Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 08:10:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068071.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_SRR6068071 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068071.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 08:10:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068071.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,838,550
Mapped reads	4,555,290 / 94.15%
Unmapped reads	283,260 / 5.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	41,088 / 0.85%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	963,031 / 19.9%
Duplication rate	15.4%
Clipped reads	2,460,432 / 50.85%

2.2. ACGT Content

Number/percentage of A's	74,920,933 / 25.65%
Number/percentage of C's	53,294,305 / 18.24%
Number/percentage of T's	94,636,367 / 32.4%
Number/percentage of G's	69,245,020 / 23.7%
Number/percentage of N's	33,362 / 0.01%
GC Percentage	41.95%

2.3. Coverage

Mean	0.0944

Standard Deviation	1.0975

2.4. Mapping Quality

Mean Mapping Quality	45.12

2.5. Mismatches and indels

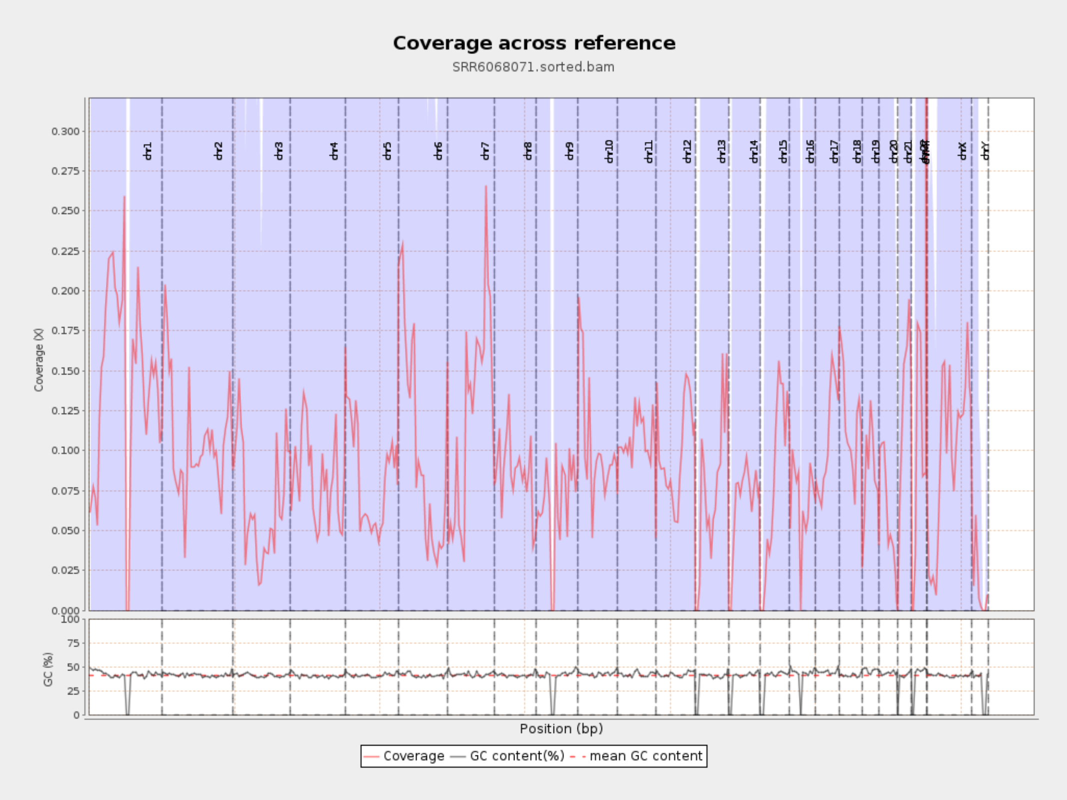
General error rate	0.58%
Mismatches	1,668,990
Insertions	19,257
Mapped reads with at least one insertion	0.42%
Deletions	63,156
Mapped reads with at least one deletion	1.37%
Homopolymer indels	43.47%

2.6. Chromosome stats

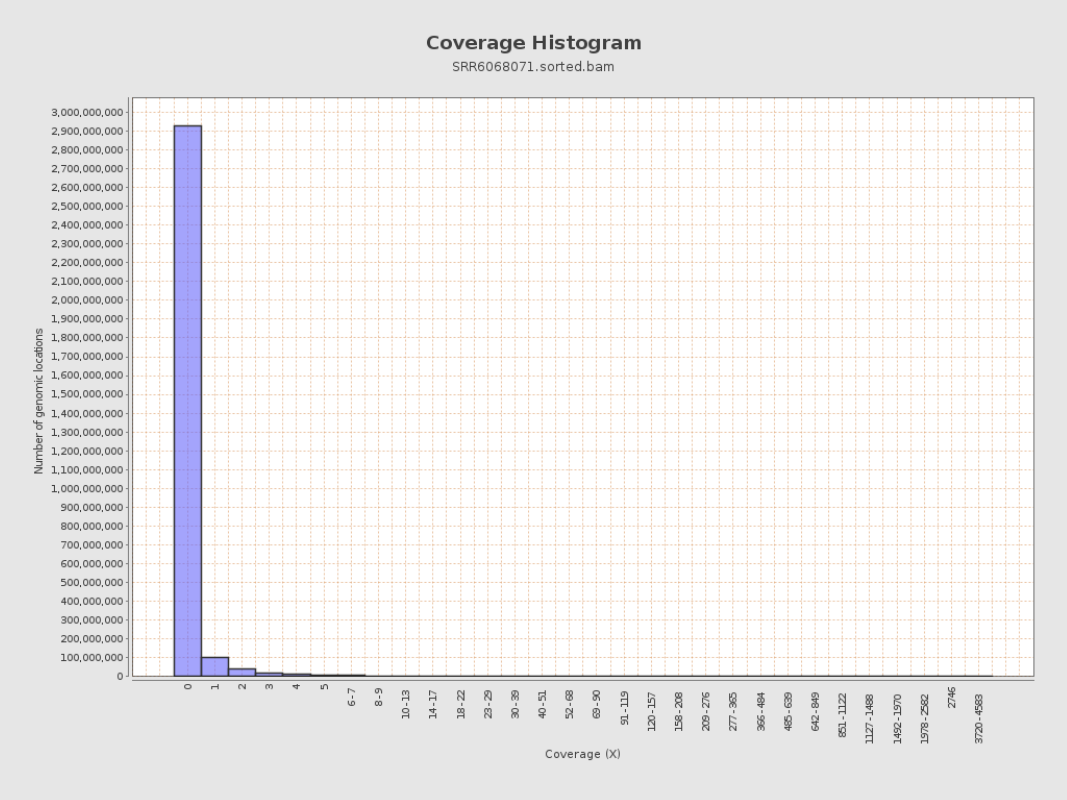
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	36088097	0.1448	2.1418
chr2	243199373	26261895	0.108	2.1839
chr3	198022430	13304058	0.0672	0.4164
chr4	191154276	15469211	0.0809	0.5408
chr5	180915260	14966706	0.0827	0.4687
chr6	171115067	17443532	0.1019	0.8081
chr7	159138663	19832152	0.1246	1.159

chr8	146364022	12708151	0.0868	1.0278
chr9	141213431	9416232	0.0667	0.7498
chr10	135534747	14290954	0.1054	0.7535
chr11	135006516	14499376	0.1074	0.7102
chr12	133851895	13362089	0.0998	0.5446
chr13	115169878	8668039	0.0753	0.5339
chr14	107349540	7087367	0.066	0.4847
chr15	102531392	8155391	0.0795	0.5132
chr16	90354753	6287543	0.0696	0.4786
chr17	81195210	8763356	0.1079	0.5787
chr18	78077248	9332577	0.1195	1.5002
chr19	59128983	5239482	0.0886	1.295
chr20	63025520	3971030	0.063	0.4436
chr21	48129895	6063758	0.126	0.6212
chr22	51304566	4487625	0.0875	0.4713
chrMT	16571	310361	18.7292	13.8699
chrX	155270560	15309273	0.0986	0.6179
chrY	59373566	921418	0.0155	0.7245

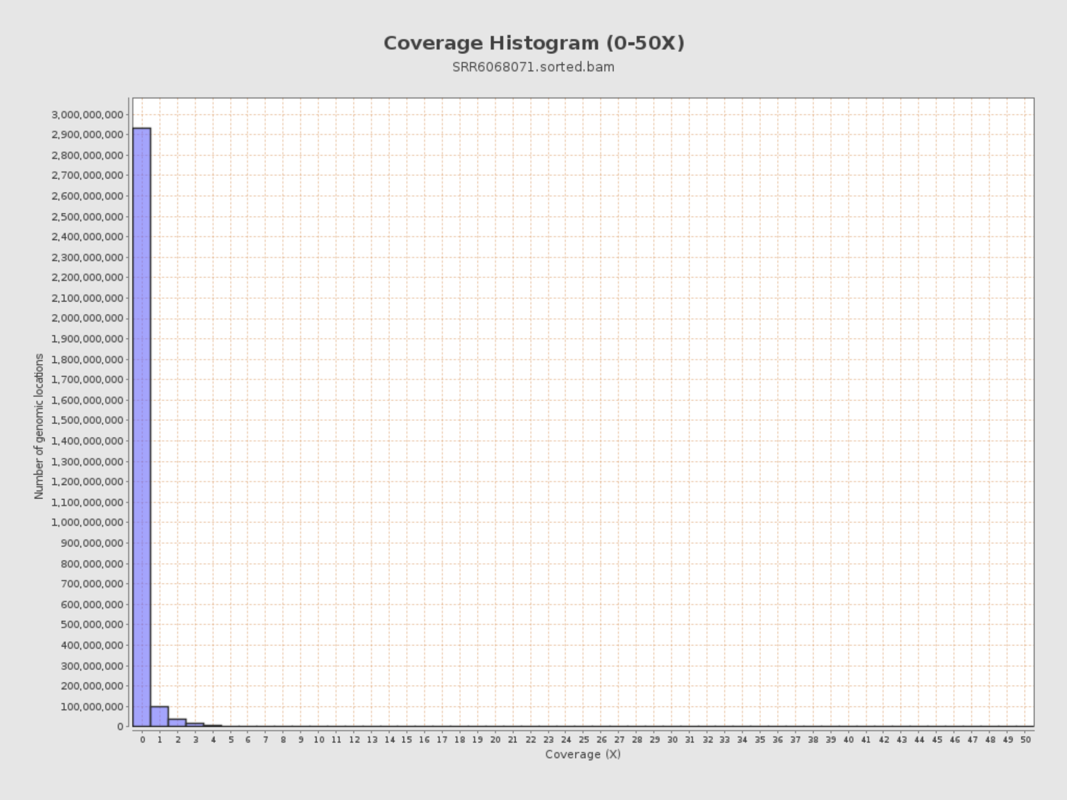
3. Results : Coverage across reference



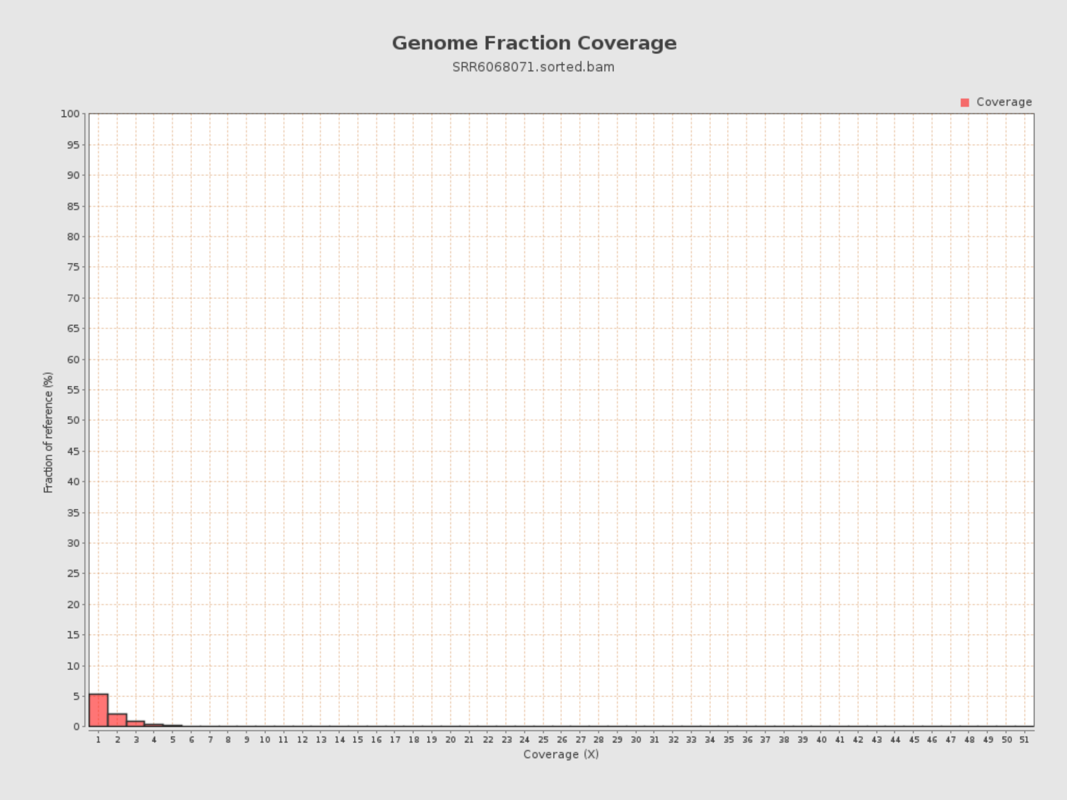
4. Results : Coverage Histogram



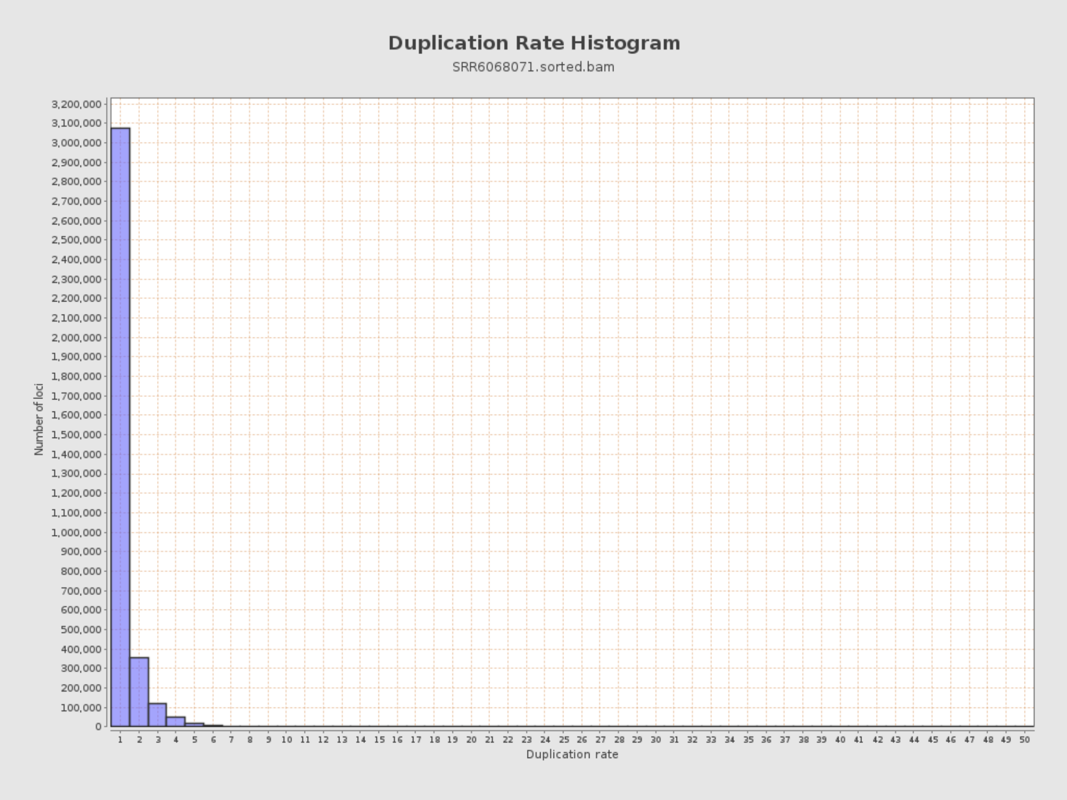
5. Results : Coverage Histogram (0-50X)



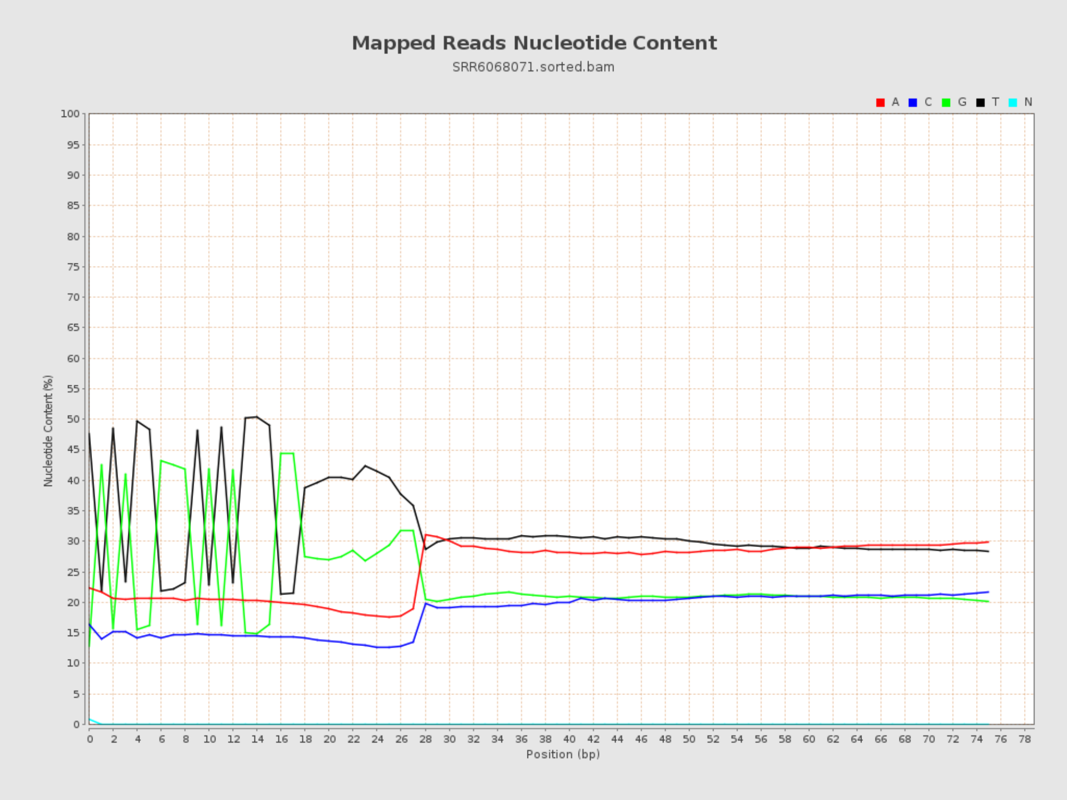
6. Results : Genome Fraction Coverage



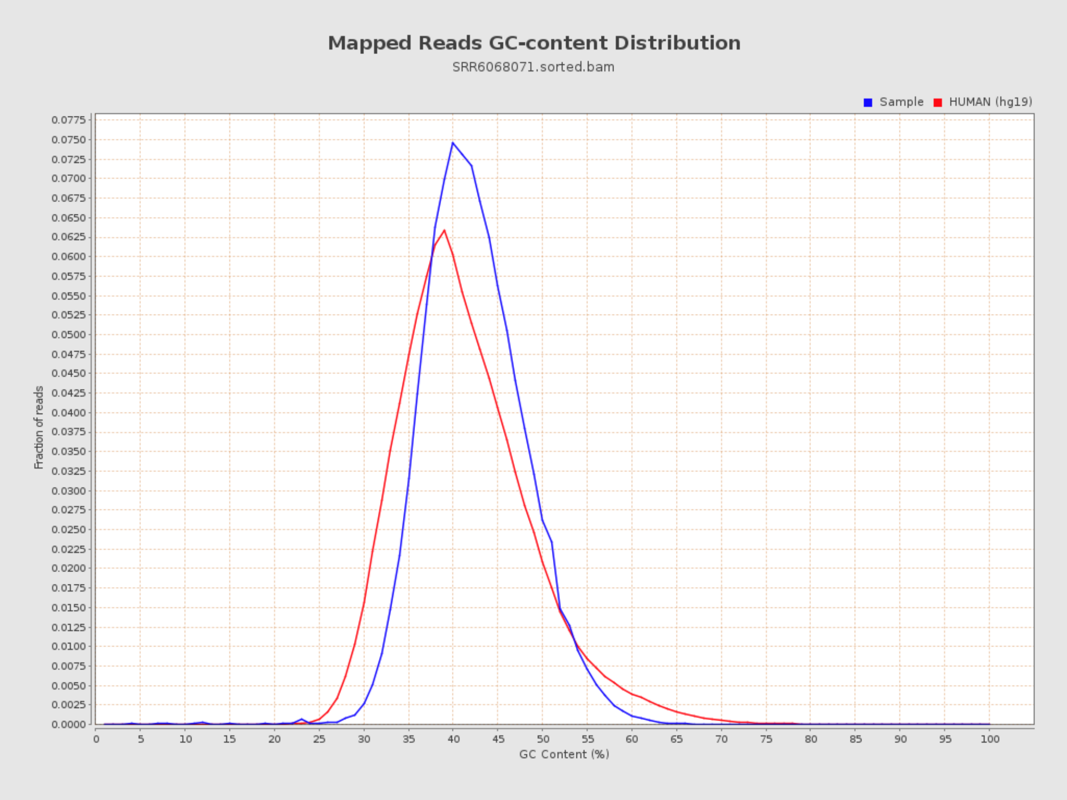
7. Results : Duplication Rate Histogram



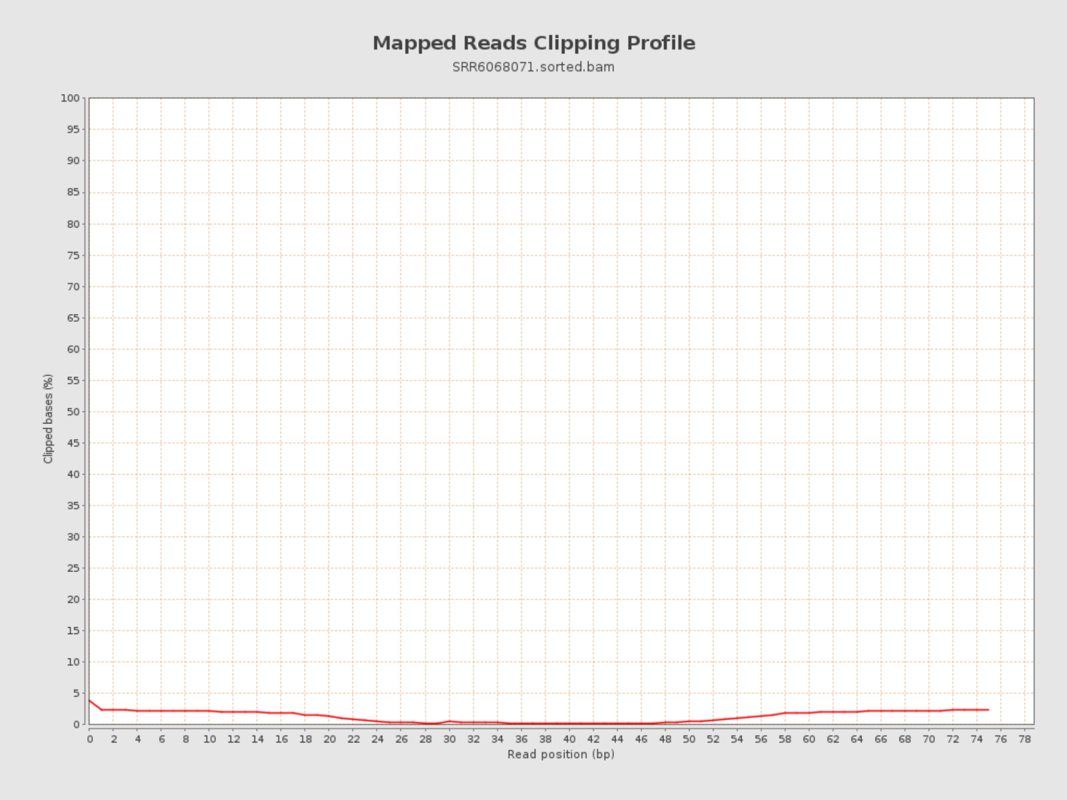
8. Results : Mapped Reads Nucleotide Content



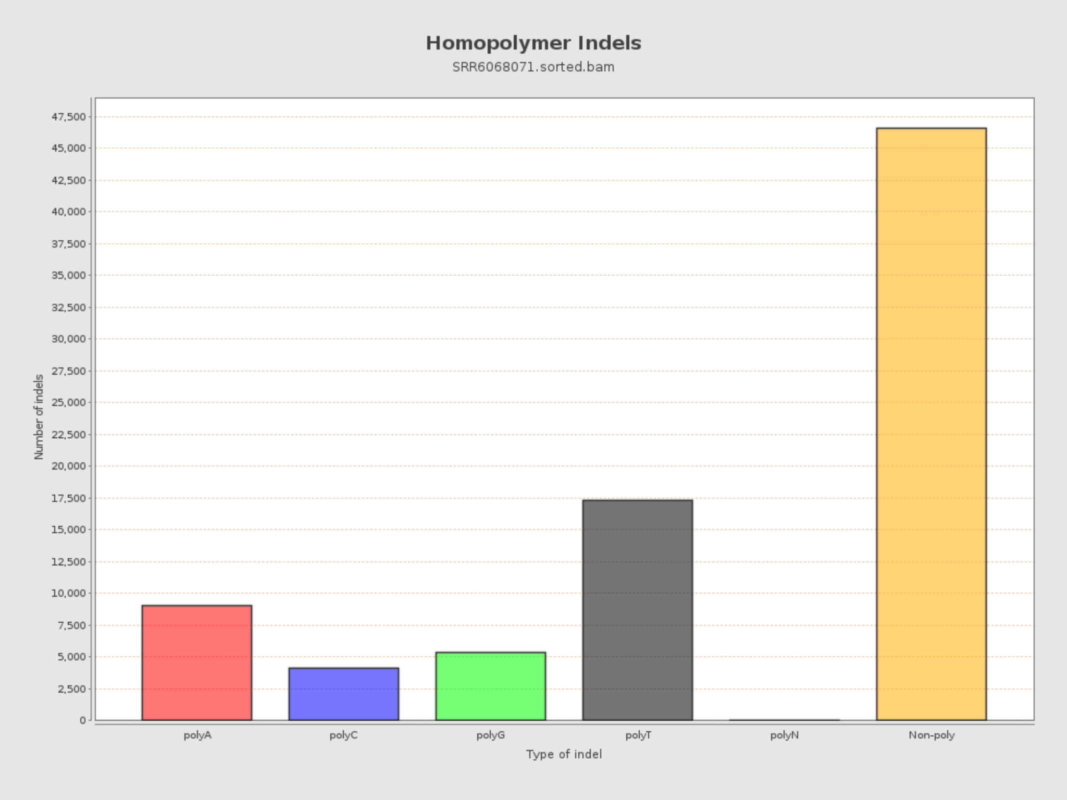
9. Results : Mapped Reads GC-content Distribution



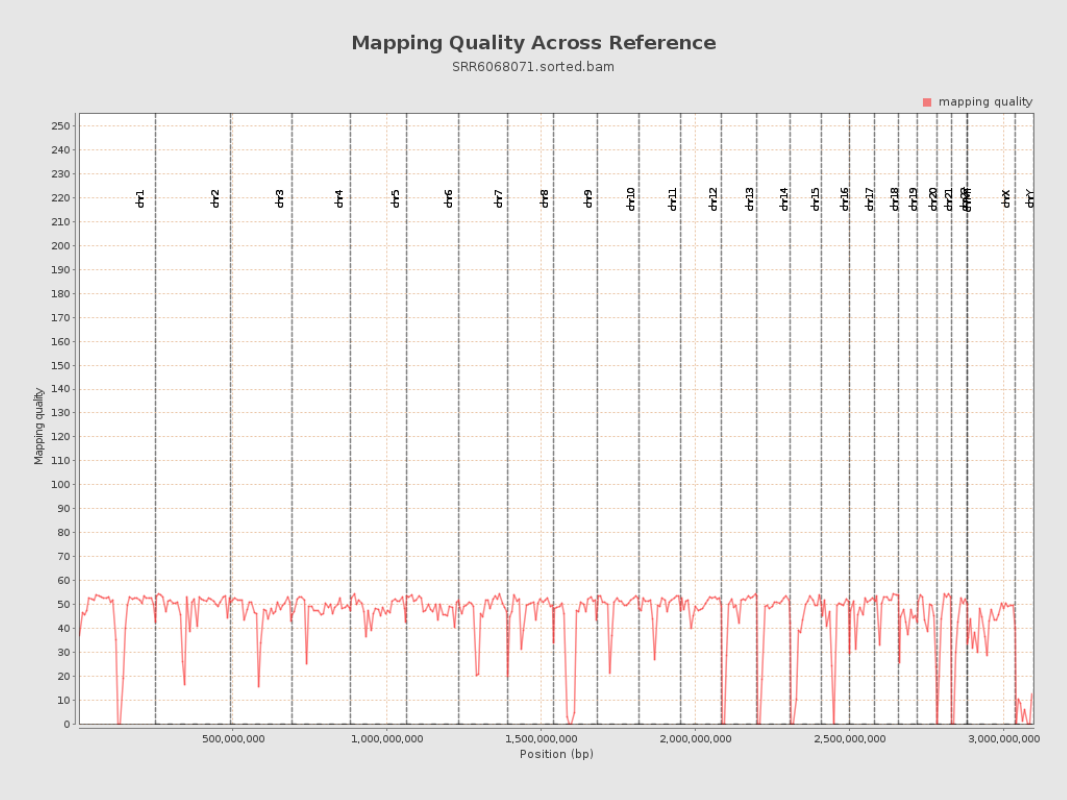
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram