Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 10:53:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716768.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_SRR9716768 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716768.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 10:53:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716768.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,234,073
Mapped reads	1,078,688 / 87.41%
Unmapped reads	155,385 / 12.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,707 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	23,384 / 1.89%
Duplication rate	1.46%
Clipped reads	1,080,719 / 87.57%

2.2. ACGT Content

Number/percentage of A's	14,854,199 / 24.33%
Number/percentage of C's	11,739,871 / 19.23%
Number/percentage of T's	19,403,813 / 31.79%
Number/percentage of G's	15,047,702 / 24.65%
Number/percentage of N's	521 / 0%
GC Percentage	43.88%

2.3. Coverage

Mean	0.0197

Standard Deviation	0.1914

2.4. Mapping Quality

Mean Mapping Quality	42.05

2.5. Mismatches and indels

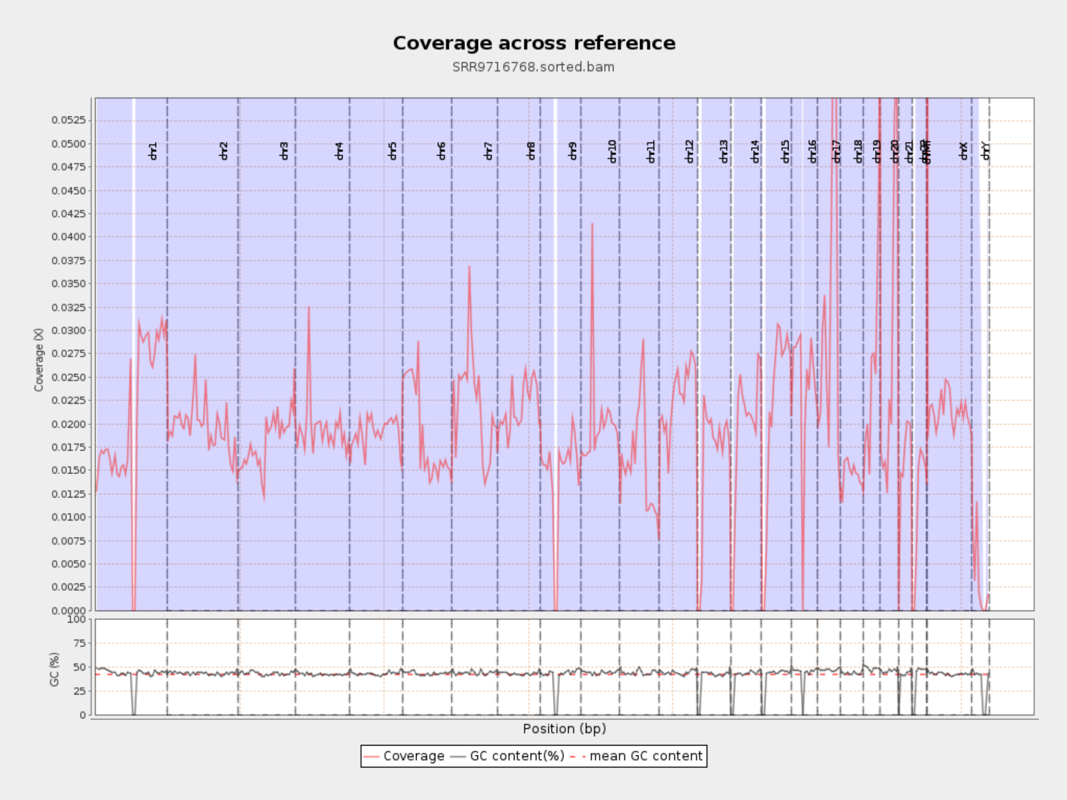
General error rate	0.54%
Mismatches	320,011
Insertions	4,977
Mapped reads with at least one insertion	0.46%
Deletions	11,309
Mapped reads with at least one deletion	1.04%
Homopolymer indels	38.62%

2.6. Chromosome stats

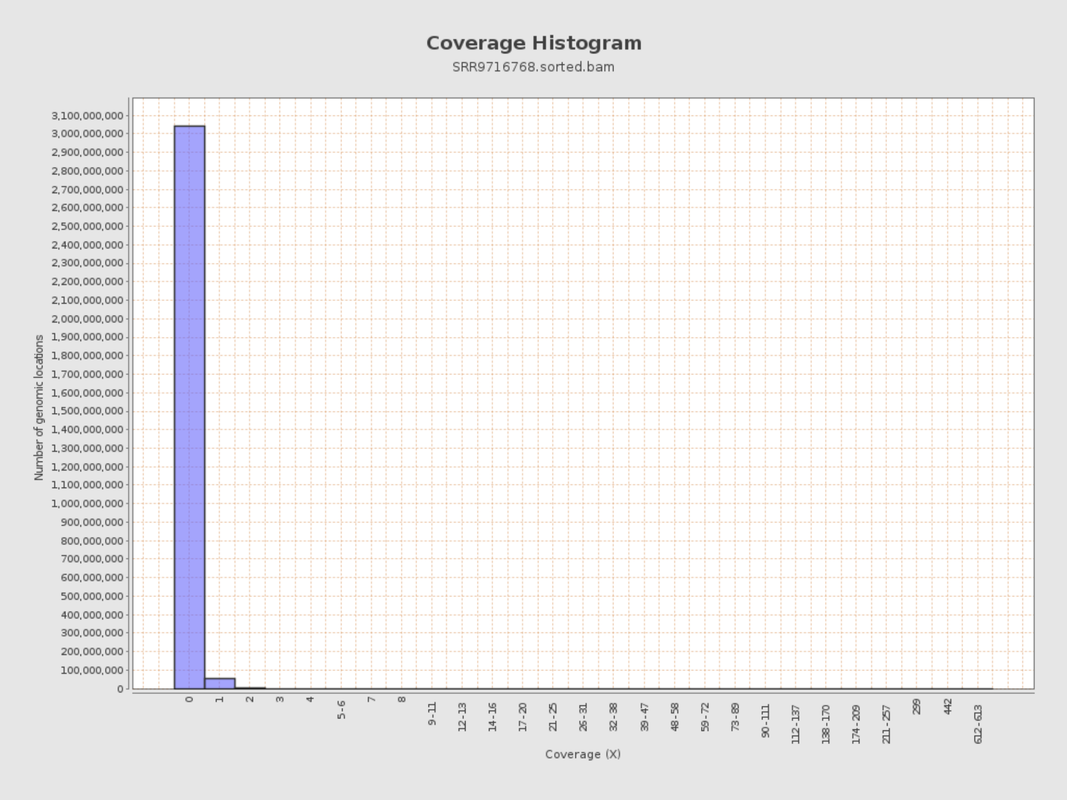
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5174069	0.0208	0.238
chr2	243199373	4782045	0.0197	0.2869
chr3	198022430	3577072	0.0181	0.1454
chr4	191154276	3738112	0.0196	0.1606
chr5	180915260	3473746	0.0192	0.1461
chr6	171115067	3247245	0.019	0.1636
chr7	159138663	3549822	0.0223	0.2592

chr8	146364022	3195633	0.0218	0.1844
chr9	141213431	2053041	0.0145	0.1471
chr10	135534747	2723749	0.0201	0.232
chr11	135006516	2172959	0.0161	0.1619
chr12	133851895	3056227	0.0228	0.1605
chr13	115169878	1859498	0.0161	0.1339
chr14	107349540	2039489	0.019	0.1494
chr15	102531392	2196096	0.0214	0.1573
chr16	90354753	2136075	0.0236	0.174
chr17	81195210	2729258	0.0336	0.2021
chr18	78077248	1136672	0.0146	0.22
chr19	59128983	1574692	0.0266	0.2338
chr20	63025520	1779024	0.0282	0.1838
chr21	48129895	760901	0.0158	0.1409
chr22	51304566	575672	0.0112	0.1129
chrMT	16571	10451	0.6307	0.8958
chrX	155270560	3327532	0.0214	0.1652
chrY	59373566	195112	0.0033	0.1018

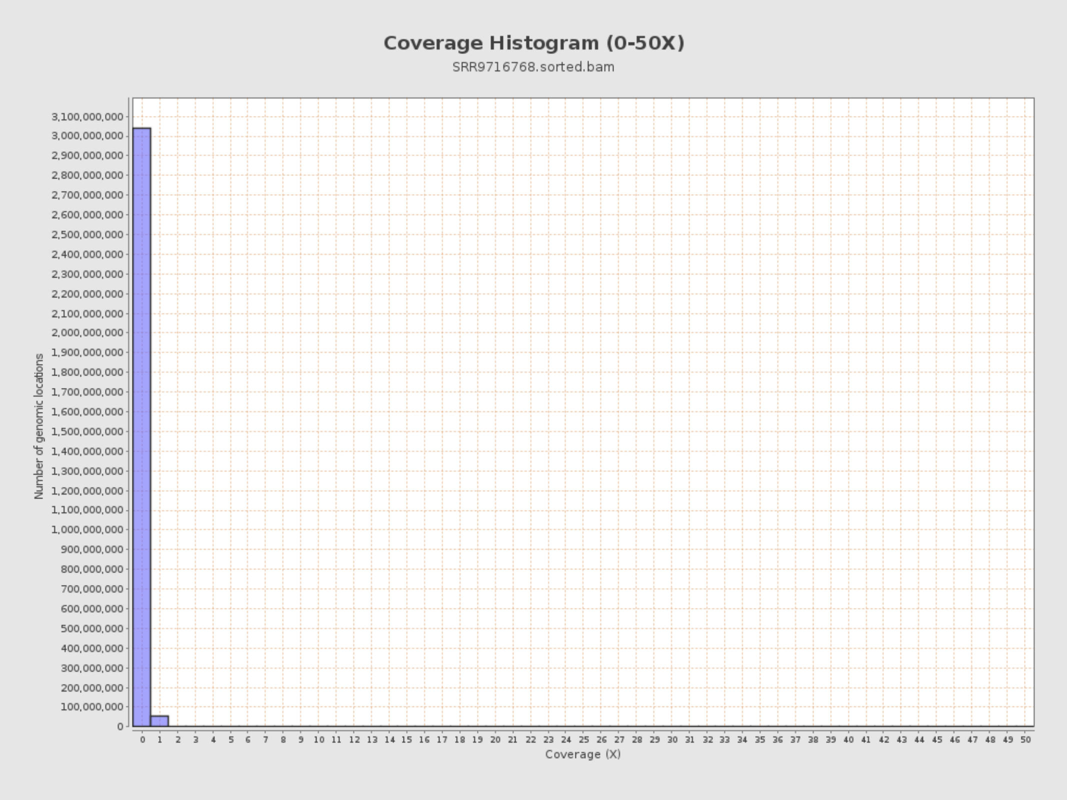
3. Results : Coverage across reference



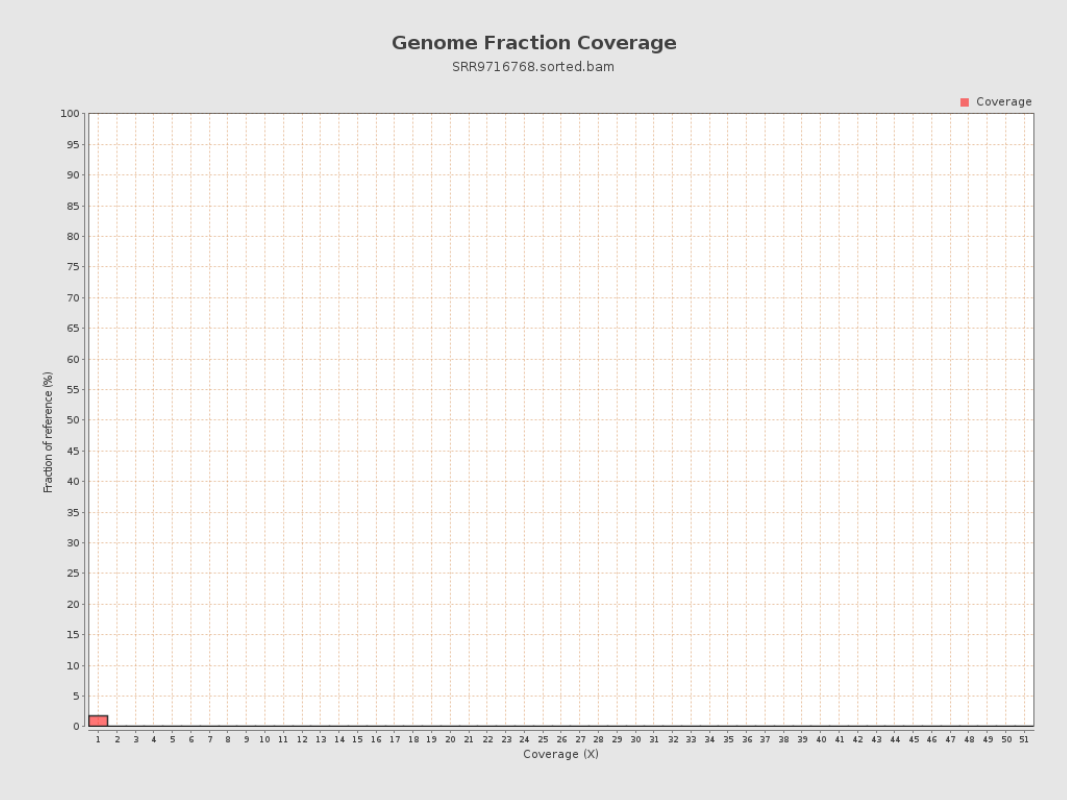
4. Results : Coverage Histogram



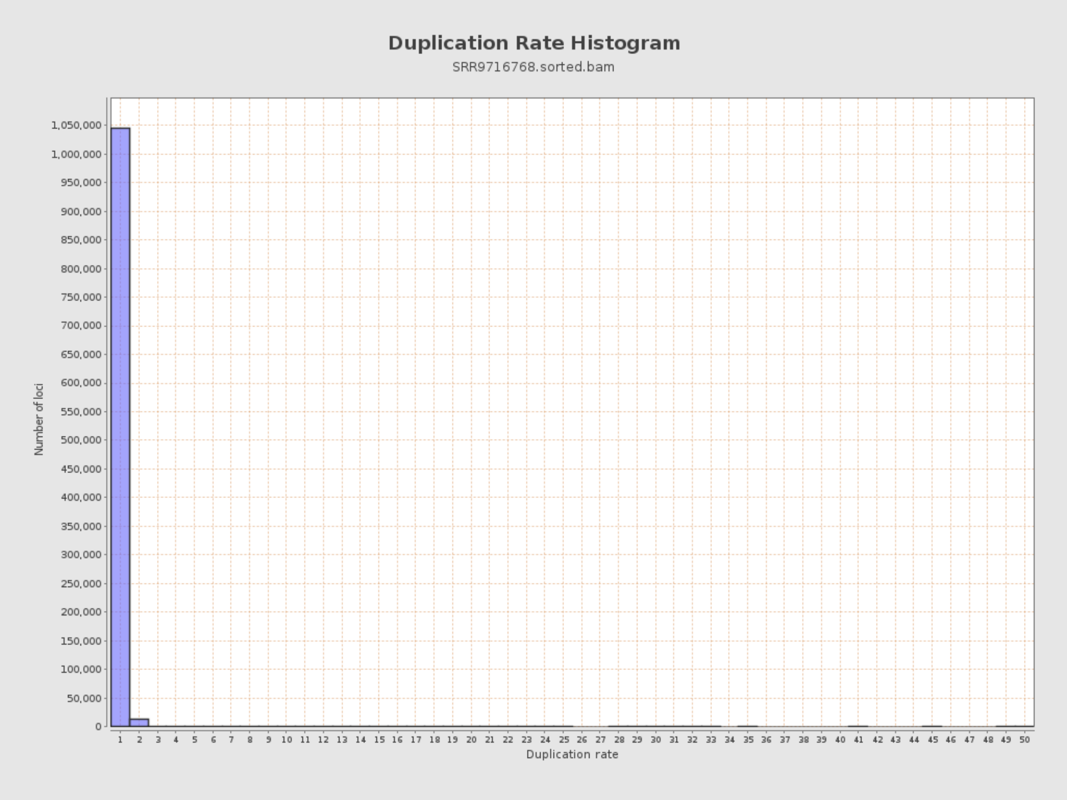
5. Results : Coverage Histogram (0-50X)



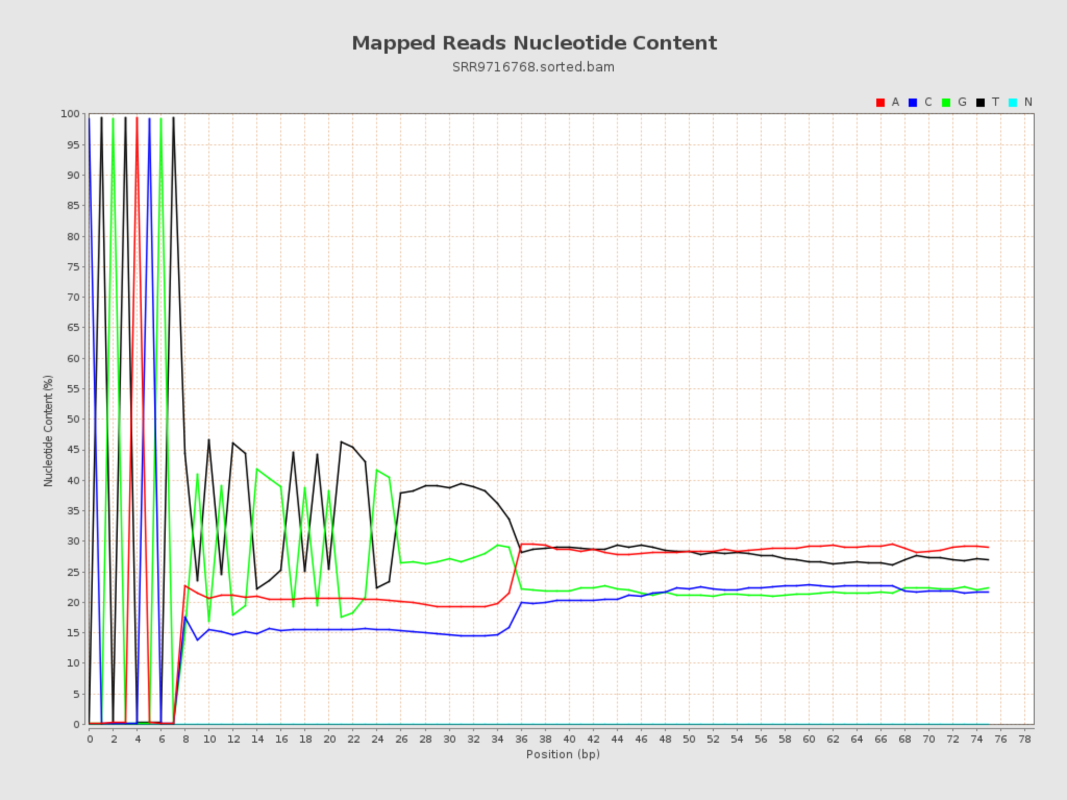
6. Results : Genome Fraction Coverage



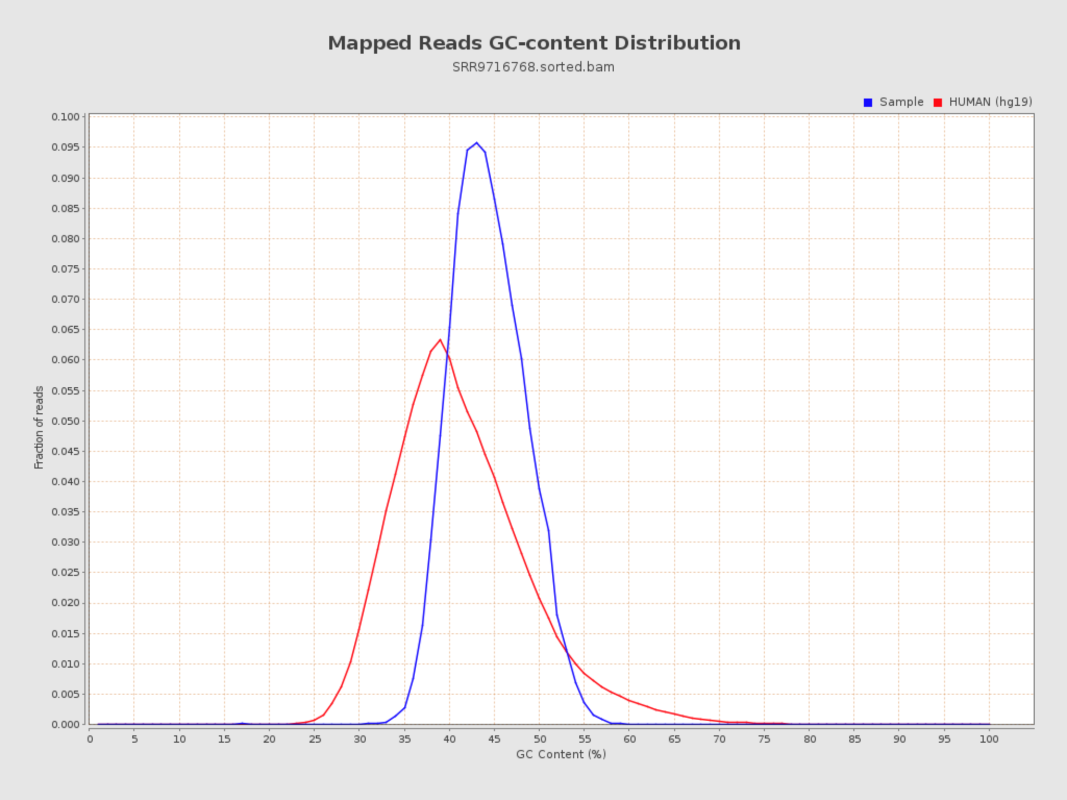
7. Results : Duplication Rate Histogram



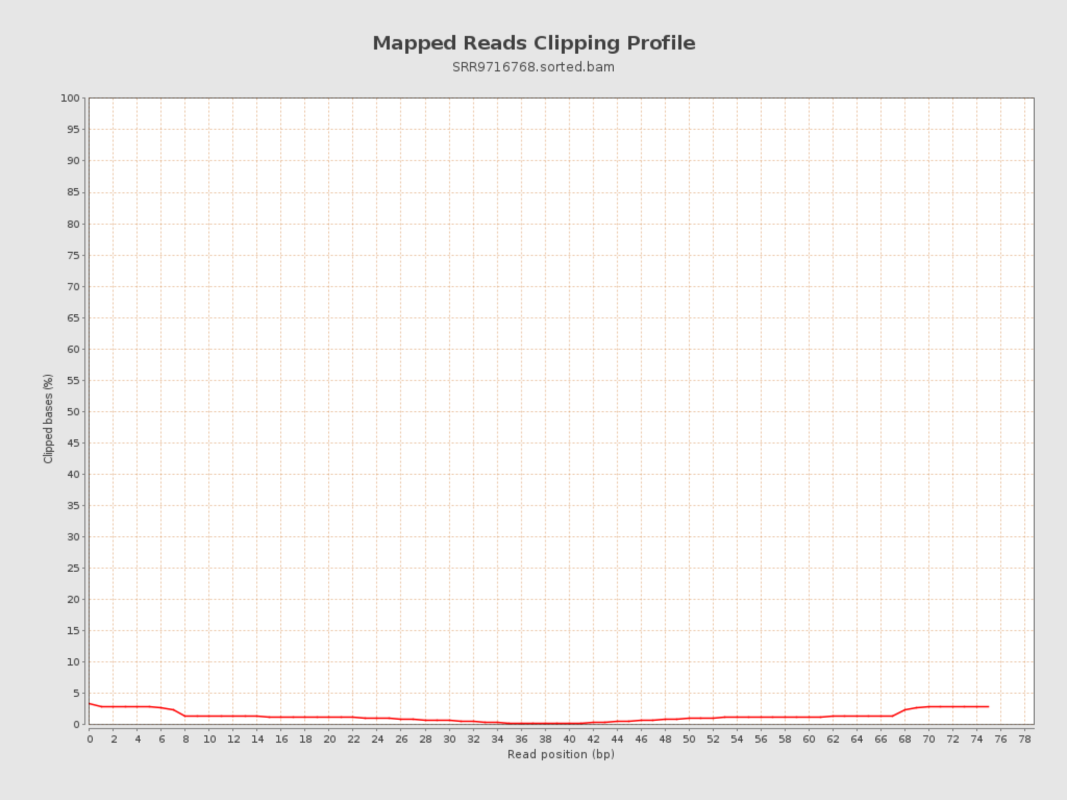
8. Results : Mapped Reads Nucleotide Content



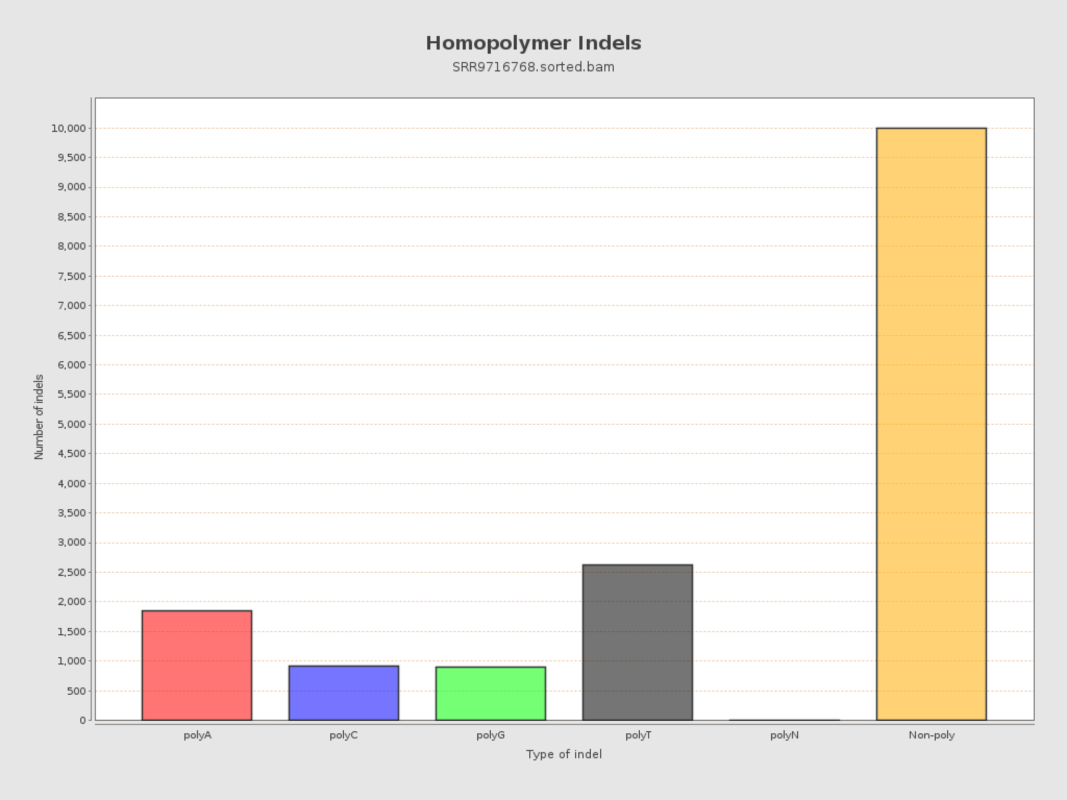
9. Results : Mapped Reads GC-content Distribution



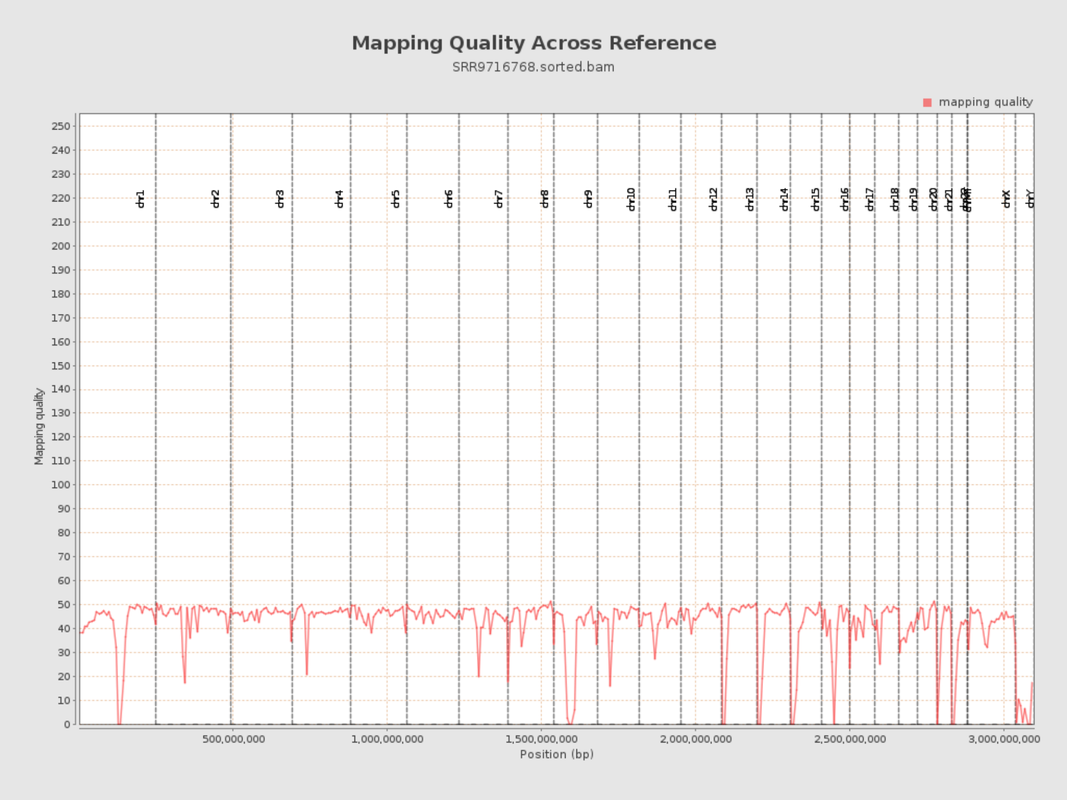
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram