Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 10:00:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068100.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_SRR6068100 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068100.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 10:00:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068100.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,994,990
Mapped reads	1,163,862 / 58.34%
Unmapped reads	831,128 / 41.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,458 / 0.47%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	59,423 / 2.98%
Duplication rate	3.93%
Clipped reads	569,048 / 28.52%

2.2. ACGT Content

Number/percentage of A's	20,997,444 / 27.56%
Number/percentage of C's	14,108,908 / 18.52%
Number/percentage of T's	24,004,279 / 31.51%
Number/percentage of G's	17,070,288 / 22.41%
Number/percentage of N's	1,399 / 0%
GC Percentage	40.93%

2.3. Coverage

Mean	0.0246

Standard Deviation	0.3023

2.4. Mapping Quality

Mean Mapping Quality	41.85

2.5. Mismatches and indels

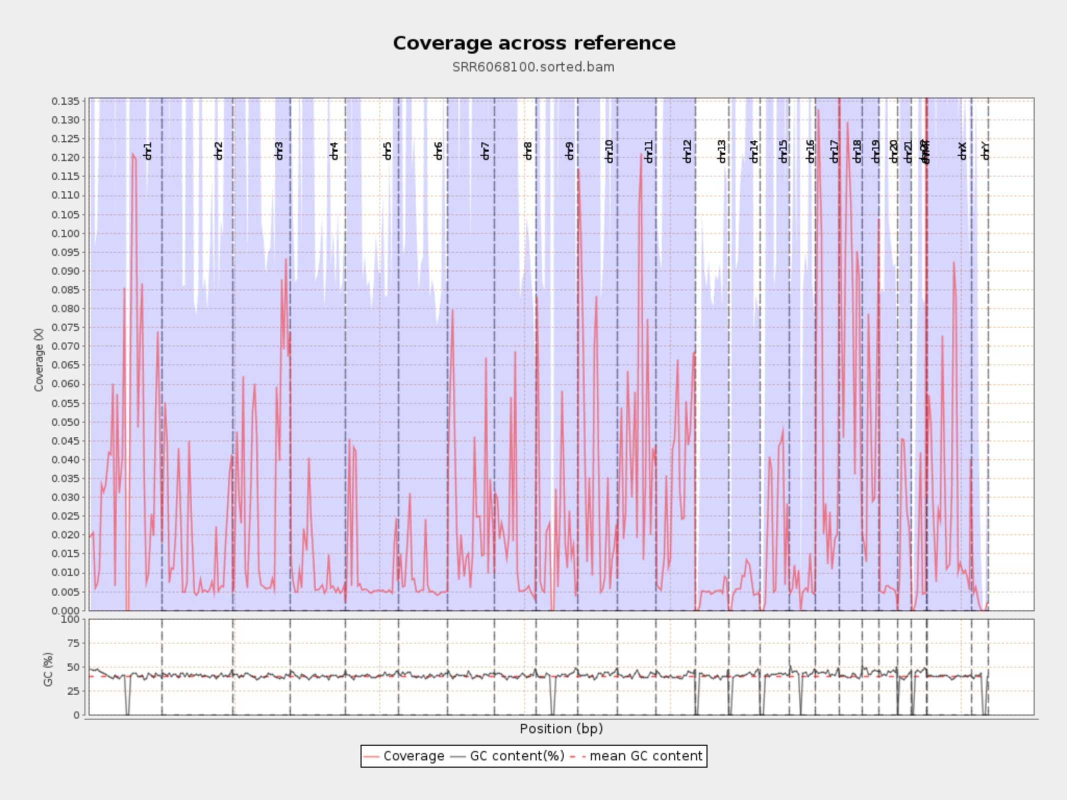
General error rate	0.78%
Mismatches	582,510
Insertions	6,197
Mapped reads with at least one insertion	0.52%
Deletions	20,254
Mapped reads with at least one deletion	1.7%
Homopolymer indels	46.88%

2.6. Chromosome stats

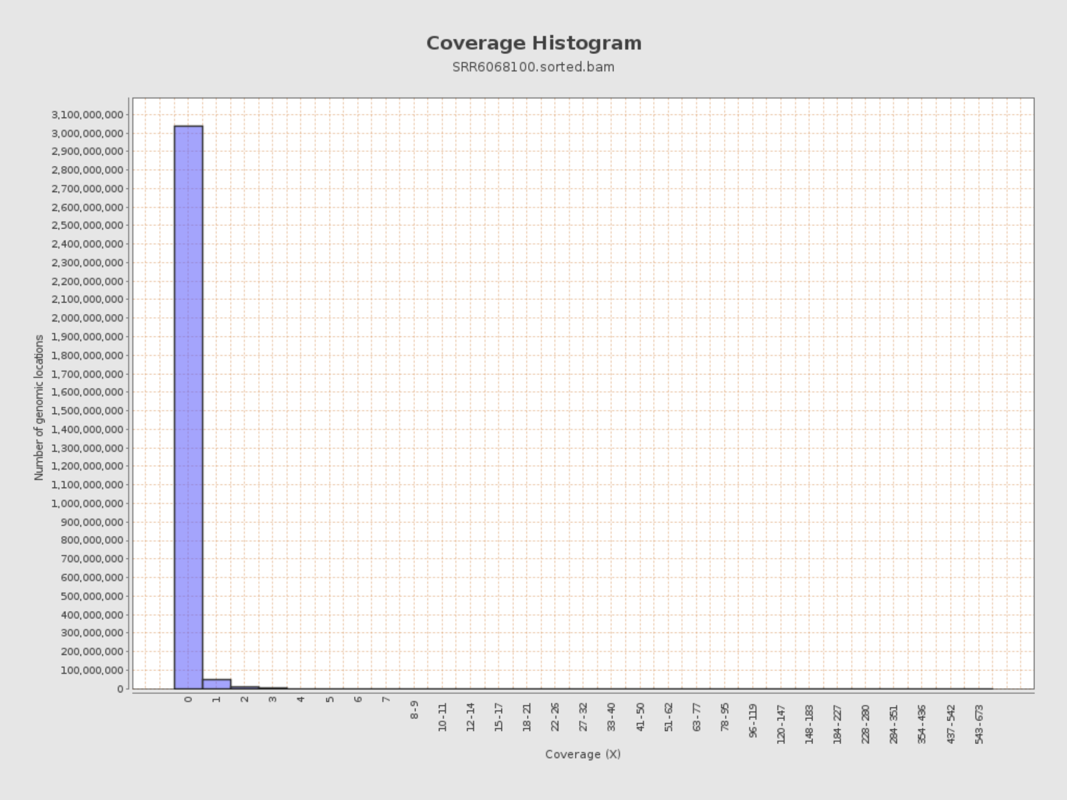
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10246426	0.0411	0.6043
chr2	243199373	4125810	0.017	0.4155
chr3	198022430	6682175	0.0337	0.2252
chr4	191154276	1939397	0.0101	0.1237
chr5	180915260	2118802	0.0117	0.2713
chr6	171115067	1501724	0.0088	0.1494
chr7	159138663	4464162	0.0281	0.2188

chr8	146364022	2717682	0.0186	0.2585
chr9	141213431	2741298	0.0194	0.2857
chr10	135534747	5223474	0.0385	0.3289
chr11	135006516	6207544	0.046	0.2832
chr12	133851895	4401224	0.0329	0.2282
chr13	115169878	535172	0.0046	0.0802
chr14	107349540	669582	0.0062	0.1581
chr15	102531392	2201039	0.0215	0.1768
chr16	90354753	606189	0.0067	0.1265
chr17	81195210	3552694	0.0438	0.2956
chr18	78077248	6624892	0.0849	0.4689
chr19	59128983	2615593	0.0442	0.3963
chr20	63025520	346408	0.0055	0.0994
chr21	48129895	1188219	0.0247	0.1998
chr22	51304566	456013	0.0089	0.1119
chrMT	16571	17932	1.0821	1.224
chrX	155270560	4847346	0.0312	0.2816
chrY	59373566	185303	0.0031	0.0751

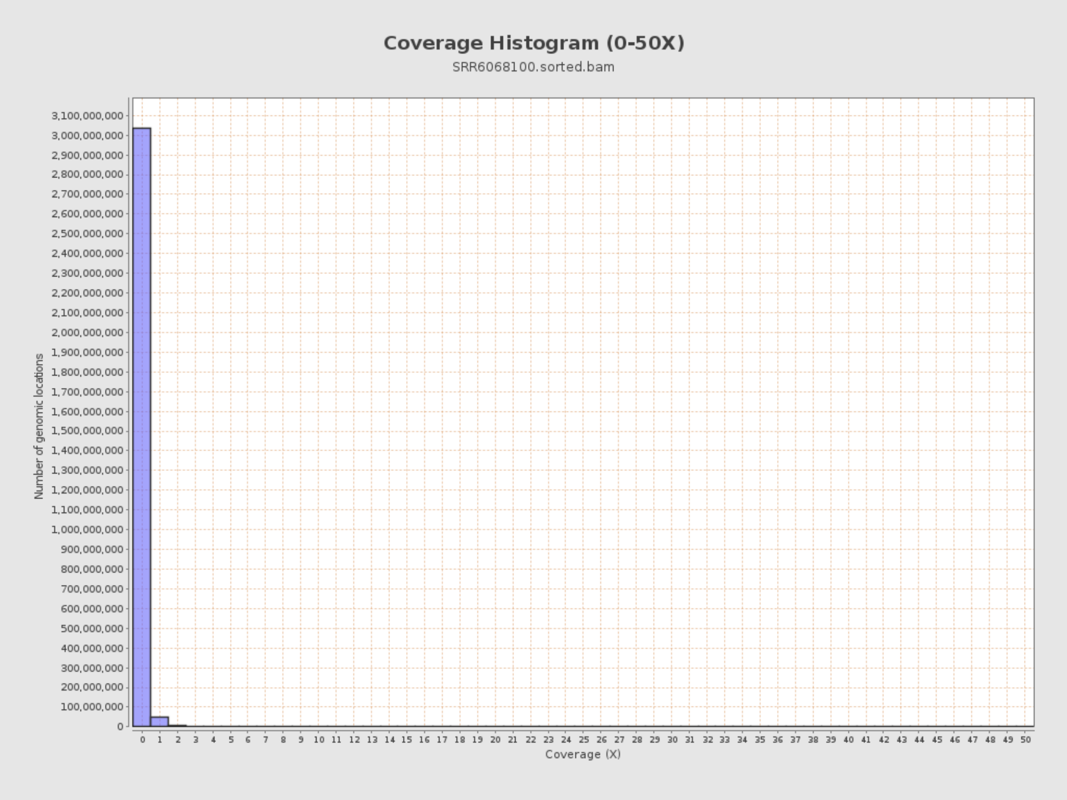
3. Results : Coverage across reference



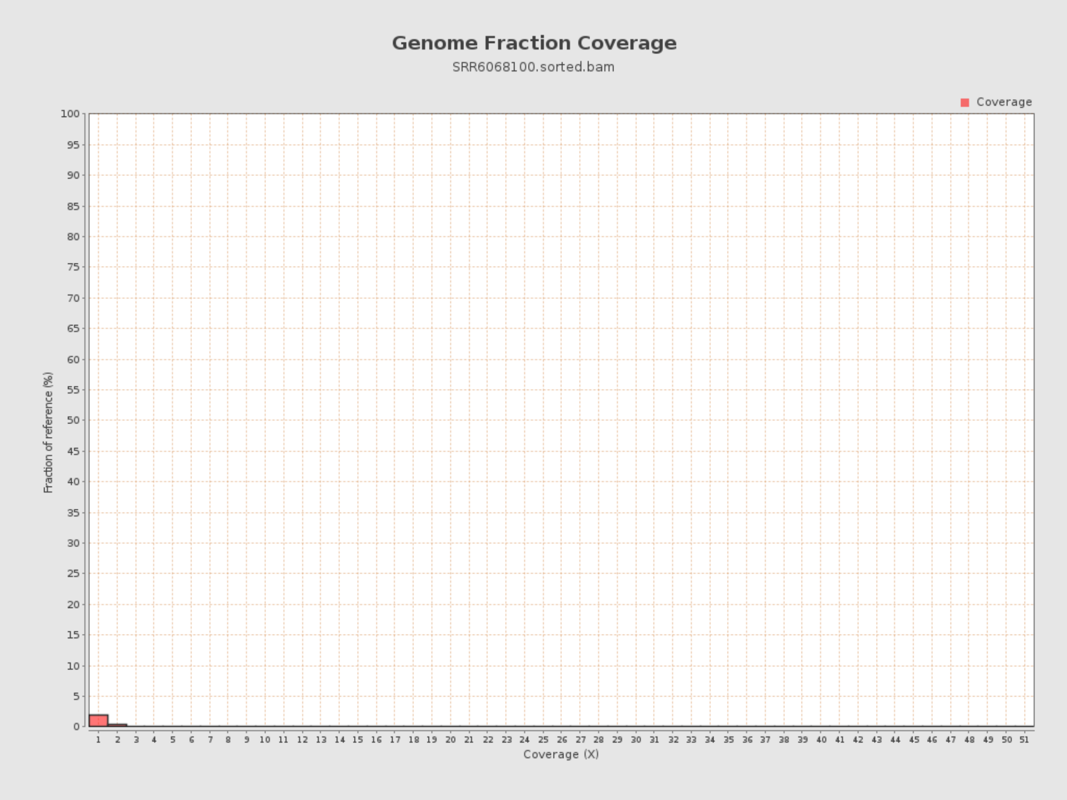
4. Results : Coverage Histogram



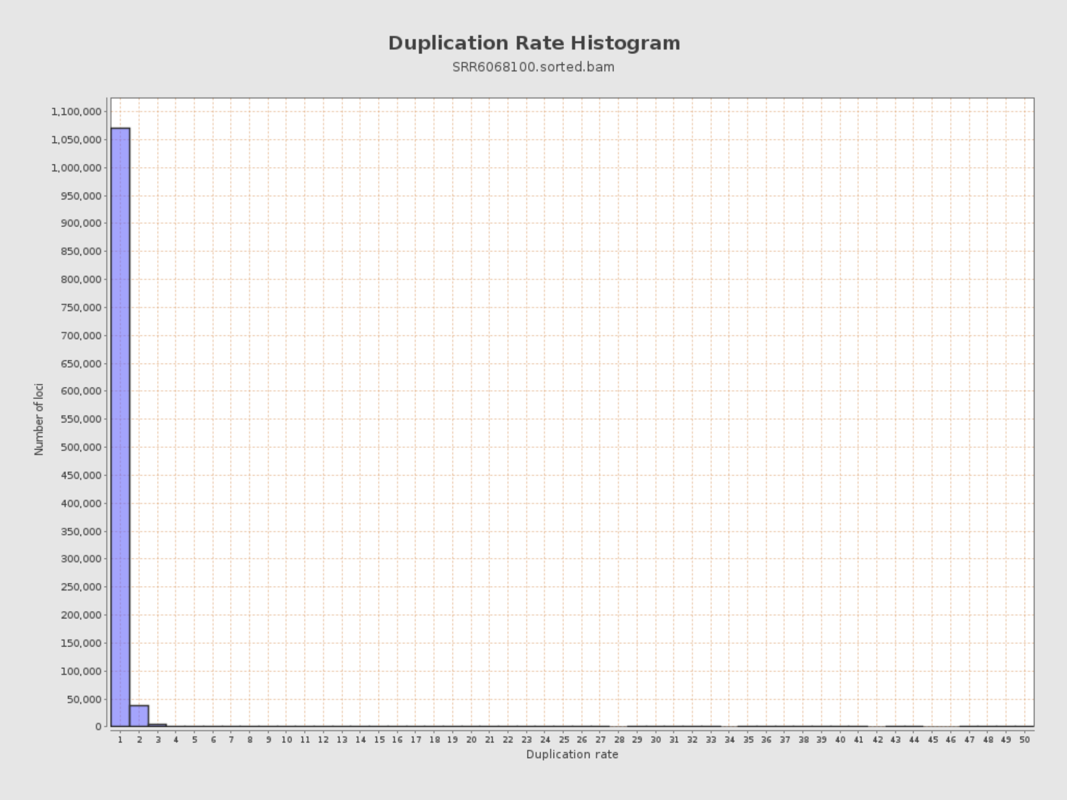
5. Results : Coverage Histogram (0-50X)



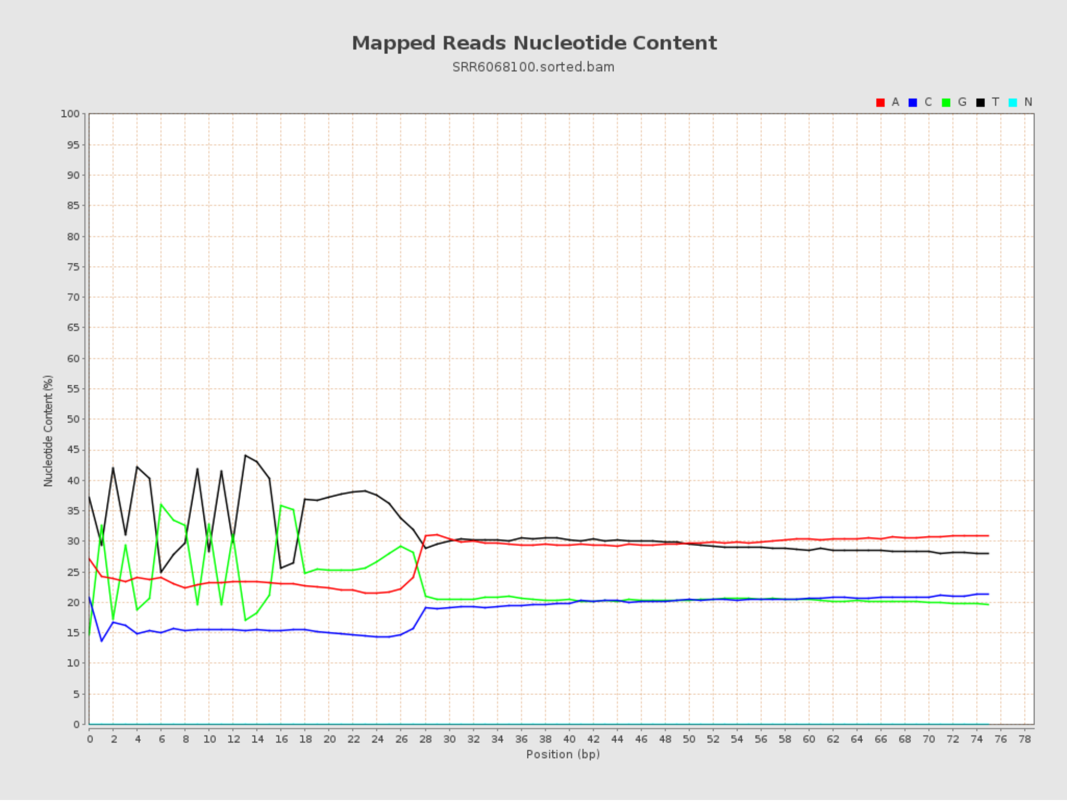
6. Results : Genome Fraction Coverage



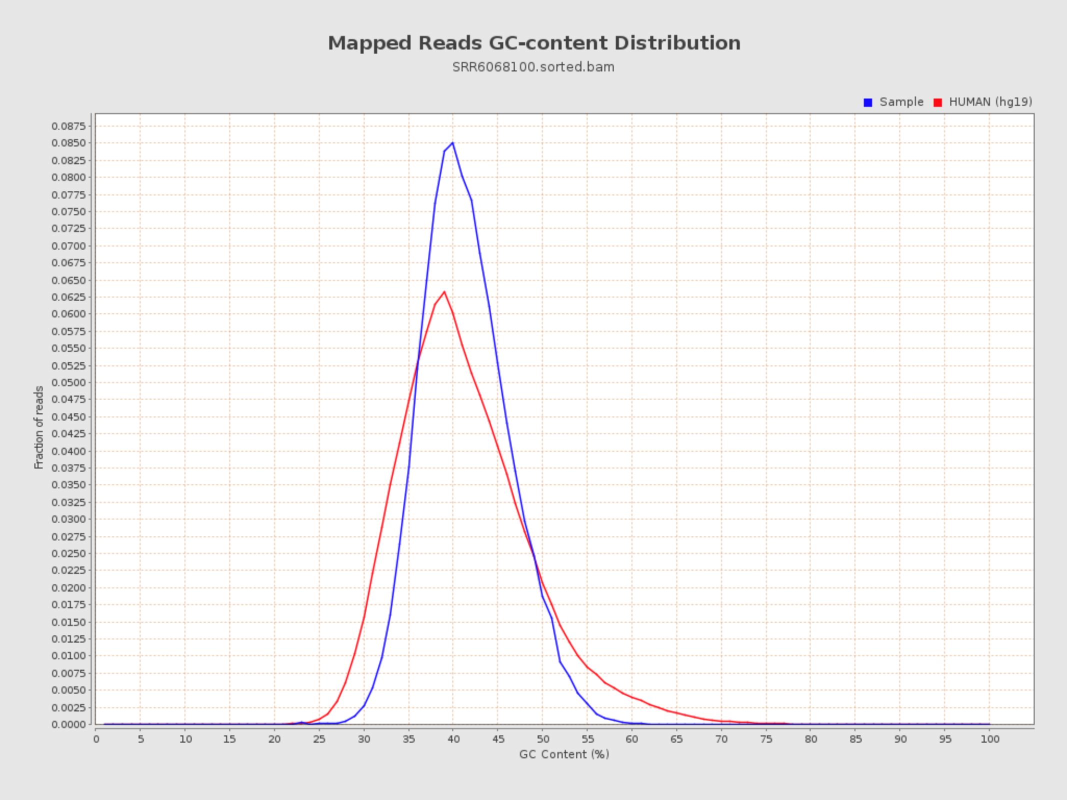
7. Results : Duplication Rate Histogram



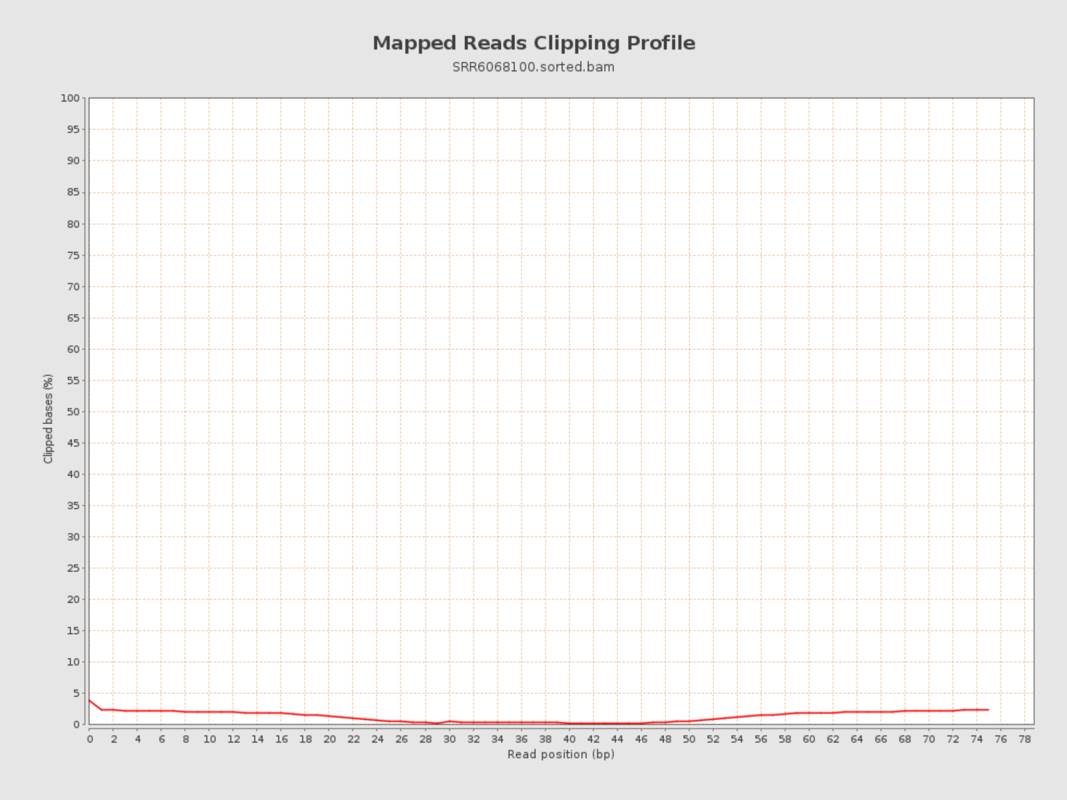
8. Results : Mapped Reads Nucleotide Content



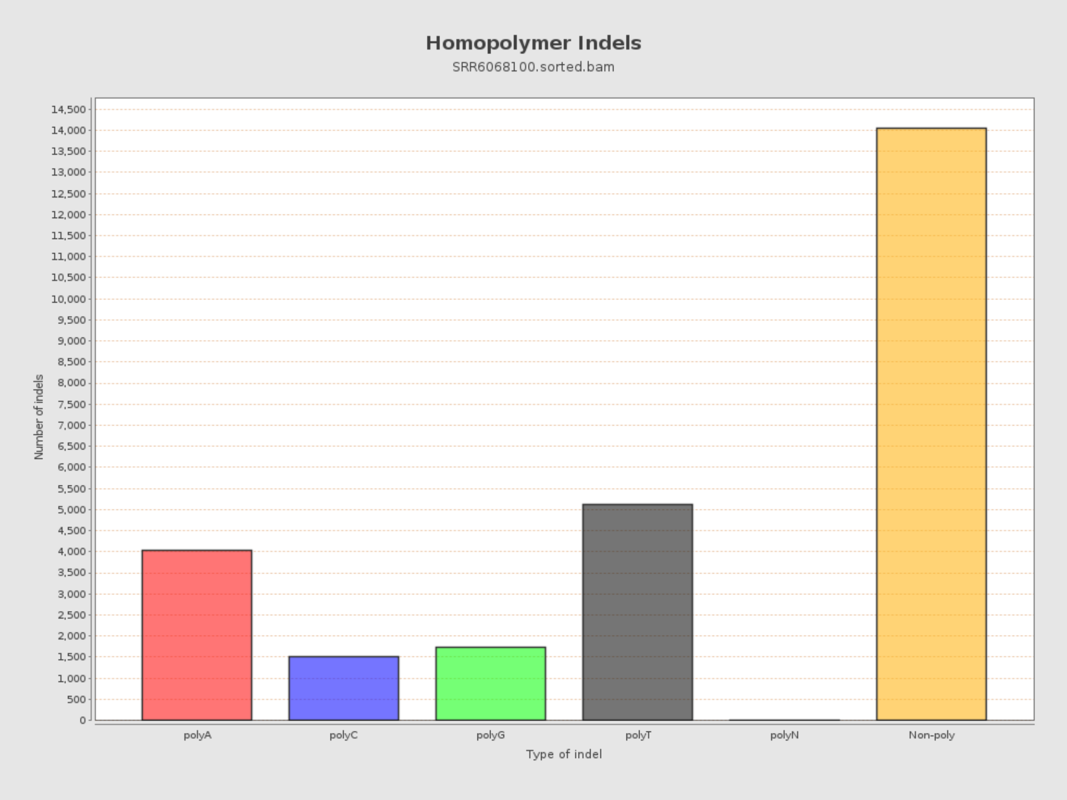
9. Results : Mapped Reads GC-content Distribution



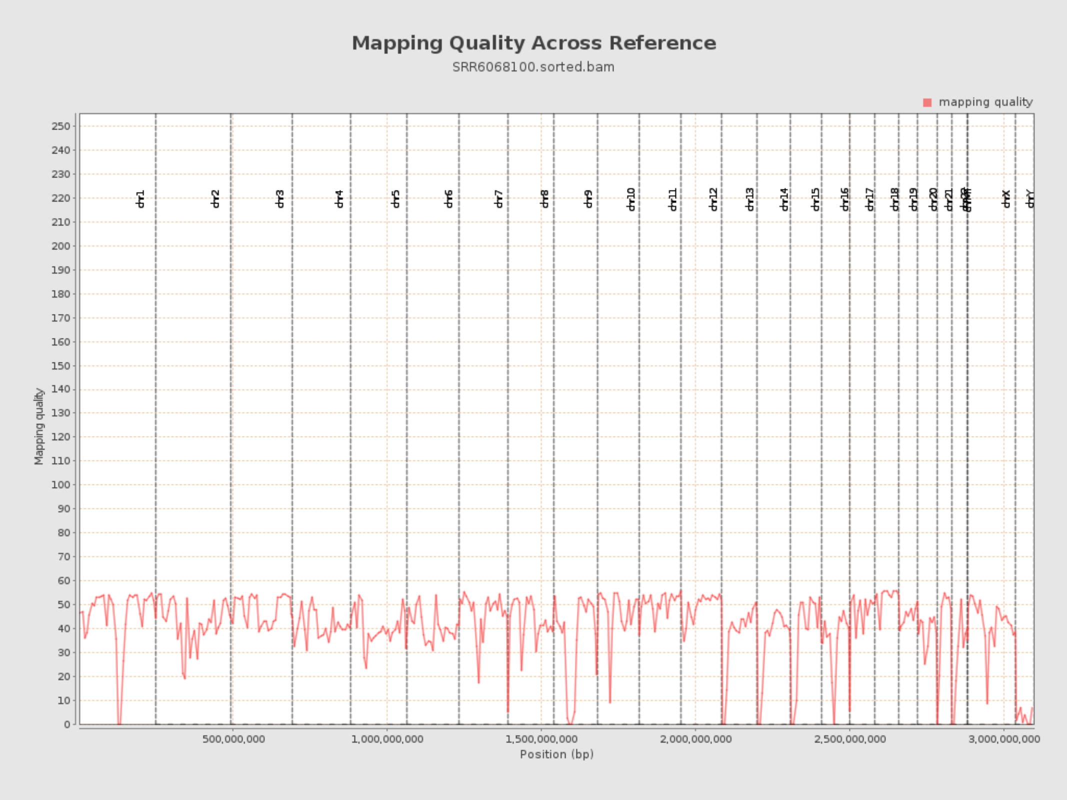
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram