Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 08:15:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068072.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_SRR6068072 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068072.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 08:15:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068072.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,998,330
Mapped reads	3,774,802 / 94.41%
Unmapped reads	223,528 / 5.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,154 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	778,669 / 19.47%
Duplication rate	15.3%
Clipped reads	1,958,629 / 48.99%

2.2. ACGT Content

Number/percentage of A's	62,573,625 / 25.67%
Number/percentage of C's	44,297,317 / 18.17%
Number/percentage of T's	78,963,524 / 32.39%
Number/percentage of G's	57,925,207 / 23.76%
Number/percentage of N's	26,983 / 0.01%
GC Percentage	41.93%

2.3. Coverage

Mean	0.0788

Standard Deviation	0.814

2.4. Mapping Quality

Mean Mapping Quality	45.53

2.5. Mismatches and indels

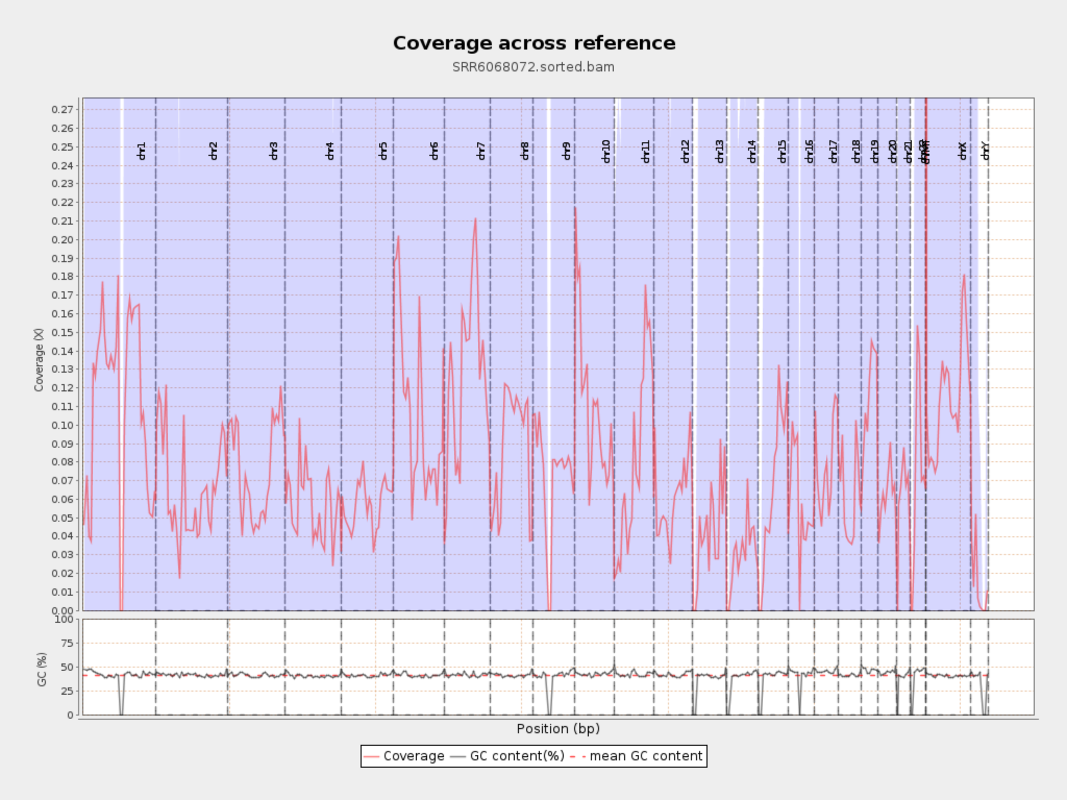
General error rate	0.56%
Mismatches	1,328,222
Insertions	16,484
Mapped reads with at least one insertion	0.43%
Deletions	55,720
Mapped reads with at least one deletion	1.46%
Homopolymer indels	44.27%

2.6. Chromosome stats

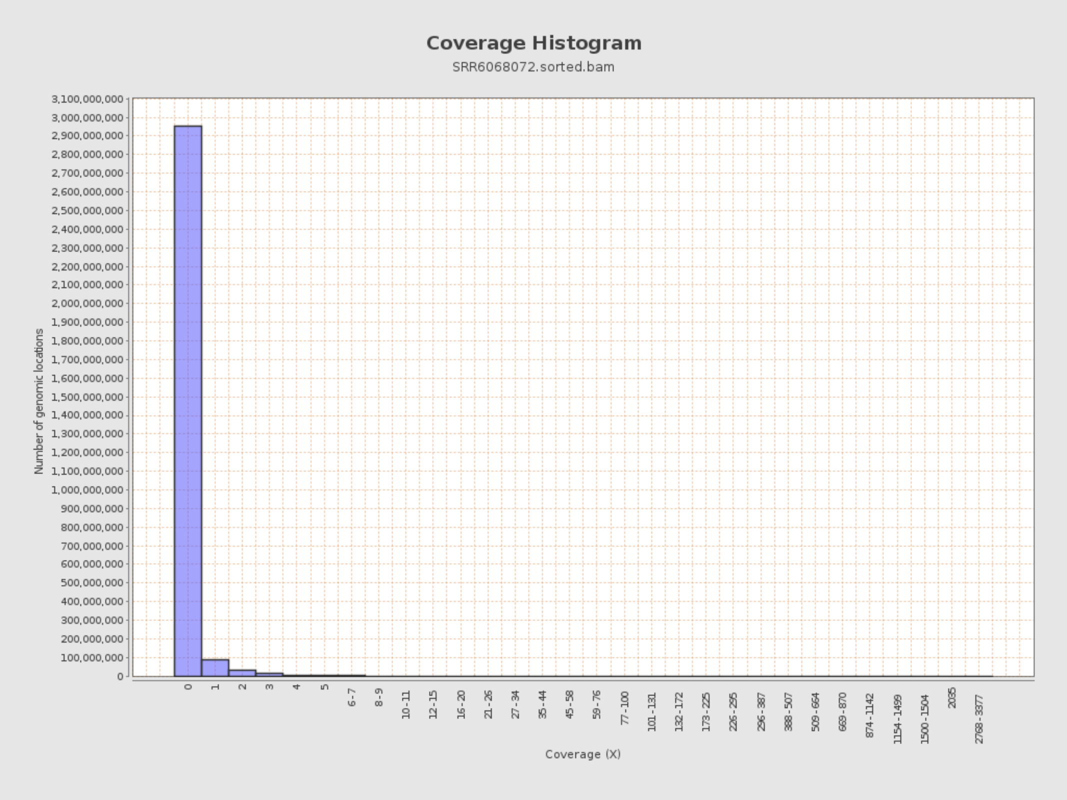
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27451652	0.1101	1.382
chr2	243199373	16119535	0.0663	1.5966
chr3	198022430	15118890	0.0763	0.4361
chr4	191154276	10993149	0.0575	0.4545
chr5	180915260	10382521	0.0574	0.376
chr6	171115067	18413807	0.1076	0.6521
chr7	159138663	20564435	0.1292	1.0321

chr8	146364022	12863711	0.0879	0.85
chr9	141213431	10246353	0.0726	0.621
chr10	135534747	14916830	0.1101	0.7063
chr11	135006516	11050797	0.0819	0.4979
chr12	133851895	8178922	0.0611	0.4048
chr13	115169878	4964032	0.0431	0.3823
chr14	107349540	3315028	0.0309	0.31
chr15	102531392	6786866	0.0662	0.4194
chr16	90354753	5079496	0.0562	0.4034
chr17	81195210	6392669	0.0787	0.4613
chr18	78077248	4849353	0.0621	1.1185
chr19	59128983	6755071	0.1142	0.955
chr20	63025520	3938914	0.0625	0.4227
chr21	48129895	2898433	0.0602	0.4403
chr22	51304566	3754800	0.0732	0.4244
chrMT	16571	134342	8.1071	6.0476
chrX	155270560	17869218	0.1151	0.5631
chrY	59373566	845678	0.0142	0.5038

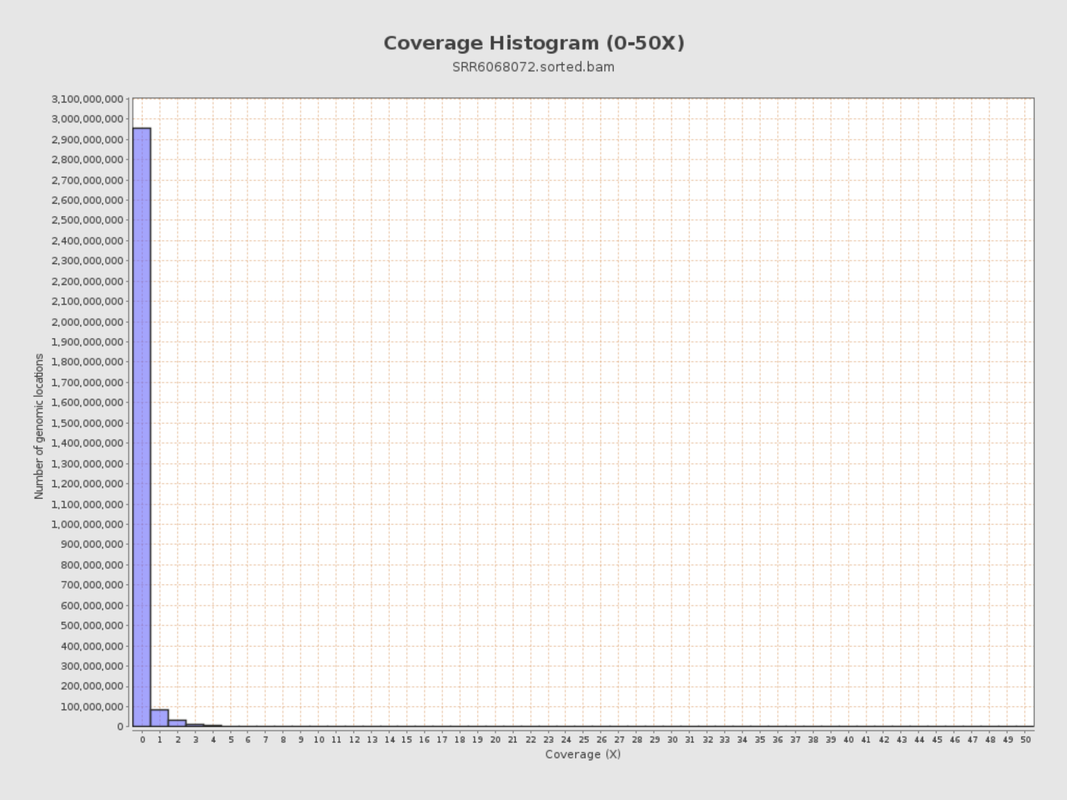
3. Results : Coverage across reference



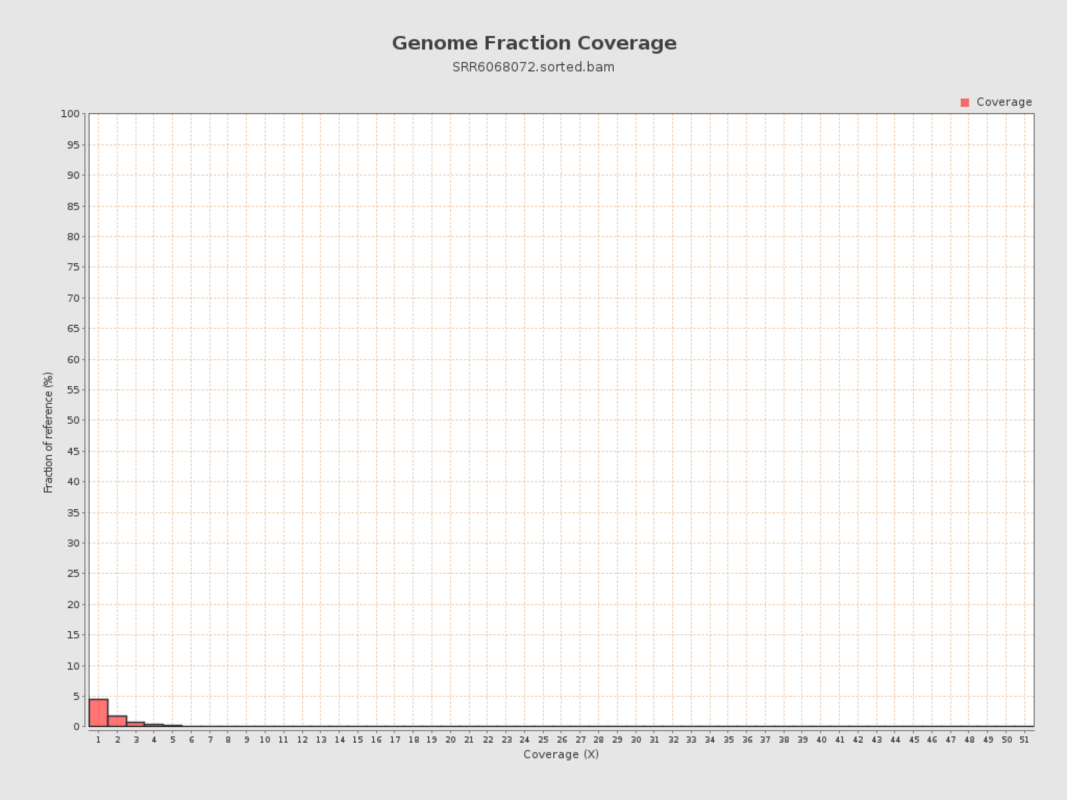
4. Results : Coverage Histogram



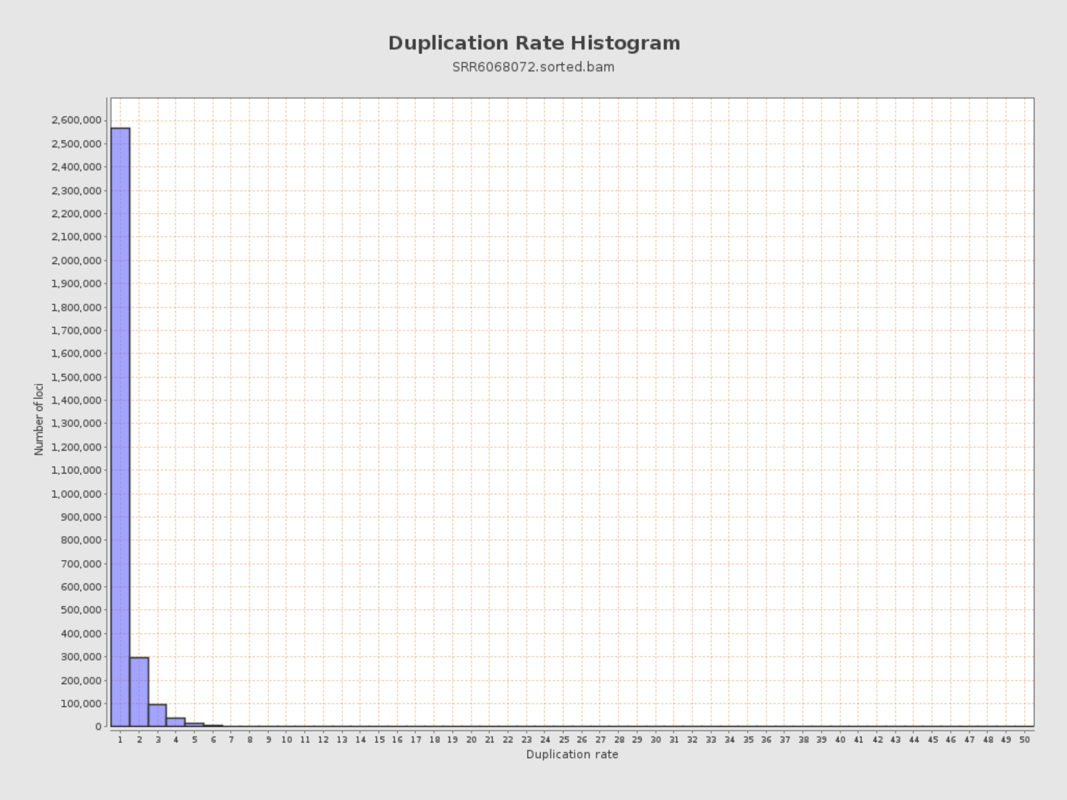
5. Results : Coverage Histogram (0-50X)



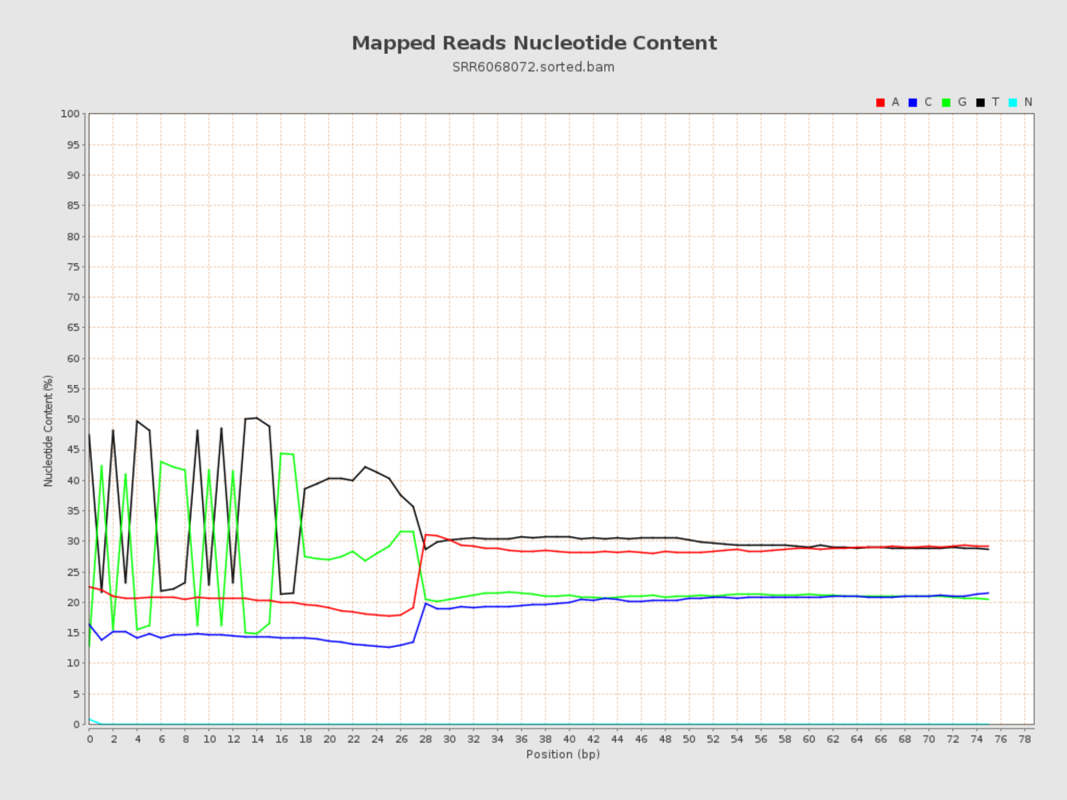
6. Results : Genome Fraction Coverage



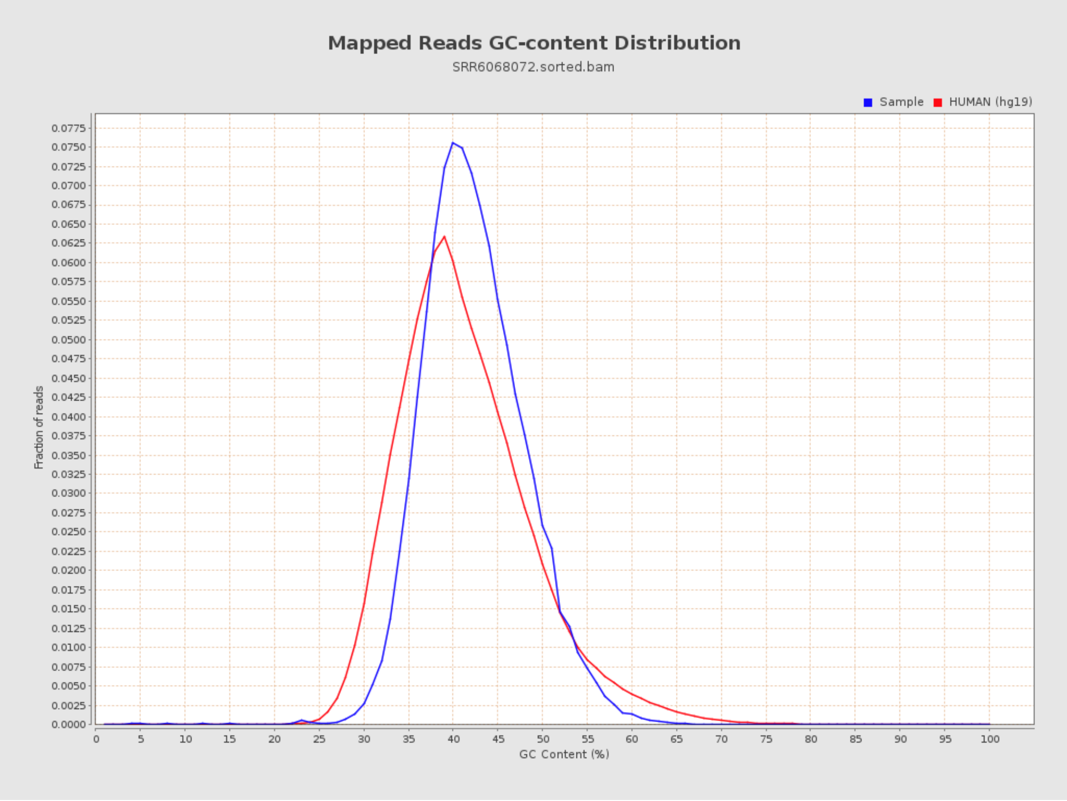
7. Results : Duplication Rate Histogram



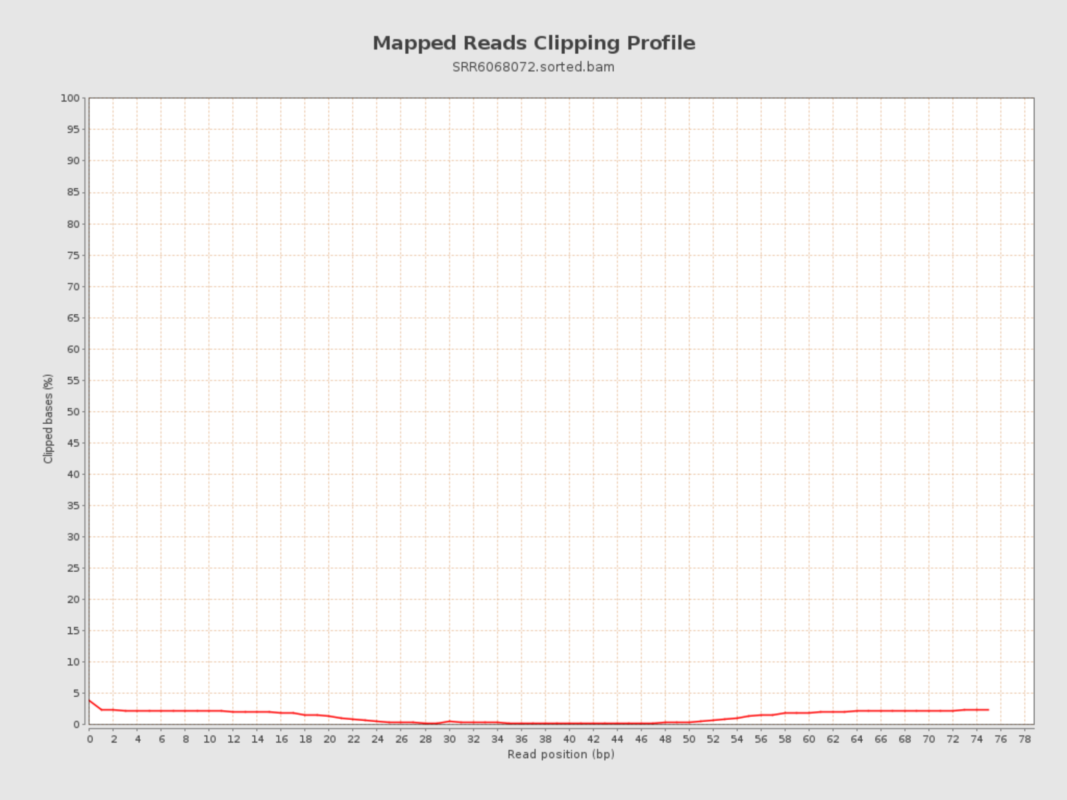
8. Results : Mapped Reads Nucleotide Content



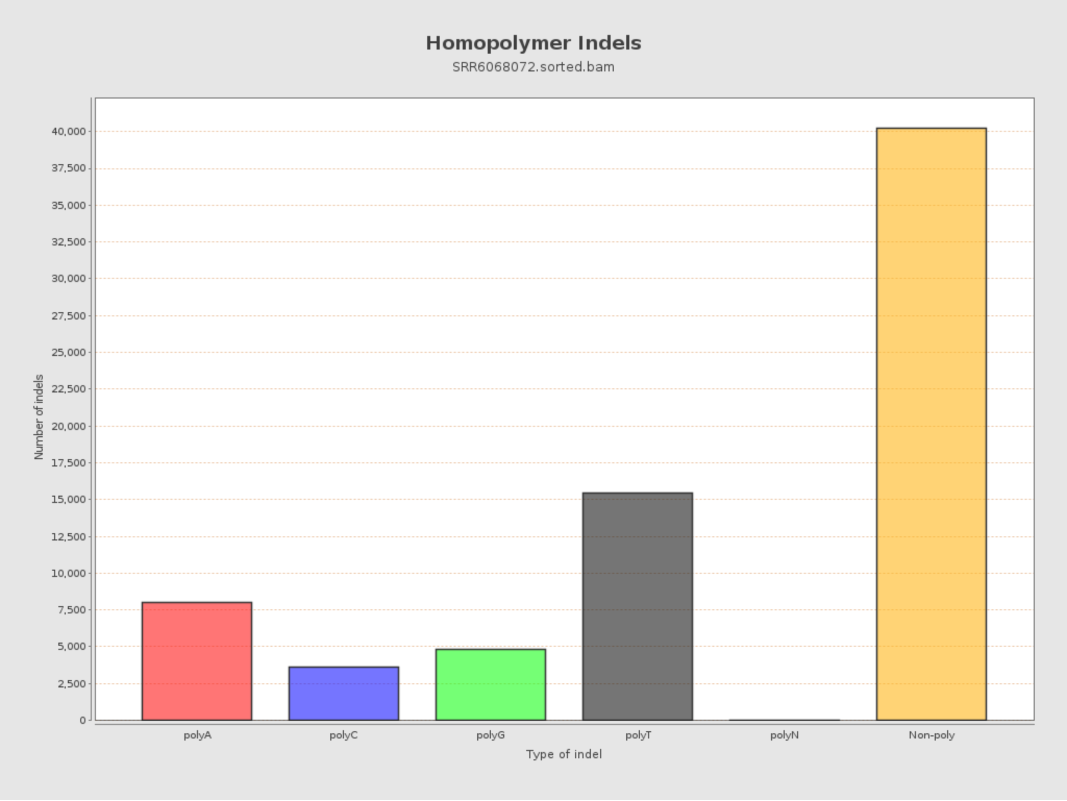
9. Results : Mapped Reads GC-content Distribution



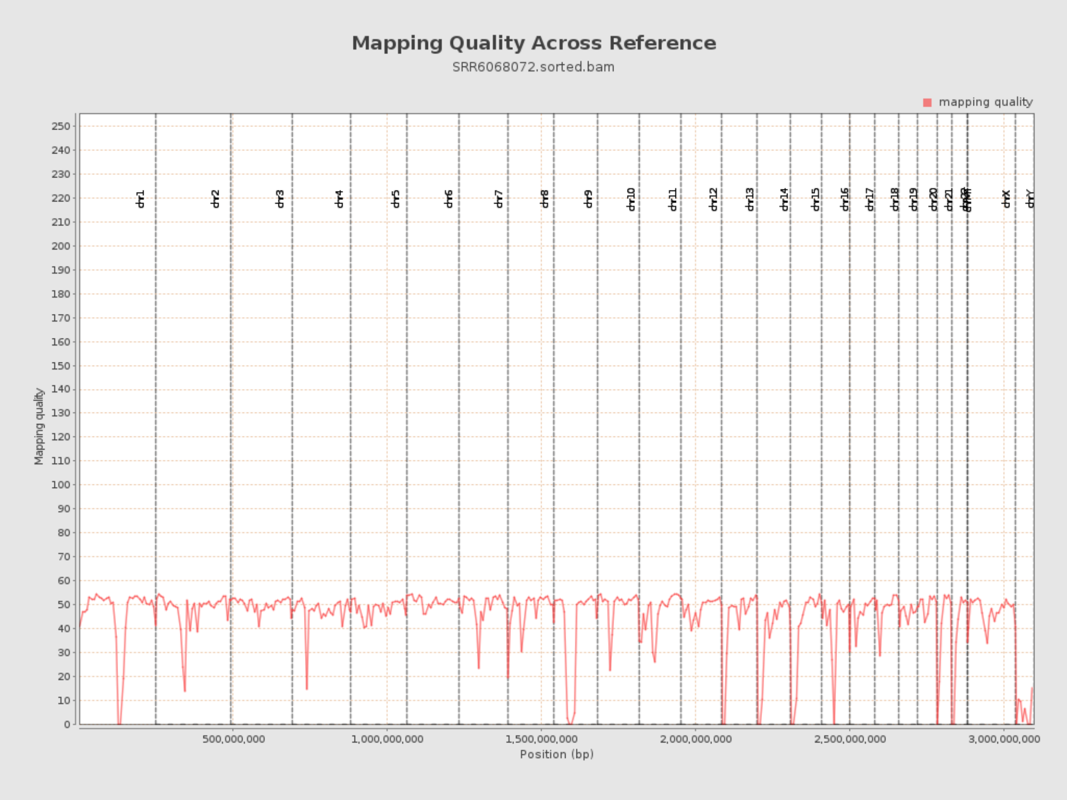
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram