Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 04:45:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716270.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_SRR9716270 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716270.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 04:45:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716270.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	541,977
Mapped reads	400,215 / 73.84%
Unmapped reads	141,762 / 26.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	415 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	17,083 / 3.15%
Duplication rate	3.83%
Clipped reads	400,084 / 73.82%

2.2. ACGT Content

Number/percentage of A's	4,382,458 / 20.86%
Number/percentage of C's	3,665,893 / 17.45%
Number/percentage of T's	7,043,049 / 33.52%
Number/percentage of G's	5,921,453 / 28.18%
Number/percentage of N's	438 / 0%
GC Percentage	45.63%

2.3. Coverage

Mean	0.0068

Standard Deviation	0.096

2.4. Mapping Quality

Mean Mapping Quality	42.33

2.5. Mismatches and indels

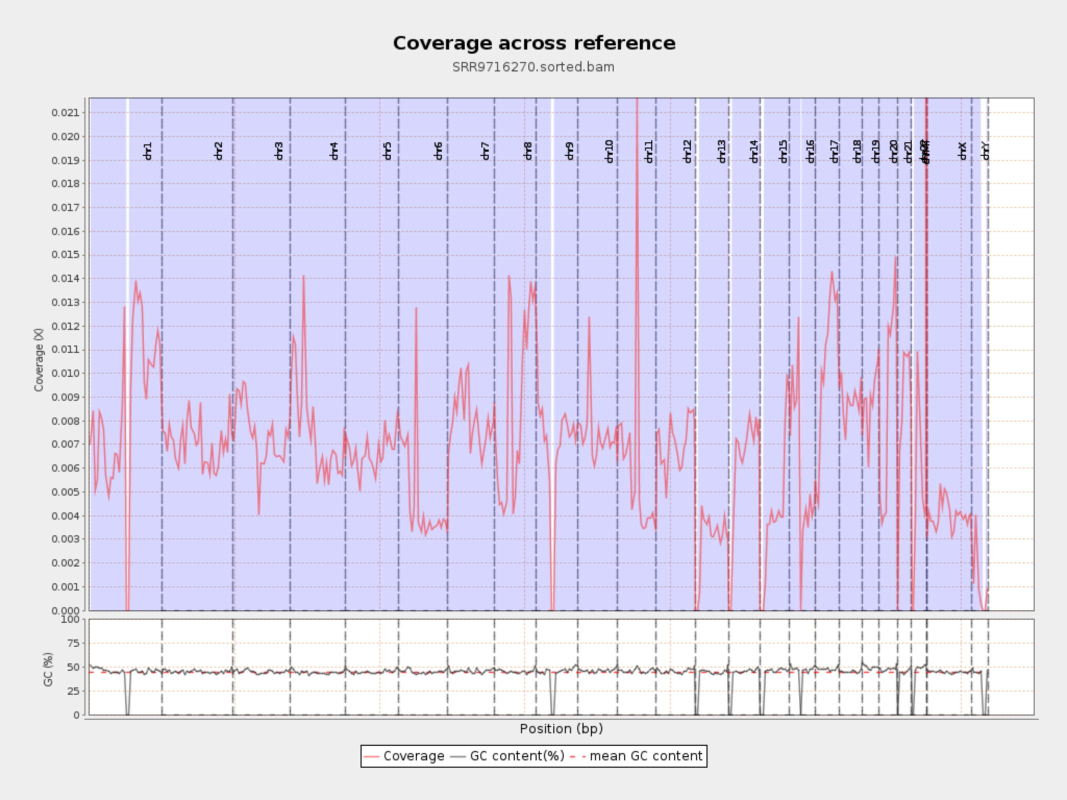
General error rate	0.72%
Mismatches	149,791
Insertions	1,317
Mapped reads with at least one insertion	0.33%
Deletions	3,196
Mapped reads with at least one deletion	0.79%
Homopolymer indels	40.84%

2.6. Chromosome stats

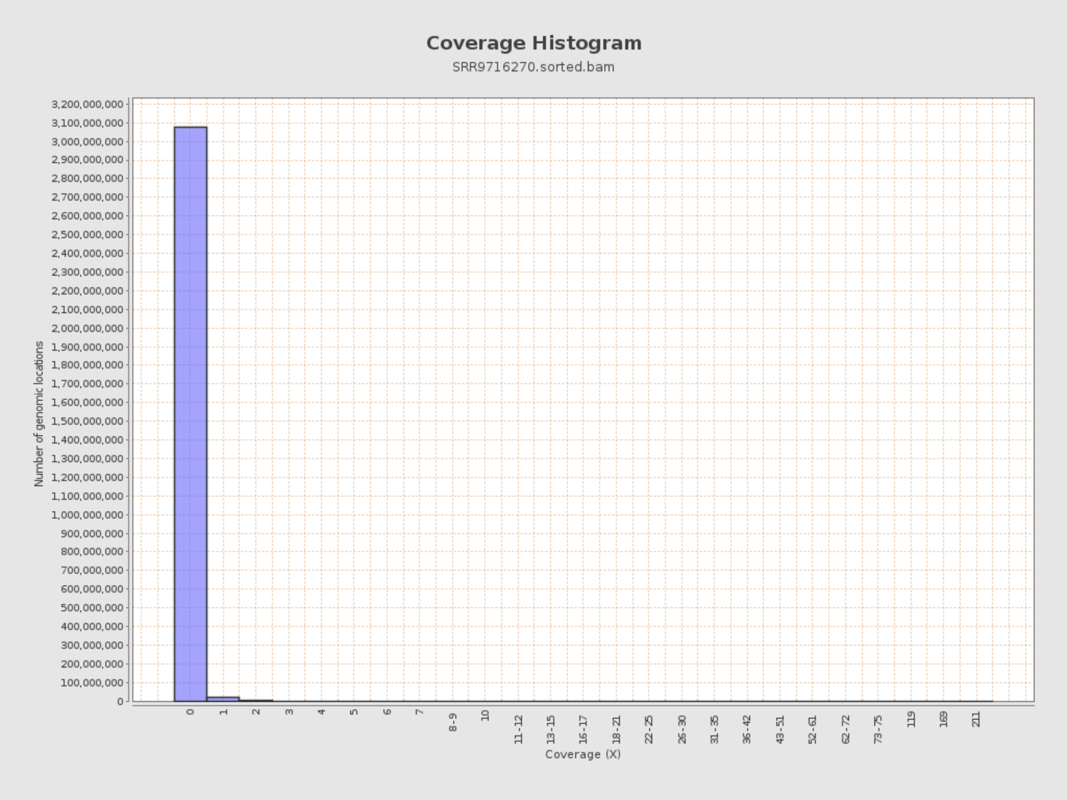
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2114280	0.0085	0.113
chr2	243199373	1716876	0.0071	0.1256
chr3	198022430	1463702	0.0074	0.0923
chr4	191154276	1454646	0.0076	0.0955
chr5	180915260	1204205	0.0067	0.0868
chr6	171115067	830566	0.0049	0.0824
chr7	159138663	1283792	0.0081	0.1059

chr8	146364022	1284648	0.0088	0.102
chr9	141213431	941340	0.0067	0.0915
chr10	135534747	1013476	0.0075	0.1043
chr11	135006516	832668	0.0062	0.091
chr12	133851895	946633	0.0071	0.0898
chr13	115169878	338998	0.0029	0.0581
chr14	107349540	648105	0.006	0.0828
chr15	102531392	414658	0.004	0.068
chr16	90354753	538332	0.006	0.0858
chr17	81195210	865674	0.0107	0.1136
chr18	78077248	688556	0.0088	0.1132
chr19	59128983	523533	0.0089	0.1099
chr20	63025520	552356	0.0088	0.1023
chr21	48129895	406181	0.0084	0.1021
chr22	51304566	248437	0.0048	0.0764
chrMT	16571	13872	0.8371	1.1636
chrX	155270560	625867	0.004	0.0703
chrY	59373566	67236	0.0011	0.0418

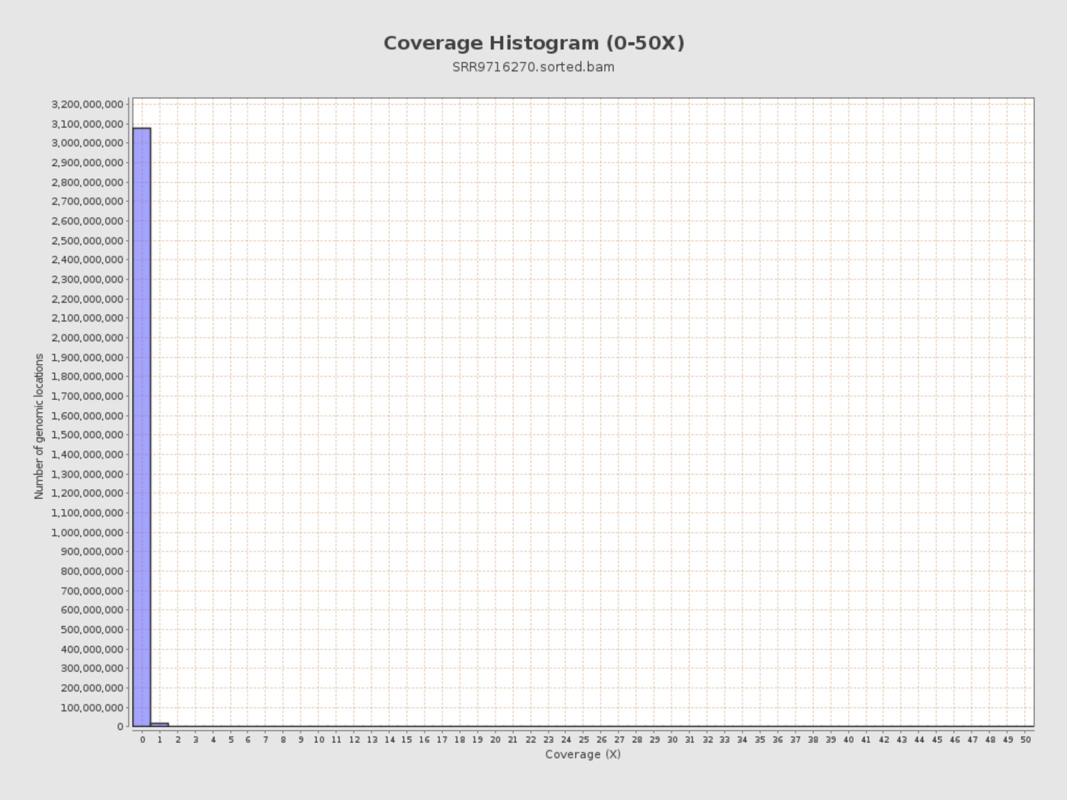
3. Results : Coverage across reference



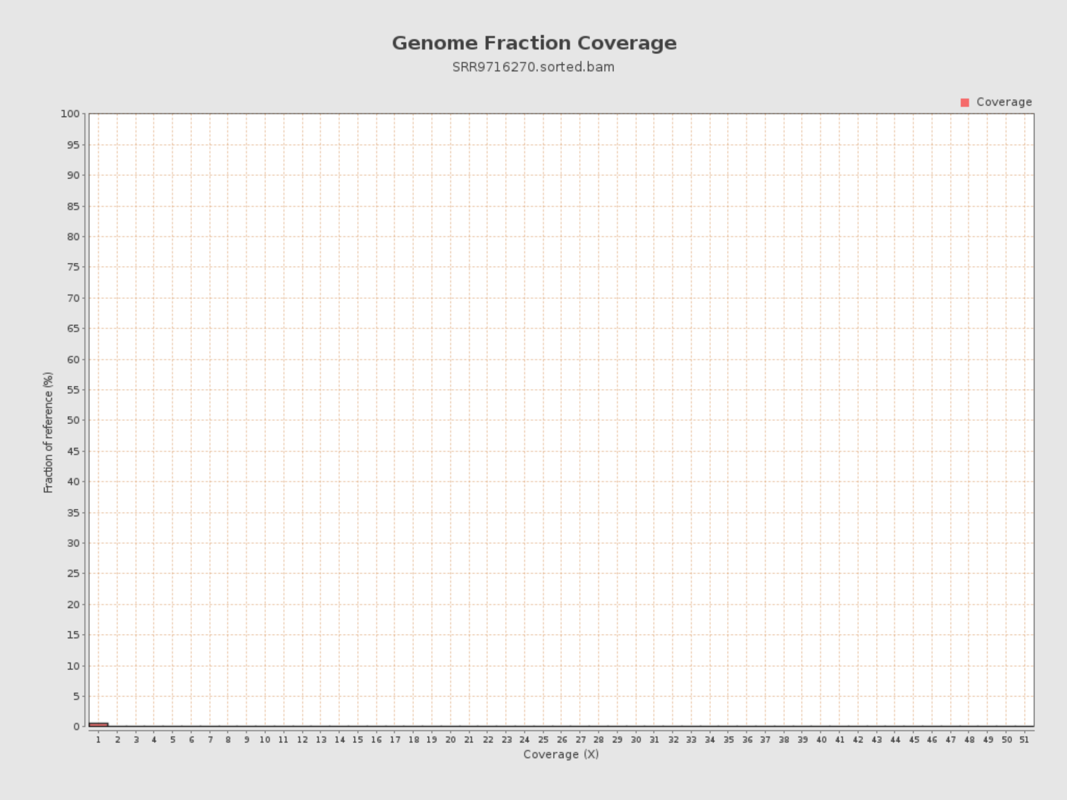
4. Results : Coverage Histogram



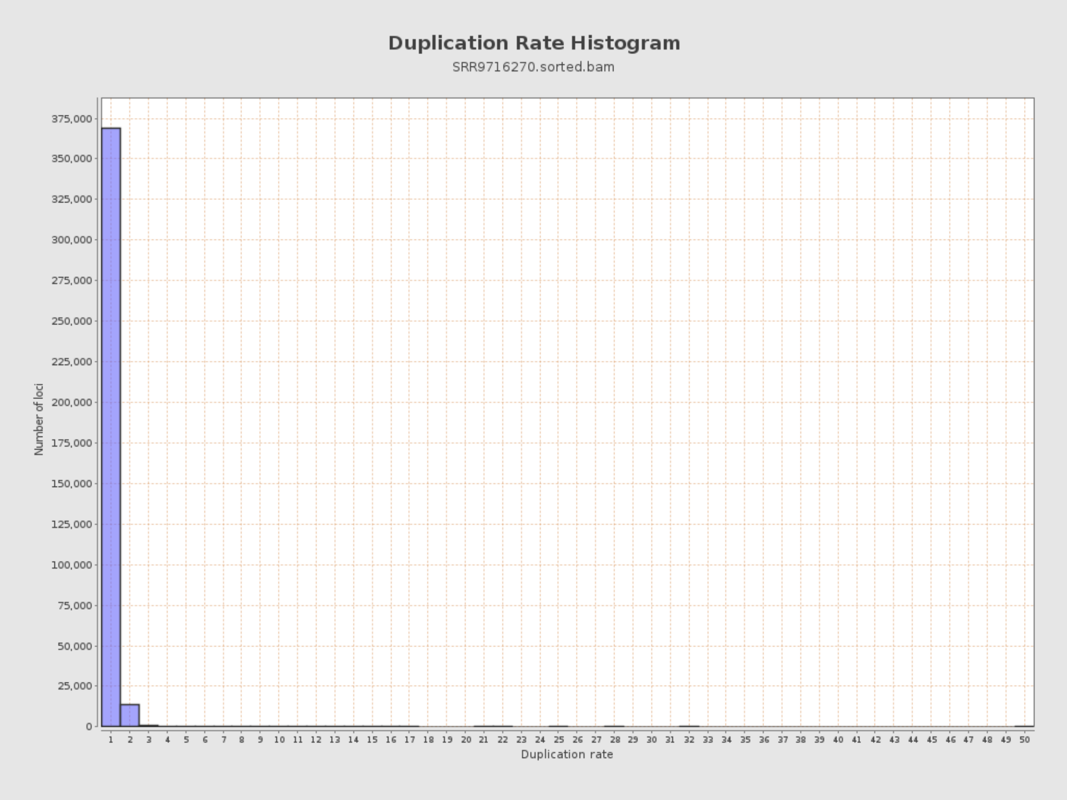
5. Results : Coverage Histogram (0-50X)



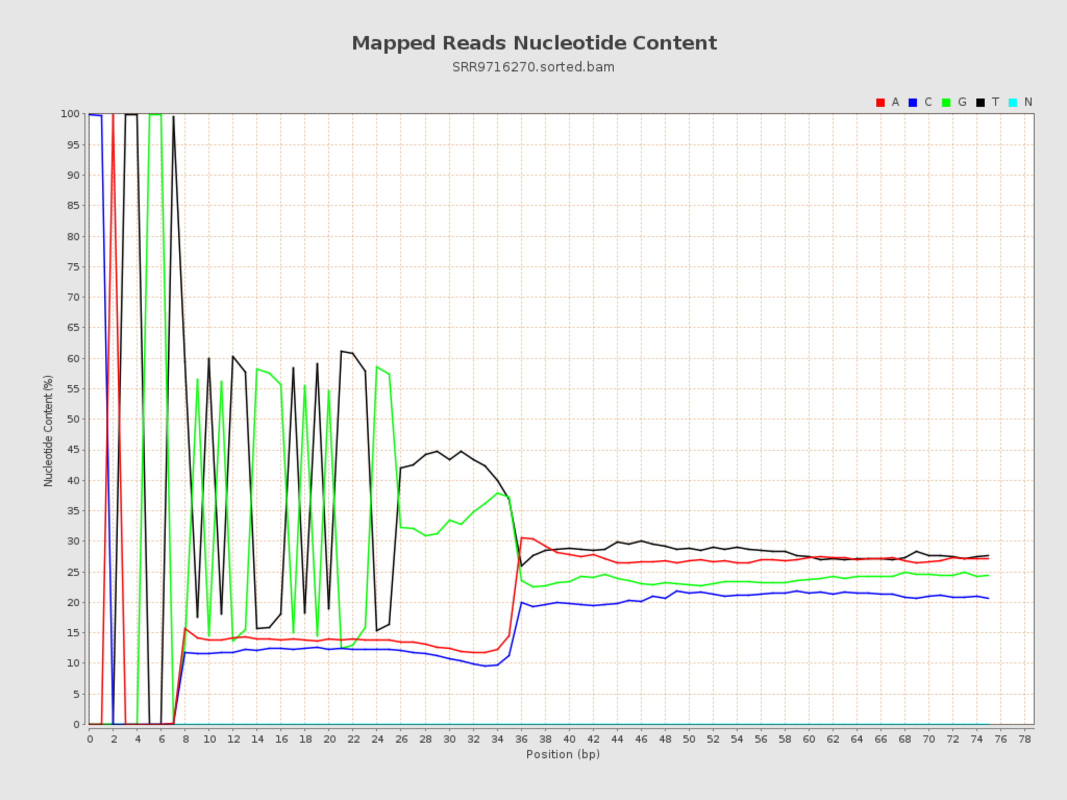
6. Results : Genome Fraction Coverage



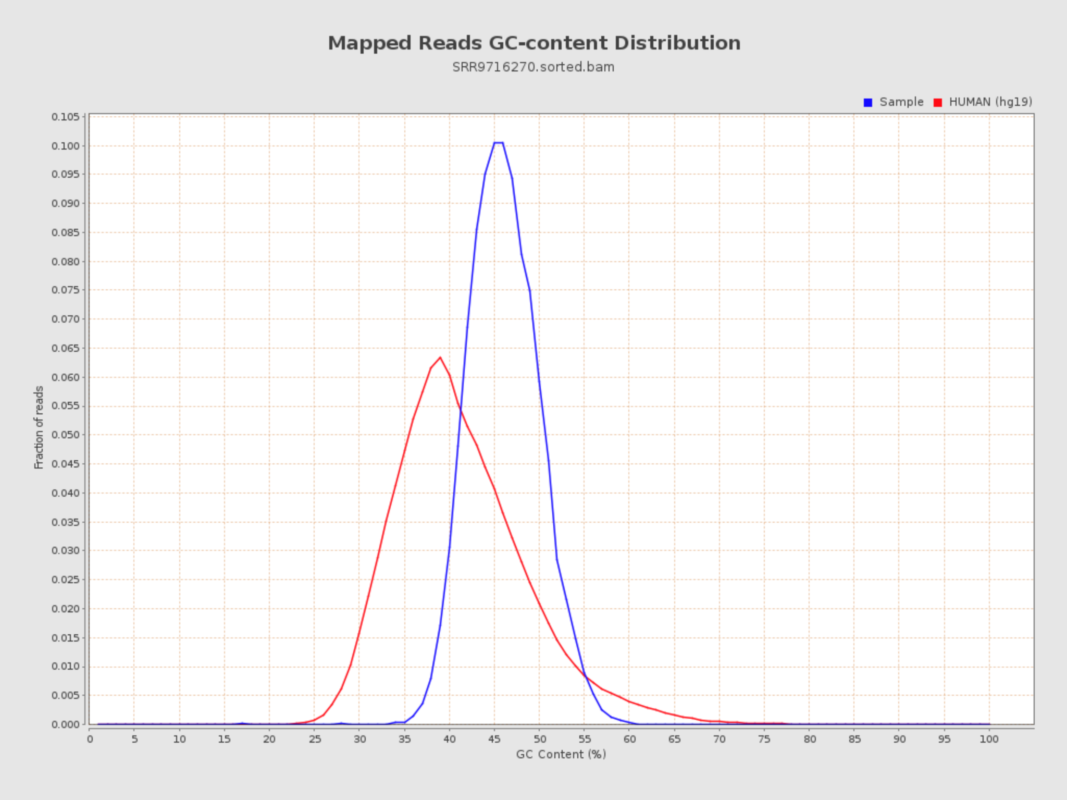
7. Results : Duplication Rate Histogram



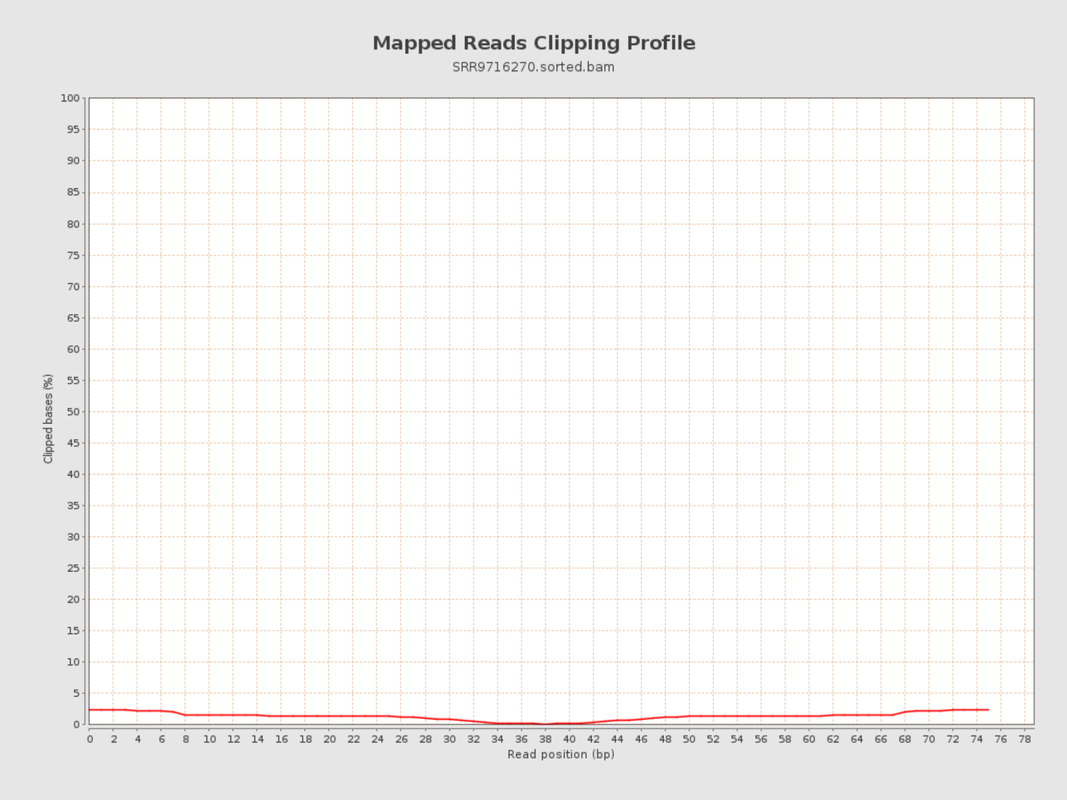
8. Results : Mapped Reads Nucleotide Content



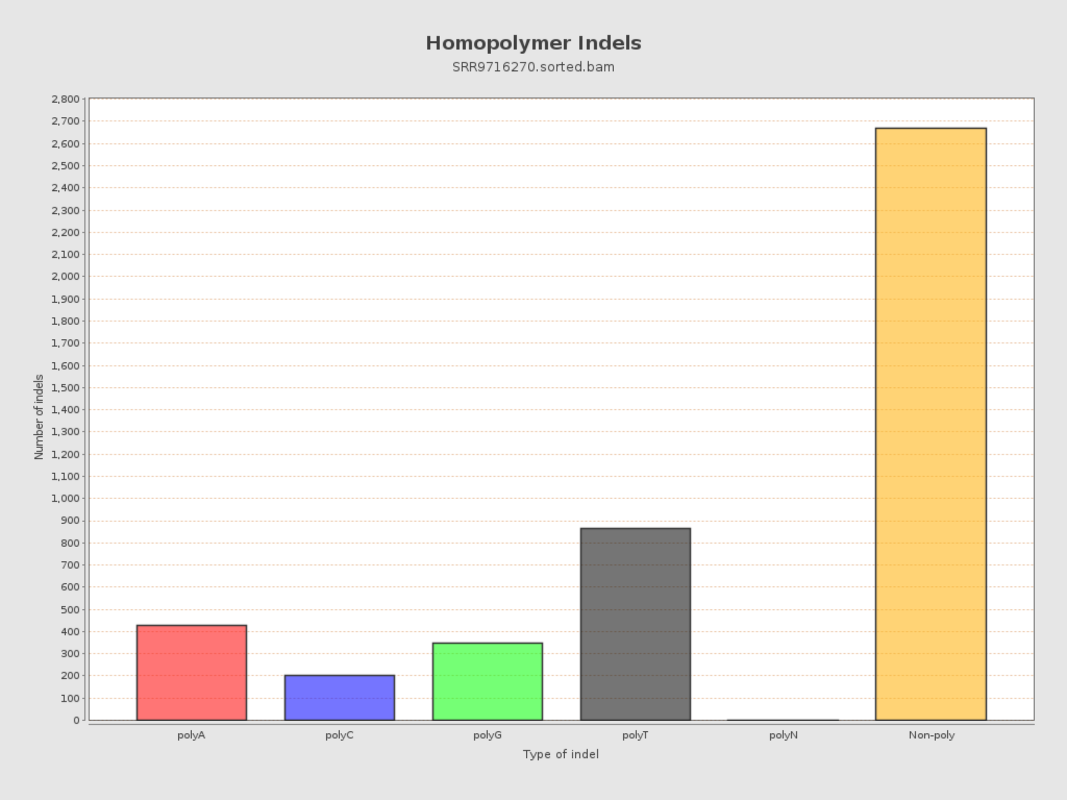
9. Results : Mapped Reads GC-content Distribution



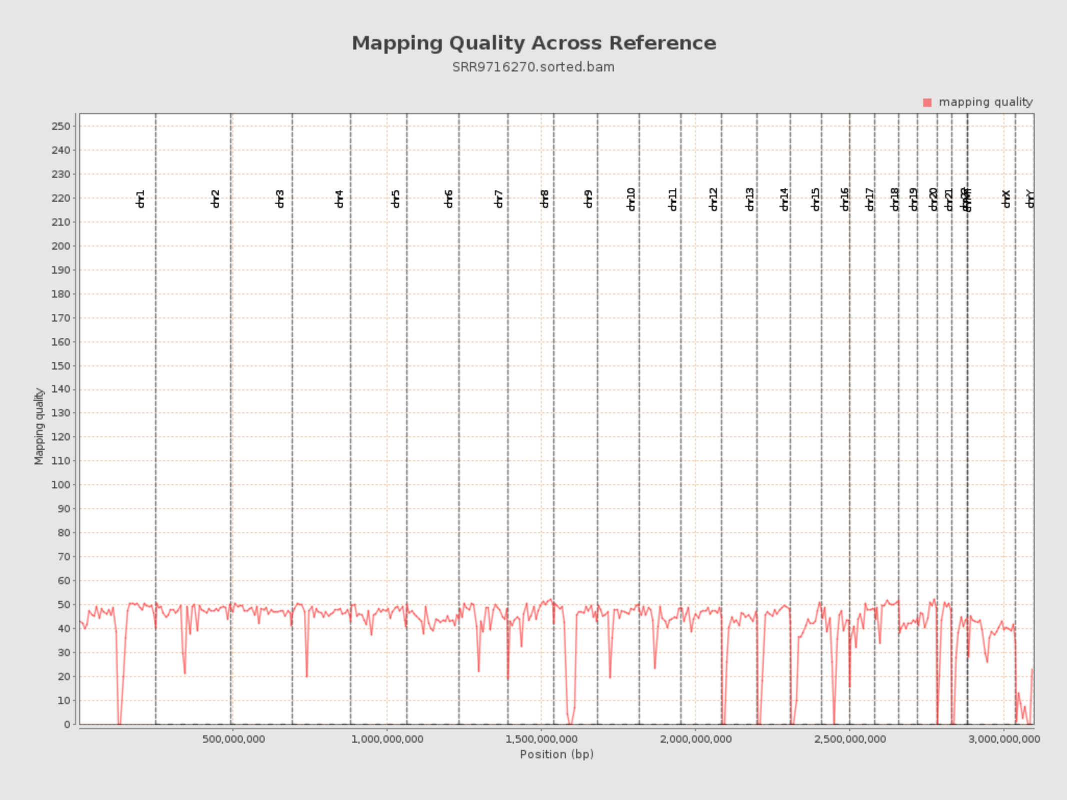
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram