Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 10:34:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716764.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_SRR9716764 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716764.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 10:34:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716764.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	851,141
Mapped reads	786,260 / 92.38%
Unmapped reads	64,881 / 7.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,159 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	25,190 / 2.96%
Duplication rate	2.38%
Clipped reads	787,794 / 92.56%

2.2. ACGT Content

Number/percentage of A's	11,316,944 / 24.71%
Number/percentage of C's	8,217,275 / 17.94%
Number/percentage of T's	14,310,698 / 31.24%
Number/percentage of G's	11,960,756 / 26.11%
Number/percentage of N's	883 / 0%
GC Percentage	44.05%

2.3. Coverage

Mean	0.0148

Standard Deviation	0.1652

2.4. Mapping Quality

Mean Mapping Quality	44.93

2.5. Mismatches and indels

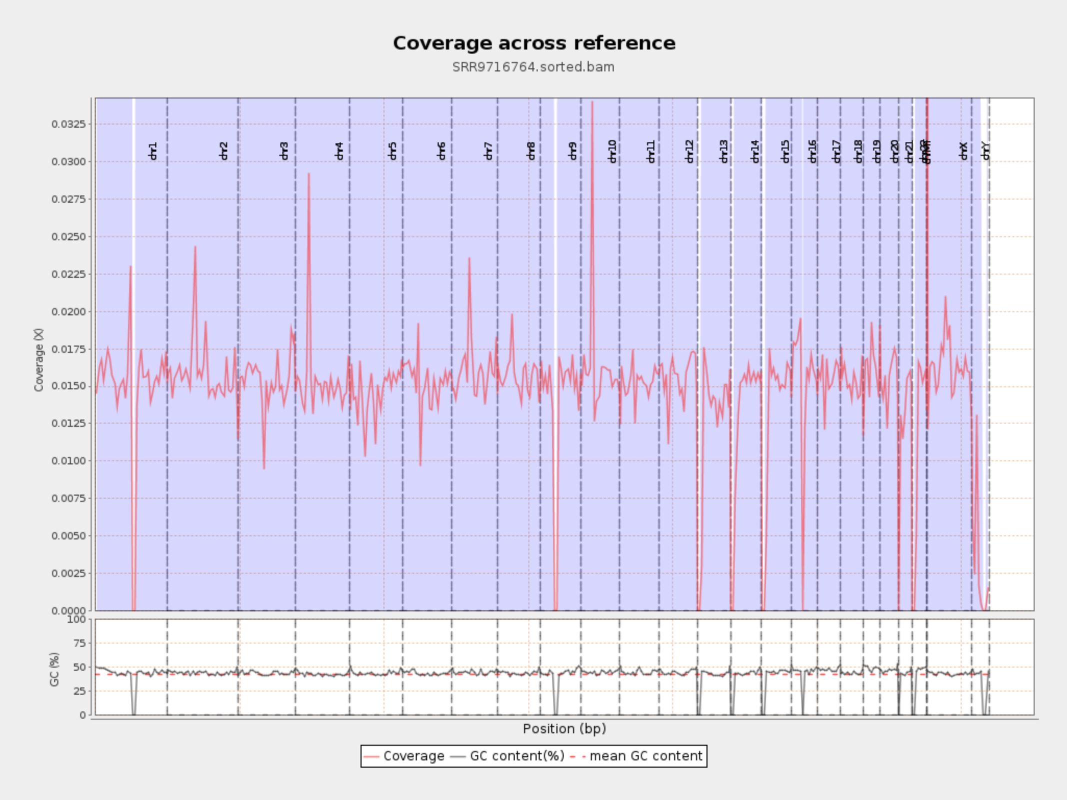
General error rate	0.52%
Mismatches	230,149
Insertions	3,309
Mapped reads with at least one insertion	0.42%
Deletions	8,498
Mapped reads with at least one deletion	1.07%
Homopolymer indels	43%

2.6. Chromosome stats

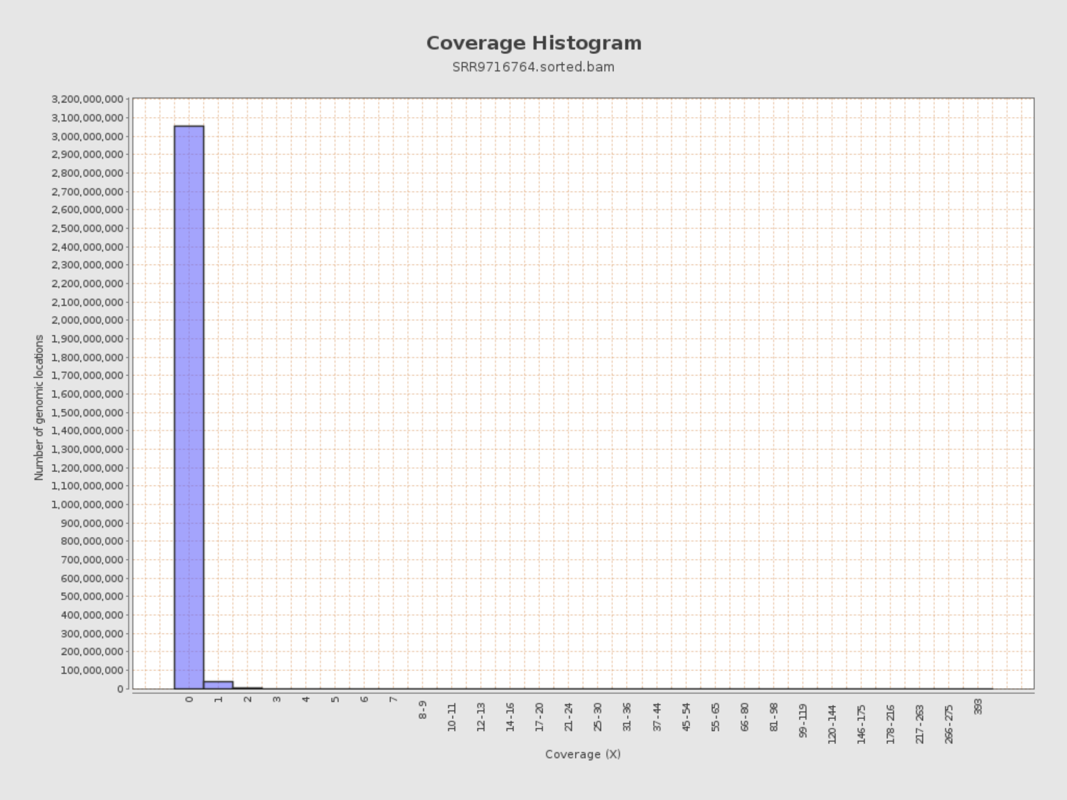
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3709823	0.0149	0.2344
chr2	243199373	3879568	0.016	0.2219
chr3	198022430	3045876	0.0154	0.1324
chr4	191154276	2950576	0.0154	0.1525
chr5	180915260	2647071	0.0146	0.1286
chr6	171115067	2604282	0.0152	0.1399
chr7	159138663	2576442	0.0162	0.1779

chr8	146364022	2305129	0.0157	0.1871
chr9	141213431	1950962	0.0138	0.1409
chr10	135534747	2238547	0.0165	0.203
chr11	135006516	2059735	0.0153	0.1437
chr12	133851895	2091248	0.0156	0.1331
chr13	115169878	1393005	0.0121	0.1166
chr14	107349540	1382346	0.0129	0.1221
chr15	102531392	1308947	0.0128	0.1203
chr16	90354753	1360305	0.0151	0.1367
chr17	81195210	1268500	0.0156	0.1379
chr18	78077248	1199444	0.0154	0.2109
chr19	59128983	960785	0.0162	0.1941
chr20	63025520	973331	0.0154	0.1344
chr21	48129895	610980	0.0127	0.1399
chr22	51304566	564142	0.011	0.1121
chrMT	16571	23237	1.4023	1.3902
chrX	155270560	2536063	0.0163	0.1416
chrY	59373566	179953	0.003	0.1491

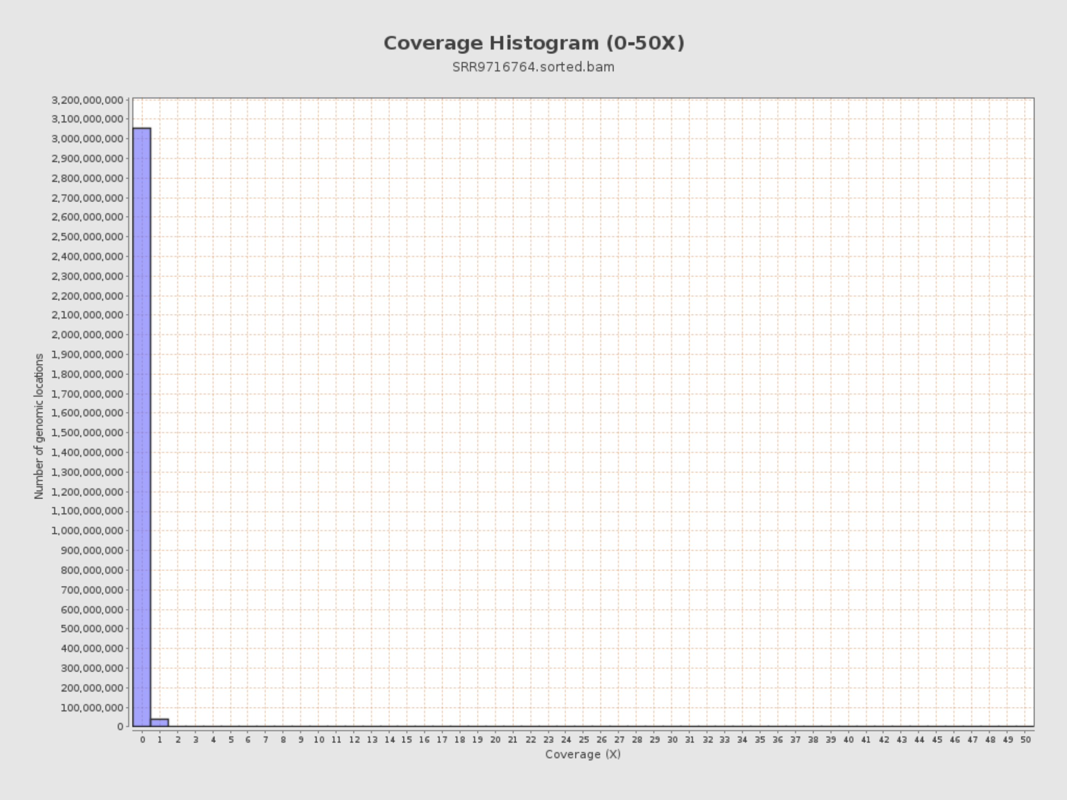
3. Results : Coverage across reference



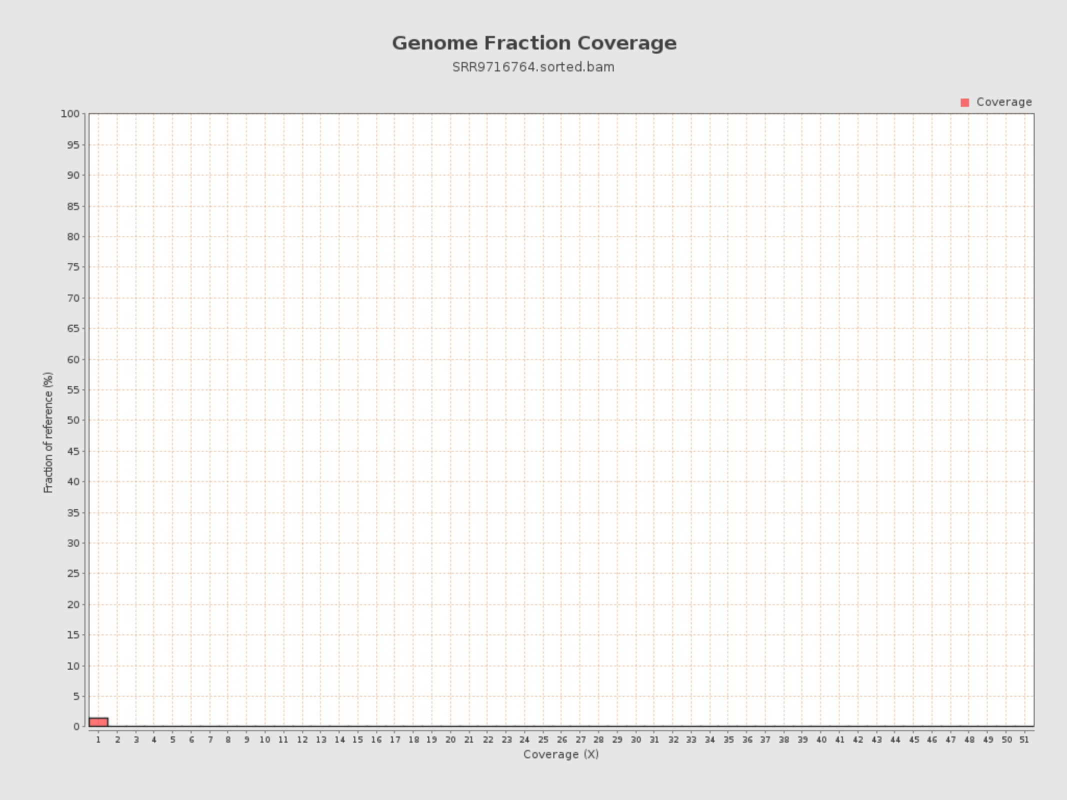
4. Results : Coverage Histogram



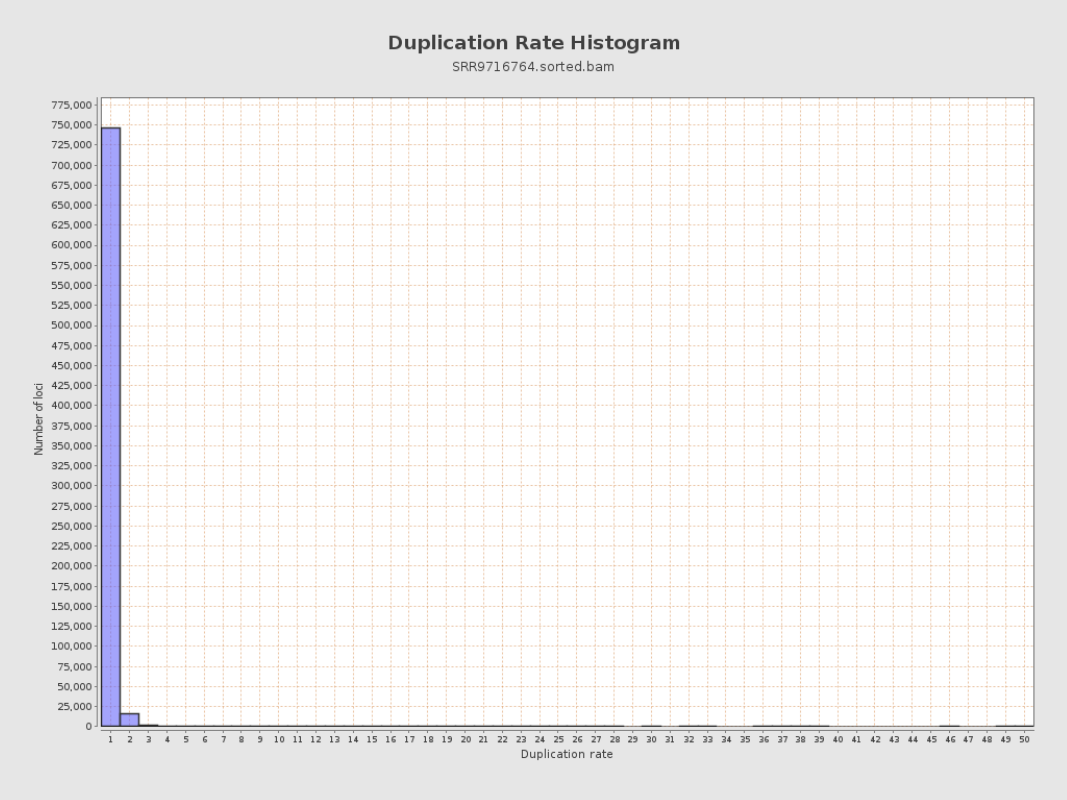
5. Results : Coverage Histogram (0-50X)



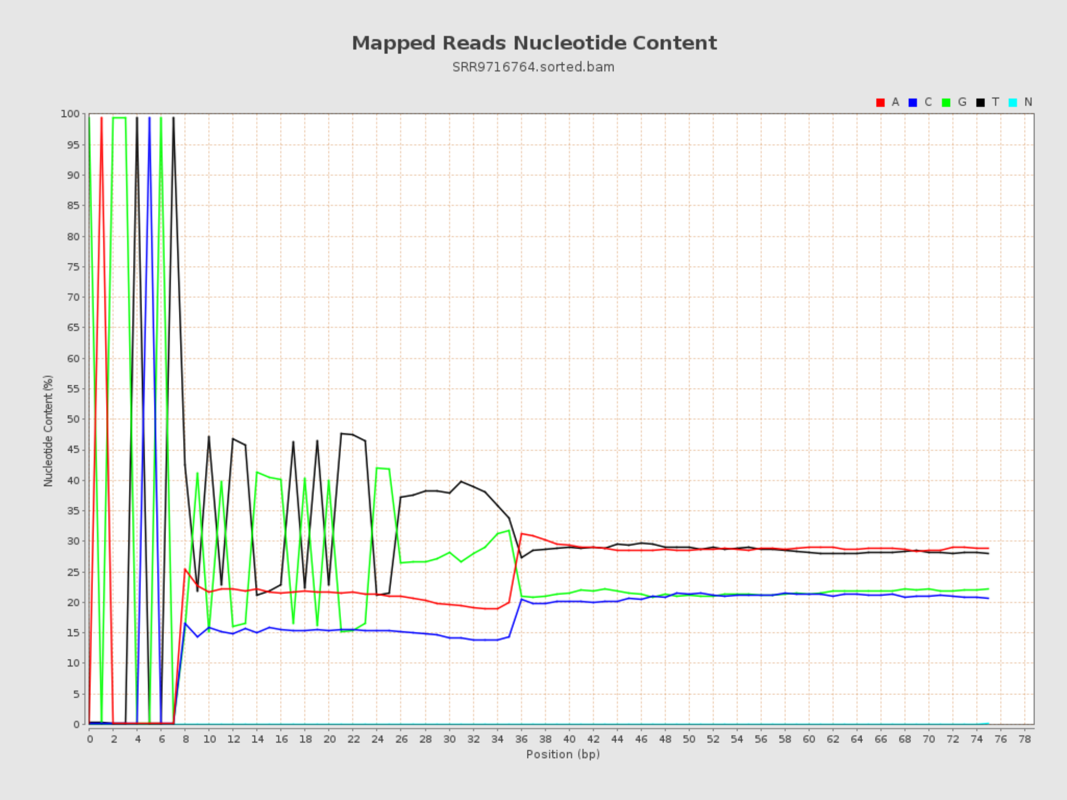
6. Results : Genome Fraction Coverage



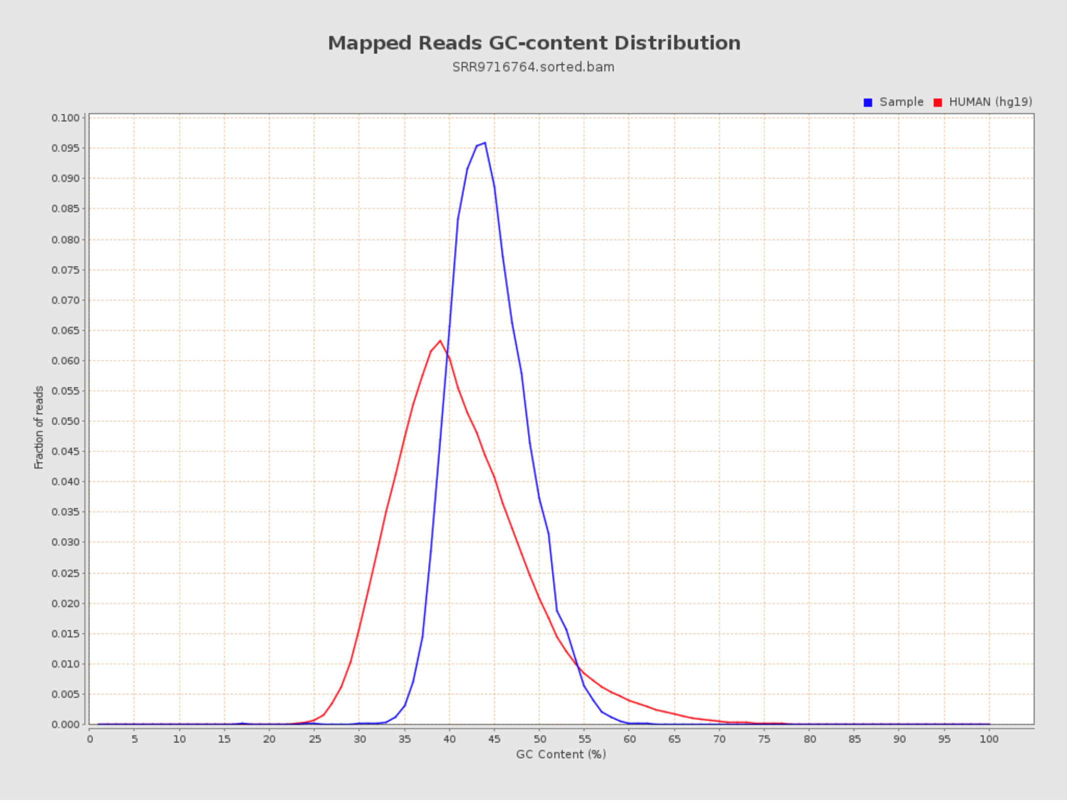
7. Results : Duplication Rate Histogram



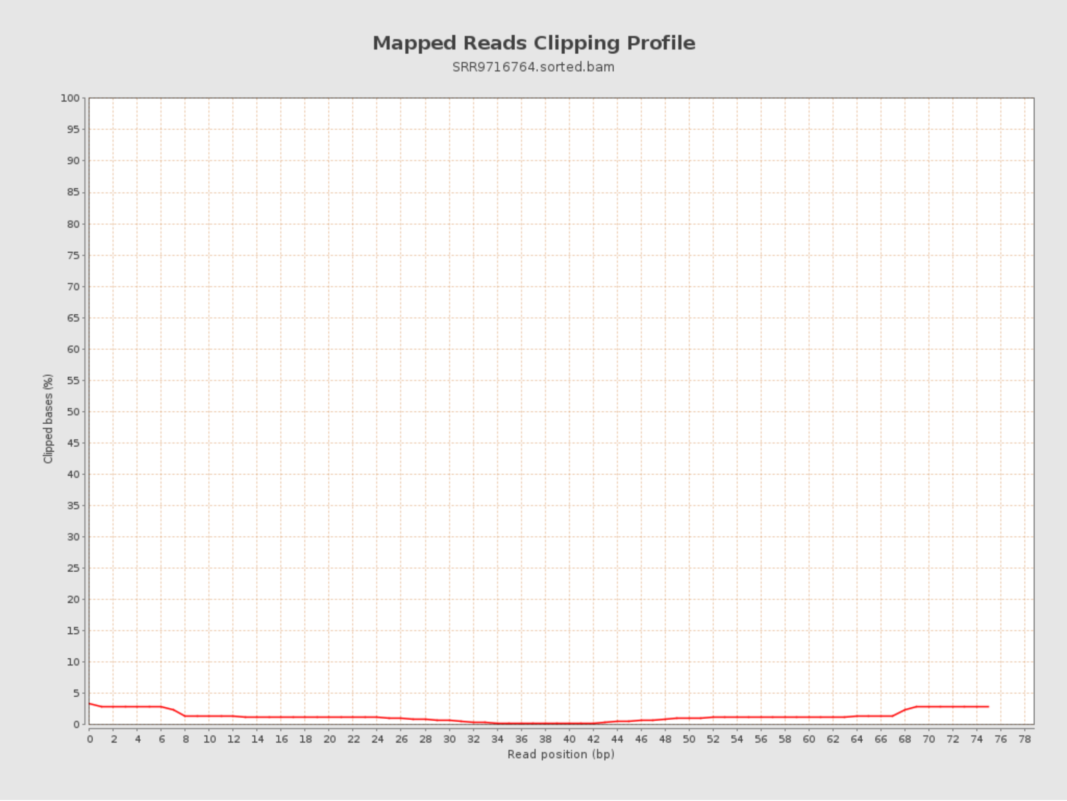
8. Results : Mapped Reads Nucleotide Content



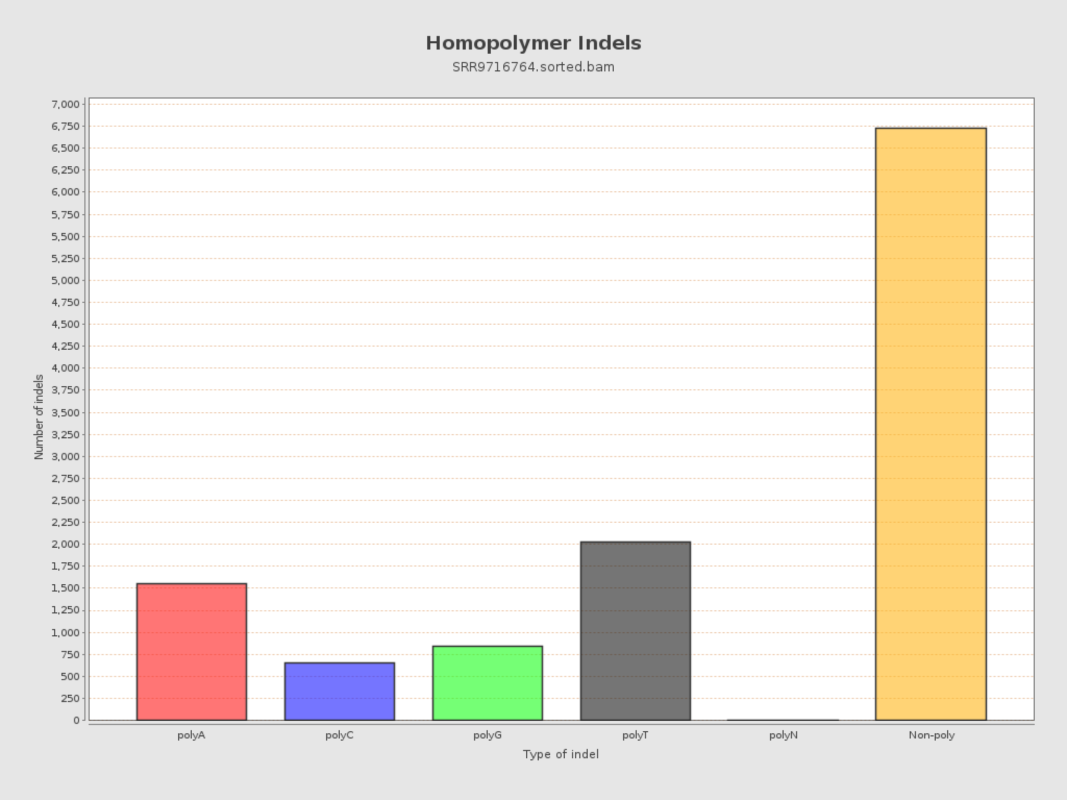
9. Results : Mapped Reads GC-content Distribution



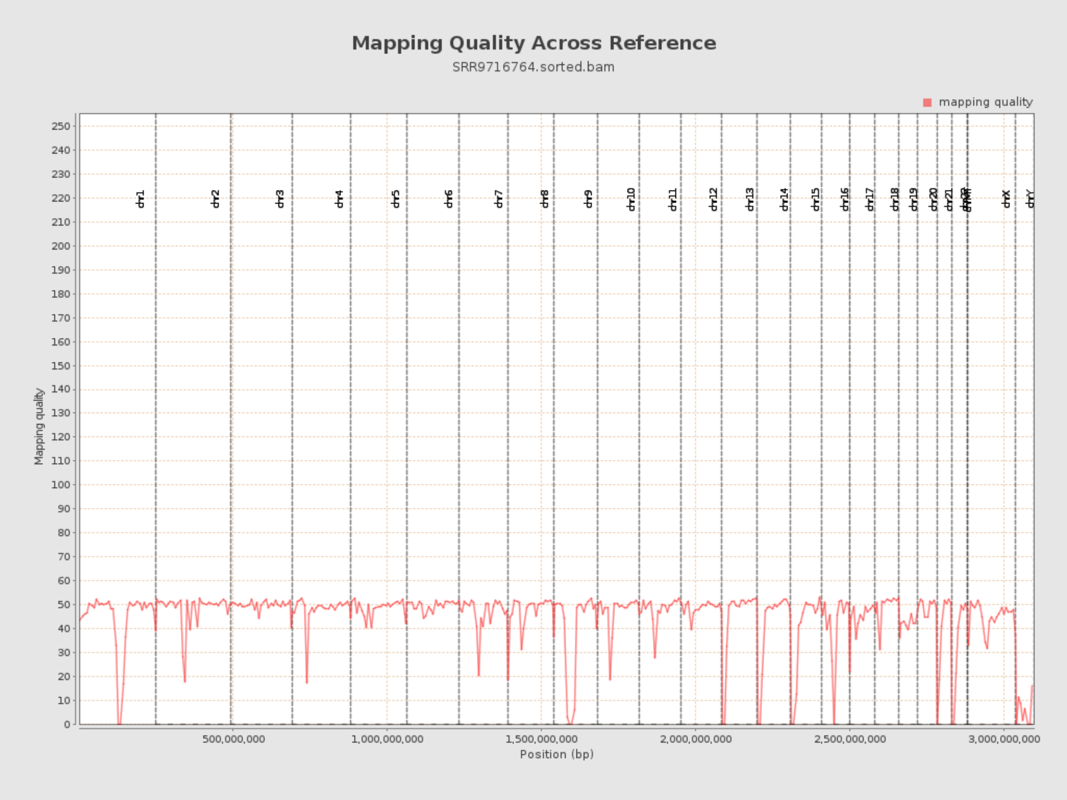
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram