Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:41:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716637.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_SRR9716637 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716637.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:41:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716637.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	688,796
Mapped reads	619,838 / 89.99%
Unmapped reads	68,958 / 10.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,368 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	11,196 / 1.63%
Duplication rate	1.43%
Clipped reads	620,756 / 90.12%

2.2. ACGT Content

Number/percentage of A's	8,885,184 / 25.13%
Number/percentage of C's	7,001,071 / 19.8%
Number/percentage of T's	10,945,522 / 30.95%
Number/percentage of G's	8,529,530 / 24.12%
Number/percentage of N's	813 / 0%
GC Percentage	43.92%

2.3. Coverage

Mean	0.0114

Standard Deviation	0.1234

2.4. Mapping Quality

Mean Mapping Quality	44.87

2.5. Mismatches and indels

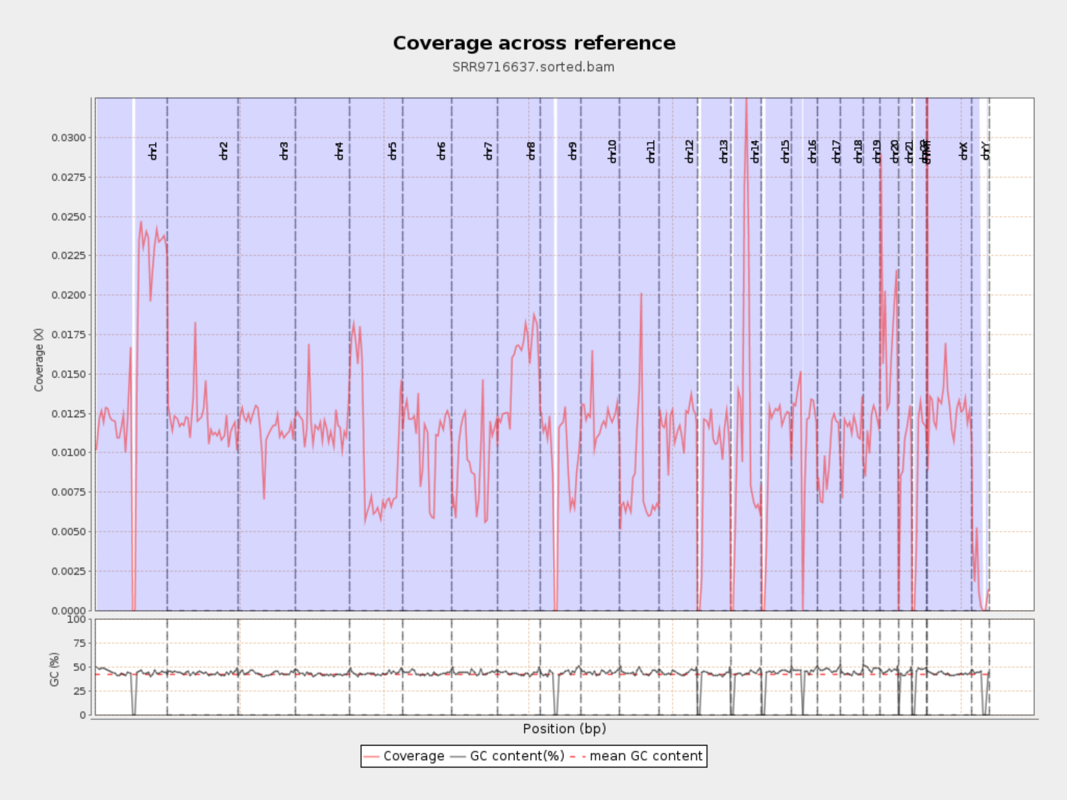
General error rate	0.5%
Mismatches	173,241
Insertions	2,006
Mapped reads with at least one insertion	0.32%
Deletions	5,664
Mapped reads with at least one deletion	0.91%
Homopolymer indels	42.24%

2.6. Chromosome stats

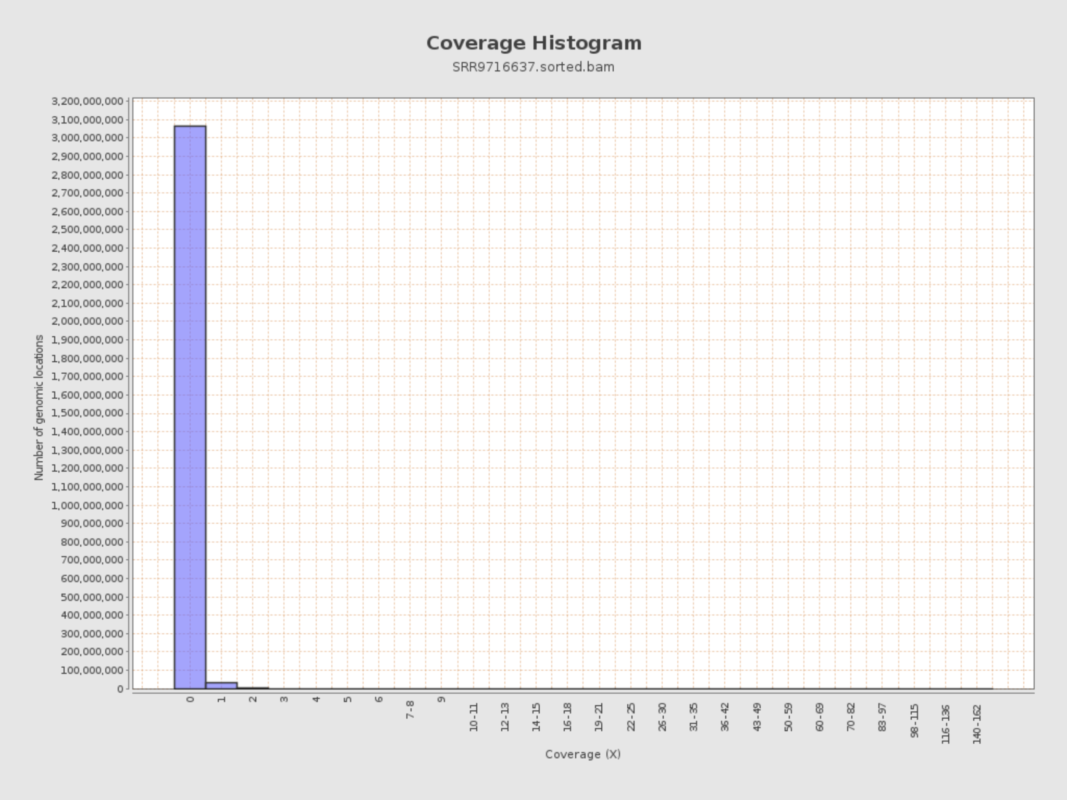
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3984508	0.016	0.173
chr2	243199373	2924780	0.012	0.1338
chr3	198022430	2288577	0.0116	0.1113
chr4	191154276	2251429	0.0118	0.1159
chr5	180915260	1791426	0.0099	0.104
chr6	171115067	1865158	0.0109	0.1124
chr7	159138663	1516416	0.0095	0.1105

chr8	146364022	2257980	0.0154	0.1387
chr9	141213431	1287326	0.0091	0.1158
chr10	135534747	1666912	0.0123	0.1248
chr11	135006516	1110126	0.0082	0.1132
chr12	133851895	1582770	0.0118	0.1138
chr13	115169878	1095959	0.0095	0.101
chr14	107349540	1241655	0.0116	0.1155
chr15	102531392	1031298	0.0101	0.1045
chr16	90354753	1027745	0.0114	0.1147
chr17	81195210	789643	0.0097	0.1032
chr18	78077248	870997	0.0112	0.1734
chr19	59128983	668920	0.0113	0.1333
chr20	63025520	1133799	0.018	0.1412
chr21	48129895	463826	0.0096	0.1048
chr22	51304566	430444	0.0084	0.0947
chrMT	16571	2279	0.1375	0.442
chrX	155270560	1989999	0.0128	0.1234
chrY	59373566	97626	0.0016	0.0511

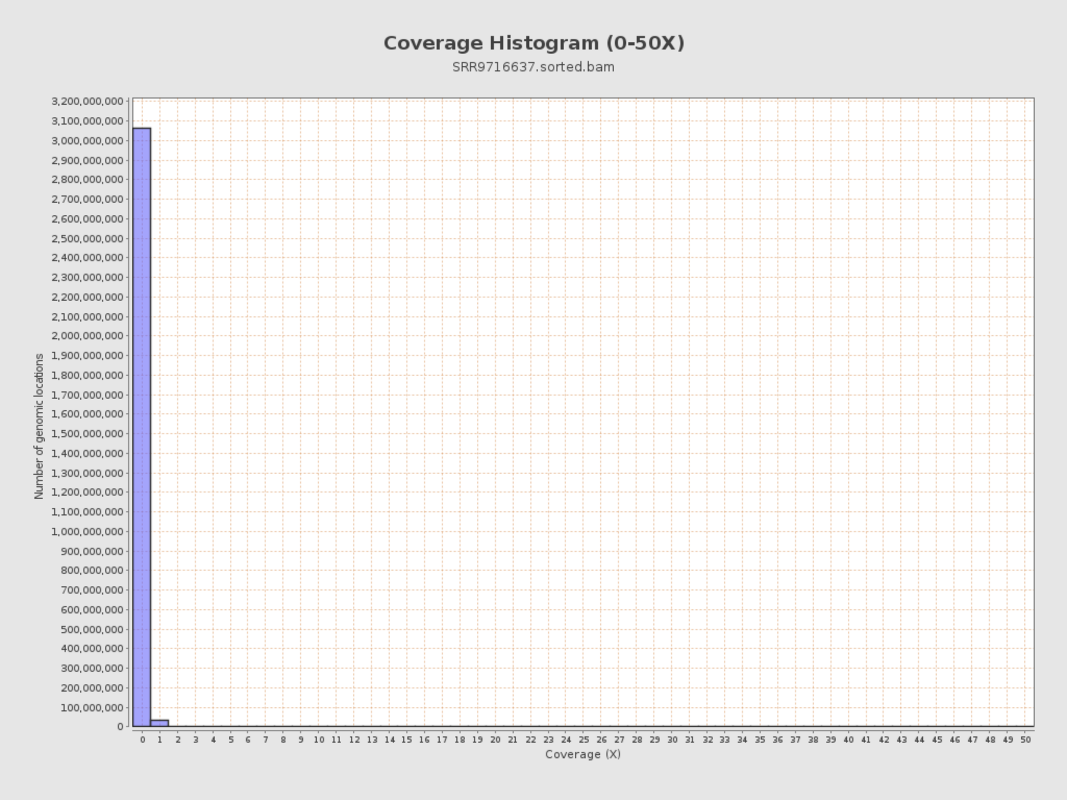
3. Results : Coverage across reference



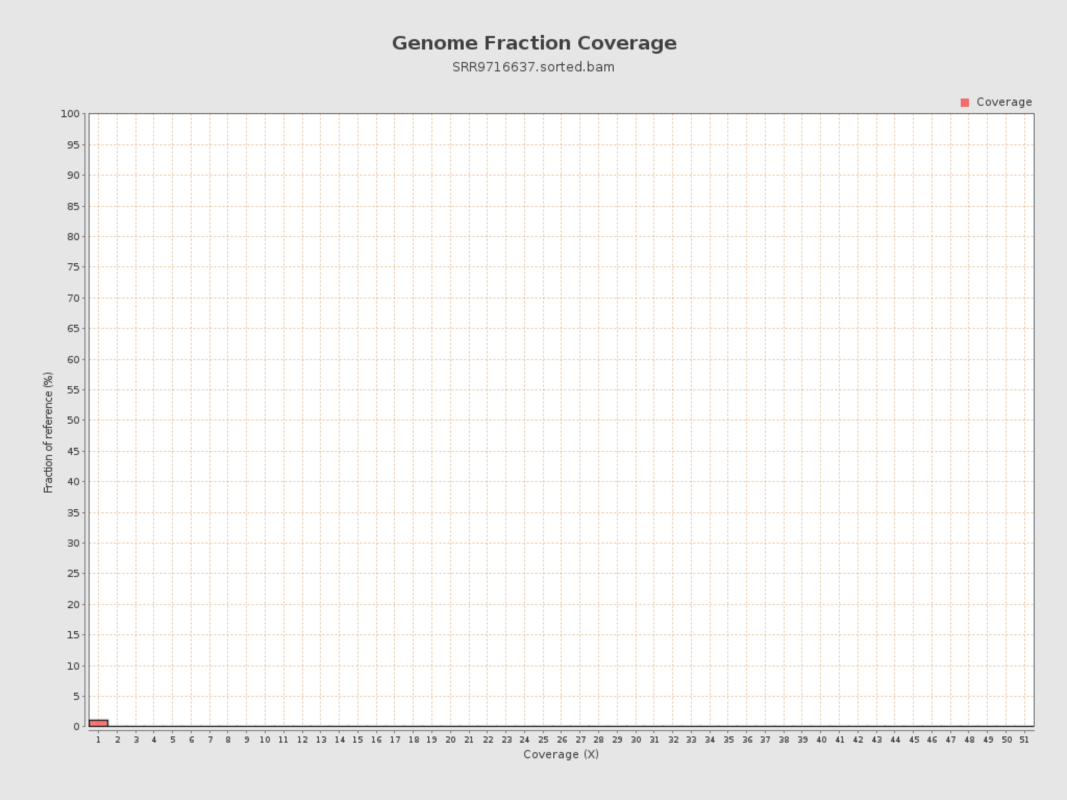
4. Results : Coverage Histogram



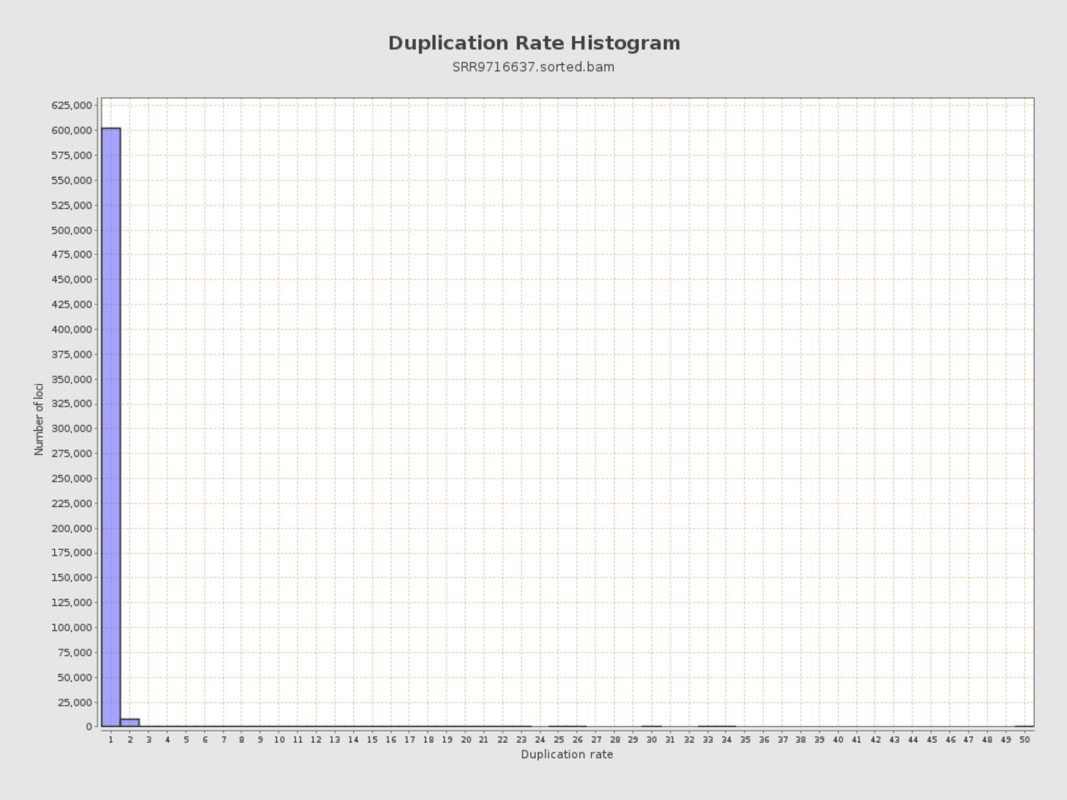
5. Results : Coverage Histogram (0-50X)



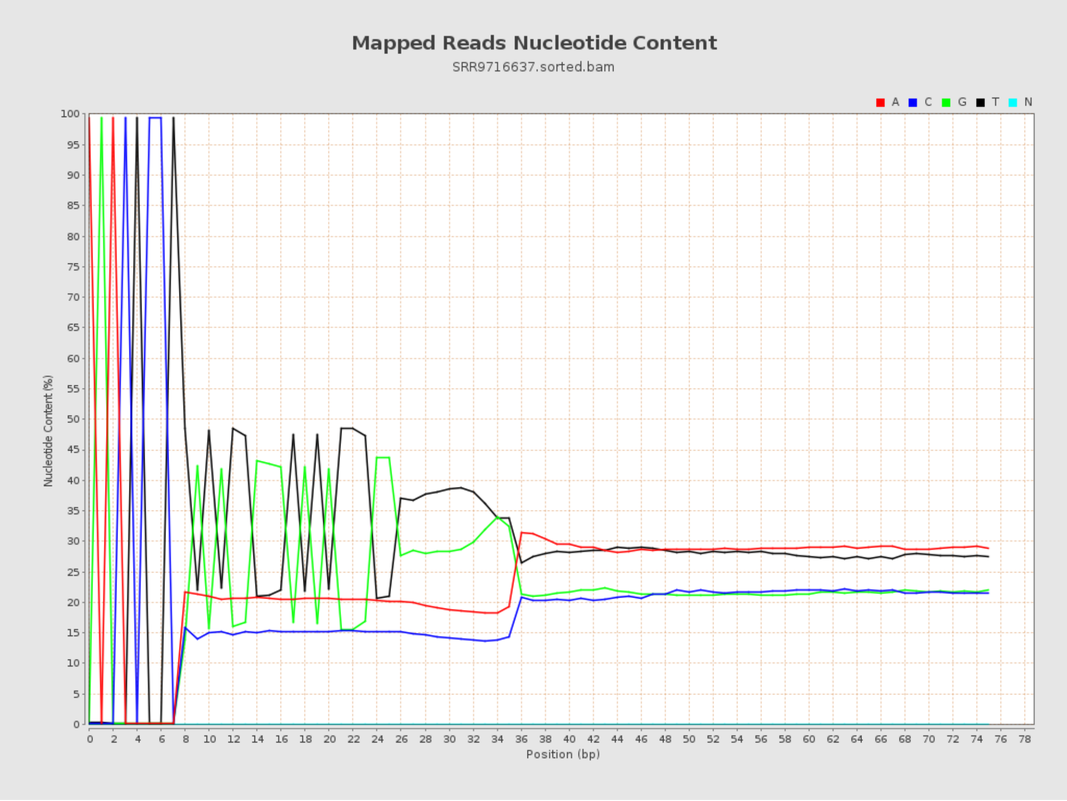
6. Results : Genome Fraction Coverage



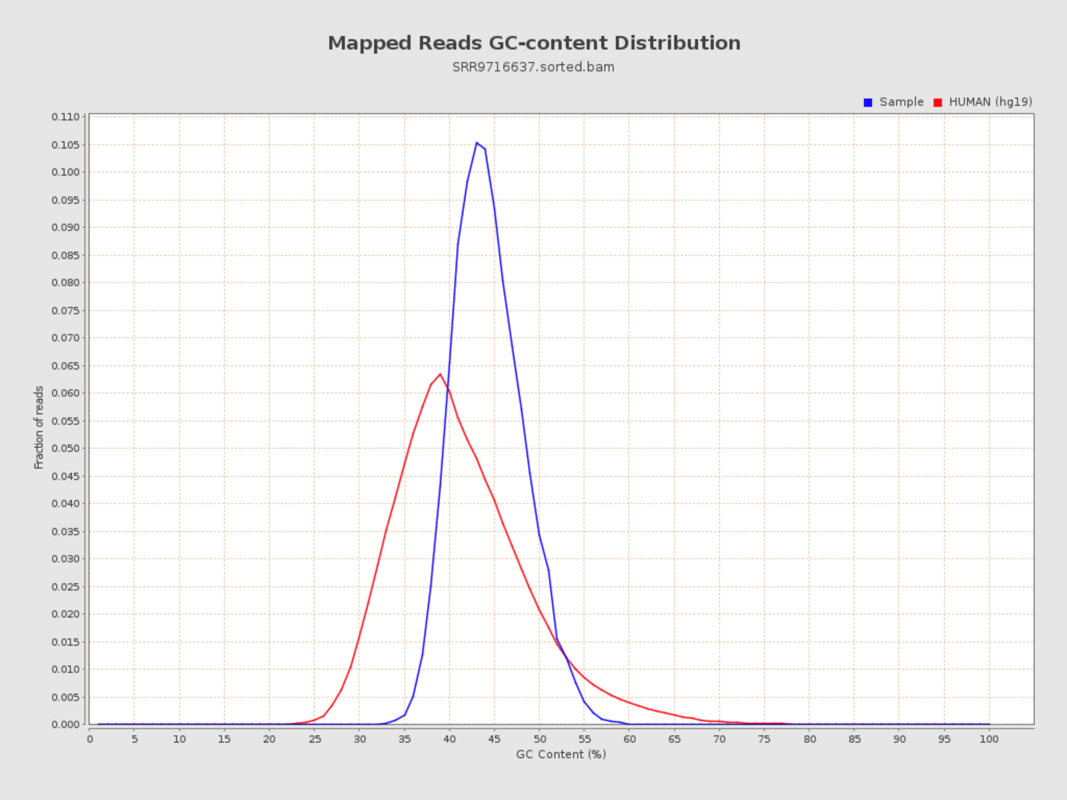
7. Results : Duplication Rate Histogram



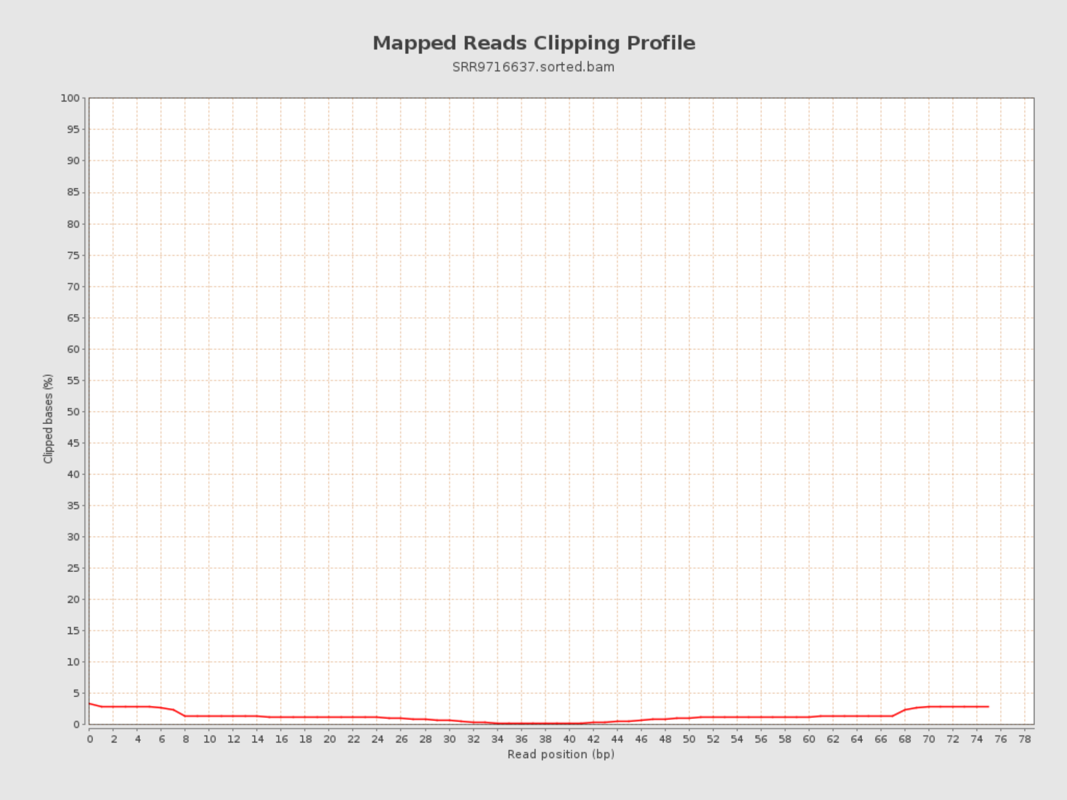
8. Results : Mapped Reads Nucleotide Content



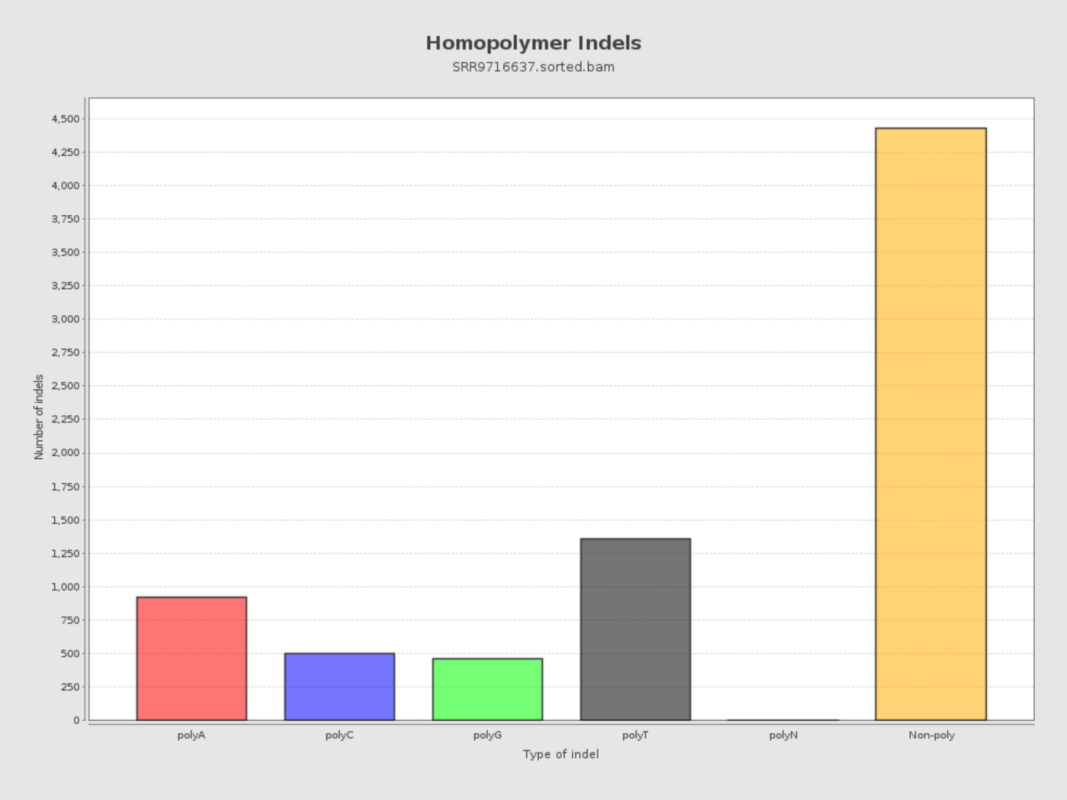
9. Results : Mapped Reads GC-content Distribution



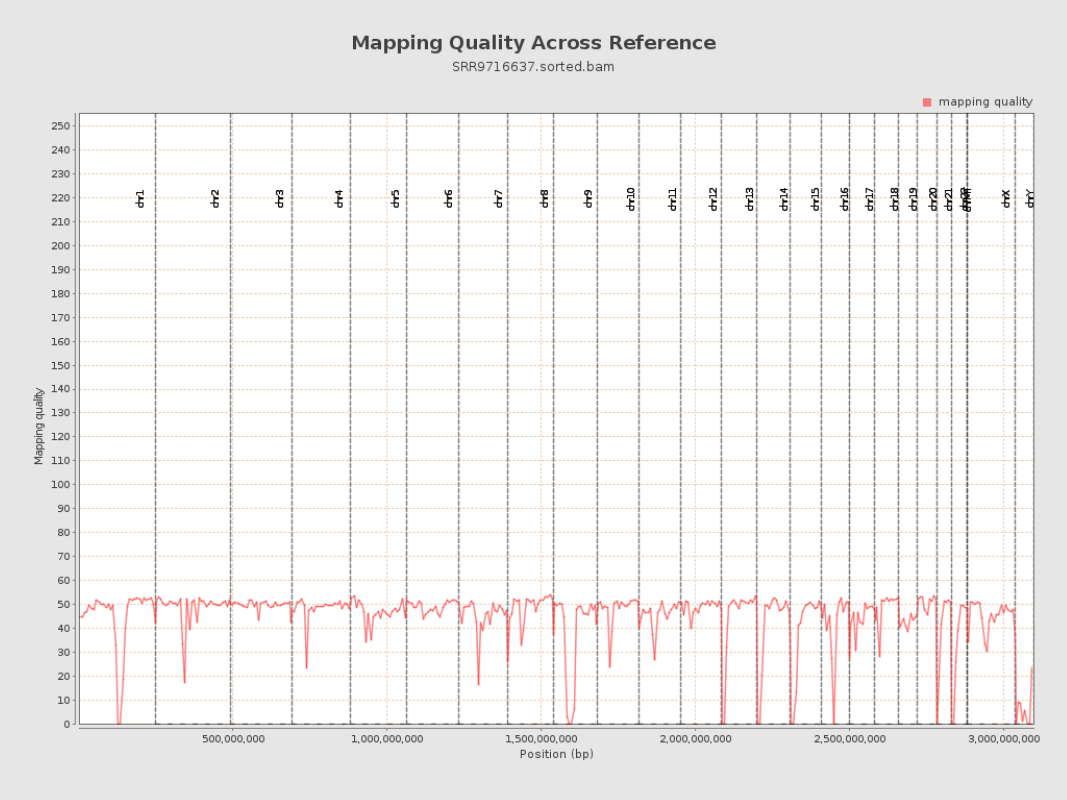
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram