Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 15:59:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716476.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_SRR9716476 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716476.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 15:59:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716476.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,802,256
Mapped reads	1,666,769 / 92.48%
Unmapped reads	135,487 / 7.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,694 / 0.54%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	78,152 / 4.34%
Duplication rate	3.74%
Clipped reads	1,674,748 / 92.93%

2.2. ACGT Content

Number/percentage of A's	24,876,007 / 25.51%
Number/percentage of C's	20,339,877 / 20.86%
Number/percentage of T's	29,145,970 / 29.89%
Number/percentage of G's	23,151,057 / 23.74%
Number/percentage of N's	690 / 0%
GC Percentage	44.6%

2.3. Coverage

Mean	0.0315

Standard Deviation	0.2703

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Mismatches and indels

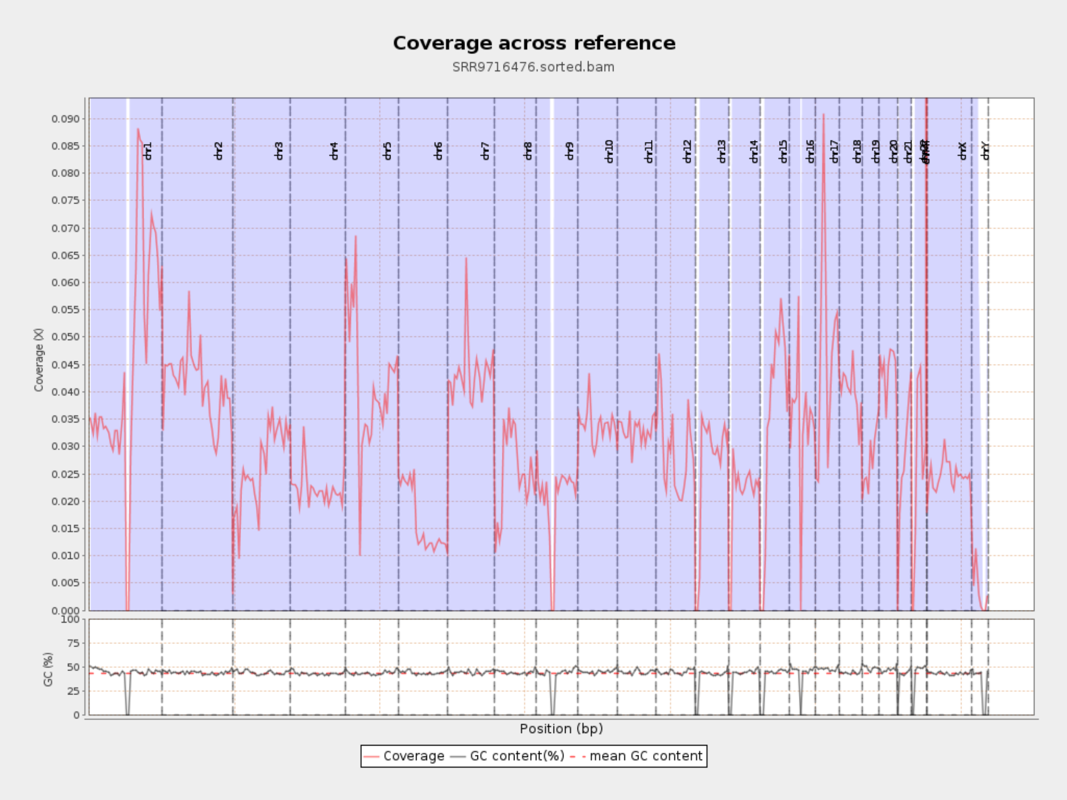
General error rate	0.49%
Mismatches	463,887
Insertions	5,368
Mapped reads with at least one insertion	0.32%
Deletions	16,787
Mapped reads with at least one deletion	1%
Homopolymer indels	44.5%

2.6. Chromosome stats

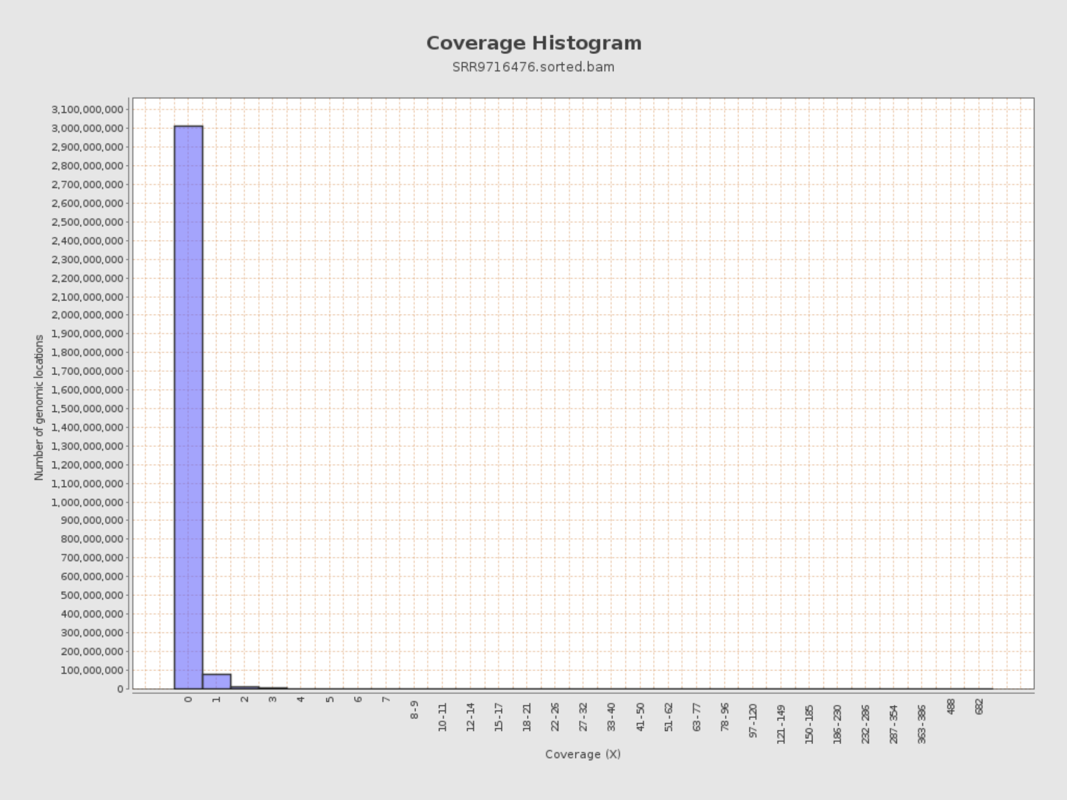
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11124558	0.0446	0.3875
chr2	243199373	10048434	0.0413	0.3859
chr3	198022430	5207002	0.0263	0.1815
chr4	191154276	4244945	0.0222	0.184
chr5	180915260	7528024	0.0416	0.2302
chr6	171115067	2816827	0.0165	0.1654
chr7	159138663	6936673	0.0436	0.4629

chr8	146364022	3651590	0.0249	0.2261
chr9	141213431	2822258	0.02	0.2071
chr10	135534747	4599337	0.0339	0.2415
chr11	135006516	4446560	0.0329	0.2654
chr12	133851895	3891514	0.0291	0.1926
chr13	115169878	3036219	0.0264	0.1822
chr14	107349540	2215817	0.0206	0.1689
chr15	102531392	3698140	0.0361	0.2132
chr16	90354753	3107589	0.0344	0.2194
chr17	81195210	3909902	0.0482	0.2682
chr18	78077248	3142980	0.0403	0.4144
chr19	59128983	1637046	0.0277	0.3107
chr20	63025520	2783448	0.0442	0.2388
chr21	48129895	1308806	0.0272	0.1943
chr22	51304566	1242608	0.0242	0.1745
chrMT	16571	96157	5.8027	4.3197
chrX	155270560	3825791	0.0246	0.1942
chrY	59373566	217599	0.0037	0.0894

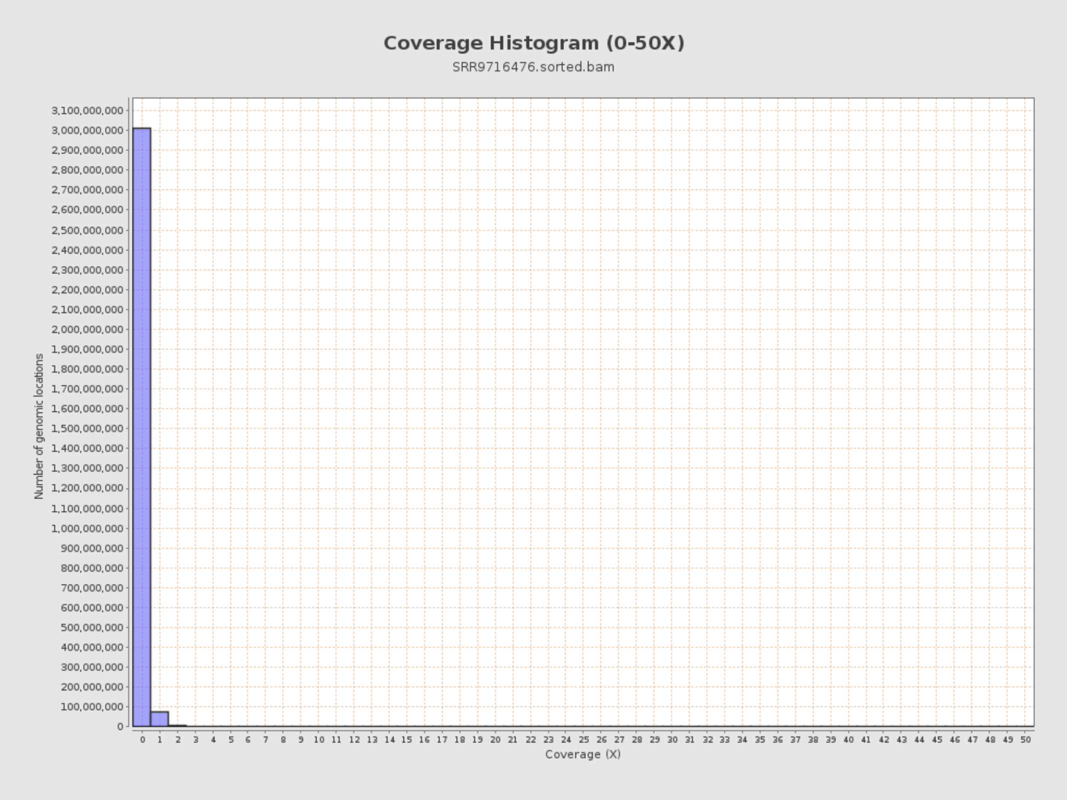
3. Results : Coverage across reference



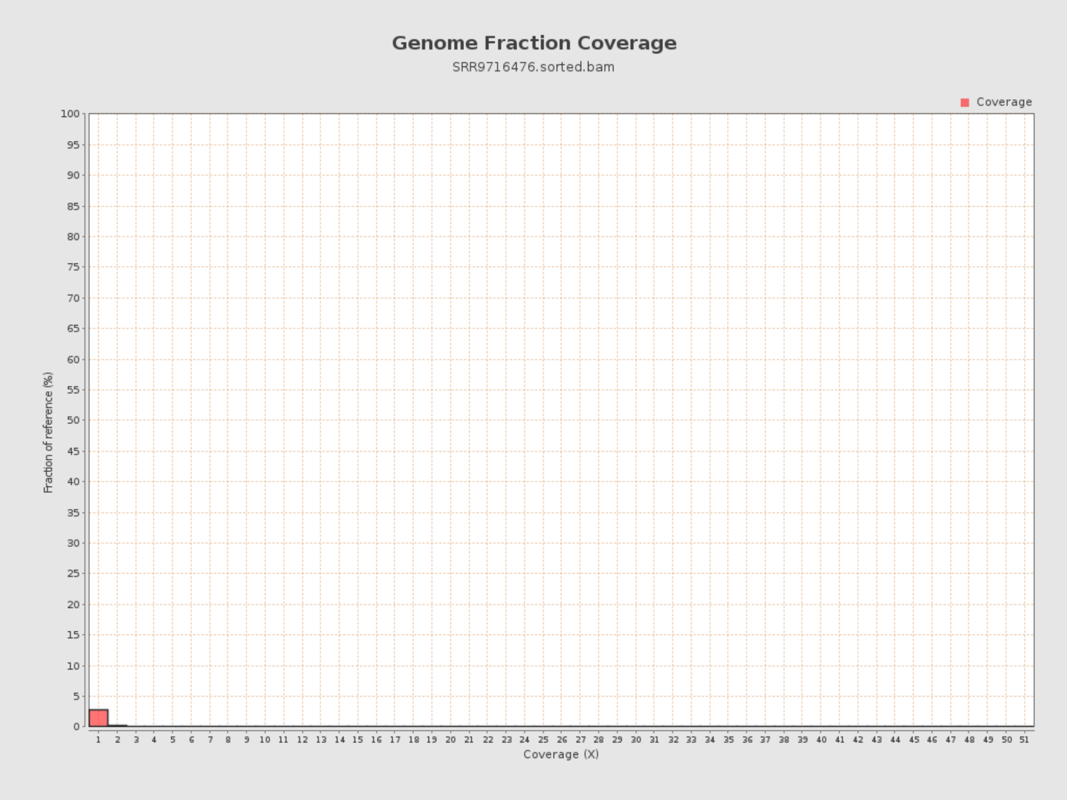
4. Results : Coverage Histogram



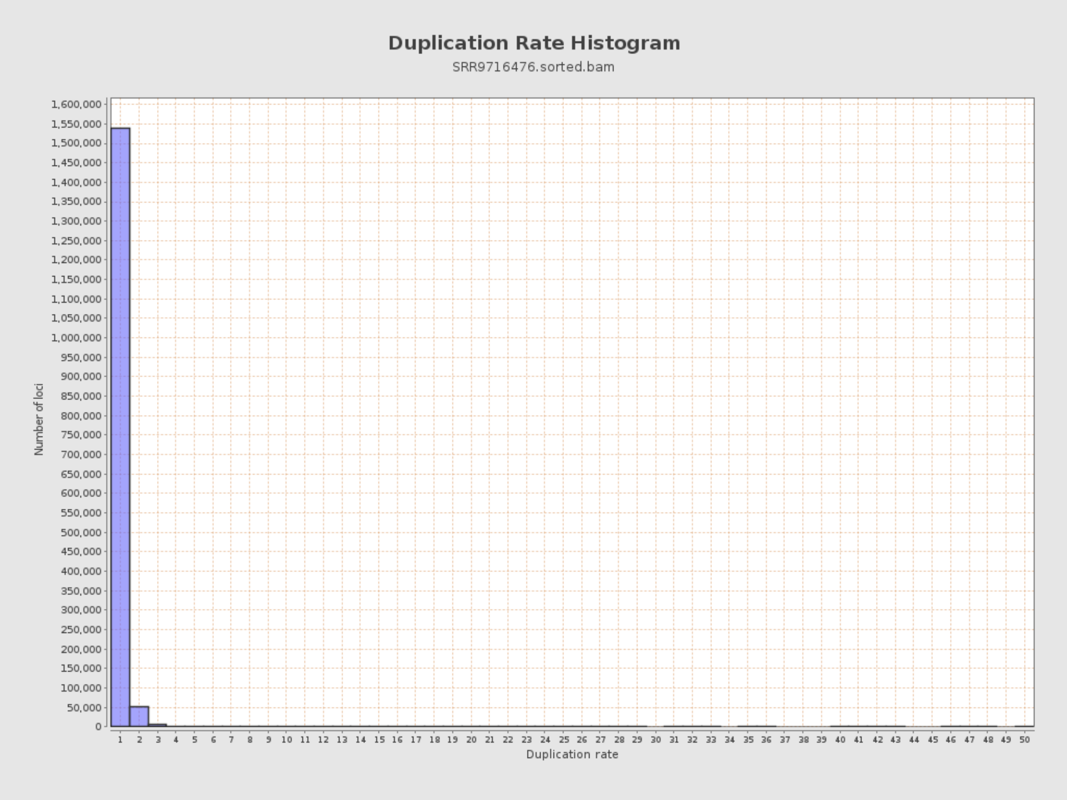
5. Results : Coverage Histogram (0-50X)



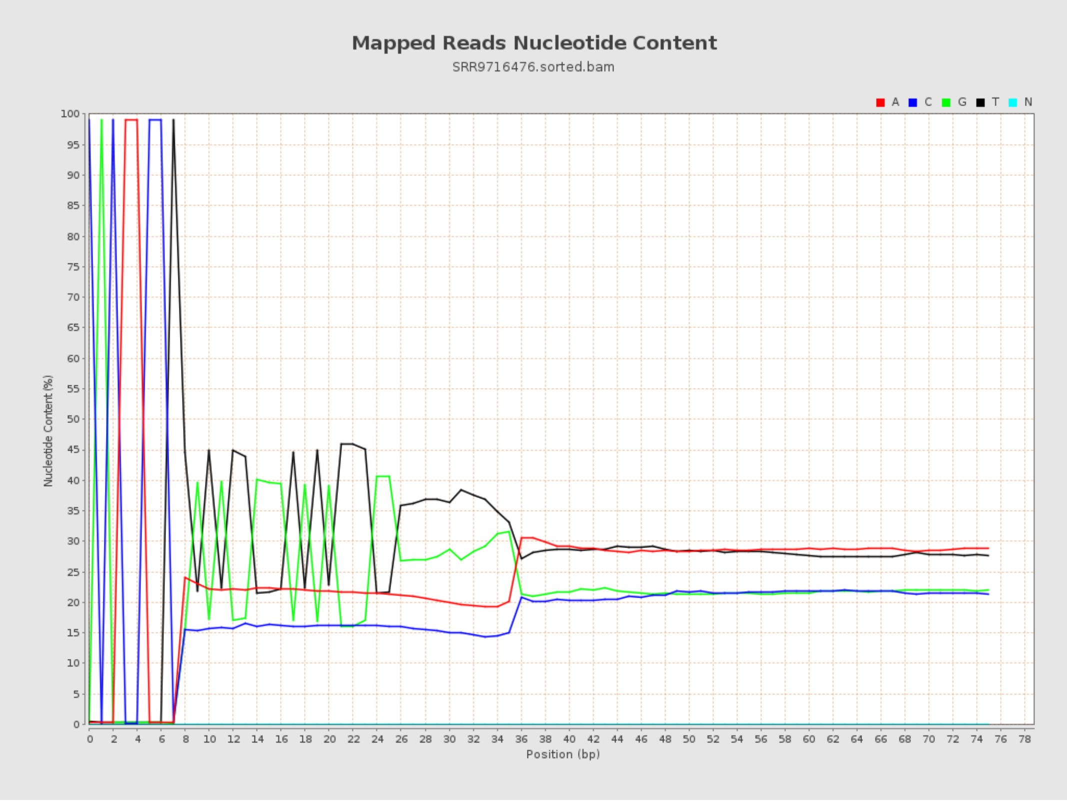
6. Results : Genome Fraction Coverage



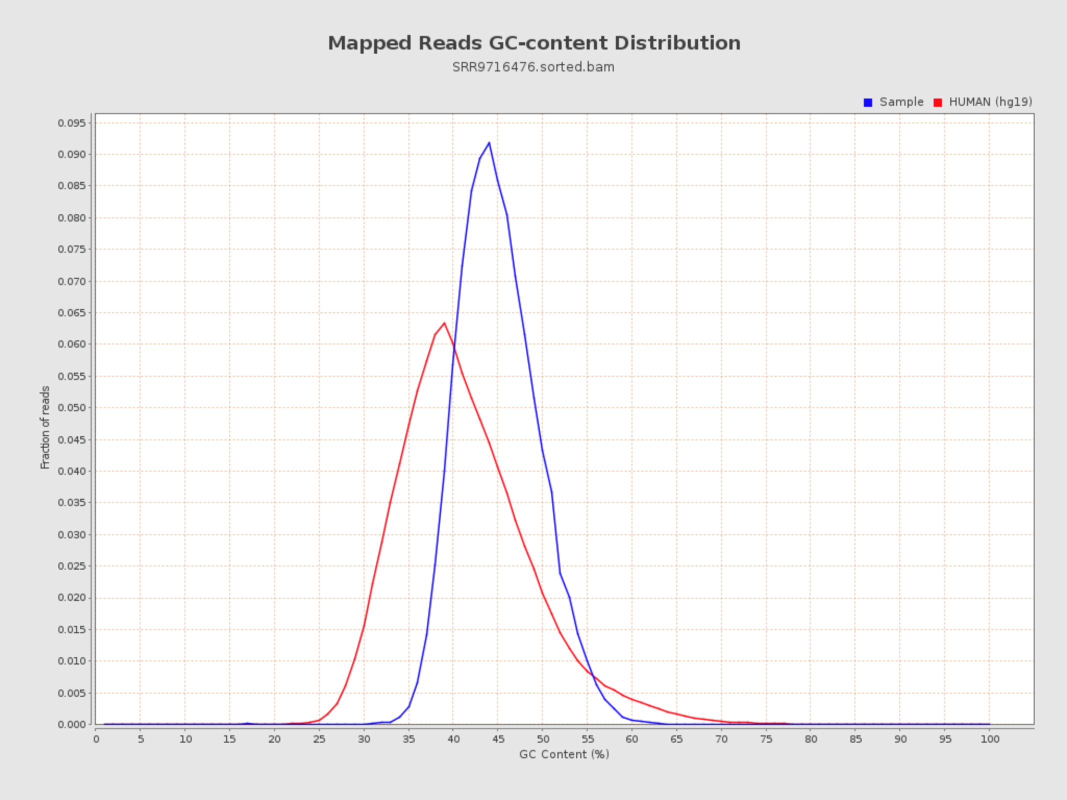
7. Results : Duplication Rate Histogram



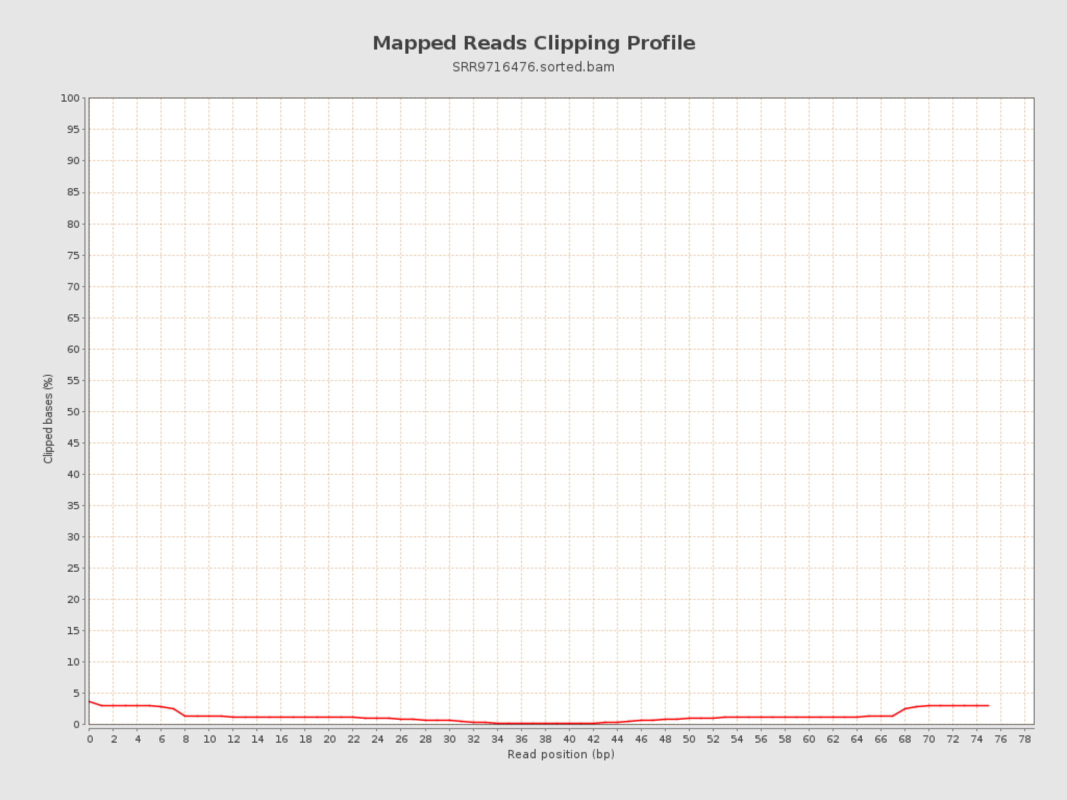
8. Results : Mapped Reads Nucleotide Content



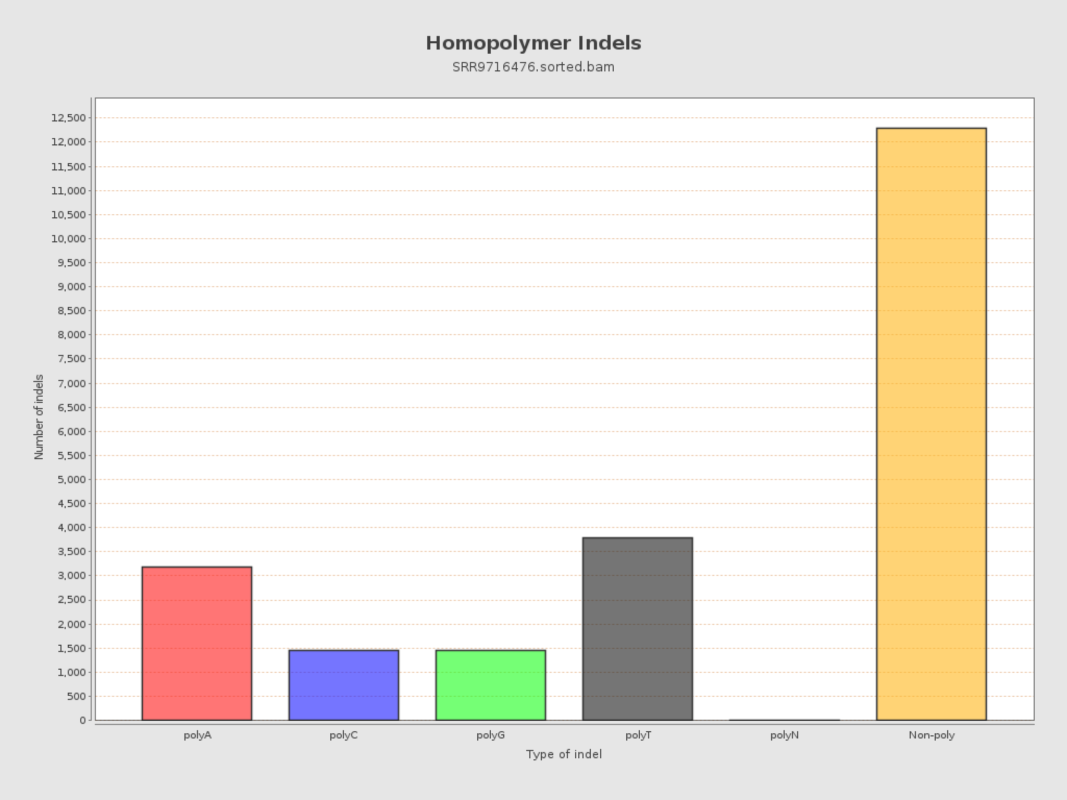
9. Results : Mapped Reads GC-content Distribution



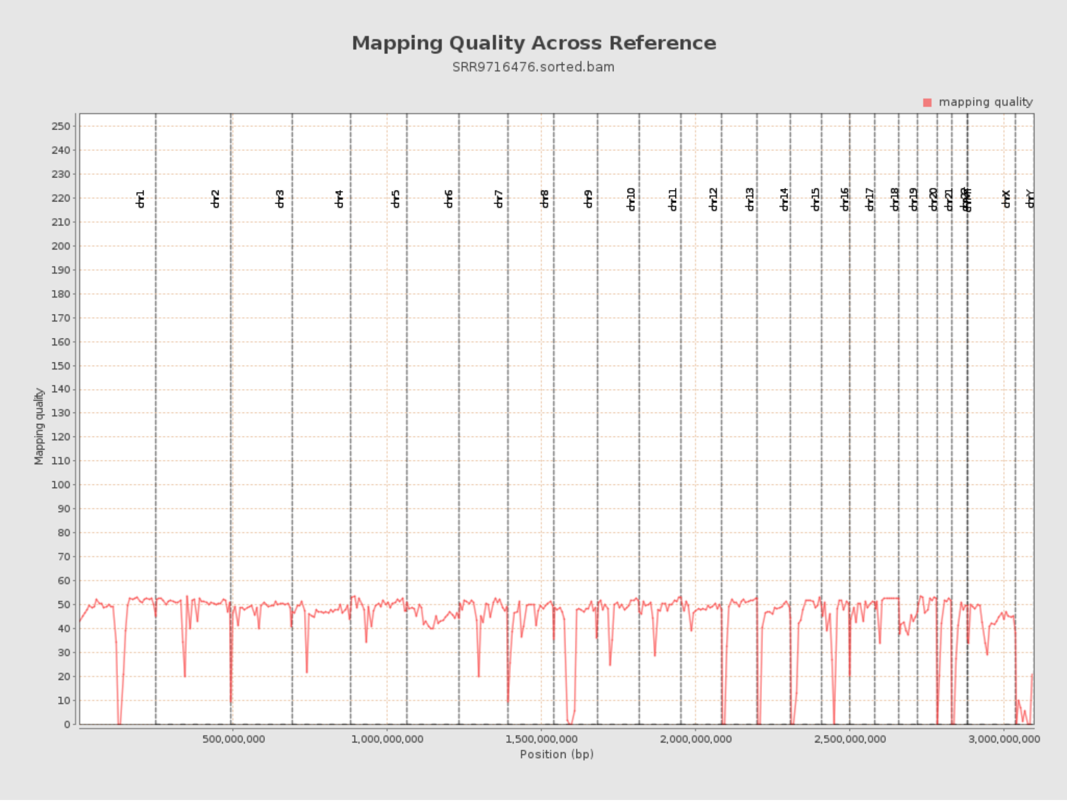
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram