Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 08:40:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716719.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_SRR9716719 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716719.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 08:40:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716719.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	535,532
Mapped reads	488,905 / 91.29%
Unmapped reads	46,627 / 8.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,440 / 0.46%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	7,198 / 1.34%
Duplication rate	1.05%
Clipped reads	489,431 / 91.39%

2.2. ACGT Content

Number/percentage of A's	7,288,976 / 25.35%
Number/percentage of C's	5,594,656 / 19.46%
Number/percentage of T's	9,032,824 / 31.42%
Number/percentage of G's	6,832,362 / 23.77%
Number/percentage of N's	299 / 0%
GC Percentage	43.23%

2.3. Coverage

Mean	0.0093

Standard Deviation	0.1175

2.4. Mapping Quality

Mean Mapping Quality	44.8

2.5. Mismatches and indels

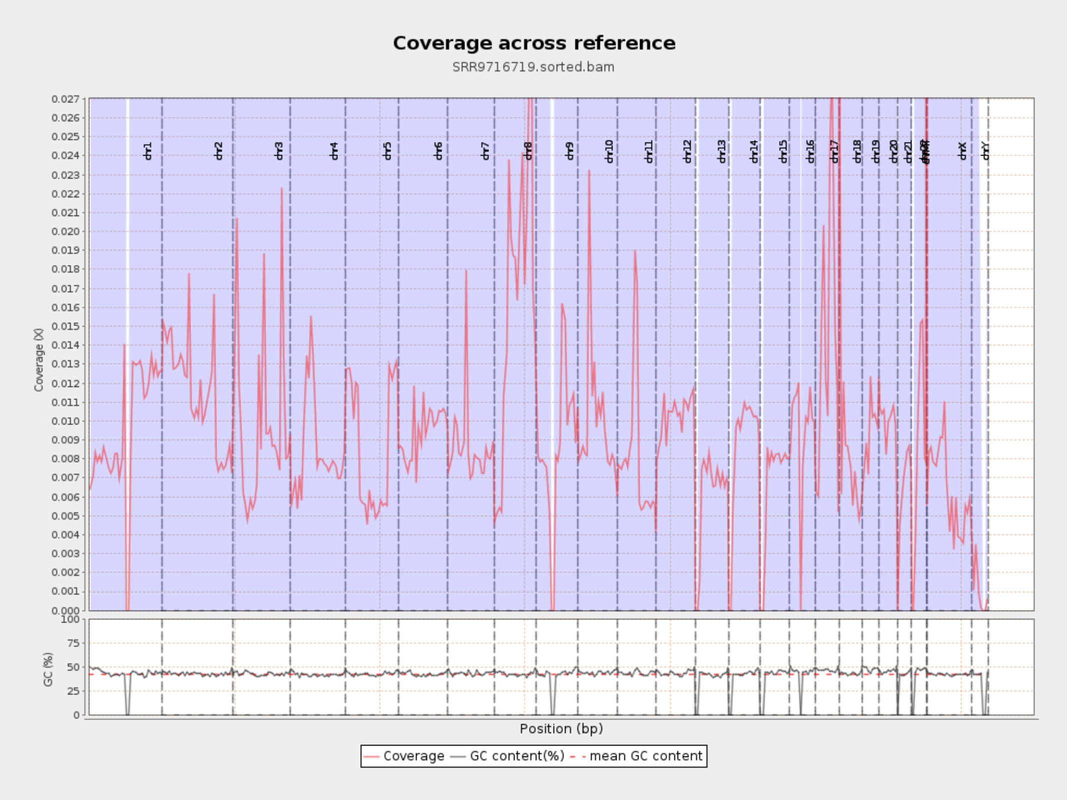
General error rate	0.51%
Mismatches	140,933
Insertions	2,393
Mapped reads with at least one insertion	0.49%
Deletions	5,446
Mapped reads with at least one deletion	1.1%
Homopolymer indels	39.65%

2.6. Chromosome stats

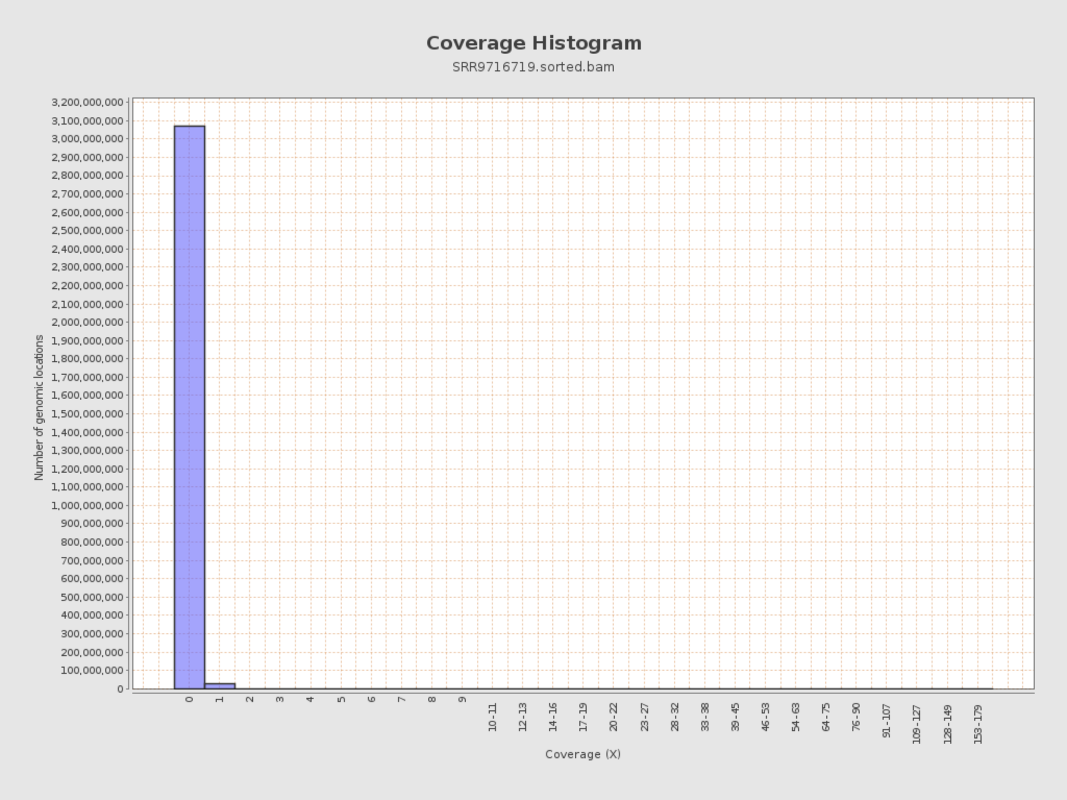
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2360083	0.0095	0.168
chr2	243199373	2823734	0.0116	0.1373
chr3	198022430	1954876	0.0099	0.1028
chr4	191154276	1619562	0.0085	0.0973
chr5	180915260	1540640	0.0085	0.0947
chr6	171115067	1615314	0.0094	0.1035
chr7	159138663	1380749	0.0087	0.156

chr8	146364022	2477653	0.0169	0.151
chr9	141213431	1201280	0.0085	0.0998
chr10	135534747	1361145	0.01	0.1364
chr11	135006516	1082768	0.008	0.0984
chr12	133851895	1367958	0.0102	0.1064
chr13	115169878	694286	0.006	0.0796
chr14	107349540	926632	0.0086	0.0959
chr15	102531392	676321	0.0066	0.0842
chr16	90354753	858123	0.0095	0.1021
chr17	81195210	1183119	0.0146	0.1256
chr18	78077248	665785	0.0085	0.1311
chr19	59128983	556019	0.0094	0.1366
chr20	63025520	624569	0.0099	0.103
chr21	48129895	303255	0.0063	0.083
chr22	51304566	410580	0.008	0.0921
chrMT	16571	3424	0.2066	0.4281
chrX	155270560	1007108	0.0065	0.0863
chrY	59373566	62820	0.0011	0.0413

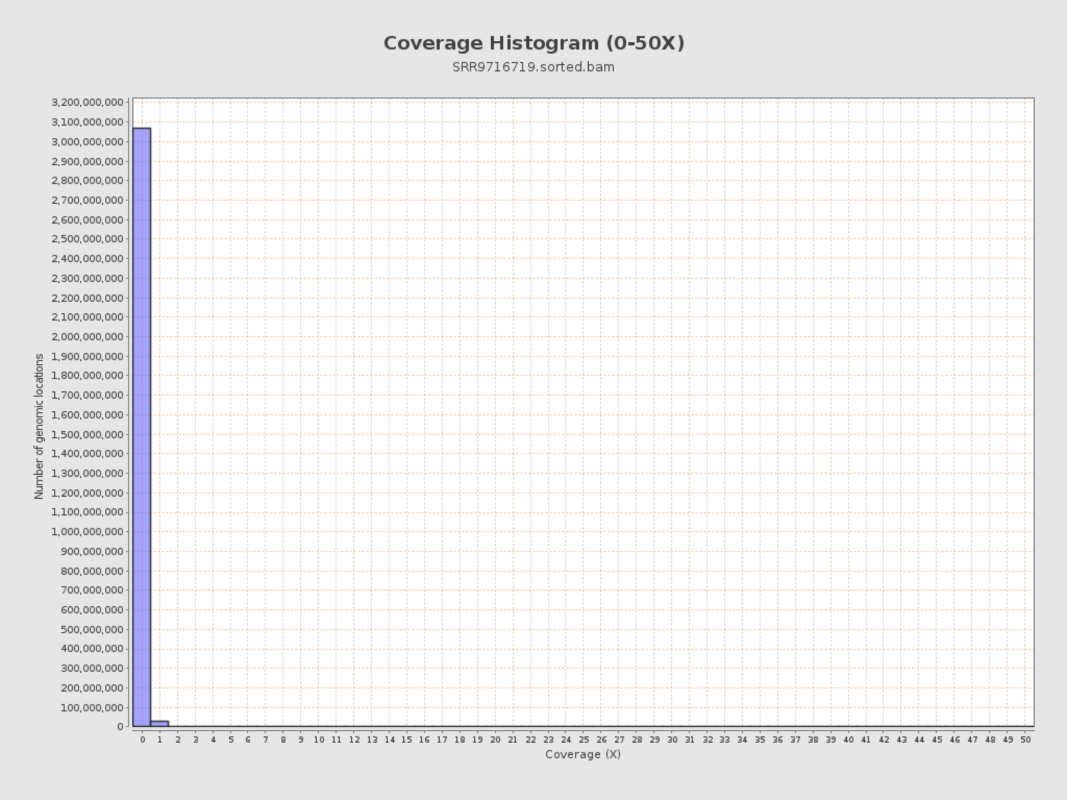
3. Results : Coverage across reference



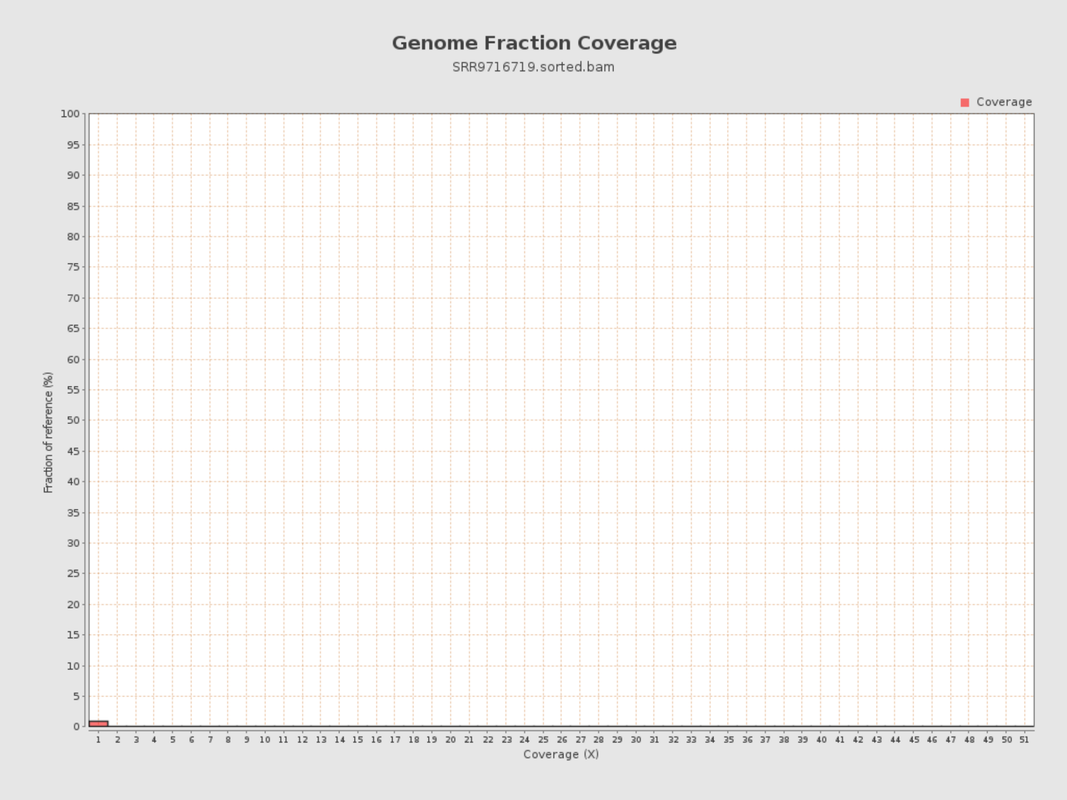
4. Results : Coverage Histogram



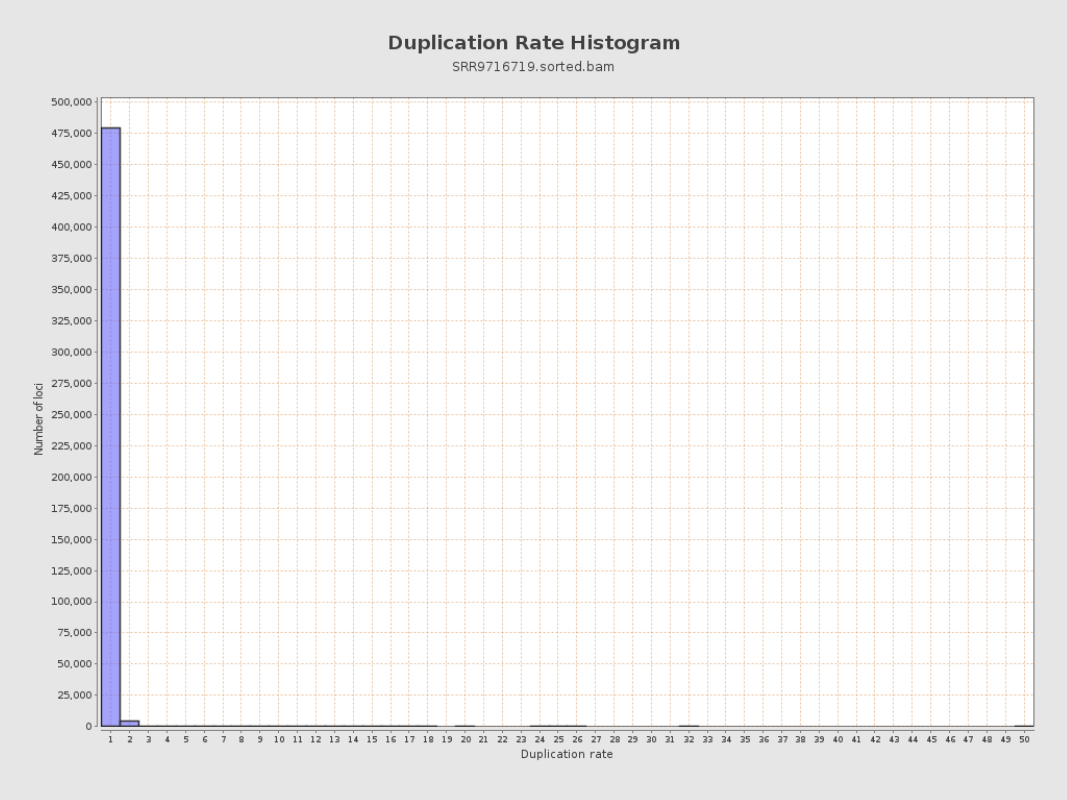
5. Results : Coverage Histogram (0-50X)



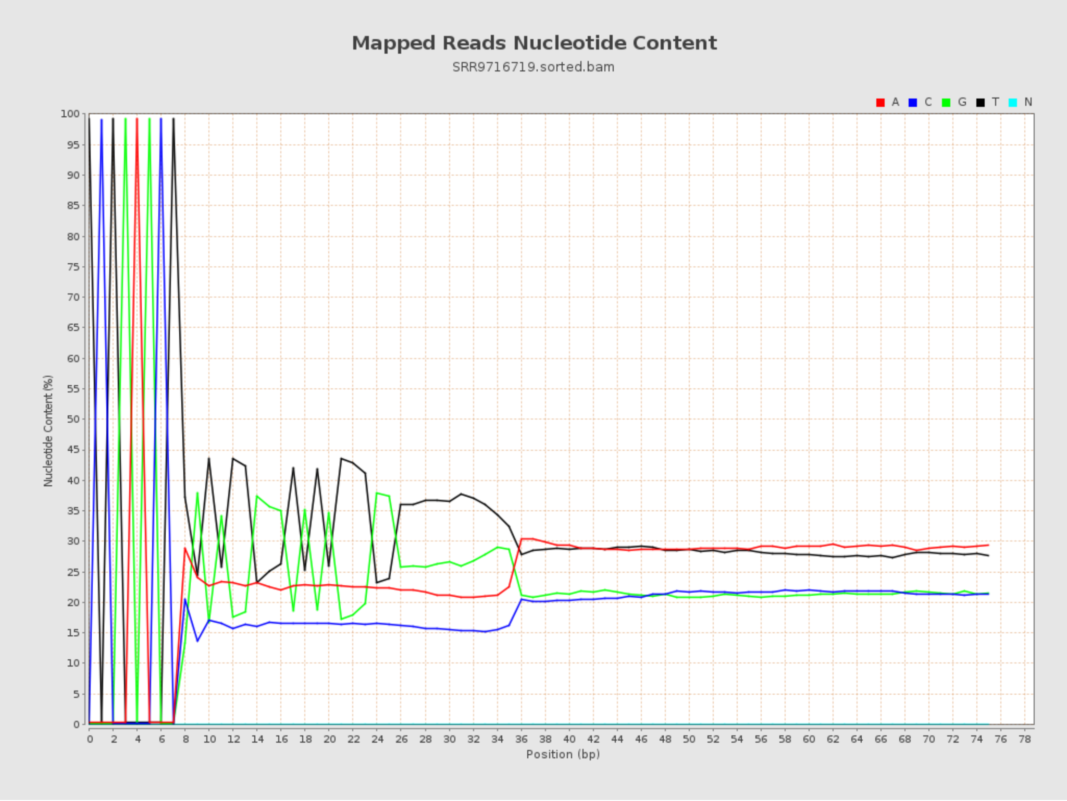
6. Results : Genome Fraction Coverage



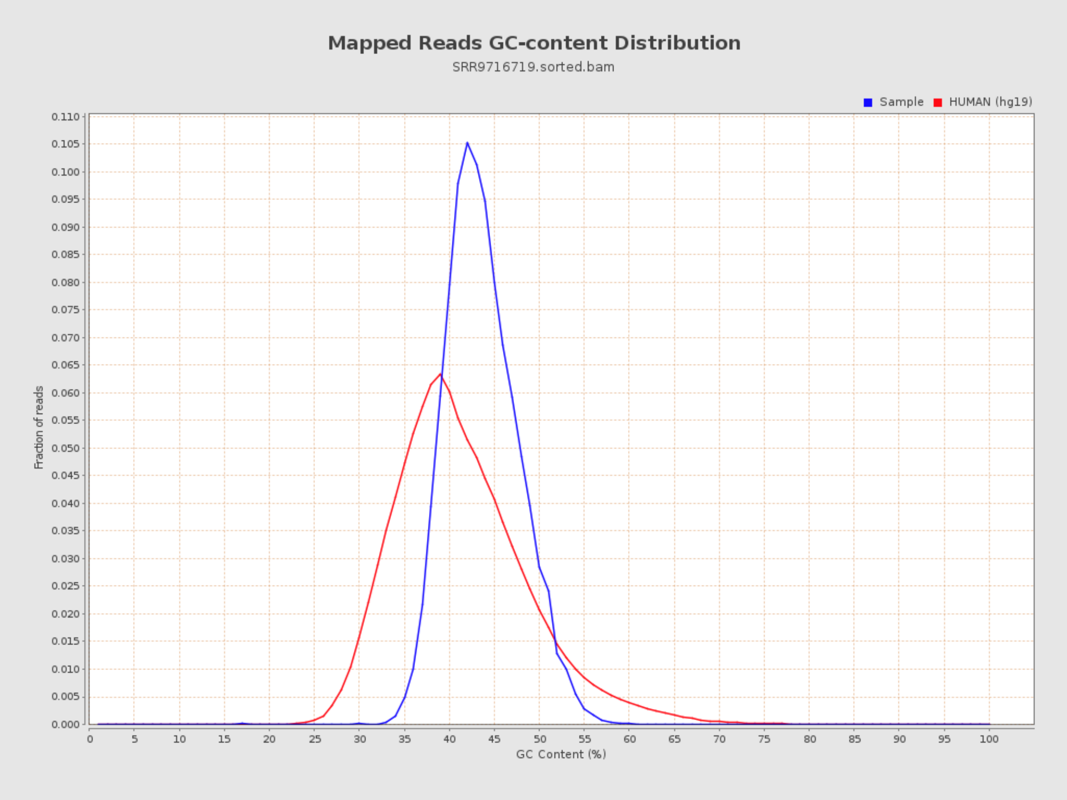
7. Results : Duplication Rate Histogram



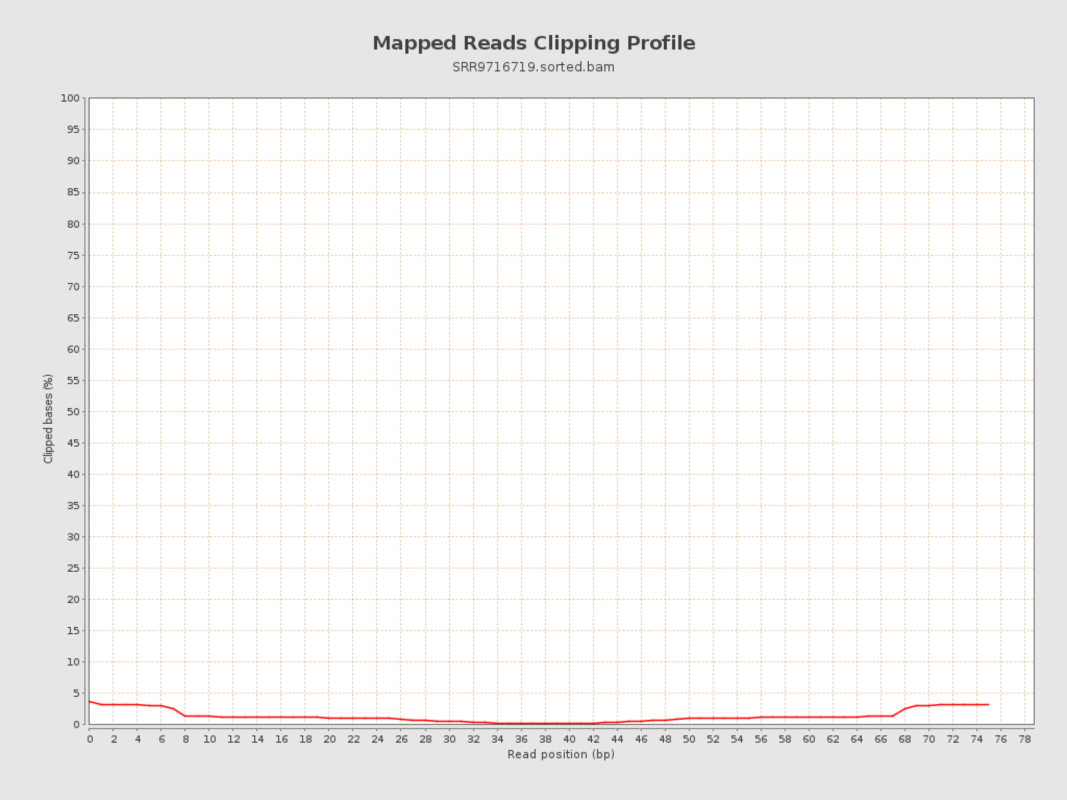
8. Results : Mapped Reads Nucleotide Content



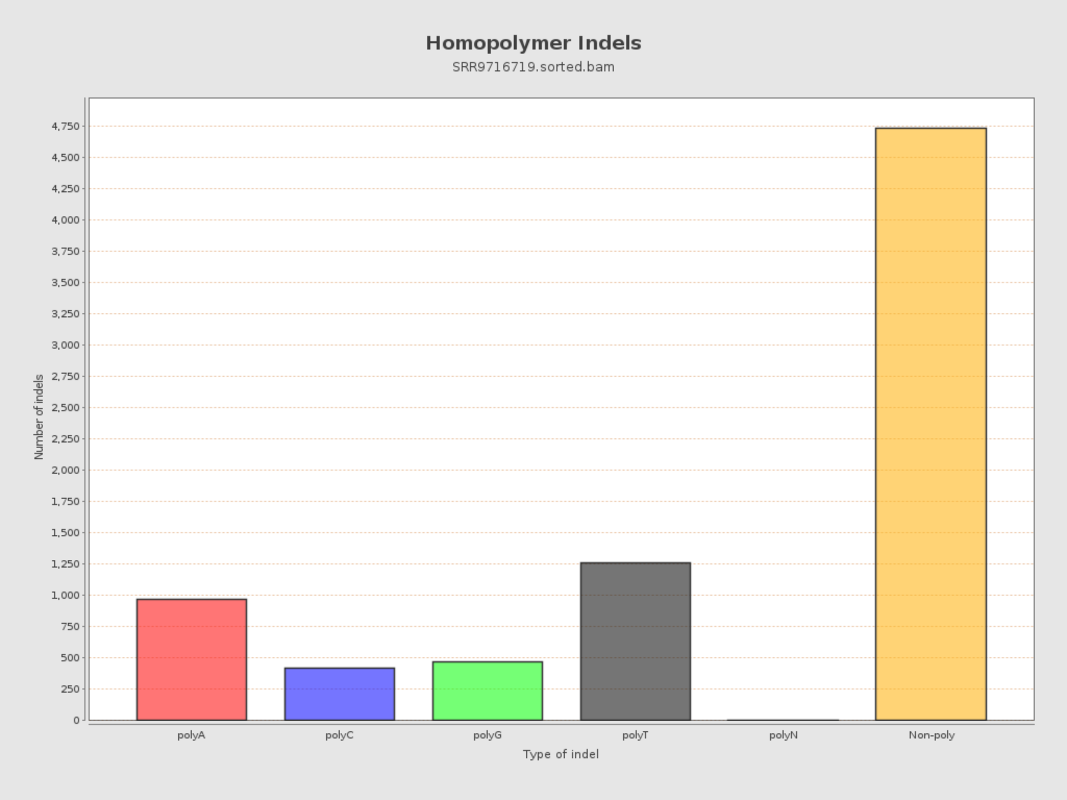
9. Results : Mapped Reads GC-content Distribution



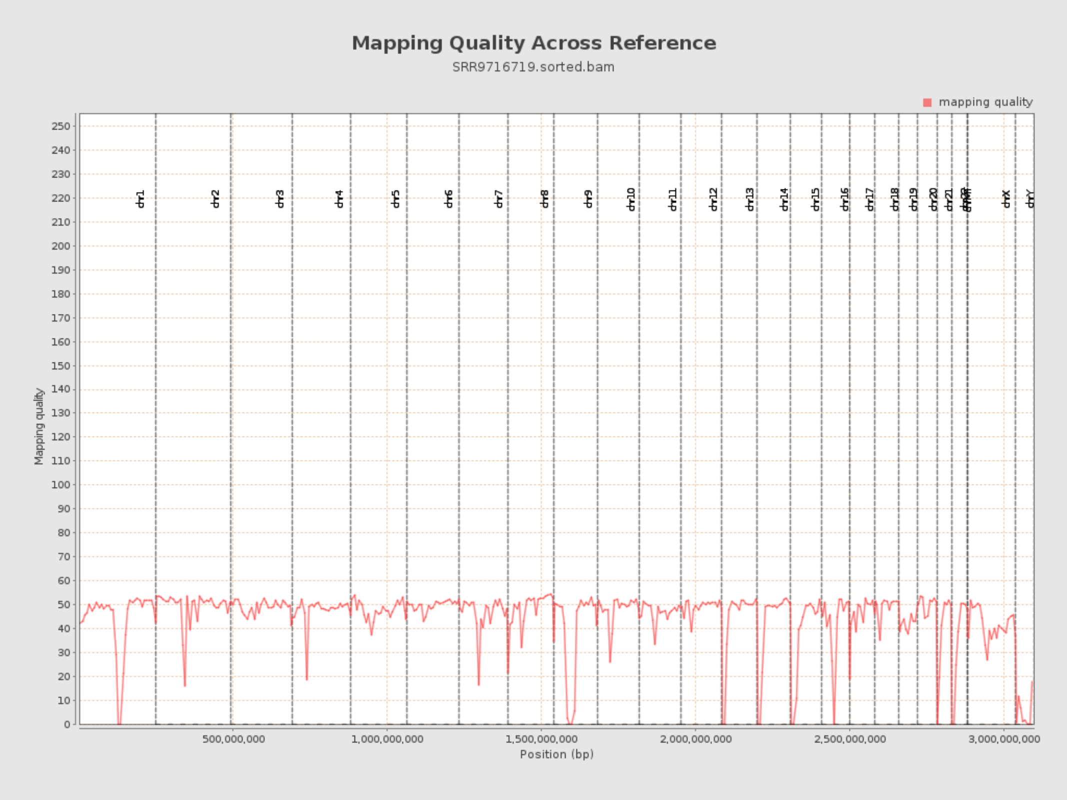
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram