Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:48:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716948.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_SRR9716948 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716948.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:48:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716948.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,241,837
Mapped reads	1,053,862 / 84.86%
Unmapped reads	187,975 / 15.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,200 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	29,566 / 2.38%
Duplication rate	2.05%
Clipped reads	1,056,994 / 85.12%

2.2. ACGT Content

Number/percentage of A's	15,035,811 / 24.76%
Number/percentage of C's	11,632,056 / 19.16%
Number/percentage of T's	19,221,619 / 31.66%
Number/percentage of G's	14,827,658 / 24.42%
Number/percentage of N's	811 / 0%
GC Percentage	43.58%

2.3. Coverage

Mean	0.0196

Standard Deviation	0.2137

2.4. Mapping Quality

Mean Mapping Quality	43.93

2.5. Mismatches and indels

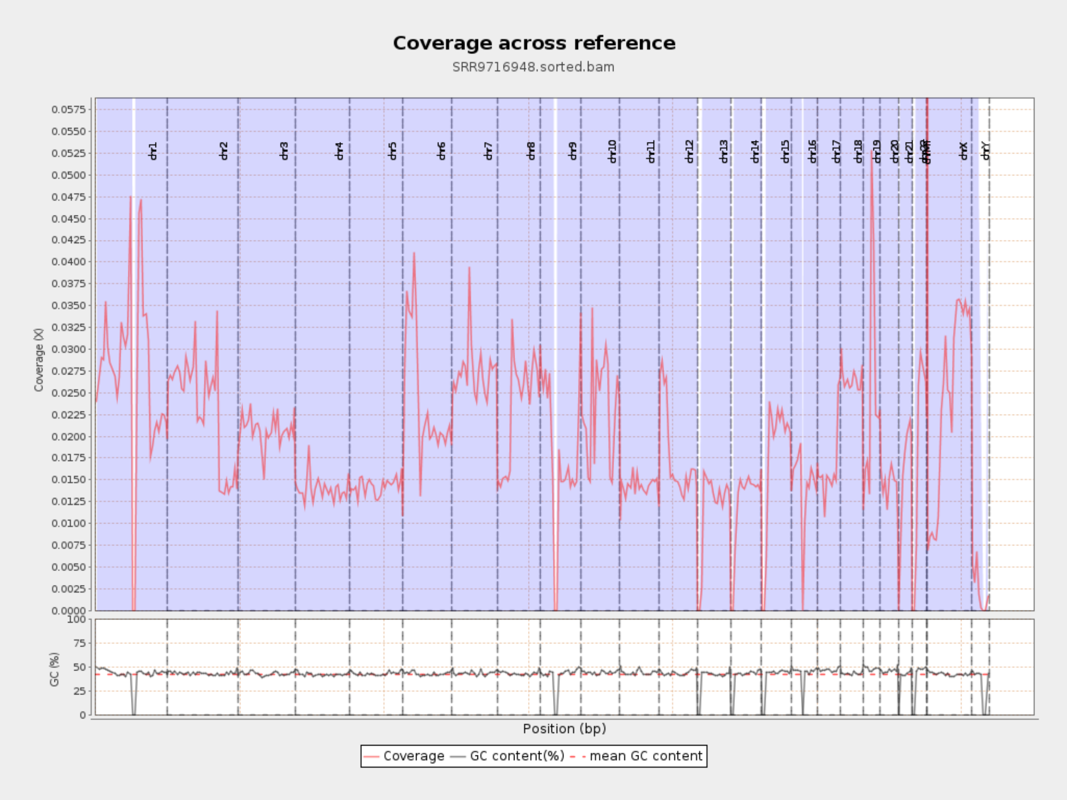
General error rate	0.51%
Mismatches	301,377
Insertions	3,901
Mapped reads with at least one insertion	0.37%
Deletions	10,449
Mapped reads with at least one deletion	0.99%
Homopolymer indels	42.93%

2.6. Chromosome stats

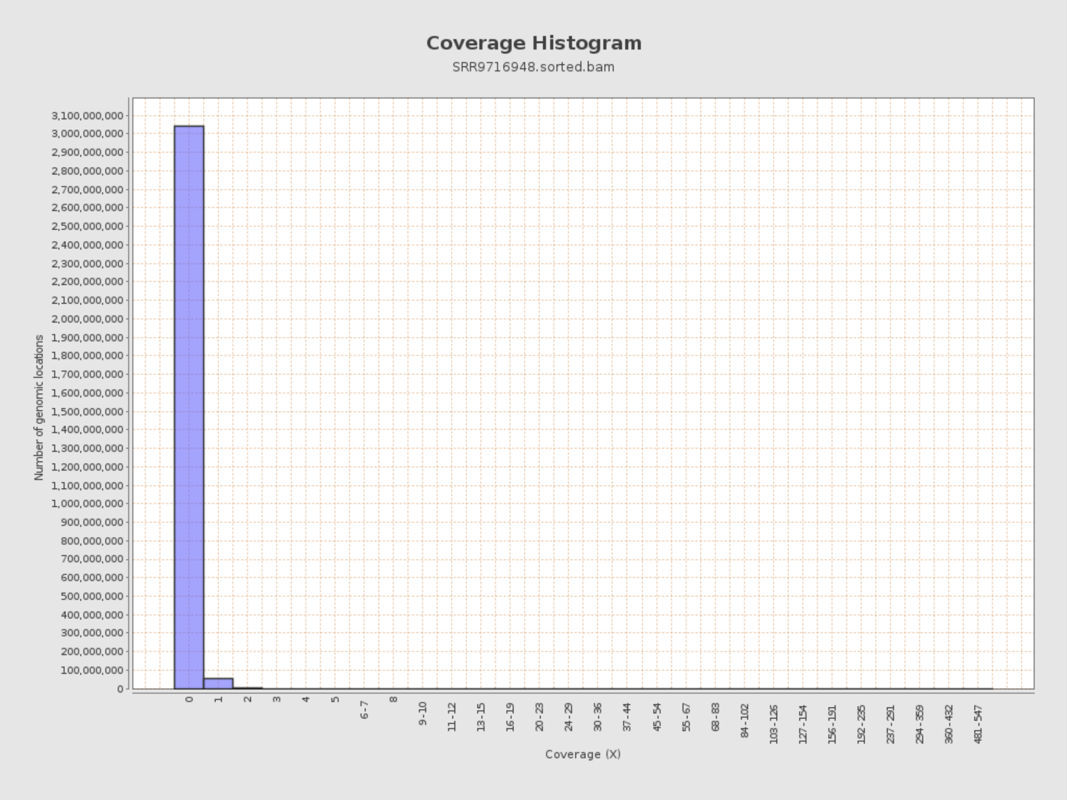
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6739081	0.027	0.4317
chr2	243199373	5633659	0.0232	0.2683
chr3	198022430	4095984	0.0207	0.1531
chr4	191154276	2672430	0.014	0.1311
chr5	180915260	2584236	0.0143	0.1293
chr6	171115067	4074218	0.0238	0.1786
chr7	159138663	4381026	0.0275	0.282

chr8	146364022	3420812	0.0234	0.1797
chr9	141213431	2453428	0.0174	0.1706
chr10	135534747	3154239	0.0233	0.1945
chr11	135006516	1937638	0.0144	0.1638
chr12	133851895	2404258	0.018	0.145
chr13	115169878	1332442	0.0116	0.1147
chr14	107349540	1295477	0.0121	0.1255
chr15	102531392	1795933	0.0175	0.1436
chr16	90354753	1266482	0.014	0.1338
chr17	81195210	1333436	0.0164	0.1389
chr18	78077248	2072113	0.0265	0.2819
chr19	59128983	1527872	0.0258	0.2781
chr20	63025520	914700	0.0145	0.1296
chr21	48129895	749127	0.0156	0.1372
chr22	51304566	952016	0.0186	0.1448
chrMT	16571	44202	2.6674	2.0047
chrX	155270560	3765473	0.0243	0.1814
chrY	59373566	134251	0.0023	0.0624

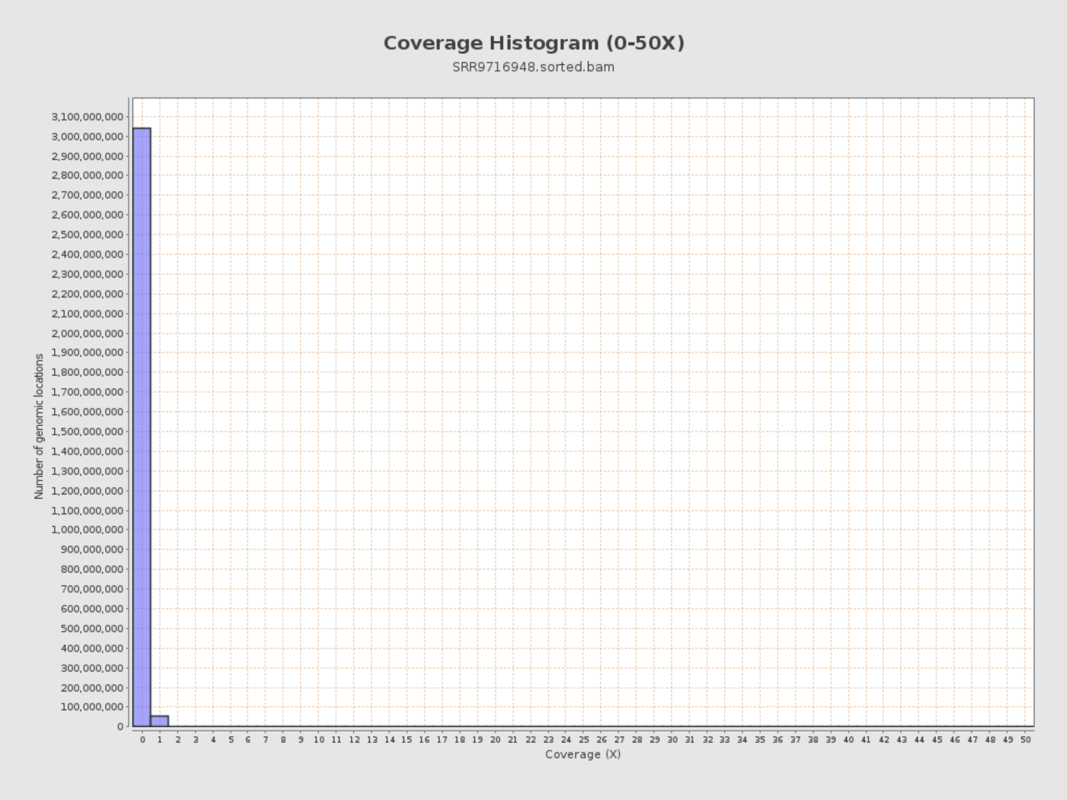
3. Results : Coverage across reference



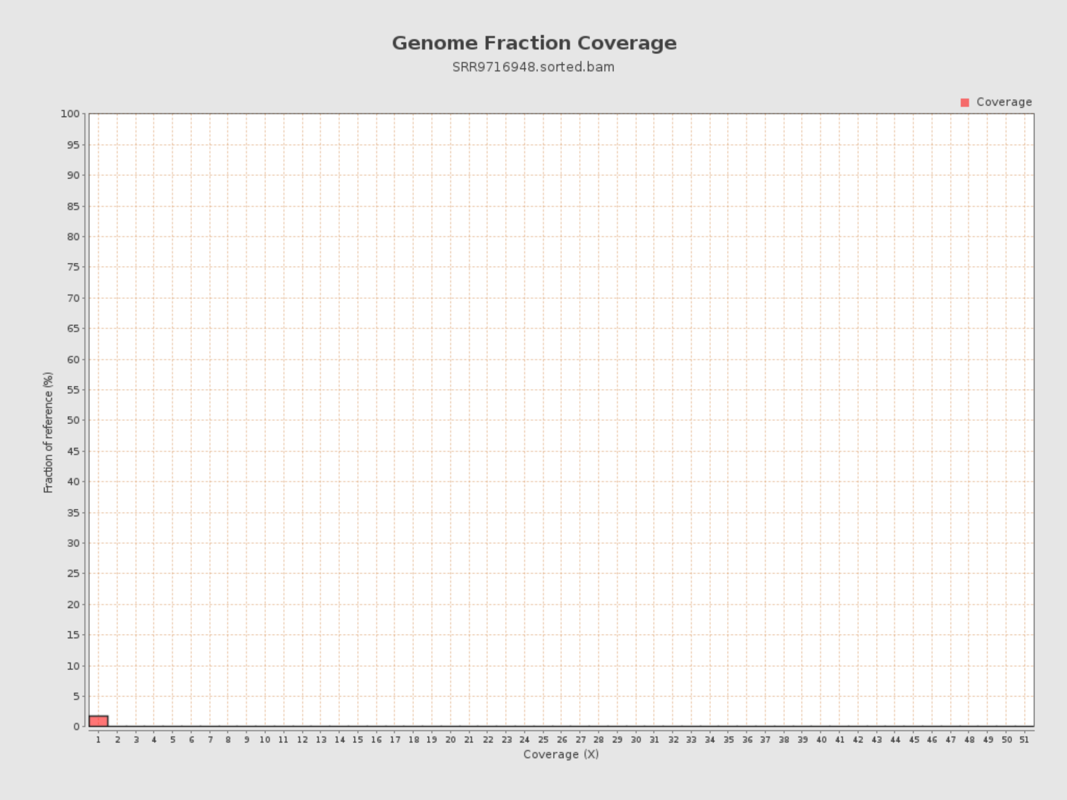
4. Results : Coverage Histogram



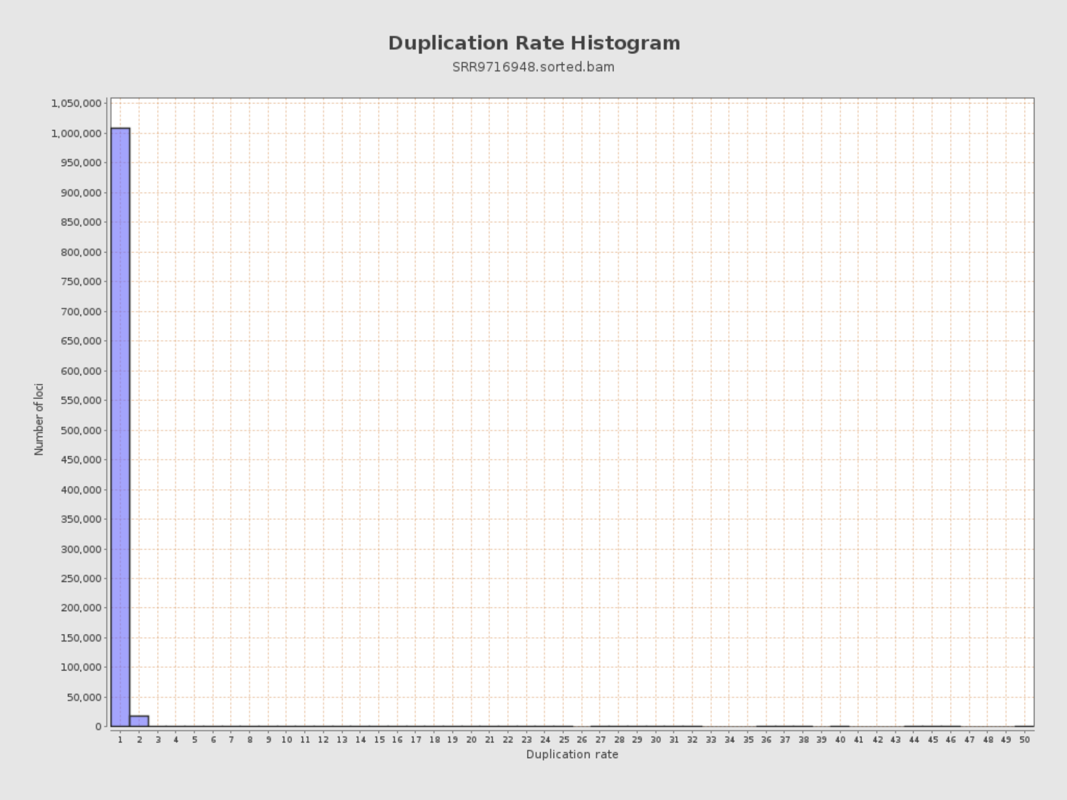
5. Results : Coverage Histogram (0-50X)



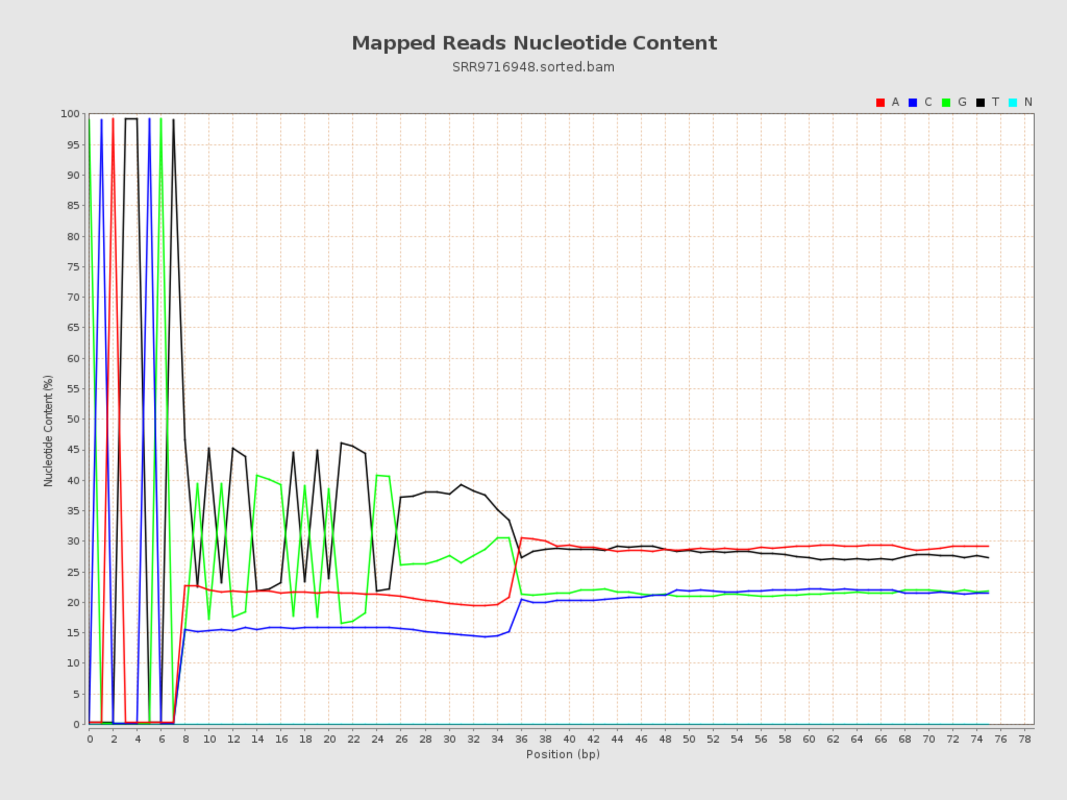
6. Results : Genome Fraction Coverage



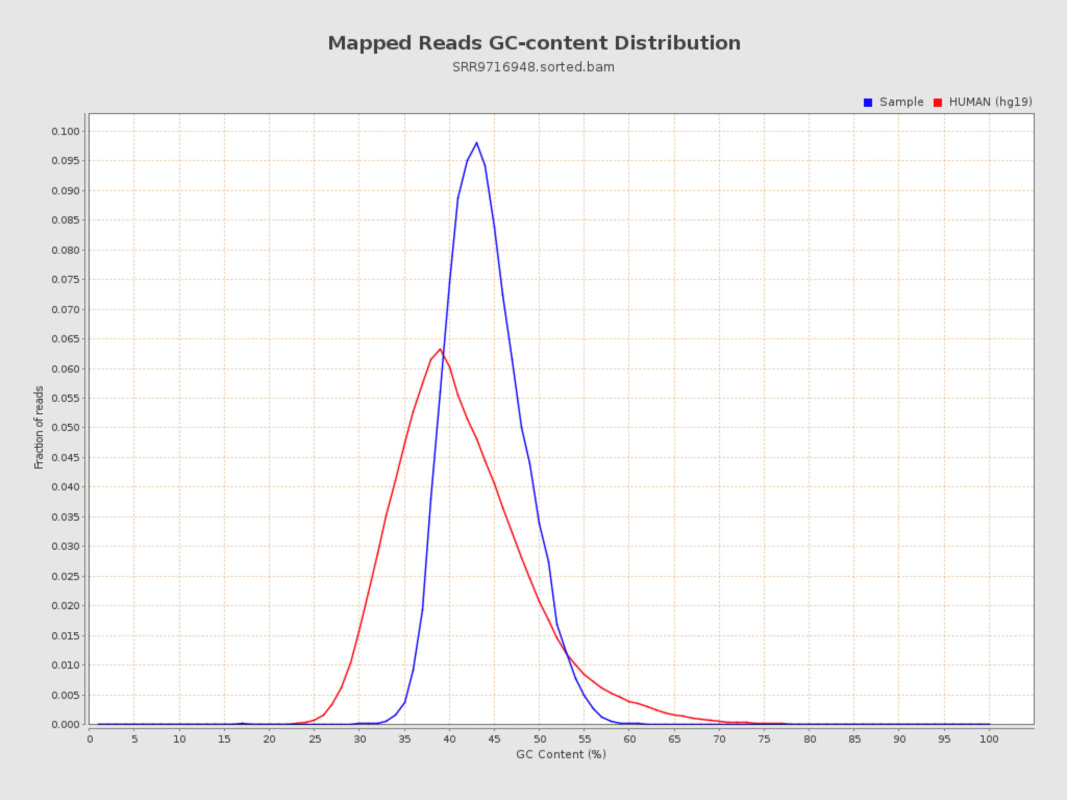
7. Results : Duplication Rate Histogram



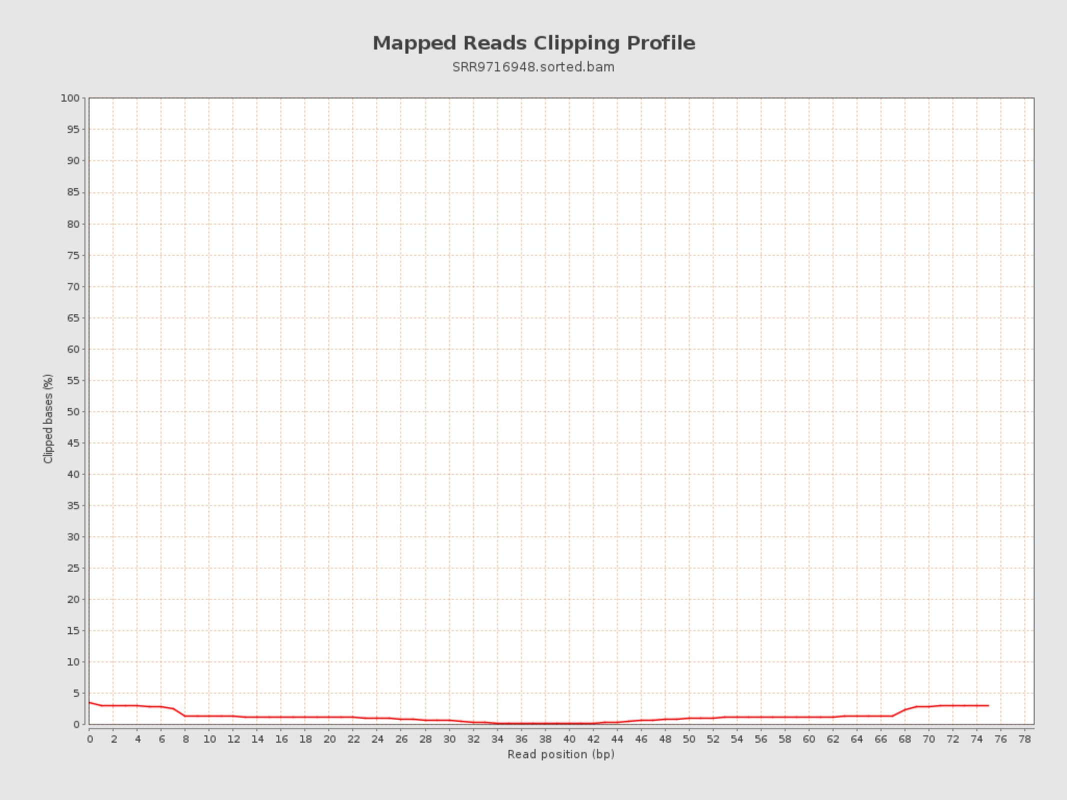
8. Results : Mapped Reads Nucleotide Content



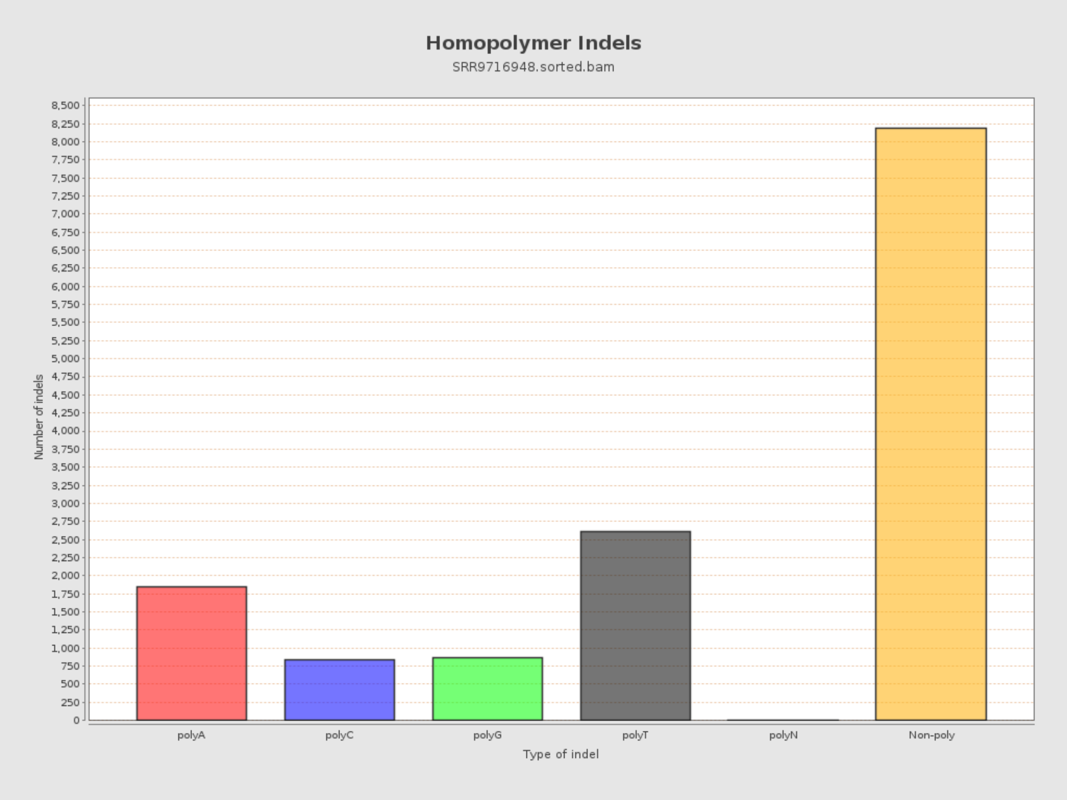
9. Results : Mapped Reads GC-content Distribution



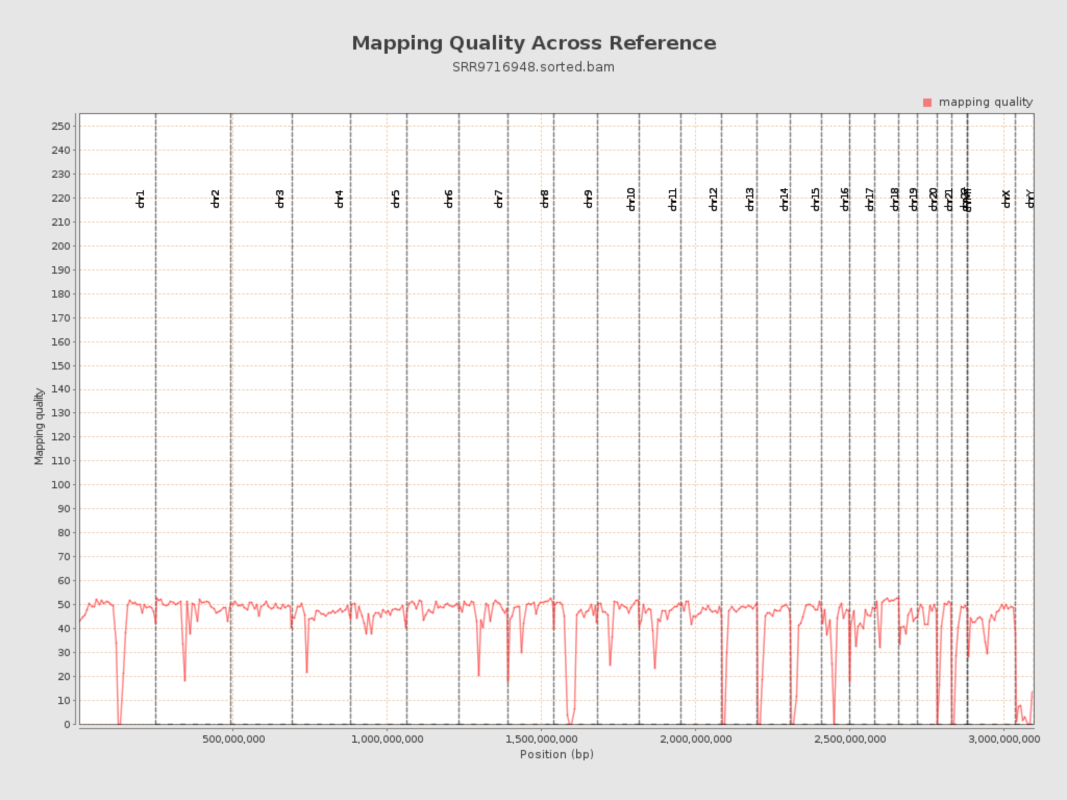
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram