Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:01:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716805.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_SRR9716805 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716805.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:01:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716805.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,003,853
Mapped reads	898,100 / 89.47%
Unmapped reads	105,753 / 10.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,034 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	23,890 / 2.38%
Duplication rate	2.04%
Clipped reads	899,563 / 89.61%

2.2. ACGT Content

Number/percentage of A's	12,883,461 / 24.87%
Number/percentage of C's	10,010,080 / 19.33%
Number/percentage of T's	16,279,773 / 31.43%
Number/percentage of G's	12,623,587 / 24.37%
Number/percentage of N's	704 / 0%
GC Percentage	43.7%

2.3. Coverage

Mean	0.0167

Standard Deviation	0.173

2.4. Mapping Quality

Mean Mapping Quality	44.74

2.5. Mismatches and indels

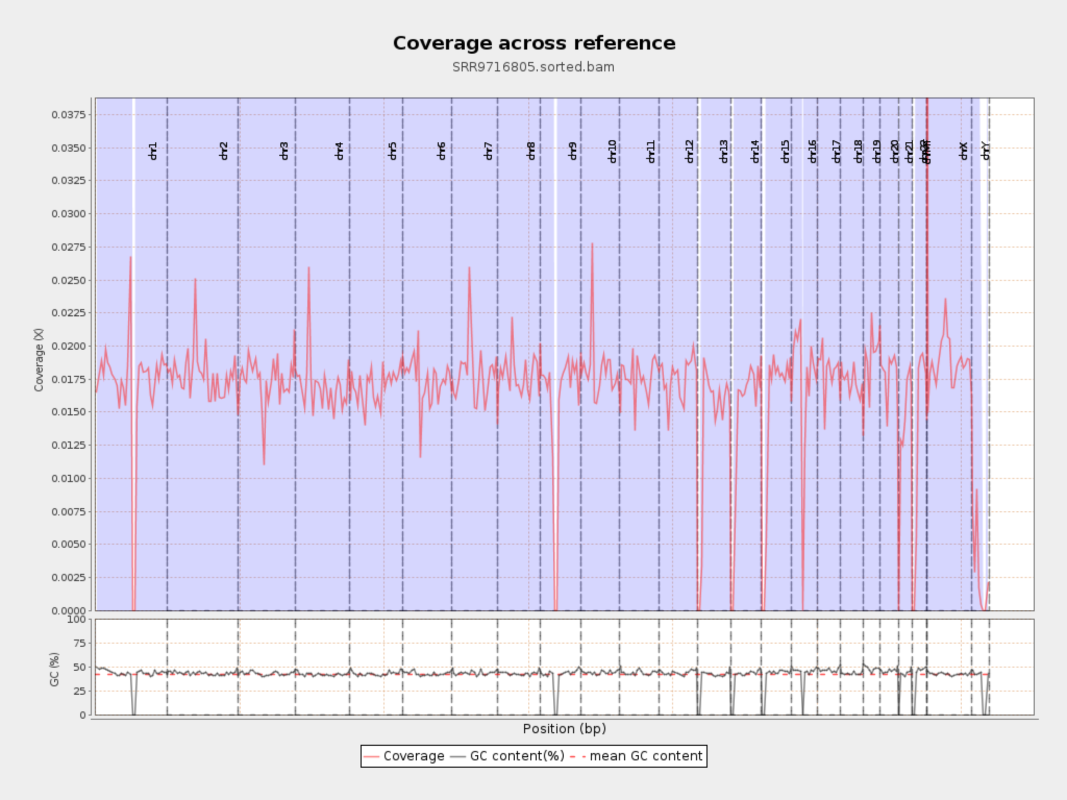
General error rate	0.52%
Mismatches	261,505
Insertions	3,603
Mapped reads with at least one insertion	0.4%
Deletions	9,694
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41.73%

2.6. Chromosome stats

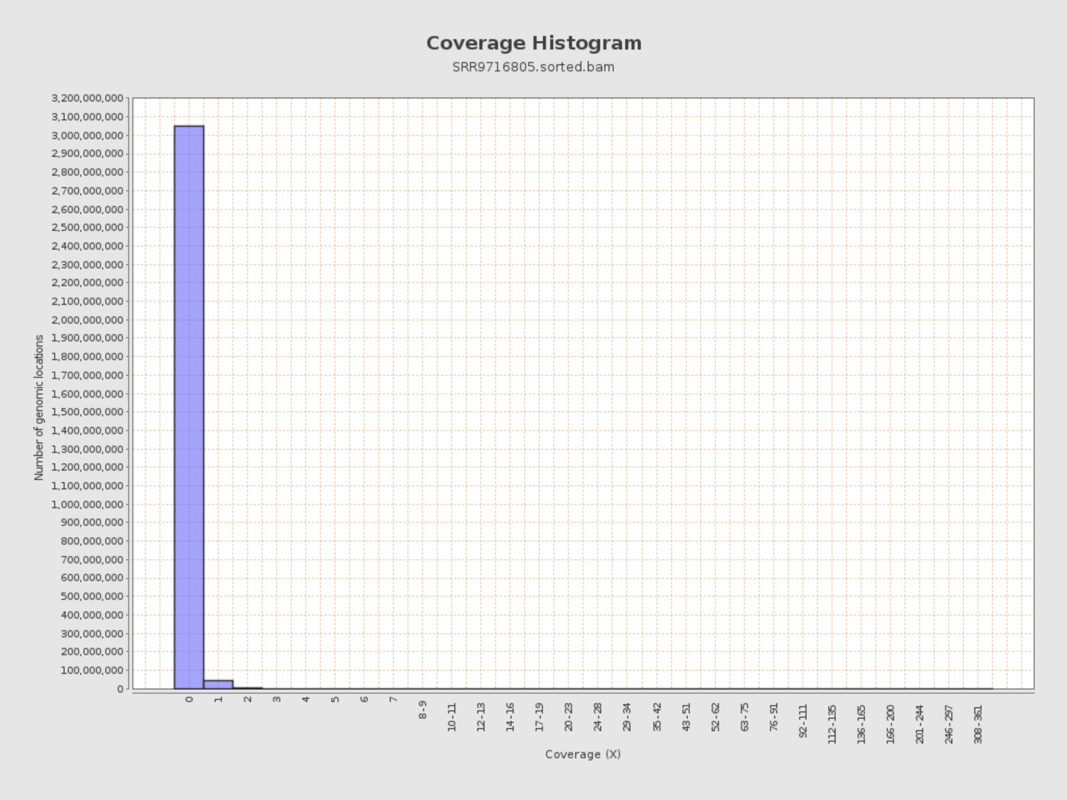
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4203546	0.0169	0.2841
chr2	243199373	4341865	0.0179	0.2118
chr3	198022430	3438896	0.0174	0.1401
chr4	191154276	3260860	0.0171	0.145
chr5	180915260	3081498	0.017	0.1387
chr6	171115067	2978545	0.0174	0.1519
chr7	159138663	2874759	0.0181	0.2015

chr8	146364022	2607860	0.0178	0.1621
chr9	141213431	2175921	0.0154	0.1527
chr10	135534747	2482758	0.0183	0.1709
chr11	135006516	2389466	0.0177	0.1606
chr12	133851895	2348965	0.0175	0.1416
chr13	115169878	1585057	0.0138	0.1246
chr14	107349540	1522295	0.0142	0.1312
chr15	102531392	1499299	0.0146	0.1292
chr16	90354753	1527224	0.0169	0.1437
chr17	81195210	1471955	0.0181	0.1484
chr18	78077248	1347628	0.0173	0.2181
chr19	59128983	1133838	0.0192	0.2194
chr20	63025520	1123792	0.0178	0.1425
chr21	48129895	668473	0.0139	0.1335
chr22	51304566	651936	0.0127	0.1192
chrMT	16571	4938	0.298	0.55
chrX	155270560	2926141	0.0188	0.1552
chrY	59373566	165381	0.0028	0.0819

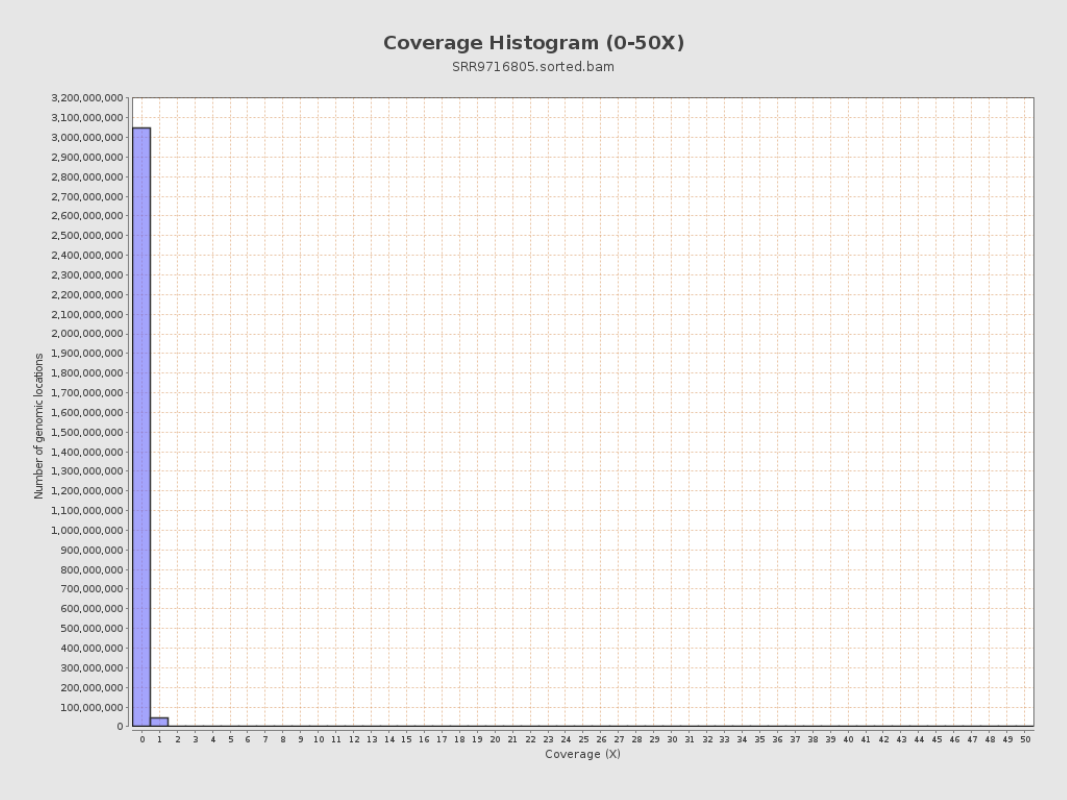
3. Results : Coverage across reference



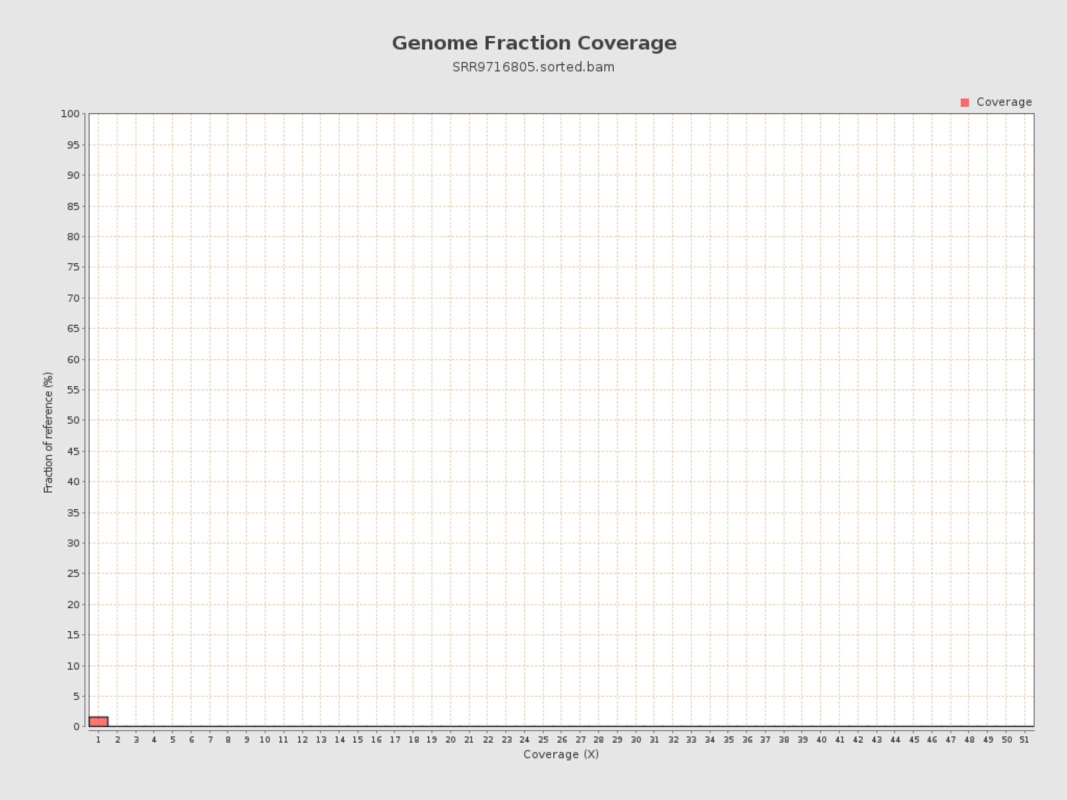
4. Results : Coverage Histogram



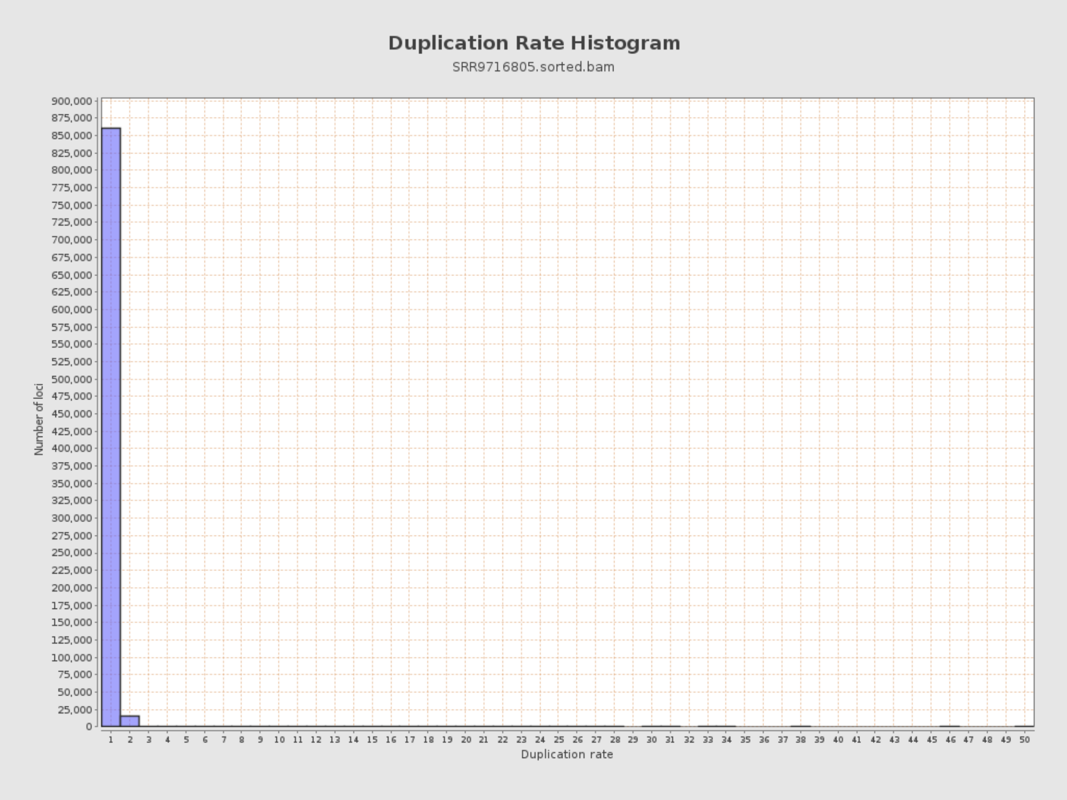
5. Results : Coverage Histogram (0-50X)



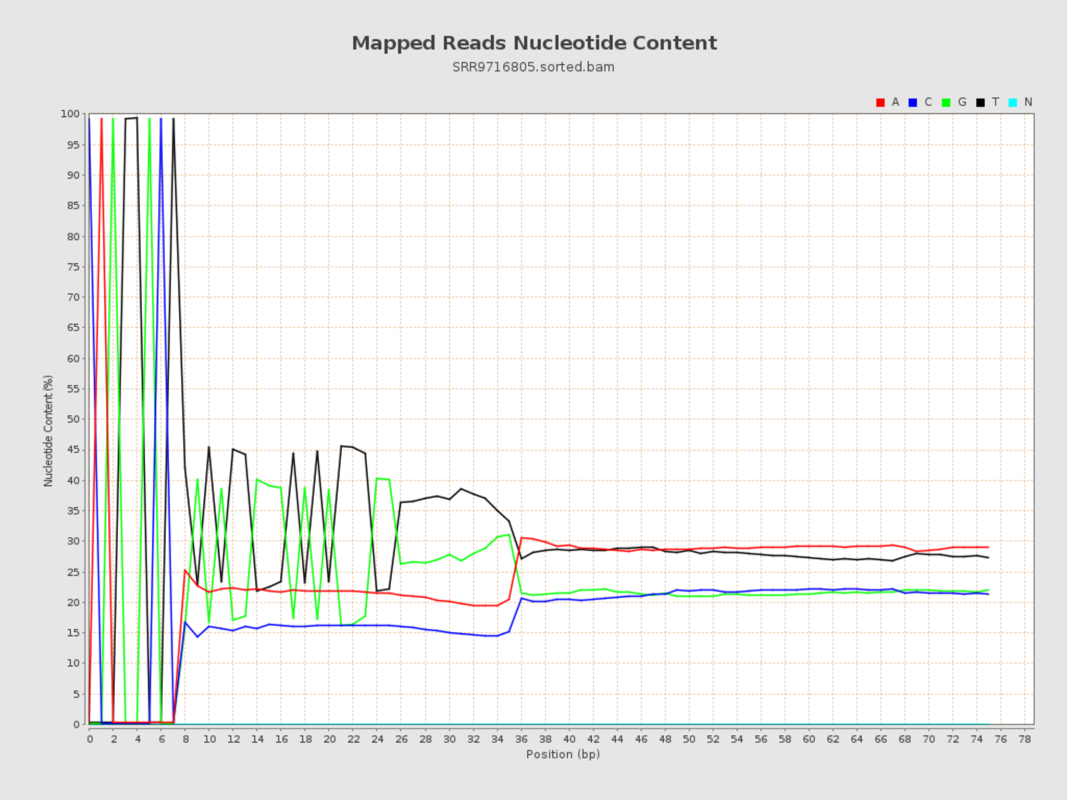
6. Results : Genome Fraction Coverage



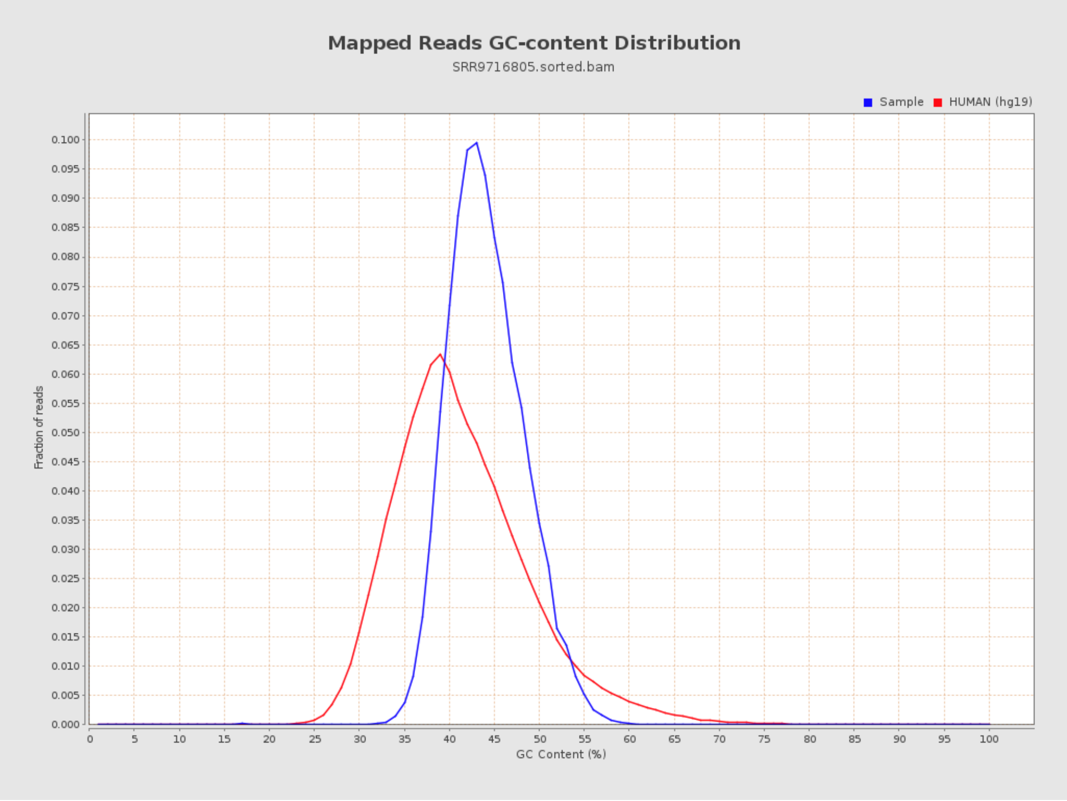
7. Results : Duplication Rate Histogram



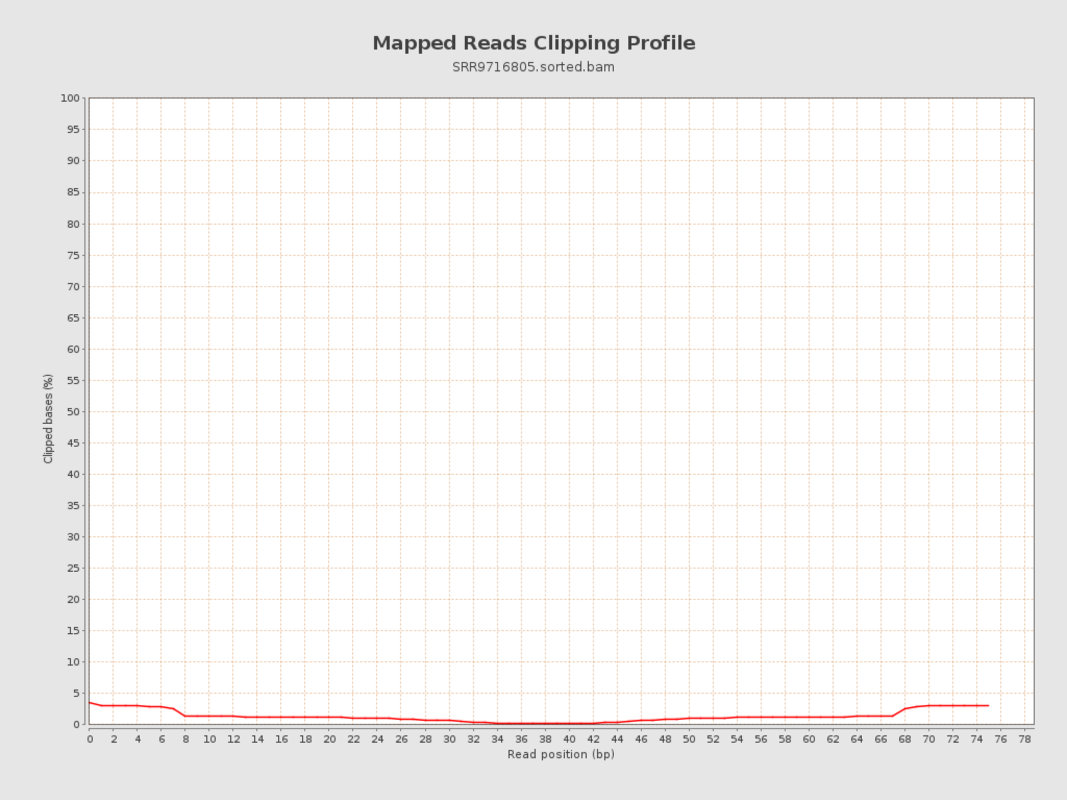
8. Results : Mapped Reads Nucleotide Content



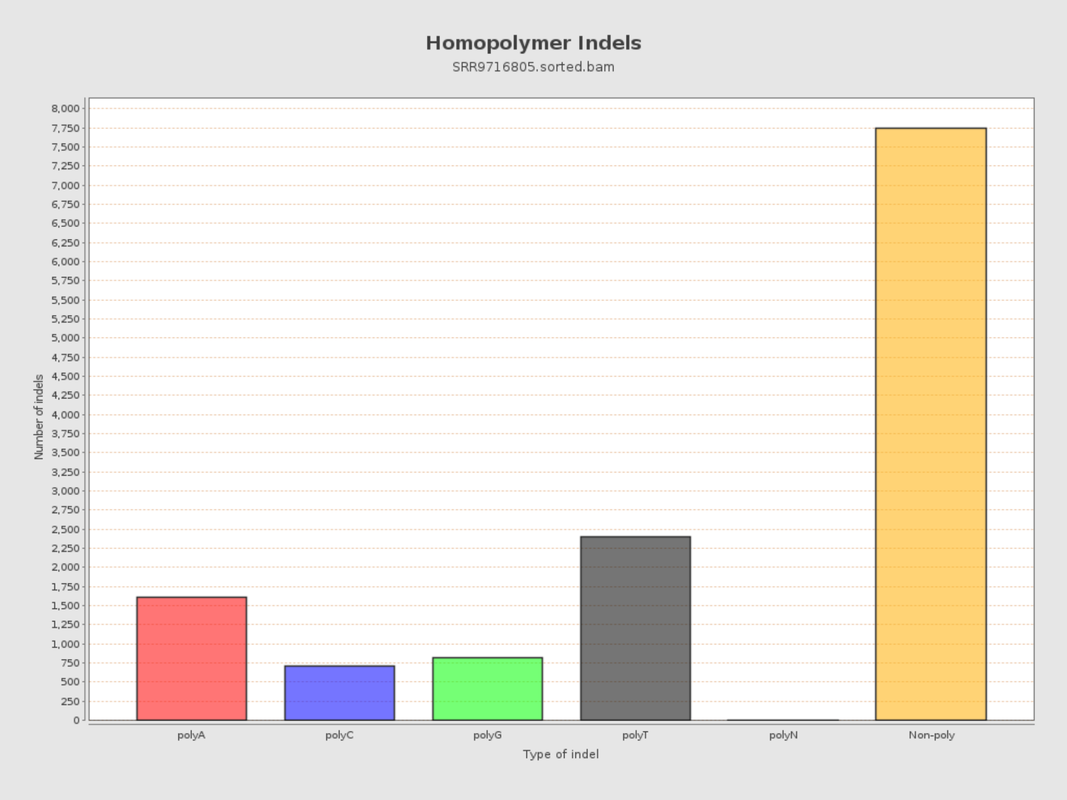
9. Results : Mapped Reads GC-content Distribution



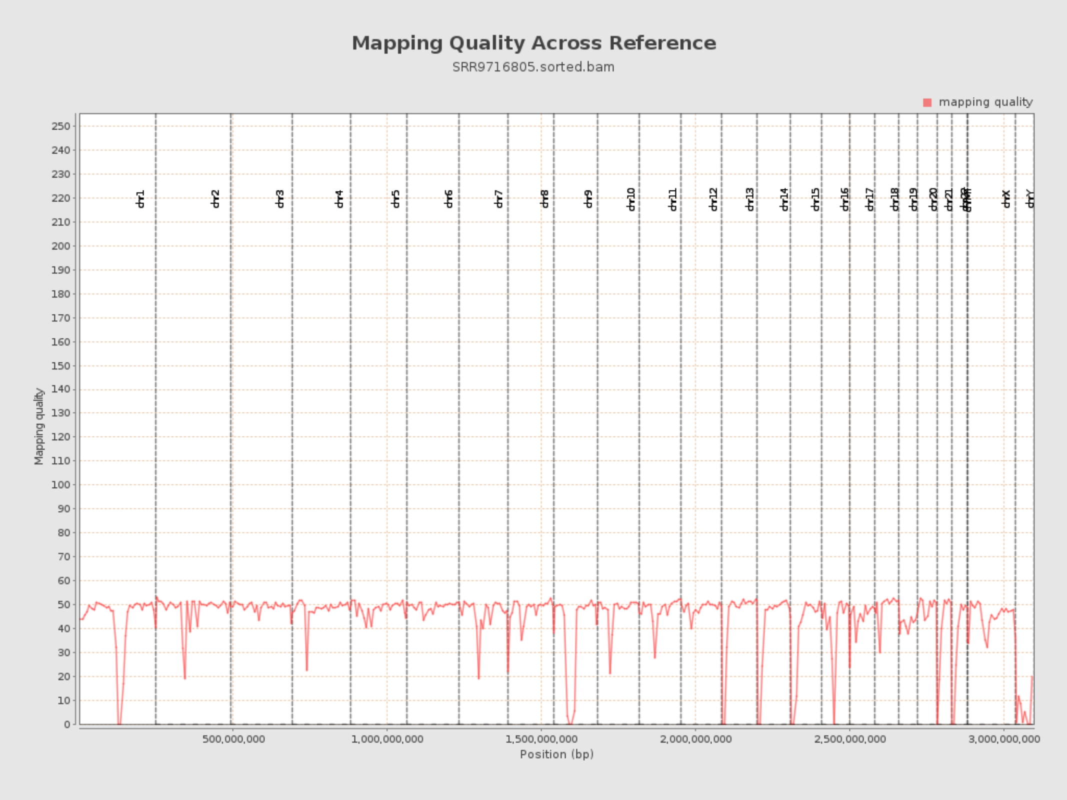
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram