Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:12:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716810.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_SRR9716810 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716810.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:12:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716810.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	545,984
Mapped reads	452,232 / 82.83%
Unmapped reads	93,752 / 17.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,893 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	8,806 / 1.61%
Duplication rate	1.54%
Clipped reads	452,975 / 82.96%

2.2. ACGT Content

Number/percentage of A's	6,374,287 / 24.65%
Number/percentage of C's	4,710,733 / 18.22%
Number/percentage of T's	8,416,859 / 32.55%
Number/percentage of G's	6,355,525 / 24.58%
Number/percentage of N's	370 / 0%
GC Percentage	42.8%

2.3. Coverage

Mean	0.0084

Standard Deviation	0.1069

2.4. Mapping Quality

Mean Mapping Quality	44.59

2.5. Mismatches and indels

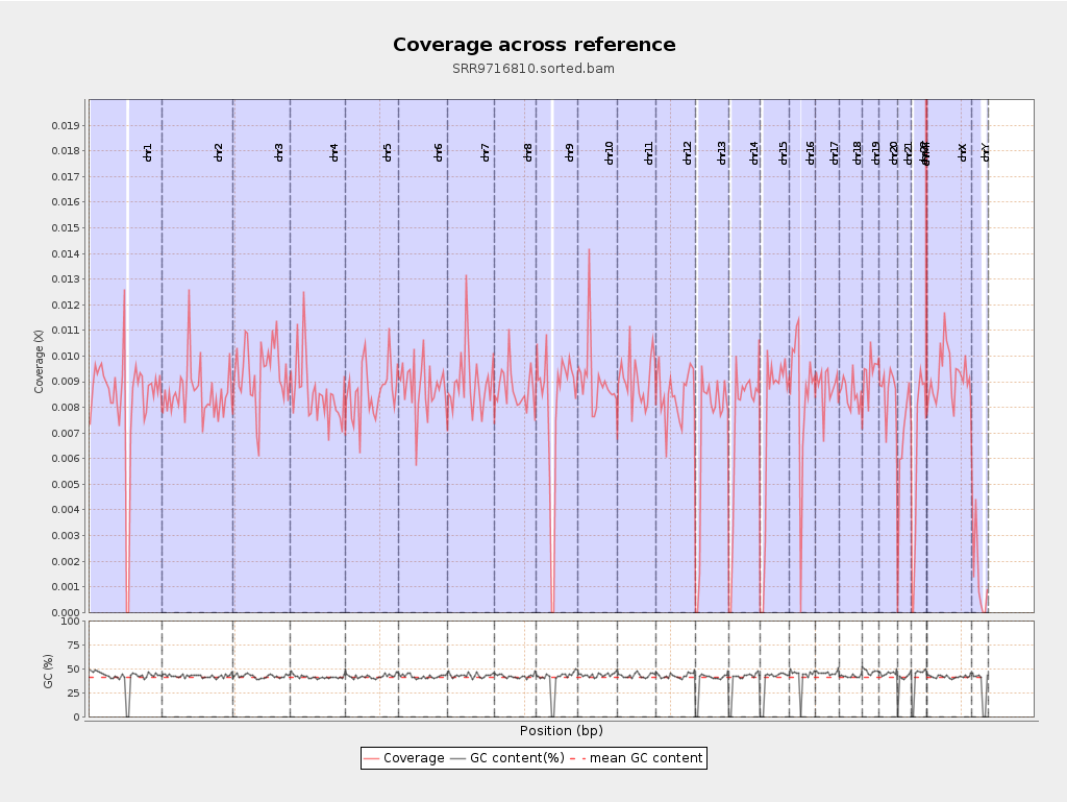
General error rate	0.51%
Mismatches	129,123
Insertions	1,968
Mapped reads with at least one insertion	0.43%
Deletions	4,609
Mapped reads with at least one deletion	1.01%
Homopolymer indels	42.48%

2.6. Chromosome stats

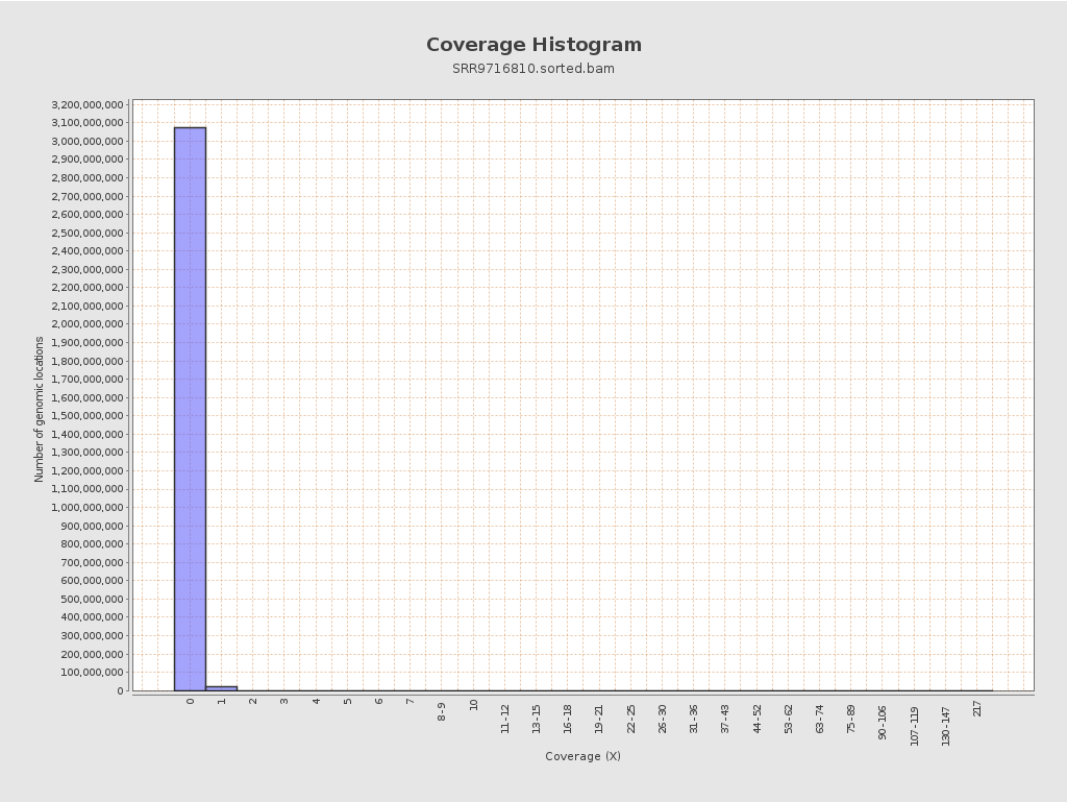
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2067917	0.0083	0.1403
chr2	243199373	2083601	0.0086	0.1314
chr3	198022430	1846056	0.0093	0.1003
chr4	191154276	1635577	0.0086	0.0977
chr5	180915260	1553090	0.0086	0.0959
chr6	171115067	1502897	0.0088	0.1022
chr7	159138663	1432125	0.009	0.1192

chr8	146364022	1276054	0.0087	0.1038
chr9	141213431	1124890	0.008	0.098
chr10	135534747	1222784	0.009	0.1093
chr11	135006516	1221671	0.009	0.1058
chr12	133851895	1137510	0.0085	0.0959
chr13	115169878	812442	0.0071	0.0872
chr14	107349540	778015	0.0072	0.0889
chr15	102531392	767555	0.0075	0.0904
chr16	90354753	777426	0.0086	0.0989
chr17	81195210	714241	0.0088	0.0984
chr18	78077248	669535	0.0086	0.1258
chr19	59128983	553270	0.0094	0.1236
chr20	63025520	542395	0.0086	0.0967
chr21	48129895	317770	0.0066	0.0862
chr22	51304566	311108	0.0061	0.0807
chrMT	16571	3430	0.207	0.4612
chrX	155270560	1433066	0.0092	0.1037
chrY	59373566	80501	0.0014	0.0459

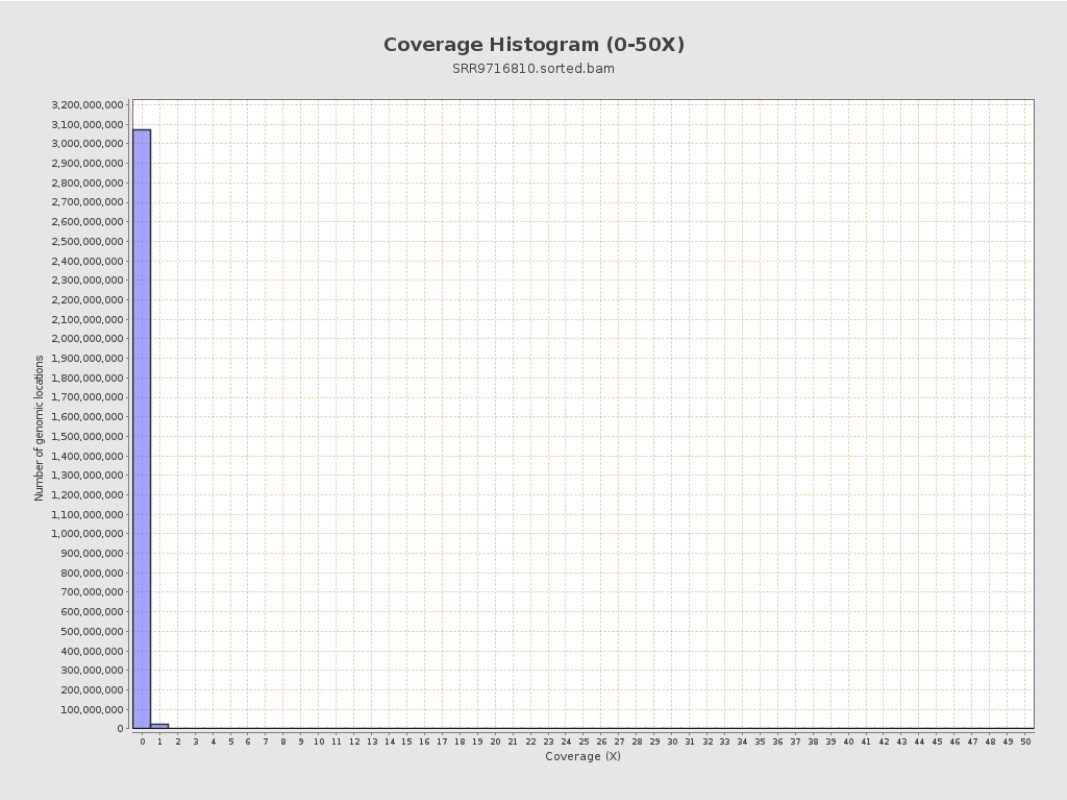
3. Results : Coverage across reference



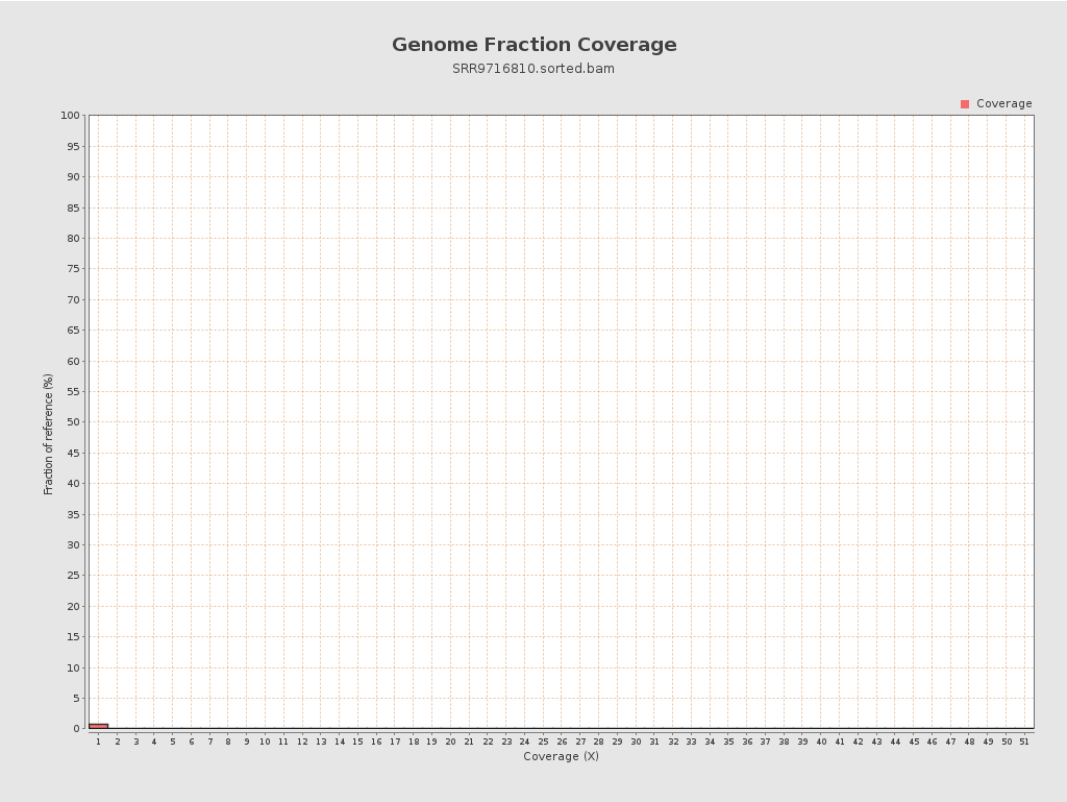
4. Results : Coverage Histogram



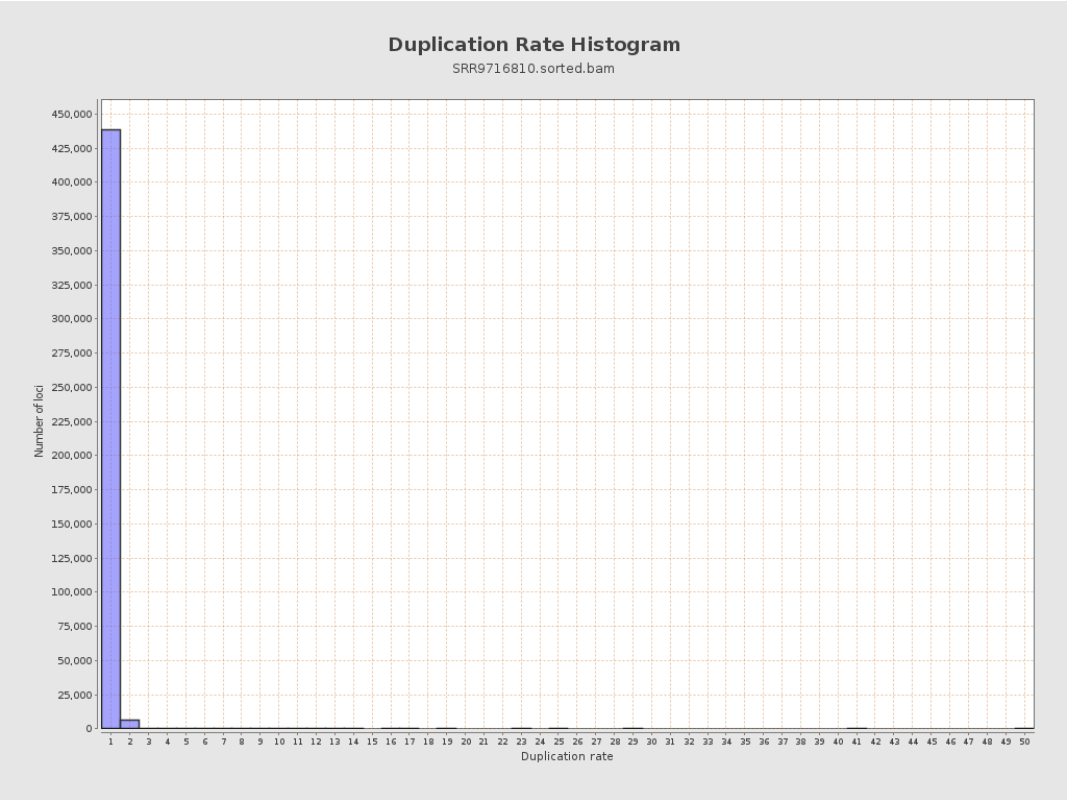
5. Results : Coverage Histogram (0-50X)



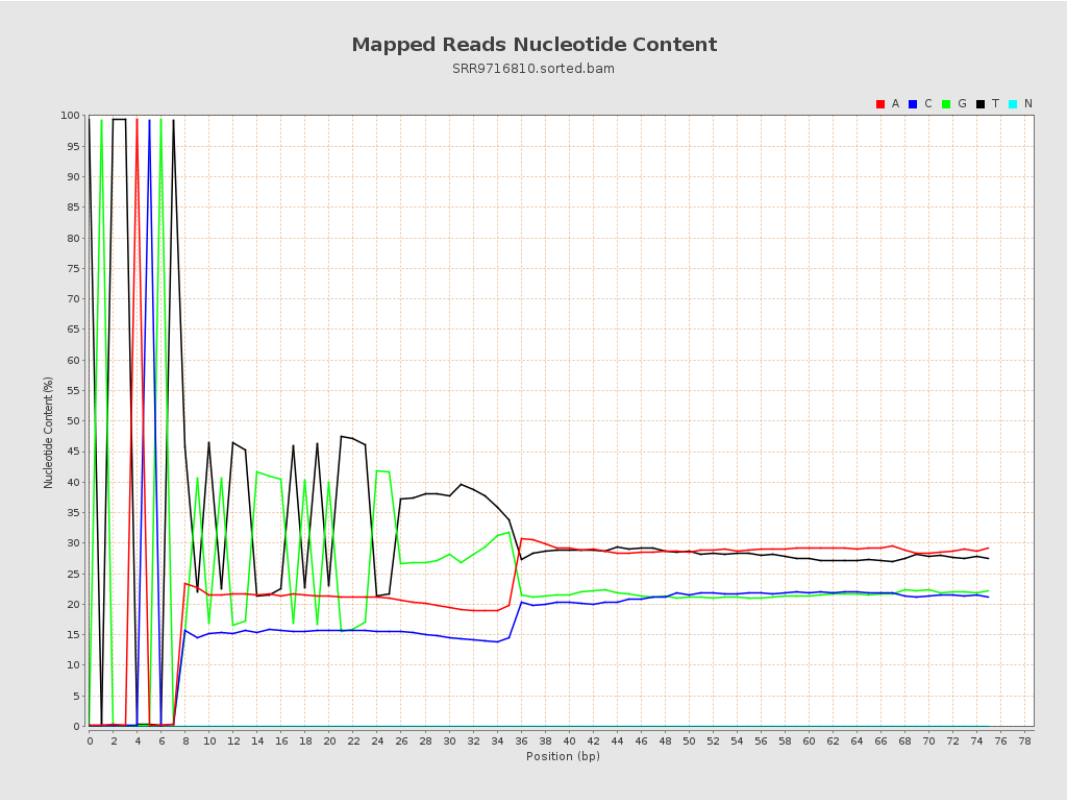
6. Results : Genome Fraction Coverage



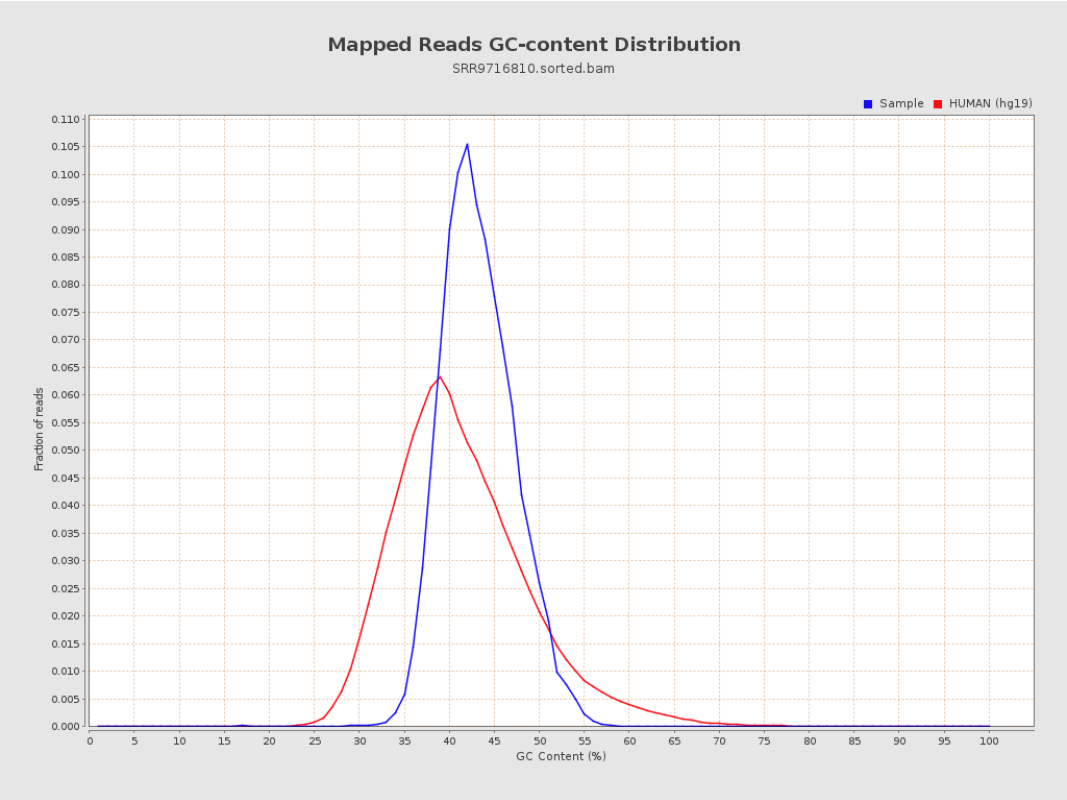
7. Results : Duplication Rate Histogram



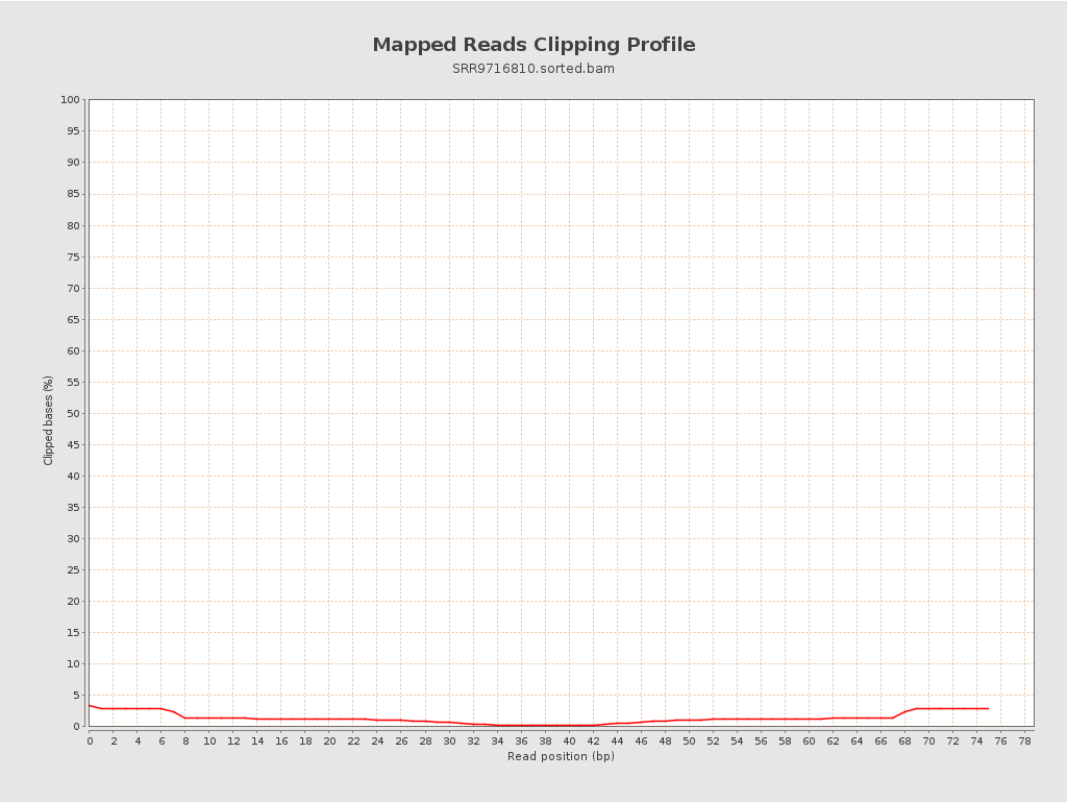
8. Results : Mapped Reads Nucleotide Content



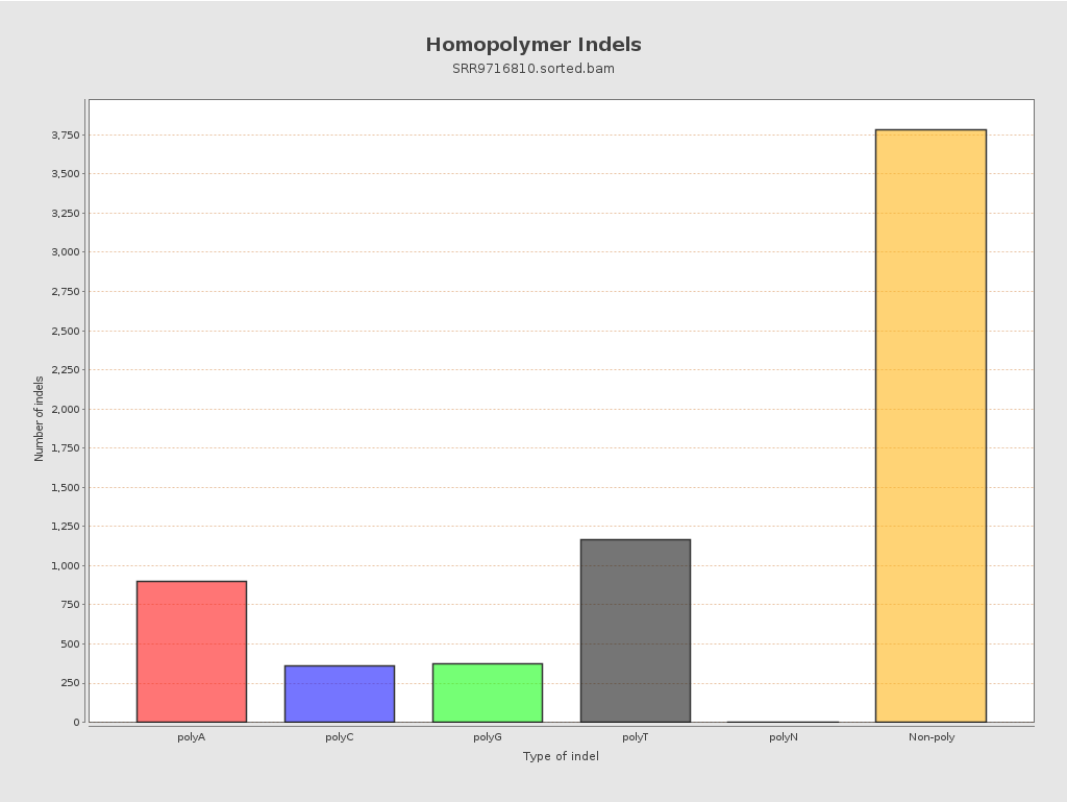
9. Results : Mapped Reads GC-content Distribution



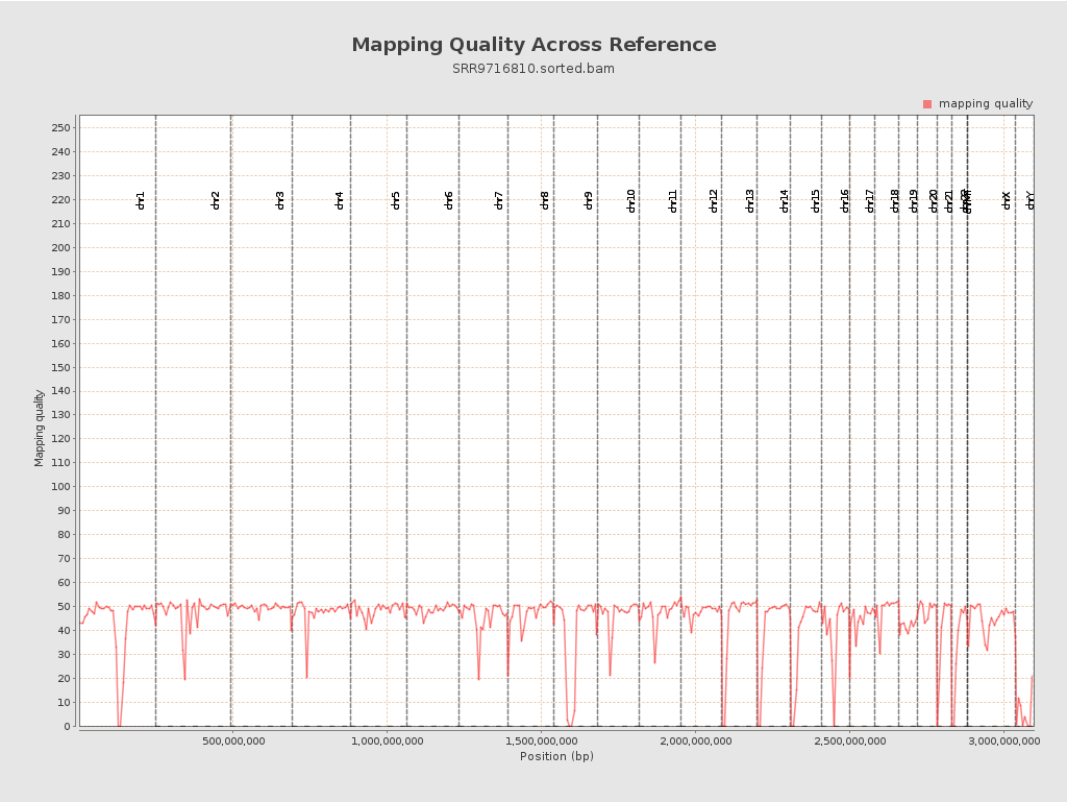
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram