Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 04:53:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716275.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_SRR9716275 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716275.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 04:53:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716275.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,380,924
Mapped reads	715,869 / 51.84%
Unmapped reads	665,055 / 48.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,642 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	25,317 / 1.83%
Duplication rate	2.91%
Clipped reads	715,812 / 51.84%

2.2. ACGT Content

Number/percentage of A's	10,274,188 / 24.65%
Number/percentage of C's	8,544,378 / 20.5%
Number/percentage of T's	13,294,875 / 31.9%
Number/percentage of G's	9,558,514 / 22.94%
Number/percentage of N's	1,143 / 0%
GC Percentage	43.44%

2.3. Coverage

Mean	0.0135

Standard Deviation	0.1491

2.4. Mapping Quality

Mean Mapping Quality	45.25

2.5. Mismatches and indels

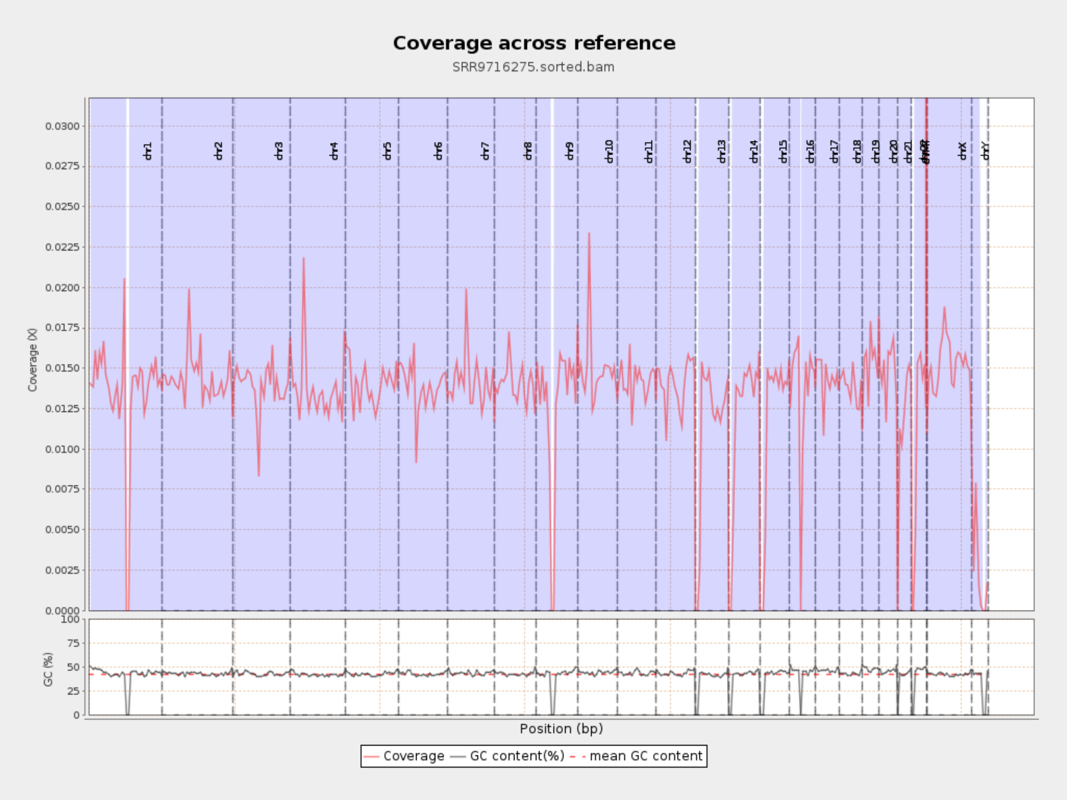
General error rate	0.51%
Mismatches	204,035
Insertions	3,611
Mapped reads with at least one insertion	0.5%
Deletions	7,744
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41.6%

2.6. Chromosome stats

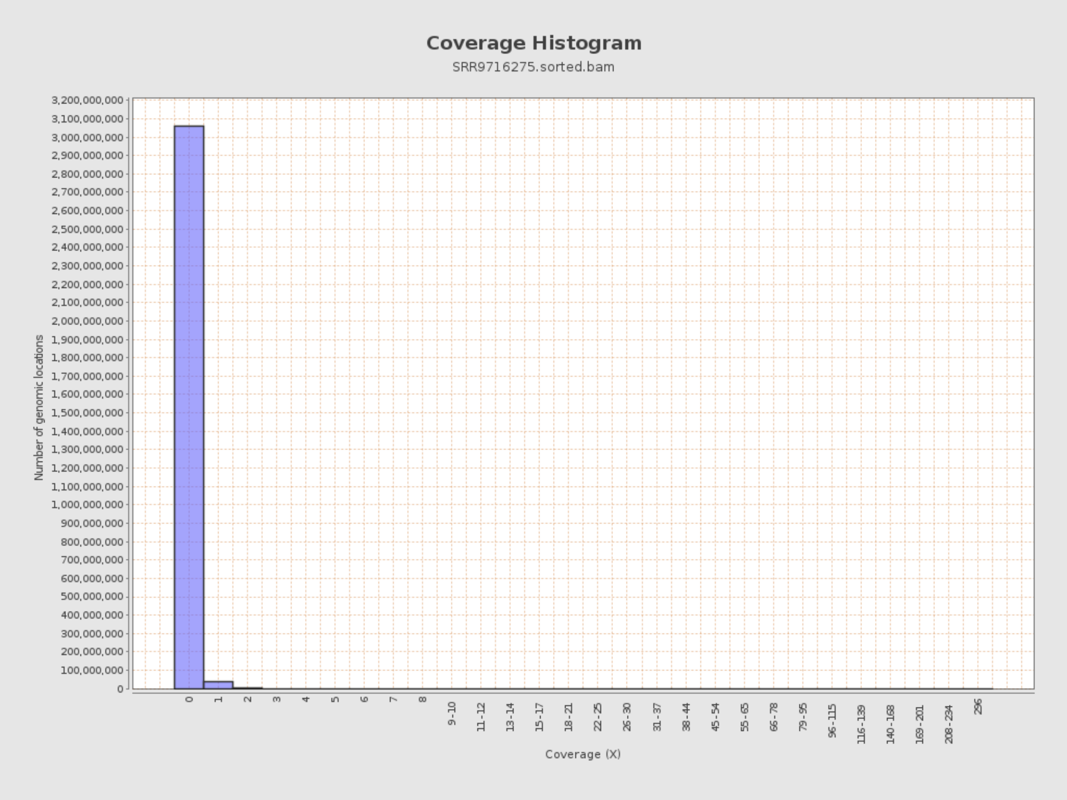
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3361797	0.0135	0.2177
chr2	243199373	3509743	0.0144	0.1823
chr3	198022430	2741680	0.0138	0.1262
chr4	191154276	2608218	0.0136	0.1312
chr5	180915260	2531979	0.014	0.1276
chr6	171115067	2378370	0.0139	0.1369
chr7	159138663	2276590	0.0143	0.1707

chr8	146364022	2054534	0.014	0.1493
chr9	141213431	1761722	0.0125	0.136
chr10	135534747	2015993	0.0149	0.1546
chr11	135006516	1915636	0.0142	0.1406
chr12	133851895	1880590	0.014	0.1284
chr13	115169878	1286321	0.0112	0.1146
chr14	107349540	1255997	0.0117	0.1178
chr15	102531392	1189764	0.0116	0.1161
chr16	90354753	1219672	0.0135	0.1287
chr17	81195210	1165959	0.0144	0.1326
chr18	78077248	1085295	0.0139	0.1893
chr19	59128983	910029	0.0154	0.1734
chr20	63025520	933927	0.0148	0.1333
chr21	48129895	560328	0.0116	0.1223
chr22	51304566	532237	0.0104	0.1096
chrMT	16571	8089	0.4881	0.7604
chrX	155270560	2361629	0.0152	0.1399
chrY	59373566	139358	0.0023	0.0717

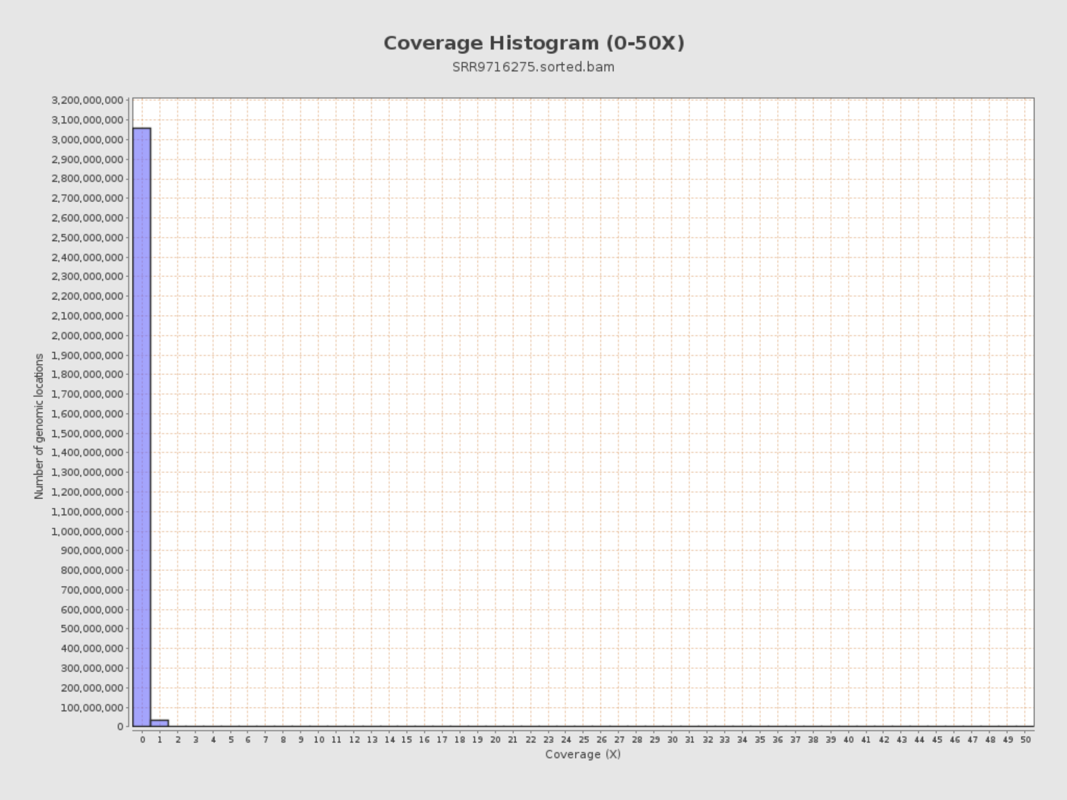
3. Results : Coverage across reference



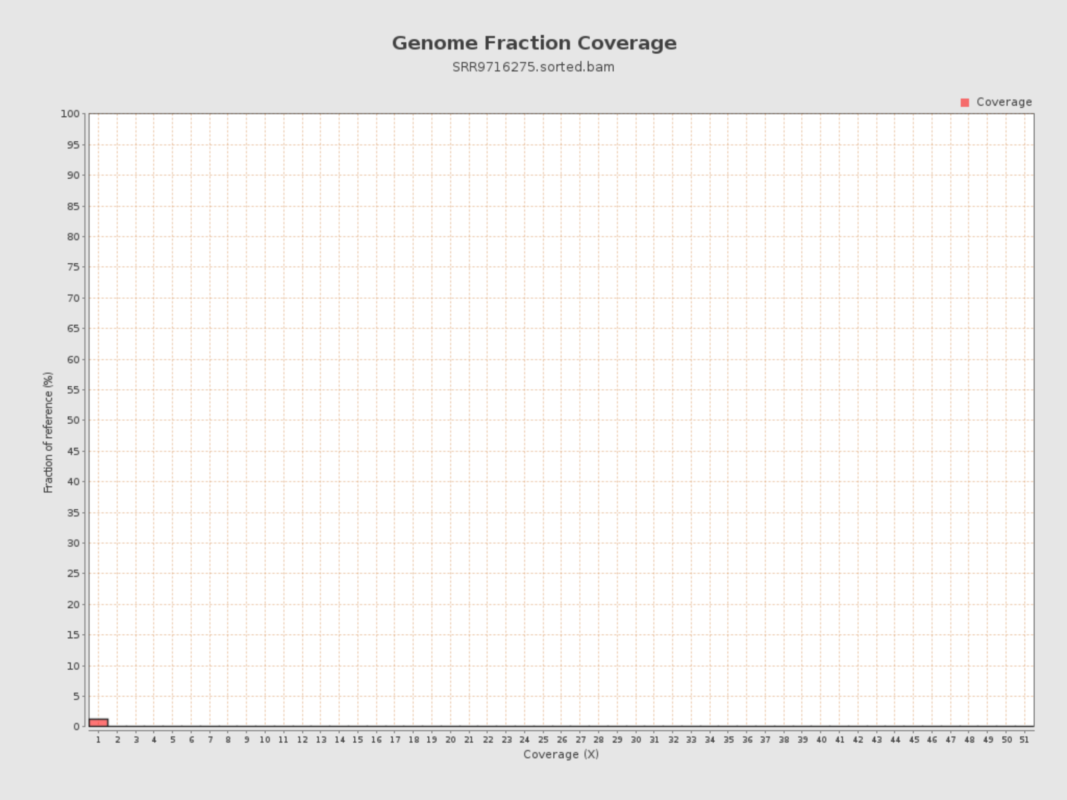
4. Results : Coverage Histogram



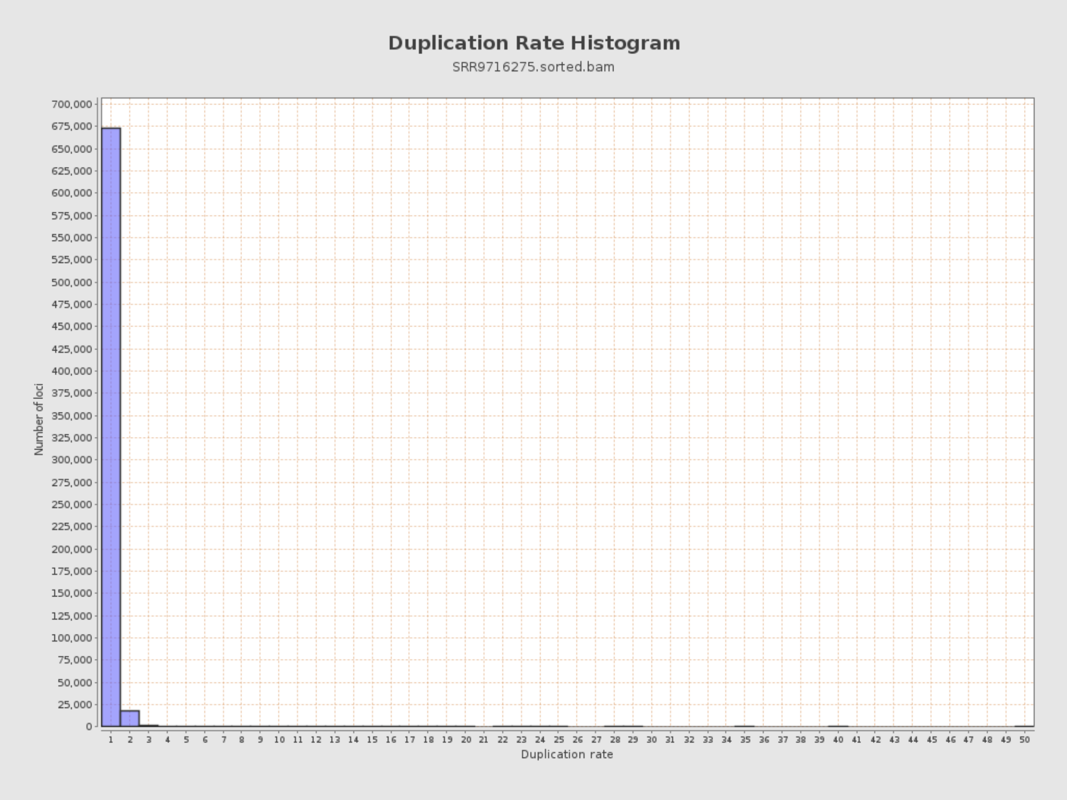
5. Results : Coverage Histogram (0-50X)



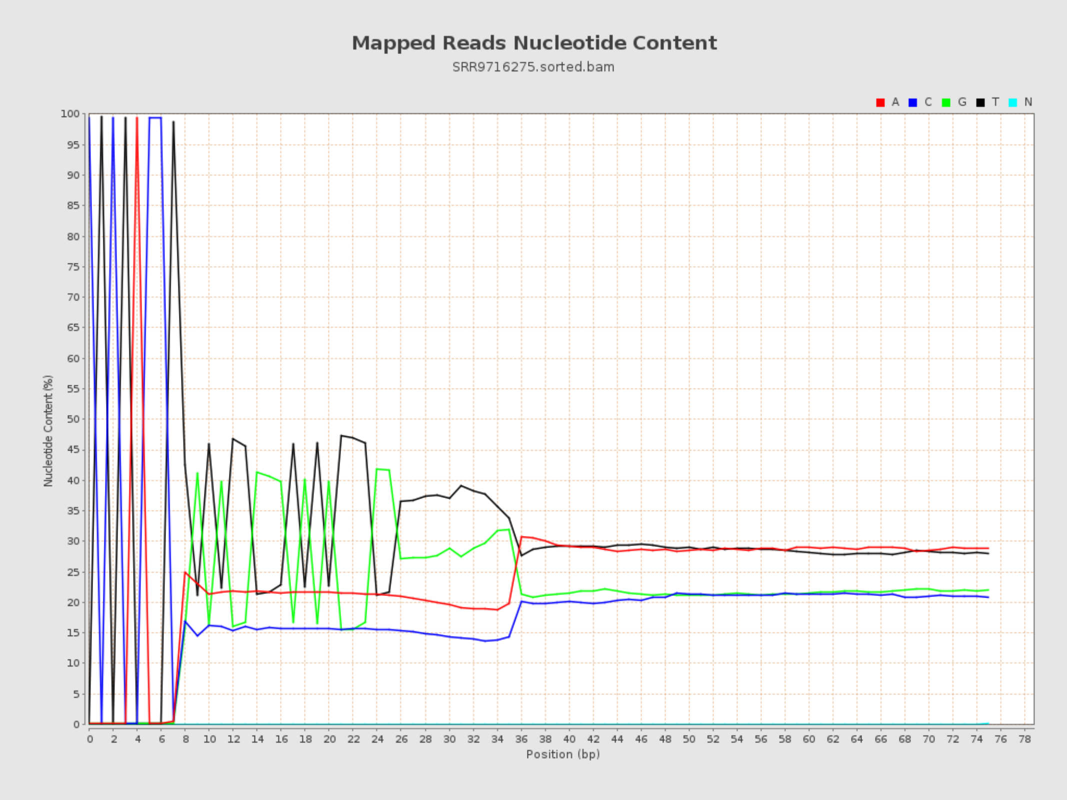
6. Results : Genome Fraction Coverage



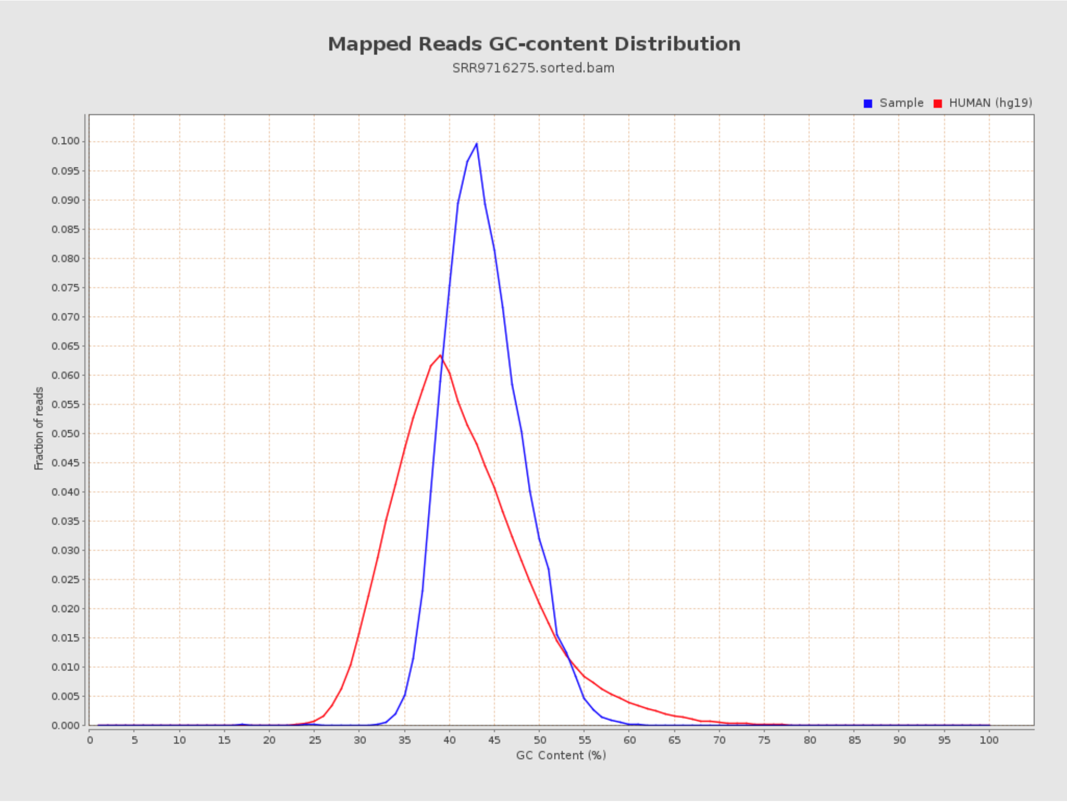
7. Results : Duplication Rate Histogram



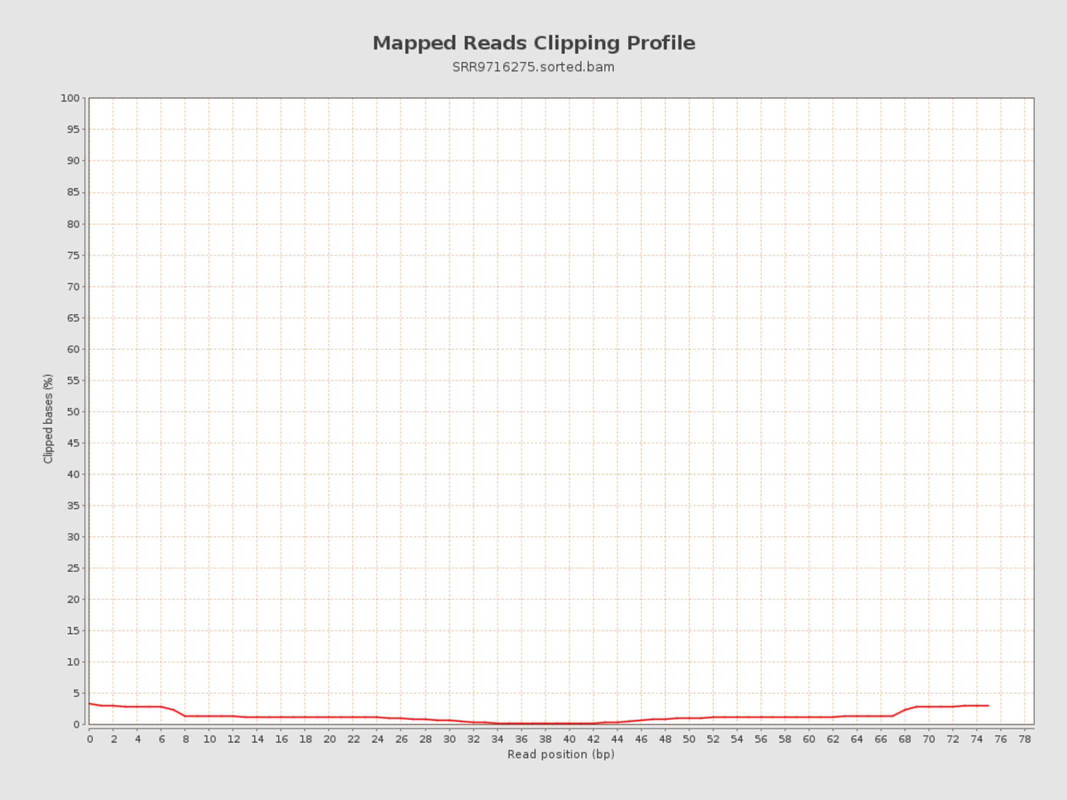
8. Results : Mapped Reads Nucleotide Content



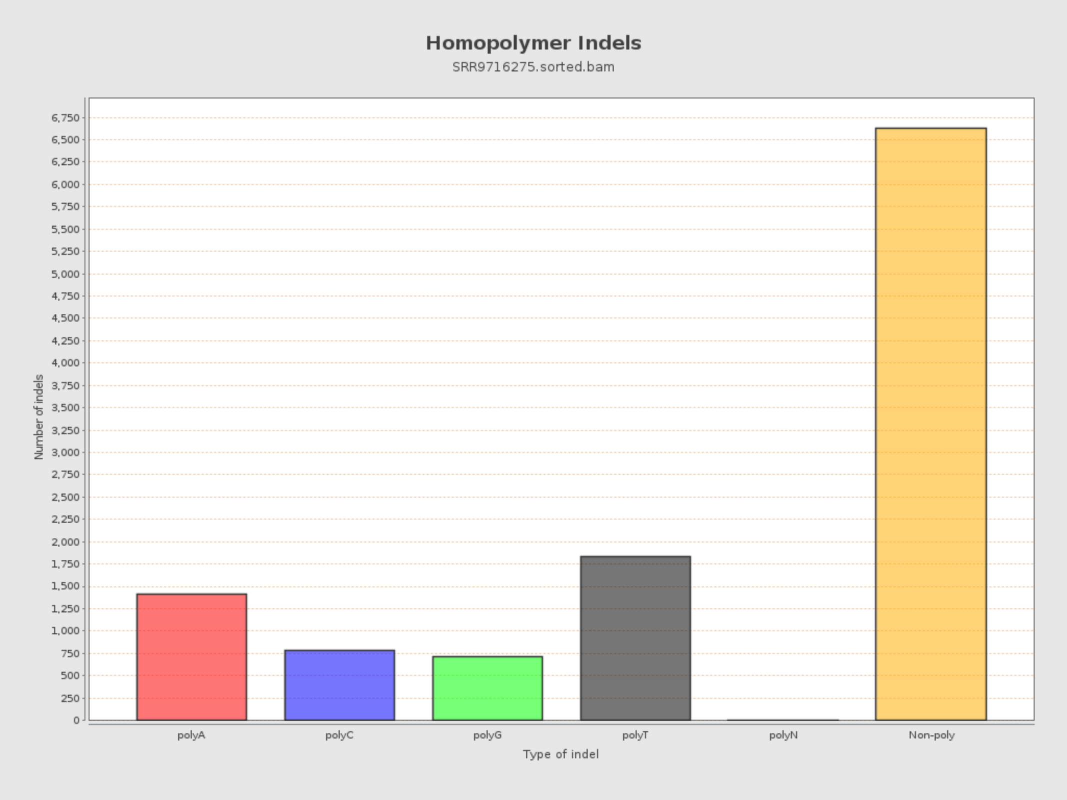
9. Results : Mapped Reads GC-content Distribution



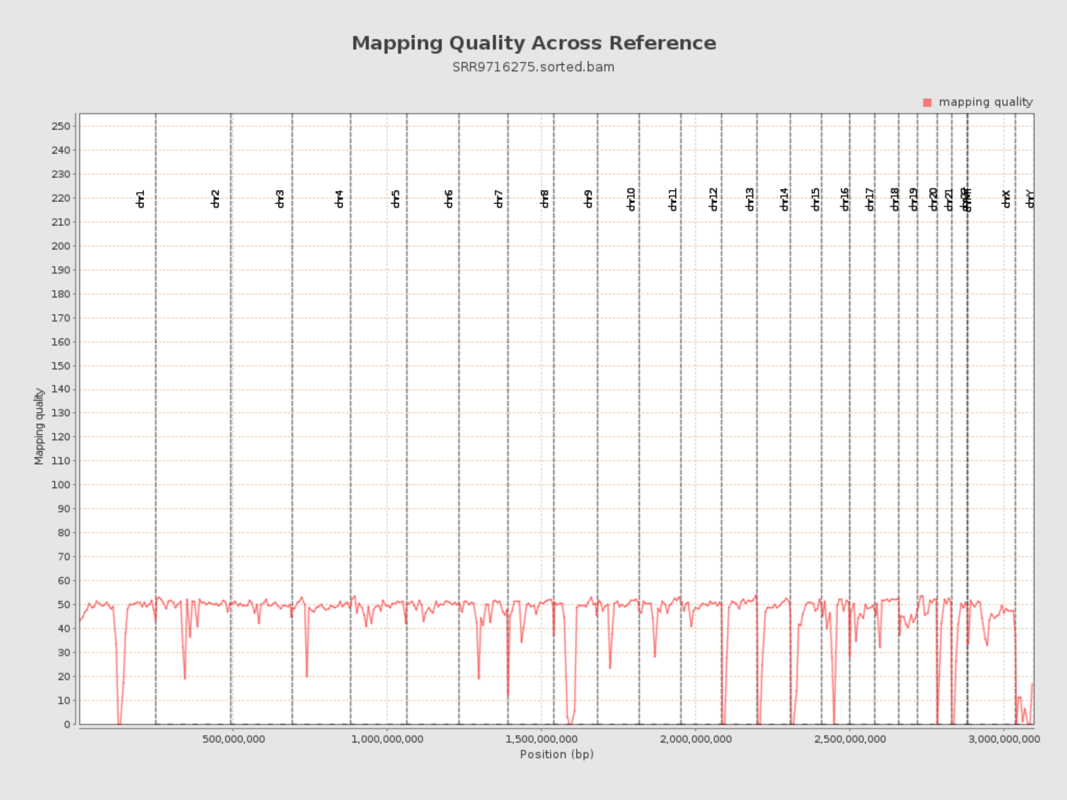
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram