Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 16:10:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716876.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_SRR9716876 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716876.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 16:10:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716876.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	831,982
Mapped reads	757,996 / 91.11%
Unmapped reads	73,986 / 8.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,401 / 0.17%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	19,911 / 2.39%
Duplication rate	2.02%
Clipped reads	757,945 / 91.1%

2.2. ACGT Content

Number/percentage of A's	10,565,246 / 24.33%
Number/percentage of C's	8,297,784 / 19.11%
Number/percentage of T's	13,889,625 / 31.99%
Number/percentage of G's	10,672,244 / 24.58%
Number/percentage of N's	435 / 0%
GC Percentage	43.68%

2.3. Coverage

Mean	0.014

Standard Deviation	0.1545

2.4. Mapping Quality

Mean Mapping Quality	44.57

2.5. Mismatches and indels

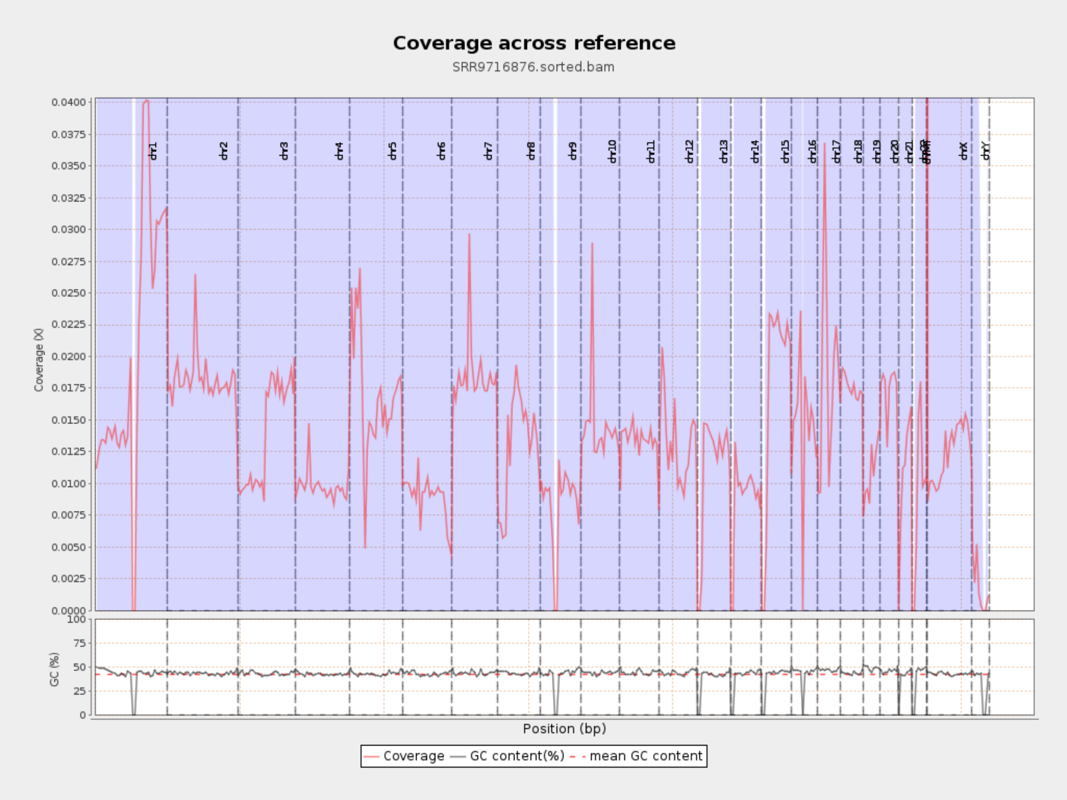
General error rate	0.49%
Mismatches	210,024
Insertions	2,754
Mapped reads with at least one insertion	0.36%
Deletions	8,505
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.4%

2.6. Chromosome stats

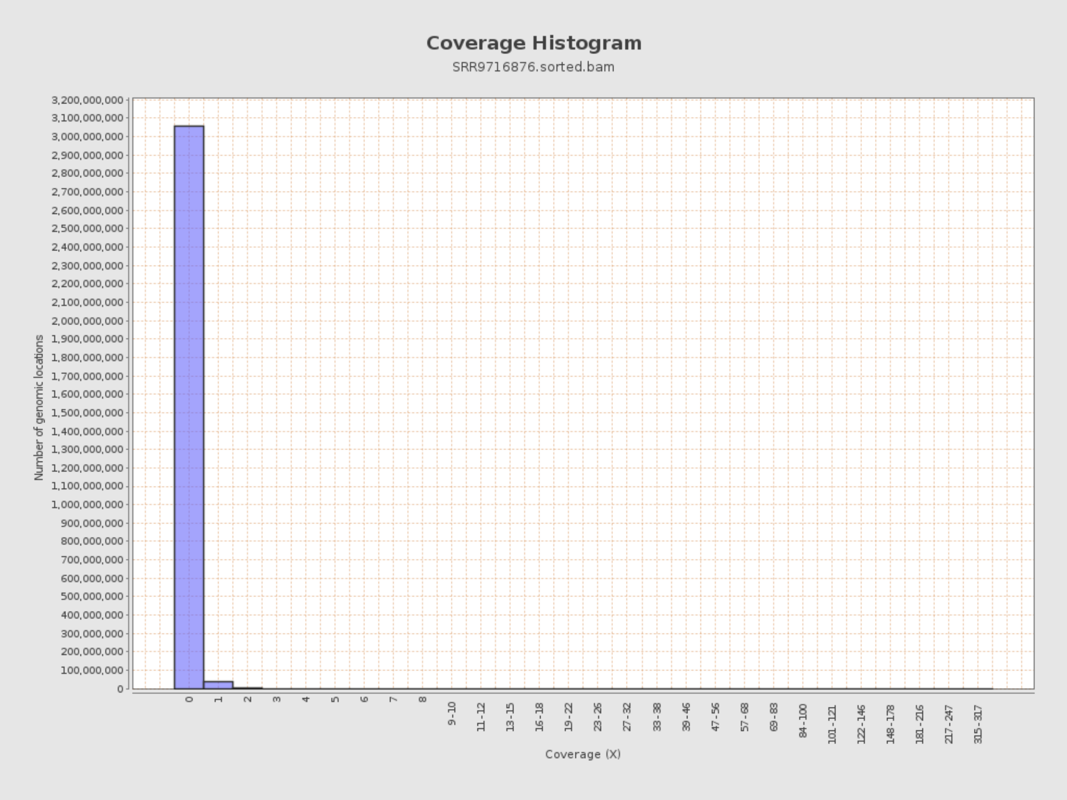
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5034913	0.0202	0.2135
chr2	243199373	4430856	0.0182	0.2052
chr3	198022430	2753039	0.0139	0.1258
chr4	191154276	1868936	0.0098	0.1067
chr5	180915260	3099445	0.0171	0.1375
chr6	171115067	1528309	0.0089	0.1079
chr7	159138663	2953727	0.0186	0.2388

chr8	146364022	1930738	0.0132	0.133
chr9	141213431	1174513	0.0083	0.1212
chr10	135534747	1981320	0.0146	0.1815
chr11	135006516	1832451	0.0136	0.1491
chr12	133851895	1766704	0.0132	0.1215
chr13	115169878	1286534	0.0112	0.1117
chr14	107349540	926446	0.0086	0.1003
chr15	102531392	1832862	0.0179	0.1411
chr16	90354753	1307402	0.0145	0.1396
chr17	81195210	1544587	0.019	0.1505
chr18	78077248	1375933	0.0176	0.2179
chr19	59128983	650402	0.011	0.1553
chr20	63025520	1088272	0.0173	0.1384
chr21	48129895	536605	0.0111	0.1124
chr22	51304566	475865	0.0093	0.1007
chrMT	16571	21414	1.2923	1.3668
chrX	155270560	1931566	0.0124	0.1278
chrY	59373566	105580	0.0018	0.0519

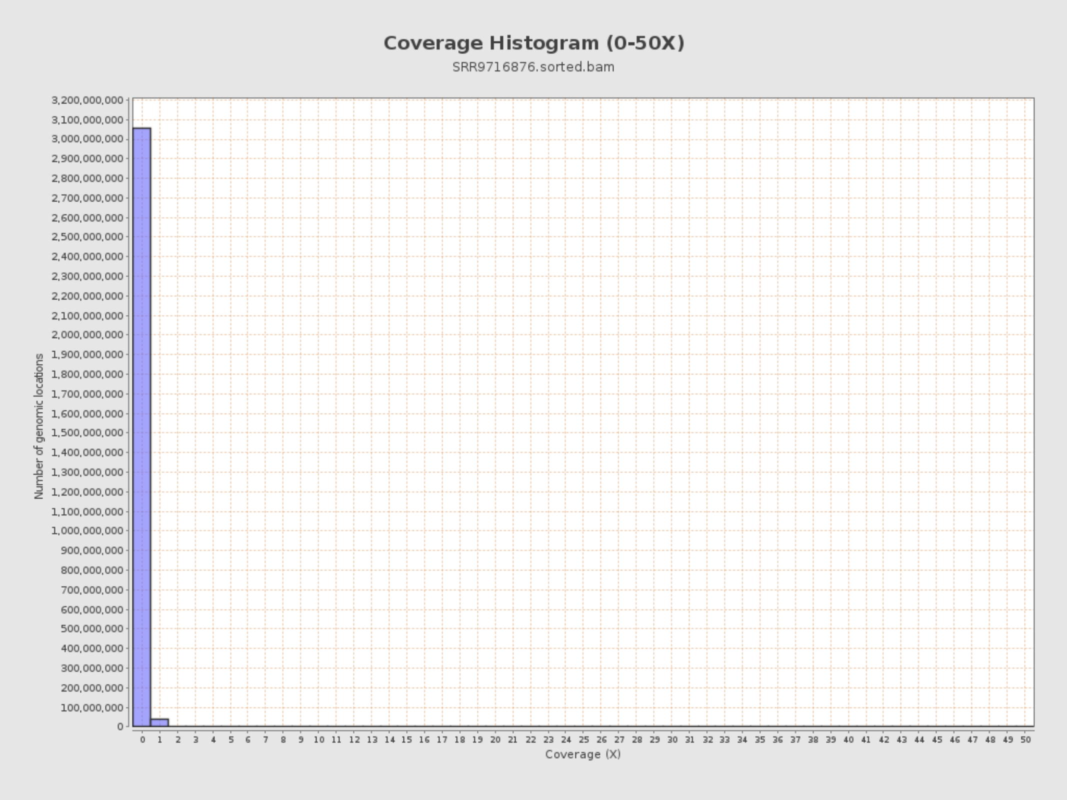
3. Results : Coverage across reference



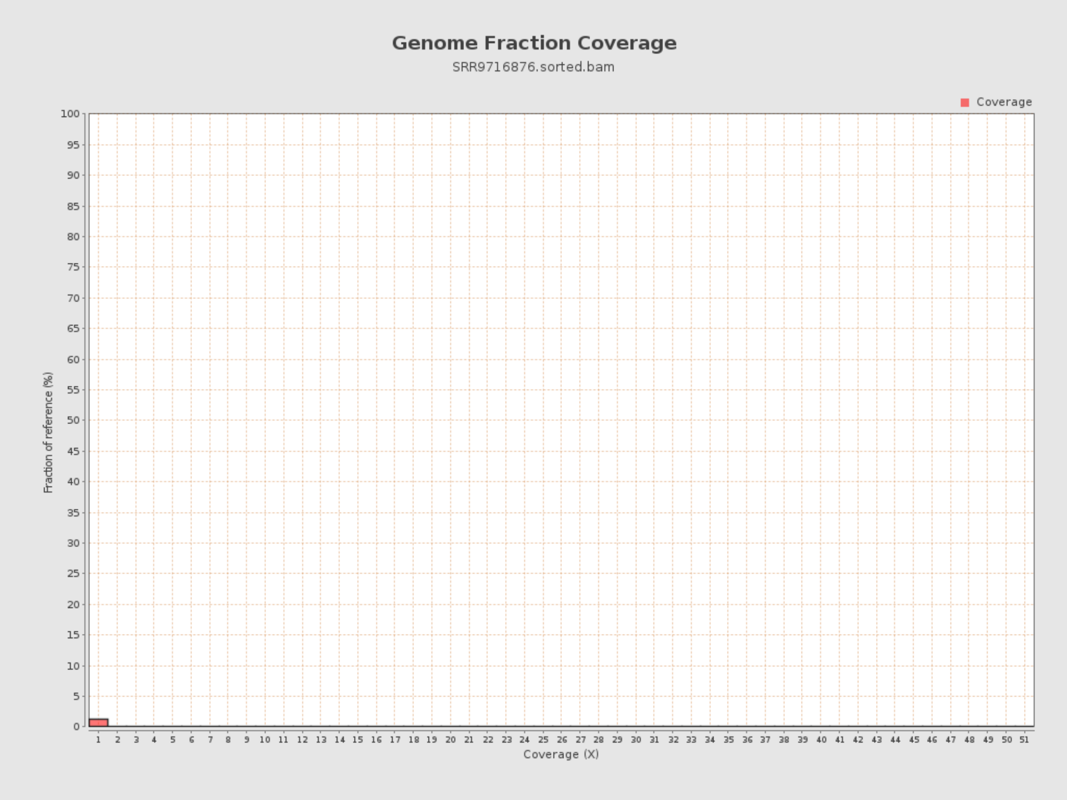
4. Results : Coverage Histogram



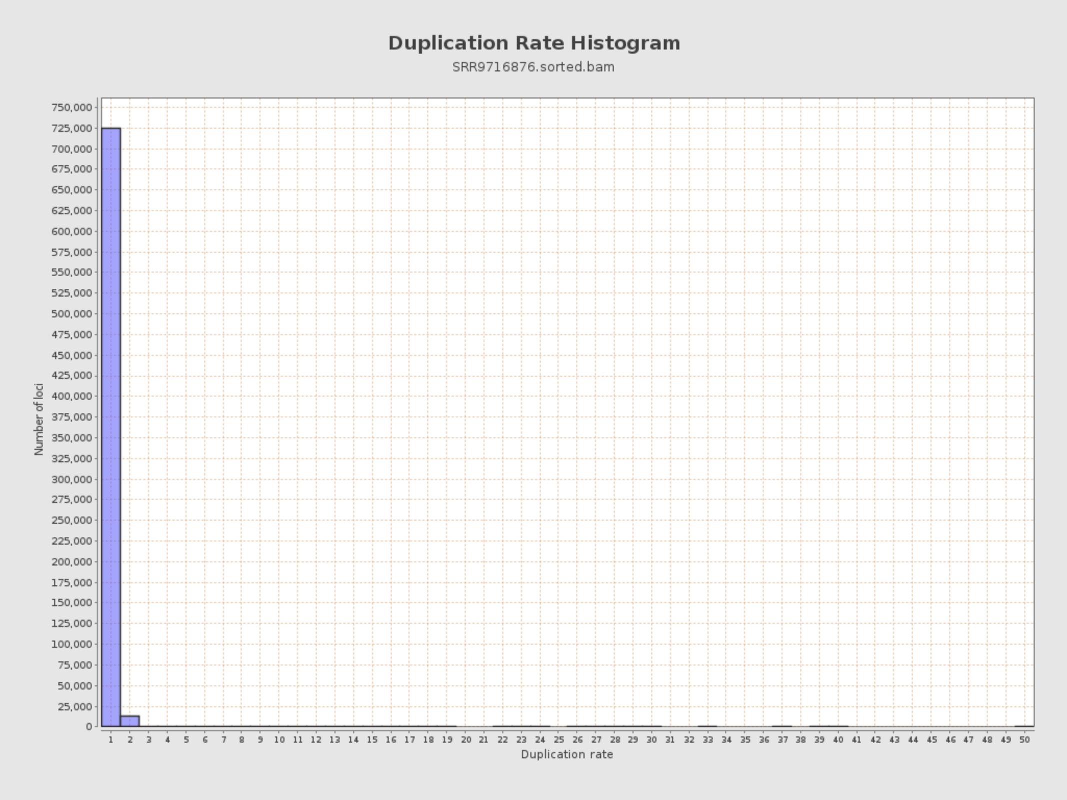
5. Results : Coverage Histogram (0-50X)



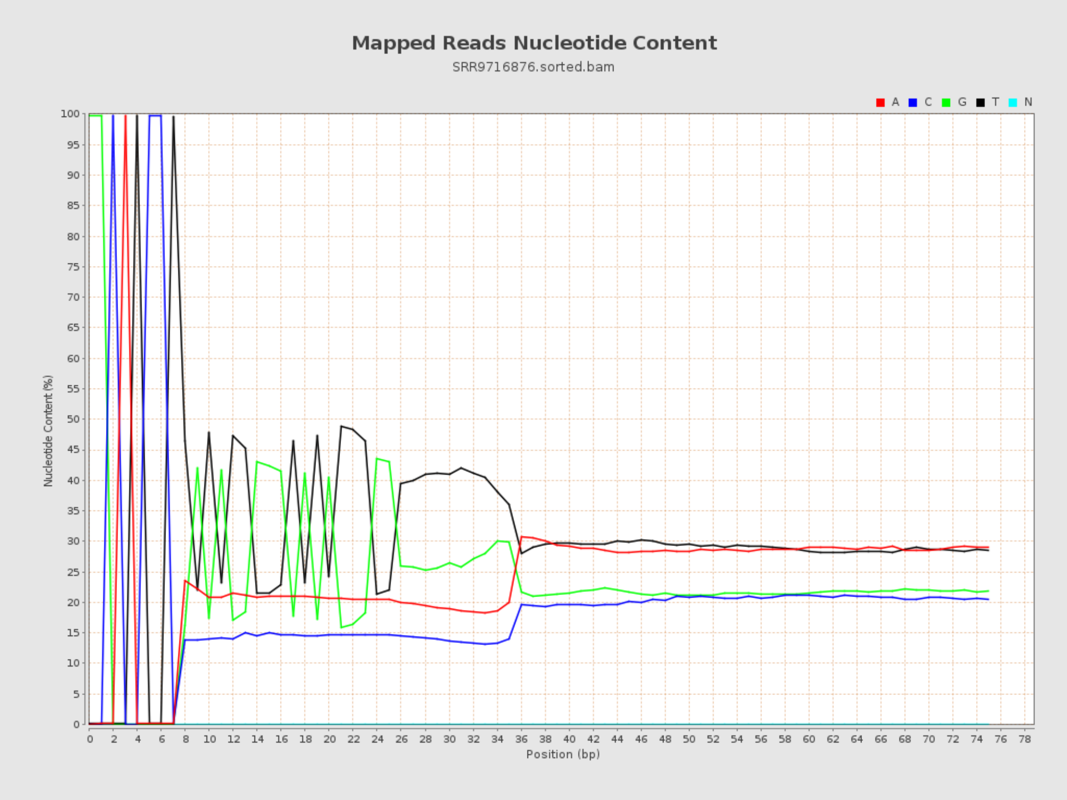
6. Results : Genome Fraction Coverage



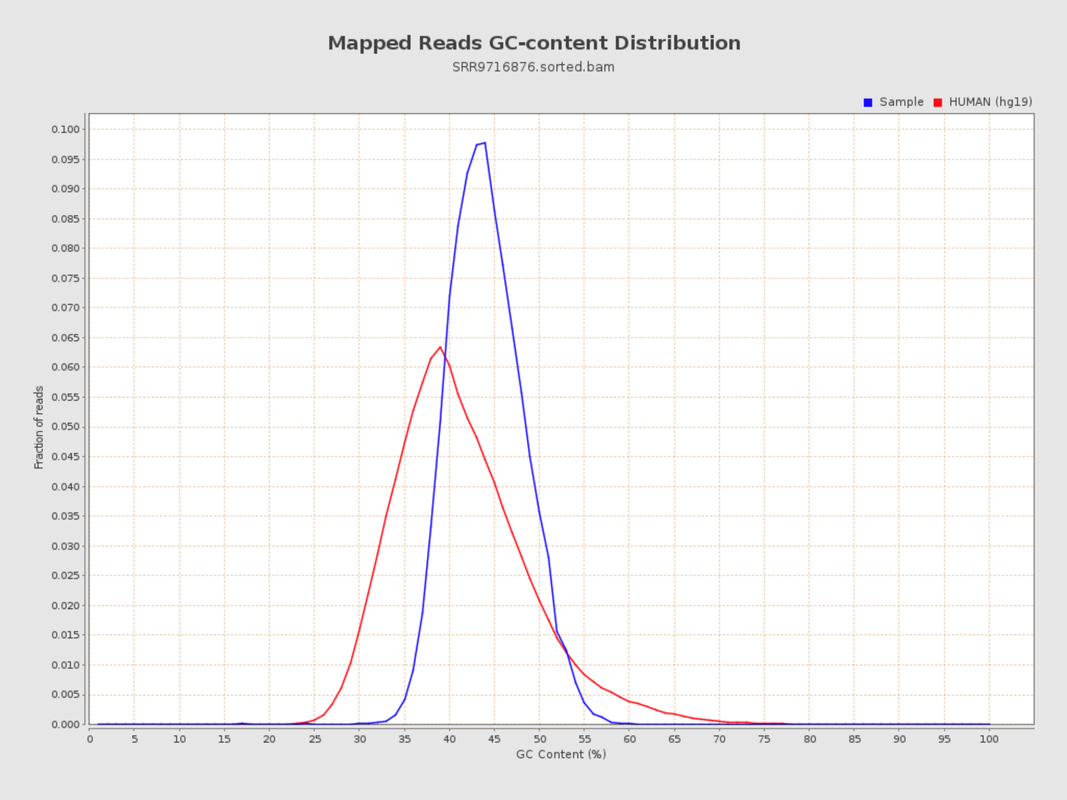
7. Results : Duplication Rate Histogram



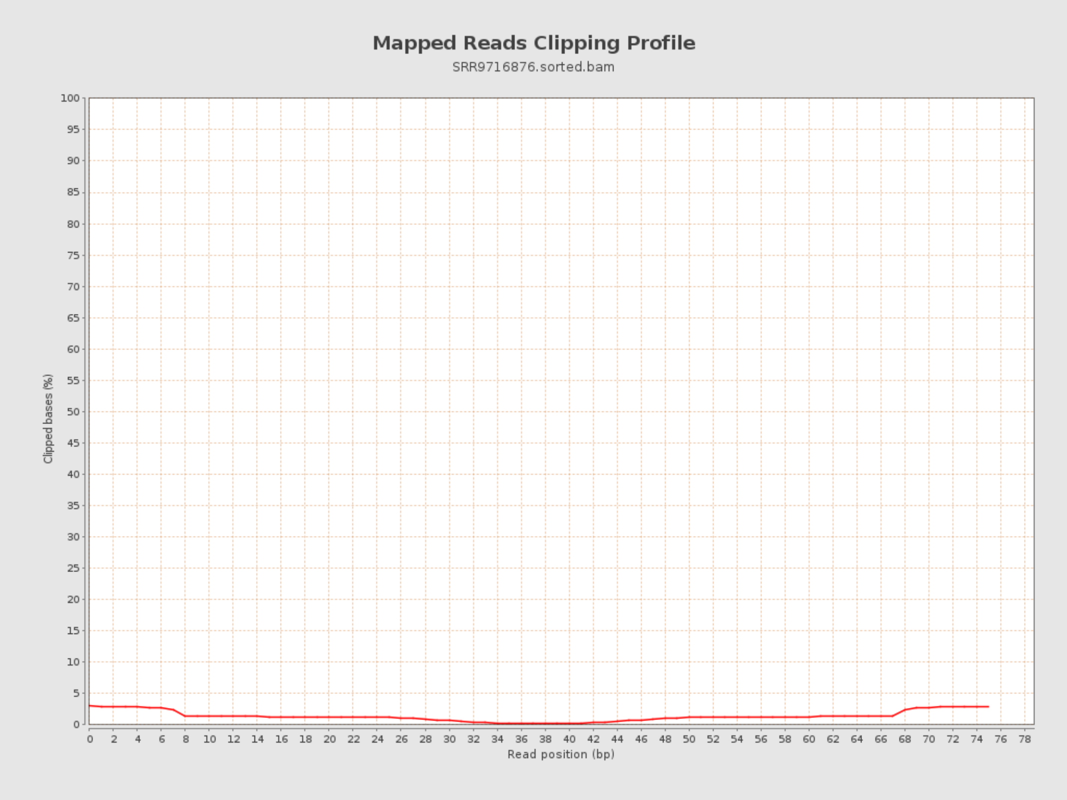
8. Results : Mapped Reads Nucleotide Content



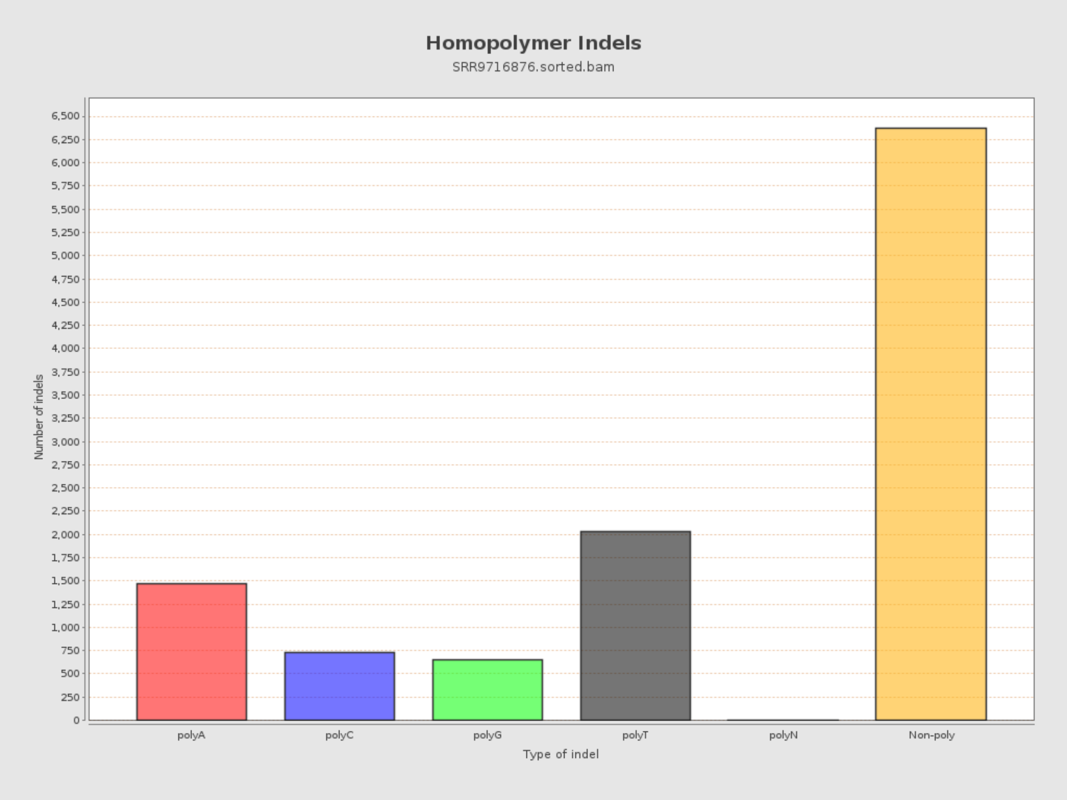
9. Results : Mapped Reads GC-content Distribution



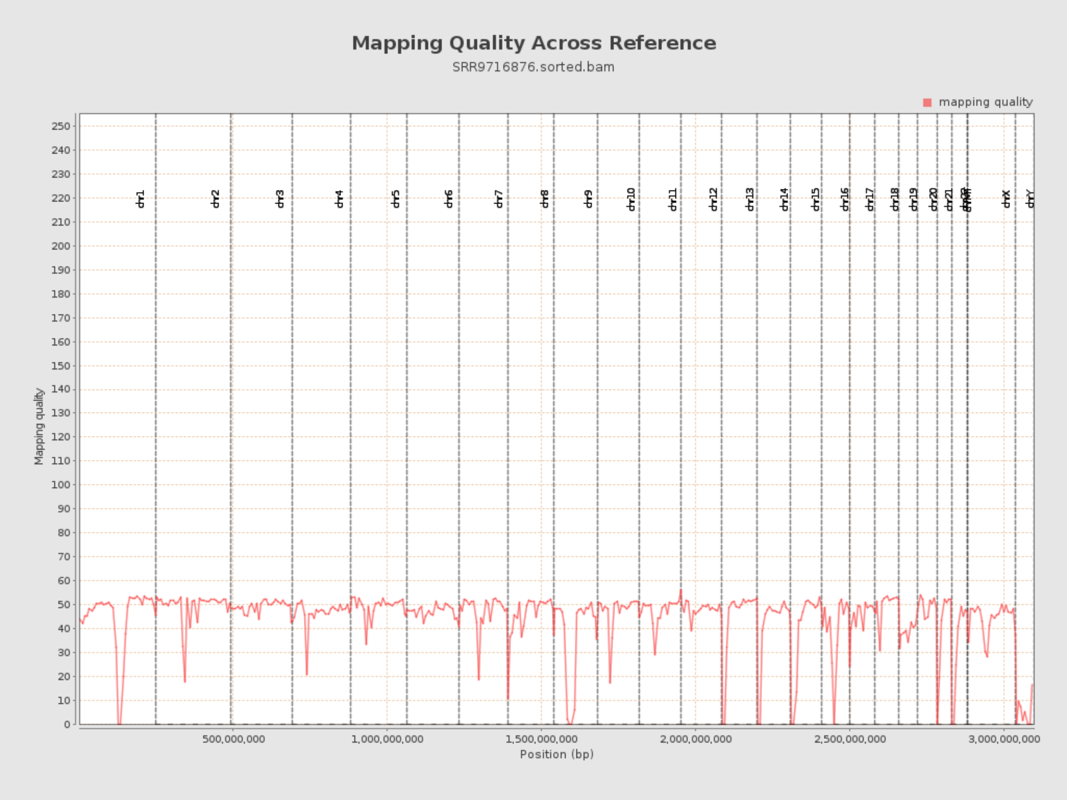
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram