Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 05:32:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716281.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_SRR9716281 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716281.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 05:32:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716281.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,351,282
Mapped reads	1,224,984 / 90.65%
Unmapped reads	126,298 / 9.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,127 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	30,507 / 2.26%
Duplication rate	1.92%
Clipped reads	1,228,857 / 90.94%

2.2. ACGT Content

Number/percentage of A's	17,135,519 / 24.52%
Number/percentage of C's	13,515,266 / 19.34%
Number/percentage of T's	21,955,258 / 31.42%
Number/percentage of G's	17,270,041 / 24.71%
Number/percentage of N's	1,516 / 0%
GC Percentage	44.06%

2.3. Coverage

Mean	0.0226

Standard Deviation	0.199

2.4. Mapping Quality

Mean Mapping Quality	44.74

2.5. Mismatches and indels

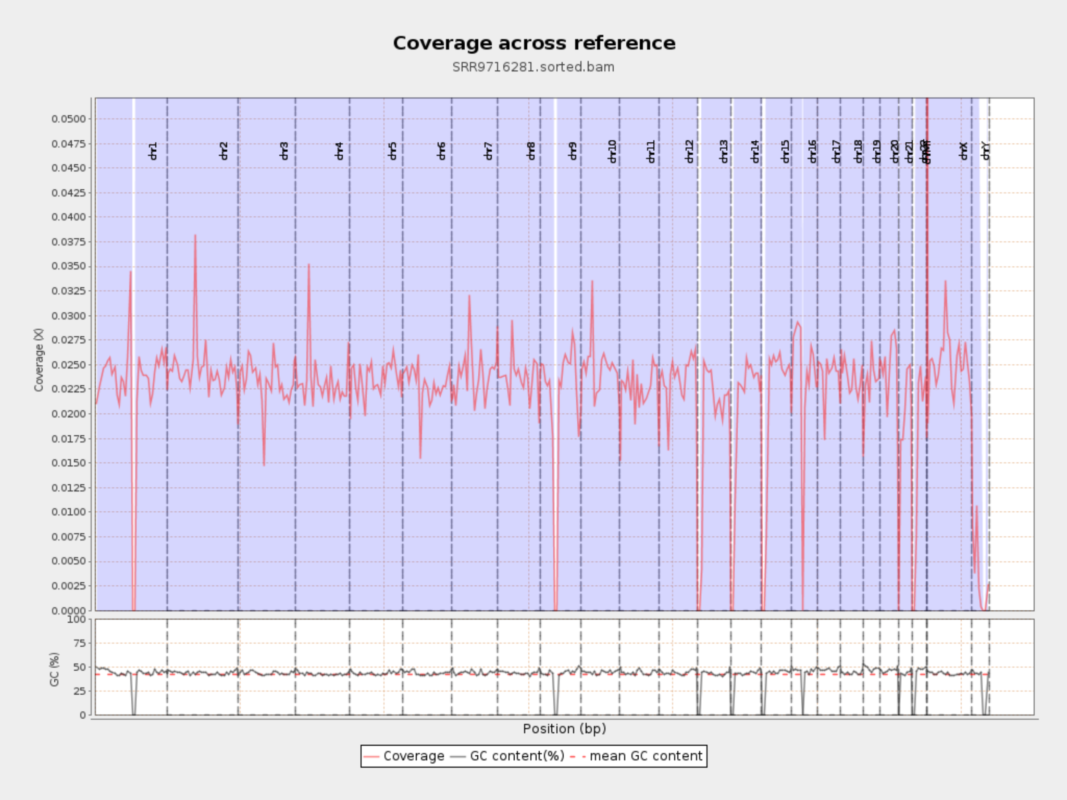
General error rate	0.49%
Mismatches	339,293
Insertions	3,685
Mapped reads with at least one insertion	0.3%
Deletions	10,056
Mapped reads with at least one deletion	0.82%
Homopolymer indels	41.82%

2.6. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5673086	0.0228	0.3114
chr2	243199373	5992386	0.0246	0.2191
chr3	198022430	4588311	0.0232	0.1628
chr4	191154276	4474059	0.0234	0.1747
chr5	180915260	4297672	0.0238	0.1664
chr6	171115067	3925656	0.0229	0.1681
chr7	159138663	3835779	0.0241	0.218

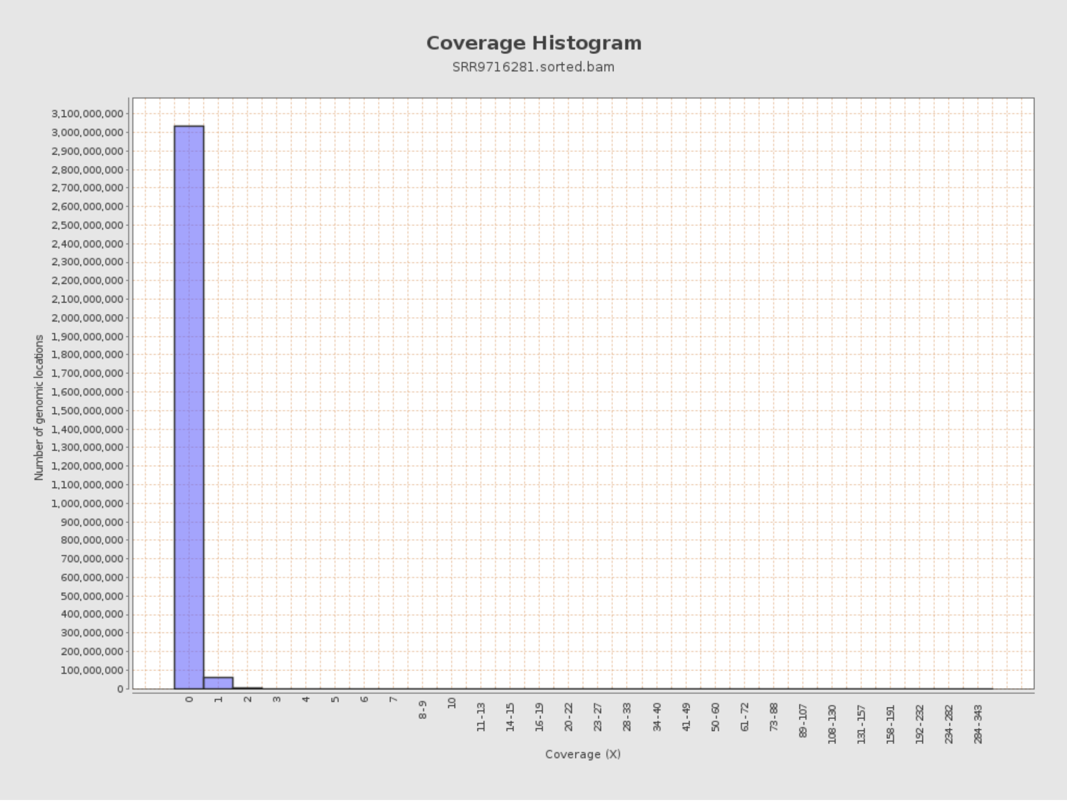
chr8	146364022	3460709	0.0236	0.19
chr9	141213431	2983683	0.0211	0.1968
chr10	135534747	3365553	0.0248	0.1941
chr11	135006516	3074213	0.0228	0.1936
chr12	133851895	3157489	0.0236	0.1655
chr13	115169878	2146901	0.0186	0.1457
chr14	107349540	2124639	0.0198	0.1558
chr15	102531392	2077597	0.0203	0.1539
chr16	90354753	2105978	0.0233	0.1718
chr17	81195210	1942452	0.0239	0.17
chr18	78077248	1850500	0.0237	0.3238
chr19	59128983	1389676	0.0235	0.2319
chr20	63025520	1563344	0.0248	0.171
chr21	48129895	912917	0.019	0.1576
chr22	51304566	816304	0.0159	0.1346
chrMT	16571	11428	0.6896	0.941
chrX	155270560	3926137	0.0253	0.1869
chrY	59373566	198192	0.0033	0.0824

3. Results : Coverage across reference

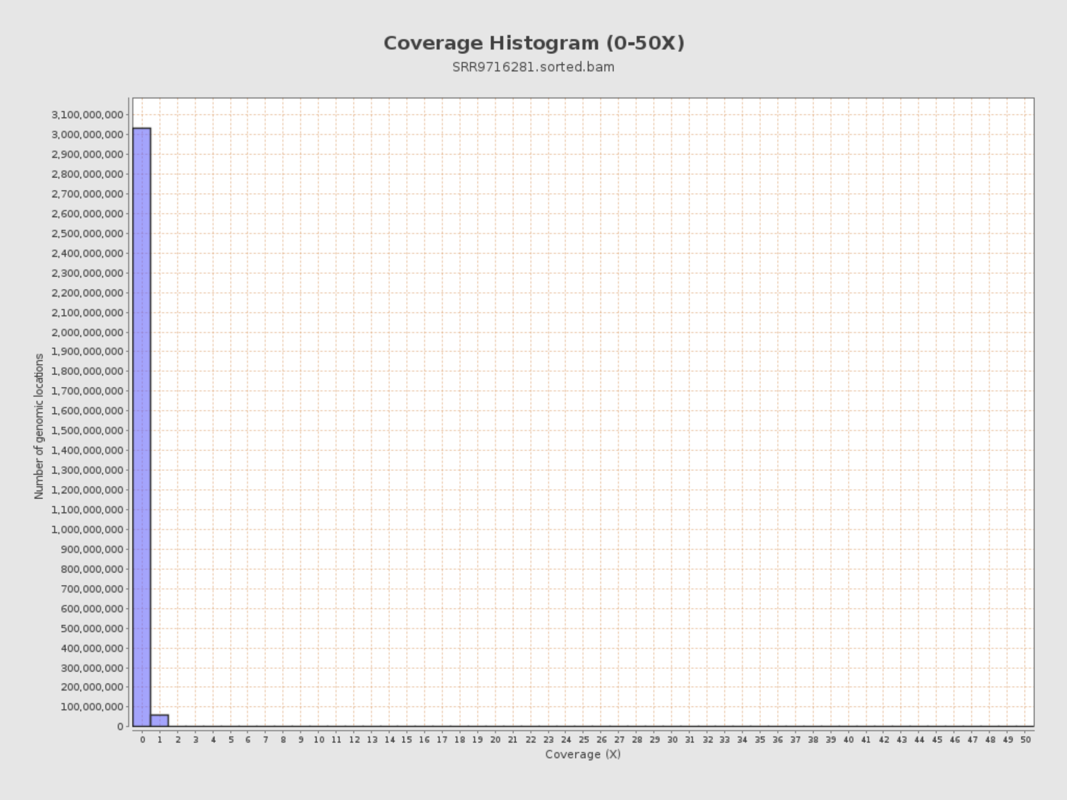


]

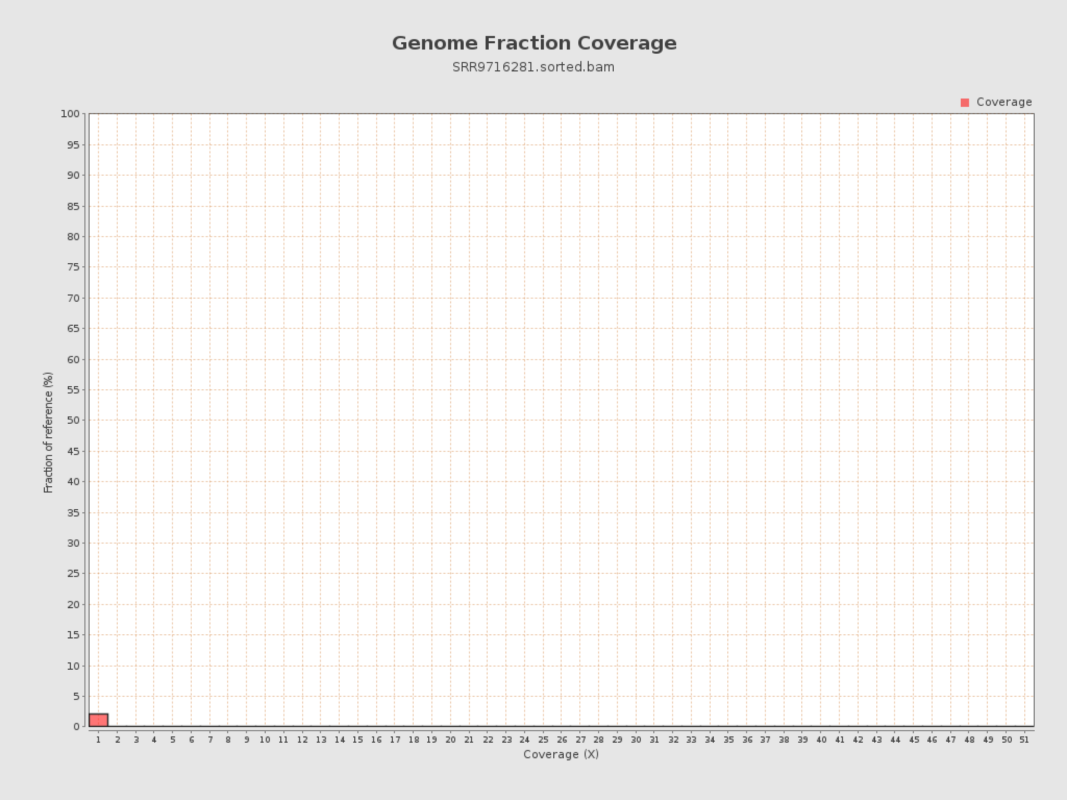
4. Results : Coverage Histogram



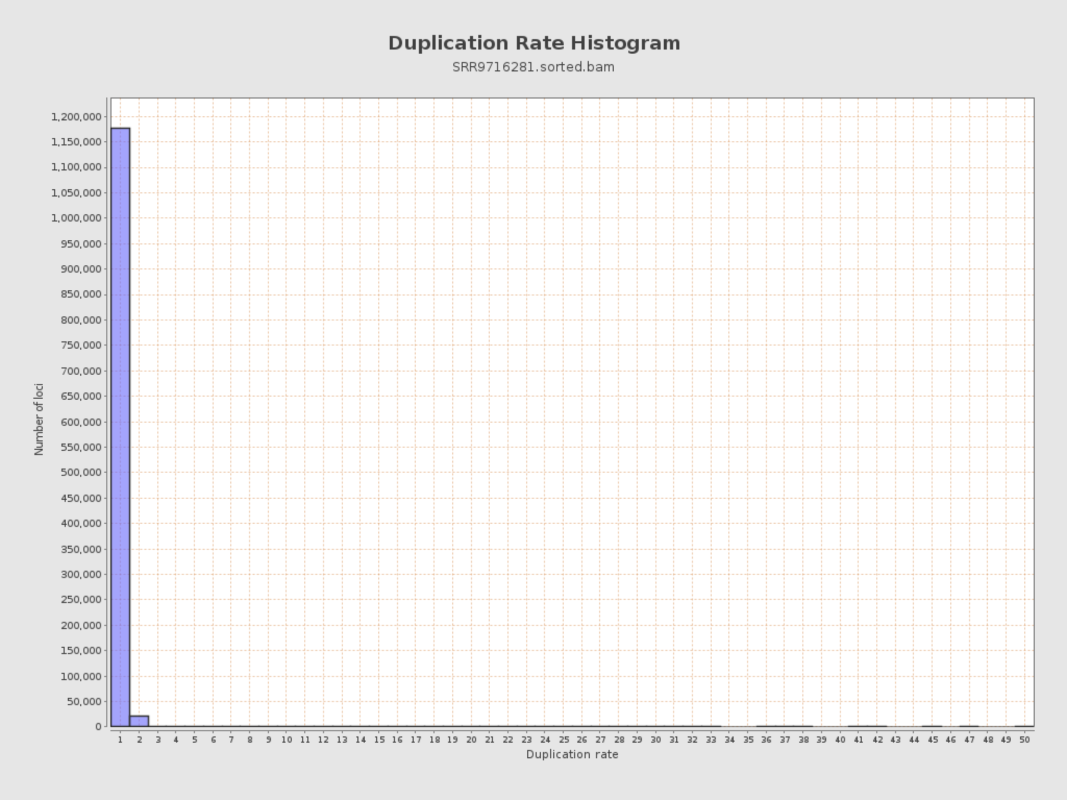
5. Results : Coverage Histogram (0-50X)



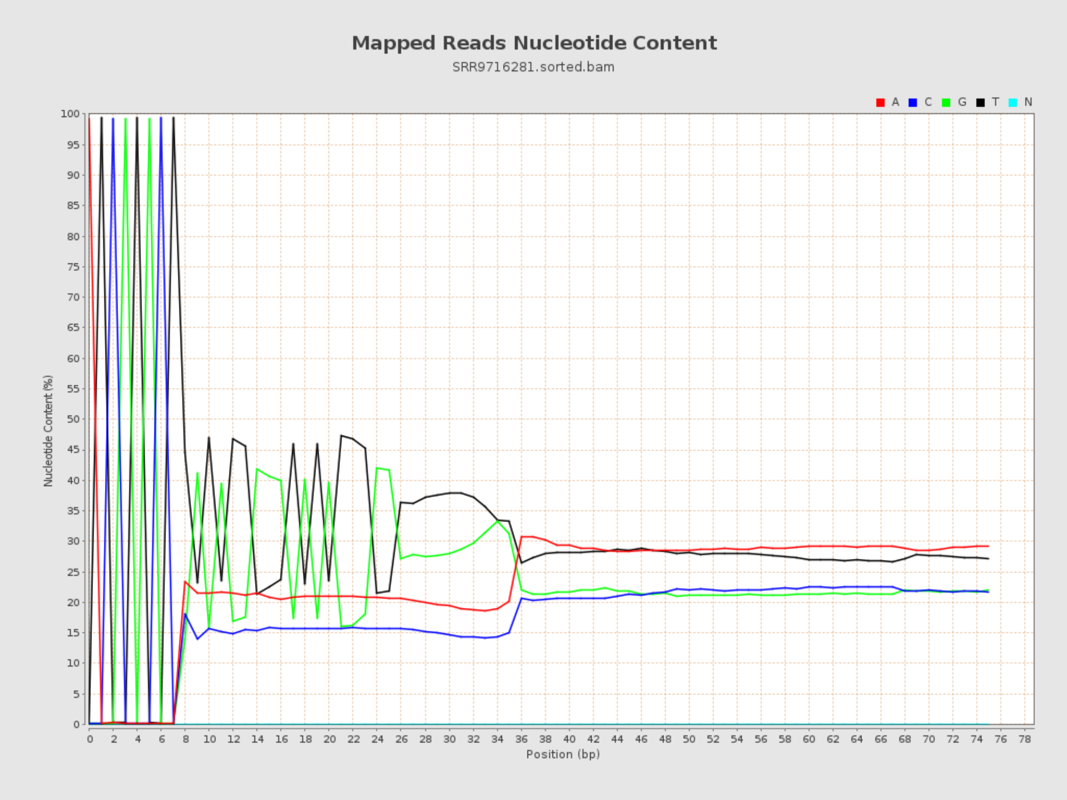
6. Results : Genome Fraction Coverage



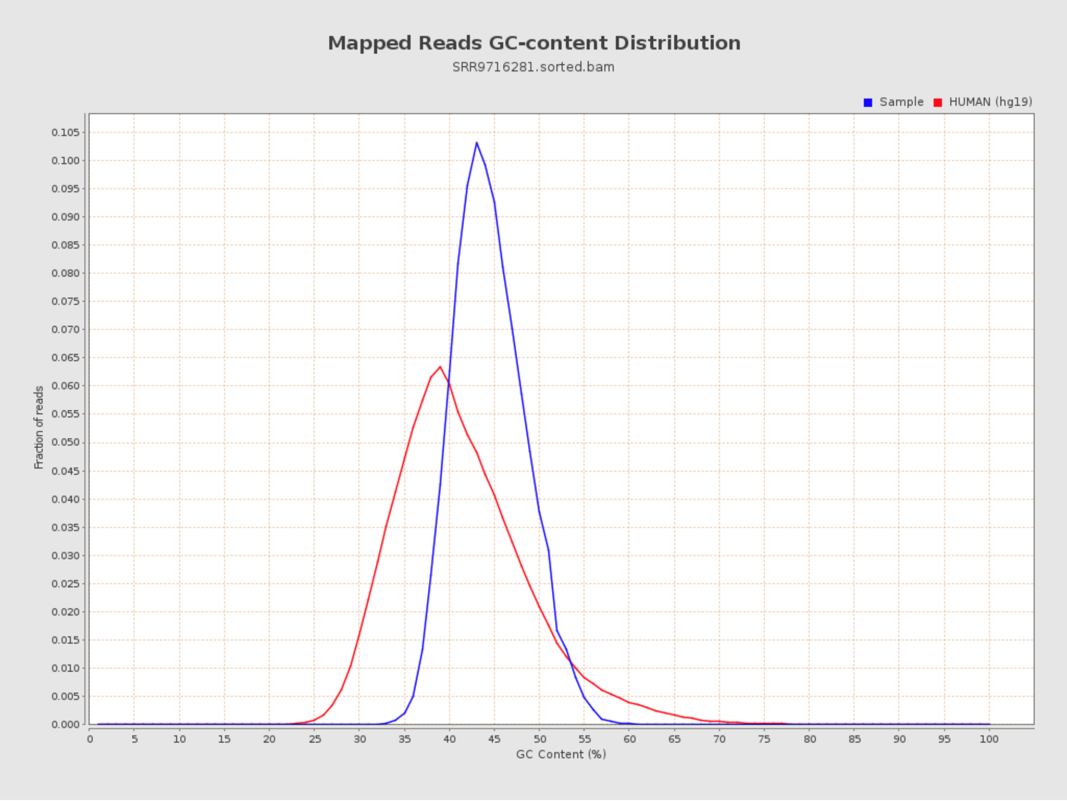
7. Results : Duplication Rate Histogram



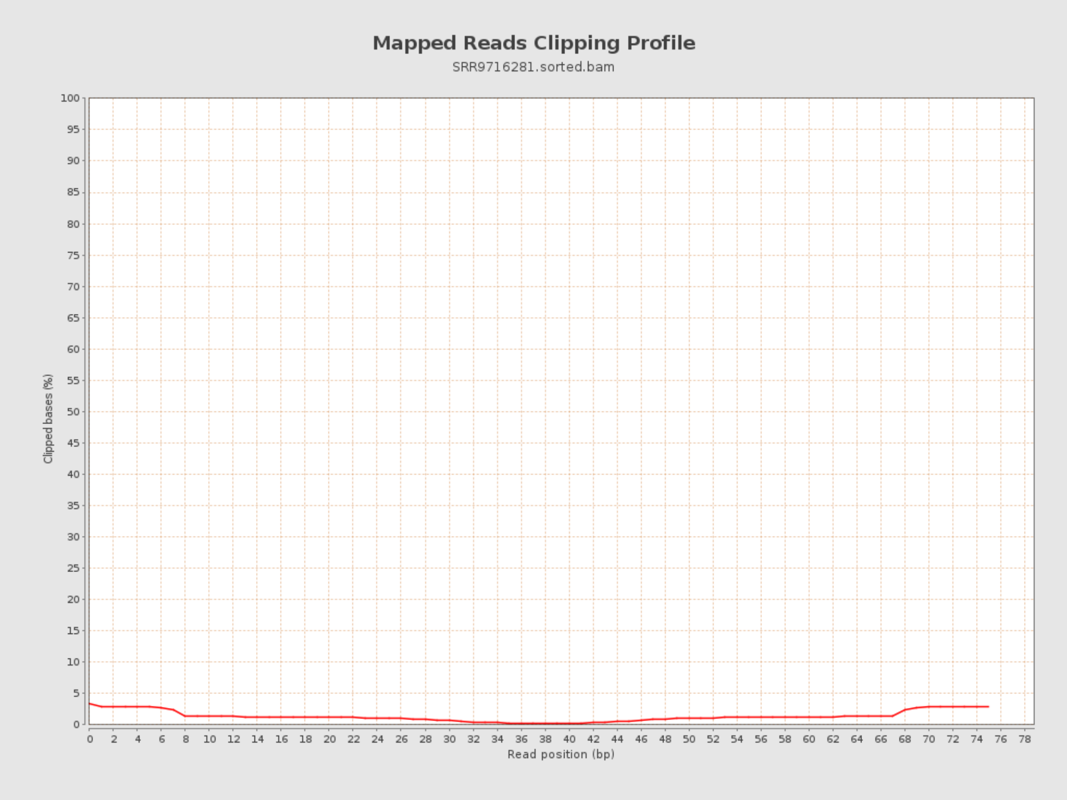
8. Results : Mapped Reads Nucleotide Content



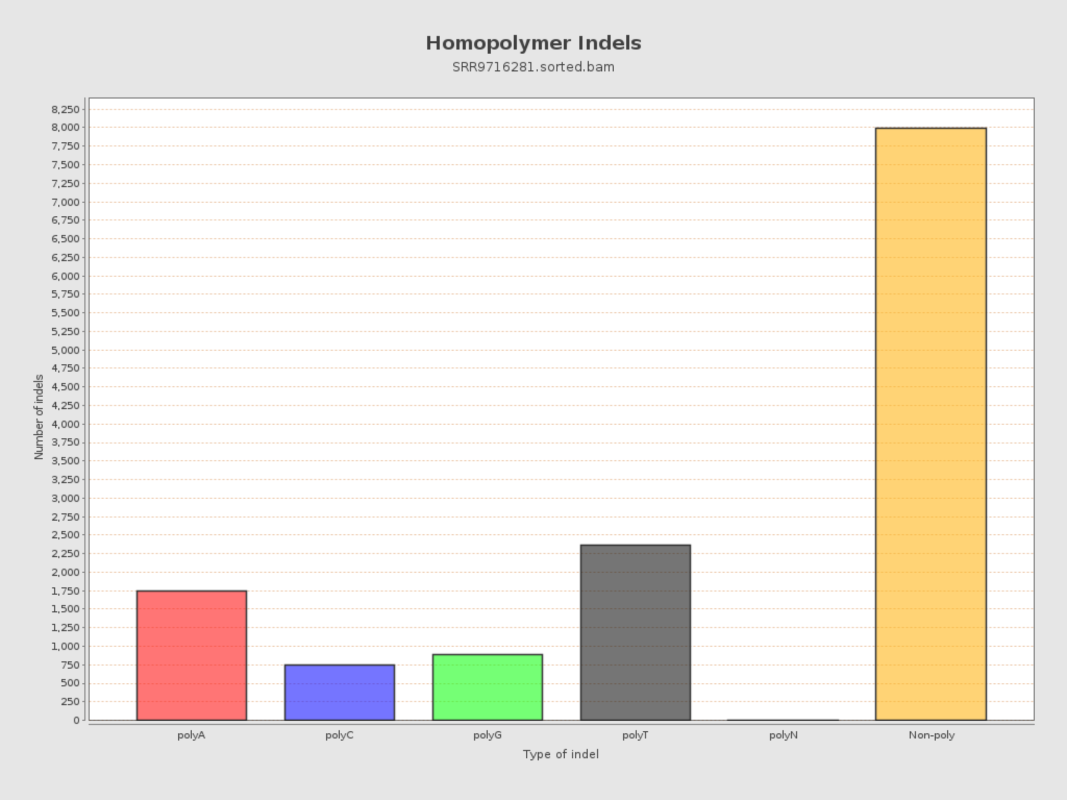
9. Results : Mapped Reads GC-content Distribution



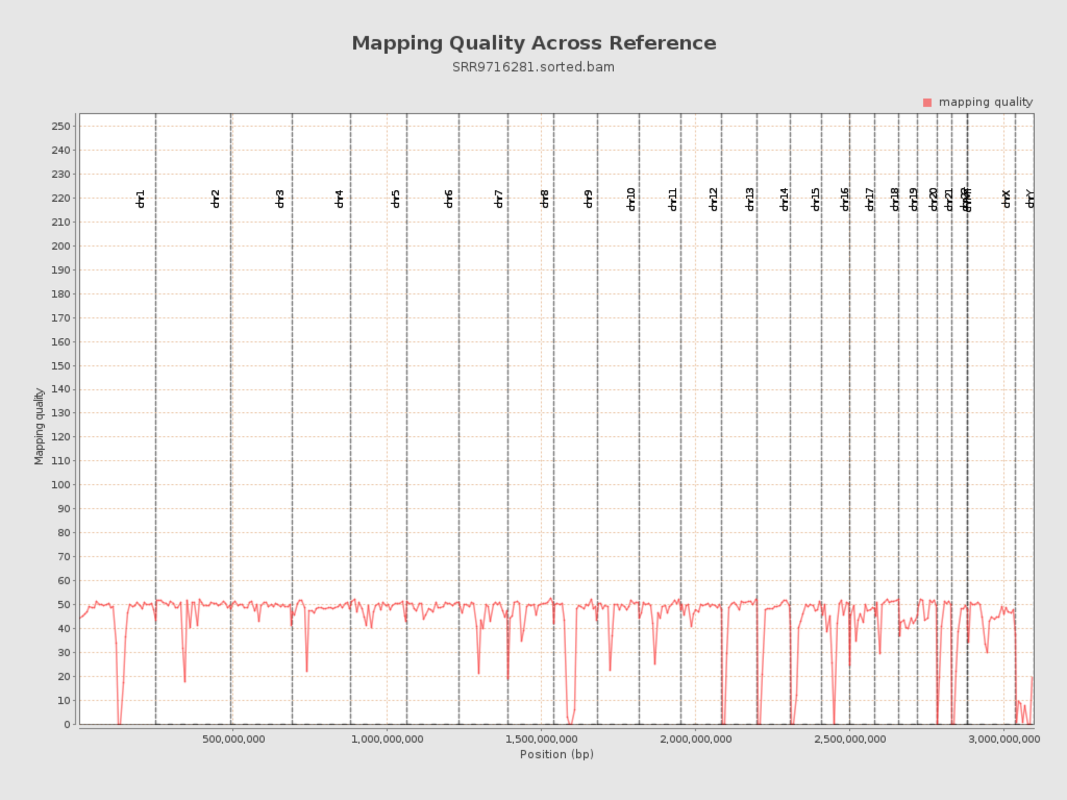
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram