Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 08:52:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068081.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_SRR6068081 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068081.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 08:52:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068081.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,995,449
Mapped reads	1,804,931 / 90.45%
Unmapped reads	190,518 / 9.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,607 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	95,172 / 4.77%
Duplication rate	4.13%
Clipped reads	775,123 / 38.84%

2.2. ACGT Content

Number/percentage of A's	33,808,653 / 27.93%
Number/percentage of C's	22,190,414 / 18.34%
Number/percentage of T's	38,624,256 / 31.91%
Number/percentage of G's	26,400,687 / 21.81%
Number/percentage of N's	2,755 / 0%
GC Percentage	40.15%

2.3. Coverage

Mean	0.0391

Standard Deviation	0.4263

2.4. Mapping Quality

Mean Mapping Quality	45.51

2.5. Mismatches and indels

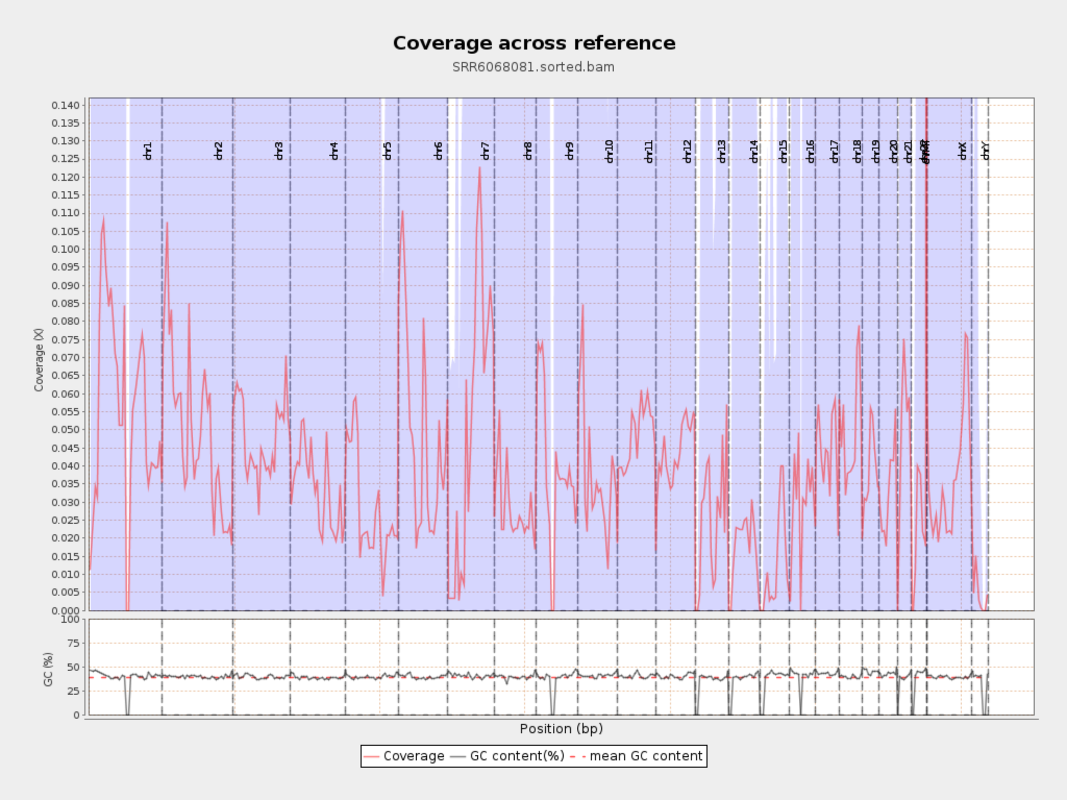
General error rate	0.78%
Mismatches	925,553
Insertions	9,945
Mapped reads with at least one insertion	0.55%
Deletions	32,011
Mapped reads with at least one deletion	1.75%
Homopolymer indels	47.22%

2.6. Chromosome stats

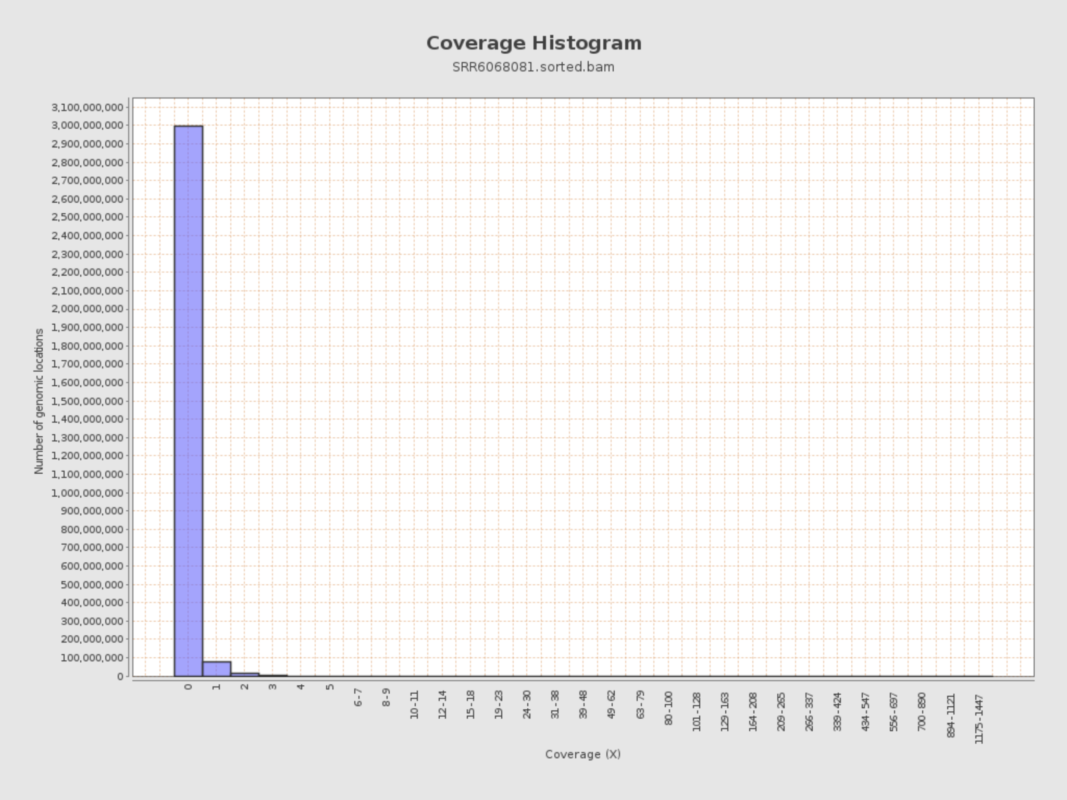
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13954782	0.056	0.8591
chr2	243199373	12167340	0.05	0.4437
chr3	198022430	9474362	0.0478	0.2592
chr4	191154276	6481643	0.0339	0.2299
chr5	180915260	5048196	0.0279	0.1998
chr6	171115067	8561471	0.05	0.2937
chr7	159138663	8090756	0.0508	0.4897

chr8	146364022	4144872	0.0283	0.8515
chr9	141213431	5527528	0.0391	0.3664
chr10	135534747	5164147	0.0381	0.3111
chr11	135006516	6448953	0.0478	0.3504
chr12	133851895	5888589	0.044	0.2575
chr13	115169878	2852652	0.0248	0.1889
chr14	107349540	1926631	0.0179	0.1851
chr15	102531392	1307846	0.0128	0.1422
chr16	90354753	2730223	0.0302	0.2241
chr17	81195210	3547188	0.0437	0.2826
chr18	78077248	3898994	0.0499	0.5537
chr19	59128983	2324338	0.0393	0.5713
chr20	63025520	2044519	0.0324	0.2298
chr21	48129895	2284227	0.0475	0.2671
chr22	51304566	1043241	0.0203	0.165
chrMT	16571	12887	0.7777	1.1603
chrX	155270560	5849018	0.0377	0.2525
chrY	59373566	304583	0.0051	0.1118

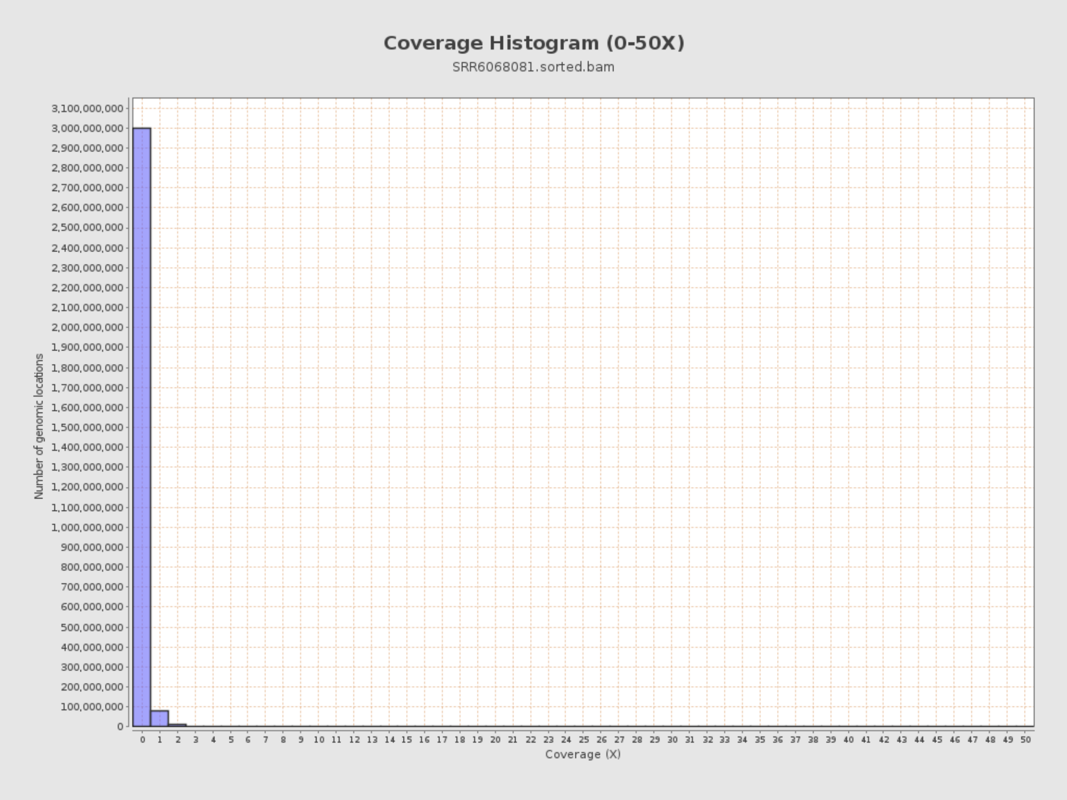
3. Results : Coverage across reference



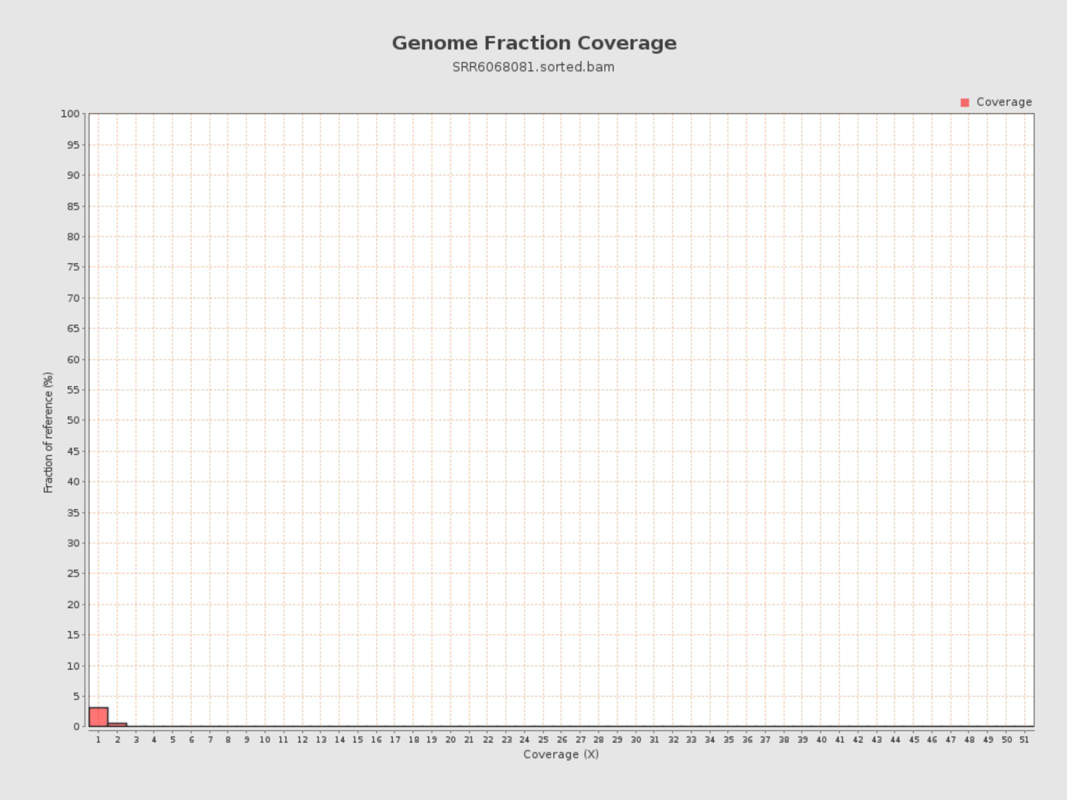
4. Results : Coverage Histogram



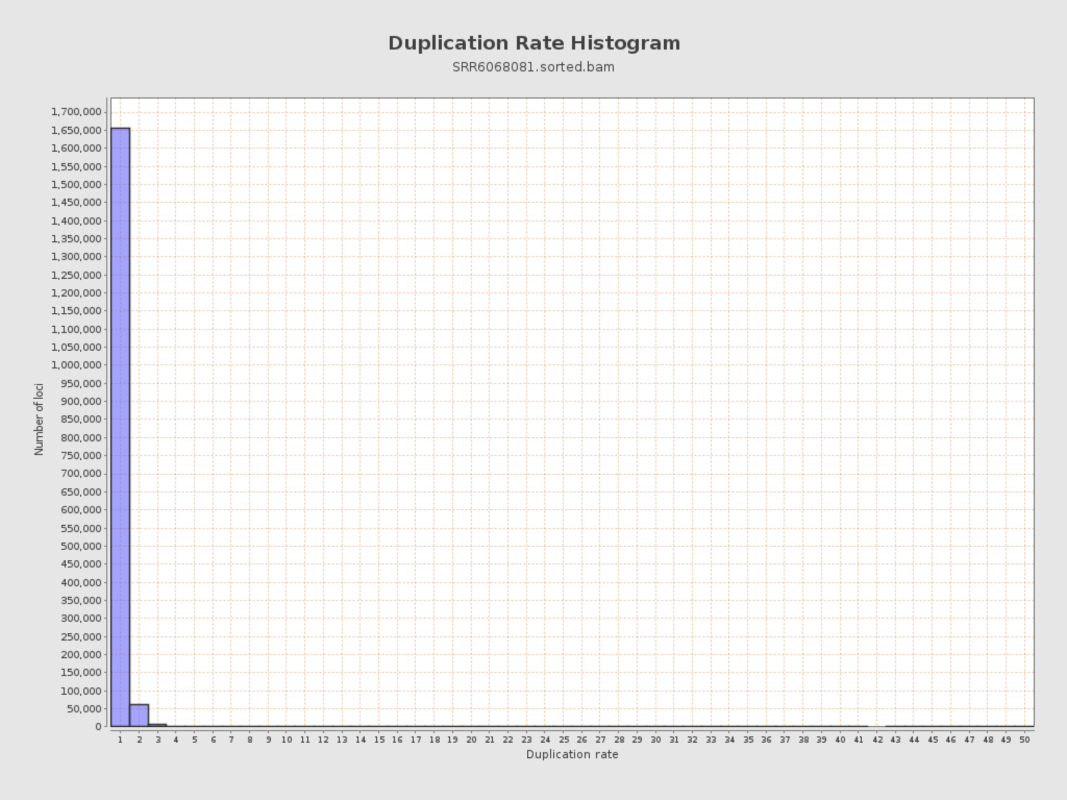
5. Results : Coverage Histogram (0-50X)



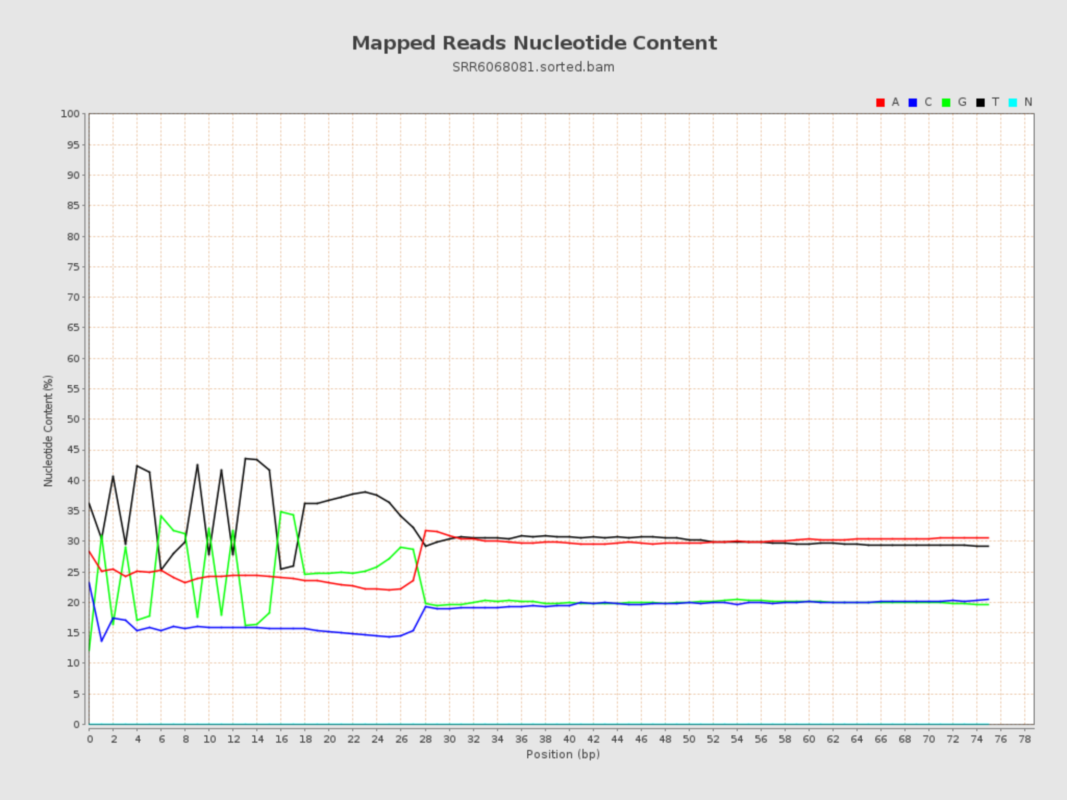
6. Results : Genome Fraction Coverage



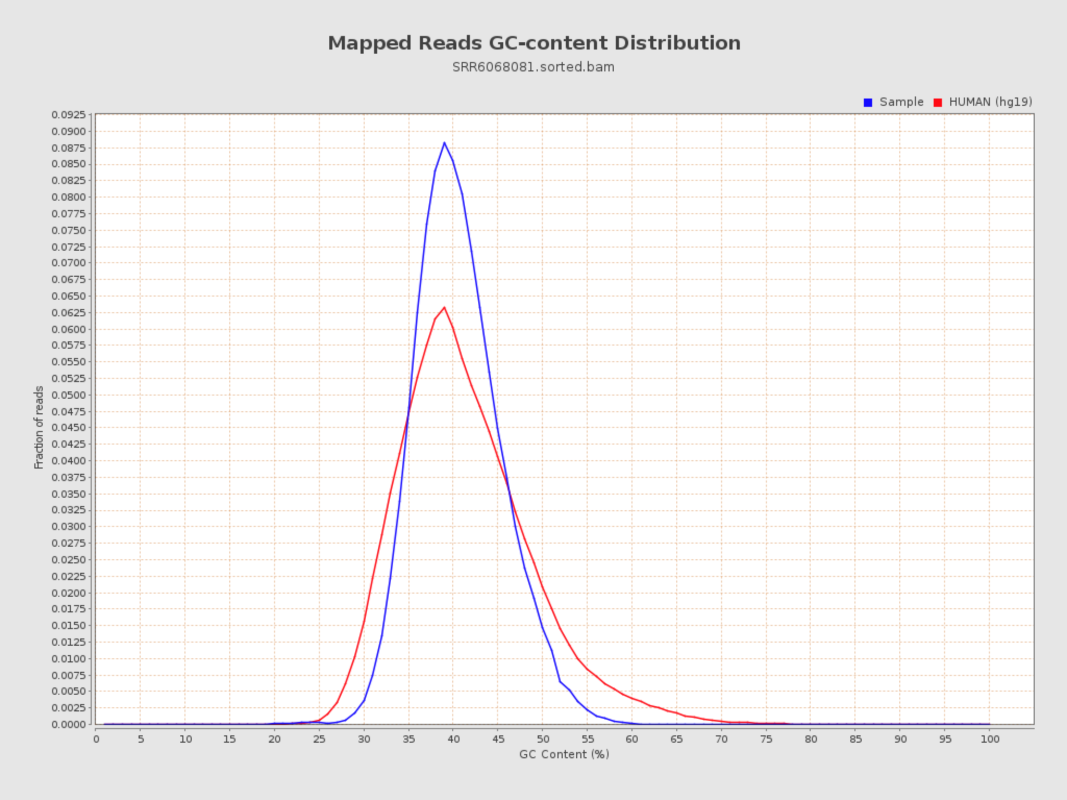
7. Results : Duplication Rate Histogram



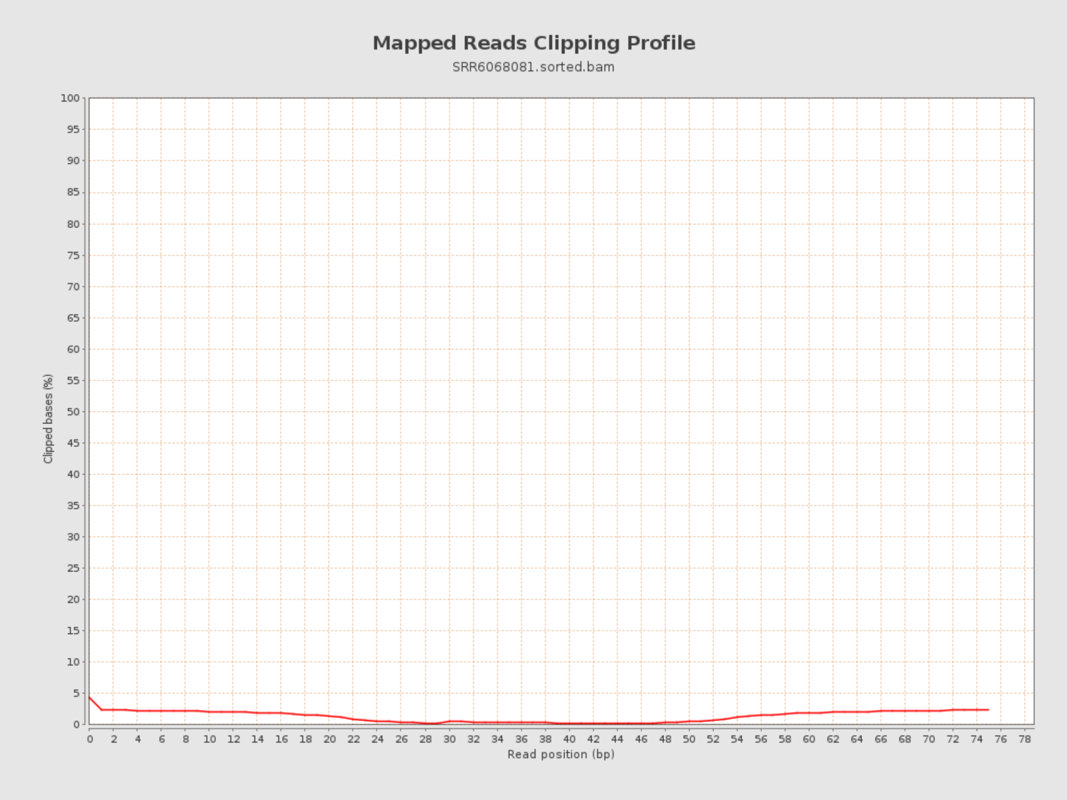
8. Results : Mapped Reads Nucleotide Content



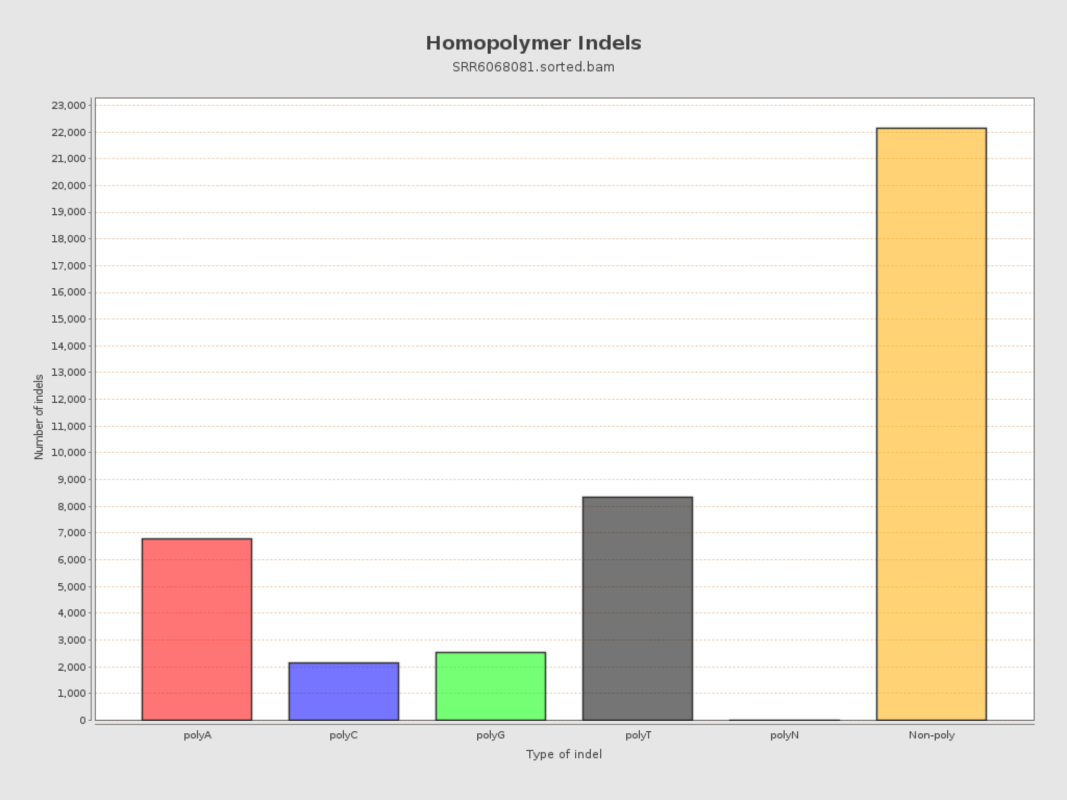
9. Results : Mapped Reads GC-content Distribution



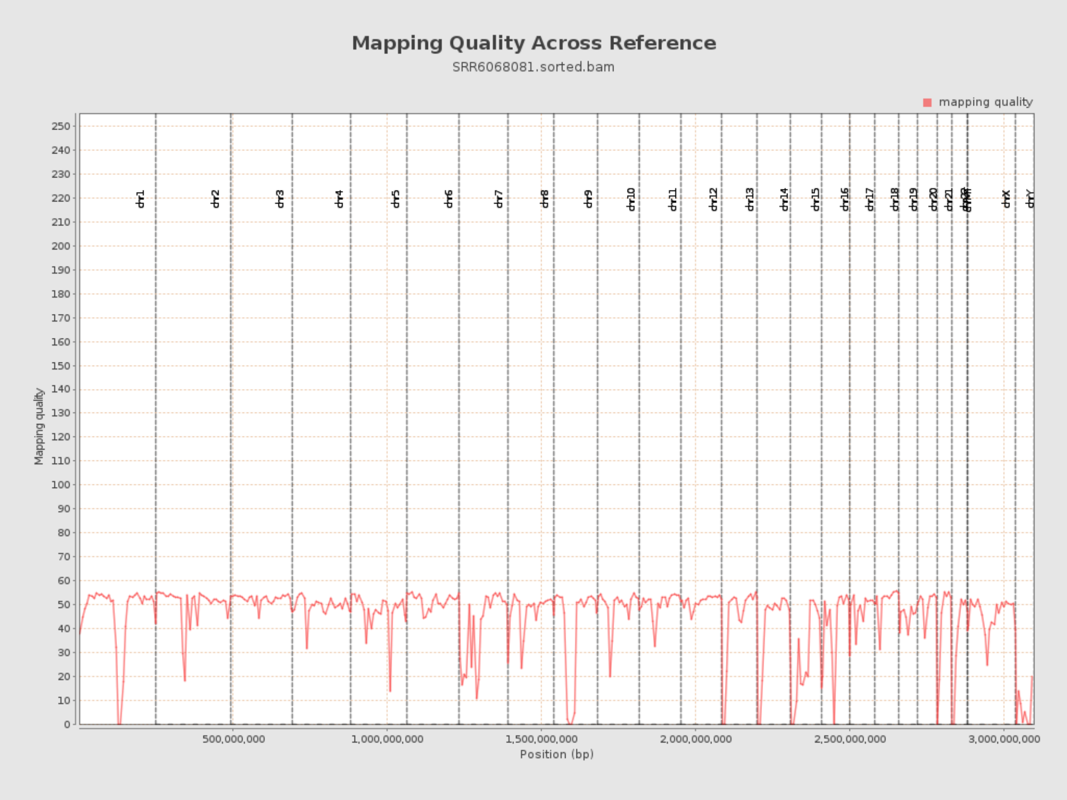
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram