Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:26:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716417.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_SRR9716417 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716417.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:26:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716417.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,068,348
Mapped reads	963,101 / 90.15%
Unmapped reads	105,247 / 9.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,839 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	27,025 / 2.53%
Duplication rate	2.05%
Clipped reads	965,216 / 90.35%

2.2. ACGT Content

Number/percentage of A's	13,475,213 / 24.04%
Number/percentage of C's	10,267,156 / 18.32%
Number/percentage of T's	18,203,760 / 32.48%
Number/percentage of G's	14,098,001 / 25.15%
Number/percentage of N's	816 / 0%
GC Percentage	43.47%

2.3. Coverage

Mean	0.0181

Standard Deviation	0.2002

2.4. Mapping Quality

Mean Mapping Quality	44.44

2.5. Mismatches and indels

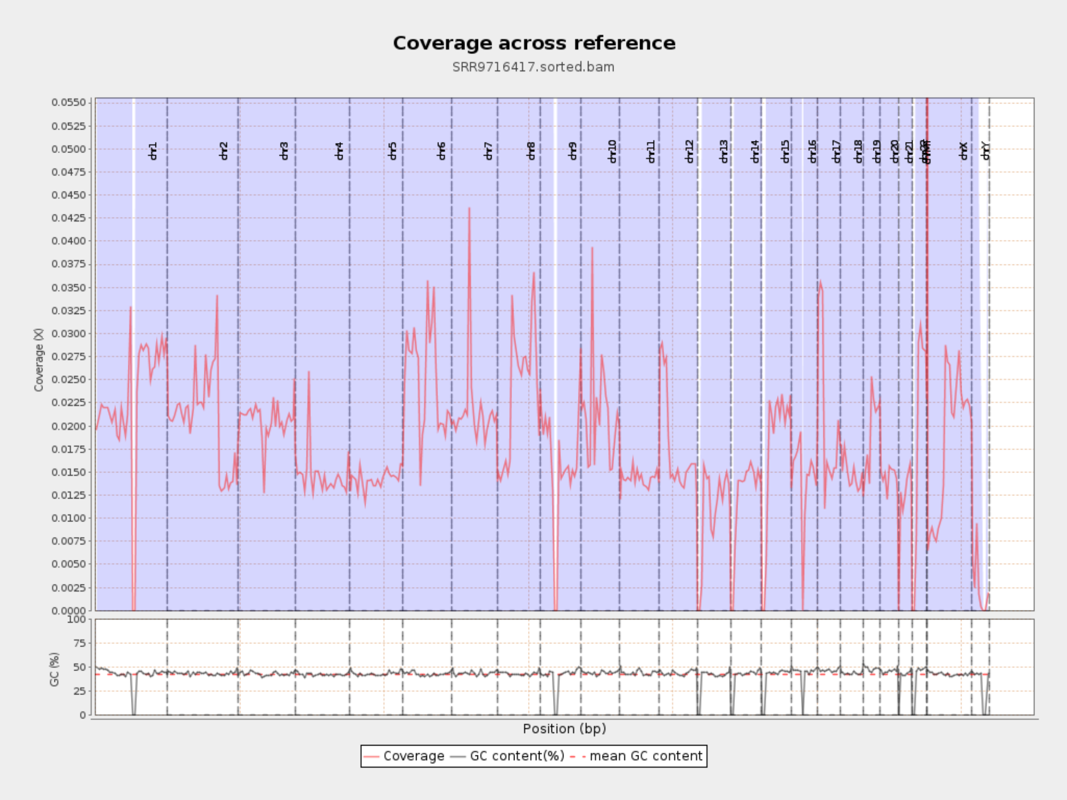
General error rate	0.52%
Mismatches	283,493
Insertions	4,046
Mapped reads with at least one insertion	0.42%
Deletions	10,040
Mapped reads with at least one deletion	1.03%
Homopolymer indels	40.86%

2.6. Chromosome stats

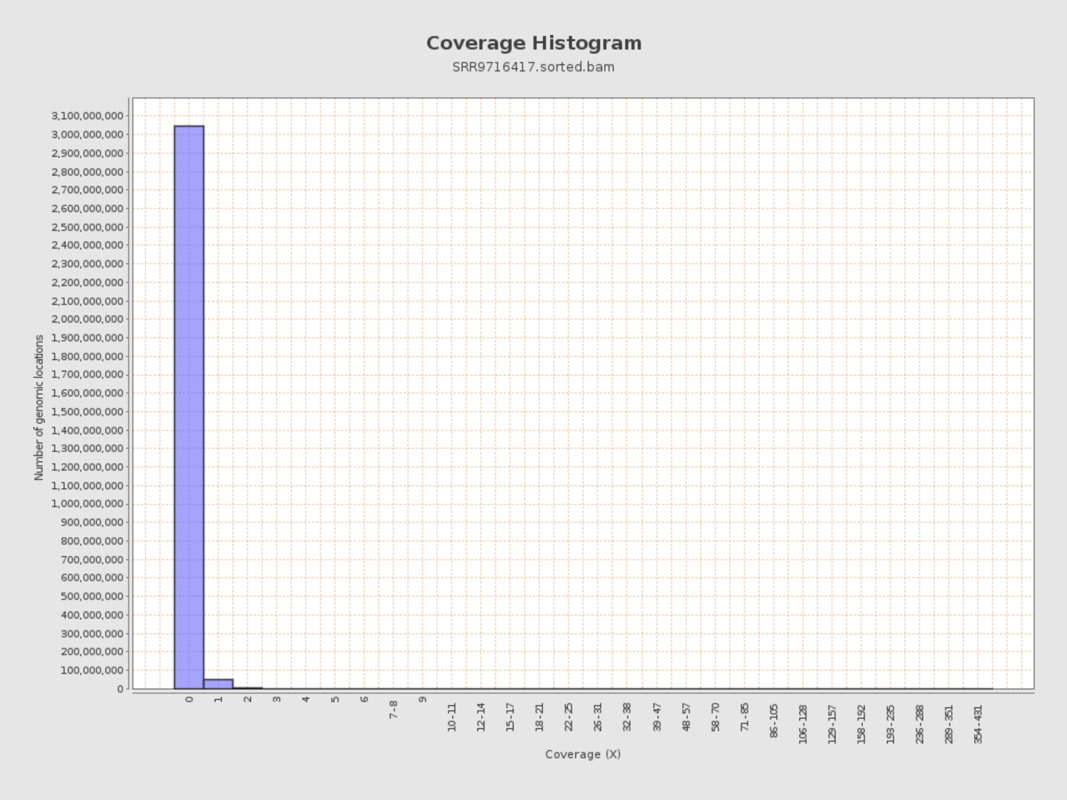
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5703421	0.0229	0.3378
chr2	243199373	5070992	0.0209	0.2284
chr3	198022430	4071208	0.0206	0.1529
chr4	191154276	2817030	0.0147	0.1372
chr5	180915260	2581661	0.0143	0.1269
chr6	171115067	4252282	0.0249	0.1892
chr7	159138663	3480233	0.0219	0.3681

chr8	146364022	3508591	0.024	0.19
chr9	141213431	2170805	0.0154	0.158
chr10	135534747	2901739	0.0214	0.1888
chr11	135006516	1939198	0.0144	0.1624
chr12	133851895	2401260	0.0179	0.1438
chr13	115169878	1225920	0.0106	0.1096
chr14	107349540	1310843	0.0122	0.1227
chr15	102531392	1785284	0.0174	0.1398
chr16	90354753	1270111	0.0141	0.1337
chr17	81195210	1706839	0.021	0.158
chr18	78077248	1149490	0.0147	0.2561
chr19	59128983	1148437	0.0194	0.2229
chr20	63025520	910289	0.0144	0.128
chr21	48129895	580781	0.0121	0.1273
chr22	51304566	1010357	0.0197	0.1497
chrMT	16571	63792	3.8496	2.8399
chrX	155270560	2848186	0.0183	0.1557
chrY	59373566	152202	0.0026	0.0691

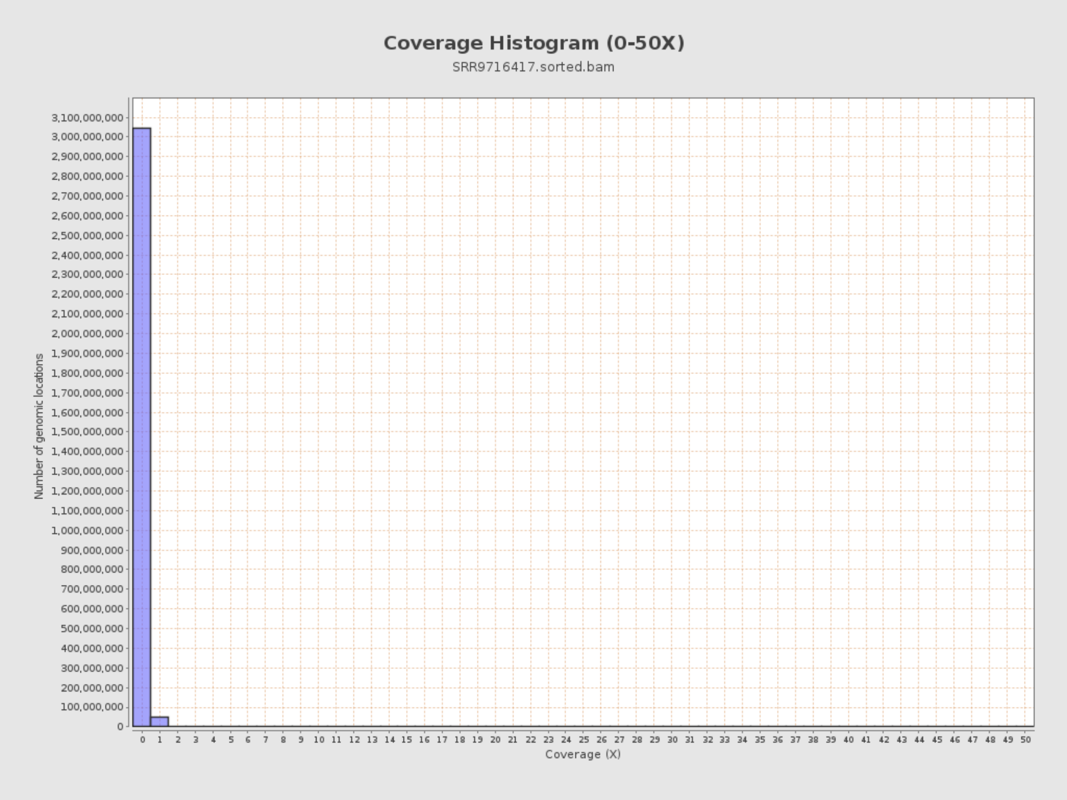
3. Results : Coverage across reference



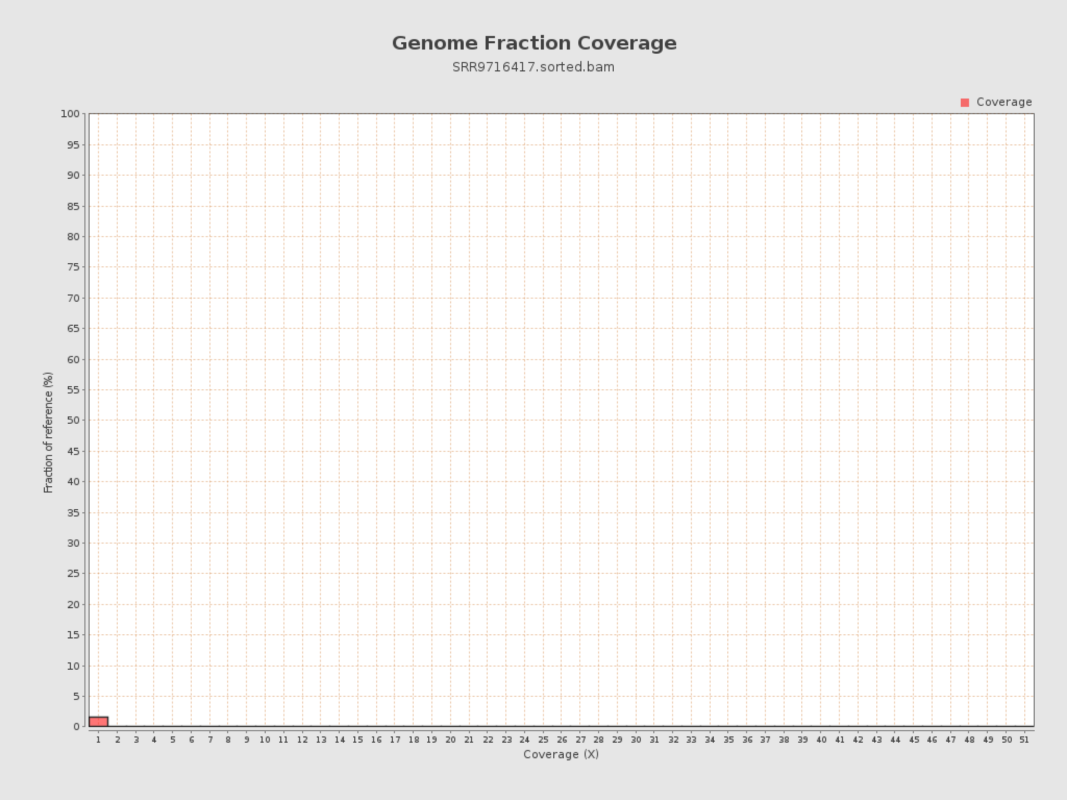
4. Results : Coverage Histogram



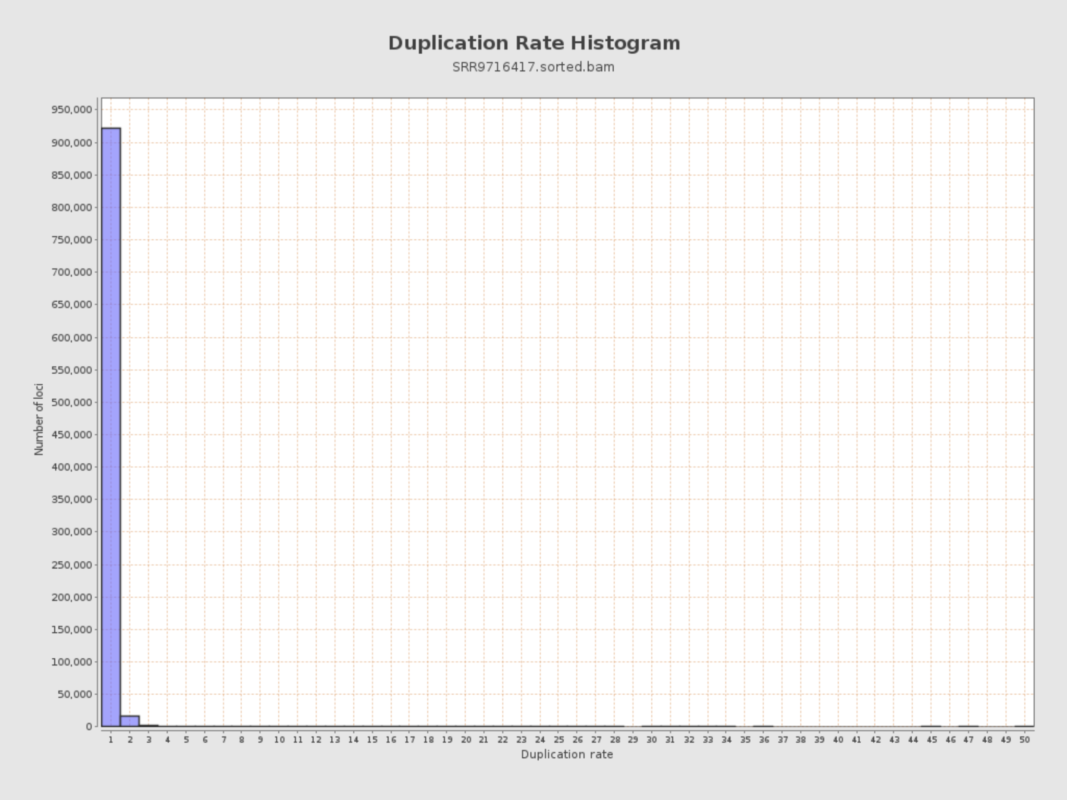
5. Results : Coverage Histogram (0-50X)



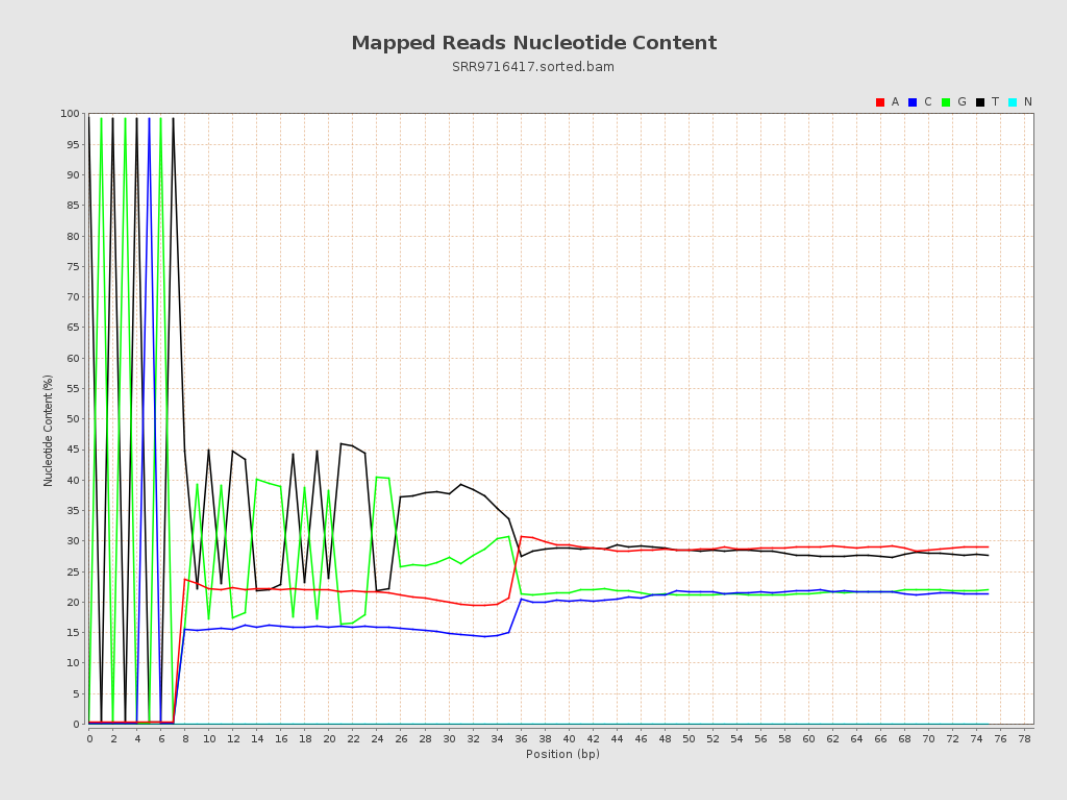
6. Results : Genome Fraction Coverage



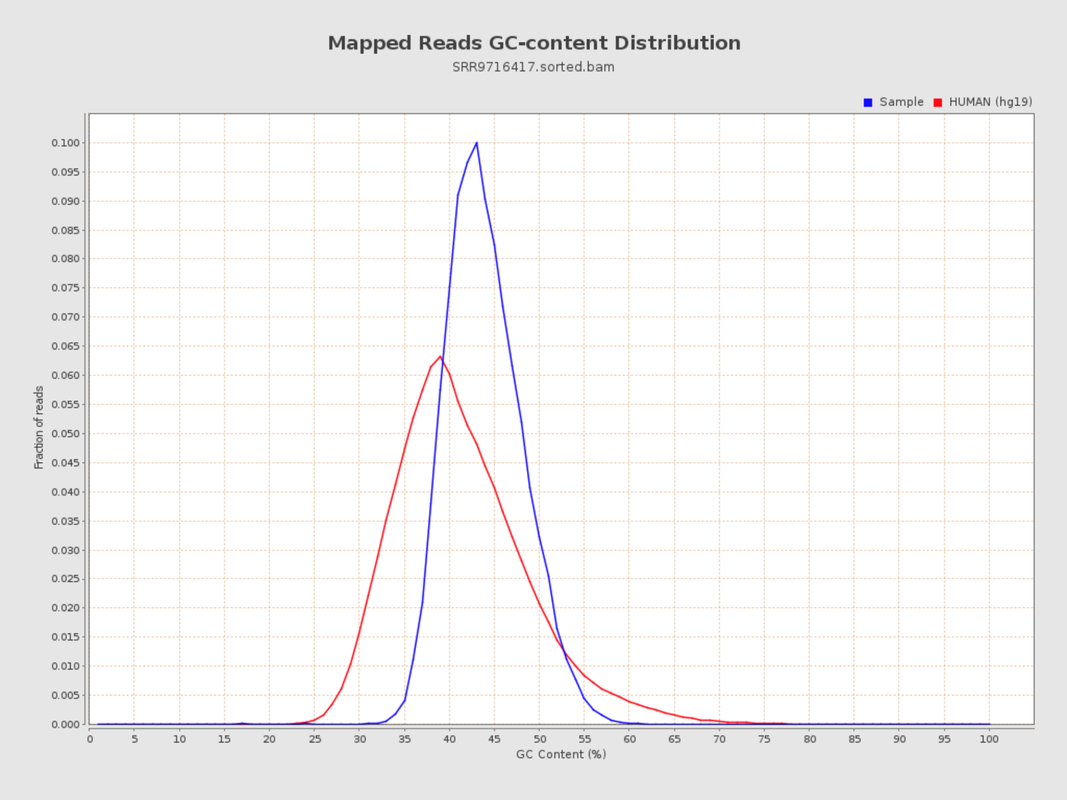
7. Results : Duplication Rate Histogram



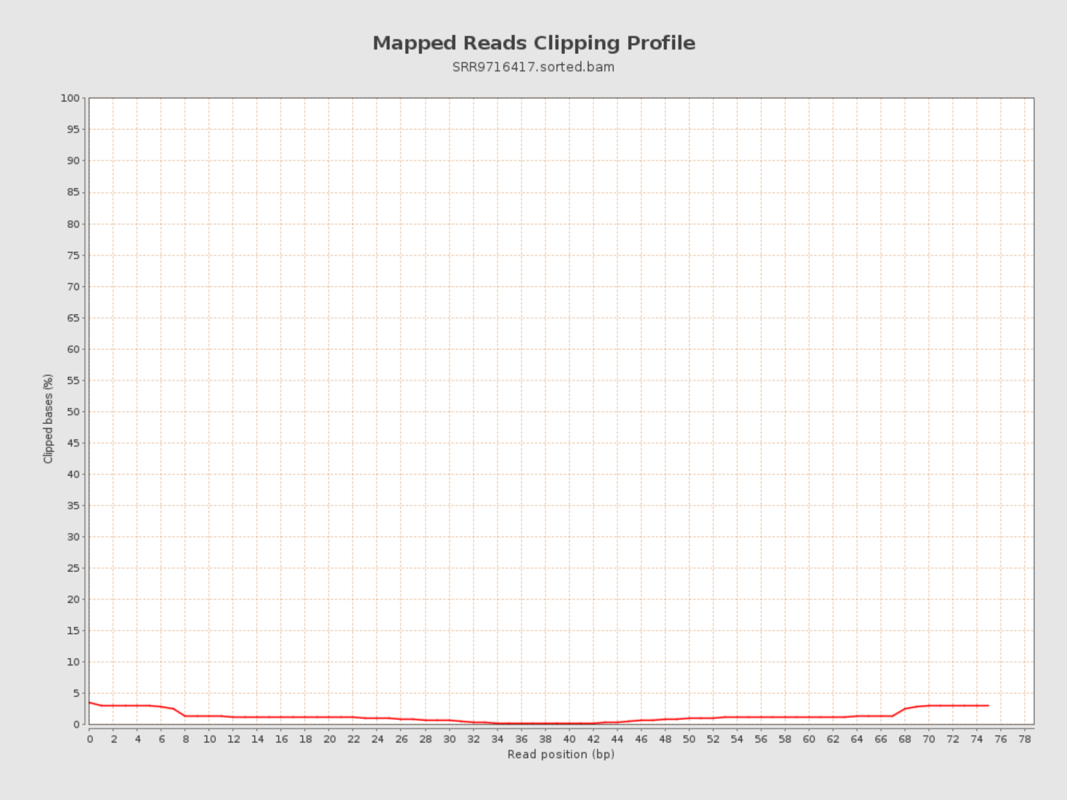
8. Results : Mapped Reads Nucleotide Content



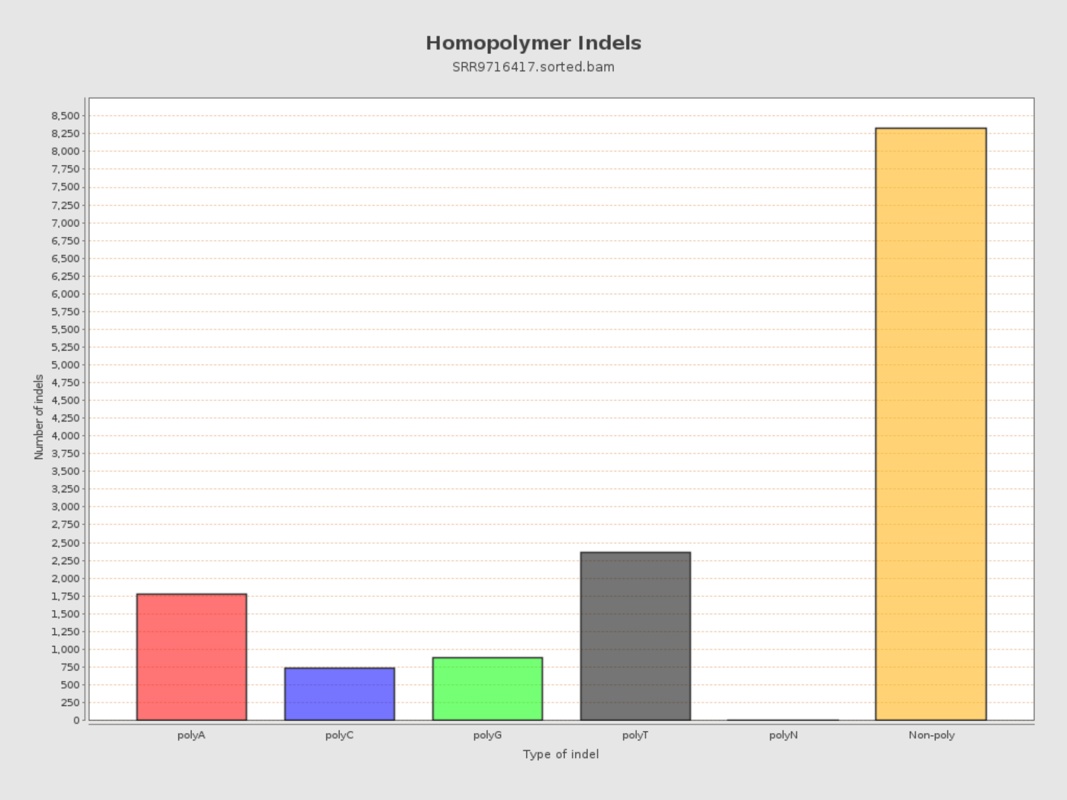
9. Results : Mapped Reads GC-content Distribution



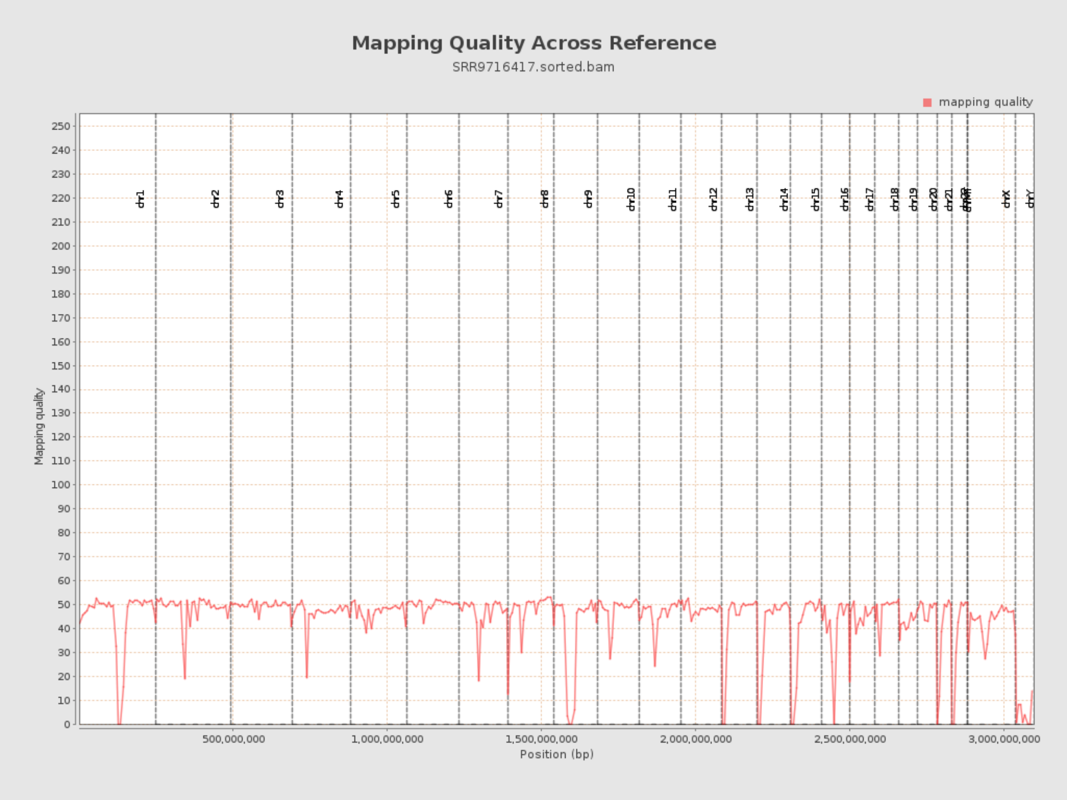
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram