Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:20:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716108.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_SRR9716108 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716108.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:20:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716108.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	717,840
Mapped reads	626,495 / 87.28%
Unmapped reads	91,345 / 12.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,272 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	9,613 / 1.34%
Duplication rate	1.08%
Clipped reads	627,134 / 87.36%

2.2. ACGT Content

Number/percentage of A's	8,917,179 / 25.05%
Number/percentage of C's	6,898,211 / 19.38%
Number/percentage of T's	11,241,995 / 31.58%
Number/percentage of G's	8,538,462 / 23.99%
Number/percentage of N's	266 / 0%
GC Percentage	43.37%

2.3. Coverage

Mean	0.0115

Standard Deviation	0.1291

2.4. Mapping Quality

Mean Mapping Quality	42.08

2.5. Mismatches and indels

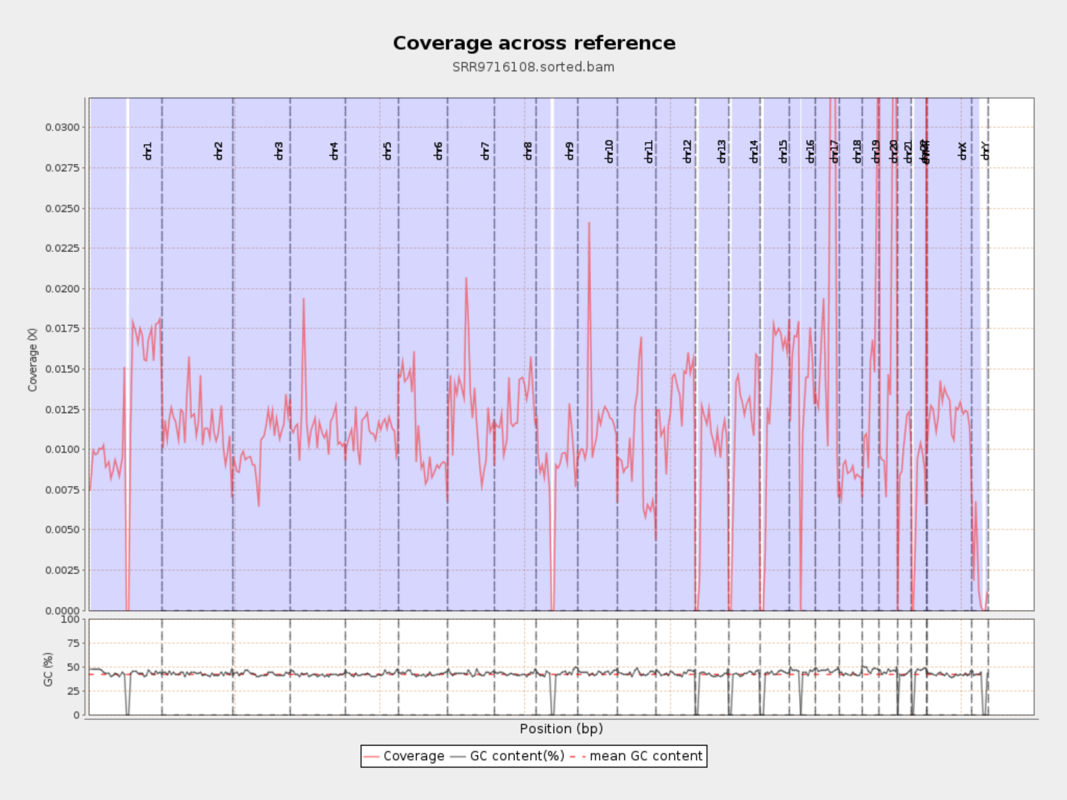
General error rate	0.54%
Mismatches	187,287
Insertions	2,763
Mapped reads with at least one insertion	0.44%
Deletions	6,930
Mapped reads with at least one deletion	1.1%
Homopolymer indels	38.35%

2.6. Chromosome stats

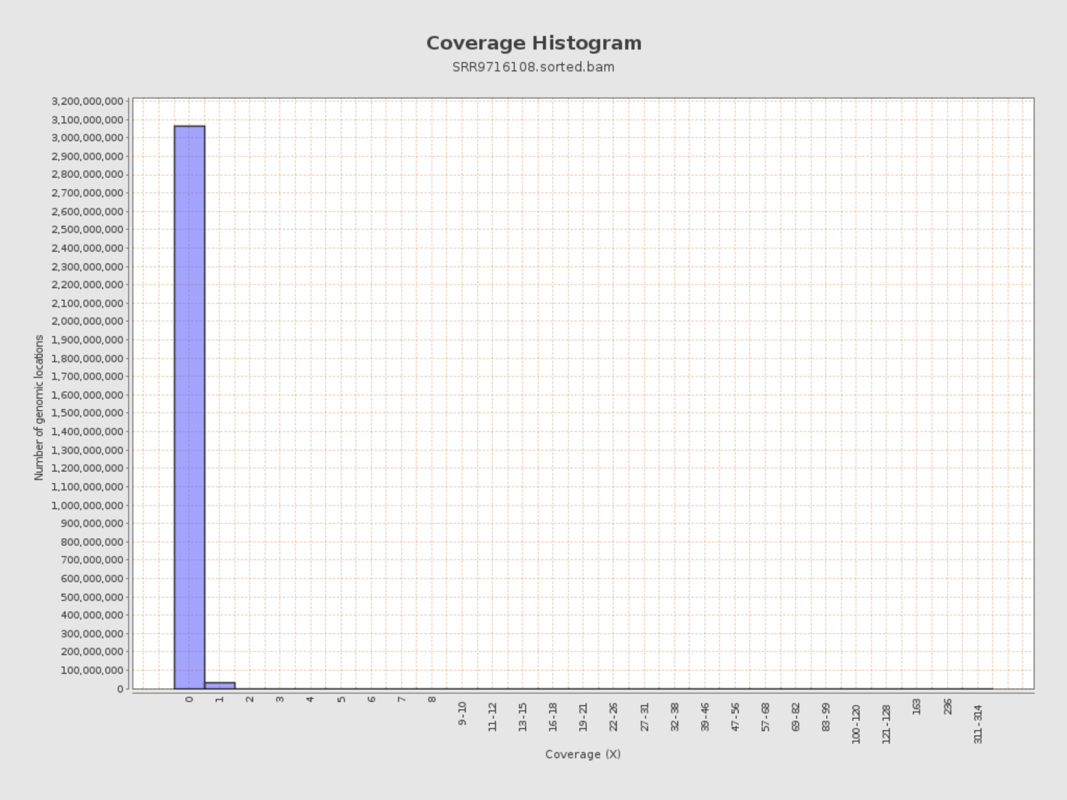
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3012005	0.0121	0.1521
chr2	243199373	2793751	0.0115	0.1699
chr3	198022430	2045410	0.0103	0.1063
chr4	191154276	2179794	0.0114	0.1162
chr5	180915260	2007605	0.0111	0.1089
chr6	171115067	1880905	0.011	0.1168
chr7	159138663	2016019	0.0127	0.1652

chr8	146364022	1838926	0.0126	0.1276
chr9	141213431	1186125	0.0084	0.1006
chr10	135534747	1592937	0.0118	0.1509
chr11	135006516	1262674	0.0094	0.109
chr12	133851895	1754018	0.0131	0.119
chr13	115169878	1076871	0.0094	0.1005
chr14	107349540	1201469	0.0112	0.1111
chr15	102531392	1299593	0.0127	0.1187
chr16	90354753	1256493	0.0139	0.1259
chr17	81195210	1595575	0.0197	0.1492
chr18	78077248	660162	0.0085	0.1383
chr19	59128983	975550	0.0165	0.1591
chr20	63025520	1156766	0.0184	0.1431
chr21	48129895	451679	0.0094	0.1037
chr22	51304566	342464	0.0067	0.0845
chrMT	16571	1258	0.0759	0.3062
chrX	155270560	1905448	0.0123	0.1181
chrY	59373566	113687	0.0019	0.067

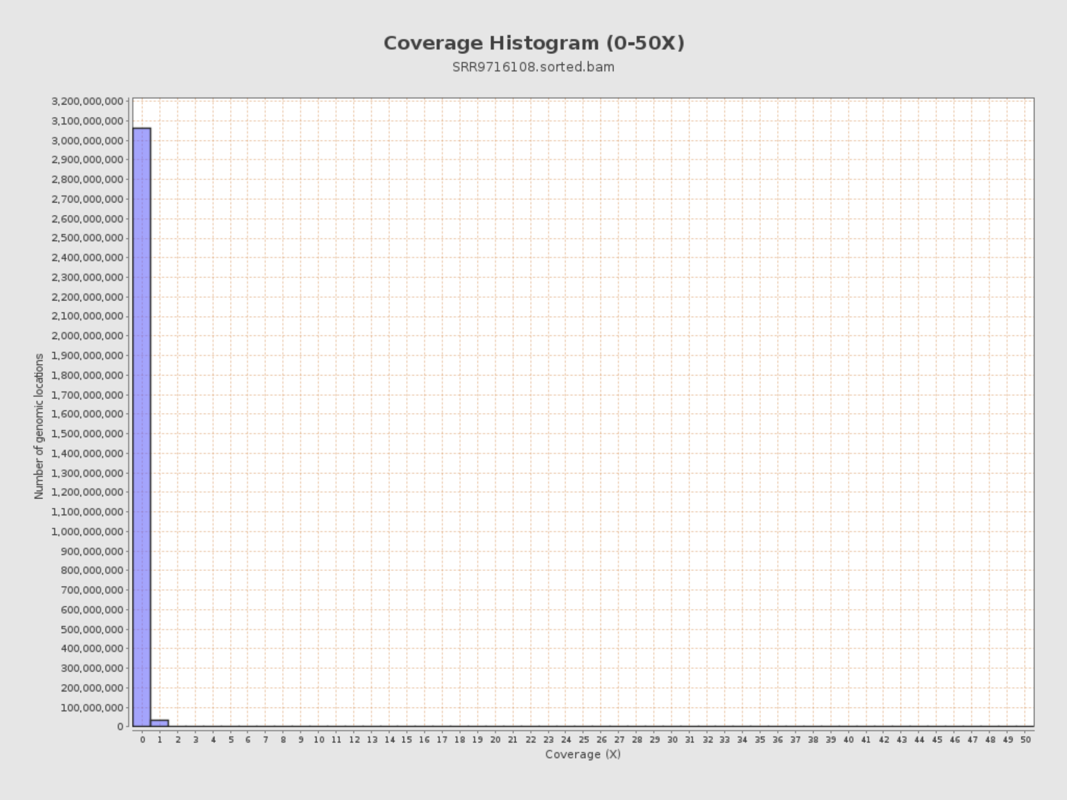
3. Results : Coverage across reference



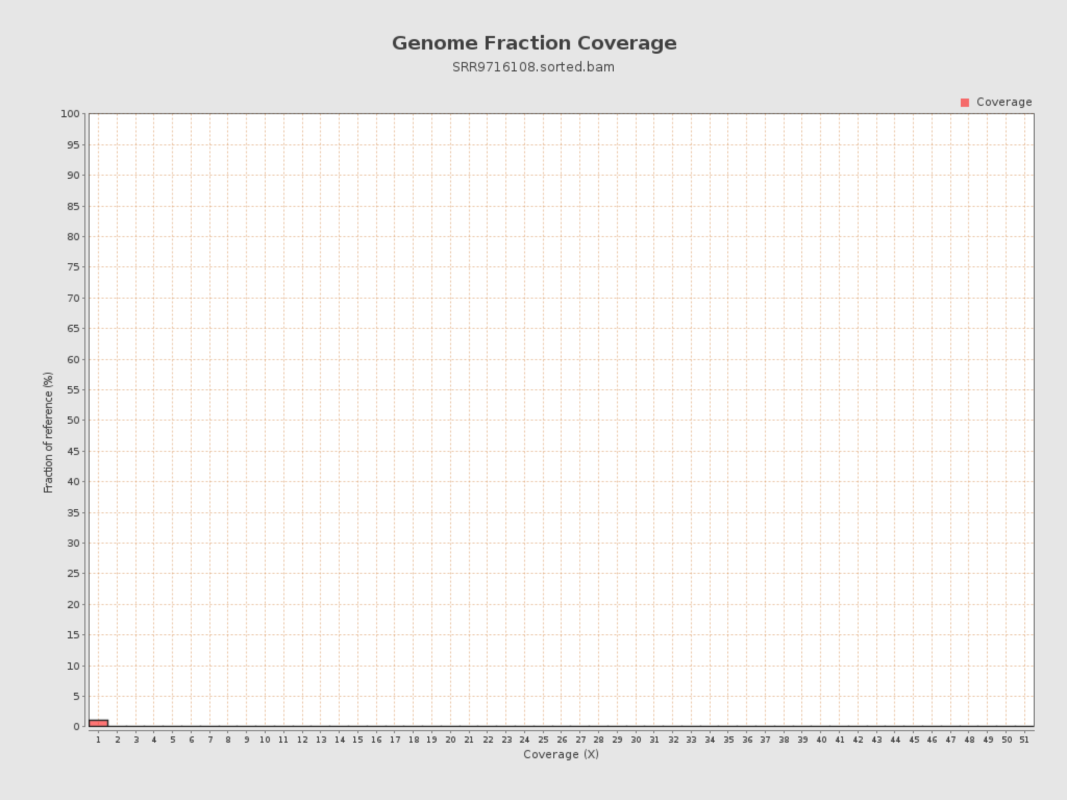
4. Results : Coverage Histogram



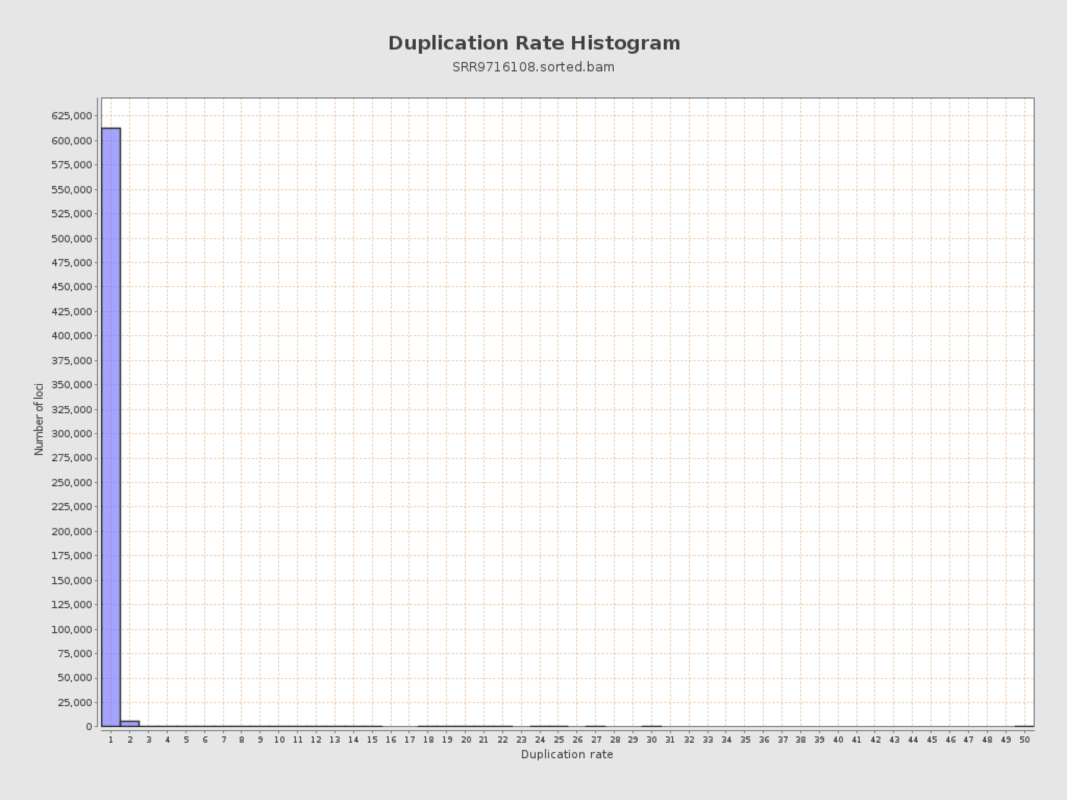
5. Results : Coverage Histogram (0-50X)



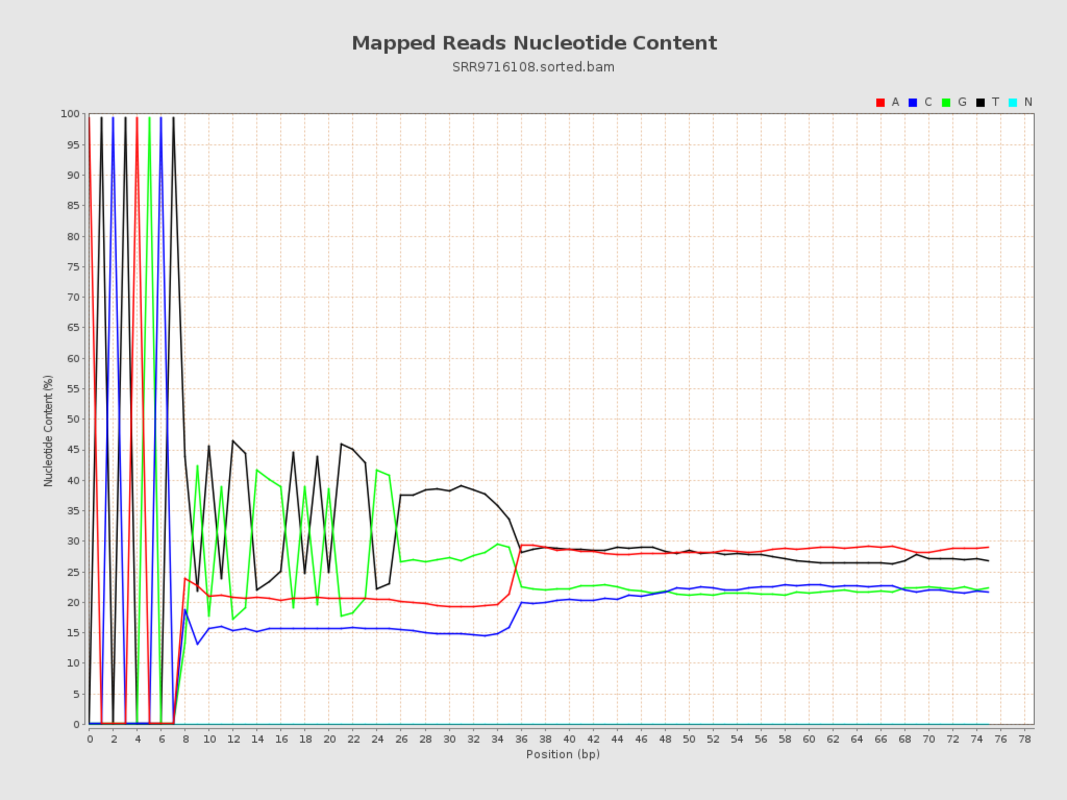
6. Results : Genome Fraction Coverage



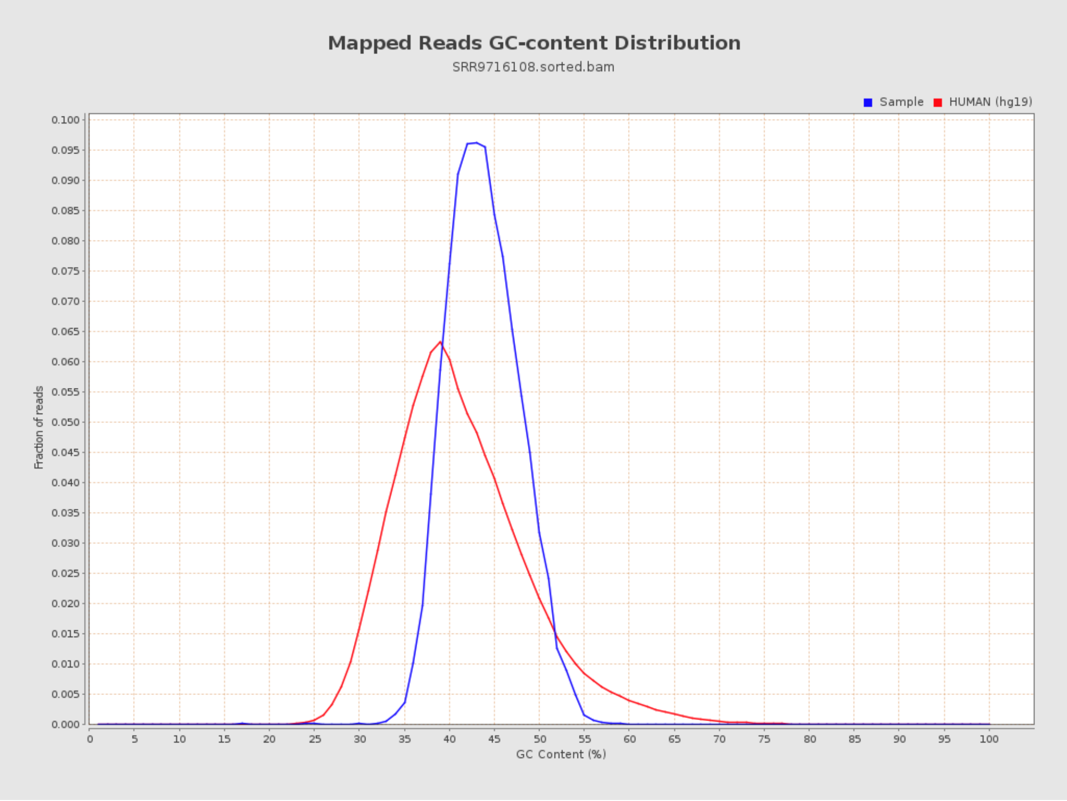
7. Results : Duplication Rate Histogram



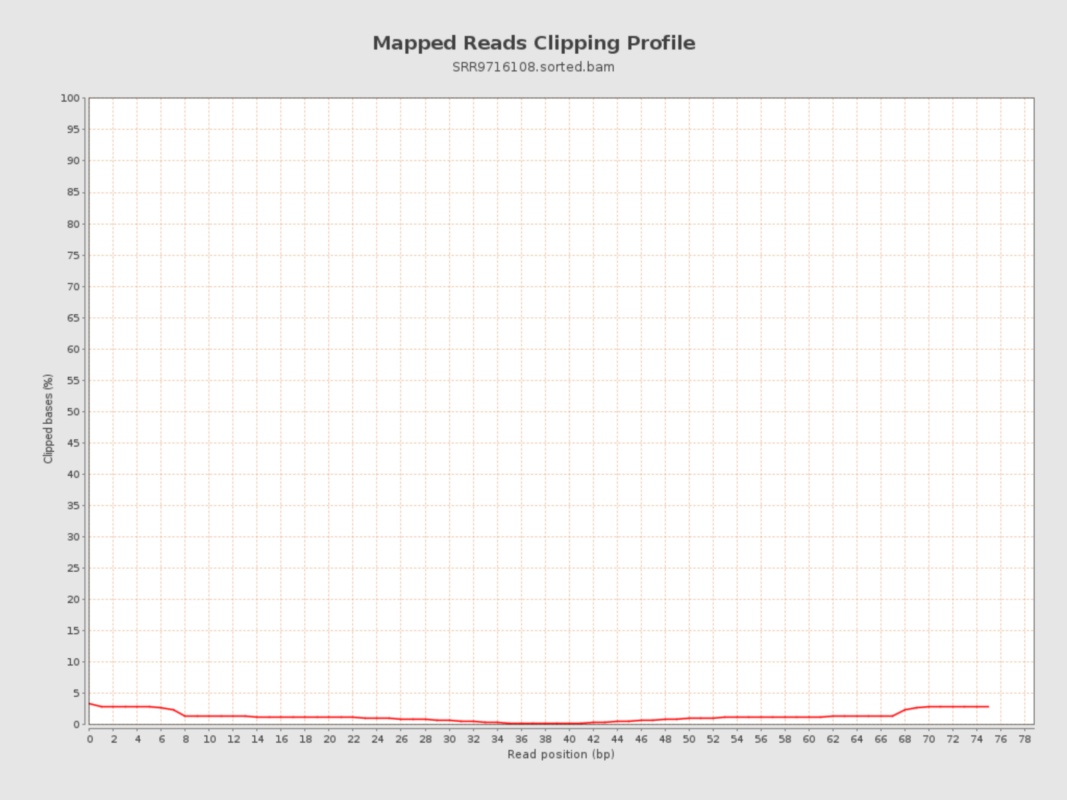
8. Results : Mapped Reads Nucleotide Content



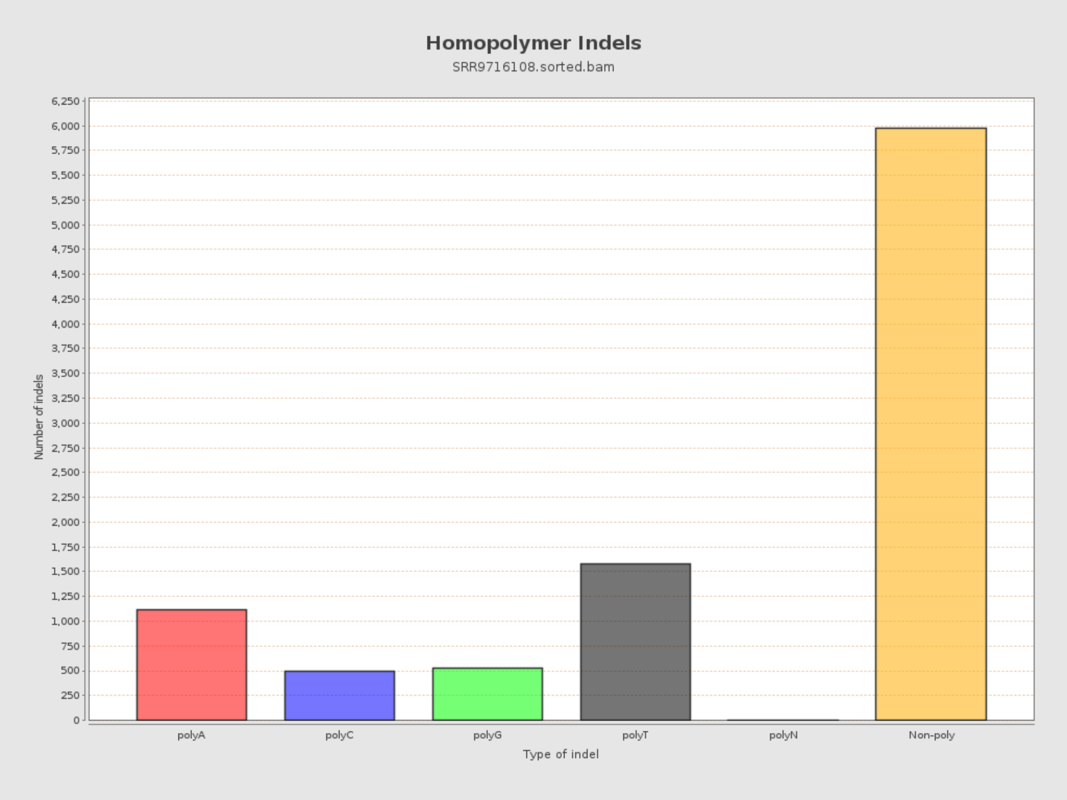
9. Results : Mapped Reads GC-content Distribution



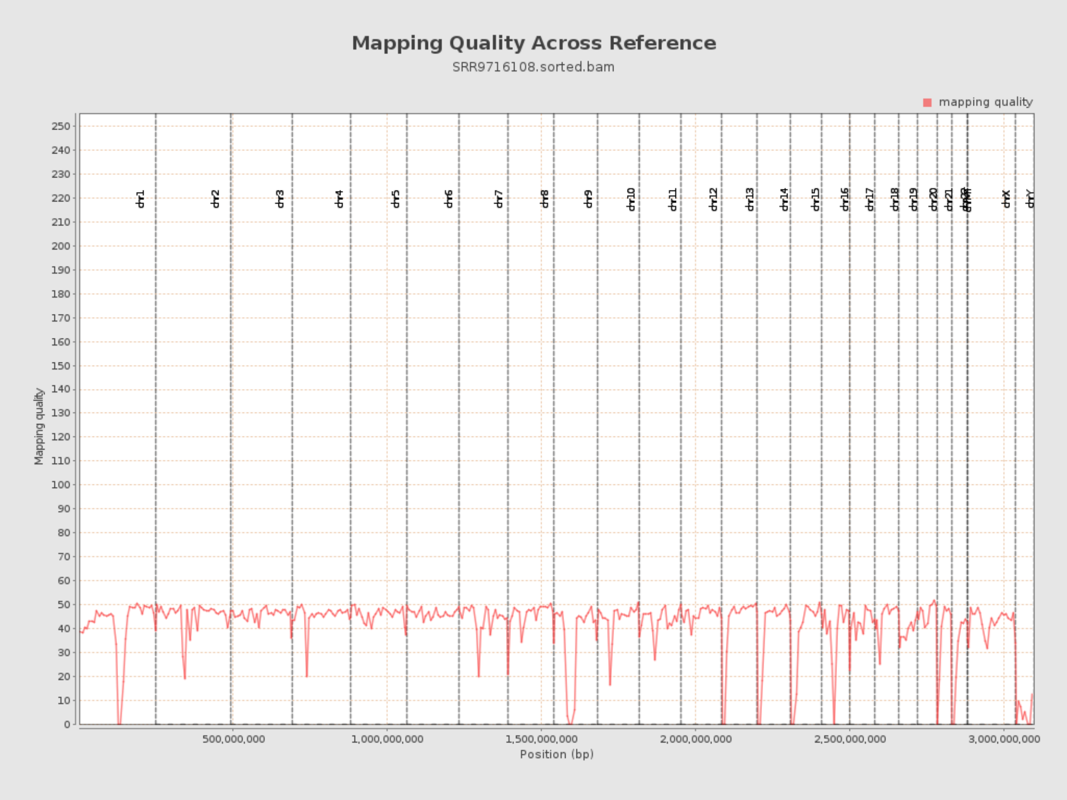
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram