Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:59:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716972.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_SRR9716972 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716972.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:59:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716972.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,310,217
Mapped reads	2,554,719 / 77.18%
Unmapped reads	755,498 / 22.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,043 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	92,720 / 2.8%
Duplication rate	2.52%
Clipped reads	2,566,275 / 77.53%

2.2. ACGT Content

Number/percentage of A's	37,759,951 / 25.91%
Number/percentage of C's	26,636,244 / 18.28%
Number/percentage of T's	45,273,170 / 31.06%
Number/percentage of G's	36,074,869 / 24.75%
Number/percentage of N's	2,344 / 0%
GC Percentage	43.03%

2.3. Coverage

Mean	0.0471

Standard Deviation	0.4116

2.4. Mapping Quality

Mean Mapping Quality	43.37

2.5. Mismatches and indels

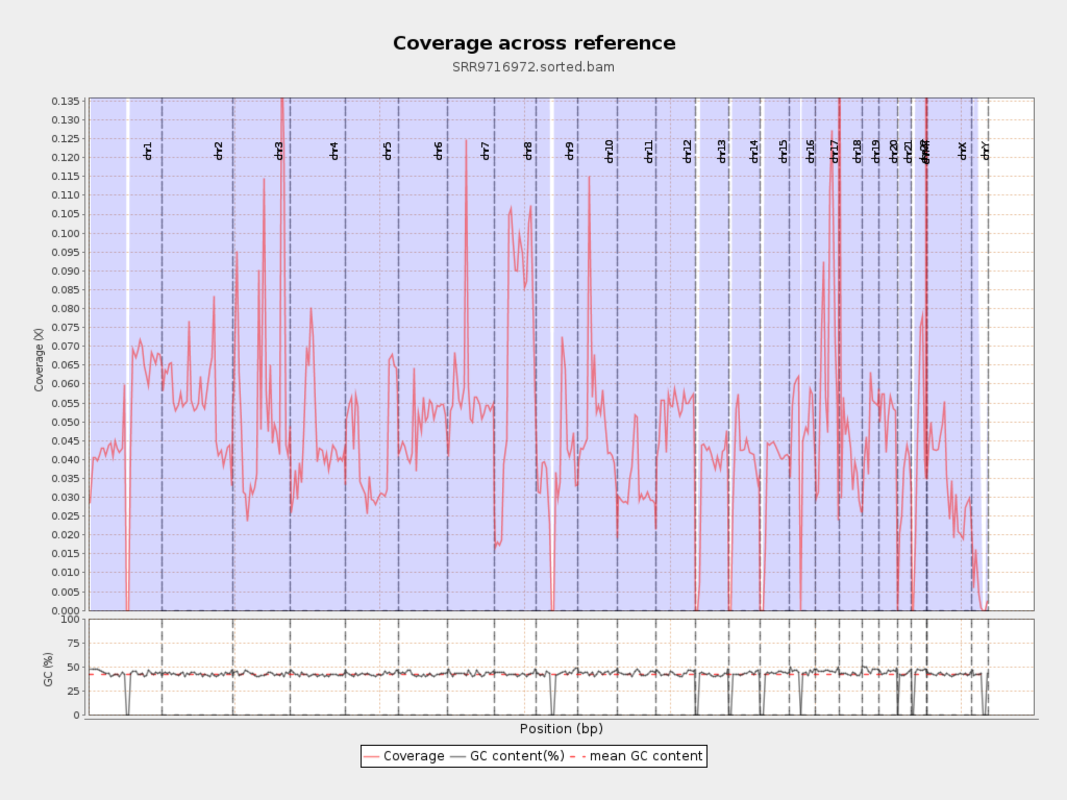
General error rate	0.5%
Mismatches	718,546
Insertions	8,584
Mapped reads with at least one insertion	0.33%
Deletions	27,241
Mapped reads with at least one deletion	1.06%
Homopolymer indels	42.66%

2.6. Chromosome stats

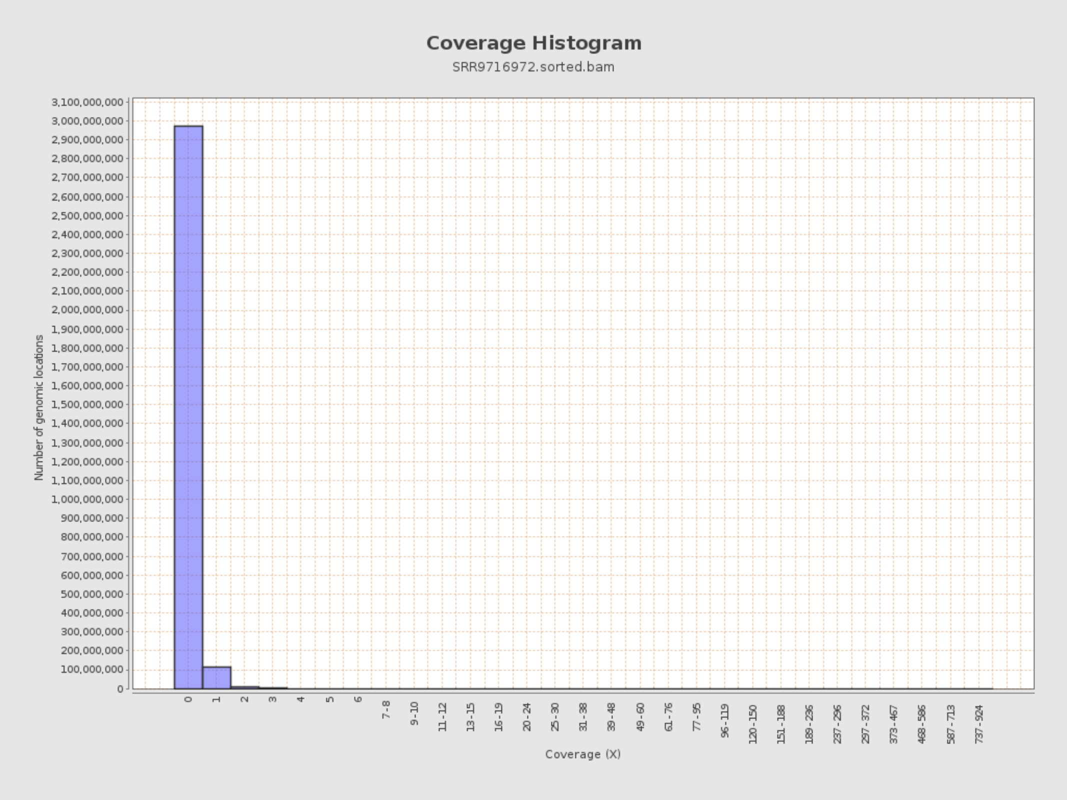
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12436144	0.0499	0.5083
chr2	243199373	13482309	0.0554	0.4907
chr3	198022430	11446159	0.0578	0.302
chr4	191154276	8565699	0.0448	0.2513
chr5	180915260	7722866	0.0427	0.2326
chr6	171115067	8429241	0.0493	0.2923
chr7	159138663	9296499	0.0584	1.0507

chr8	146364022	10489407	0.0717	0.3876
chr9	141213431	5067656	0.0359	0.2737
chr10	135534747	6978802	0.0515	0.5221
chr11	135006516	4399088	0.0326	0.2737
chr12	133851895	7080867	0.0529	0.2843
chr13	115169878	4017747	0.0349	0.208
chr14	107349540	3971768	0.037	0.2253
chr15	102531392	3533411	0.0345	0.2153
chr16	90354753	4353057	0.0482	0.2705
chr17	81195210	5467618	0.0673	0.3077
chr18	78077248	3633639	0.0465	0.4752
chr19	59128983	2909449	0.0492	0.4685
chr20	63025520	3257614	0.0517	0.2666
chr21	48129895	1461323	0.0304	0.2024
chr22	51304566	2045849	0.0399	0.228
chrMT	16571	32401	1.9553	1.9355
chrX	155270560	5395470	0.0347	0.2587
chrY	59373566	315226	0.0053	0.117

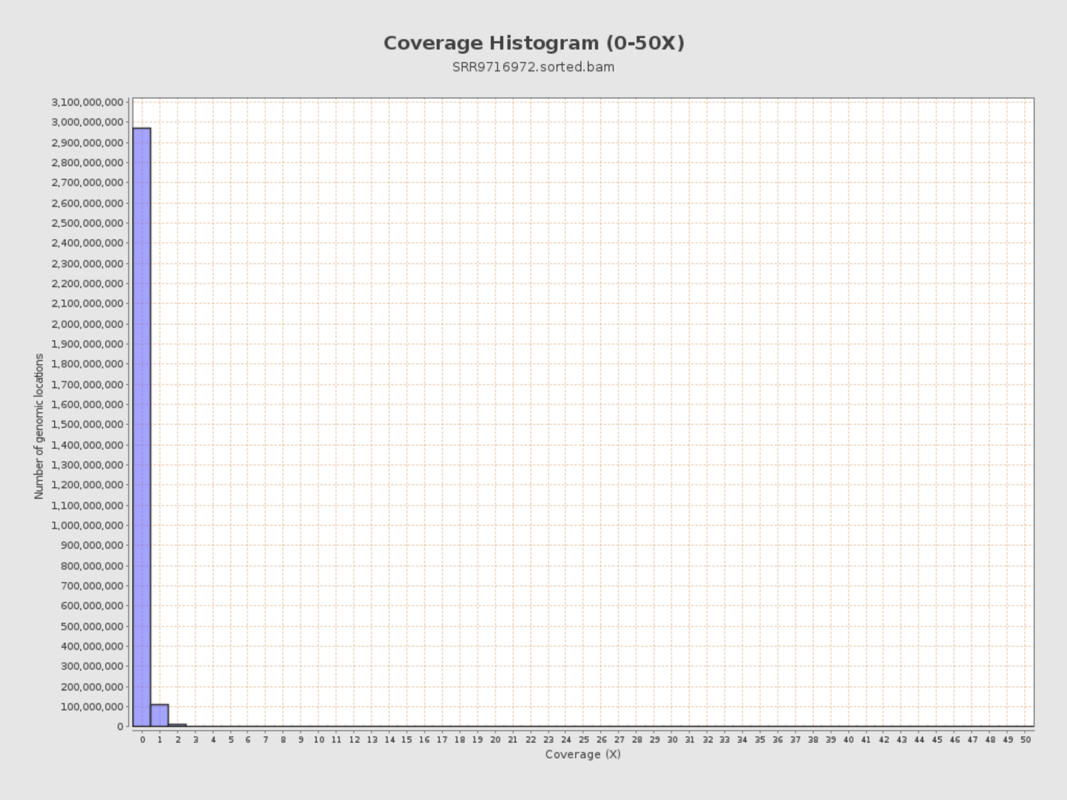
3. Results : Coverage across reference



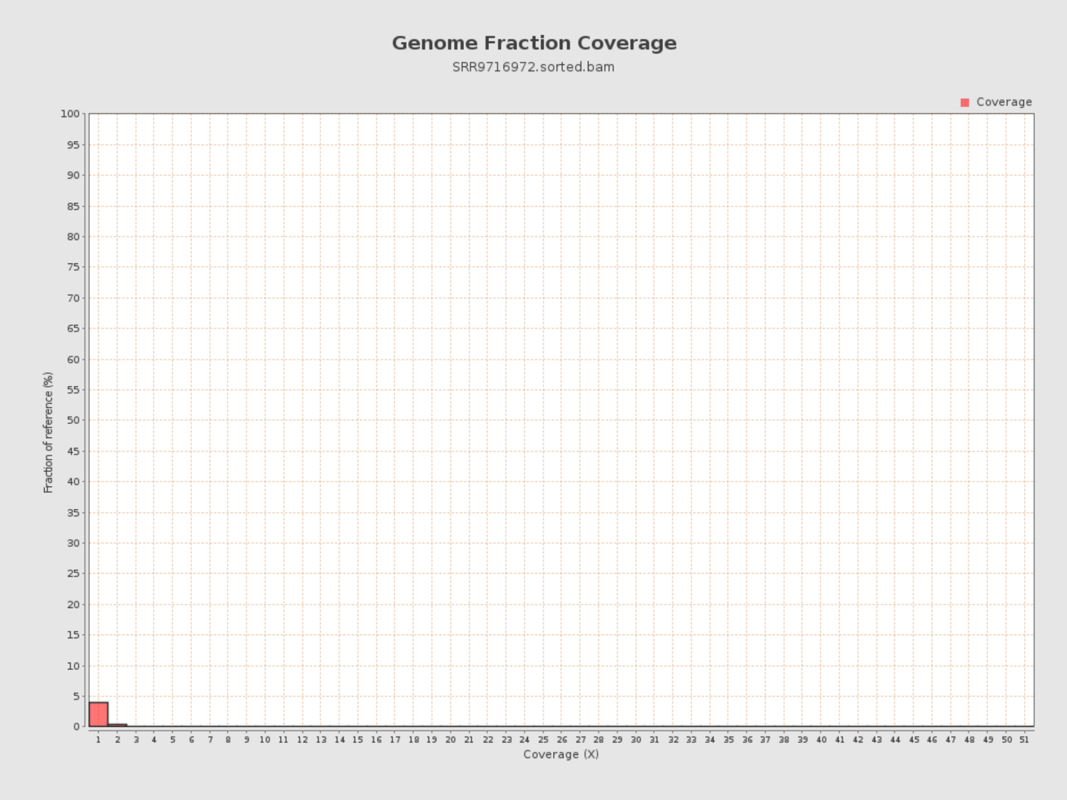
4. Results : Coverage Histogram



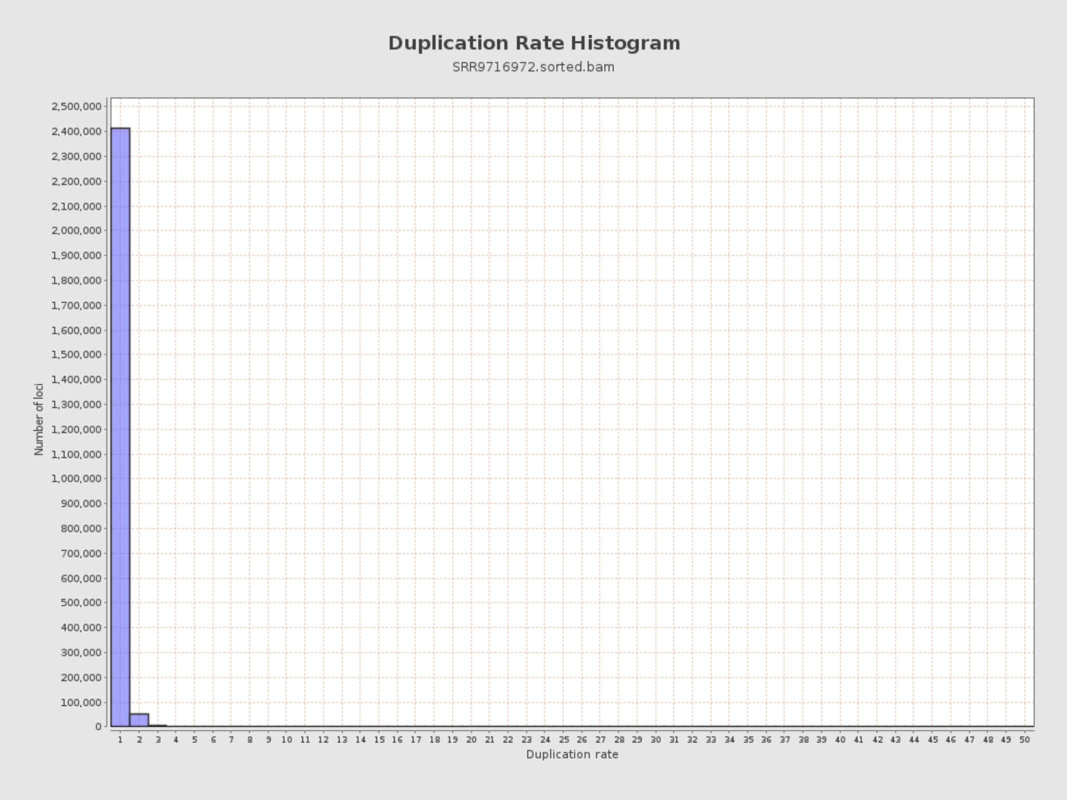
5. Results : Coverage Histogram (0-50X)



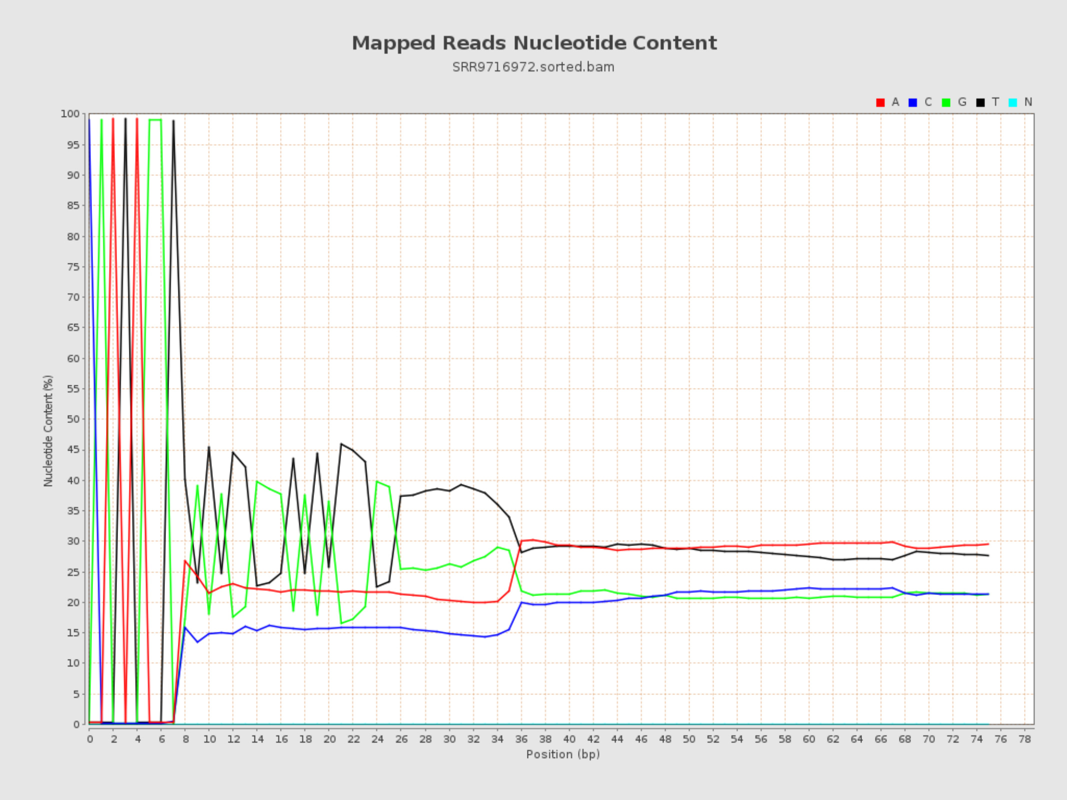
6. Results : Genome Fraction Coverage



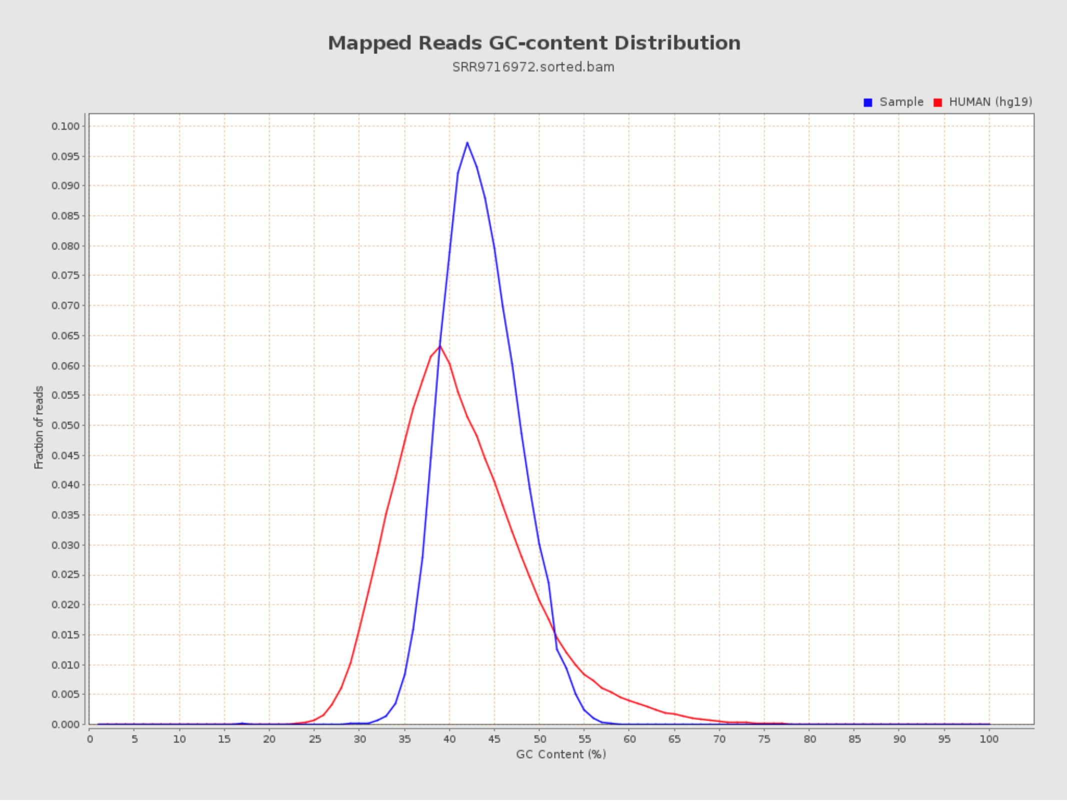
7. Results : Duplication Rate Histogram



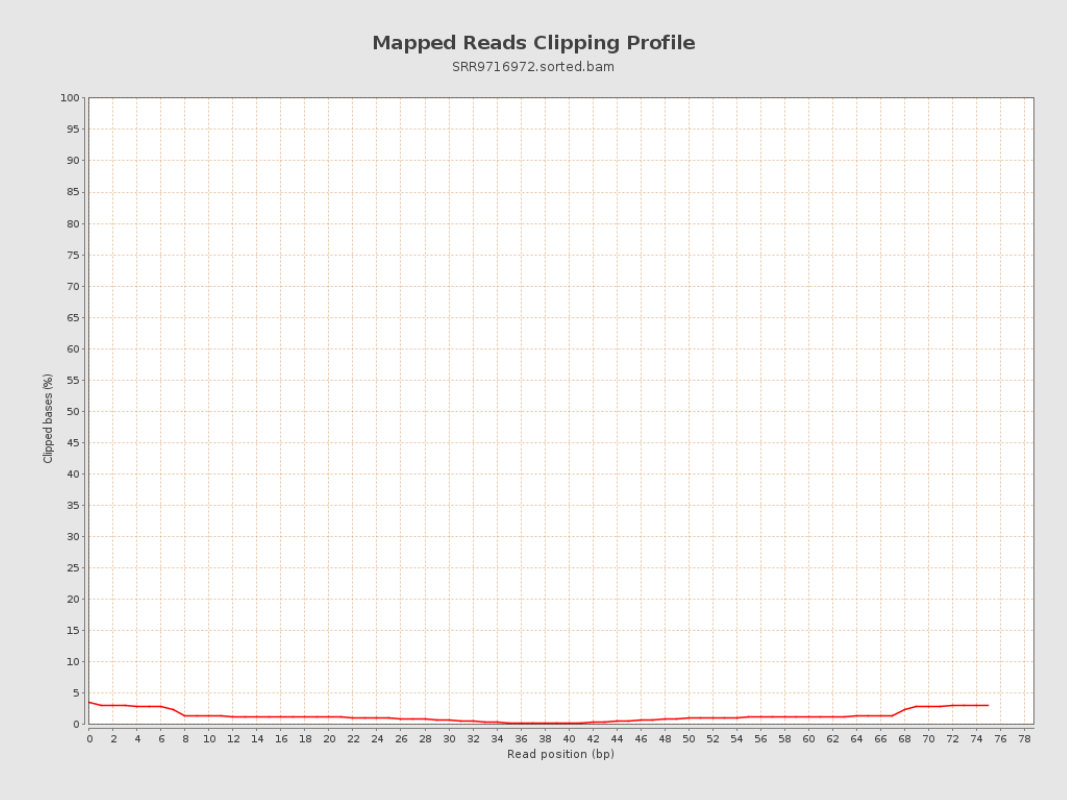
8. Results : Mapped Reads Nucleotide Content



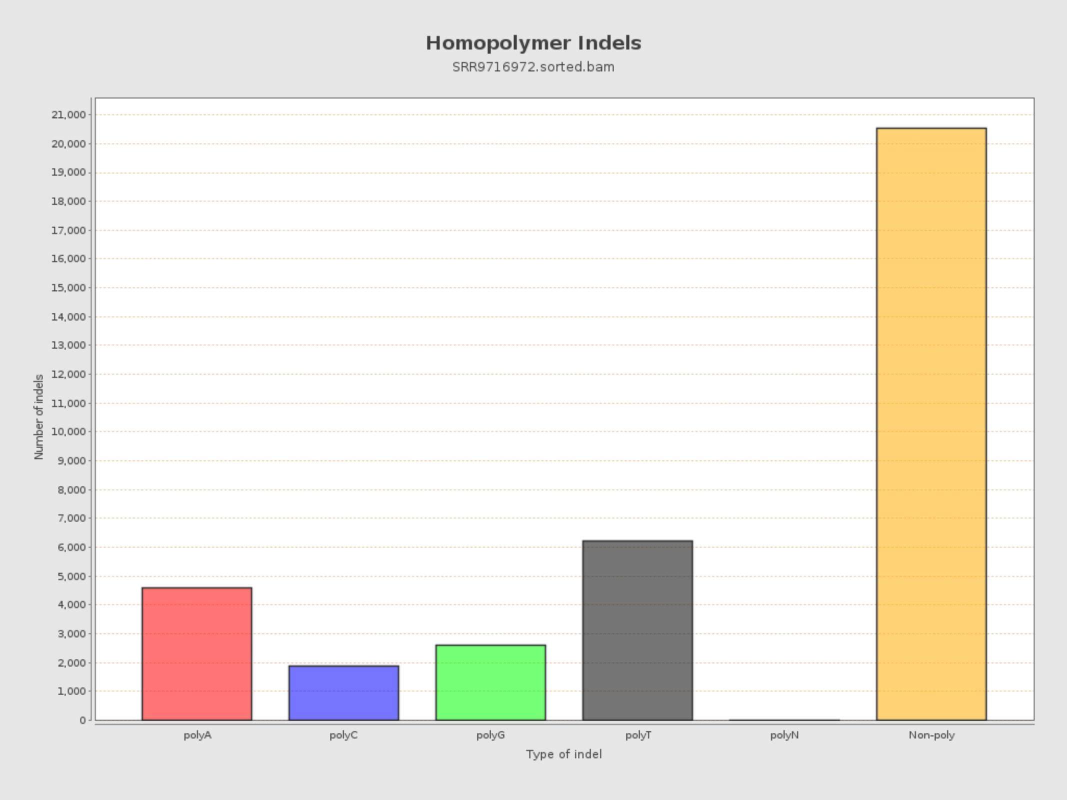
9. Results : Mapped Reads GC-content Distribution



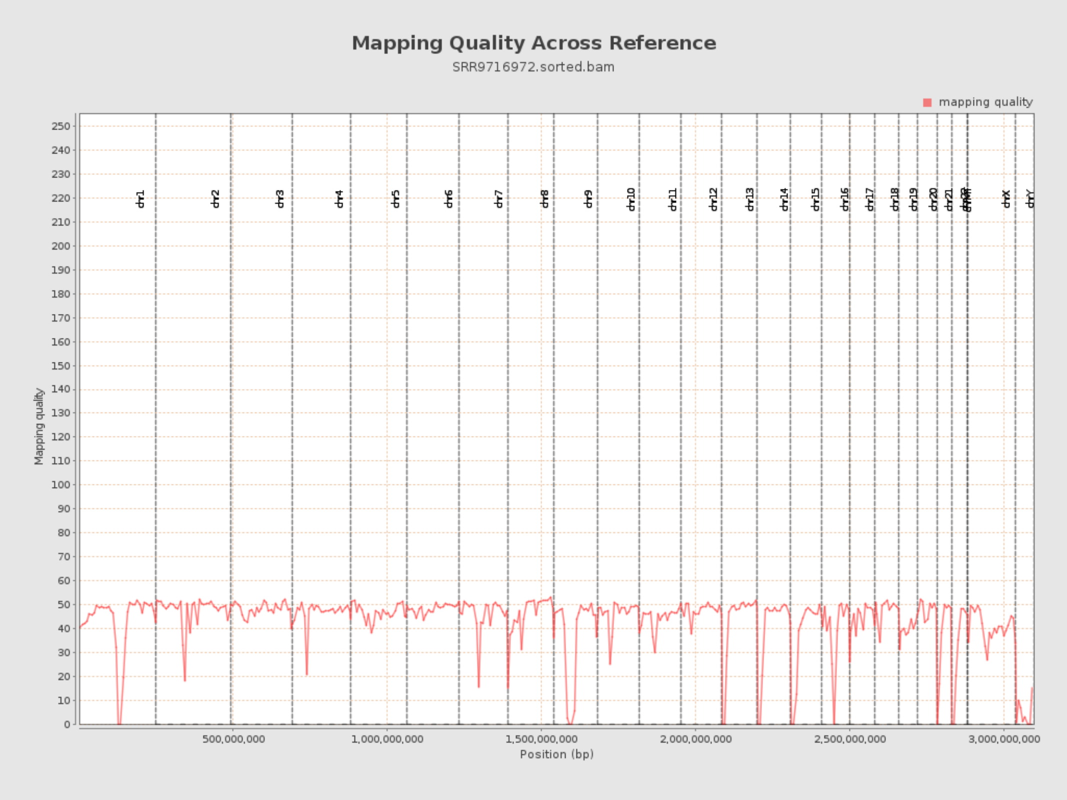
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram