Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:35:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716820.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_SRR9716820 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716820.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:35:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716820.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	527,192
Mapped reads	457,729 / 86.82%
Unmapped reads	69,463 / 13.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,435 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	9,868 / 1.87%
Duplication rate	1.68%
Clipped reads	459,936 / 87.24%

2.2. ACGT Content

Number/percentage of A's	6,632,177 / 24.91%
Number/percentage of C's	5,338,234 / 20.05%
Number/percentage of T's	8,163,463 / 30.66%
Number/percentage of G's	6,489,891 / 24.38%
Number/percentage of N's	142 / 0%
GC Percentage	44.43%

2.3. Coverage

Mean	0.0086

Standard Deviation	0.1123

2.4. Mapping Quality

Mean Mapping Quality	44.75

2.5. Mismatches and indels

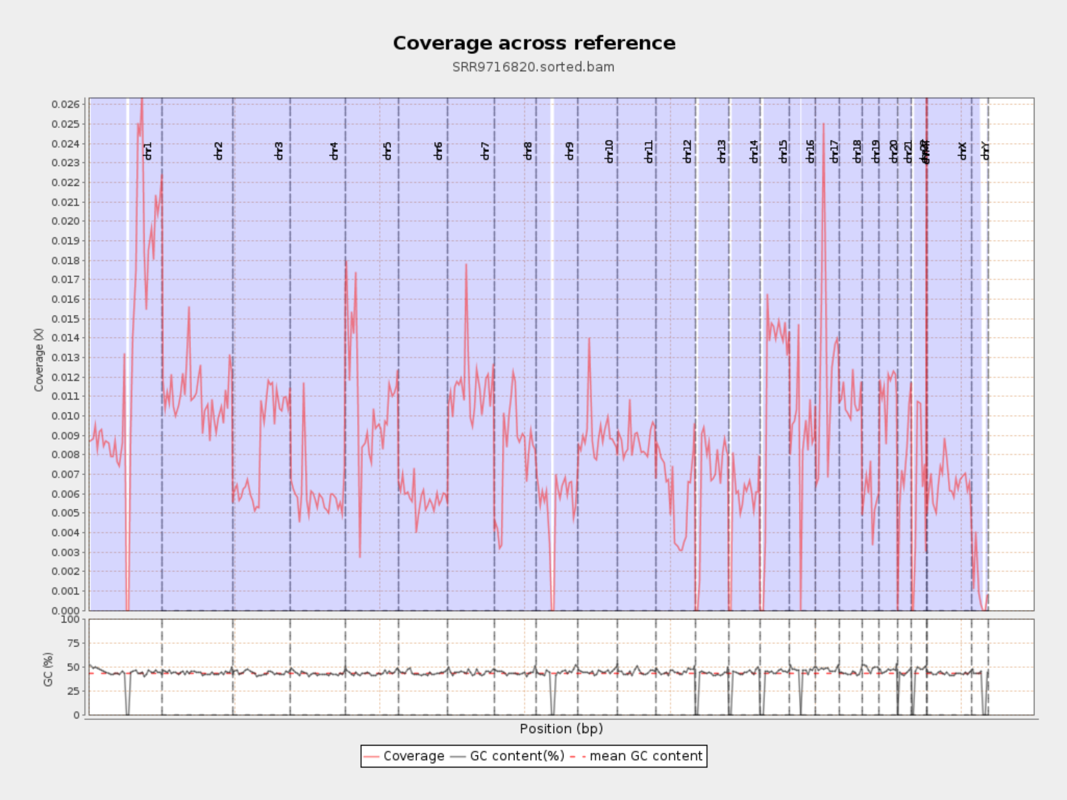
General error rate	0.51%
Mismatches	132,911
Insertions	1,541
Mapped reads with at least one insertion	0.33%
Deletions	4,646
Mapped reads with at least one deletion	1.01%
Homopolymer indels	42.4%

2.6. Chromosome stats

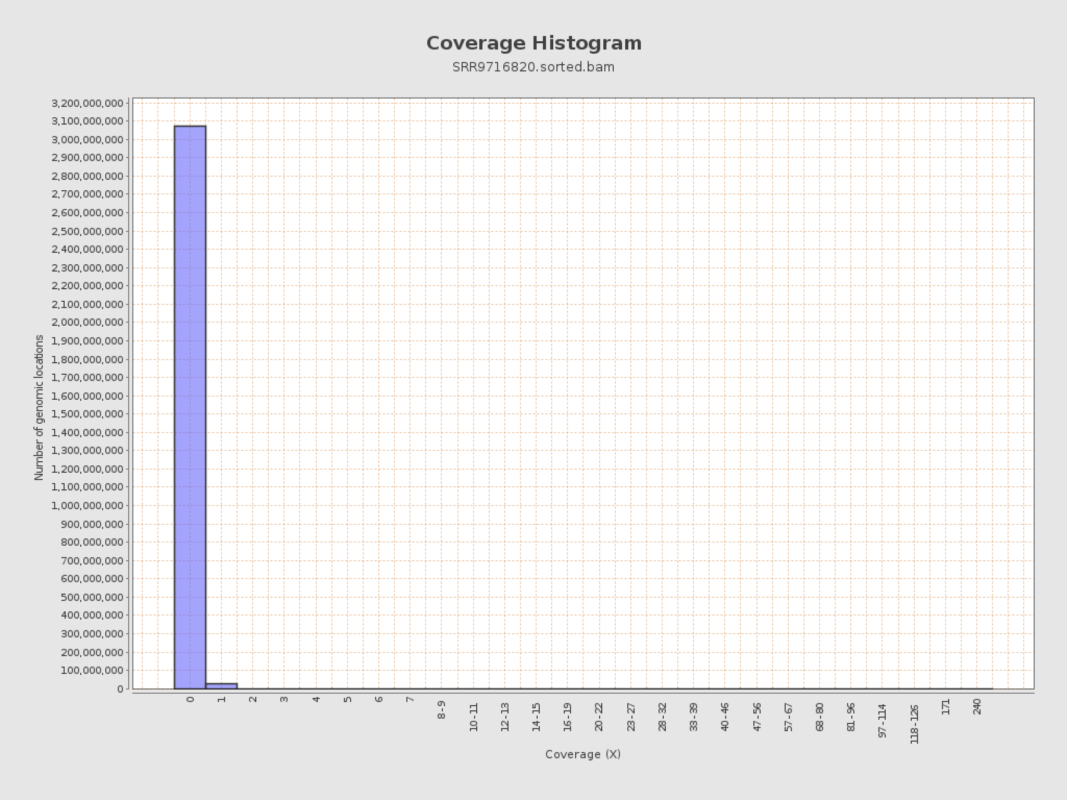
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3215377	0.0129	0.1562
chr2	243199373	2682252	0.011	0.1523
chr3	198022430	1667864	0.0084	0.095
chr4	191154276	1135364	0.0059	0.0871
chr5	180915260	1926936	0.0107	0.1075
chr6	171115067	990054	0.0058	0.0824
chr7	159138663	1836763	0.0115	0.1536

chr8	146364022	1195264	0.0082	0.107
chr9	141213431	746895	0.0053	0.0845
chr10	135534747	1229050	0.0091	0.1117
chr11	135006516	1177366	0.0087	0.1093
chr12	133851895	795387	0.0059	0.0802
chr13	115169878	767788	0.0067	0.0847
chr14	107349540	575479	0.0054	0.0765
chr15	102531392	1186271	0.0116	0.1119
chr16	90354753	809042	0.009	0.1001
chr17	81195210	1046846	0.0129	0.1209
chr18	78077248	842492	0.0108	0.1536
chr19	59128983	344638	0.0058	0.1108
chr20	63025520	716558	0.0114	0.1114
chr21	48129895	352569	0.0073	0.0913
chr22	51304566	304071	0.0059	0.0801
chrMT	16571	622	0.0375	0.2085
chrX	155270560	1017732	0.0066	0.0868
chrY	59373566	68755	0.0012	0.0469

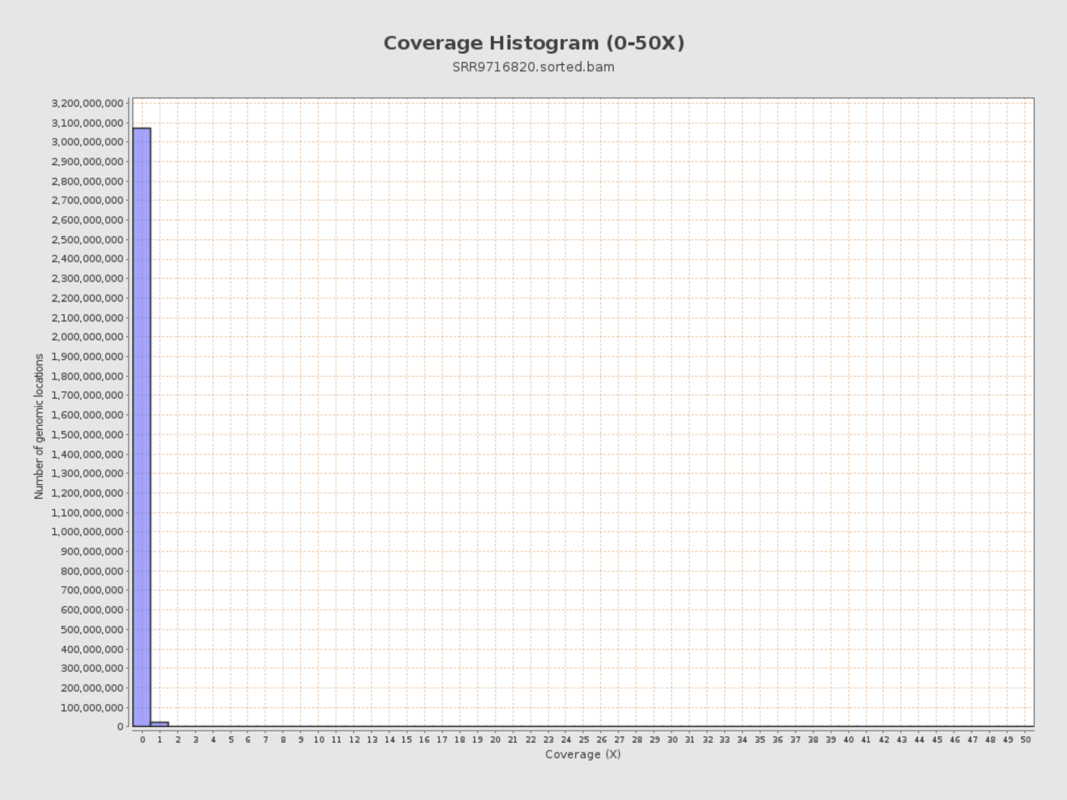
3. Results : Coverage across reference



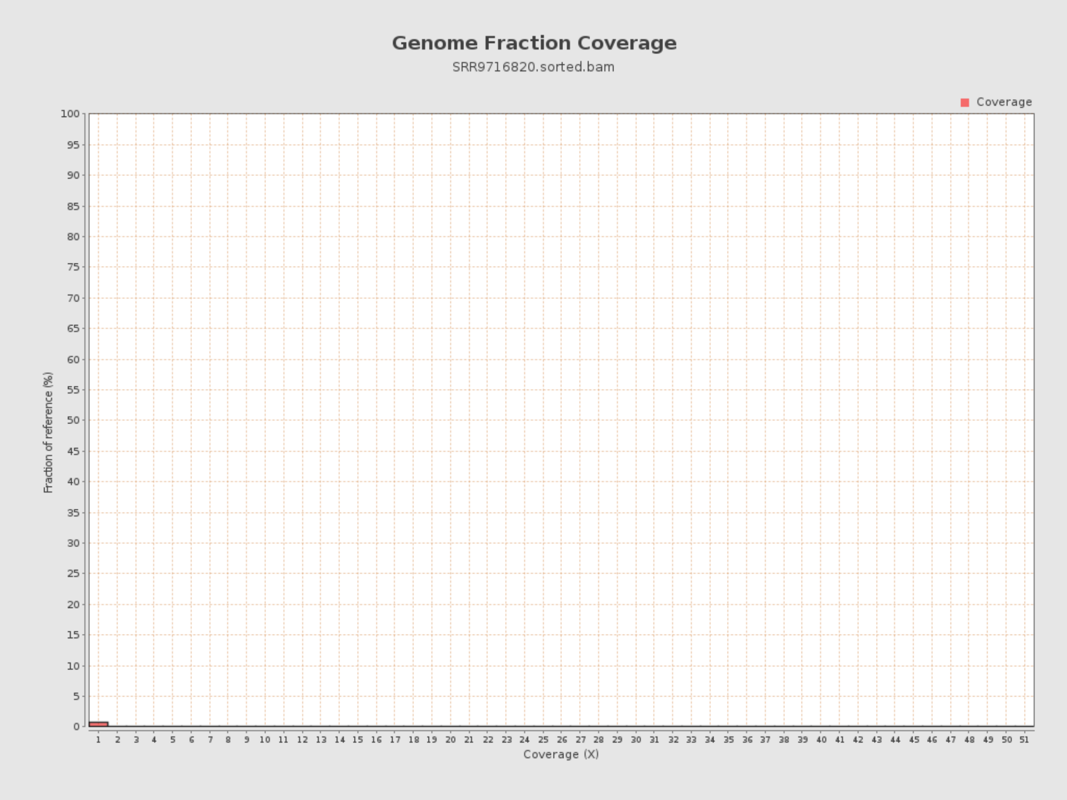
4. Results : Coverage Histogram



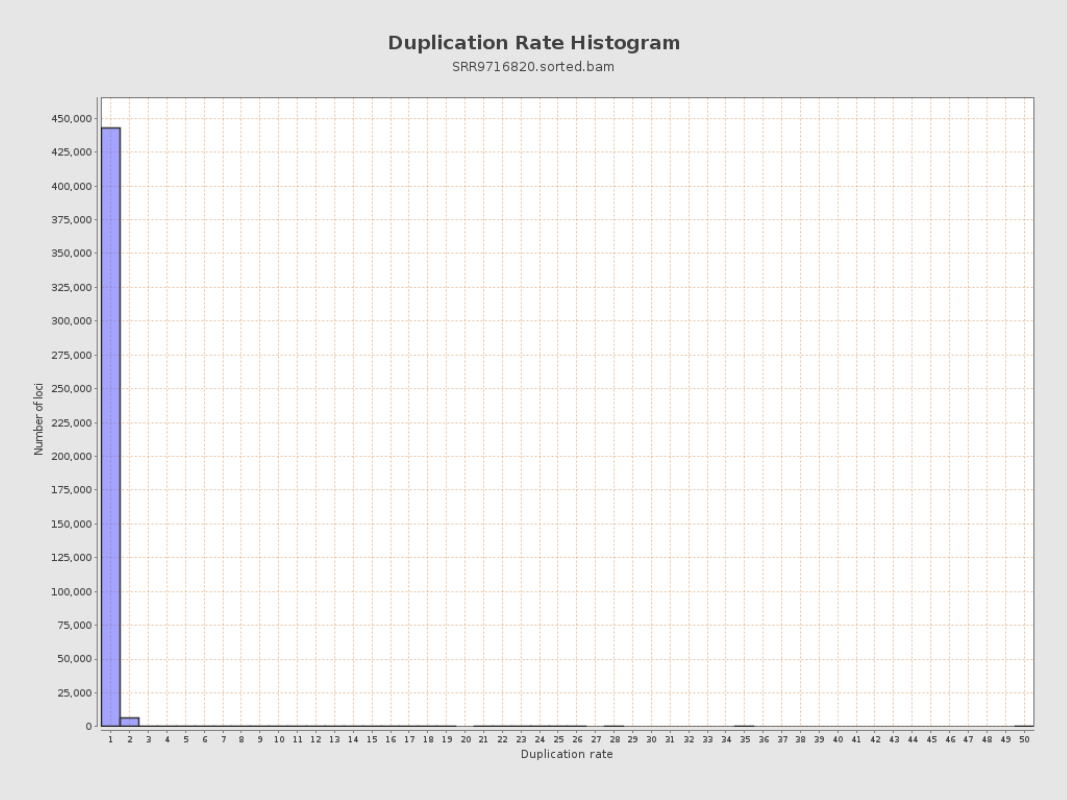
5. Results : Coverage Histogram (0-50X)



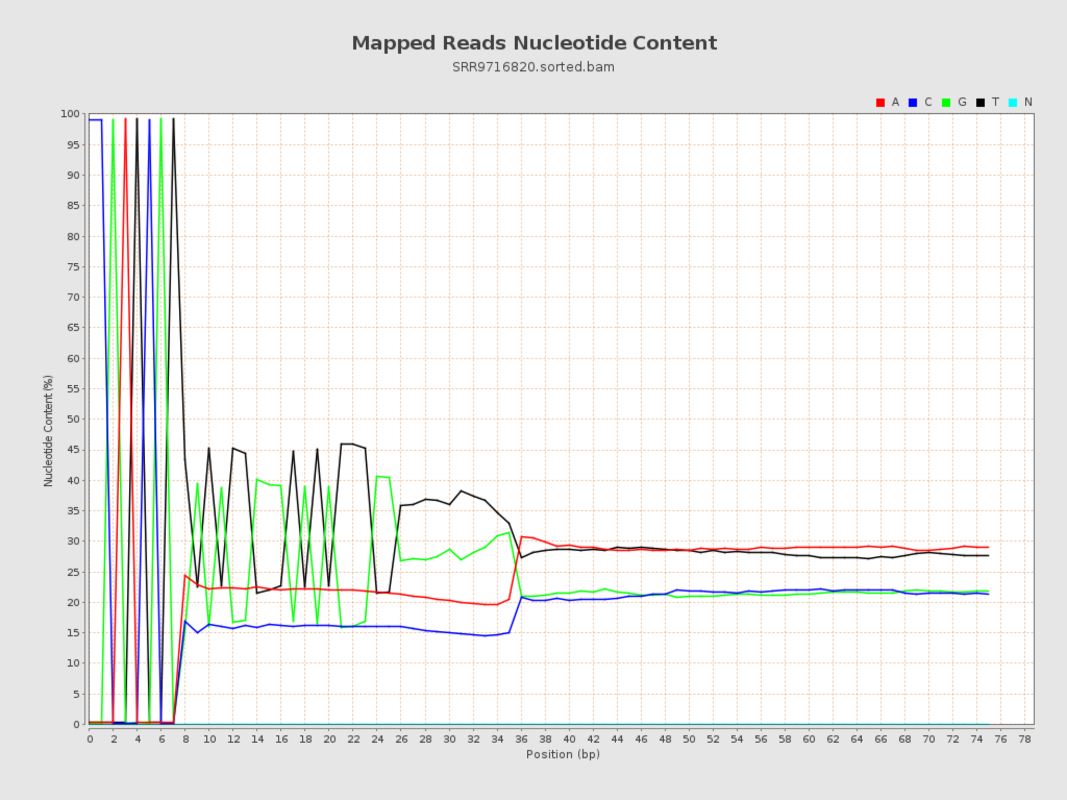
6. Results : Genome Fraction Coverage



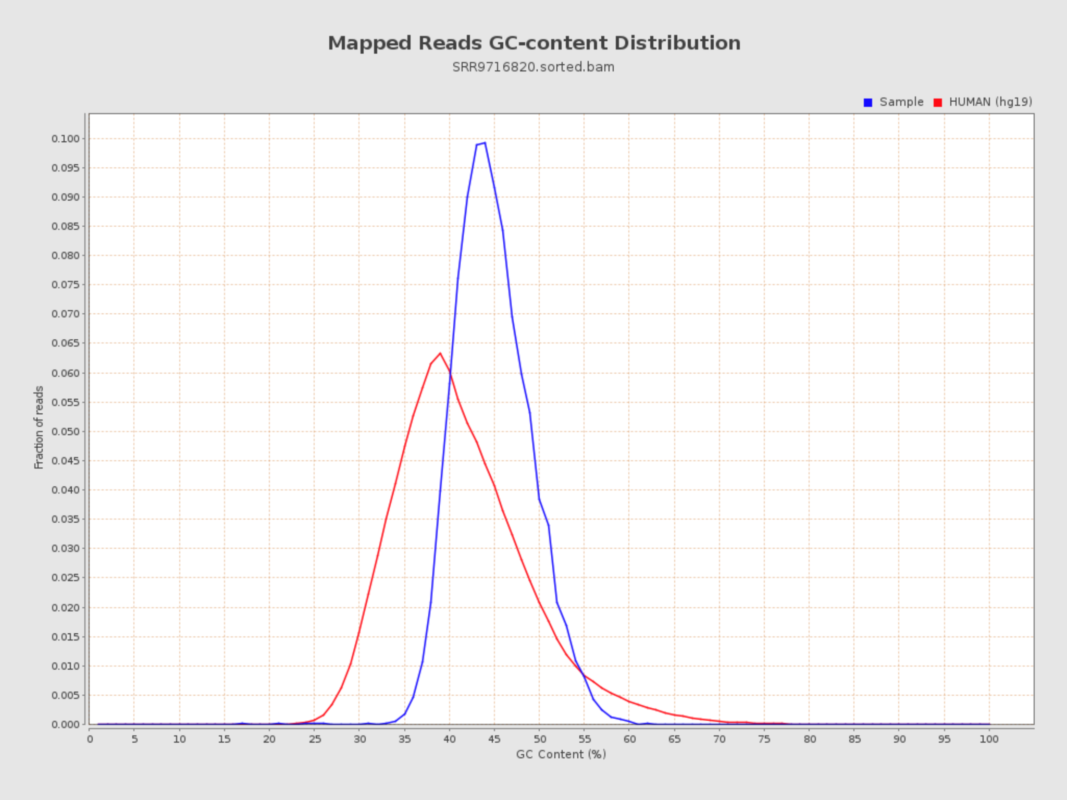
7. Results : Duplication Rate Histogram



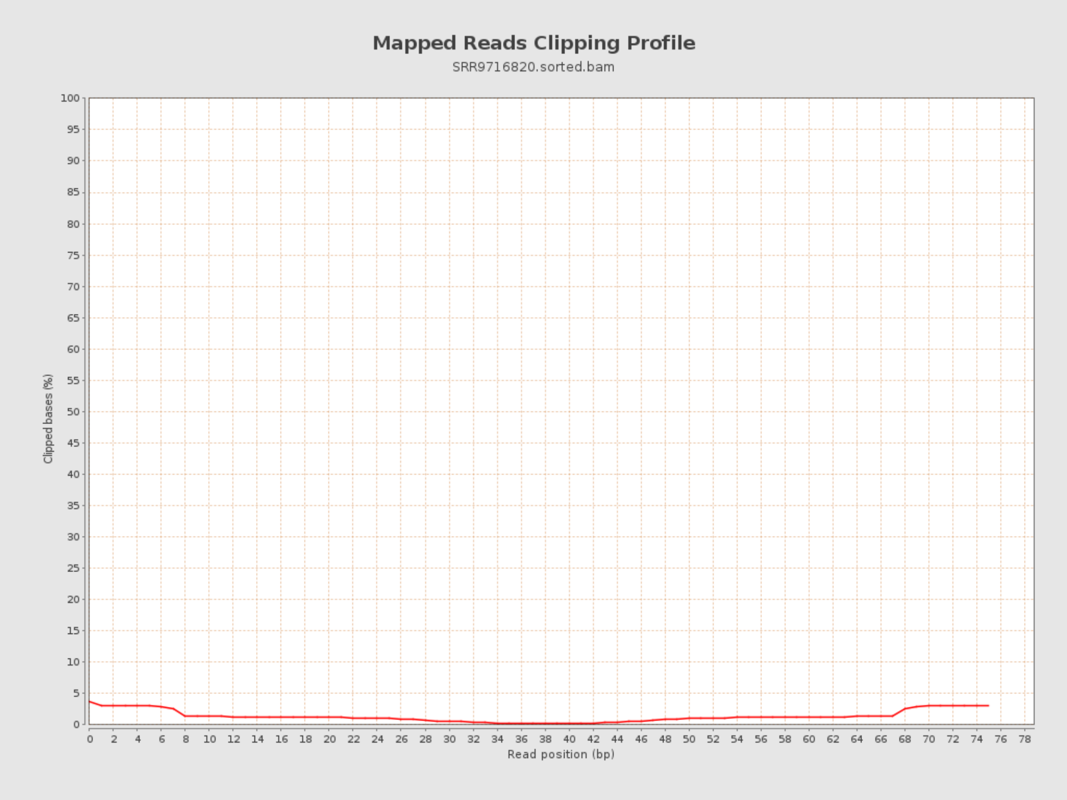
8. Results : Mapped Reads Nucleotide Content



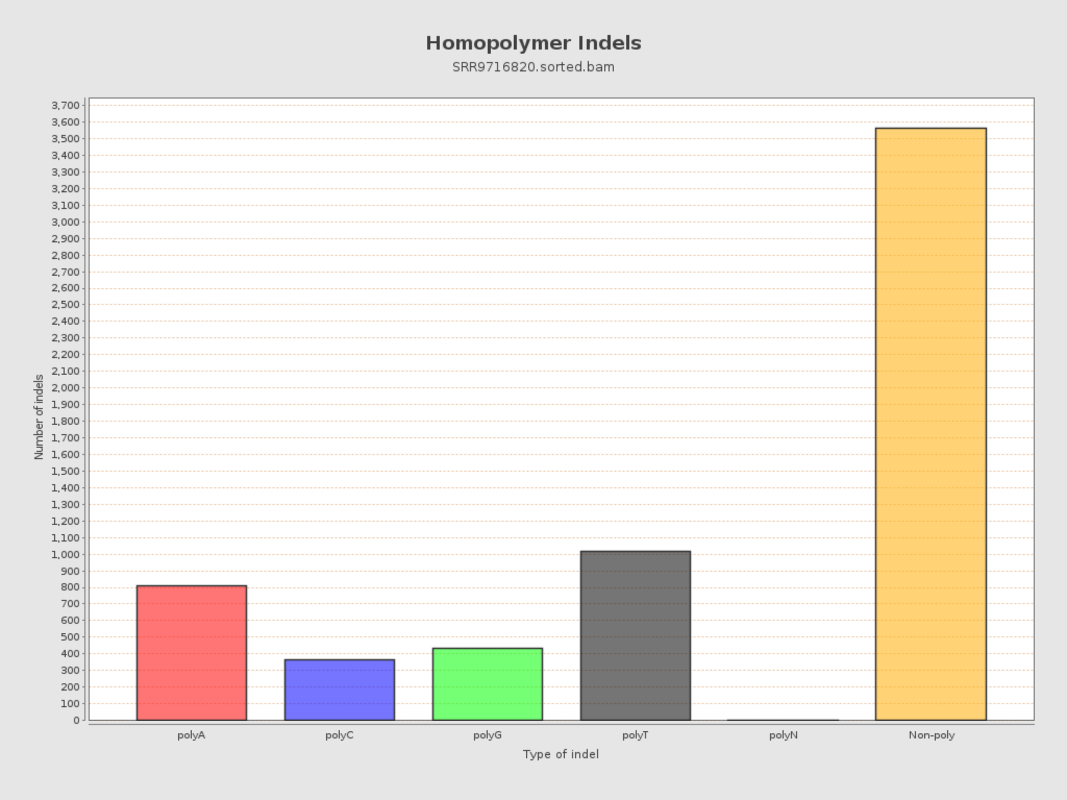
9. Results : Mapped Reads GC-content Distribution



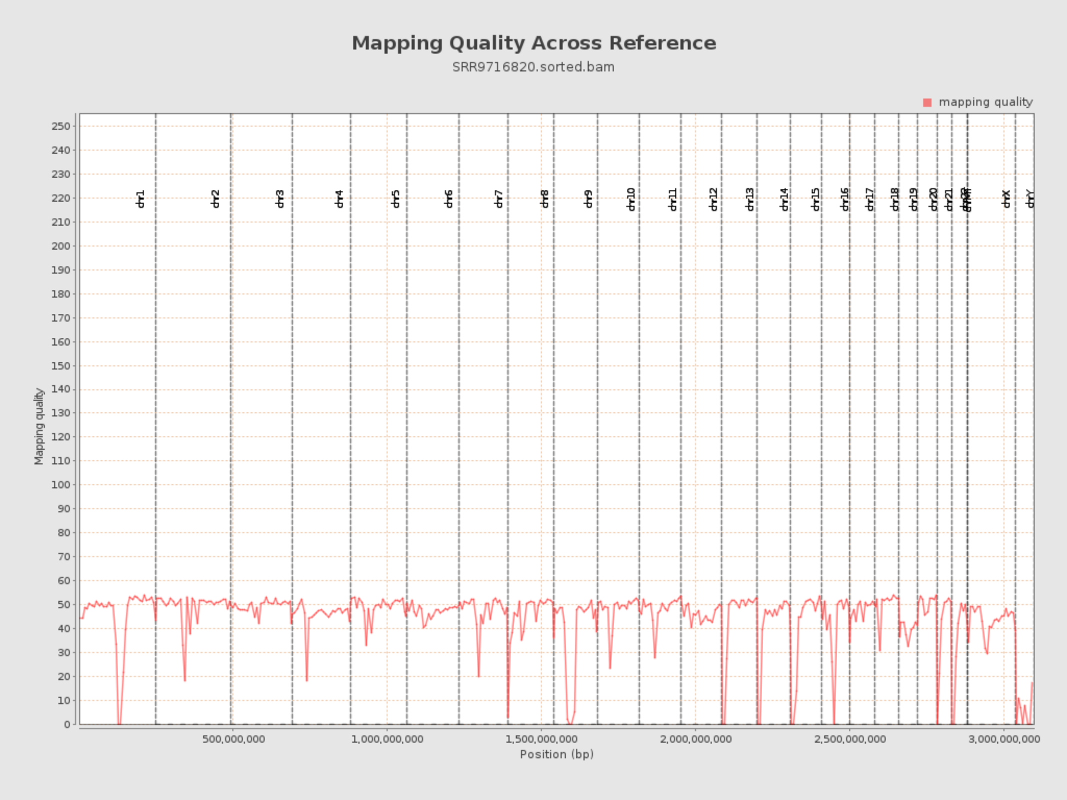
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram