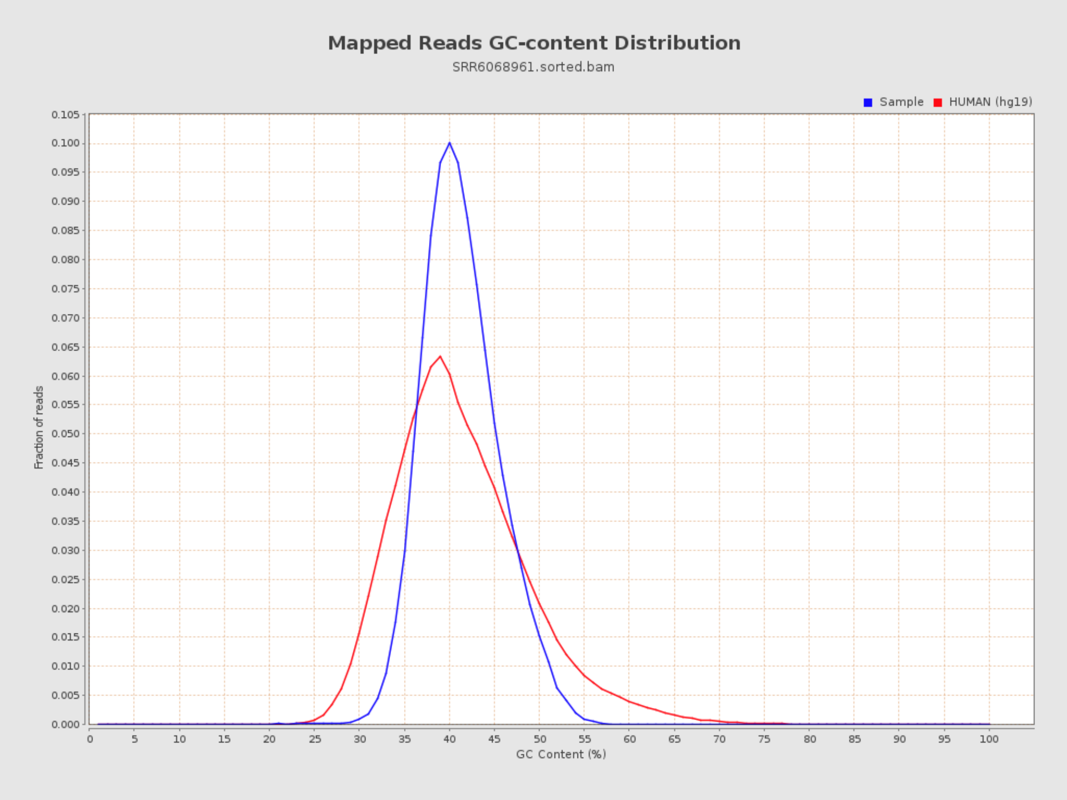
7. Results : Duplication Rate Histogram



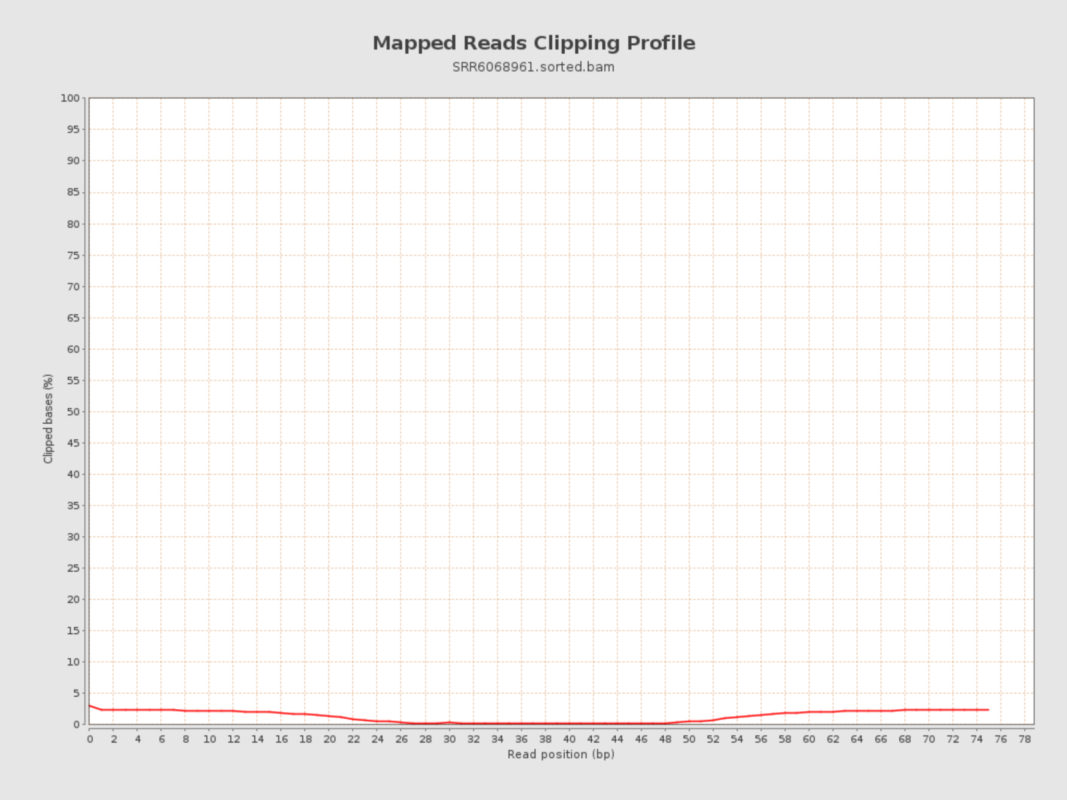
8. Results : Mapped Reads Nucleotide Content



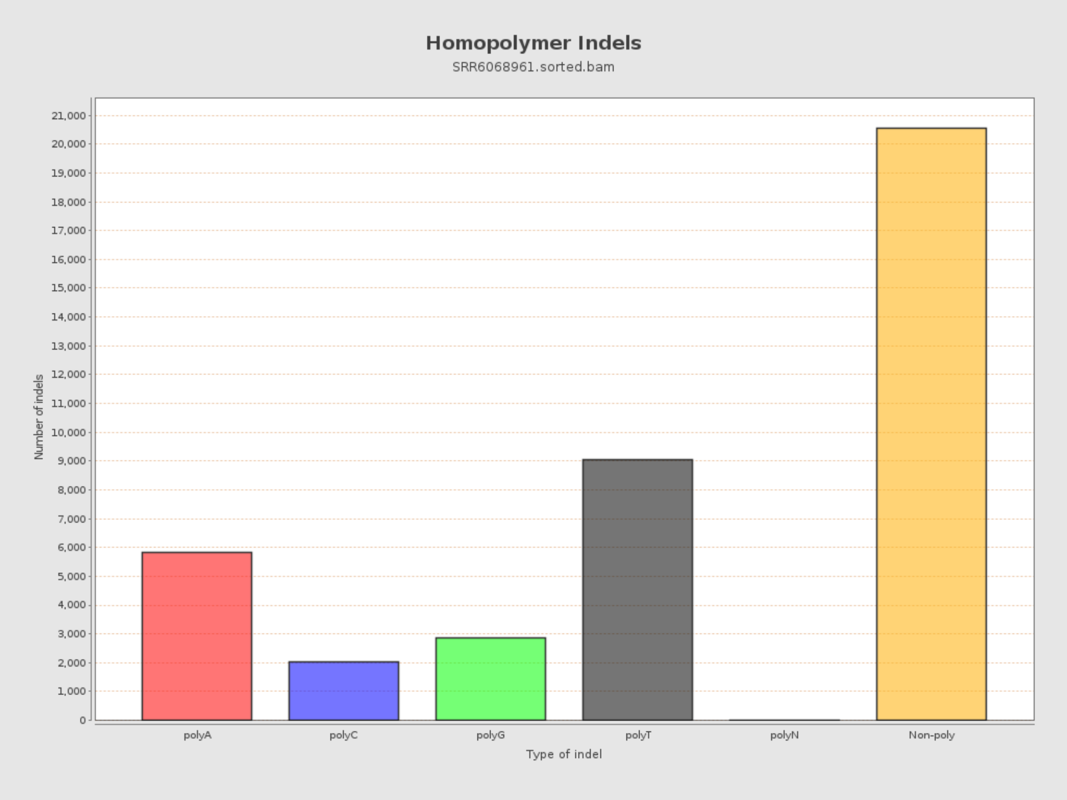
9. Results : Mapped Reads GC-content Distribution



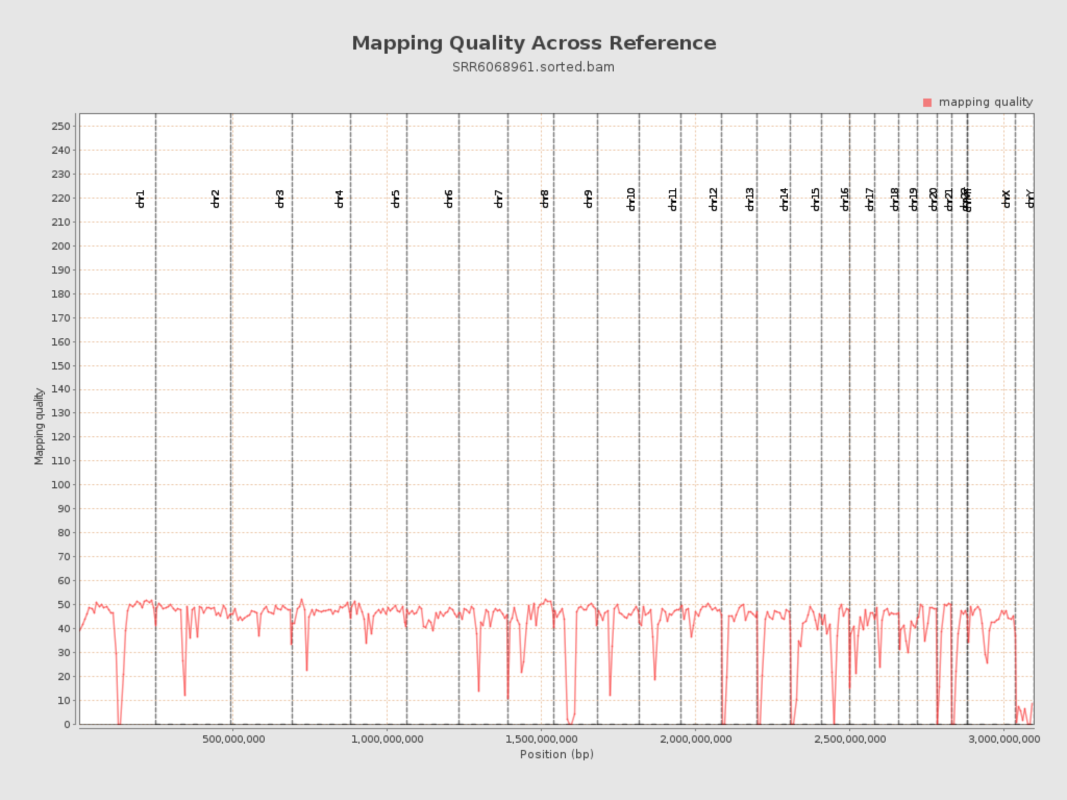
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram