Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:50:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716827.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_SRR9716827 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716827.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:50:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716827.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	600,679
Mapped reads	505,290 / 84.12%
Unmapped reads	95,389 / 15.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	707 / 0.12%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	30,682 / 5.11%
Duplication rate	5.45%
Clipped reads	505,687 / 84.19%

2.2. ACGT Content

Number/percentage of A's	5,302,297 / 19.79%
Number/percentage of C's	4,986,794 / 18.62%
Number/percentage of T's	8,627,176 / 32.21%
Number/percentage of G's	7,869,289 / 29.38%
Number/percentage of N's	596 / 0%
GC Percentage	48%

2.3. Coverage

Mean	0.0087

Standard Deviation	0.1084

2.4. Mapping Quality

Mean Mapping Quality	43.63

2.5. Mismatches and indels

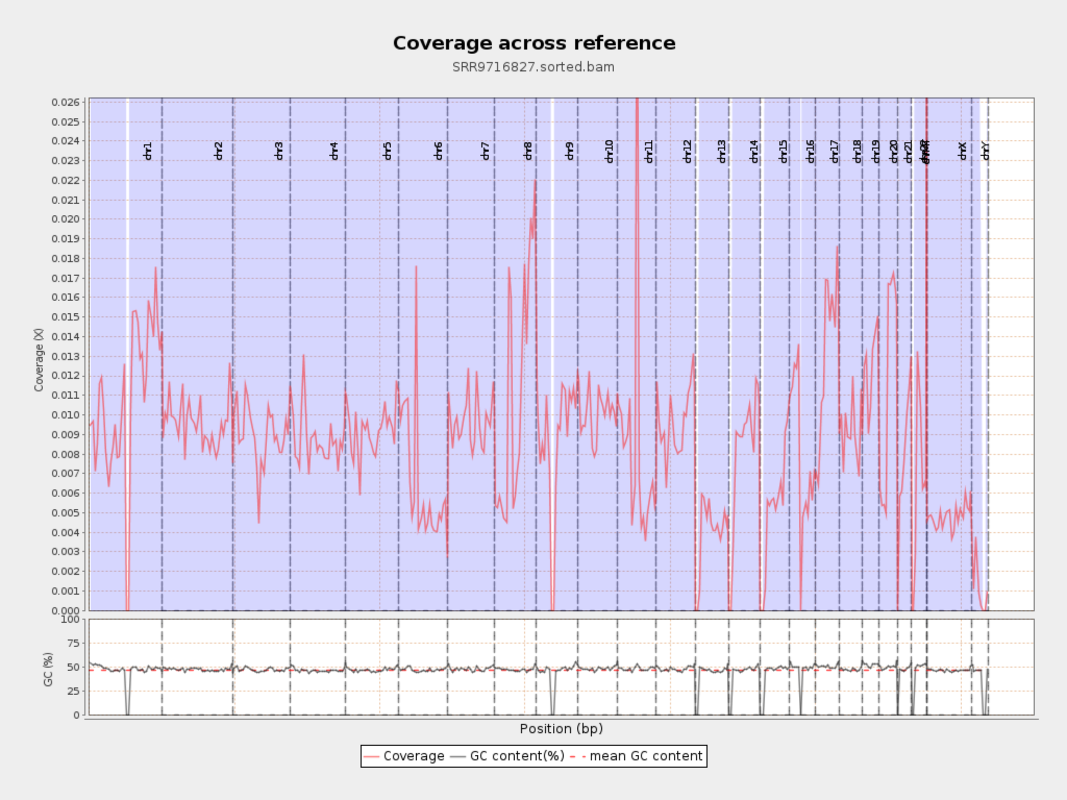
General error rate	0.62%
Mismatches	163,362
Insertions	1,293
Mapped reads with at least one insertion	0.25%
Deletions	3,677
Mapped reads with at least one deletion	0.73%
Homopolymer indels	41.03%

2.6. Chromosome stats

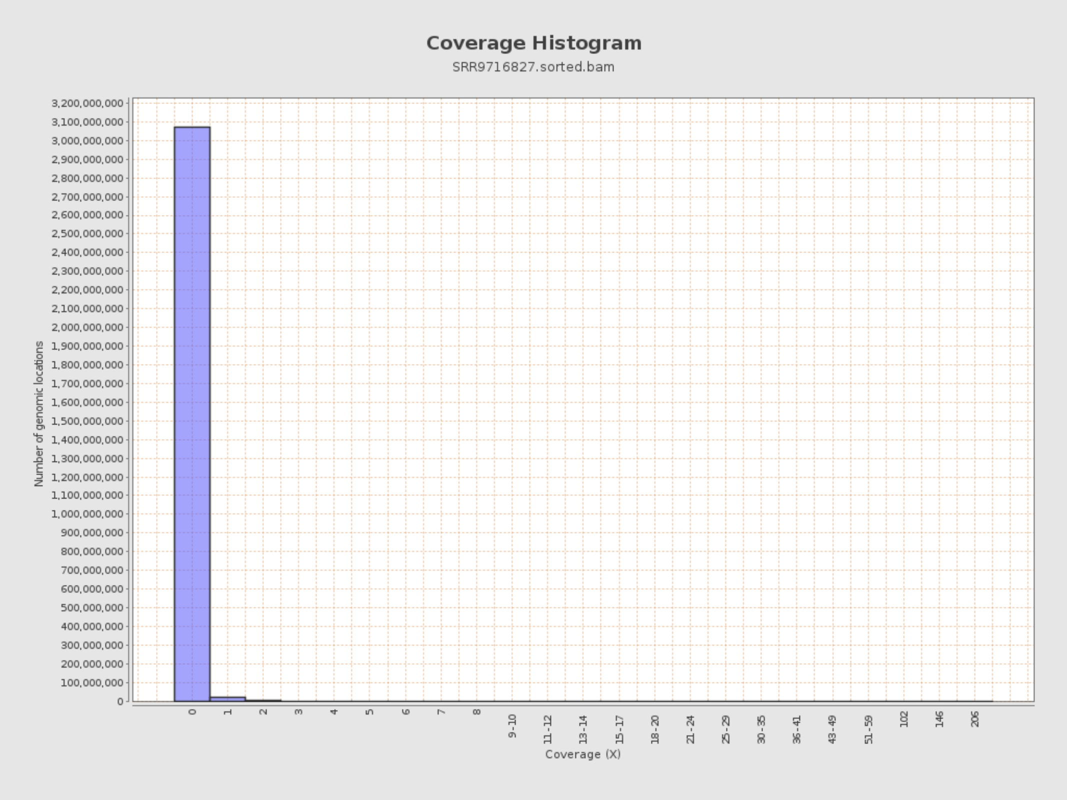
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2671239	0.0107	0.1226
chr2	243199373	2334071	0.0096	0.1341
chr3	198022430	1779234	0.009	0.1056
chr4	191154276	1667653	0.0087	0.1042
chr5	180915260	1661179	0.0092	0.1053
chr6	171115067	1135558	0.0066	0.0942
chr7	159138663	1536482	0.0097	0.1141

chr8	146364022	1647004	0.0113	0.1195
chr9	141213431	1198830	0.0085	0.1052
chr10	135534747	1362632	0.0101	0.1177
chr11	135006516	1177439	0.0087	0.1089
chr12	133851895	1291793	0.0097	0.1096
chr13	115169878	455280	0.004	0.07
chr14	107349540	856709	0.008	0.0993
chr15	102531392	537534	0.0052	0.0799
chr16	90354753	714646	0.0079	0.1017
chr17	81195210	1096318	0.0135	0.1327
chr18	78077248	710715	0.0091	0.1119
chr19	59128983	723858	0.0122	0.1343
chr20	63025520	725833	0.0115	0.1228
chr21	48129895	381394	0.0079	0.106
chr22	51304566	316347	0.0062	0.0893
chrMT	16571	656	0.0396	0.2227
chrX	155270560	743894	0.0048	0.0766
chrY	59373566	66048	0.0011	0.0425

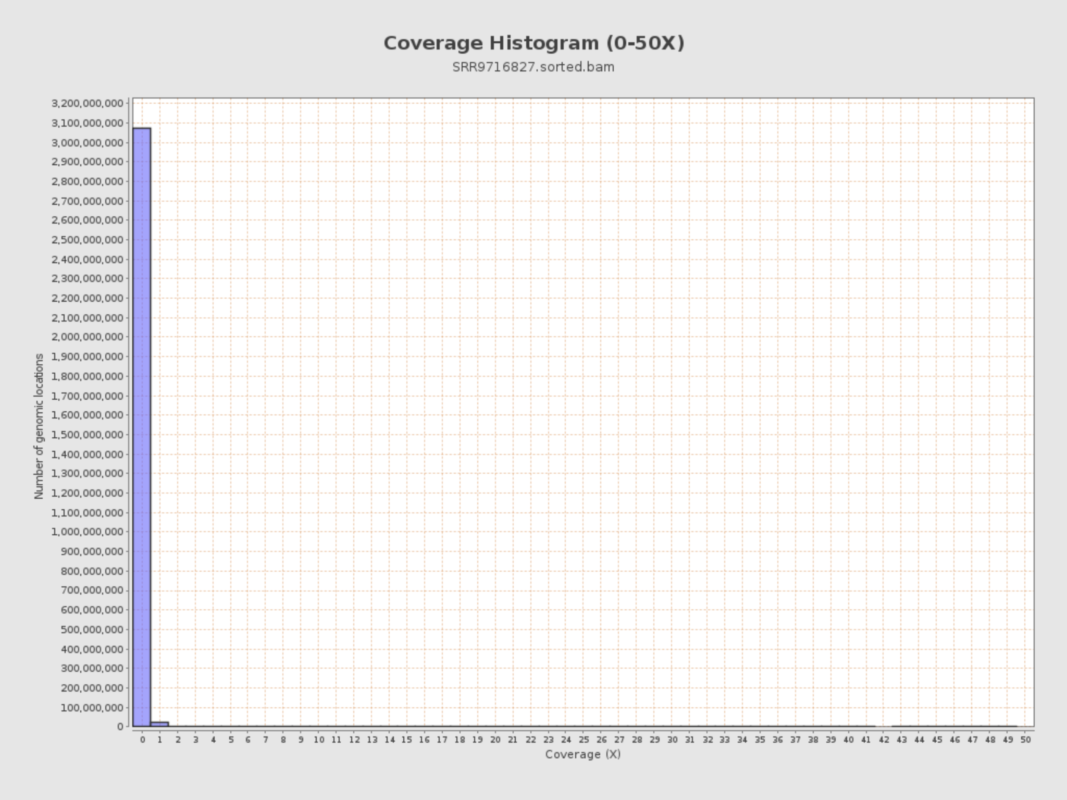
3. Results : Coverage across reference



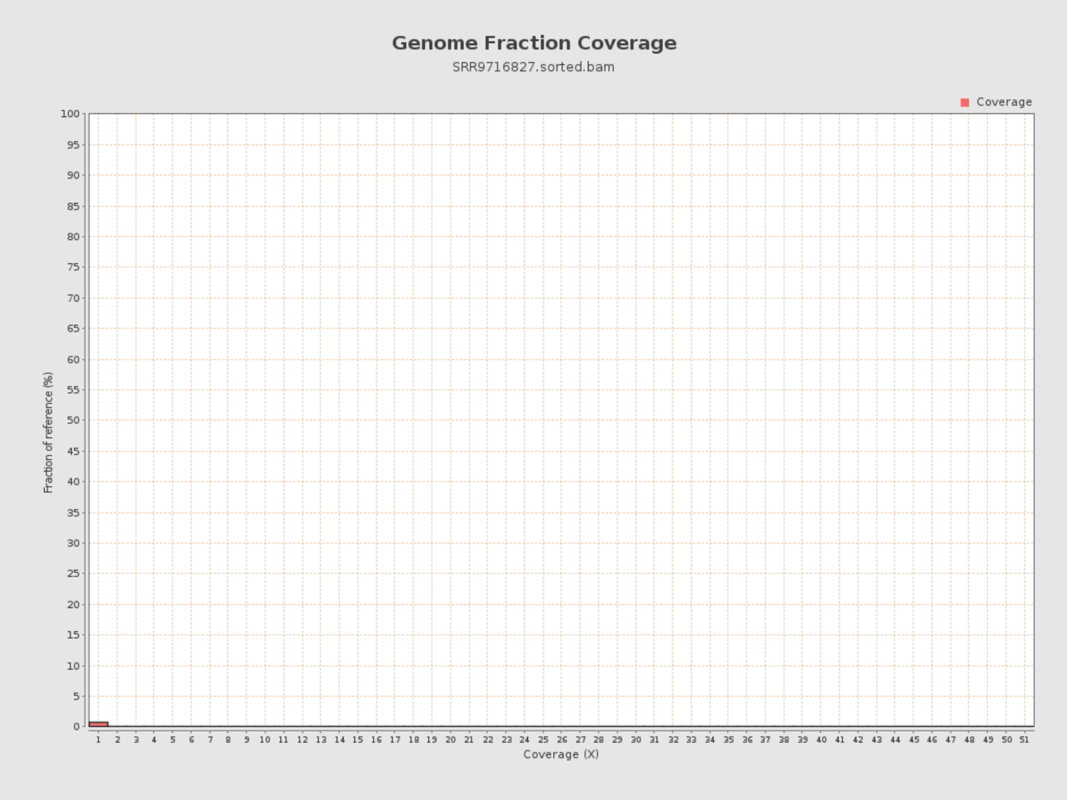
4. Results : Coverage Histogram



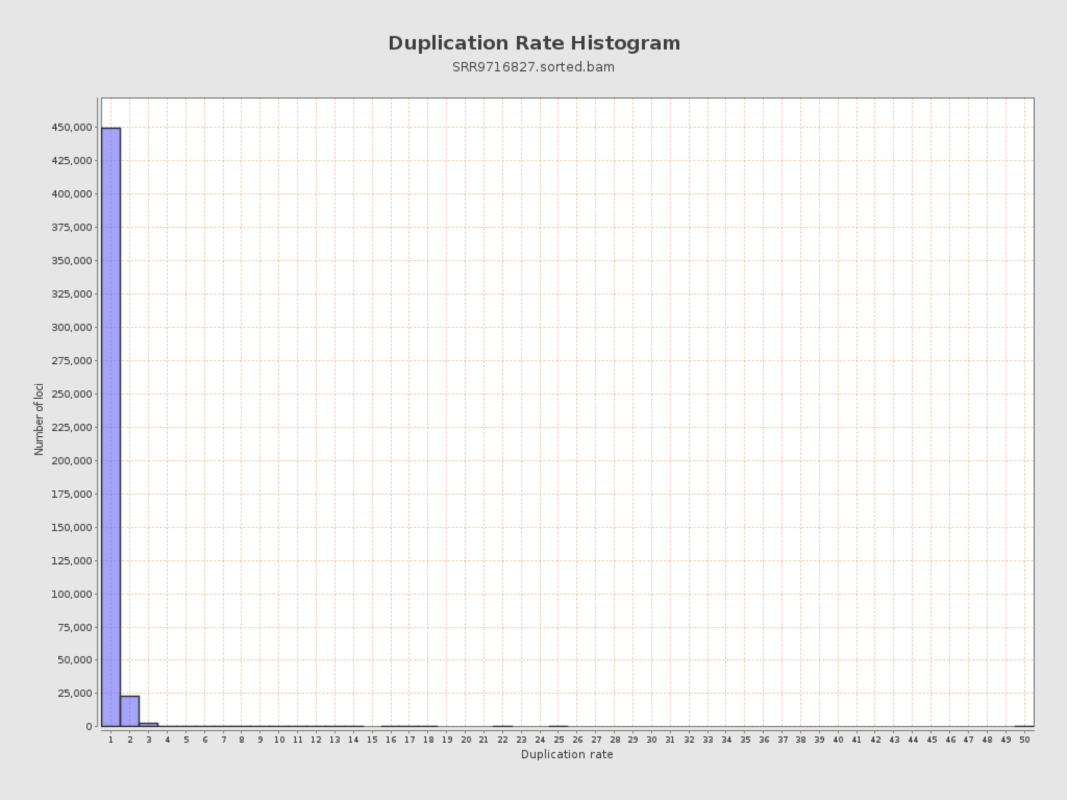
5. Results : Coverage Histogram (0-50X)



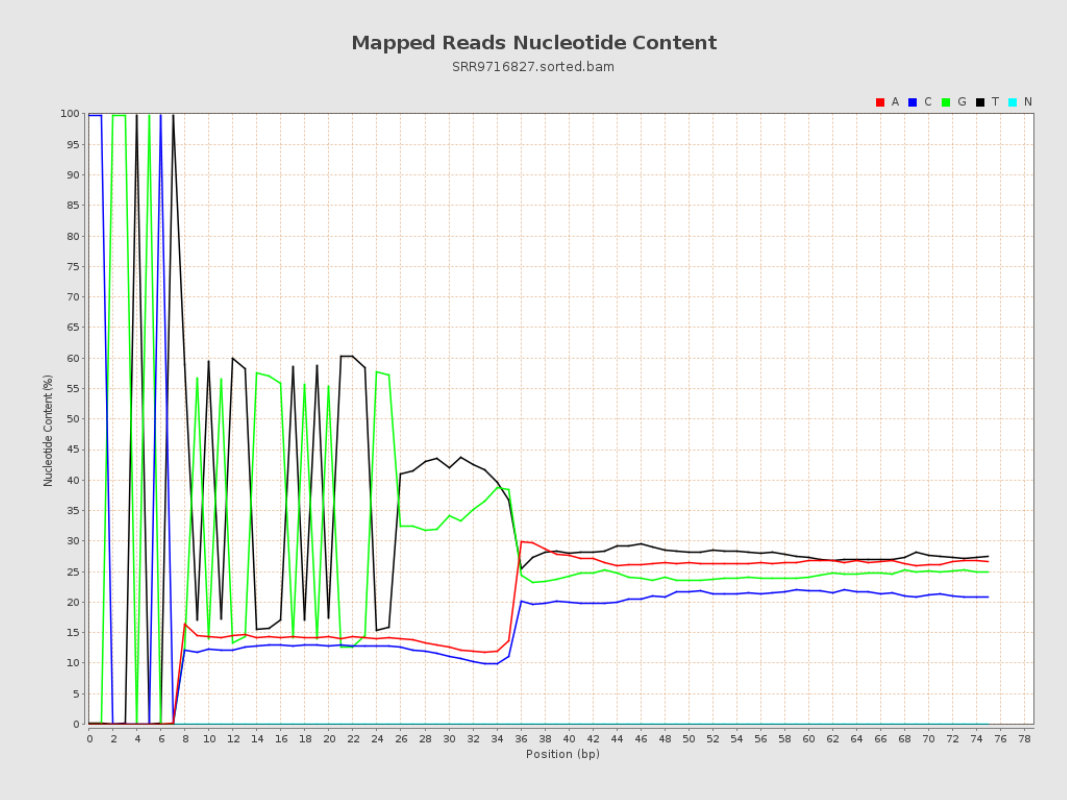
6. Results : Genome Fraction Coverage



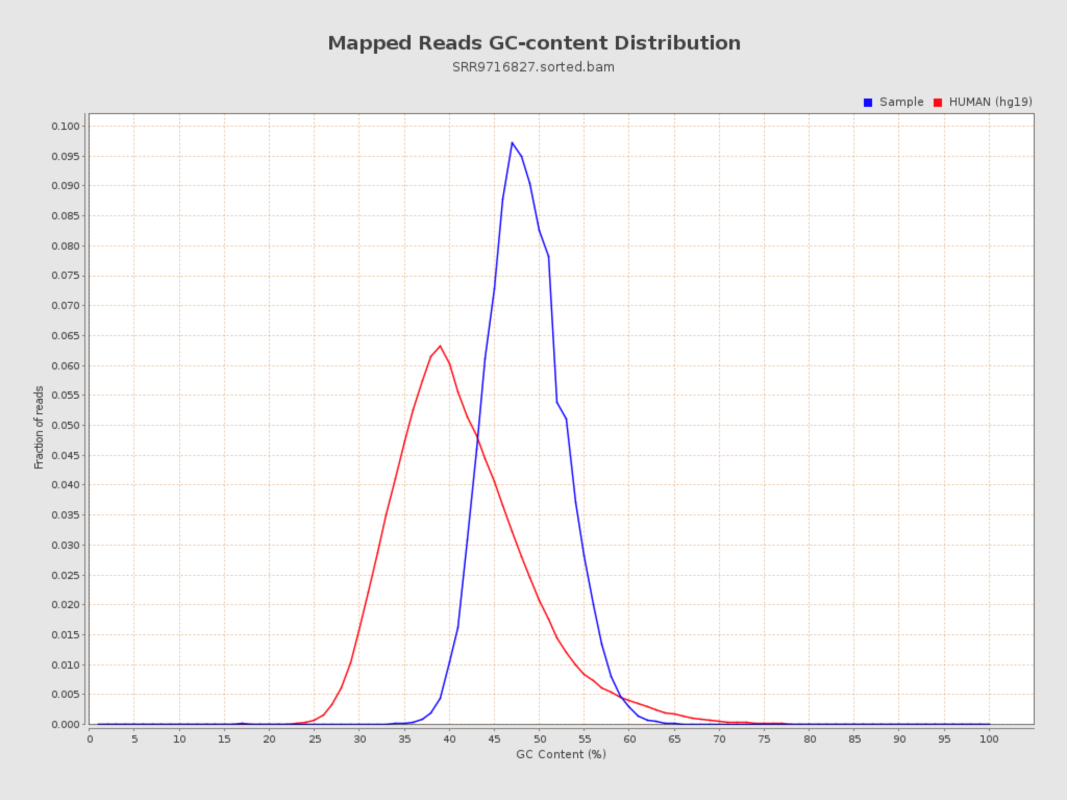
7. Results : Duplication Rate Histogram



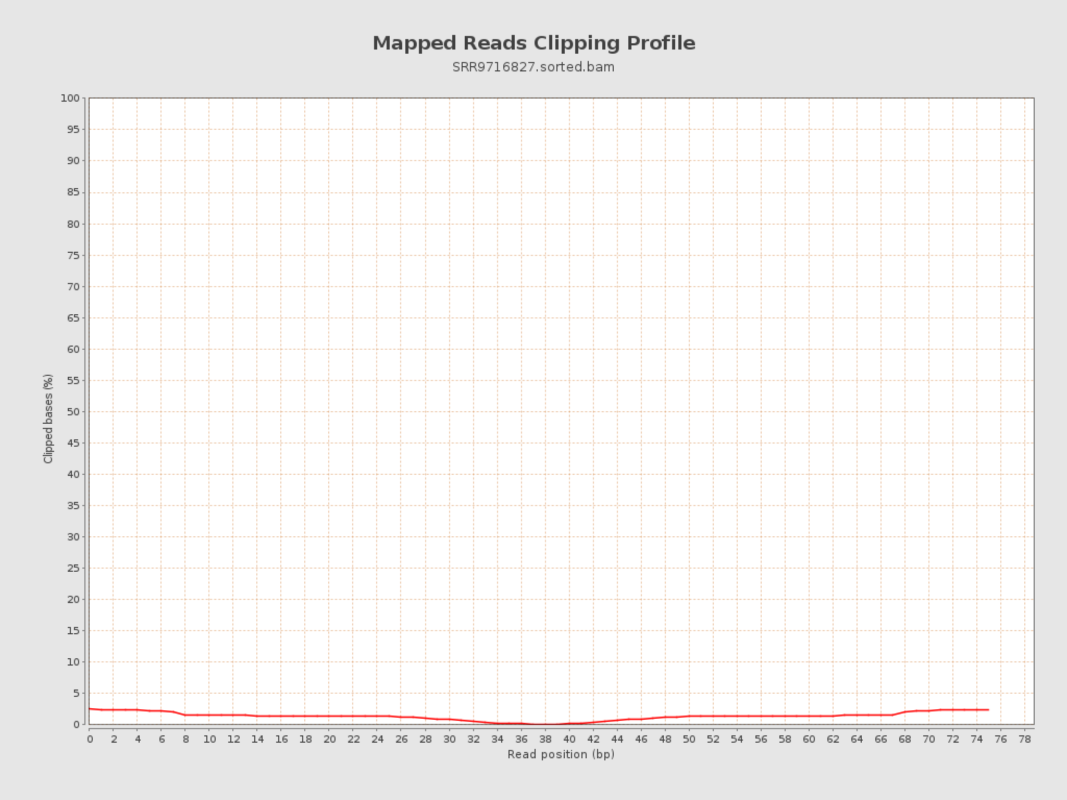
8. Results : Mapped Reads Nucleotide Content



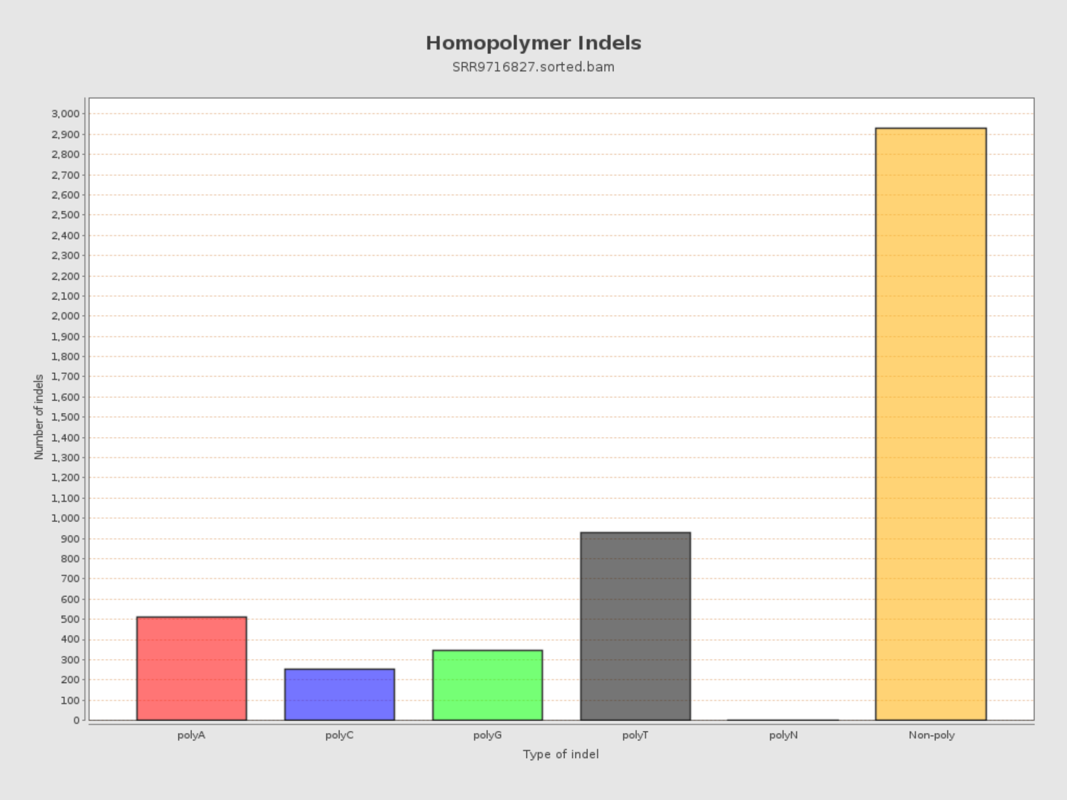
9. Results : Mapped Reads GC-content Distribution



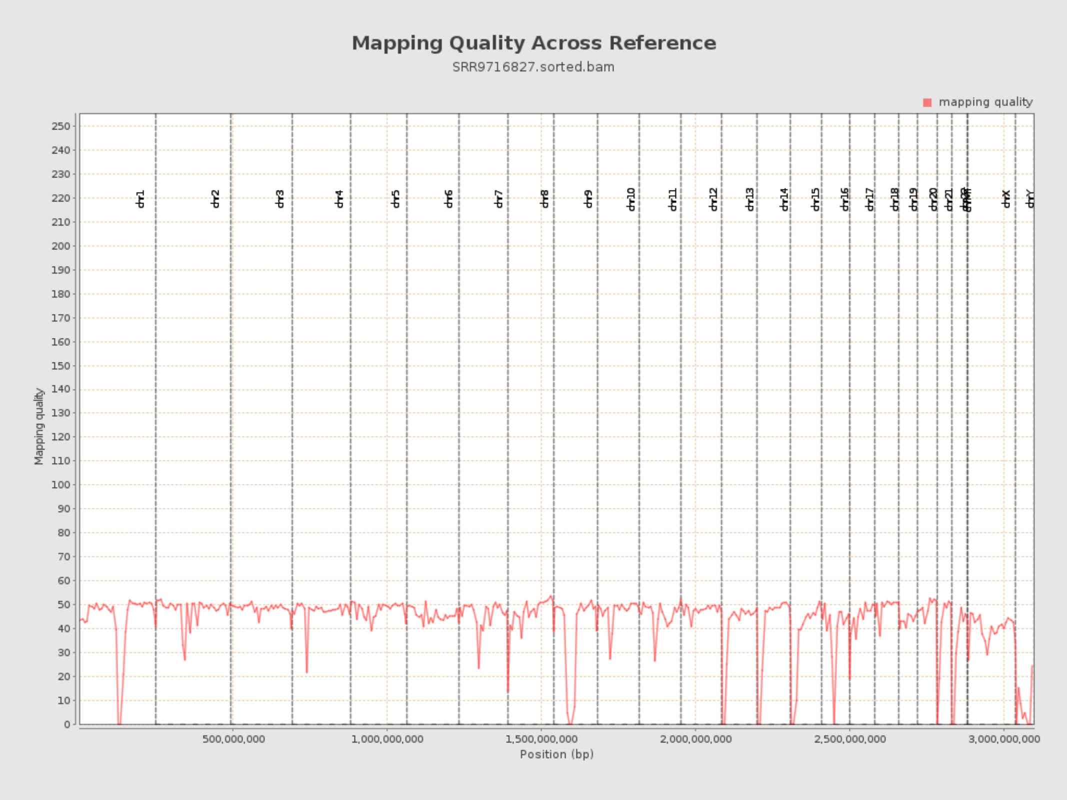
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram