Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:16:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716106.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_SRR9716106 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716106.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:16:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716106.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,446,436
Mapped reads	1,164,131 / 80.48%
Unmapped reads	282,305 / 19.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,521 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	35,220 / 2.43%
Duplication rate	2.25%
Clipped reads	1,166,077 / 80.62%

2.2. ACGT Content

Number/percentage of A's	17,194,061 / 25.61%
Number/percentage of C's	11,353,113 / 16.91%
Number/percentage of T's	21,664,673 / 32.27%
Number/percentage of G's	16,931,964 / 25.22%
Number/percentage of N's	1,854 / 0%
GC Percentage	42.12%

2.3. Coverage

Mean	0.0217

Standard Deviation	0.2123

2.4. Mapping Quality

Mean Mapping Quality	44.61

2.5. Mismatches and indels

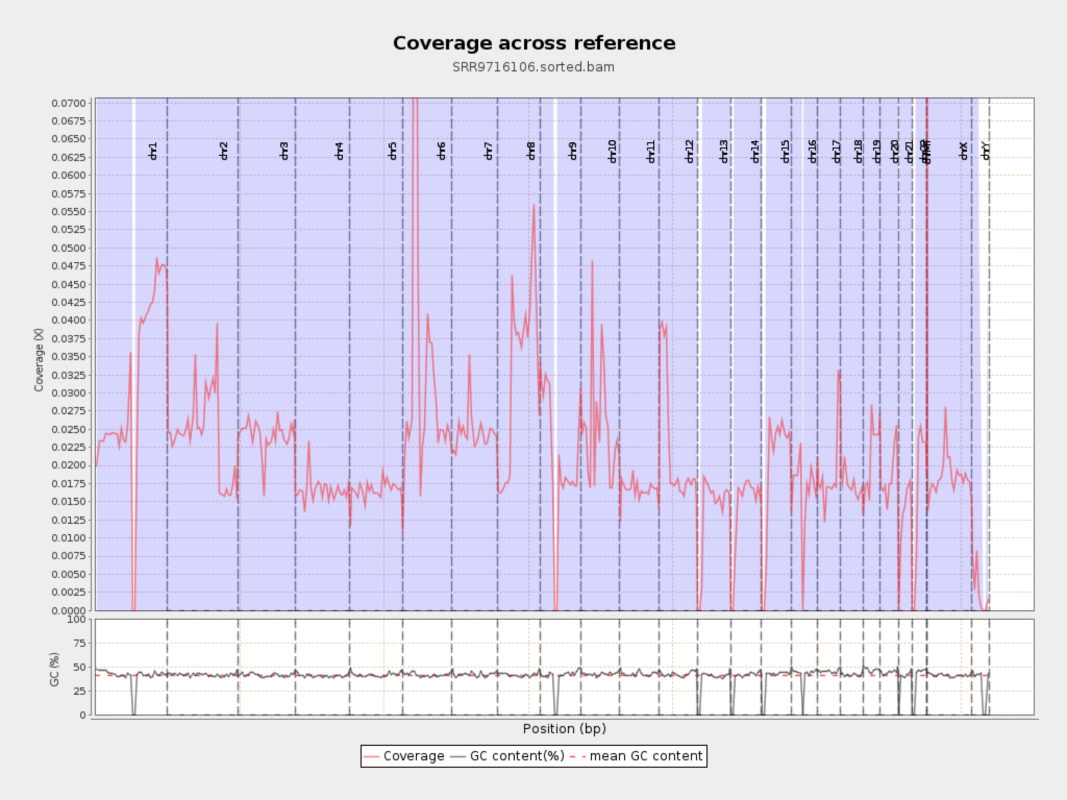
General error rate	0.52%
Mismatches	338,901
Insertions	4,692
Mapped reads with at least one insertion	0.4%
Deletions	12,772
Mapped reads with at least one deletion	1.09%
Homopolymer indels	43.74%

2.6. Chromosome stats

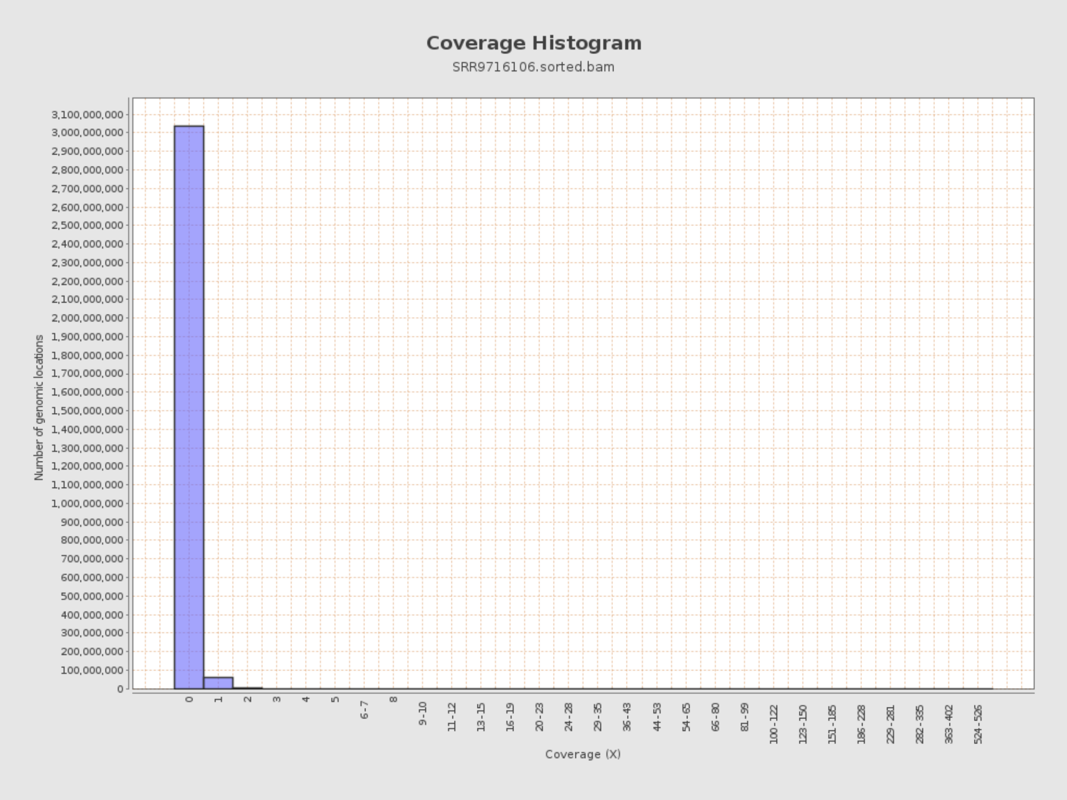
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7665019	0.0308	0.3507
chr2	243199373	5895492	0.0242	0.2757
chr3	198022430	4793066	0.0242	0.1669
chr4	191154276	3183027	0.0167	0.1437
chr5	180915260	3036618	0.0168	0.1402
chr6	171115067	5838102	0.0341	0.2381
chr7	159138663	3921919	0.0246	0.257

chr8	146364022	4855765	0.0332	0.2172
chr9	141213431	2859716	0.0203	0.1986
chr10	135534747	3445084	0.0254	0.2428
chr11	135006516	2268980	0.0168	0.171
chr12	133851895	3037324	0.0227	0.1652
chr13	115169878	1554895	0.0135	0.1245
chr14	107349540	1497066	0.0139	0.1386
chr15	102531392	2014938	0.0197	0.1522
chr16	90354753	1452555	0.0161	0.153
chr17	81195210	1544872	0.019	0.1528
chr18	78077248	1349869	0.0173	0.3105
chr19	59128983	1265598	0.0214	0.2405
chr20	63025520	1172545	0.0186	0.1474
chr21	48129895	628773	0.0131	0.1335
chr22	51304566	835477	0.0163	0.1365
chrMT	16571	1672	0.1009	0.3534
chrX	155270560	2890196	0.0186	0.165
chrY	59373566	156986	0.0026	0.0725

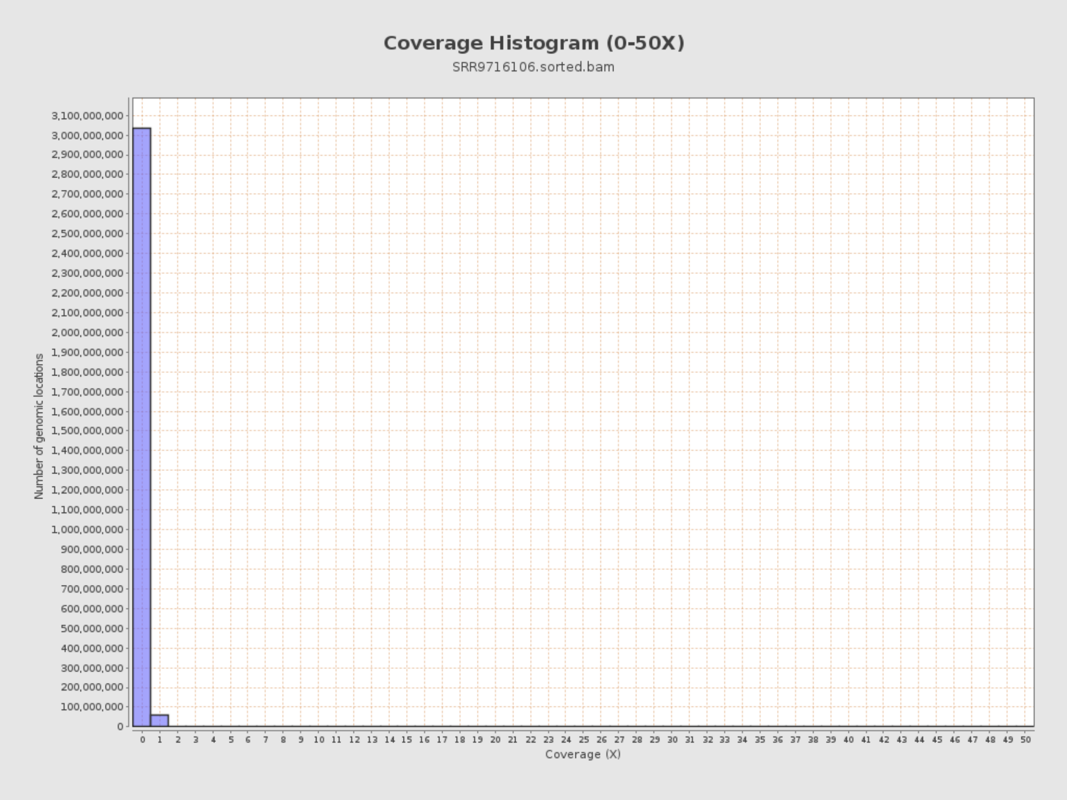
3. Results : Coverage across reference



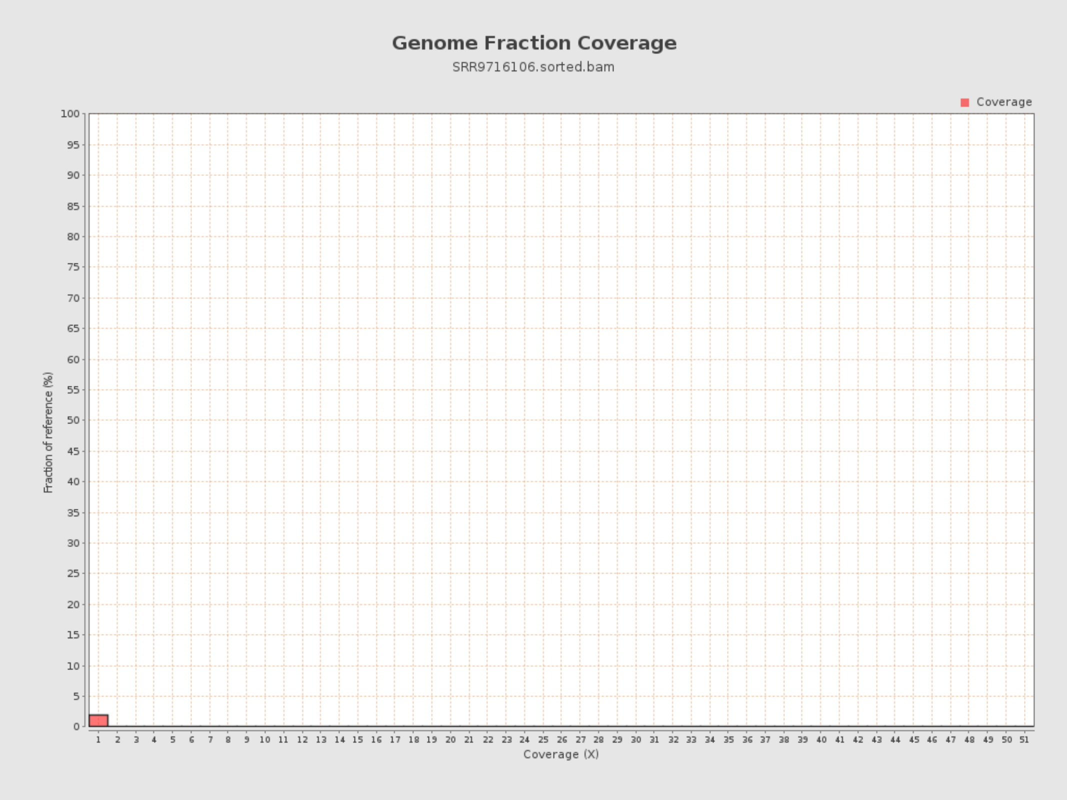
4. Results : Coverage Histogram



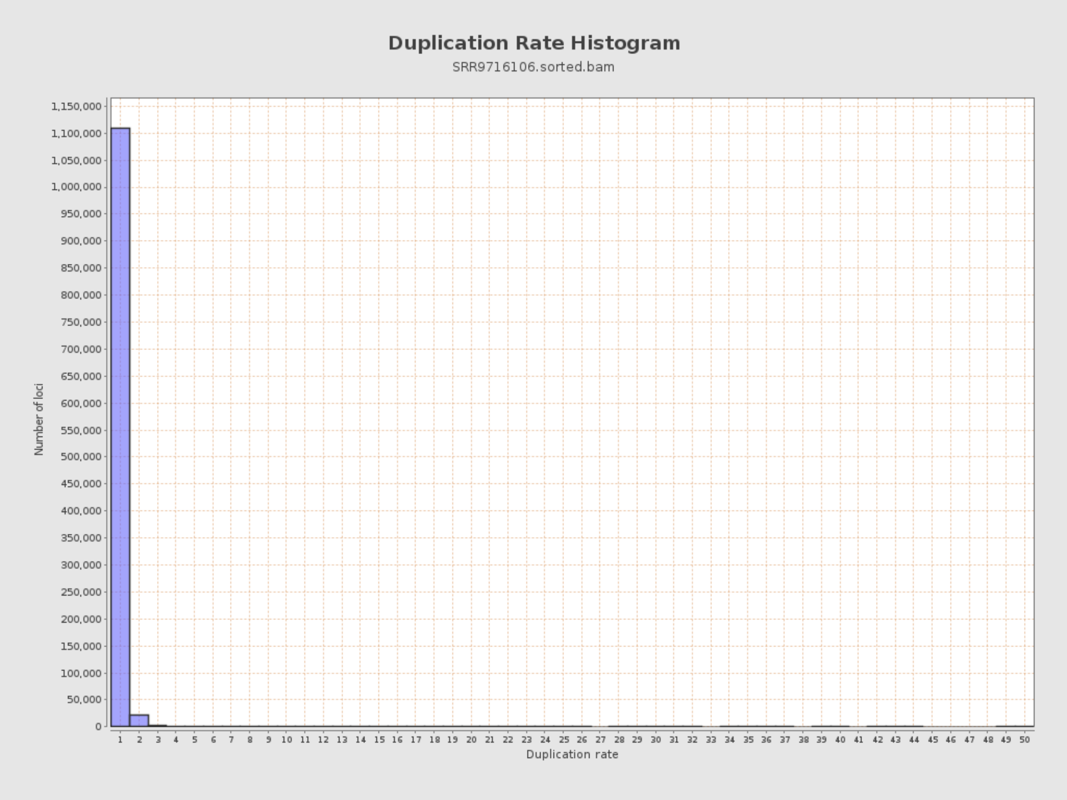
5. Results : Coverage Histogram (0-50X)



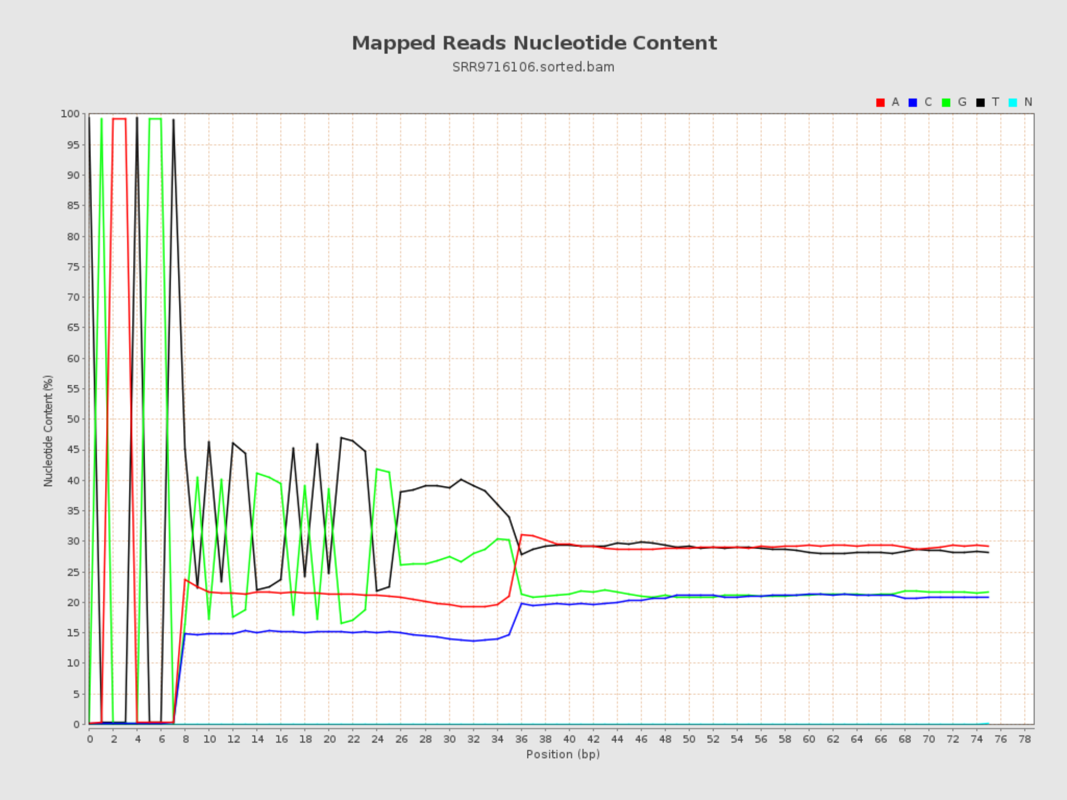
6. Results : Genome Fraction Coverage



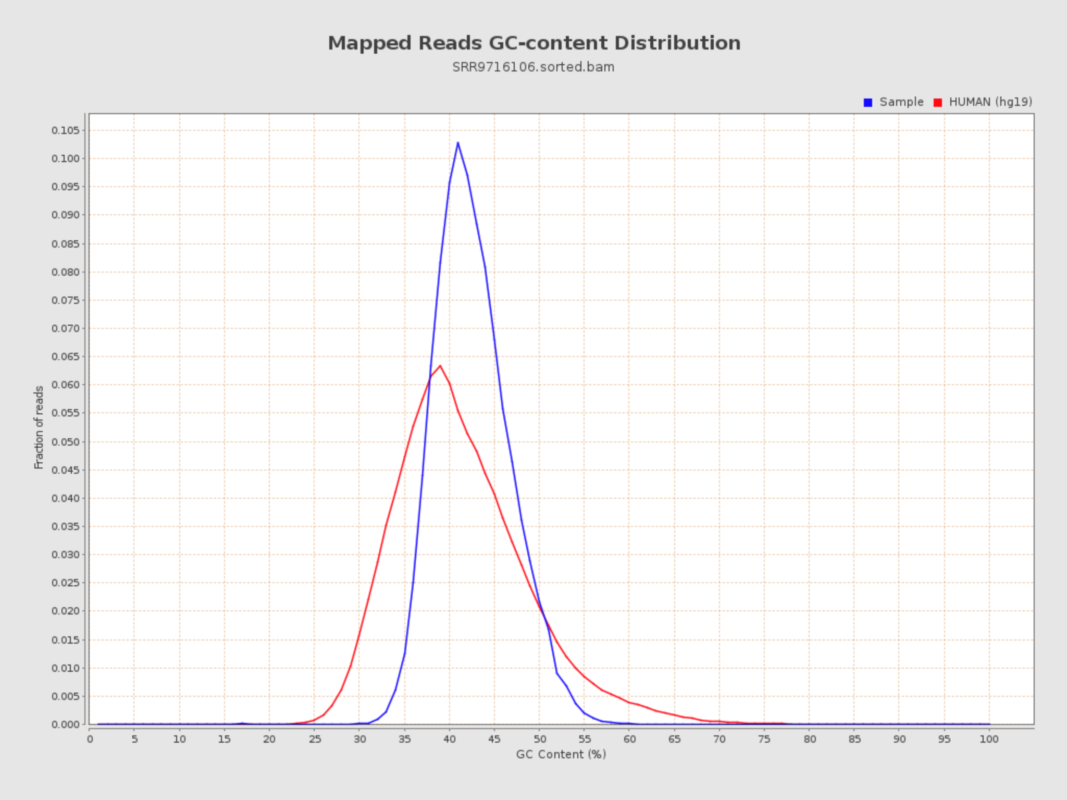
7. Results : Duplication Rate Histogram



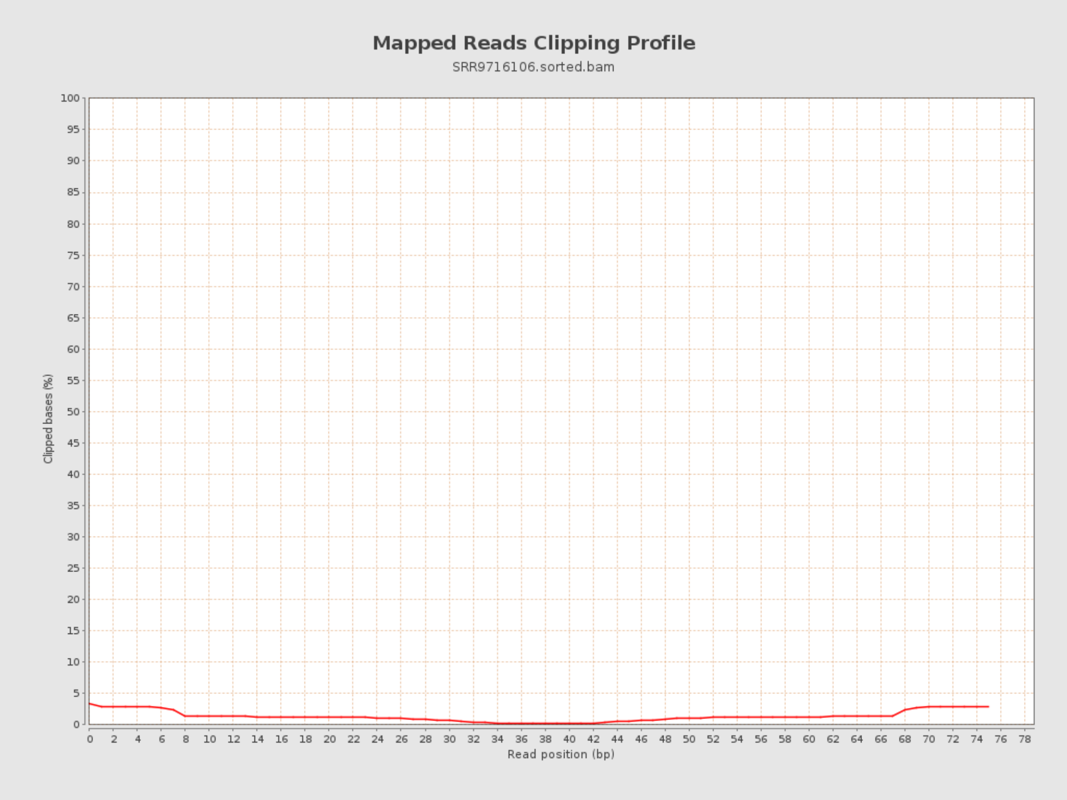
8. Results : Mapped Reads Nucleotide Content



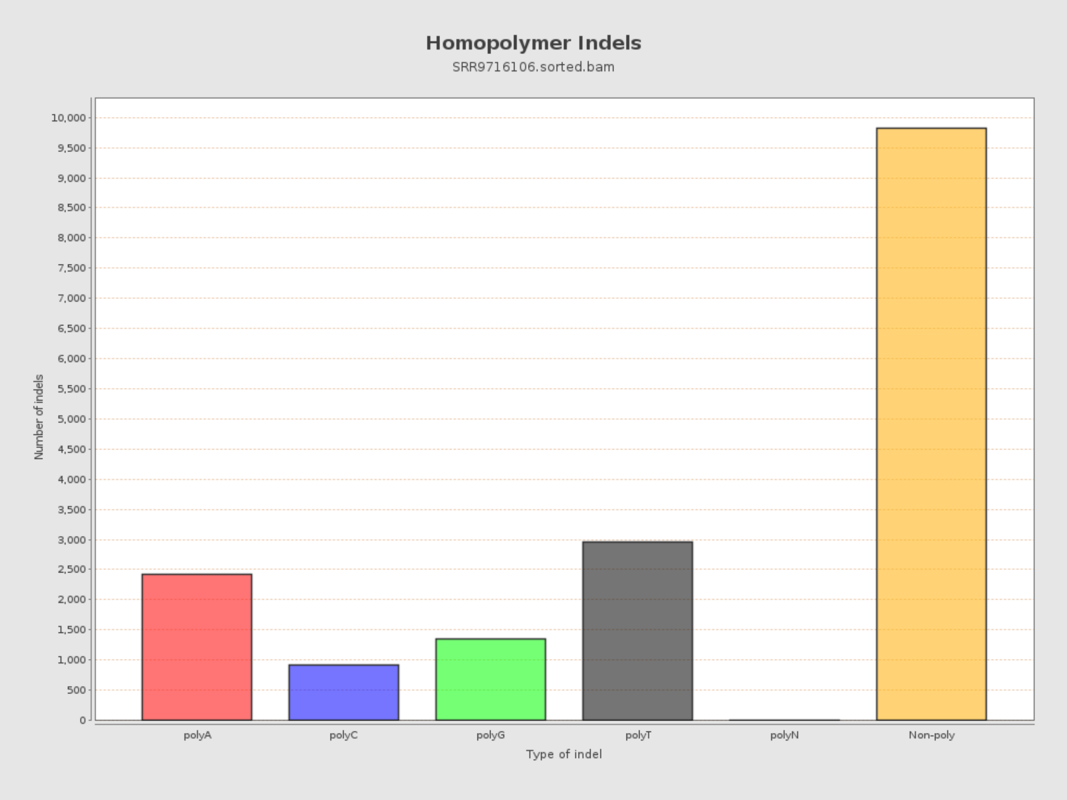
9. Results : Mapped Reads GC-content Distribution



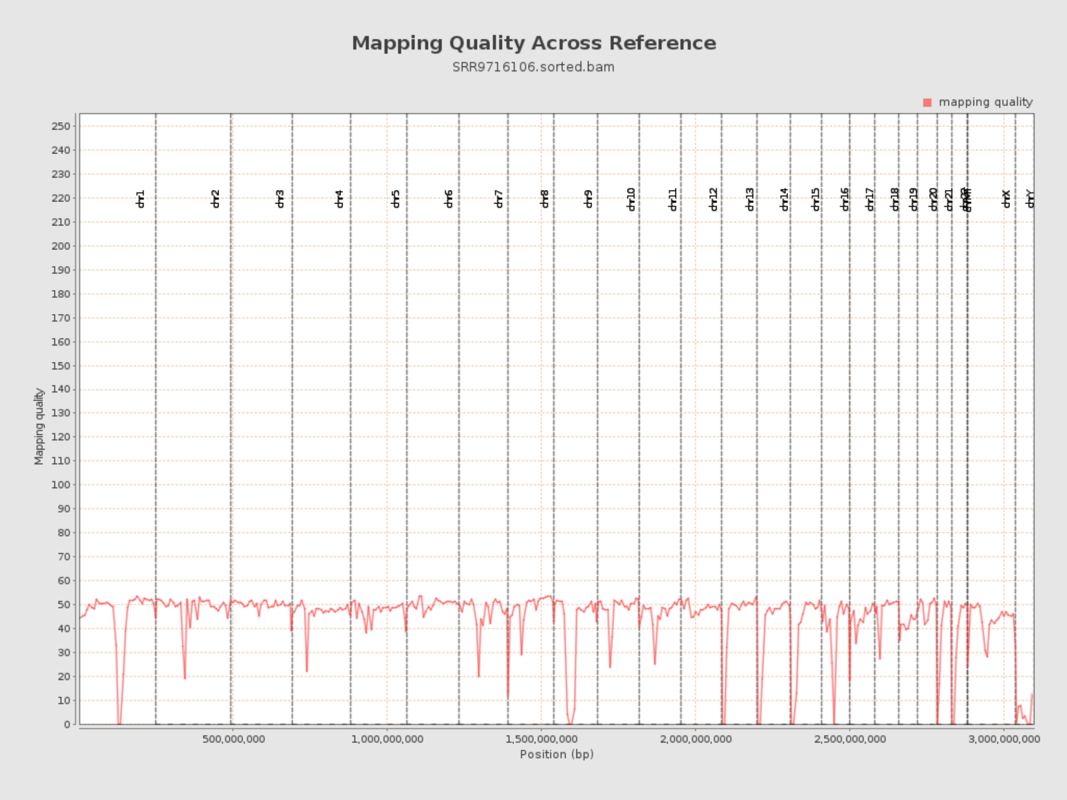
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram