Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 10:40:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716766.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_SRR9716766 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716766.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 10:40:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716766.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,160,540
Mapped reads	1,049,677 / 90.45%
Unmapped reads	110,863 / 9.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,707 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	36,048 / 3.11%
Duplication rate	2.45%
Clipped reads	1,050,006 / 90.48%

2.2. ACGT Content

Number/percentage of A's	14,623,894 / 24.35%
Number/percentage of C's	11,449,017 / 19.07%
Number/percentage of T's	20,158,308 / 33.57%
Number/percentage of G's	13,814,831 / 23.01%
Number/percentage of N's	1,126 / 0%
GC Percentage	42.07%

2.3. Coverage

Mean	0.0194

Standard Deviation	0.2106

2.4. Mapping Quality

Mean Mapping Quality	44.44

2.5. Mismatches and indels

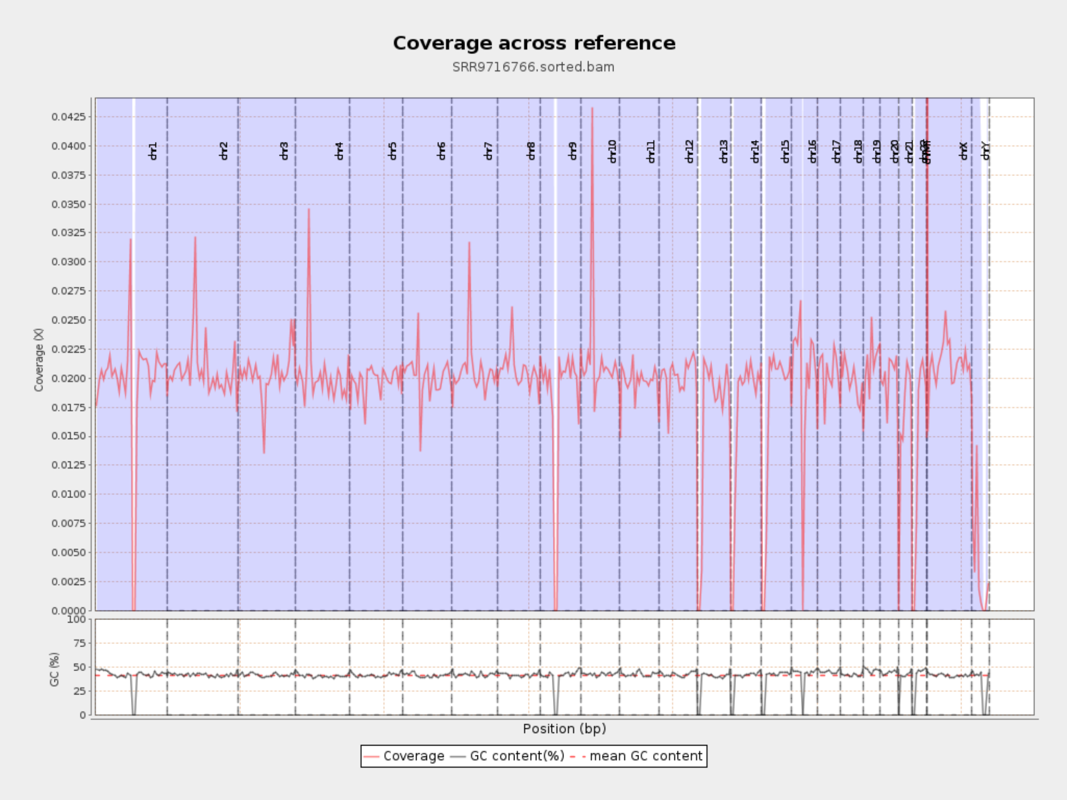
General error rate	0.54%
Mismatches	317,746
Insertions	4,206
Mapped reads with at least one insertion	0.4%
Deletions	11,882
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.72%

2.6. Chromosome stats

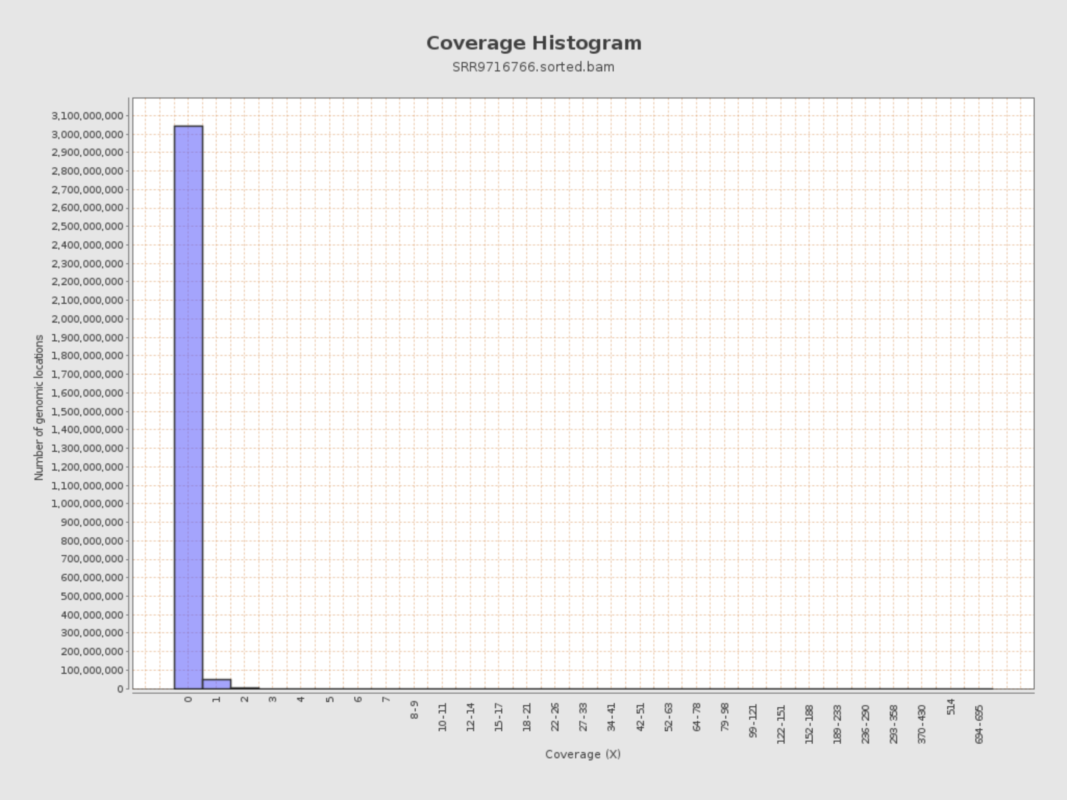
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4869622	0.0195	0.3282
chr2	243199373	5046609	0.0208	0.328
chr3	198022430	4039974	0.0204	0.1552
chr4	191154276	3887859	0.0203	0.1699
chr5	180915260	3598563	0.0199	0.1504
chr6	171115067	3450101	0.0202	0.173
chr7	159138663	3304228	0.0208	0.2347

chr8	146364022	3037474	0.0208	0.2276
chr9	141213431	2532312	0.0179	0.1751
chr10	135534747	2952869	0.0218	0.2332
chr11	135006516	2682942	0.0199	0.1789
chr12	133851895	2704394	0.0202	0.1543
chr13	115169878	1883931	0.0164	0.1362
chr14	107349540	1796410	0.0167	0.1422
chr15	102531392	1729447	0.0169	0.1412
chr16	90354753	1782060	0.0197	0.1604
chr17	81195210	1659397	0.0204	0.1595
chr18	78077248	1545895	0.0198	0.2646
chr19	59128983	1260636	0.0213	0.2537
chr20	63025520	1263589	0.02	0.1545
chr21	48129895	785417	0.0163	0.1534
chr22	51304566	711480	0.0139	0.1261
chrMT	16571	18471	1.1147	1.1697
chrX	155270560	3308426	0.0213	0.1684
chrY	59373566	214103	0.0036	0.1447

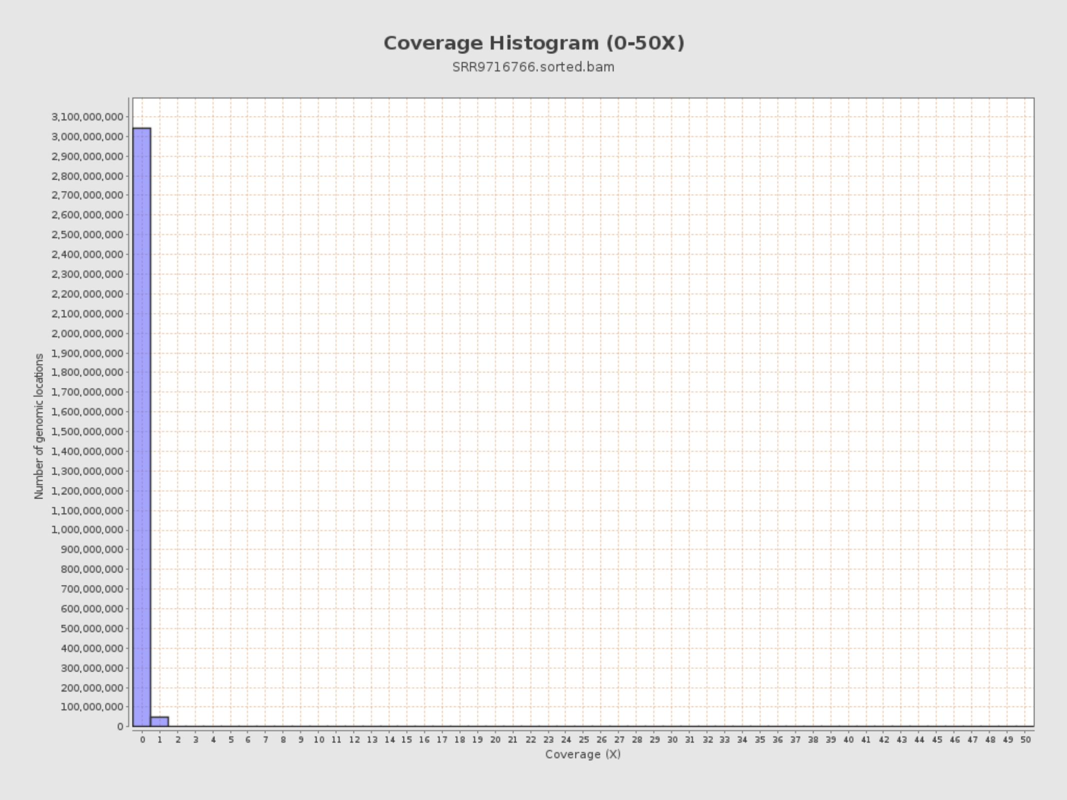
3. Results : Coverage across reference



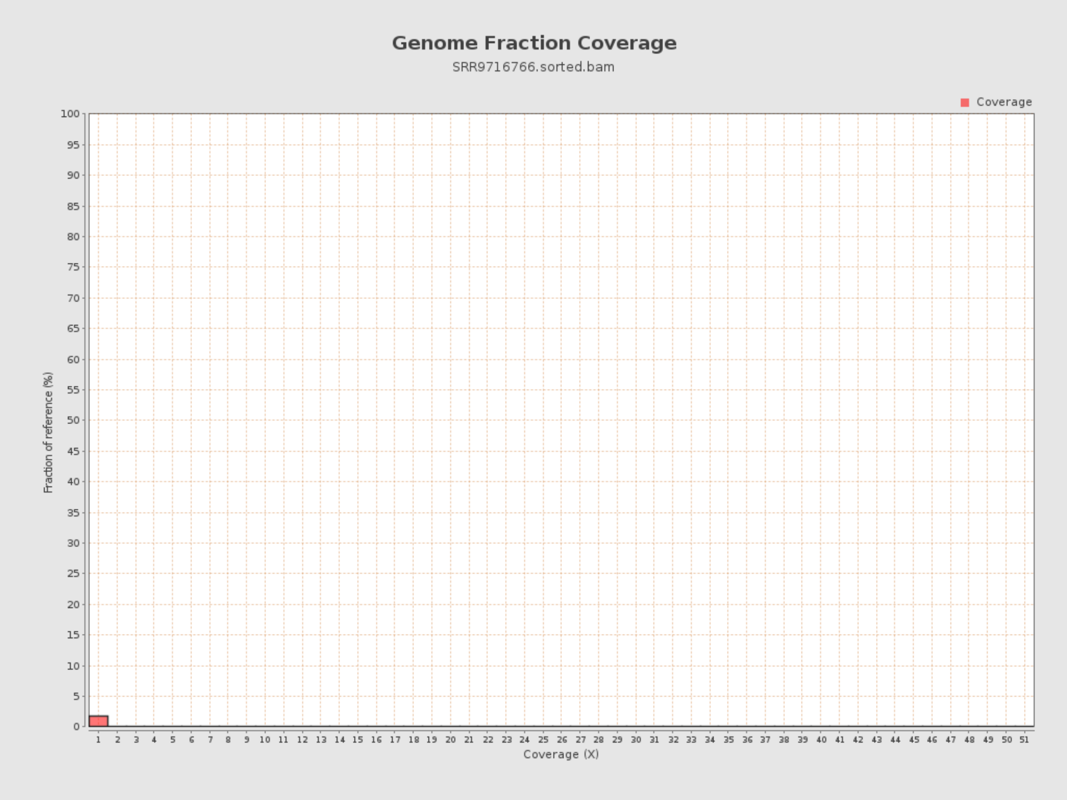
4. Results : Coverage Histogram



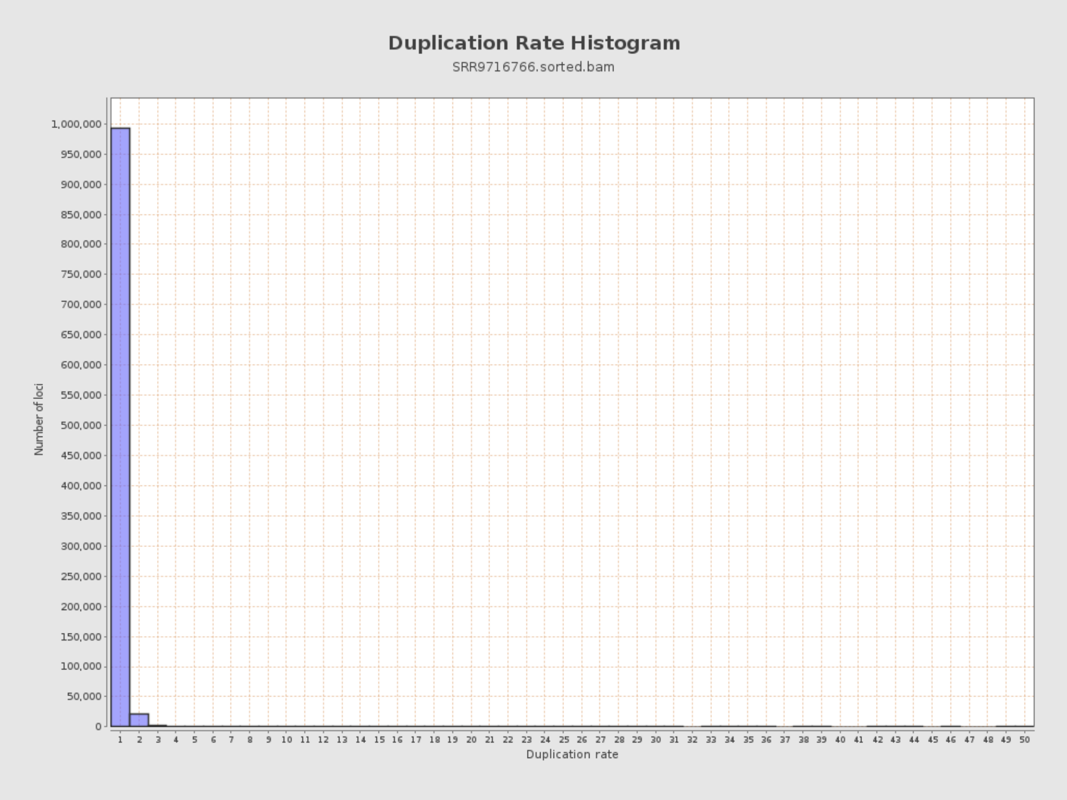
5. Results : Coverage Histogram (0-50X)



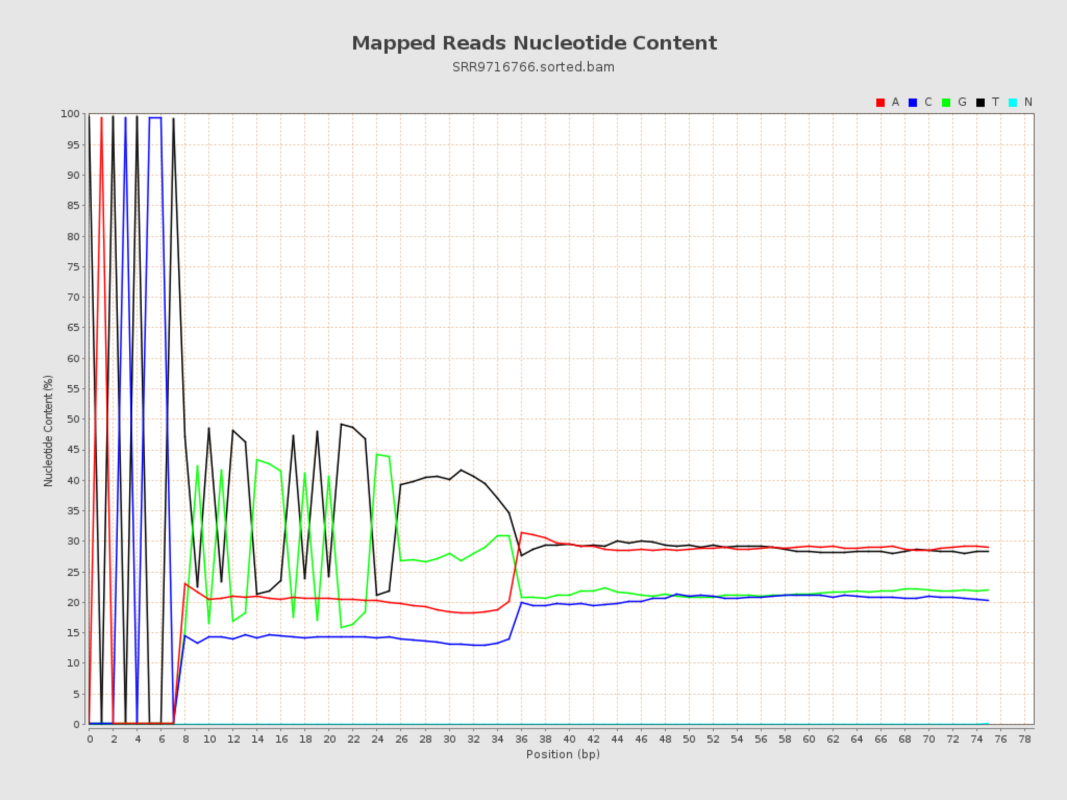
6. Results : Genome Fraction Coverage



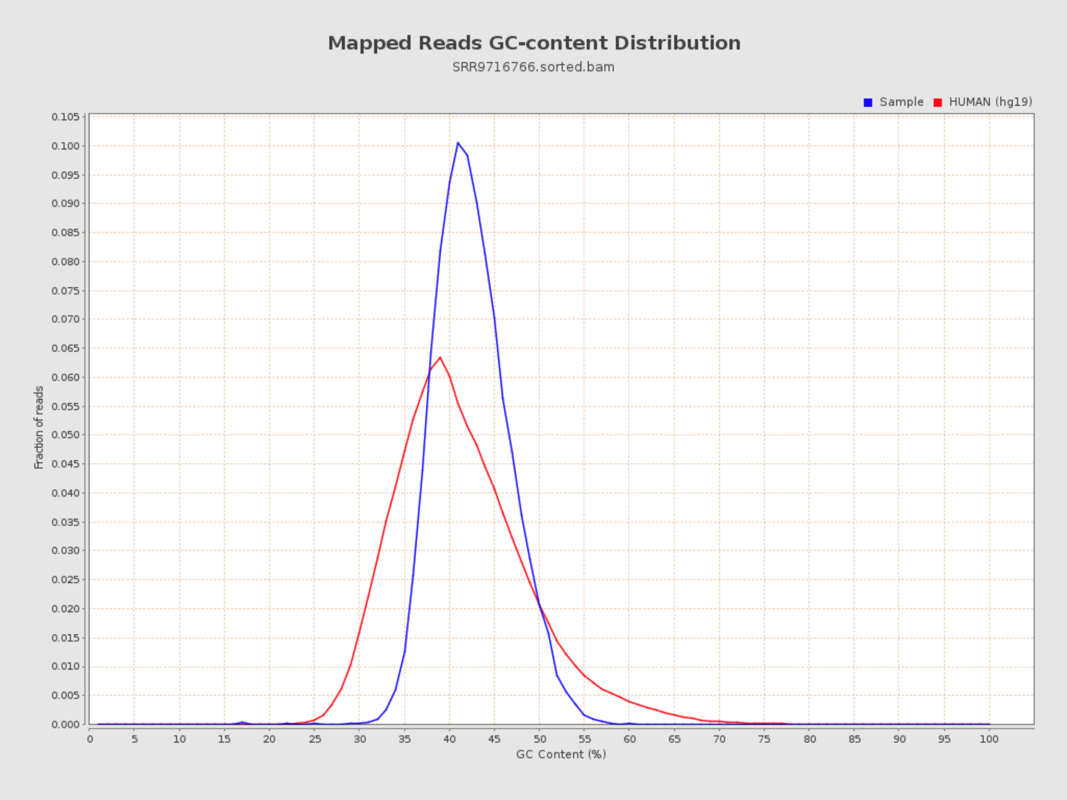
7. Results : Duplication Rate Histogram



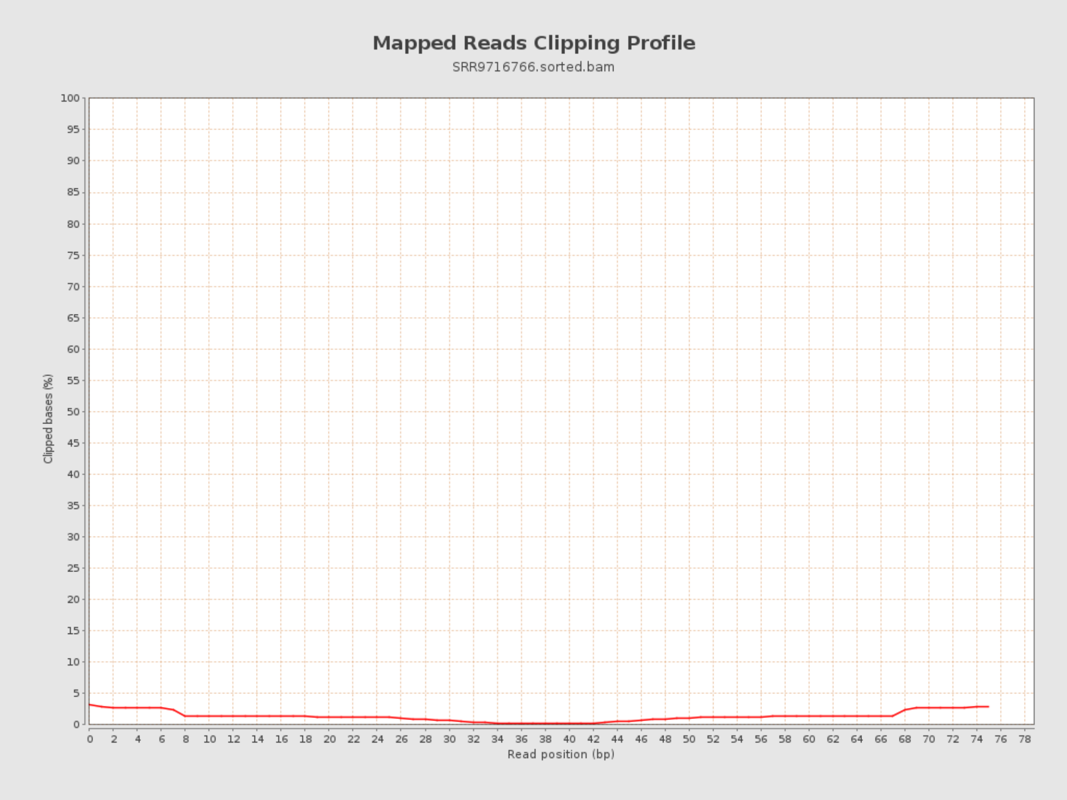
8. Results : Mapped Reads Nucleotide Content



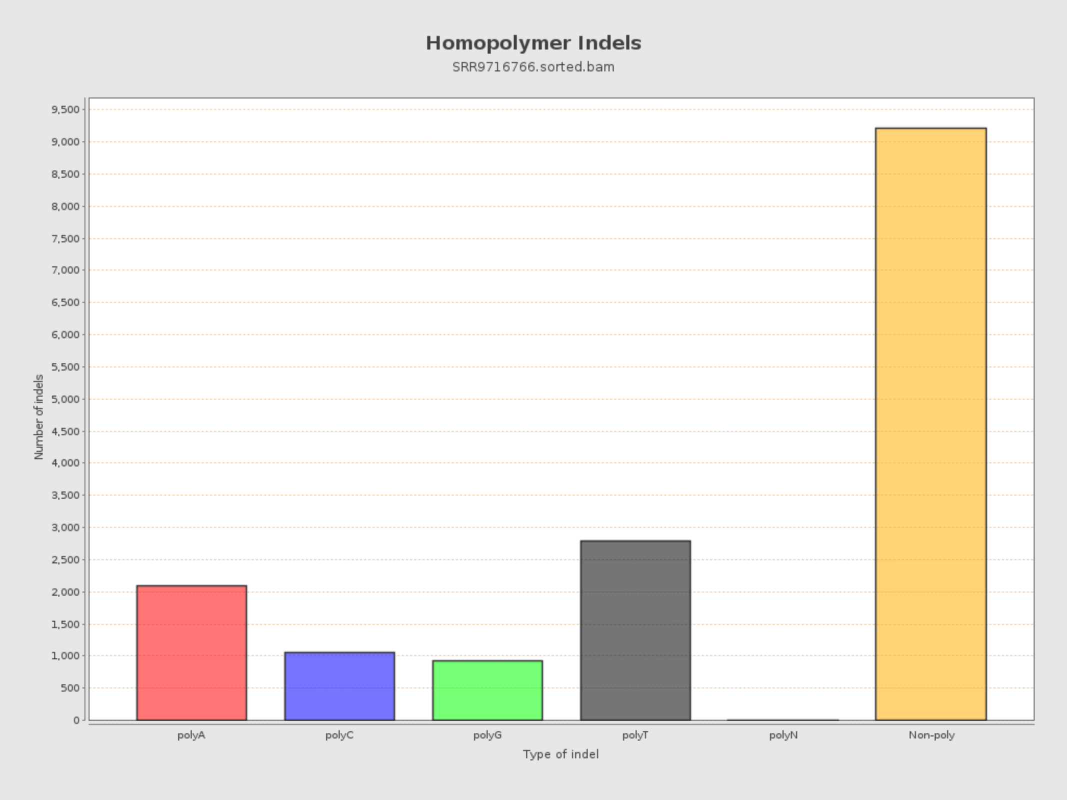
9. Results : Mapped Reads GC-content Distribution



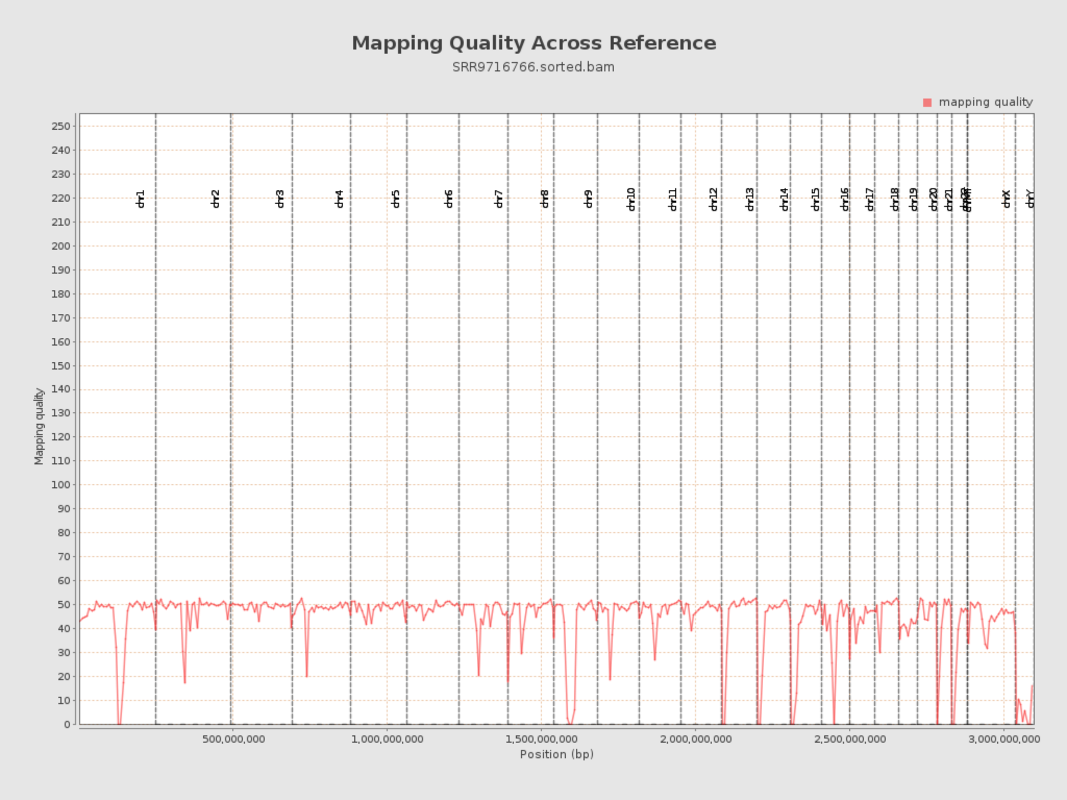
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram