Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:06:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716807.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_SRR9716807 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716807.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:06:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716807.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	936,045
Mapped reads	846,483 / 90.43%
Unmapped reads	89,562 / 9.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,222 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	27,709 / 2.96%
Duplication rate	2.62%
Clipped reads	849,898 / 90.8%

2.2. ACGT Content

Number/percentage of A's	12,609,741 / 25.63%
Number/percentage of C's	9,422,304 / 19.15%
Number/percentage of T's	14,777,523 / 30.03%
Number/percentage of G's	12,398,298 / 25.2%
Number/percentage of N's	340 / 0%
GC Percentage	44.34%

2.3. Coverage

Mean	0.0159

Standard Deviation	0.1688

2.4. Mapping Quality

Mean Mapping Quality	44.92

2.5. Mismatches and indels

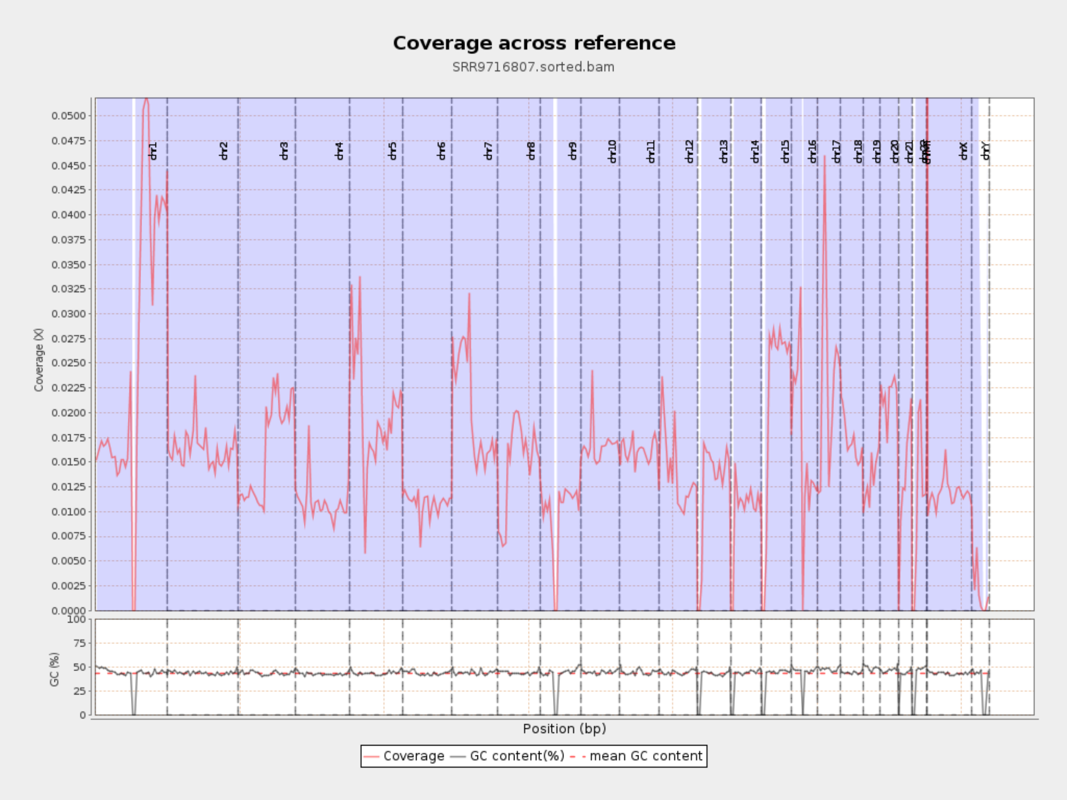
General error rate	0.49%
Mismatches	237,790
Insertions	2,986
Mapped reads with at least one insertion	0.35%
Deletions	8,171
Mapped reads with at least one deletion	0.96%
Homopolymer indels	42.97%

2.6. Chromosome stats

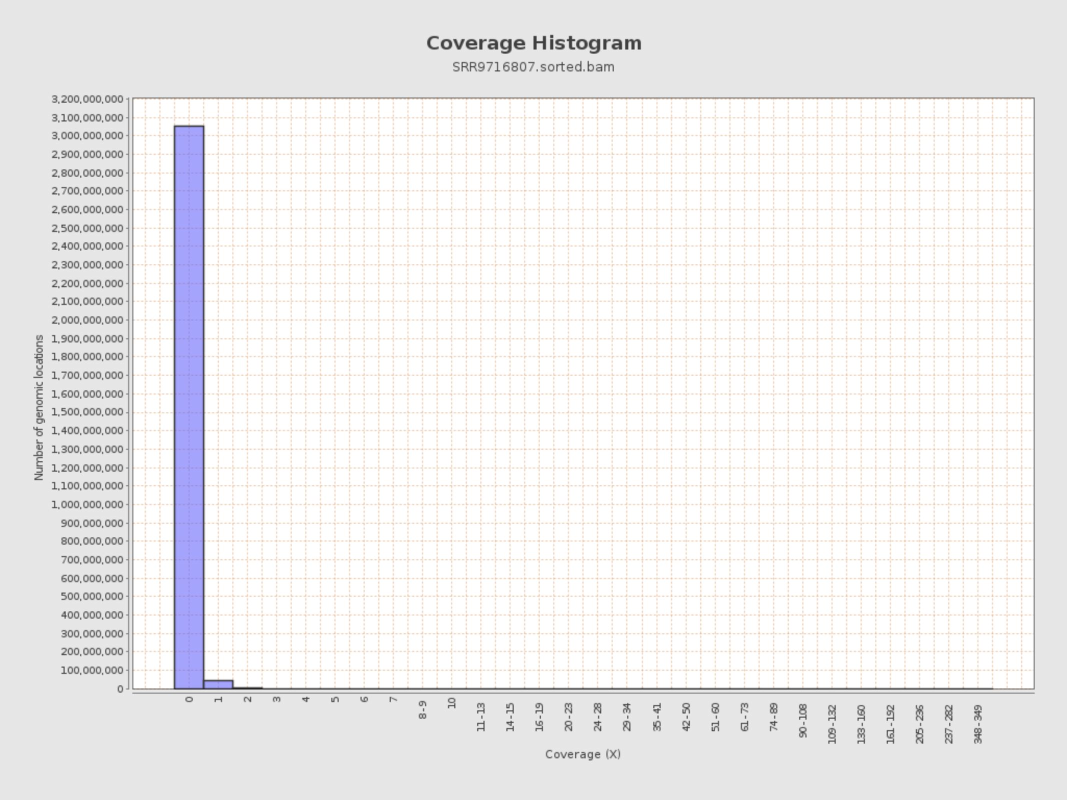
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6383105	0.0256	0.2671
chr2	243199373	3970614	0.0163	0.2052
chr3	198022430	3219087	0.0163	0.1363
chr4	191154276	2081965	0.0109	0.1218
chr5	180915260	3635052	0.0201	0.1523
chr6	171115067	1848546	0.0108	0.1172
chr7	159138663	3275572	0.0206	0.2612

chr8	146364022	2201424	0.015	0.1568
chr9	141213431	1381699	0.0098	0.1264
chr10	135534747	2274216	0.0168	0.1567
chr11	135006516	2192609	0.0162	0.1599
chr12	133851895	1889803	0.0141	0.128
chr13	115169878	1439036	0.0125	0.1209
chr14	107349540	1062290	0.0099	0.1087
chr15	102531392	2229167	0.0217	0.1581
chr16	90354753	1475324	0.0163	0.1396
chr17	81195210	1945481	0.024	0.1726
chr18	78077248	1345569	0.0172	0.222
chr19	59128983	799900	0.0135	0.1885
chr20	63025520	1353385	0.0215	0.1583
chr21	48129895	653100	0.0136	0.1289
chr22	51304566	582680	0.0114	0.1138
chrMT	16571	15403	0.9295	1.1175
chrX	155270560	1847619	0.0119	0.1247
chrY	59373566	118539	0.002	0.0628

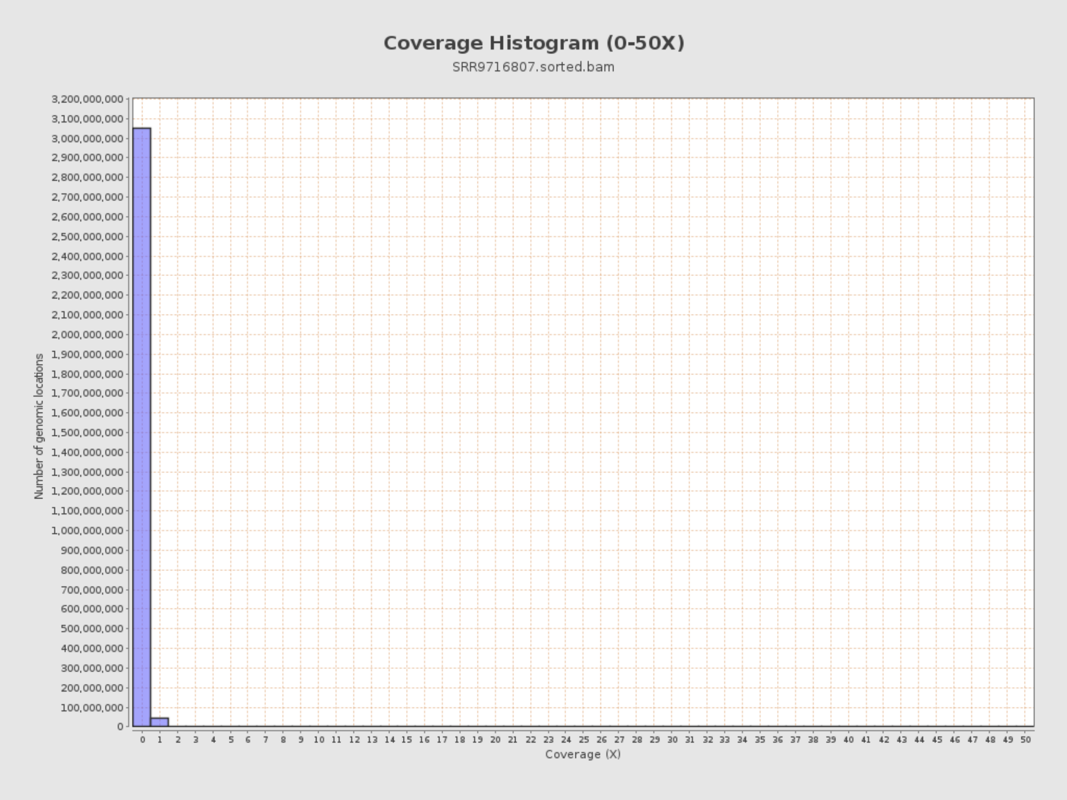
3. Results : Coverage across reference



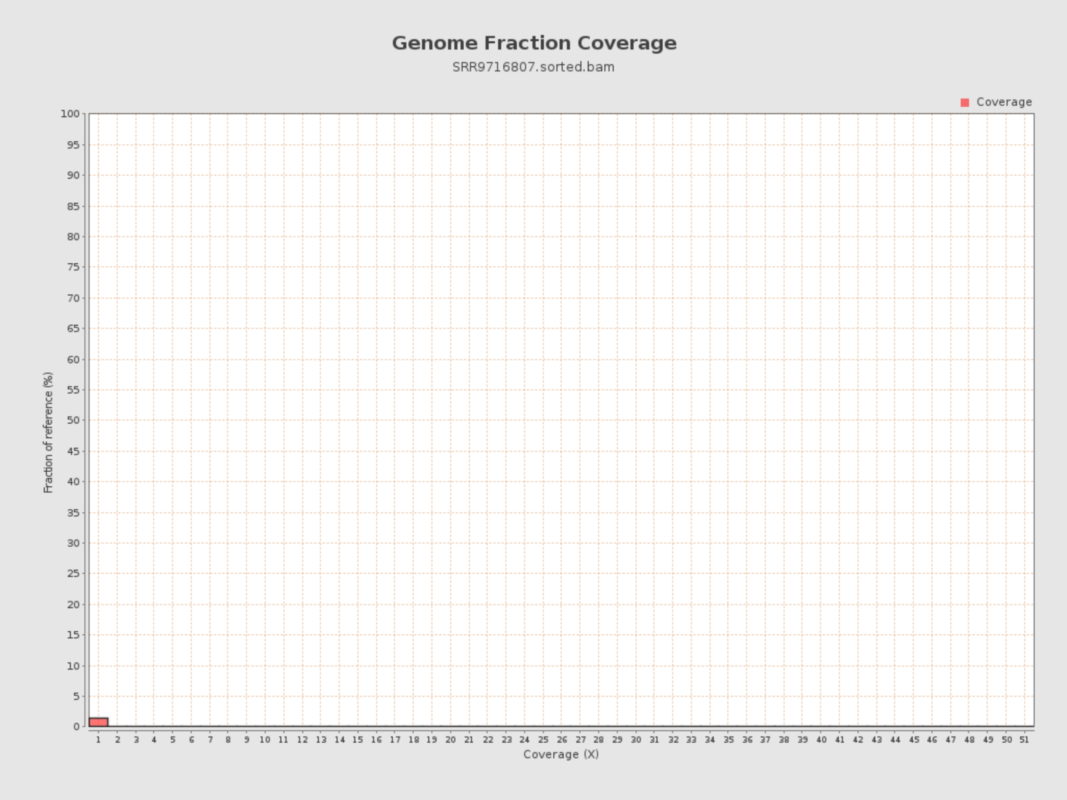
4. Results : Coverage Histogram



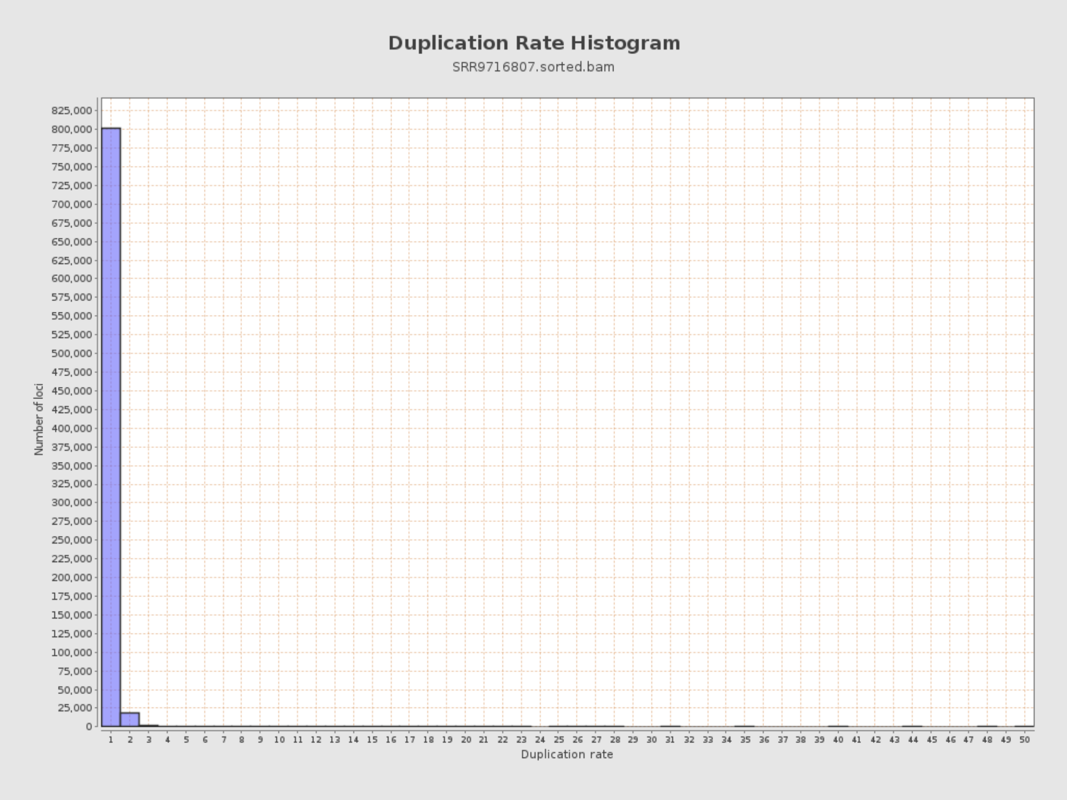
5. Results : Coverage Histogram (0-50X)



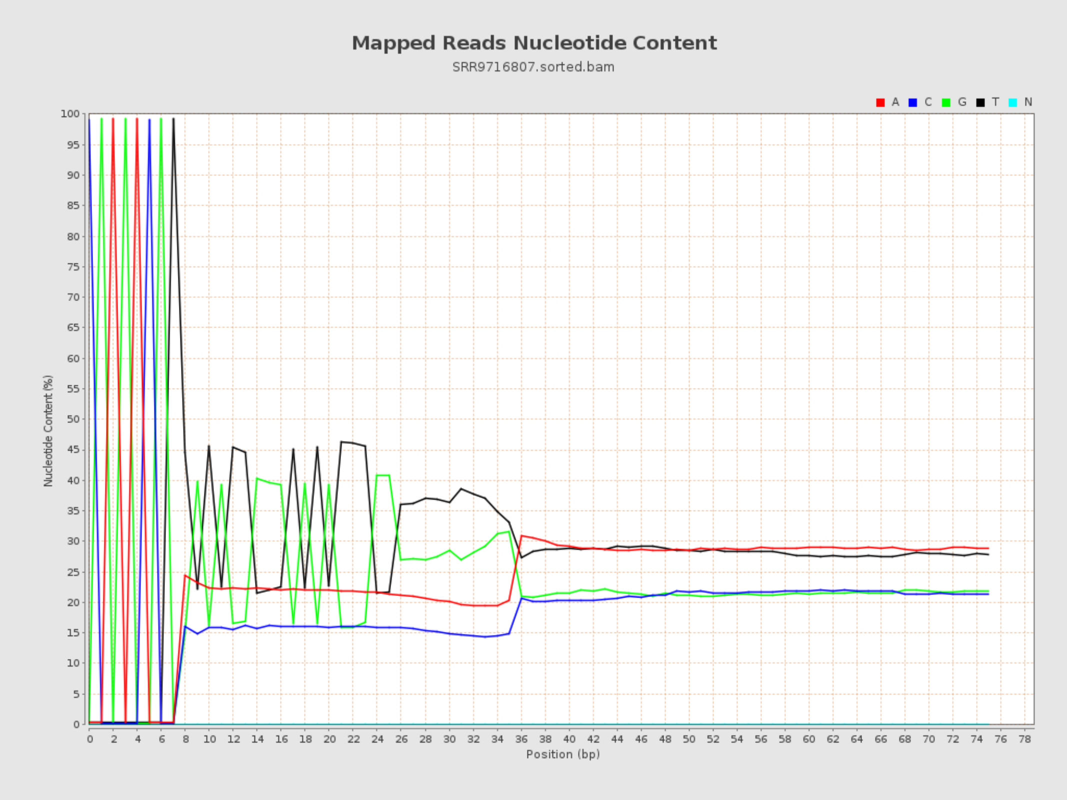
6. Results : Genome Fraction Coverage



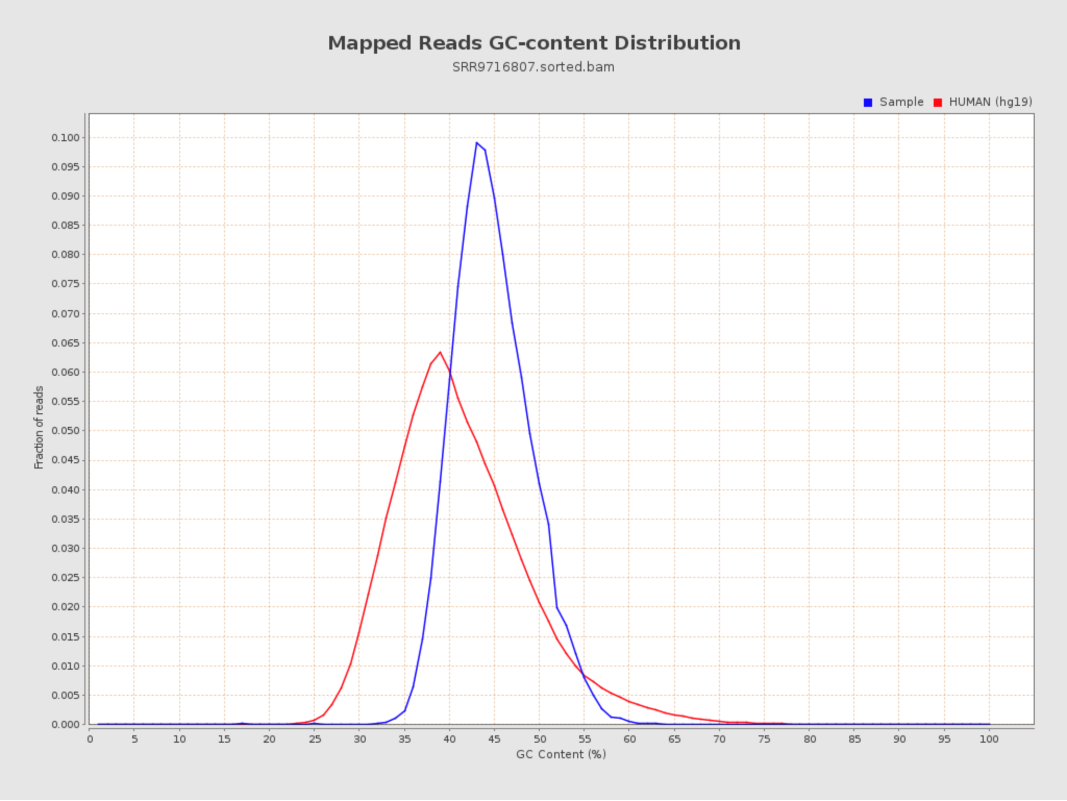
7. Results : Duplication Rate Histogram



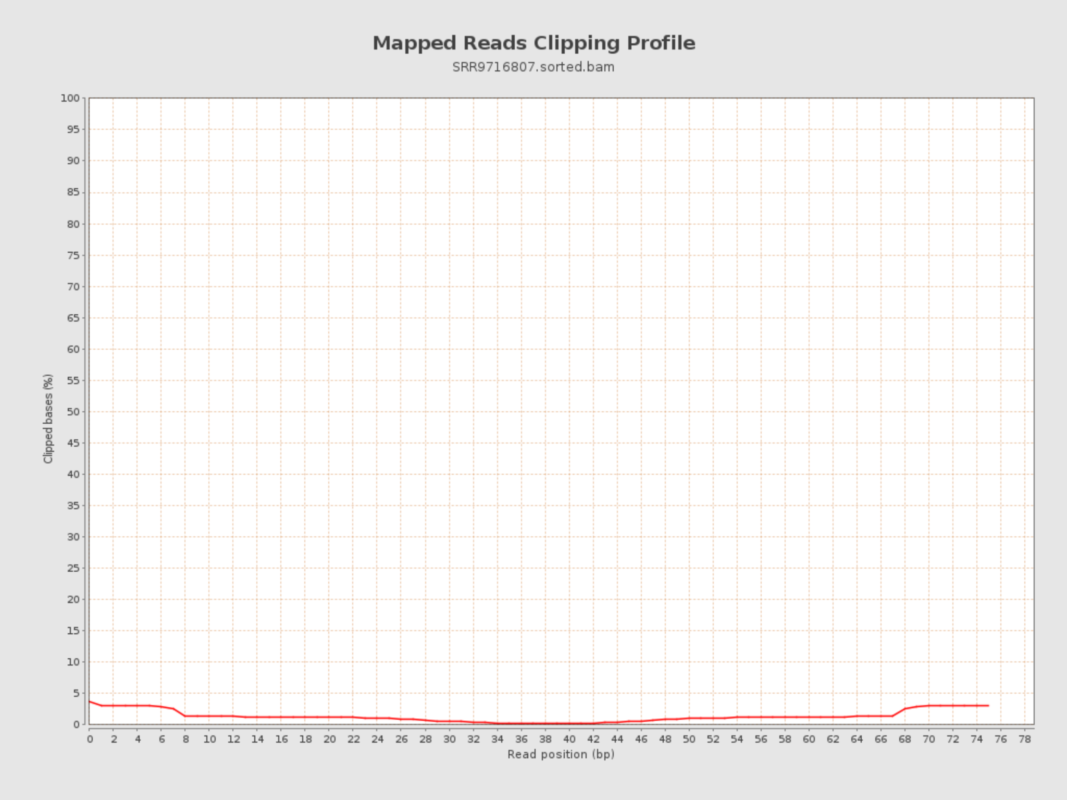
8. Results : Mapped Reads Nucleotide Content



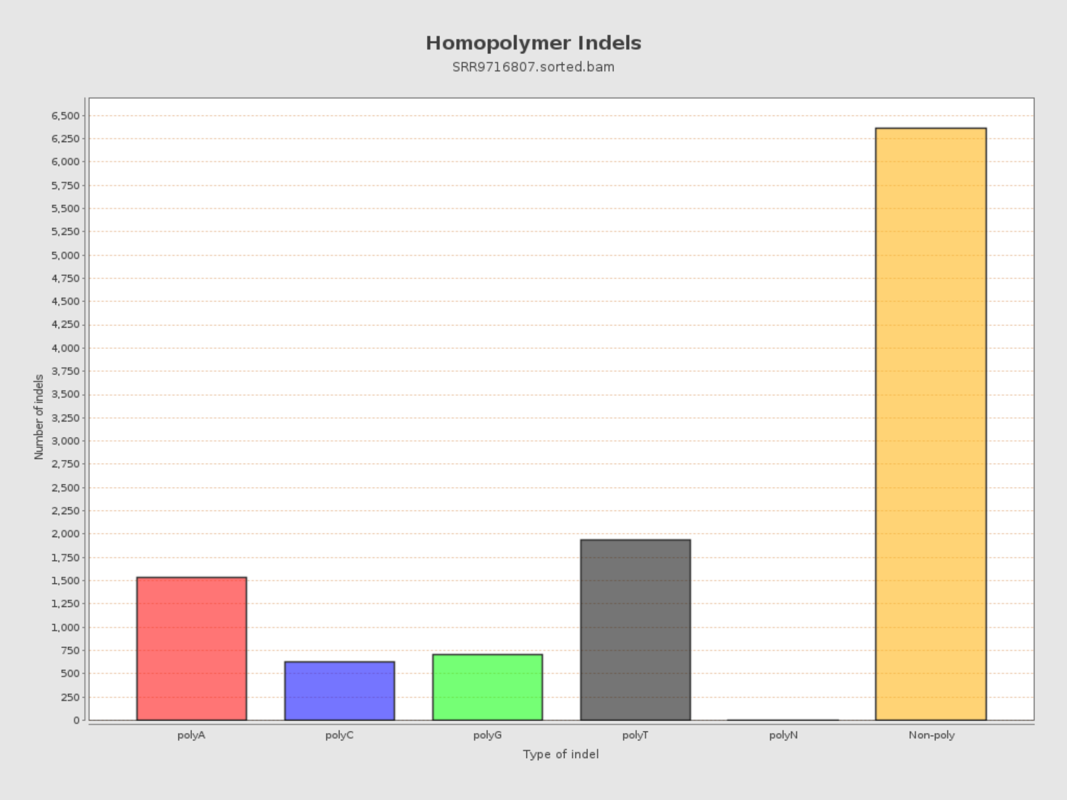
9. Results : Mapped Reads GC-content Distribution



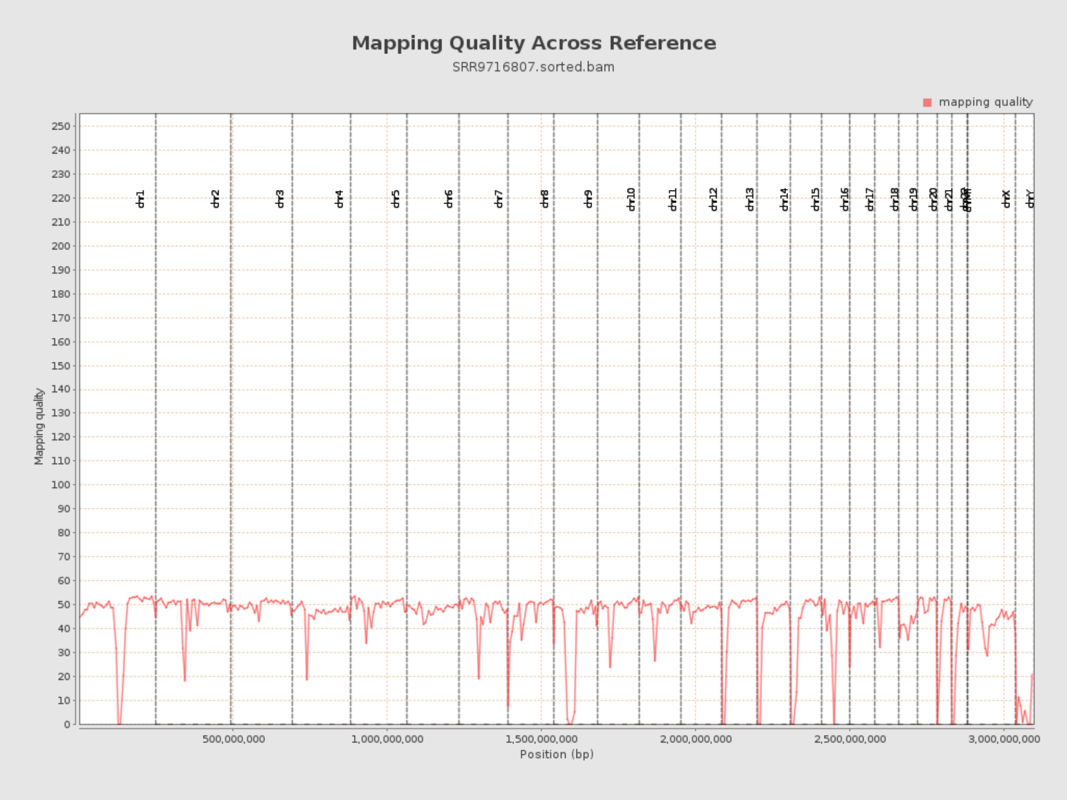
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram