Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 08:51:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716722.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_SRR9716722 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716722.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 08:51:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716722.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,013,179
Mapped reads	922,092 / 91.01%
Unmapped reads	91,087 / 8.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,454 / 0.54%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	22,379 / 2.21%
Duplication rate	1.7%
Clipped reads	925,312 / 91.33%

2.2. ACGT Content

Number/percentage of A's	13,530,379 / 25.04%
Number/percentage of C's	10,392,989 / 19.23%
Number/percentage of T's	17,059,842 / 31.57%
Number/percentage of G's	13,059,259 / 24.16%
Number/percentage of N's	750 / 0%
GC Percentage	43.4%

2.3. Coverage

Mean	0.0175

Standard Deviation	0.1893

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Mismatches and indels

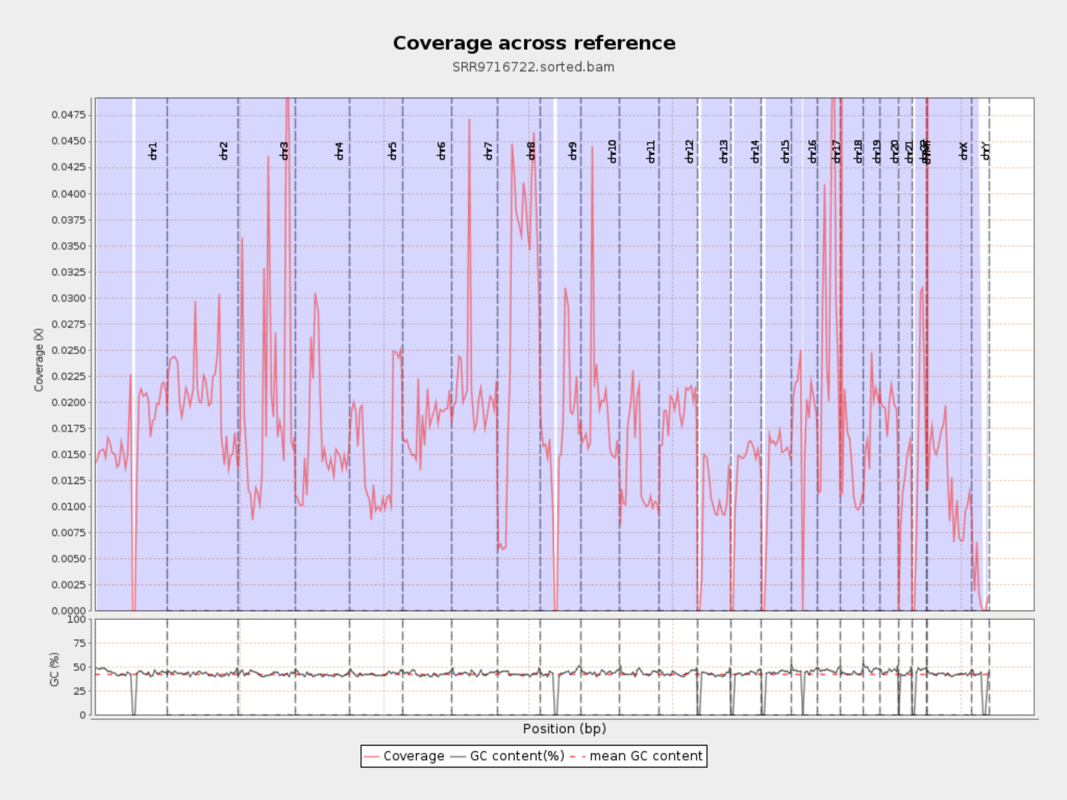
General error rate	0.49%
Mismatches	258,060
Insertions	3,719
Mapped reads with at least one insertion	0.4%
Deletions	9,241
Mapped reads with at least one deletion	1%
Homopolymer indels	42.72%

2.6. Chromosome stats

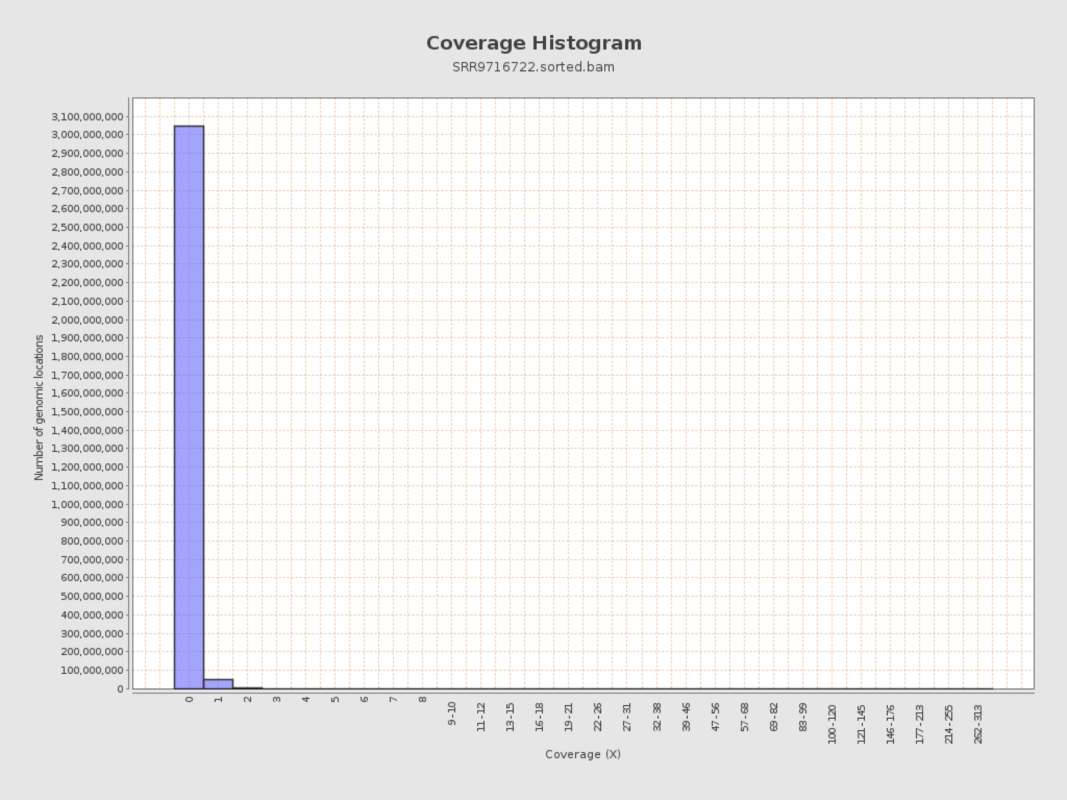
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4071487	0.0163	0.228
chr2	243199373	5013765	0.0206	0.2092
chr3	198022430	4117016	0.0208	0.1581
chr4	191154276	3065867	0.016	0.1402
chr5	180915260	2759486	0.0153	0.13
chr6	171115067	3054953	0.0179	0.1463
chr7	159138663	3432031	0.0216	0.405

chr8	146364022	4361081	0.0298	0.2219
chr9	141213431	2322807	0.0164	0.1489
chr10	135534747	2618757	0.0193	0.2419
chr11	135006516	1844753	0.0137	0.1387
chr12	133851895	2589068	0.0193	0.1576
chr13	115169878	1092415	0.0095	0.1018
chr14	107349540	1372584	0.0128	0.1209
chr15	102531392	1326303	0.0129	0.1207
chr16	90354753	1669550	0.0185	0.1475
chr17	81195210	2305900	0.0284	0.1838
chr18	78077248	1250384	0.016	0.2053
chr19	59128983	1093123	0.0185	0.23
chr20	63025520	1217639	0.0193	0.1502
chr21	48129895	559228	0.0116	0.1184
chr22	51304566	806323	0.0157	0.132
chrMT	16571	63610	3.8386	2.8691
chrX	155270560	1929184	0.0124	0.1283
chrY	59373566	120225	0.002	0.0619

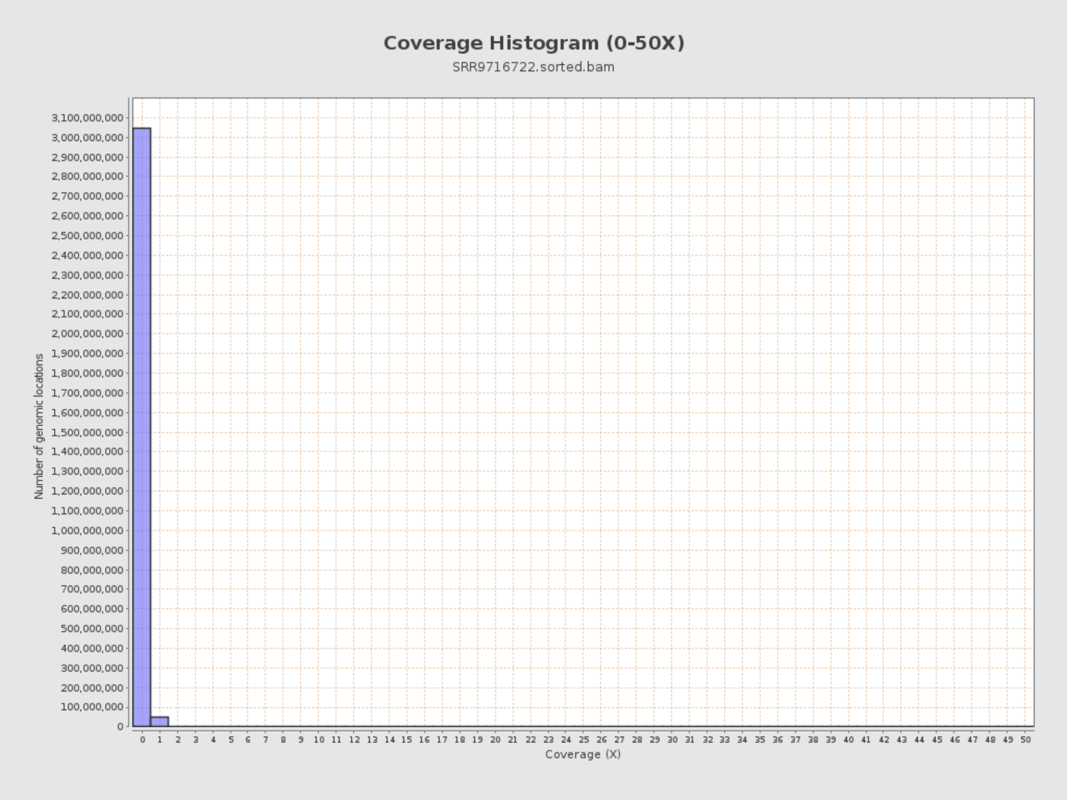
3. Results : Coverage across reference



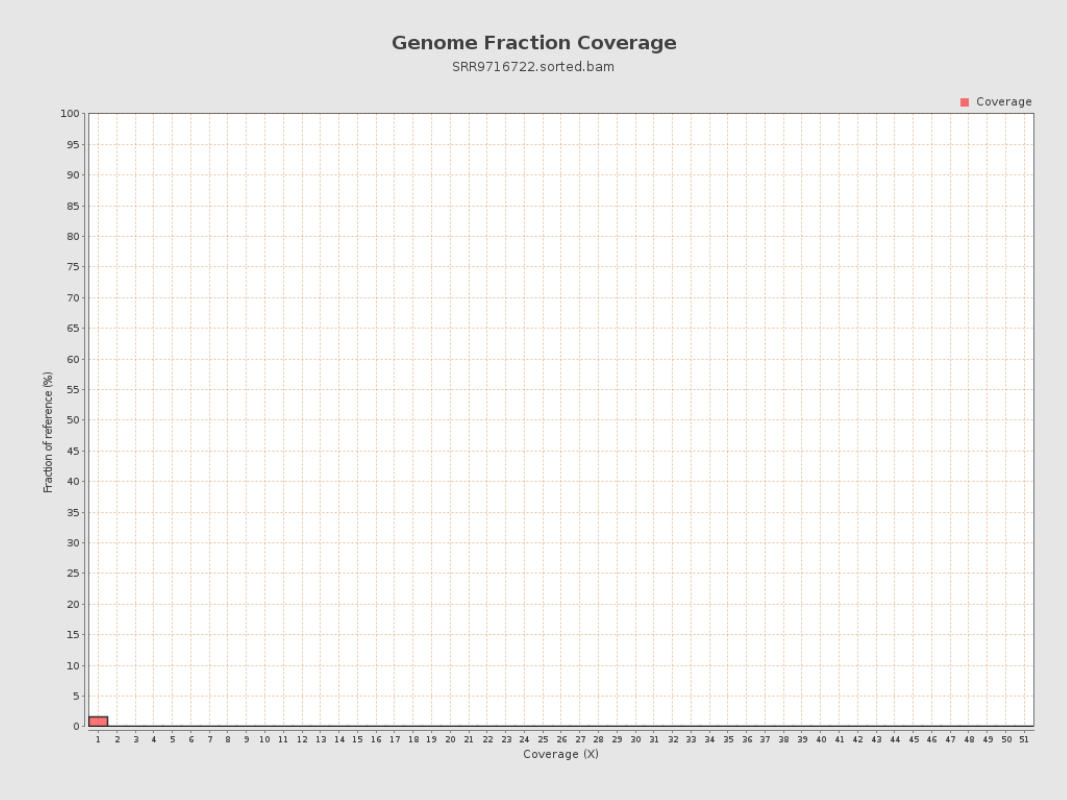
4. Results : Coverage Histogram



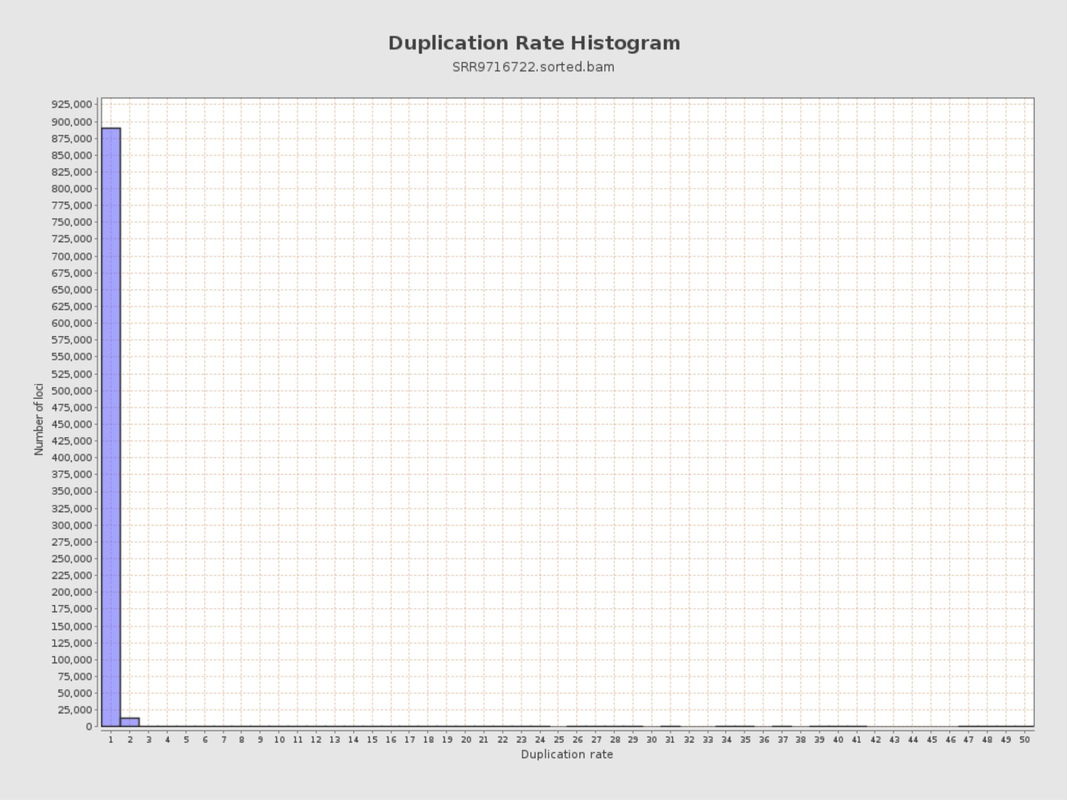
5. Results : Coverage Histogram (0-50X)



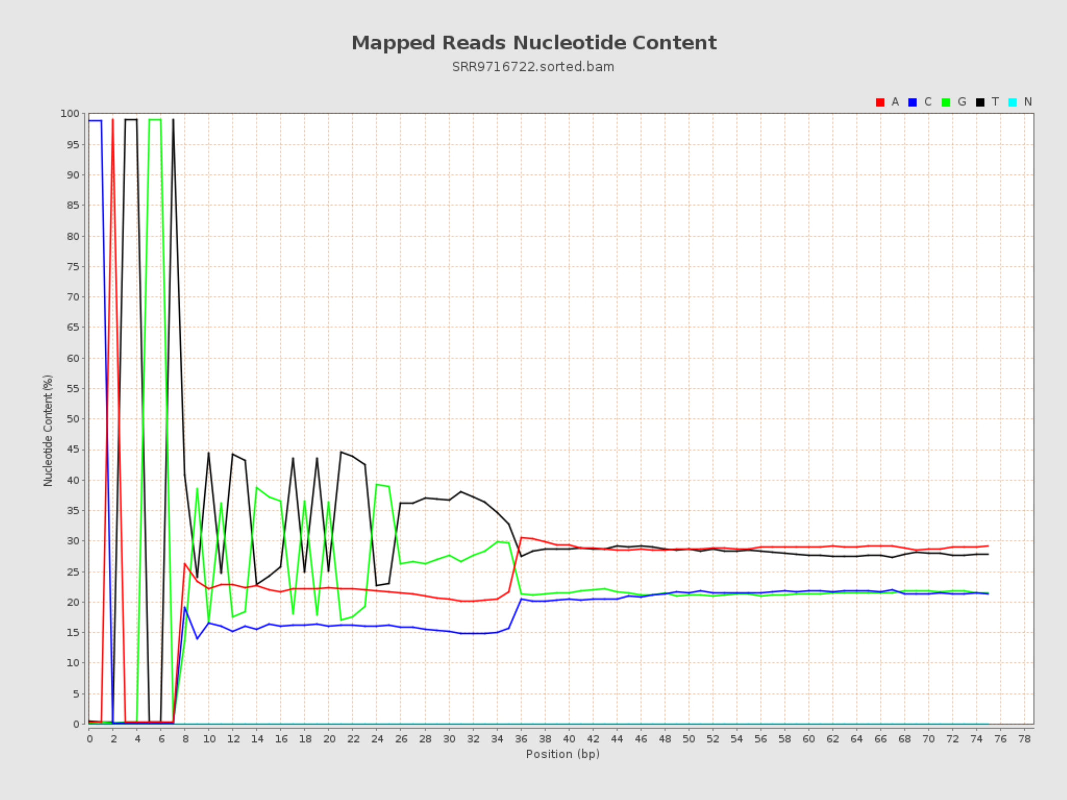
6. Results : Genome Fraction Coverage



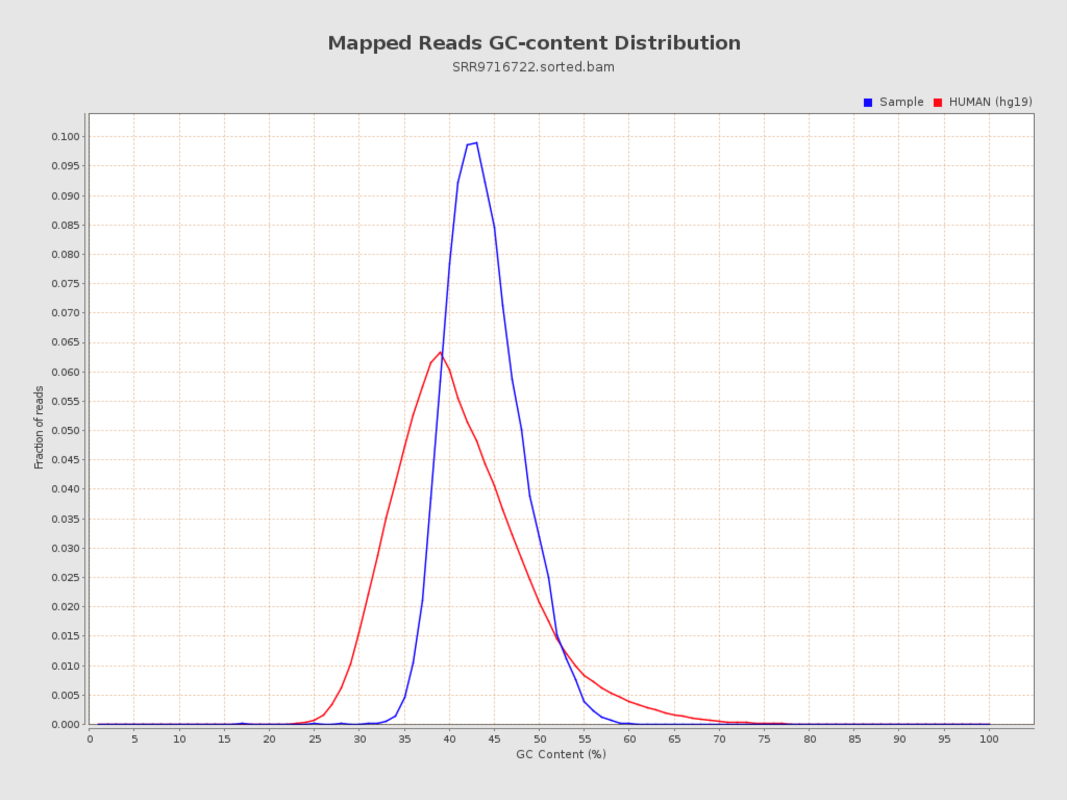
7. Results : Duplication Rate Histogram



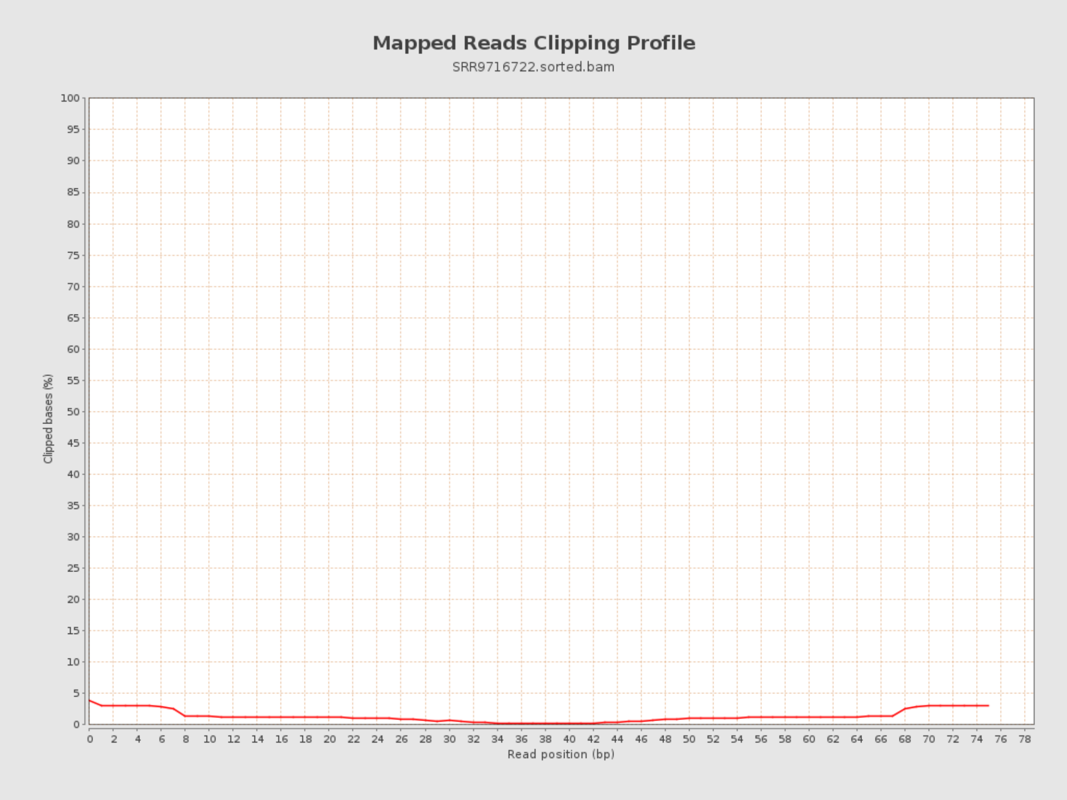
8. Results : Mapped Reads Nucleotide Content



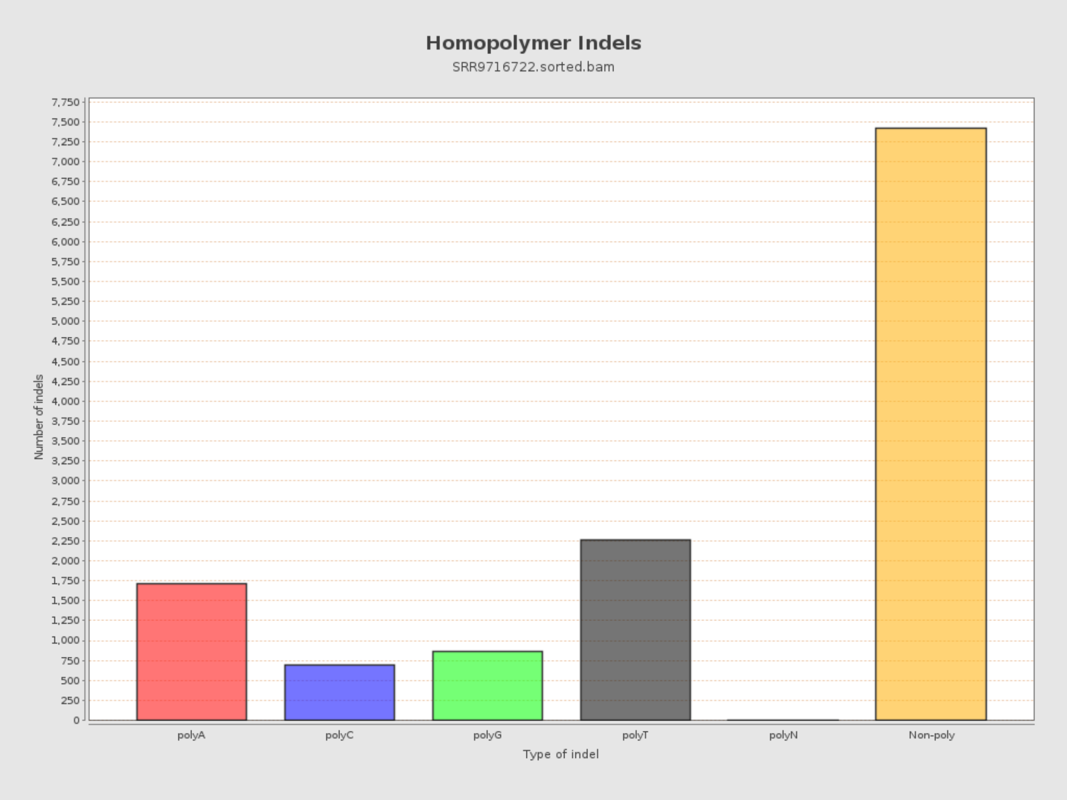
9. Results : Mapped Reads GC-content Distribution



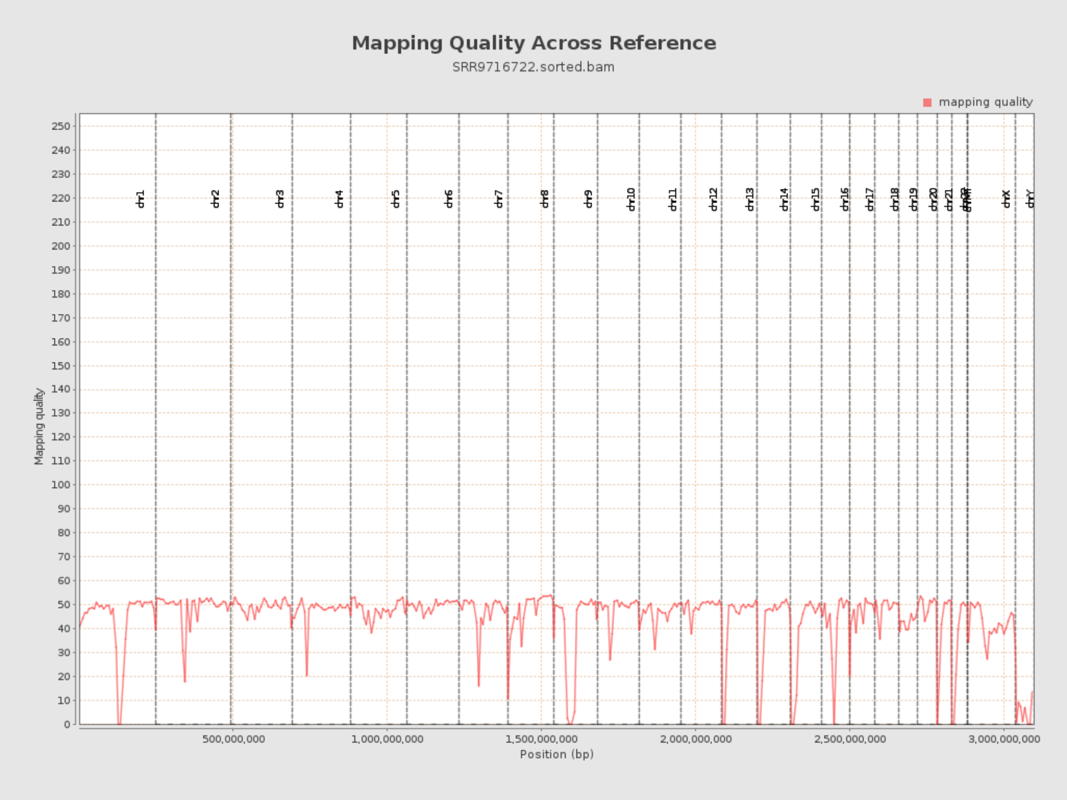
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram