Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:33:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716917.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_SRR9716917 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716917.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:33:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716917.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	670,223
Mapped reads	594,535 / 88.71%
Unmapped reads	75,688 / 11.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,372 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	12,614 / 1.88%
Duplication rate	1.57%
Clipped reads	595,052 / 88.78%

2.2. ACGT Content

Number/percentage of A's	7,999,987 / 23.84%
Number/percentage of C's	6,047,557 / 18.02%
Number/percentage of T's	11,063,681 / 32.97%
Number/percentage of G's	8,445,882 / 25.17%
Number/percentage of N's	392 / 0%
GC Percentage	43.19%

2.3. Coverage

Mean	0.0108

Standard Deviation	0.131

2.4. Mapping Quality

Mean Mapping Quality	43.57

2.5. Mismatches and indels

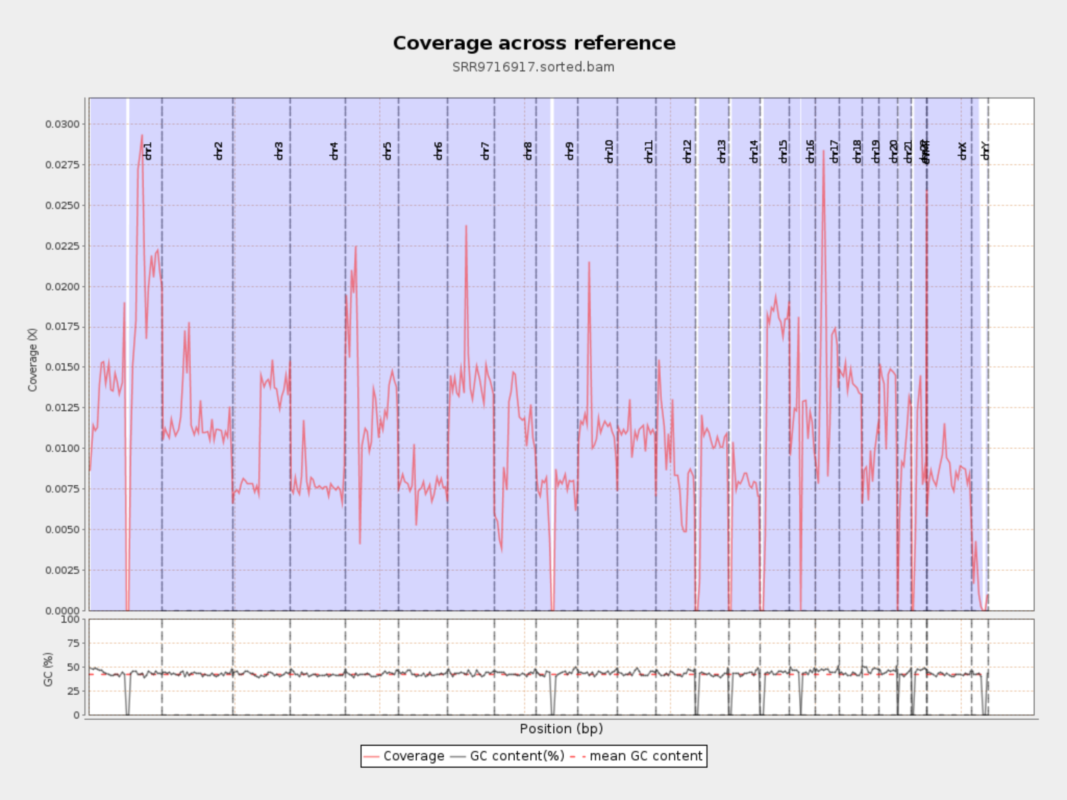
General error rate	0.52%
Mismatches	172,685
Insertions	1,991
Mapped reads with at least one insertion	0.33%
Deletions	6,378
Mapped reads with at least one deletion	1.07%
Homopolymer indels	43.29%

2.6. Chromosome stats

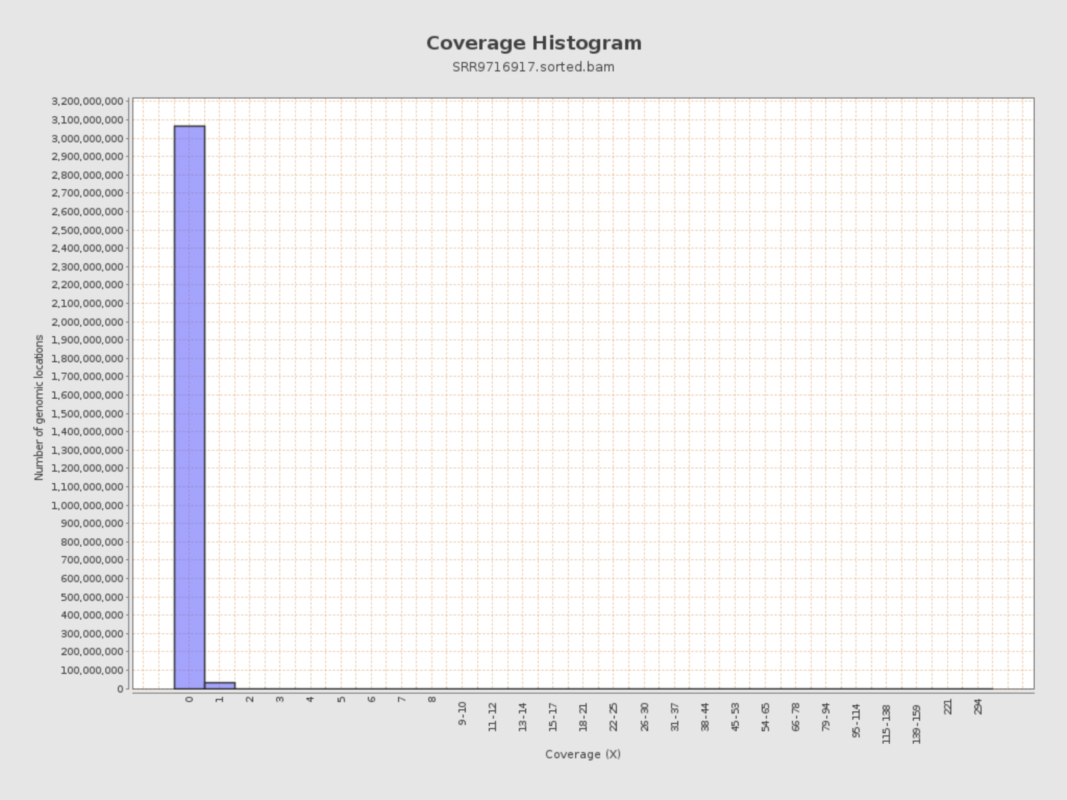
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4000560	0.0161	0.1834
chr2	243199373	2858921	0.0118	0.1716
chr3	198022430	2150226	0.0109	0.1095
chr4	191154276	1493610	0.0078	0.0942
chr5	180915260	2447792	0.0135	0.1205
chr6	171115067	1309527	0.0077	0.0984
chr7	159138663	2294971	0.0144	0.1924

chr8	146364022	1502408	0.0103	0.1147
chr9	141213431	953304	0.0068	0.1029
chr10	135534747	1584643	0.0117	0.1434
chr11	135006516	1476210	0.0109	0.1268
chr12	133851895	1225278	0.0092	0.1003
chr13	115169878	1020843	0.0089	0.0977
chr14	107349540	756454	0.007	0.089
chr15	102531392	1493140	0.0146	0.1258
chr16	90354753	1009352	0.0112	0.1181
chr17	81195210	1257772	0.0155	0.1329
chr18	78077248	1107351	0.0142	0.1785
chr19	59128983	532654	0.009	0.1384
chr20	63025520	869839	0.0138	0.1221
chr21	48129895	438335	0.0091	0.1007
chr22	51304566	384895	0.0075	0.0902
chrMT	16571	430	0.0259	0.159
chrX	155270560	1318302	0.0085	0.1064
chrY	59373566	80896	0.0014	0.0435

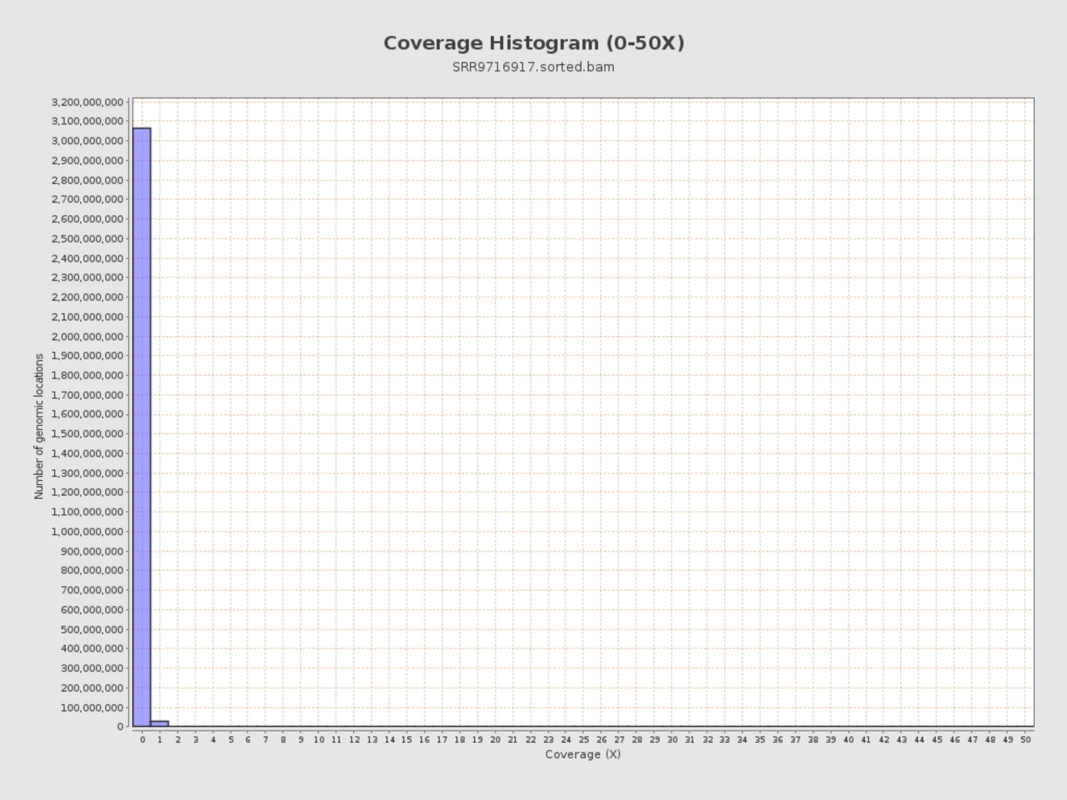
3. Results : Coverage across reference



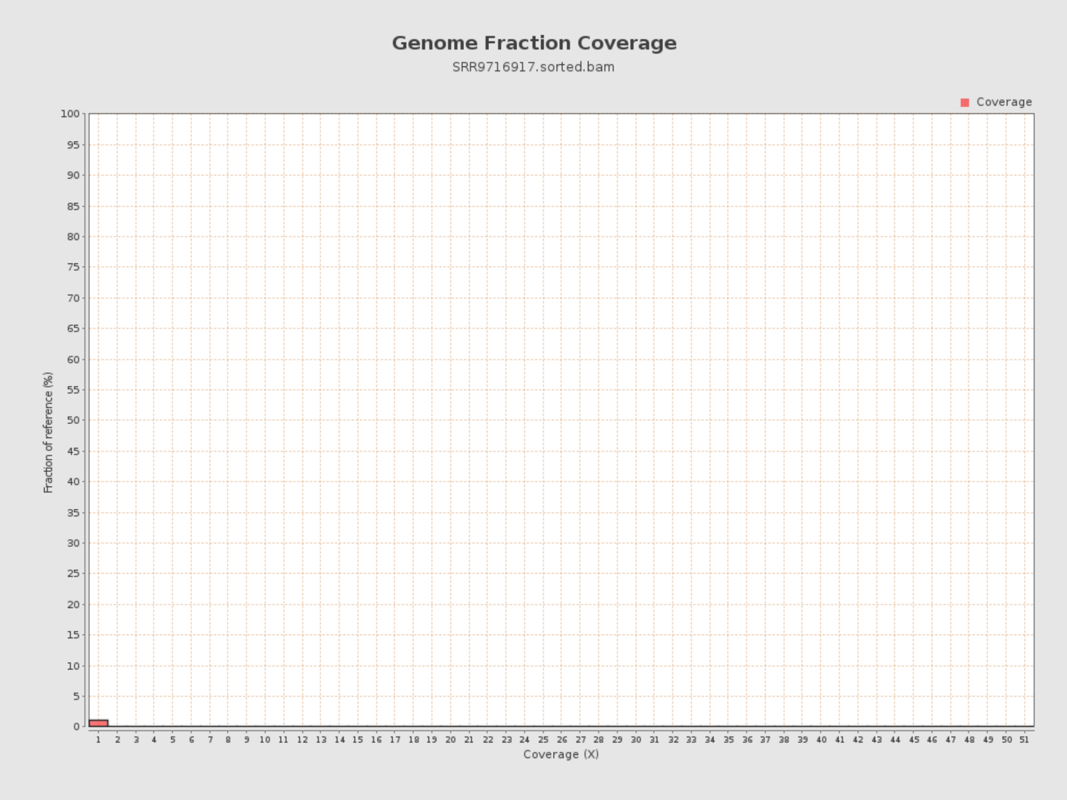
4. Results : Coverage Histogram



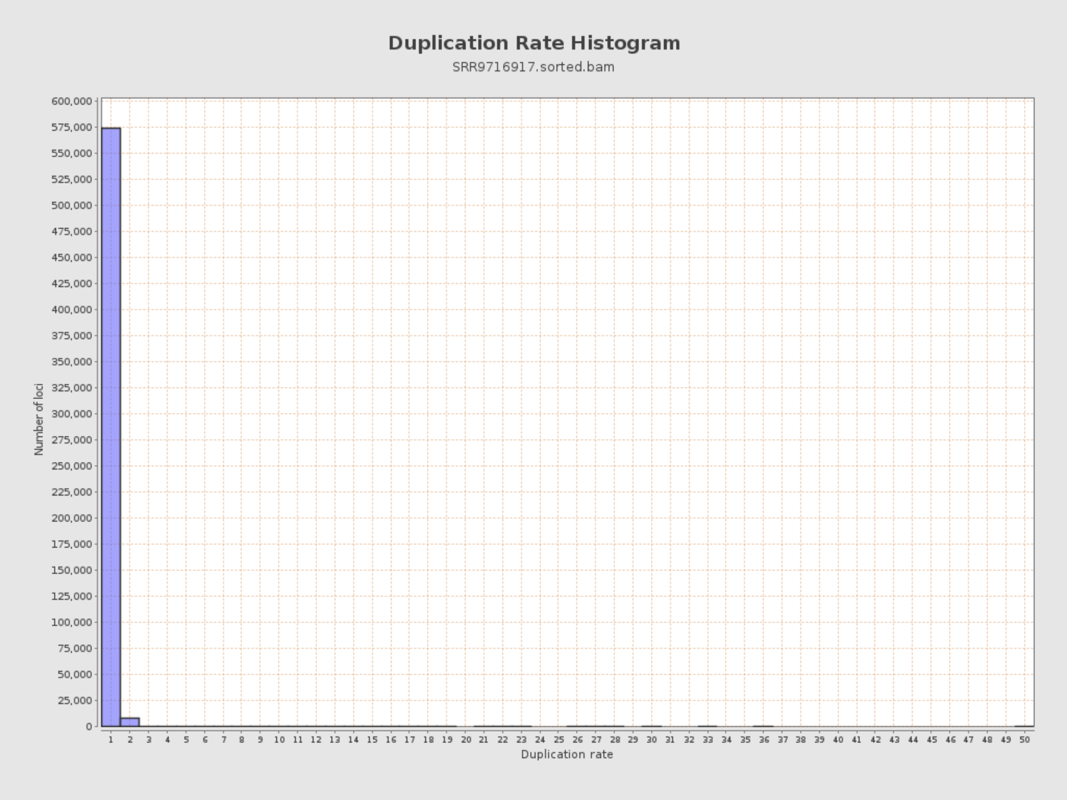
5. Results : Coverage Histogram (0-50X)



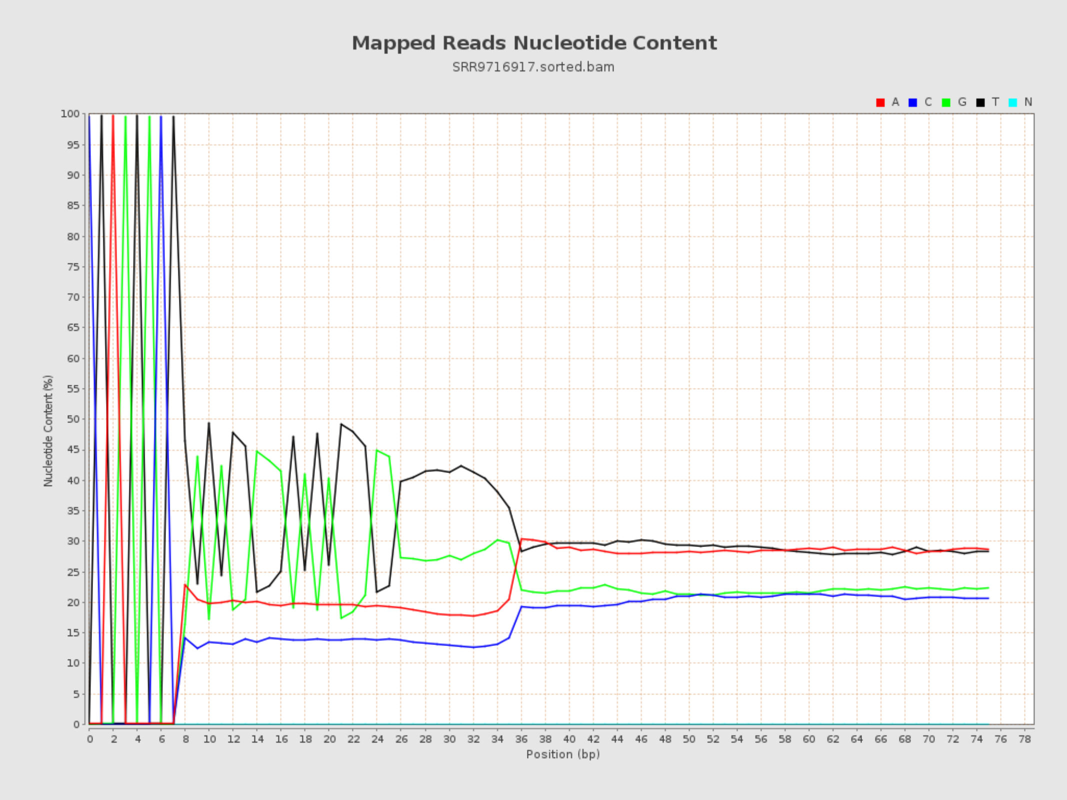
6. Results : Genome Fraction Coverage



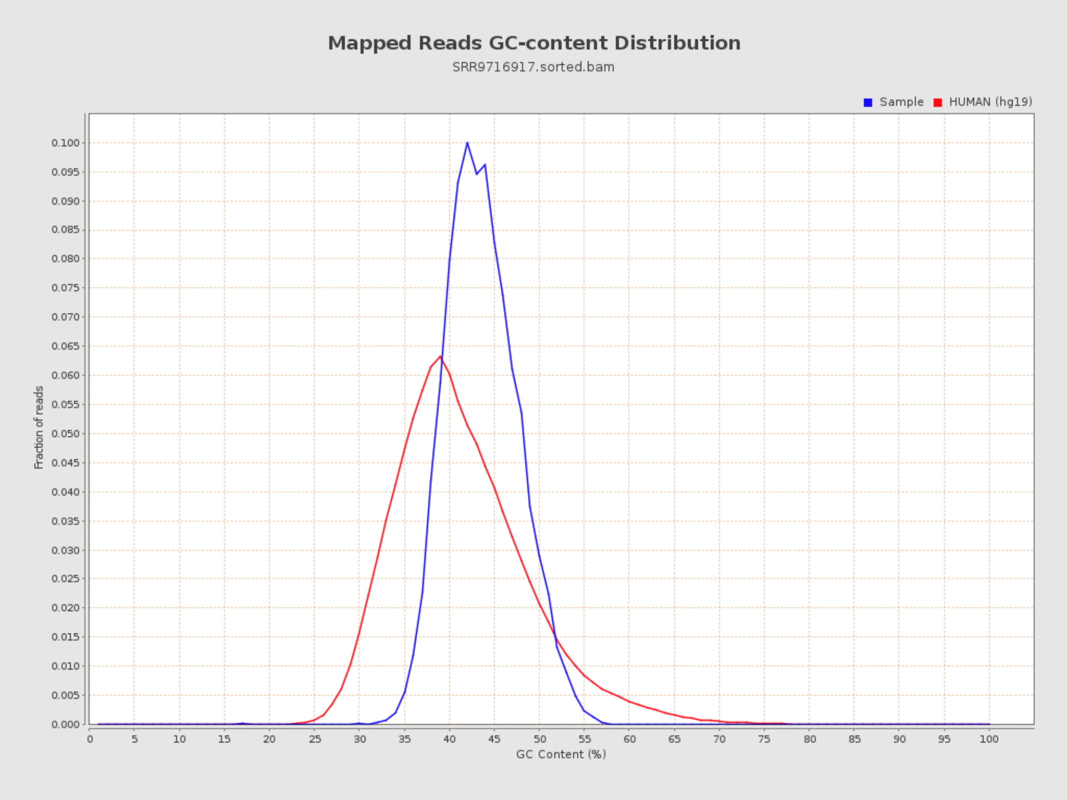
7. Results : Duplication Rate Histogram



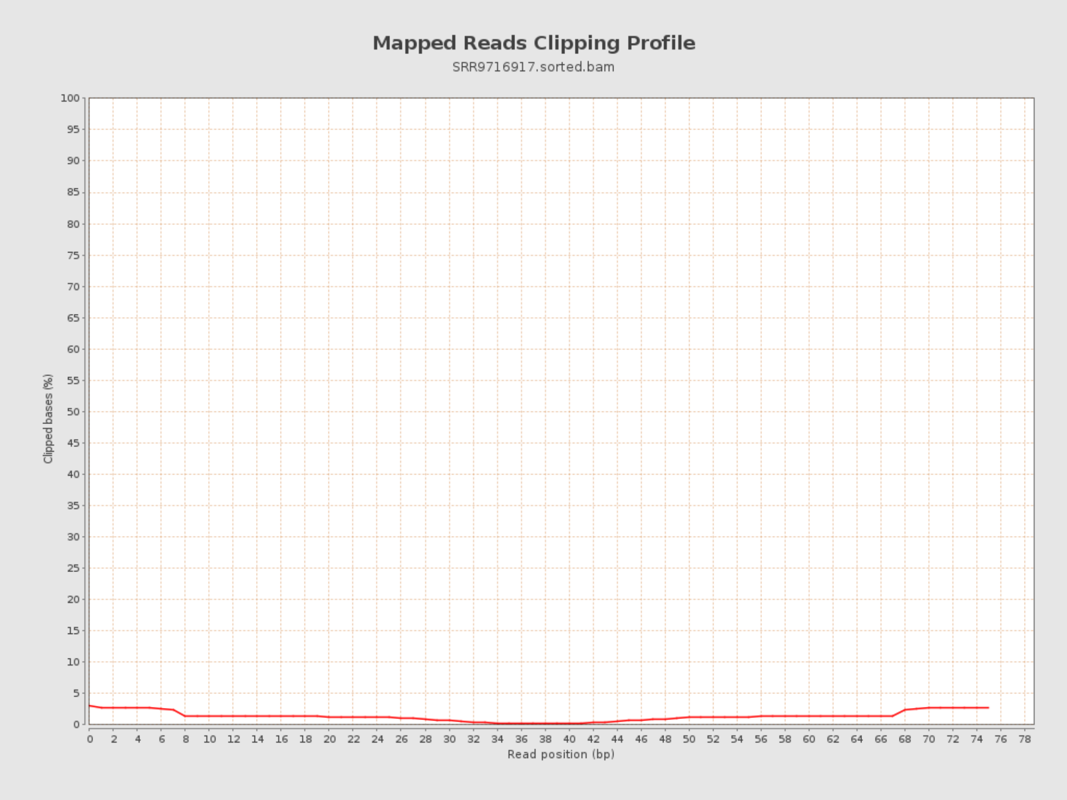
8. Results : Mapped Reads Nucleotide Content



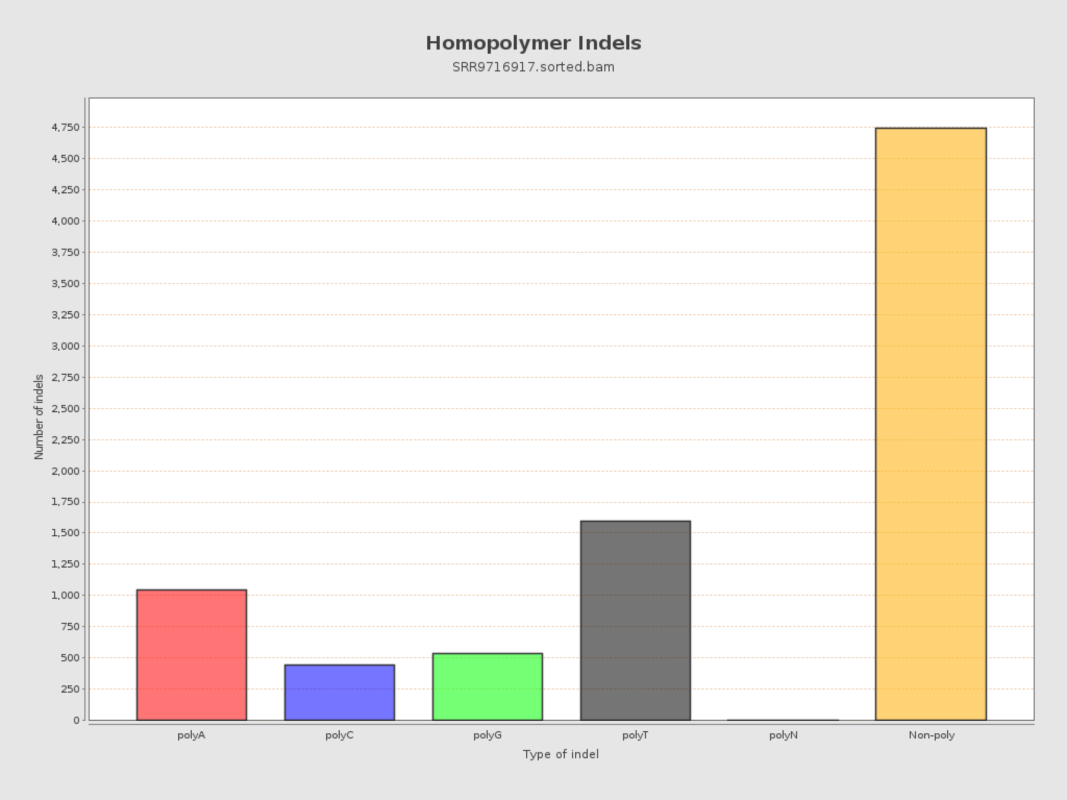
9. Results : Mapped Reads GC-content Distribution



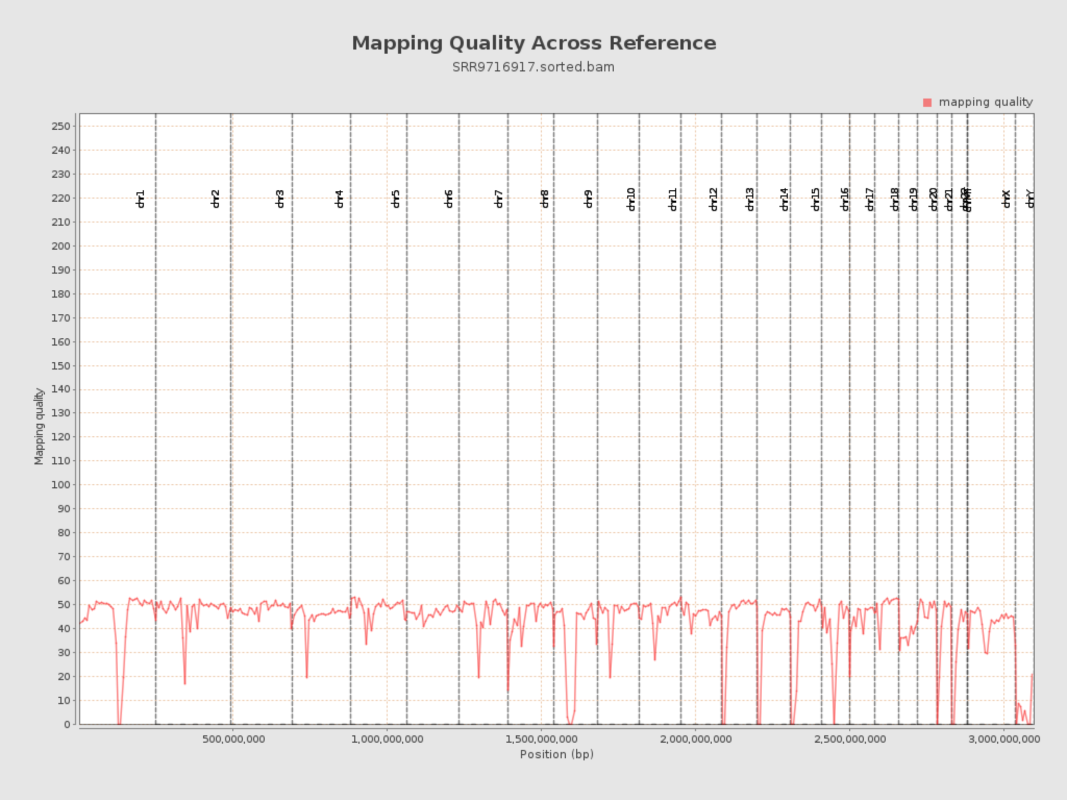
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram