Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:28:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716816.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_SRR9716816 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716816.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:28:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716816.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	545,141
Mapped reads	483,624 / 88.72%
Unmapped reads	61,517 / 11.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,176 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	8,417 / 1.54%
Duplication rate	1.28%
Clipped reads	484,501 / 88.88%

2.2. ACGT Content

Number/percentage of A's	6,977,338 / 25.02%
Number/percentage of C's	5,026,542 / 18.02%
Number/percentage of T's	9,111,797 / 32.67%
Number/percentage of G's	6,775,263 / 24.29%
Number/percentage of N's	197 / 0%
GC Percentage	42.31%

2.3. Coverage

Mean	0.009

Standard Deviation	0.1167

2.4. Mapping Quality

Mean Mapping Quality	44.48

2.5. Mismatches and indels

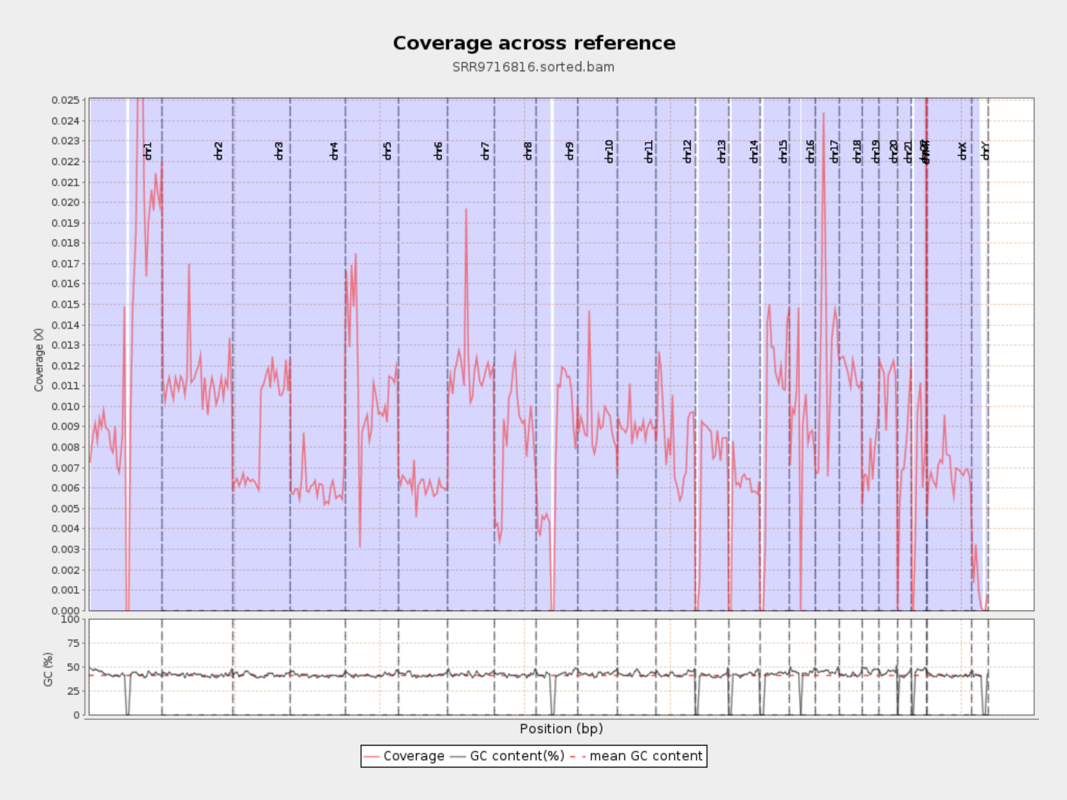
General error rate	0.51%
Mismatches	139,438
Insertions	2,162
Mapped reads with at least one insertion	0.44%
Deletions	4,993
Mapped reads with at least one deletion	1.02%
Homopolymer indels	41.82%

2.6. Chromosome stats

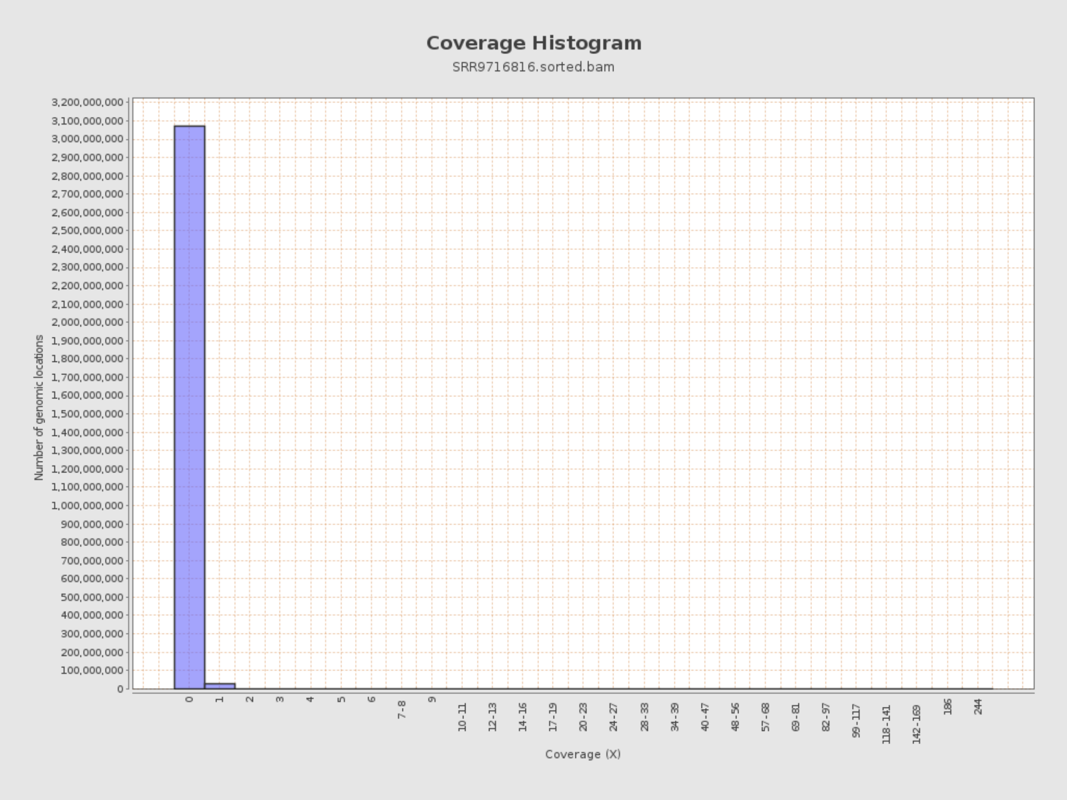
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3311290	0.0133	0.1744
chr2	243199373	2742148	0.0113	0.1512
chr3	198022430	1760973	0.0089	0.0974
chr4	191154276	1146075	0.006	0.0816
chr5	180915260	2005987	0.0111	0.1082
chr6	171115067	1049597	0.0061	0.085
chr7	159138663	1904213	0.012	0.1728

chr8	146364022	1231236	0.0084	0.105
chr9	141213431	1019041	0.0072	0.0965
chr10	135534747	1245376	0.0092	0.1093
chr11	135006516	1211782	0.009	0.1131
chr12	133851895	1112955	0.0083	0.0939
chr13	115169878	811187	0.007	0.0865
chr14	107349540	595536	0.0055	0.0776
chr15	102531392	1038697	0.0101	0.1041
chr16	90354753	799751	0.0089	0.0993
chr17	81195210	1046754	0.0129	0.1201
chr18	78077248	915712	0.0117	0.159
chr19	59128983	434859	0.0074	0.1174
chr20	63025520	712405	0.0113	0.1099
chr21	48129895	354471	0.0074	0.0898
chr22	51304566	310867	0.0061	0.0801
chrMT	16571	14561	0.8787	1.0162
chrX	155270560	1060859	0.0068	0.0897
chrY	59373566	62610	0.0011	0.0373

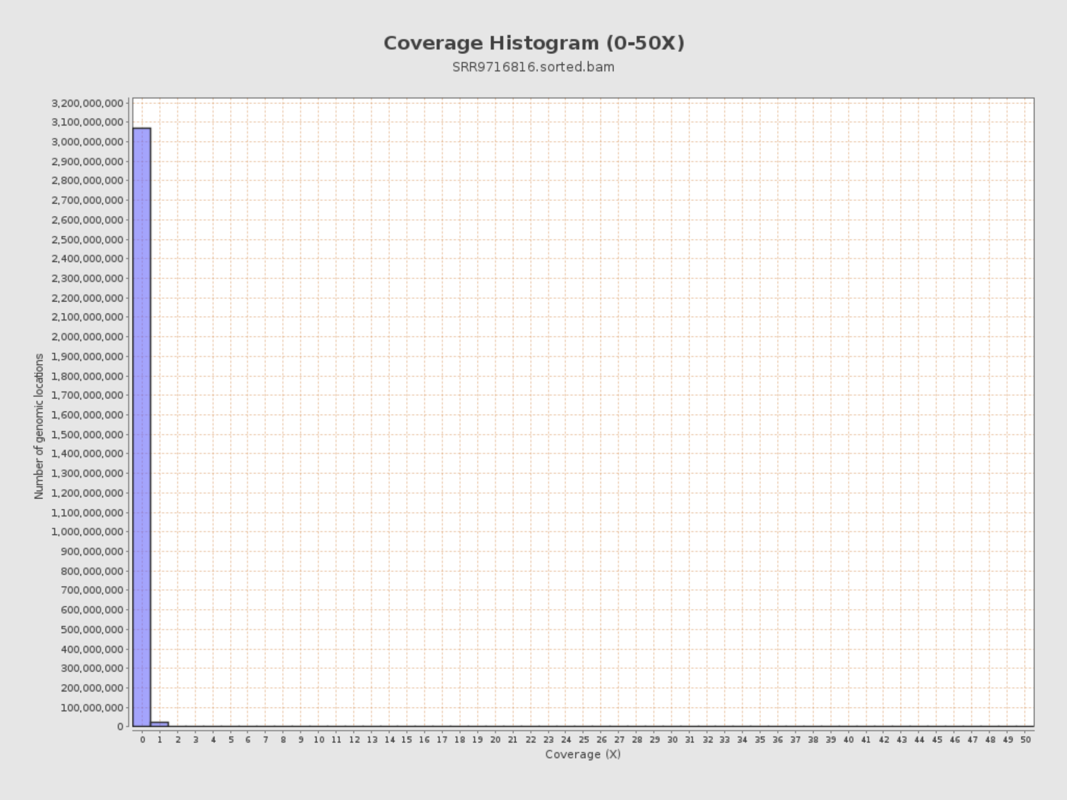
3. Results : Coverage across reference



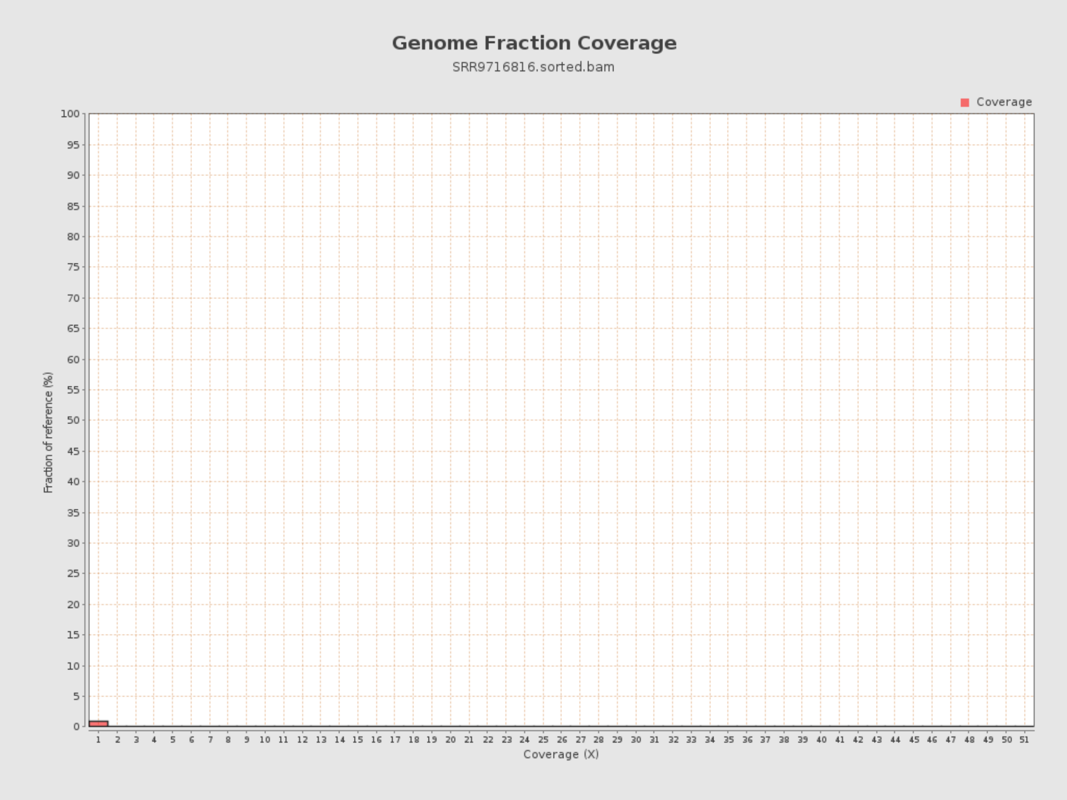
4. Results : Coverage Histogram



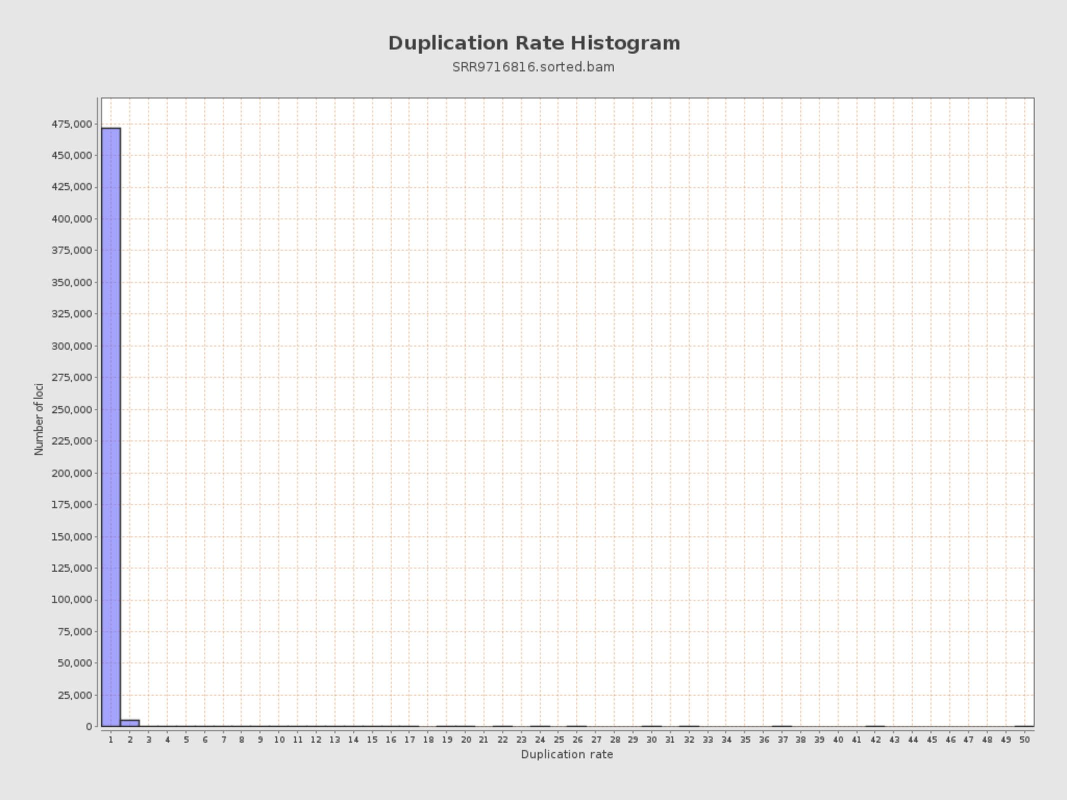
5. Results : Coverage Histogram (0-50X)



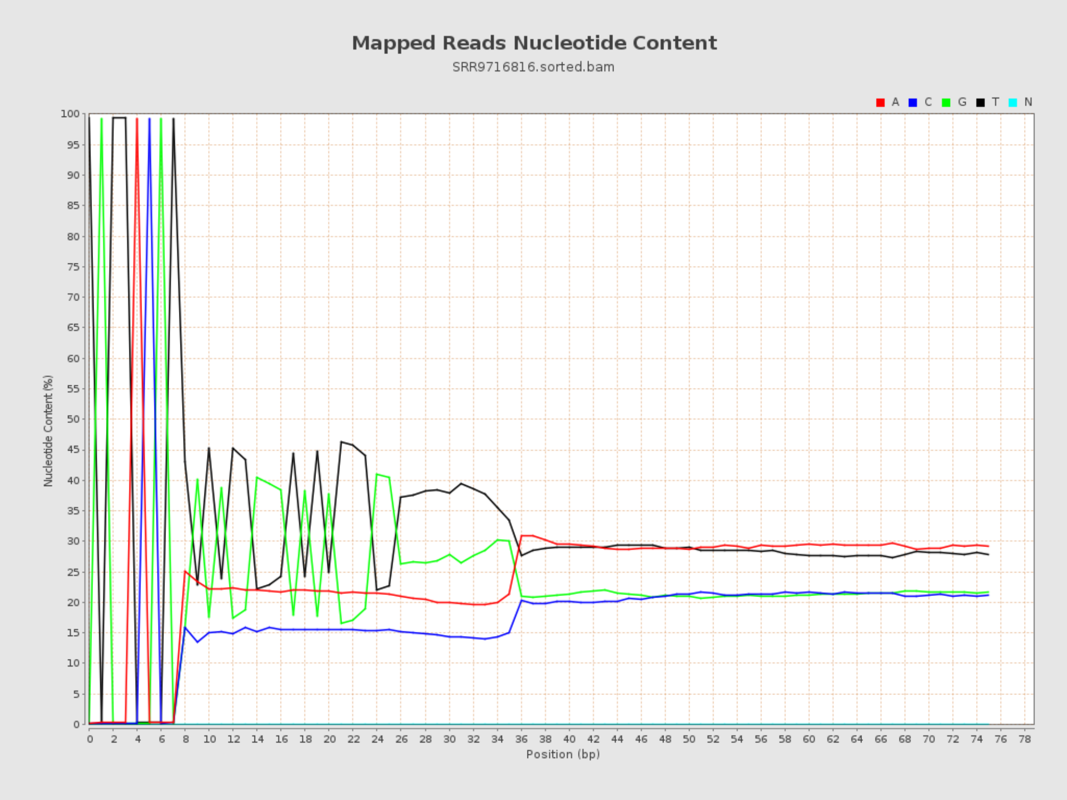
6. Results : Genome Fraction Coverage



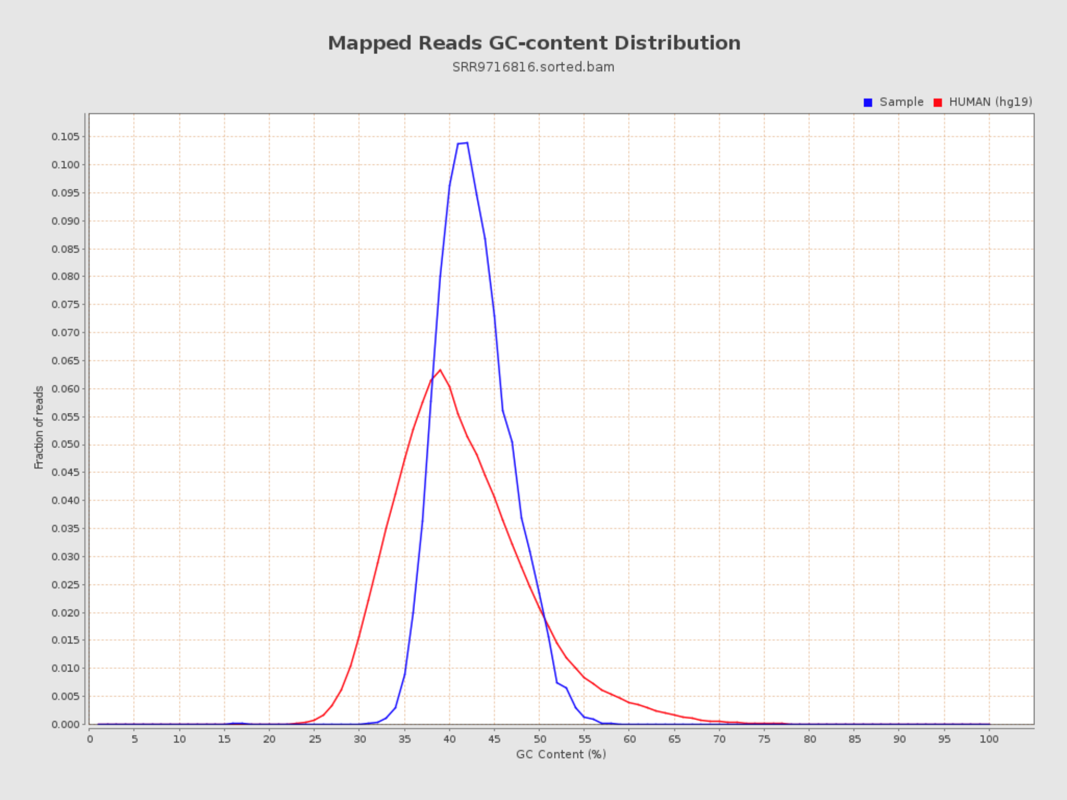
7. Results : Duplication Rate Histogram



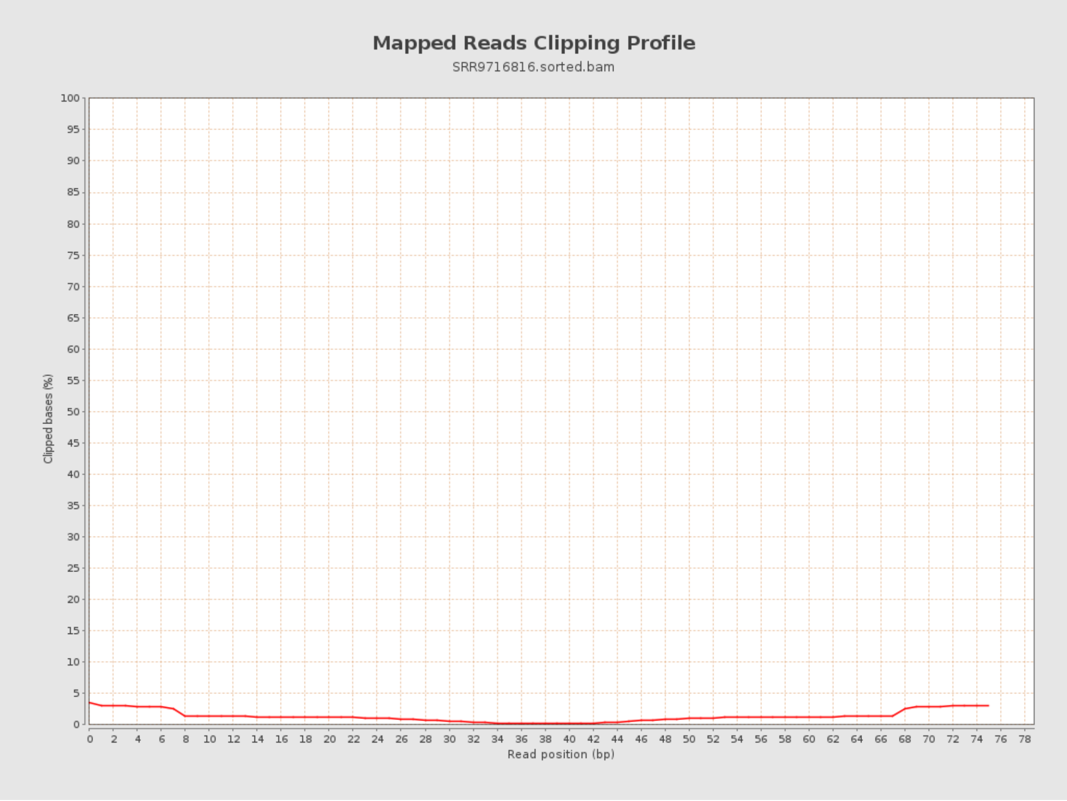
8. Results : Mapped Reads Nucleotide Content



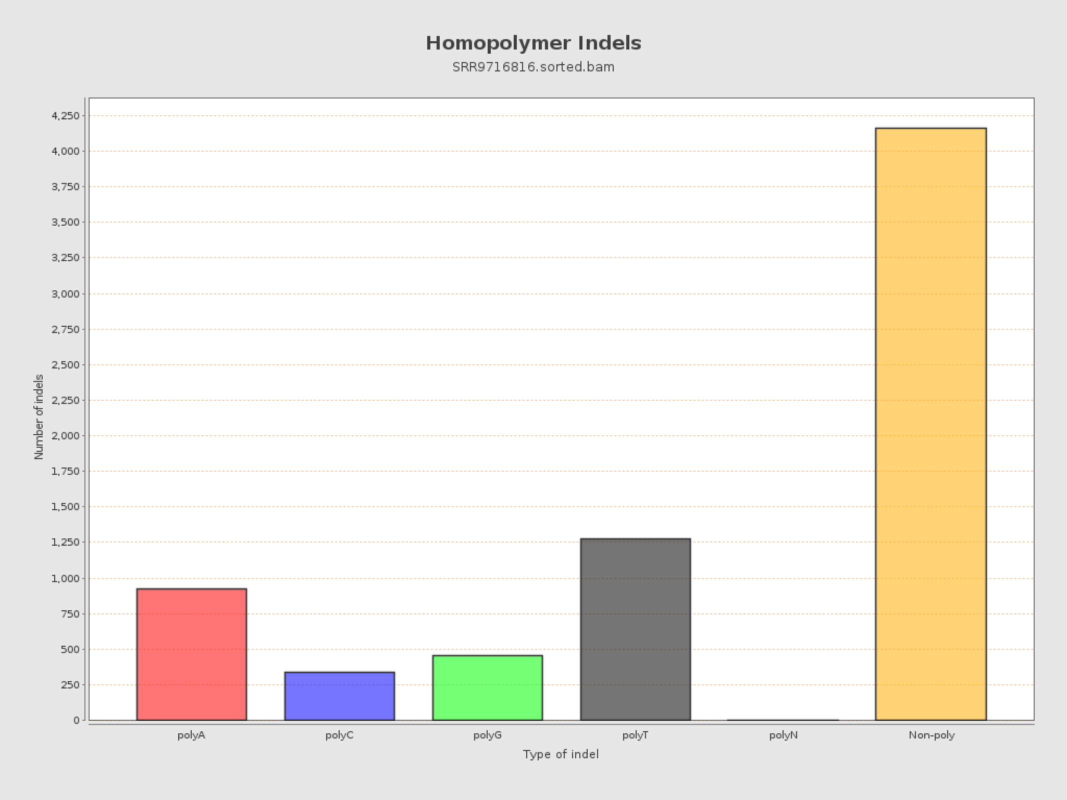
9. Results : Mapped Reads GC-content Distribution



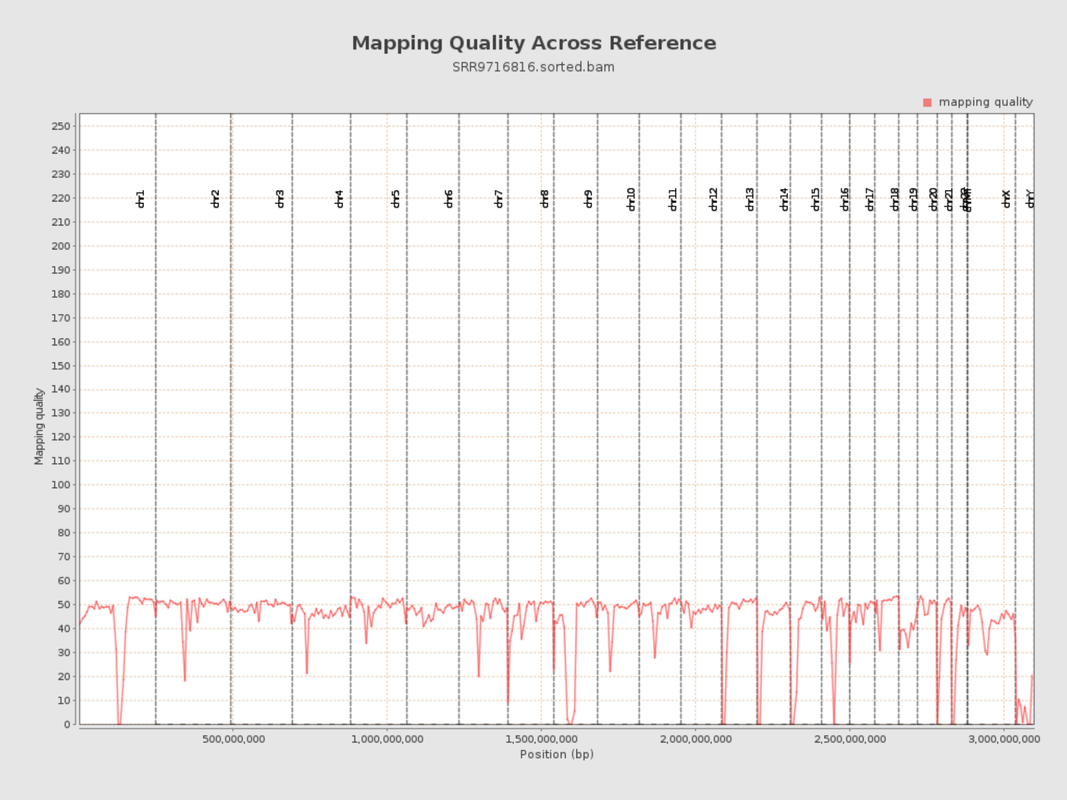
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram