Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:39:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080972.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_SRR3080972 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080972.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:39:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080972.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,659,294
Mapped reads	5,918,114 / 88.87%
Unmapped reads	741,180 / 11.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	56,373 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	432,694 / 6.5%
Duplication rate	5.69%
Clipped reads	2,537,726 / 38.11%

2.2. ACGT Content

Number/percentage of A's	111,543,998 / 28.01%
Number/percentage of C's	70,473,112 / 17.7%
Number/percentage of T's	129,089,416 / 32.42%
Number/percentage of G's	86,346,770 / 21.68%
Number/percentage of N's	783,763 / 0.2%
GC Percentage	39.38%

2.3. Coverage

Mean	0.1287

Standard Deviation	0.8595

2.4. Mapping Quality

Mean Mapping Quality	46.73

2.5. Mismatches and indels

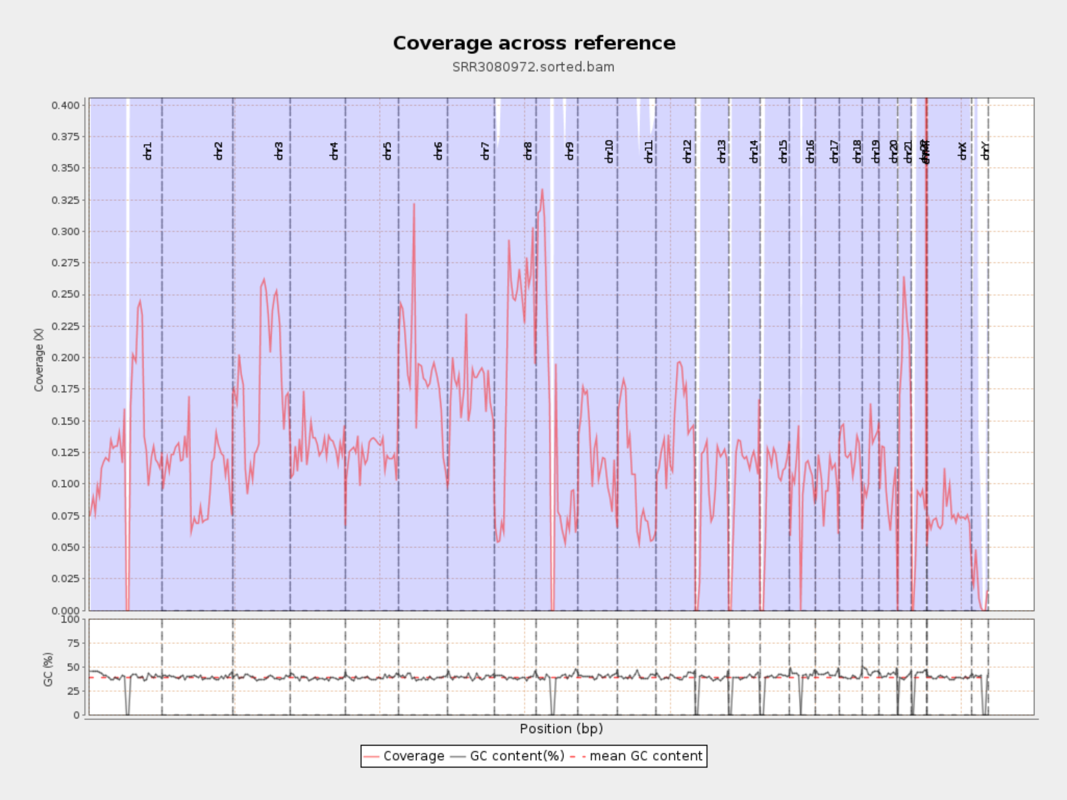
General error rate	1.01%
Mismatches	3,949,015
Insertions	32,051
Mapped reads with at least one insertion	0.54%
Deletions	88,182
Mapped reads with at least one deletion	1.47%
Homopolymer indels	49.27%

2.6. Chromosome stats

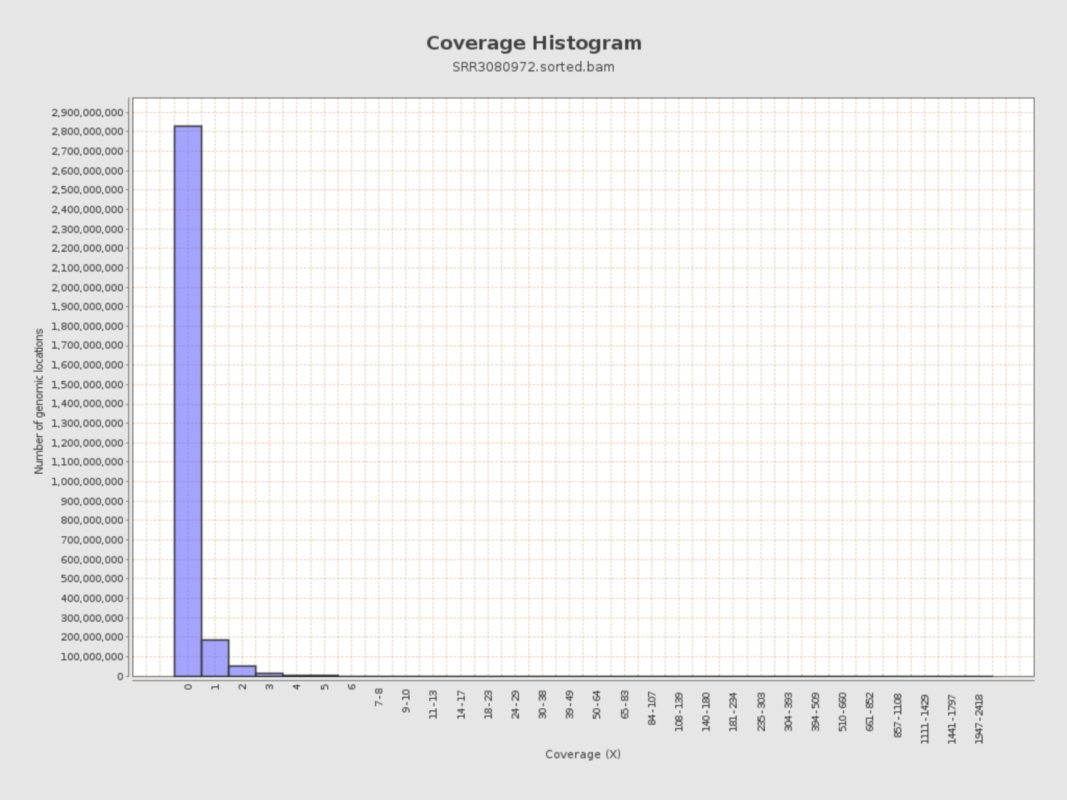
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31831876	0.1277	1.1305
chr2	243199373	26164582	0.1076	0.8076
chr3	198022430	35926187	0.1814	0.595
chr4	191154276	24785564	0.1297	0.5447
chr5	180915260	22432661	0.124	0.4875
chr6	171115067	32580220	0.1904	1.0312
chr7	159138663	28124638	0.1767	1.2905

chr8	146364022	29612749	0.2023	1.6245
chr9	141213431	20002118	0.1416	1.016
chr10	135534747	17017496	0.1256	0.72
chr11	135006516	13809696	0.1023	0.6124
chr12	133851895	19326592	0.1444	0.5542
chr13	115169878	10720823	0.0931	0.4188
chr14	107349540	10982440	0.1023	0.5878
chr15	102531392	9862893	0.0962	0.4318
chr16	90354753	8915038	0.0987	0.5547
chr17	81195210	8095849	0.0997	0.4699
chr18	78077248	9923601	0.1271	1.7583
chr19	59128983	7177248	0.1214	0.8916
chr20	63025520	6166768	0.0978	0.4792
chr21	48129895	9090987	0.1889	0.7313
chr22	51304566	3238217	0.0631	0.3407
chrMT	16571	202137	12.1982	7.264
chrX	155270560	11530884	0.0743	0.4335
chrY	59373566	861556	0.0145	0.2926

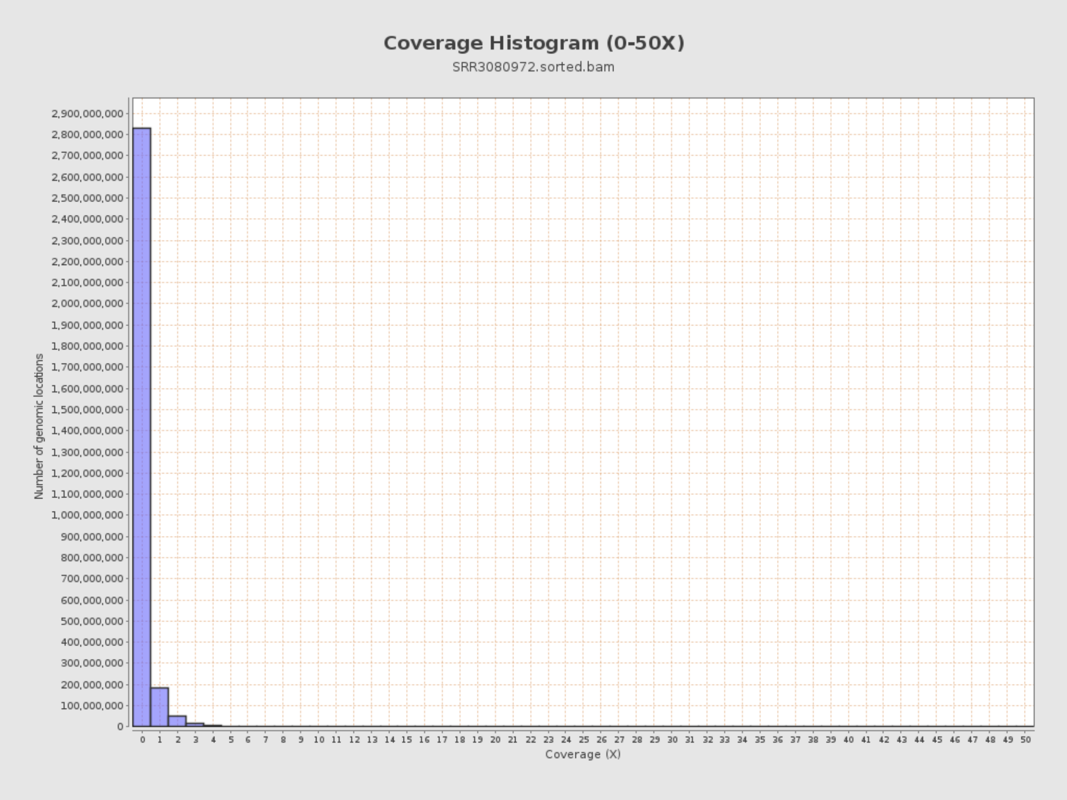
3. Results : Coverage across reference



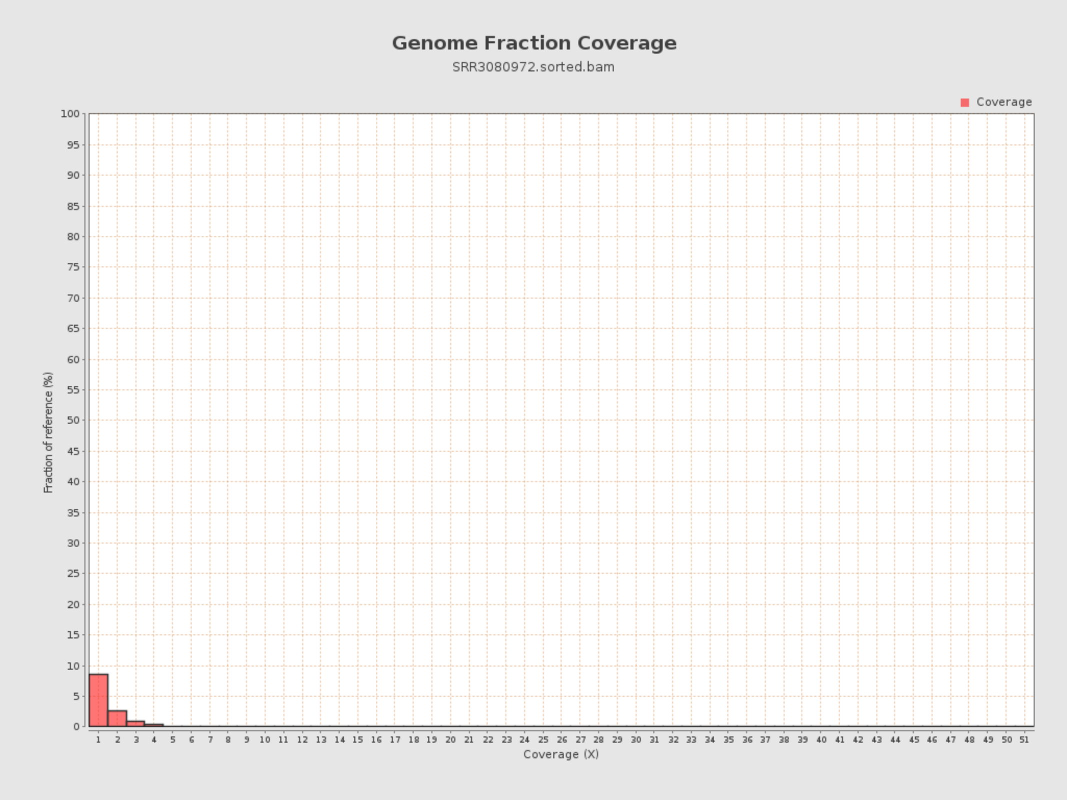
4. Results : Coverage Histogram



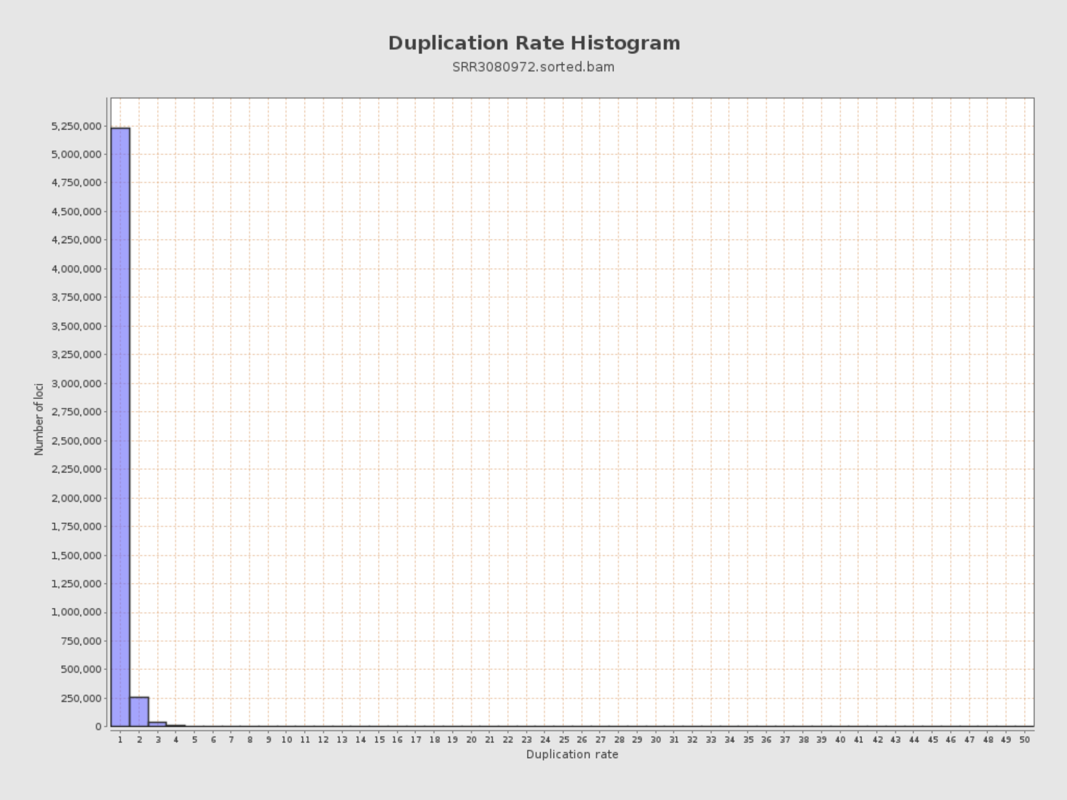
5. Results : Coverage Histogram (0-50X)



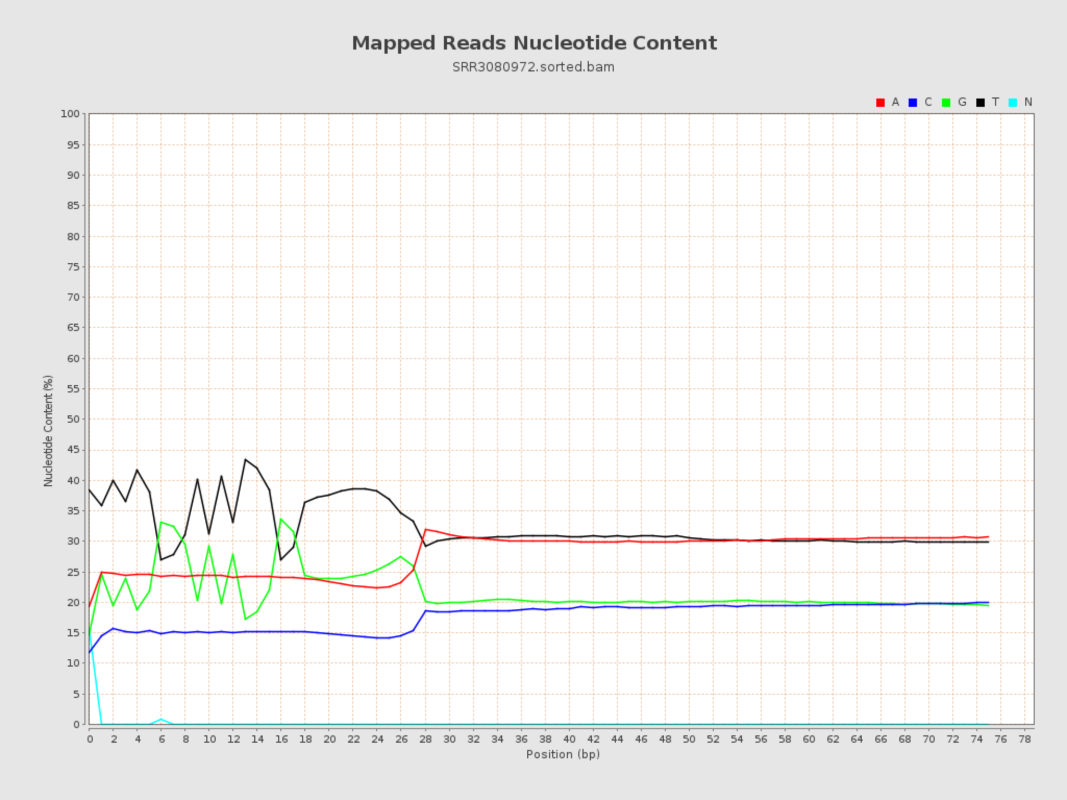
6. Results : Genome Fraction Coverage



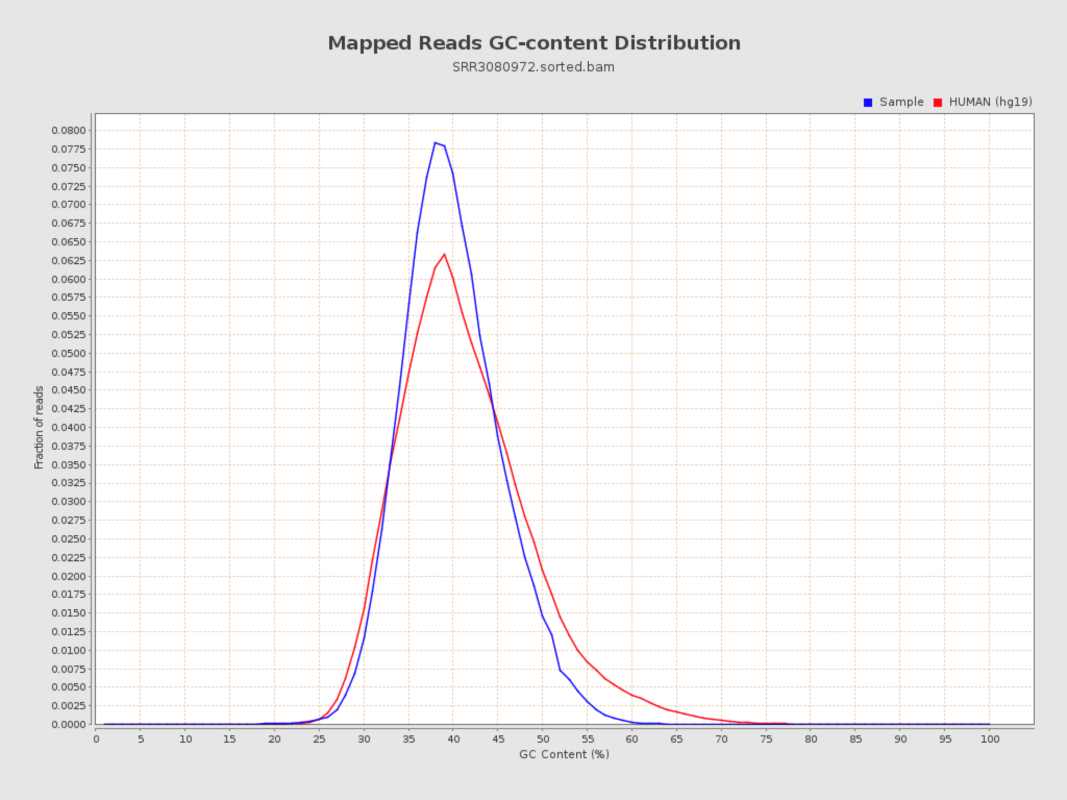
7. Results : Duplication Rate Histogram



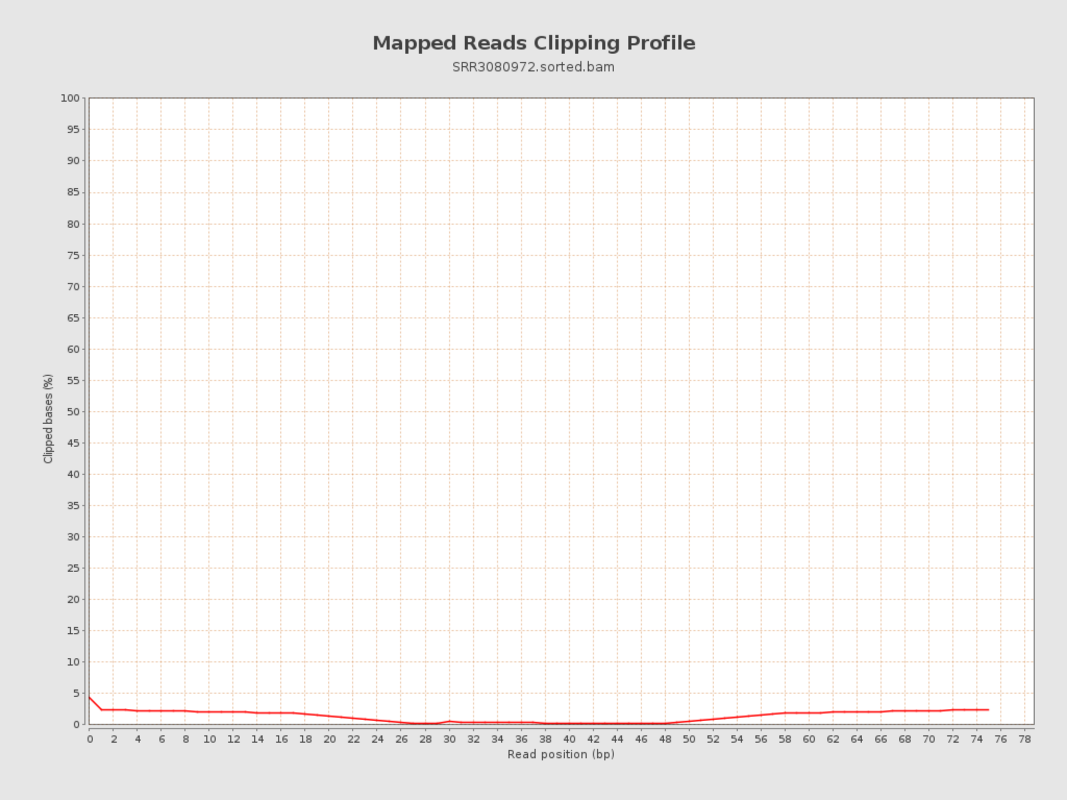
8. Results : Mapped Reads Nucleotide Content



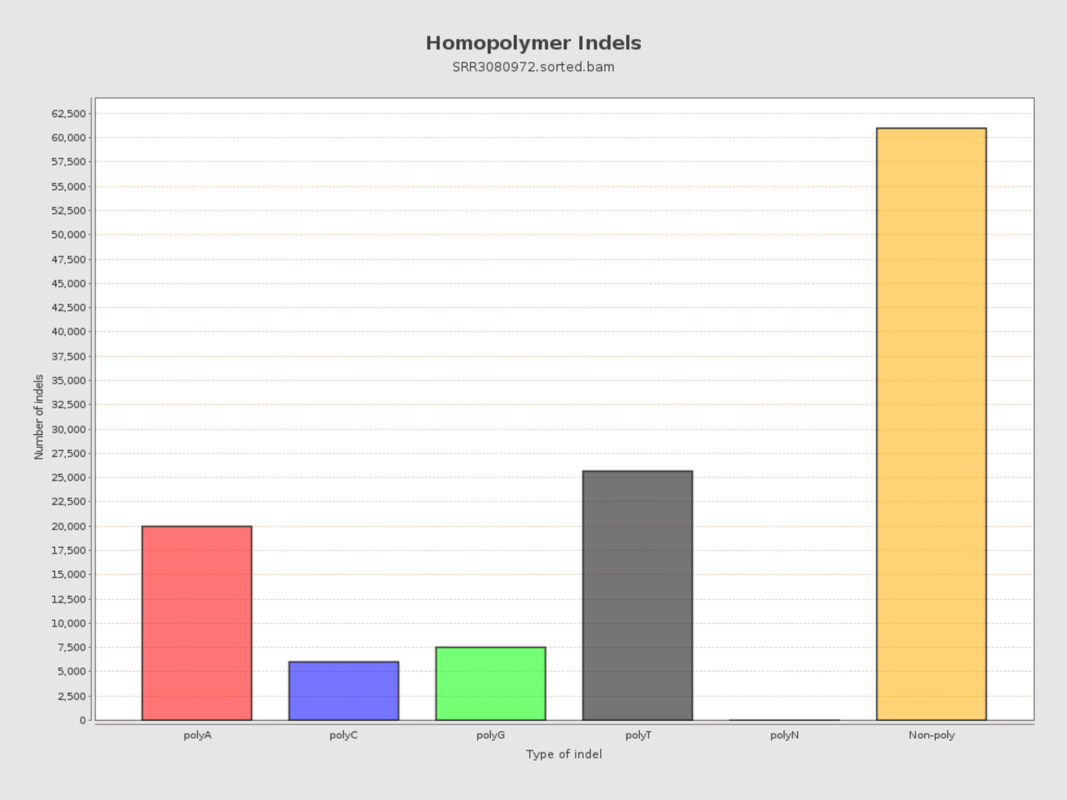
9. Results : Mapped Reads GC-content Distribution



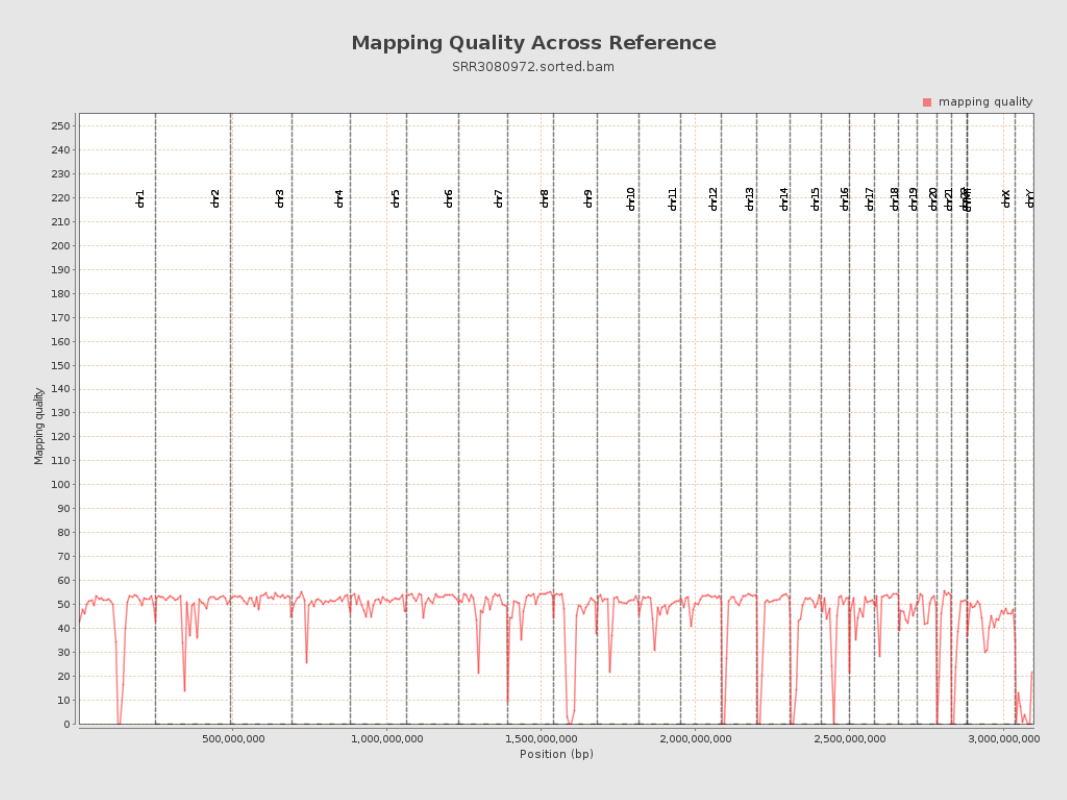
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram