Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 17:23:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068958.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_SRR6068958 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068958.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 17:23:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068958.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,192,268
Mapped reads	2,631,619 / 82.44%
Unmapped reads	560,649 / 17.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,509 / 0.45%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	122,563 / 3.84%
Duplication rate	2.82%
Clipped reads	1,547,572 / 48.48%

2.2. ACGT Content

Number/percentage of A's	43,572,959 / 26.09%
Number/percentage of C's	28,281,728 / 16.93%
Number/percentage of T's	55,567,940 / 33.27%
Number/percentage of G's	39,234,966 / 23.49%
Number/percentage of N's	384,277 / 0.23%
GC Percentage	40.42%

2.3. Coverage

Mean	0.054

Standard Deviation	0.6517

2.4. Mapping Quality

Mean Mapping Quality	43.77

2.5. Mismatches and indels

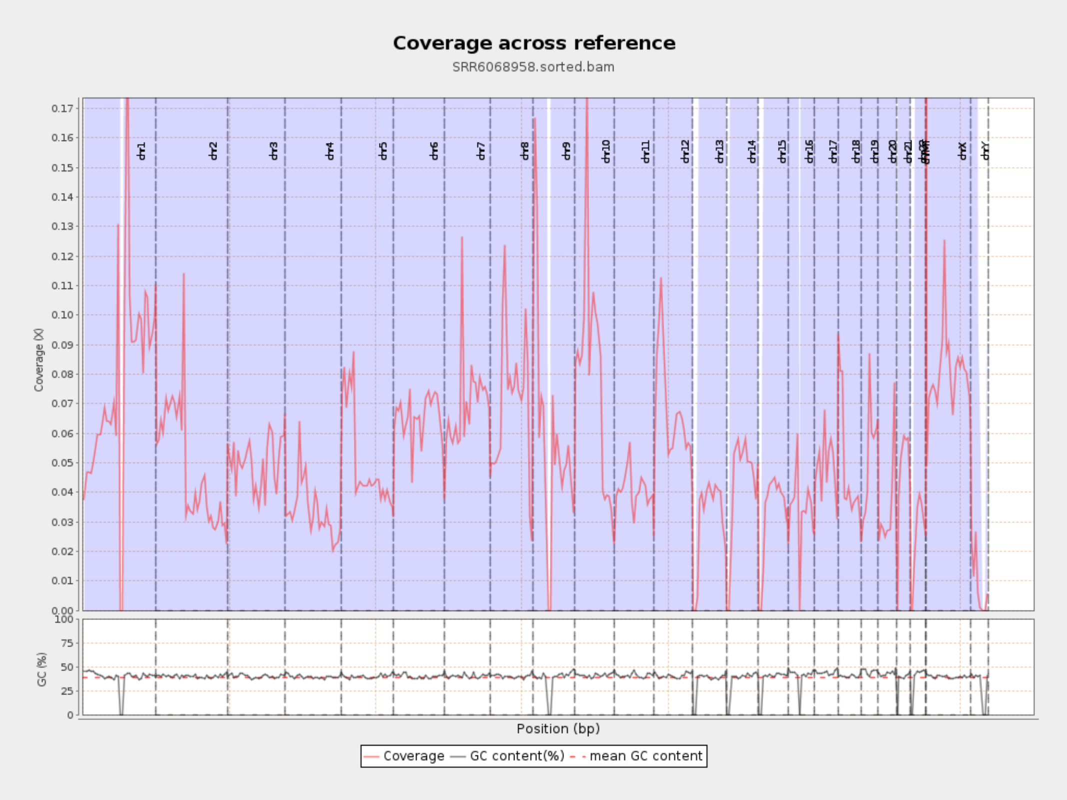
General error rate	0.97%
Mismatches	1,592,394
Insertions	15,872
Mapped reads with at least one insertion	0.6%
Deletions	46,723
Mapped reads with at least one deletion	1.76%
Homopolymer indels	47.61%

2.6. Chromosome stats

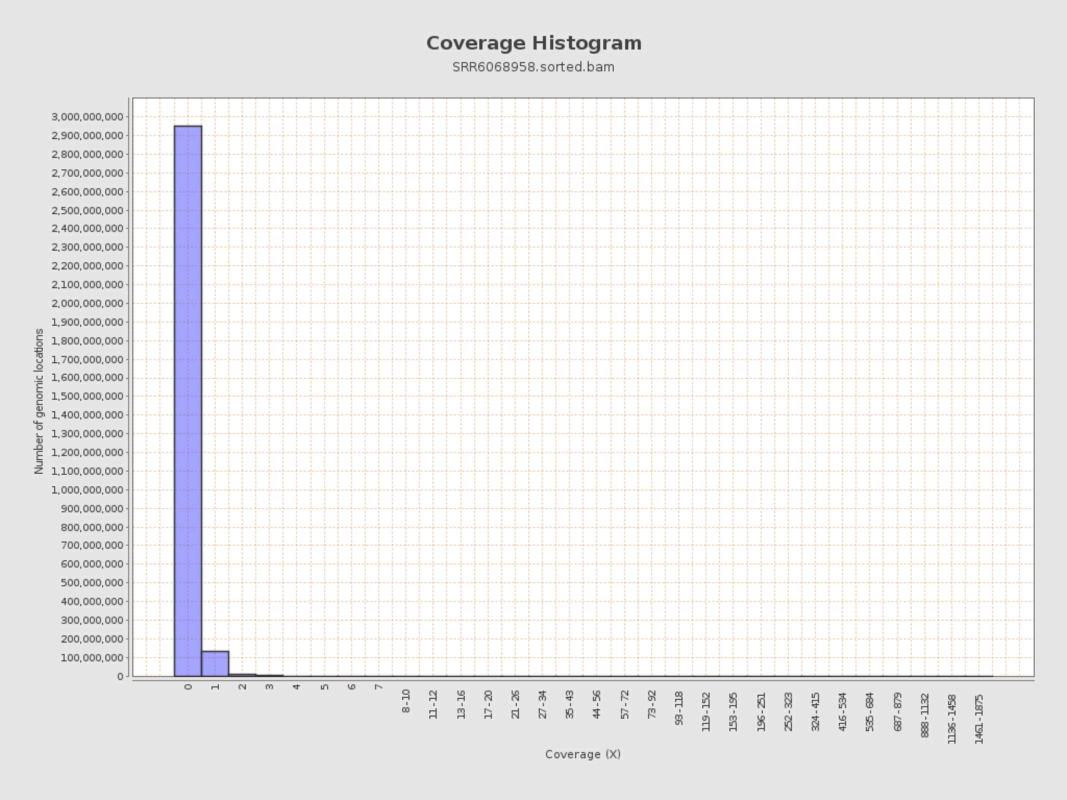
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19096510	0.0766	1.4481
chr2	243199373	11760936	0.0484	0.5829
chr3	198022430	9859694	0.0498	0.2862
chr4	191154276	6481342	0.0339	0.2626
chr5	180915260	9151633	0.0506	0.2562
chr6	171115067	11218786	0.0656	0.3821
chr7	159138663	11101889	0.0698	0.8995

chr8	146364022	10335046	0.0706	0.743
chr9	141213431	8292699	0.0587	0.6343
chr10	135534747	10740483	0.0792	0.9256
chr11	135006516	5511862	0.0408	0.476
chr12	133851895	9143454	0.0683	0.3063
chr13	115169878	3563855	0.0309	0.1926
chr14	107349540	4627290	0.0431	0.2852
chr15	102531392	3310178	0.0323	0.2001
chr16	90354753	3029775	0.0335	0.2974
chr17	81195210	4012026	0.0494	0.295
chr18	78077248	3781780	0.0484	1.0076
chr19	59128983	3080475	0.0521	1.0056
chr20	63025520	2261806	0.0359	0.2434
chr21	48129895	2253987	0.0468	0.288
chr22	51304566	1272376	0.0248	0.1772
chrMT	16571	234608	14.1577	8.7783
chrX	155270560	12477758	0.0804	0.4312
chrY	59373566	518136	0.0087	0.2079

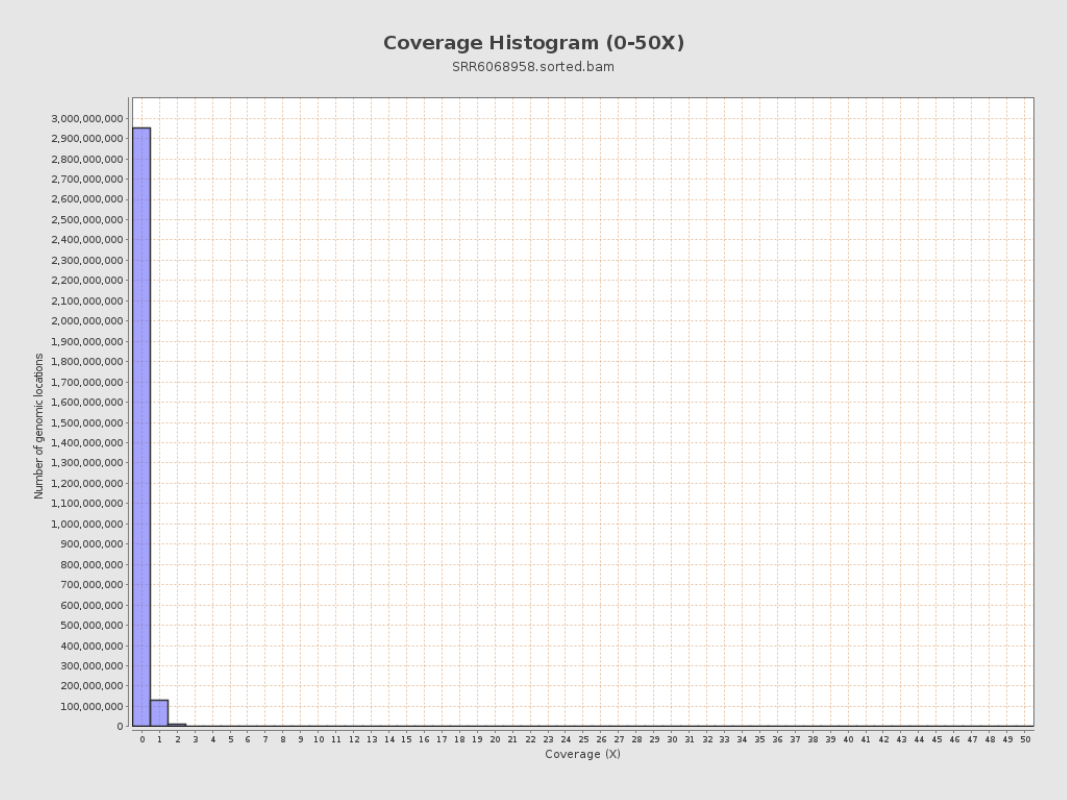
3. Results : Coverage across reference



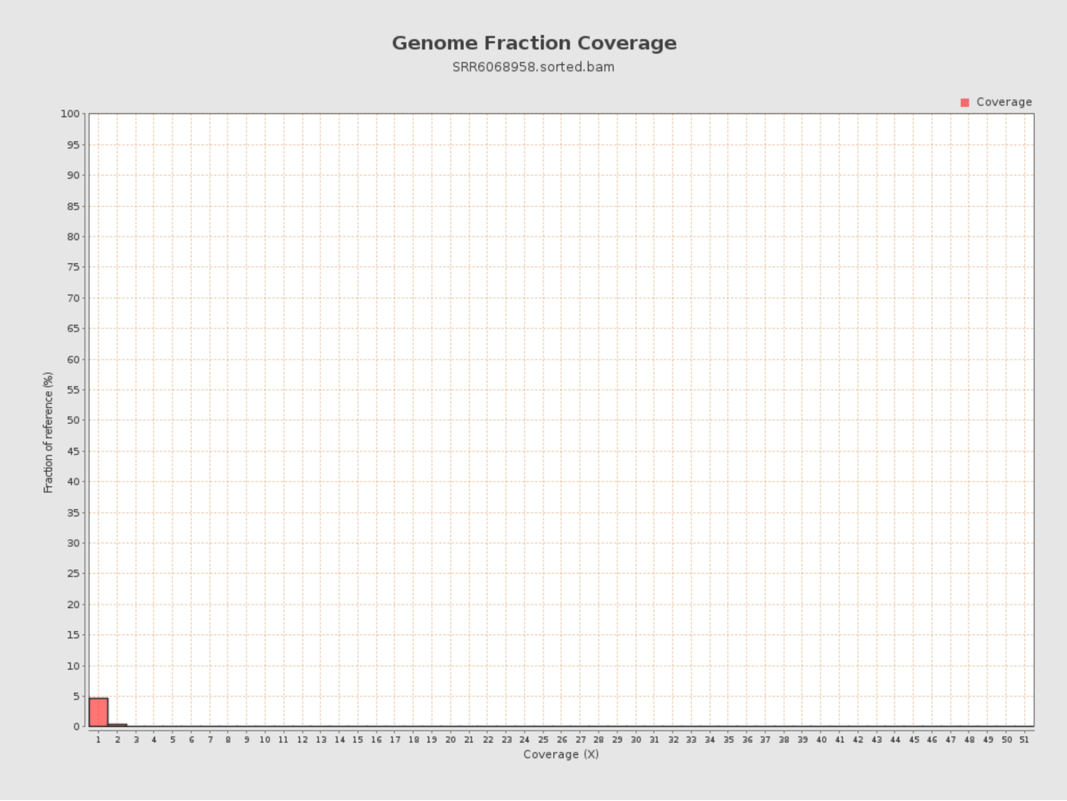
4. Results : Coverage Histogram



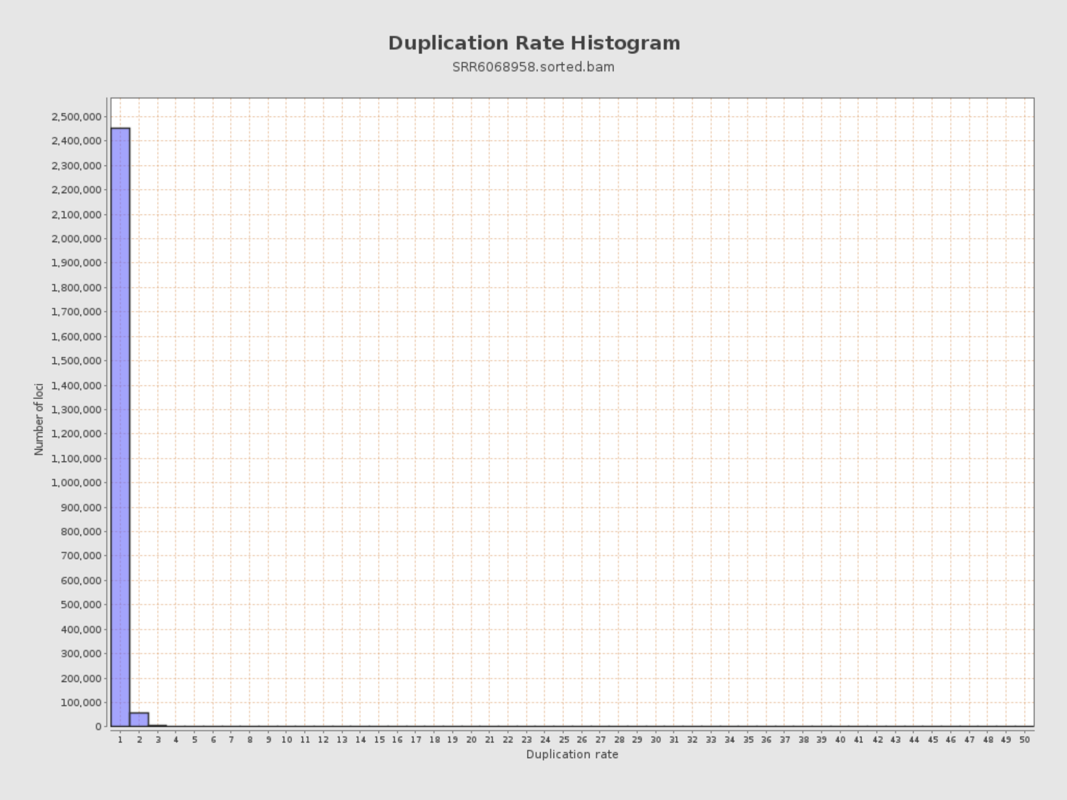
5. Results : Coverage Histogram (0-50X)



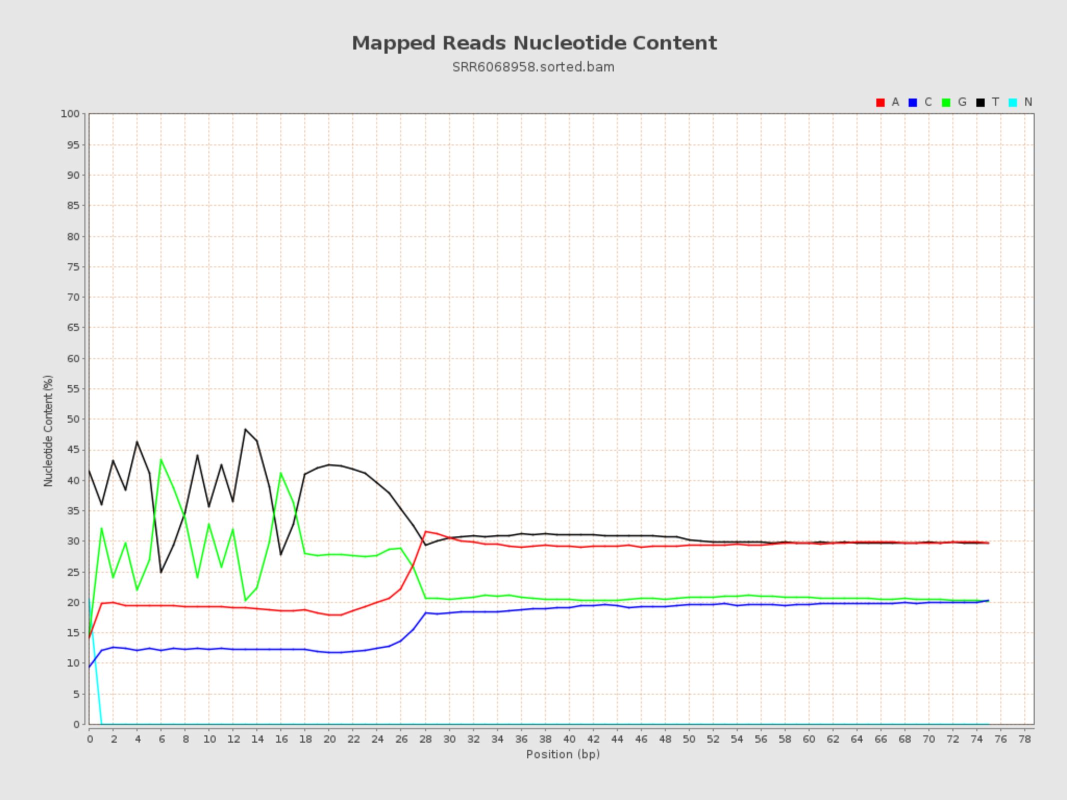
6. Results : Genome Fraction Coverage



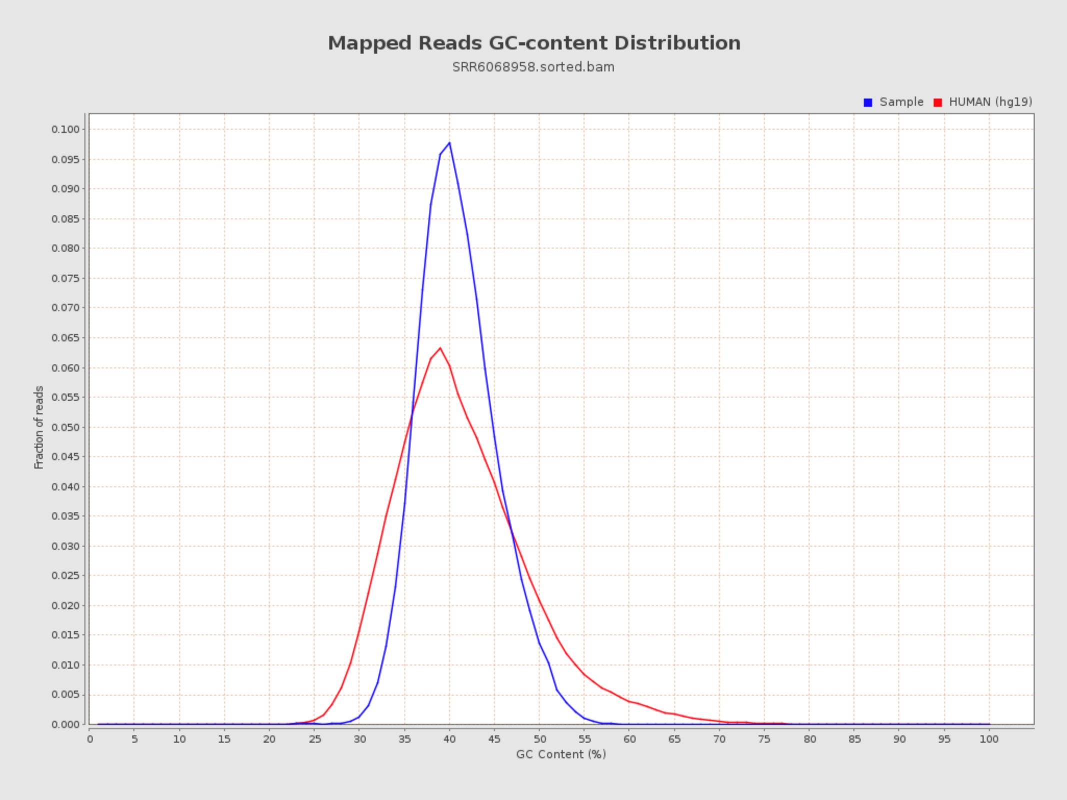
7. Results : Duplication Rate Histogram



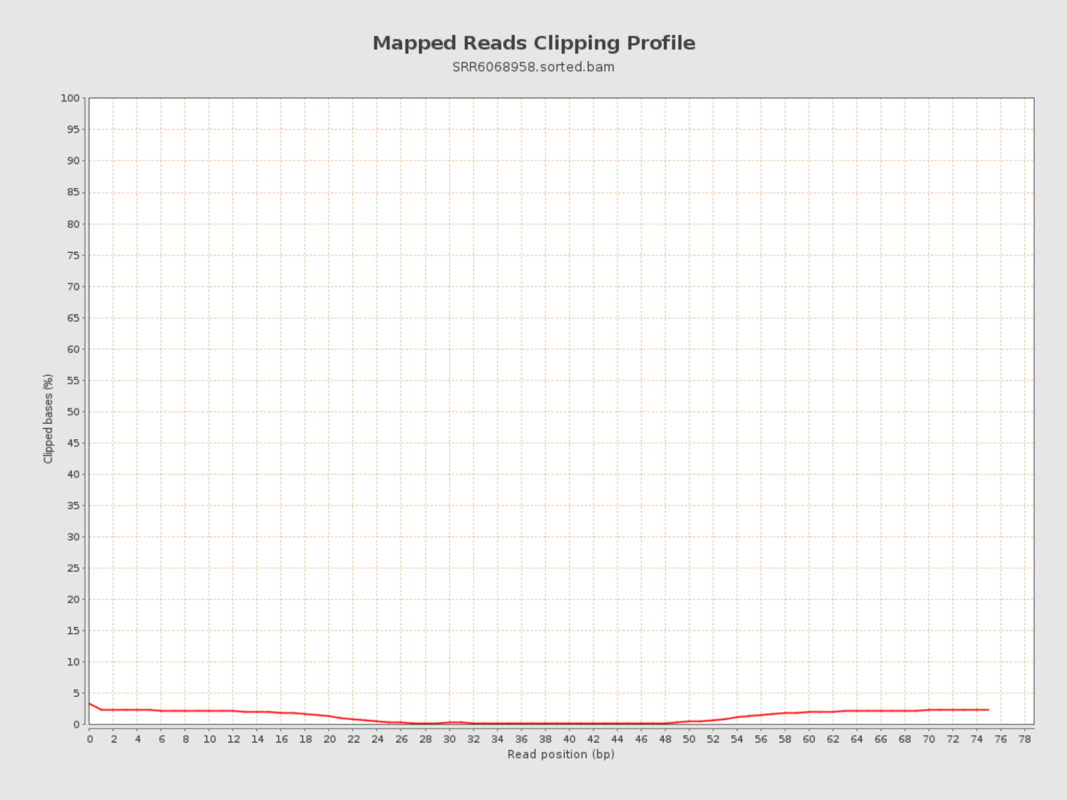
8. Results : Mapped Reads Nucleotide Content



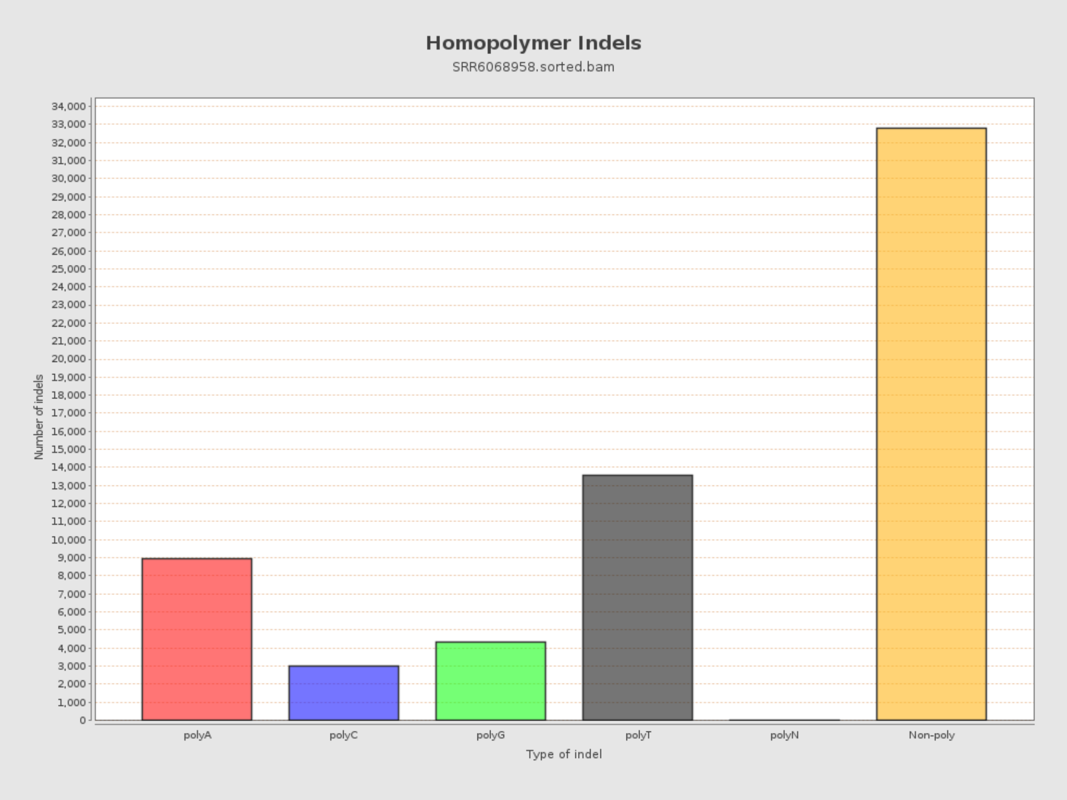
9. Results : Mapped Reads GC-content Distribution



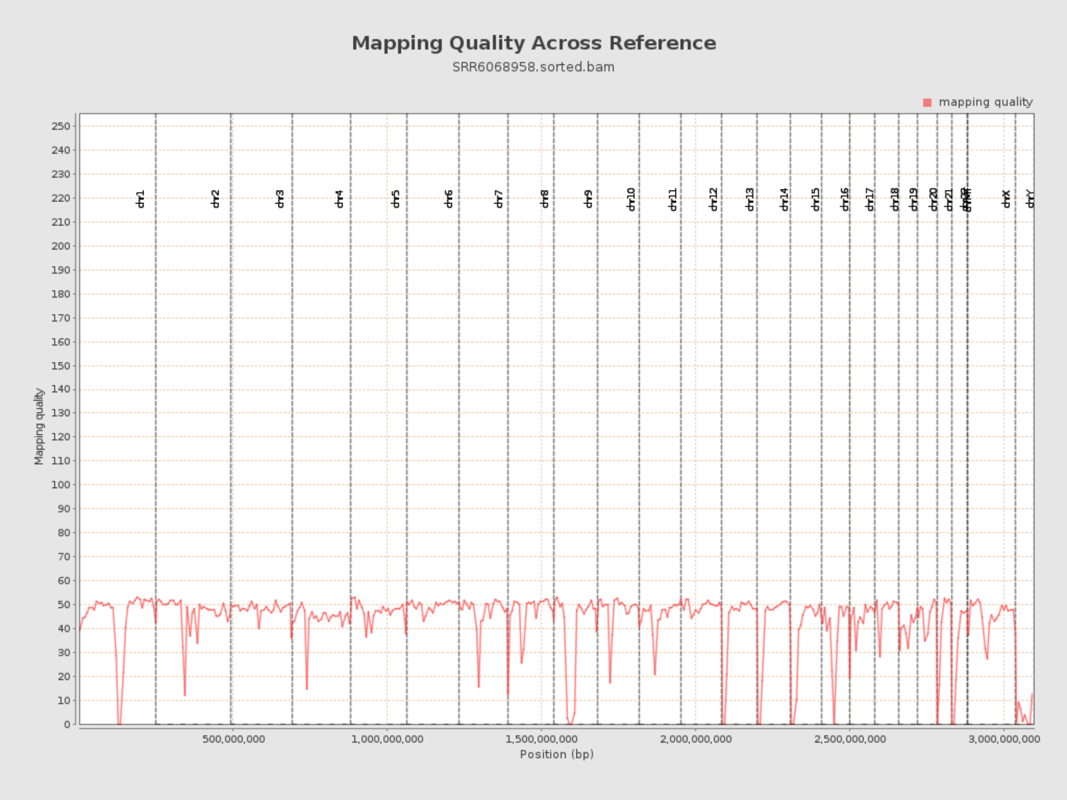
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram