Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:03:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716806.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_SRR9716806 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716806.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:03:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716806.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	601,647
Mapped reads	530,391 / 88.16%
Unmapped reads	71,256 / 11.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,597 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	11,342 / 1.89%
Duplication rate	1.69%
Clipped reads	531,267 / 88.3%

2.2. ACGT Content

Number/percentage of A's	7,289,940 / 23.84%
Number/percentage of C's	6,354,148 / 20.78%
Number/percentage of T's	9,660,421 / 31.59%
Number/percentage of G's	7,274,022 / 23.79%
Number/percentage of N's	416 / 0%
GC Percentage	44.57%

2.3. Coverage

Mean	0.0099

Standard Deviation	0.1215

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

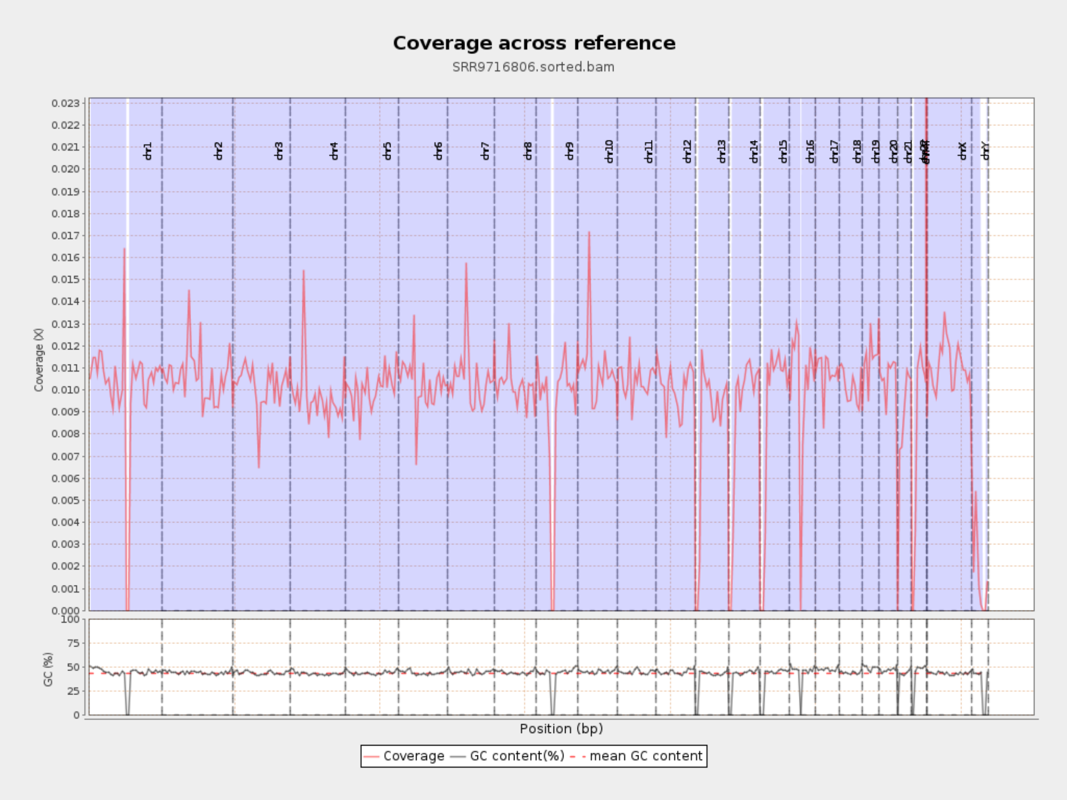
General error rate	0.52%
Mismatches	154,854
Insertions	2,238
Mapped reads with at least one insertion	0.42%
Deletions	5,812
Mapped reads with at least one deletion	1.09%
Homopolymer indels	40.32%

2.6. Chromosome stats

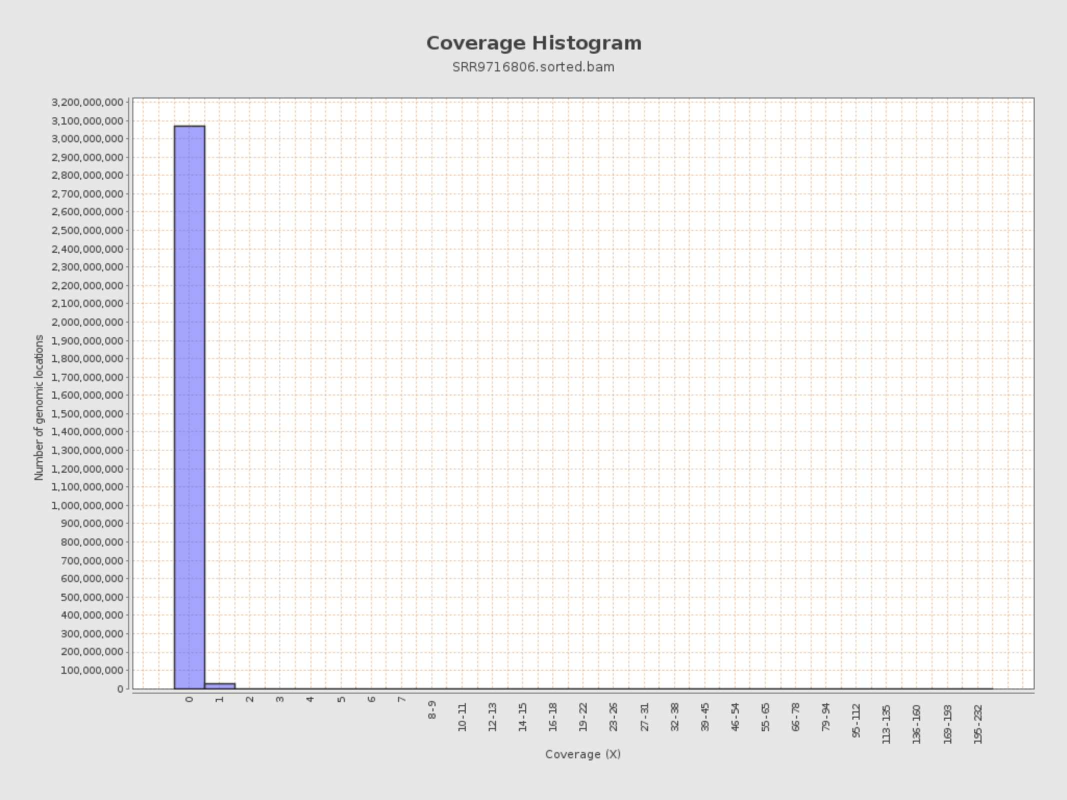
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2515135	0.0101	0.1887
chr2	243199373	2591089	0.0107	0.138
chr3	198022430	2018999	0.0102	0.1054
chr4	191154276	1850871	0.0097	0.1054
chr5	180915260	1822661	0.0101	0.1045
chr6	171115067	1759431	0.0103	0.113
chr7	159138663	1674303	0.0105	0.1372

chr8	146364022	1489994	0.0102	0.1142
chr9	141213431	1268922	0.009	0.1062
chr10	135534747	1490008	0.011	0.1229
chr11	135006516	1409333	0.0104	0.1184
chr12	133851895	1351691	0.0101	0.1051
chr13	115169878	949294	0.0082	0.094
chr14	107349540	924675	0.0086	0.0981
chr15	102531392	912085	0.0089	0.0991
chr16	90354753	916886	0.0101	0.1071
chr17	81195210	872647	0.0107	0.1097
chr18	78077248	793275	0.0102	0.1425
chr19	59128983	673186	0.0114	0.1448
chr20	63025520	663707	0.0105	0.1075
chr21	48129895	400173	0.0083	0.0985
chr22	51304566	394383	0.0077	0.0915
chrMT	16571	26365	1.591	1.5367
chrX	155270560	1719732	0.0111	0.1134
chrY	59373566	99121	0.0017	0.0545

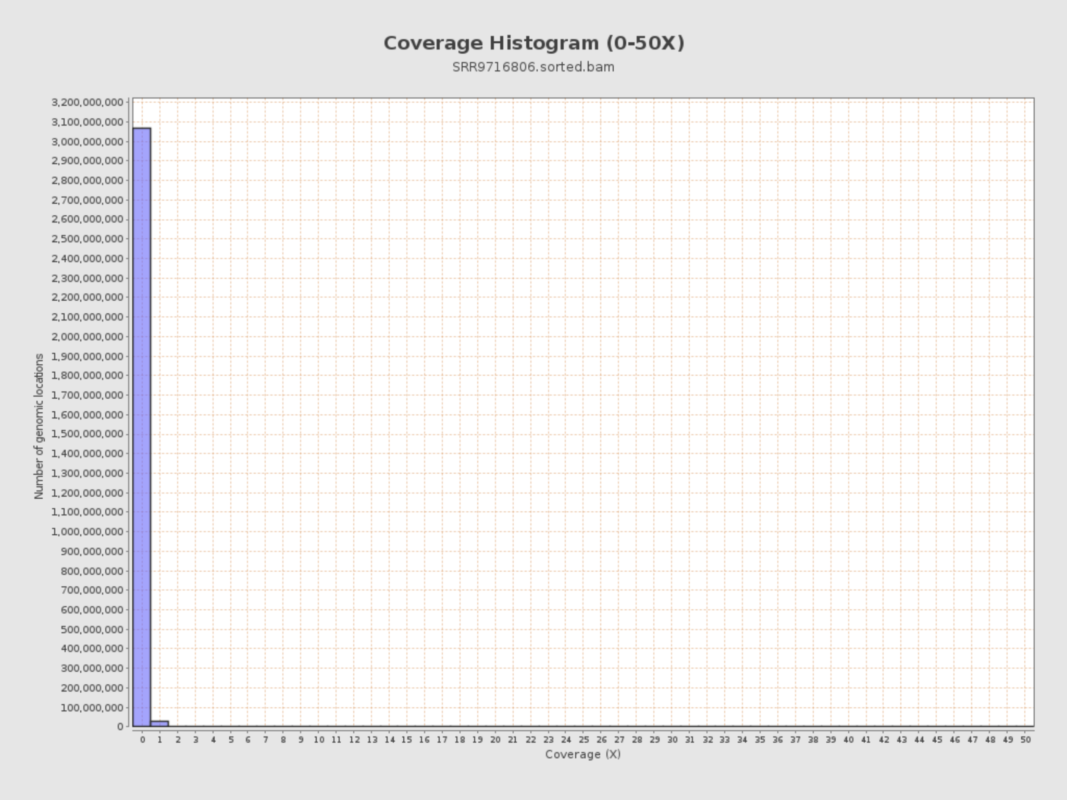
3. Results : Coverage across reference



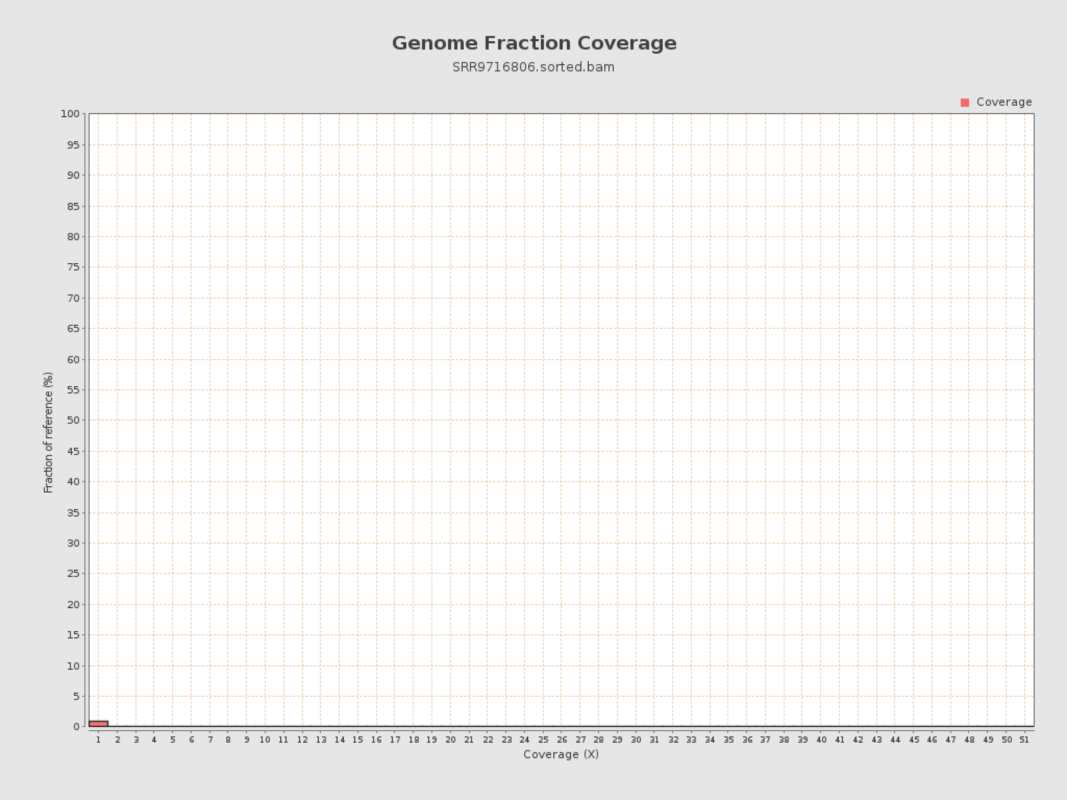
4. Results : Coverage Histogram



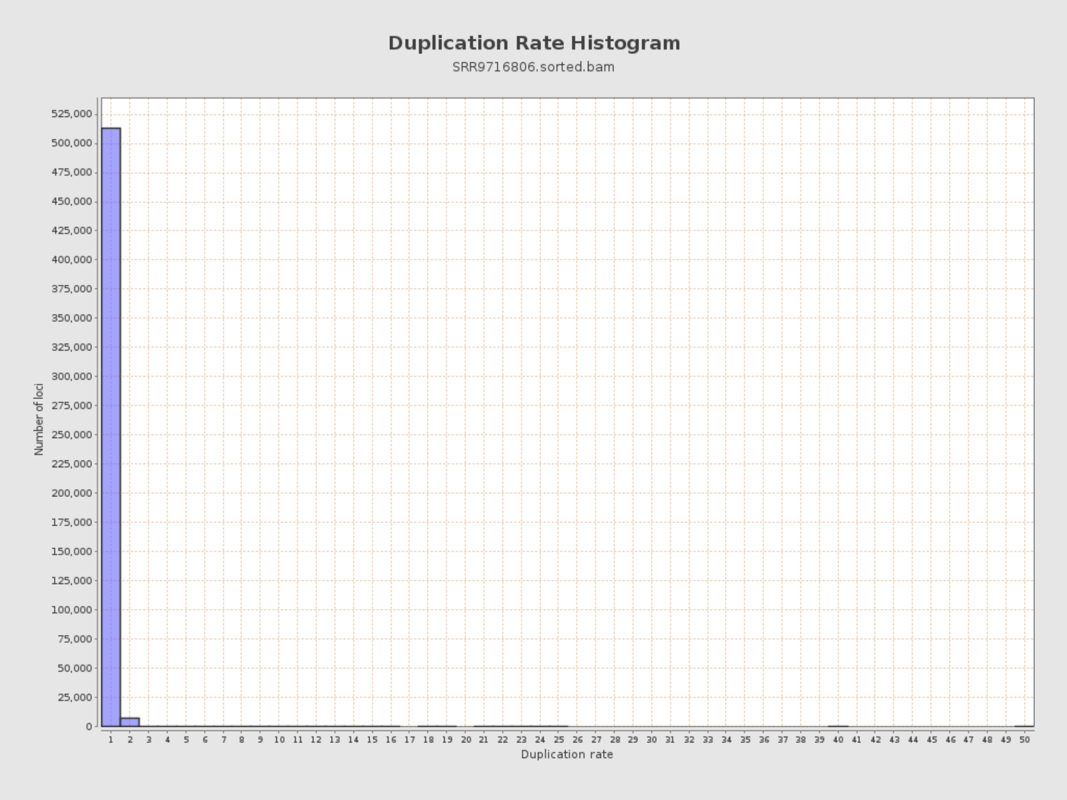
5. Results : Coverage Histogram (0-50X)



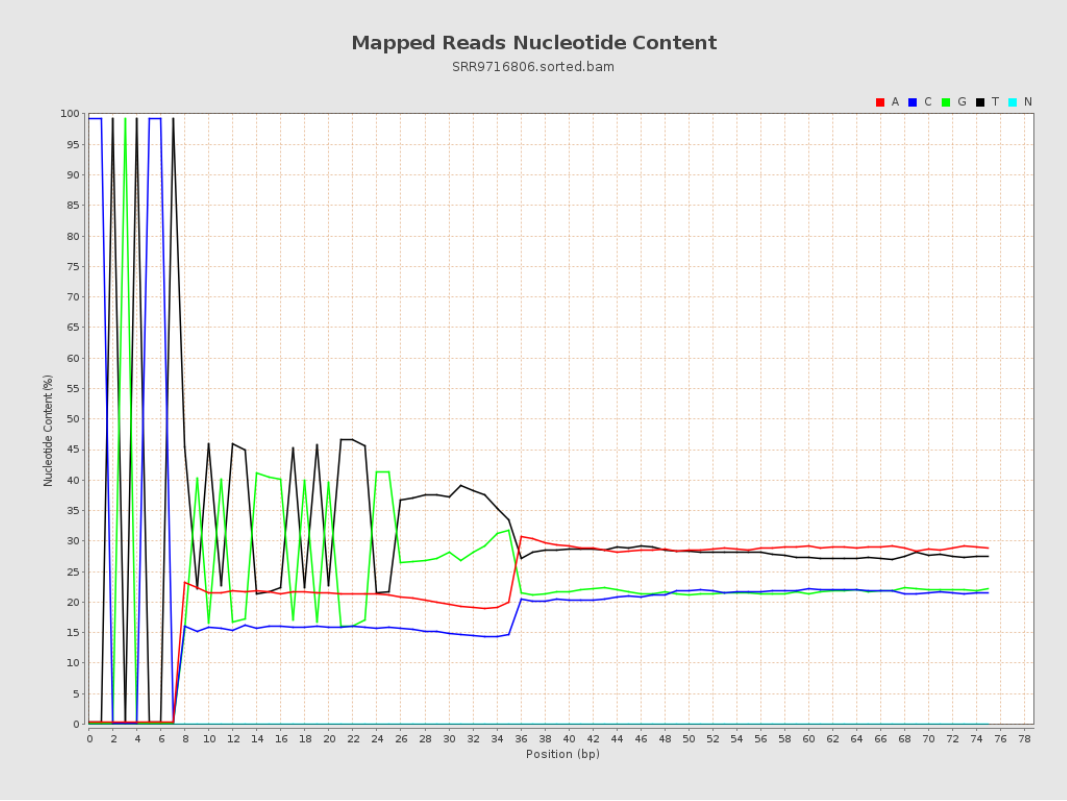
6. Results : Genome Fraction Coverage



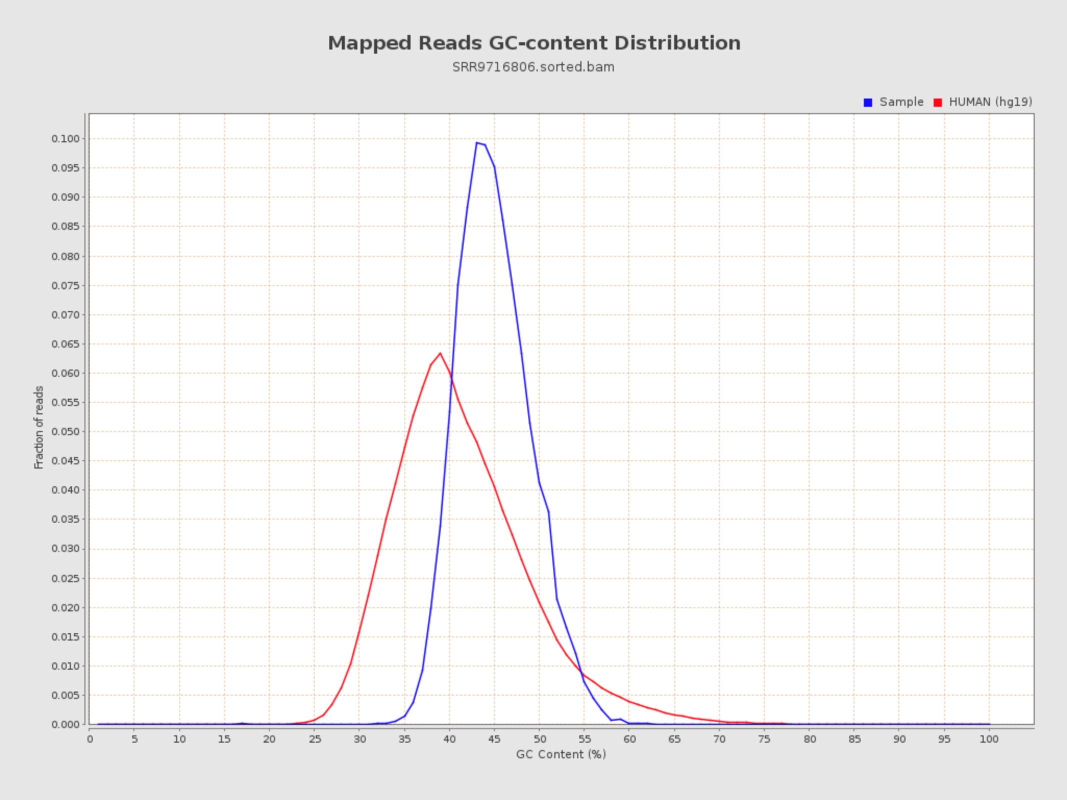
7. Results : Duplication Rate Histogram



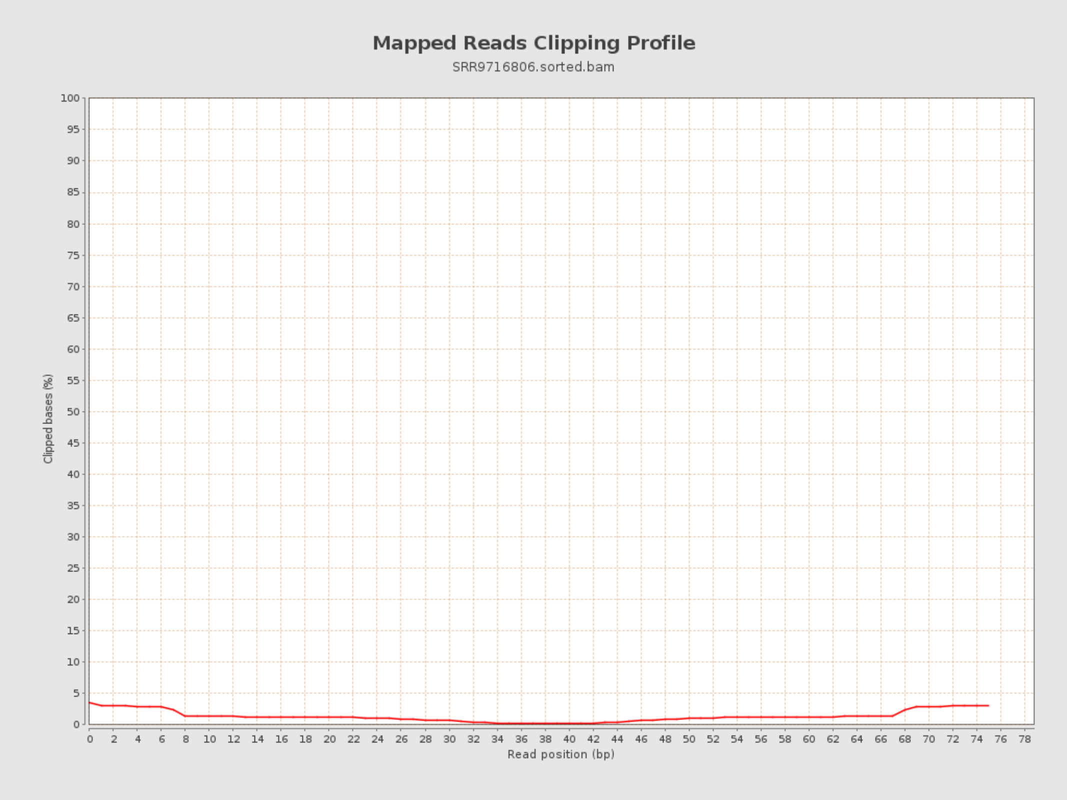
8. Results : Mapped Reads Nucleotide Content



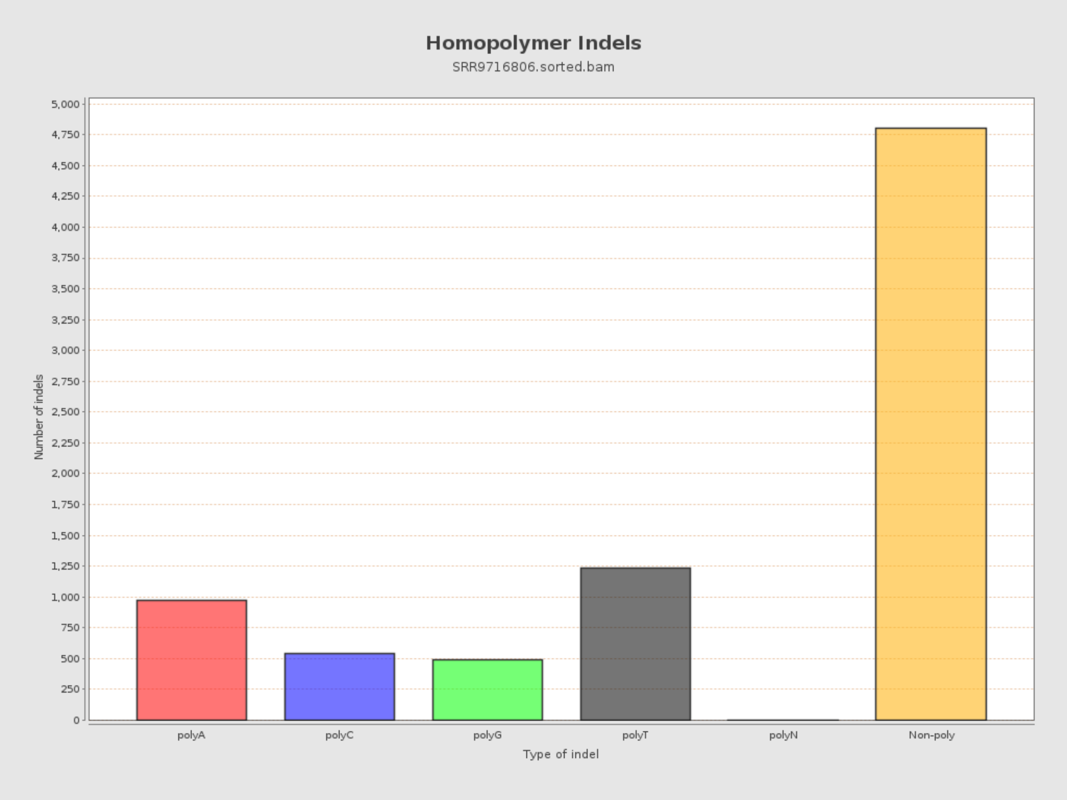
9. Results : Mapped Reads GC-content Distribution



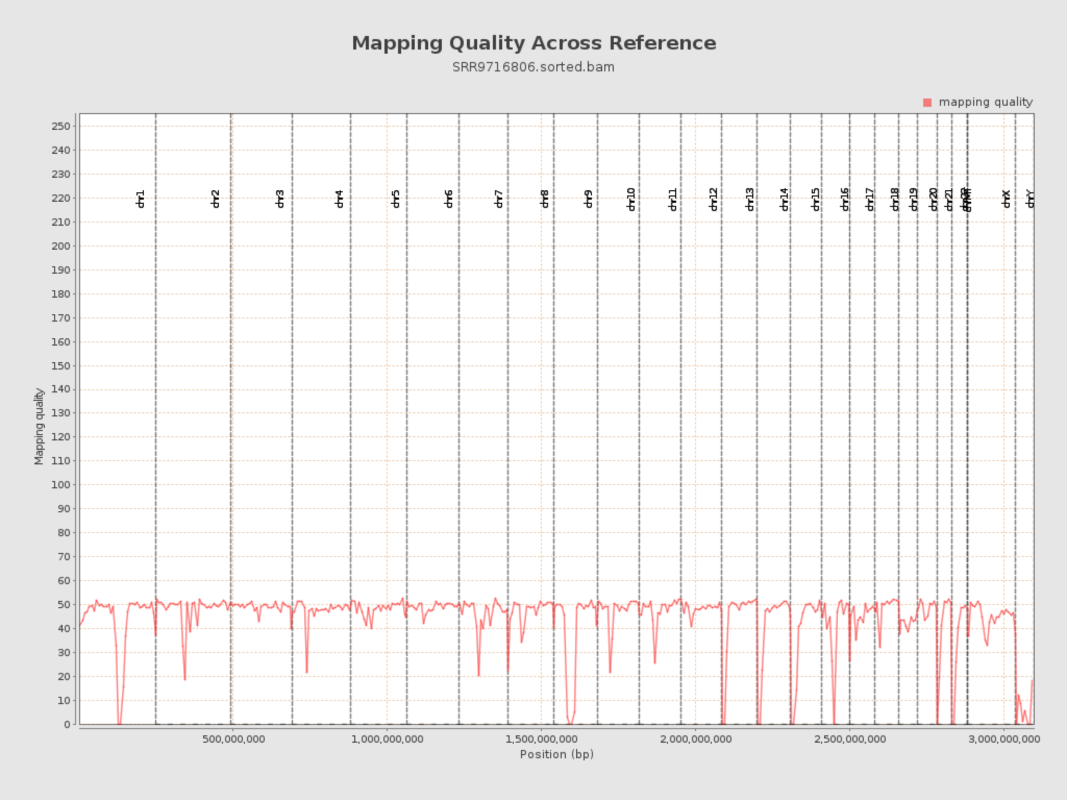
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram