Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 04:51:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716274.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_SRR9716274 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716274.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 04:51:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716274.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	643,412
Mapped reads	560,738 / 87.15%
Unmapped reads	82,674 / 12.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,603 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	8,166 / 1.27%
Duplication rate	1.13%
Clipped reads	561,974 / 87.34%

2.2. ACGT Content

Number/percentage of A's	7,534,372 / 23.69%
Number/percentage of C's	5,854,141 / 18.41%
Number/percentage of T's	10,231,283 / 32.17%
Number/percentage of G's	8,185,984 / 25.74%
Number/percentage of N's	684 / 0%
GC Percentage	44.14%

2.3. Coverage

Mean	0.0103

Standard Deviation	0.1152

2.4. Mapping Quality

Mean Mapping Quality	43.6

2.5. Mismatches and indels

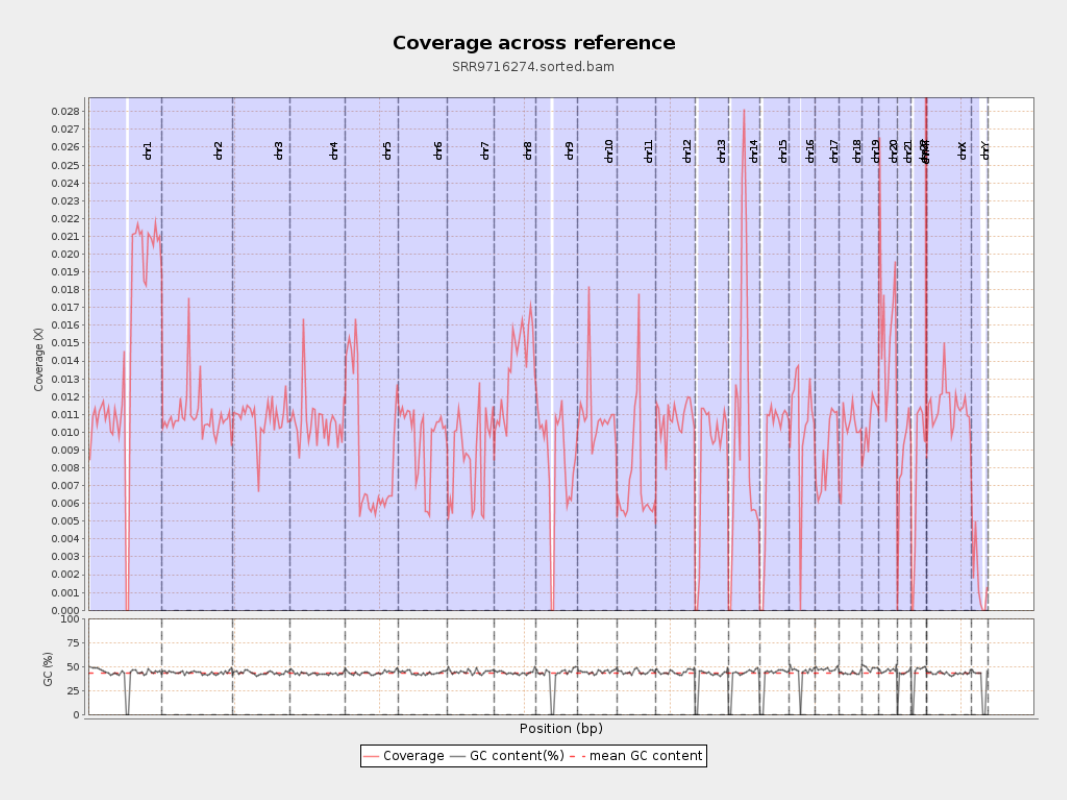
General error rate	0.5%
Mismatches	156,287
Insertions	2,030
Mapped reads with at least one insertion	0.36%
Deletions	5,057
Mapped reads with at least one deletion	0.9%
Homopolymer indels	40.61%

2.6. Chromosome stats

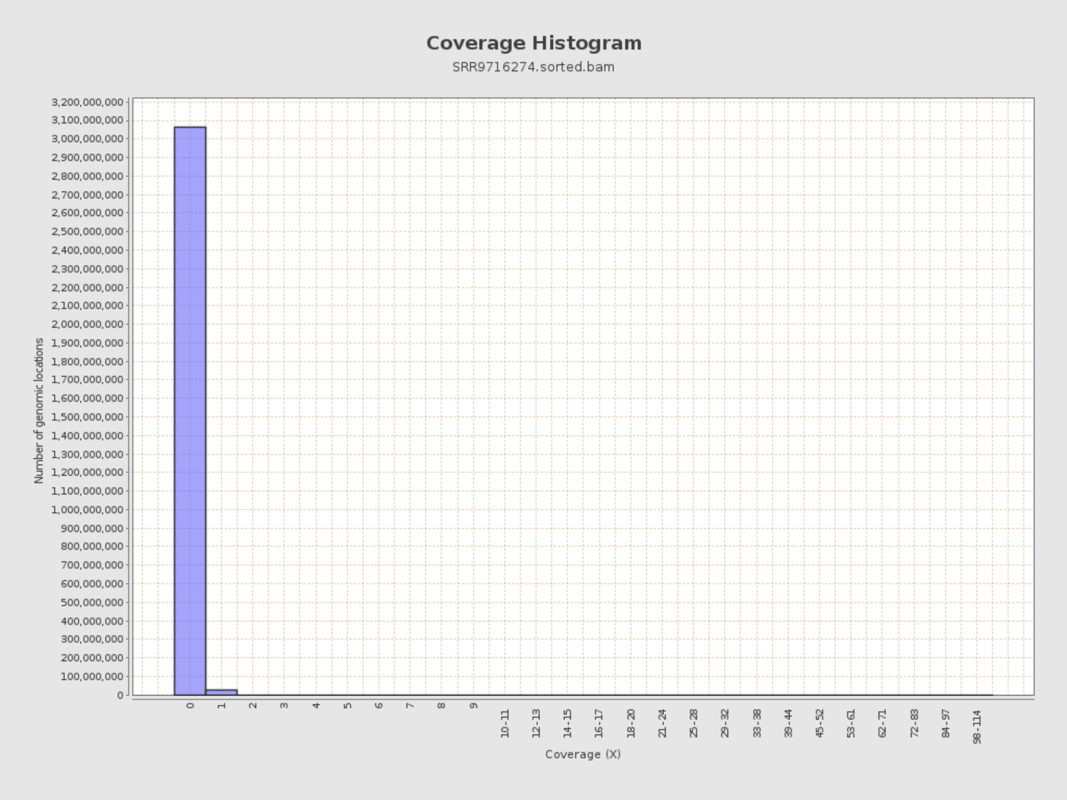
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3578706	0.0144	0.1532
chr2	243199373	2661980	0.0109	0.1262
chr3	198022430	2129853	0.0108	0.1074
chr4	191154276	2023215	0.0106	0.11
chr5	180915260	1586163	0.0088	0.0973
chr6	171115067	1658249	0.0097	0.1043
chr7	159138663	1370067	0.0086	0.1041

chr8	146364022	1991146	0.0136	0.1268
chr9	141213431	1152458	0.0082	0.107
chr10	135534747	1480364	0.0109	0.1253
chr11	135006516	995146	0.0074	0.0989
chr12	133851895	1445836	0.0108	0.1082
chr13	115169878	997710	0.0087	0.0959
chr14	107349540	1096492	0.0102	0.1077
chr15	102531392	903763	0.0088	0.097
chr16	90354753	952042	0.0105	0.1105
chr17	81195210	721292	0.0089	0.0984
chr18	78077248	780330	0.01	0.1658
chr19	59128983	619941	0.0105	0.1242
chr20	63025520	1016200	0.0161	0.1327
chr21	48129895	402449	0.0084	0.0978
chr22	51304566	379261	0.0074	0.0886
chrMT	16571	4852	0.2928	0.6231
chrX	155270560	1770332	0.0114	0.1164
chrY	59373566	97156	0.0016	0.0503

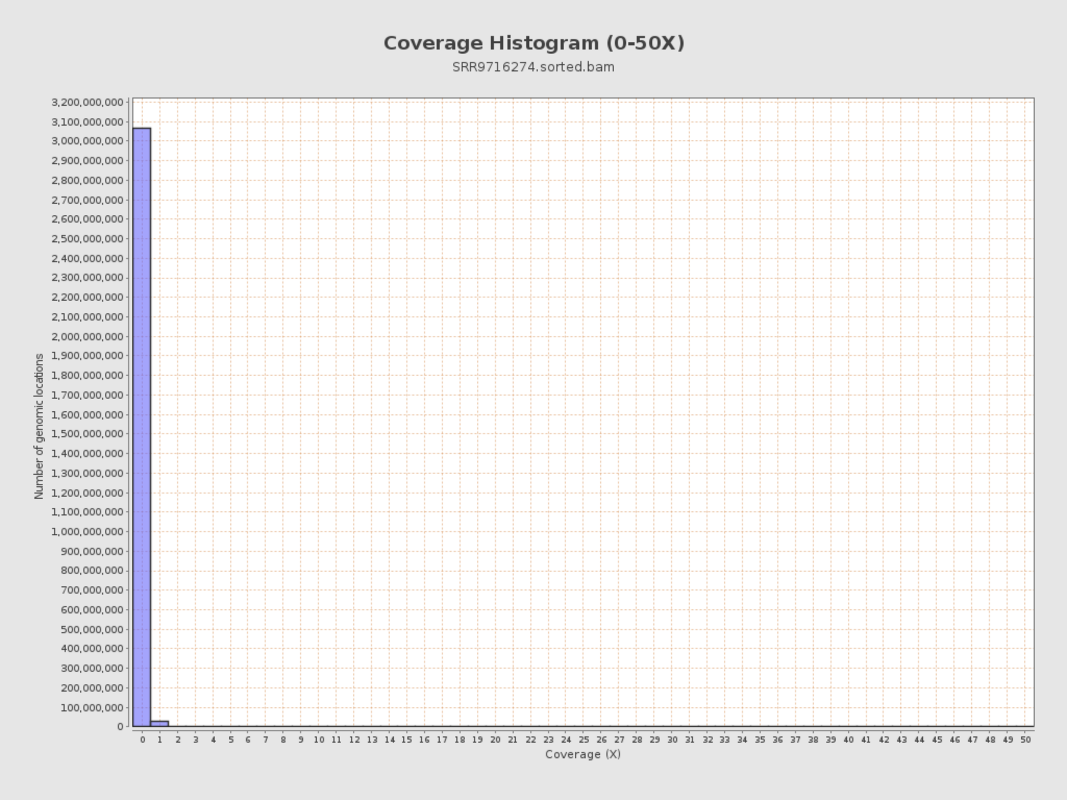
3. Results : Coverage across reference



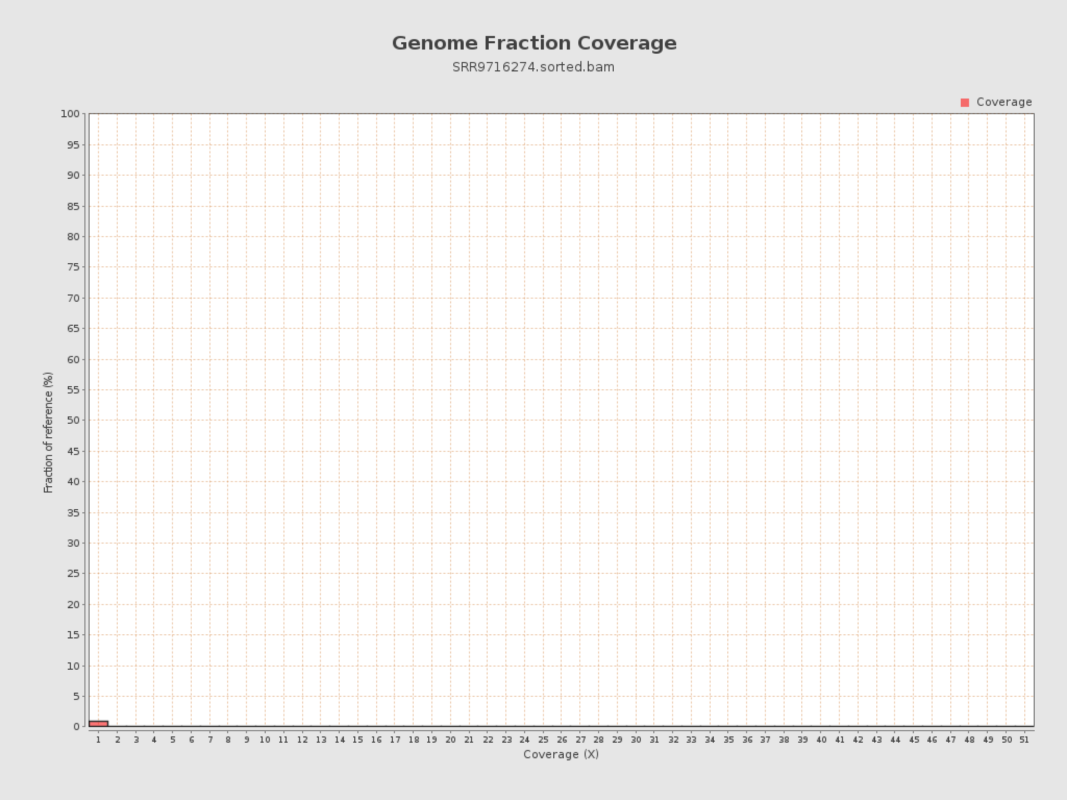
4. Results : Coverage Histogram



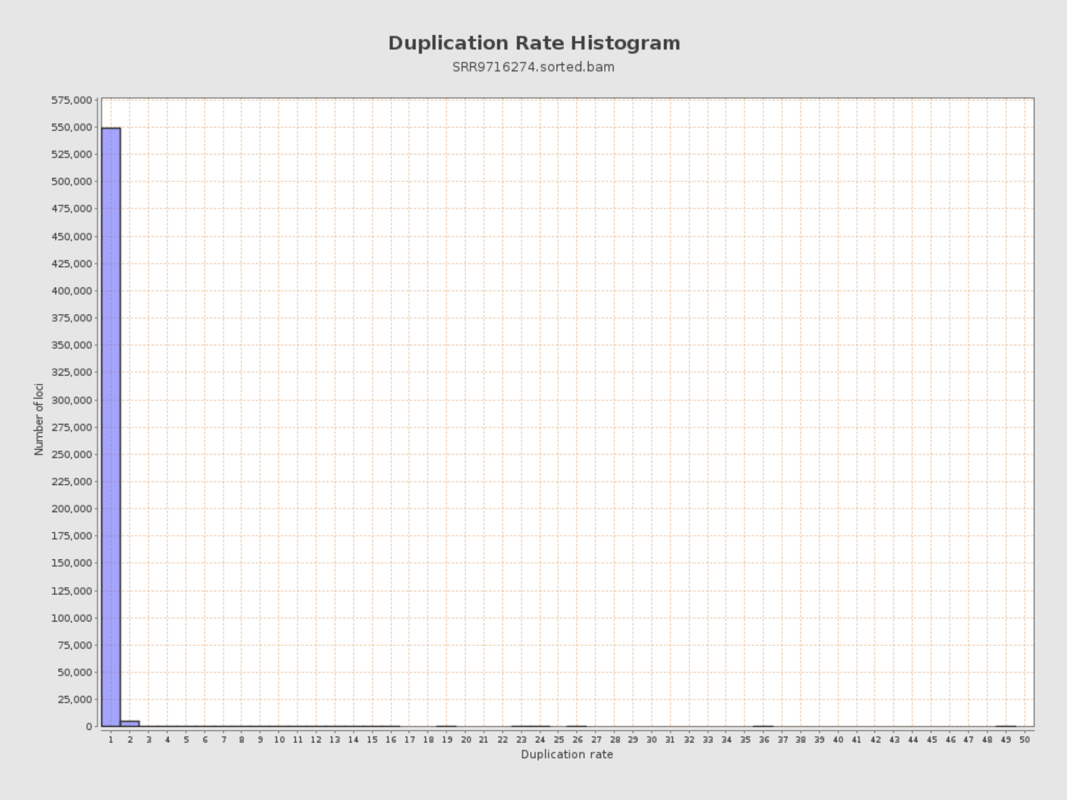
5. Results : Coverage Histogram (0-50X)



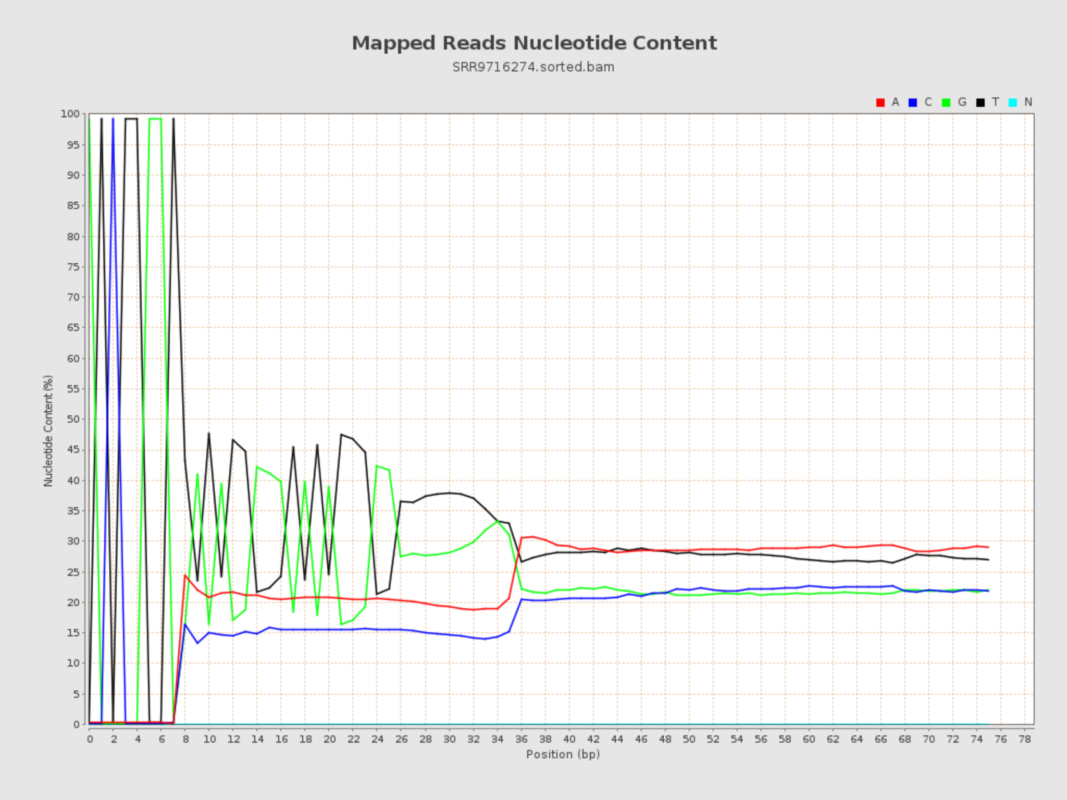
6. Results : Genome Fraction Coverage



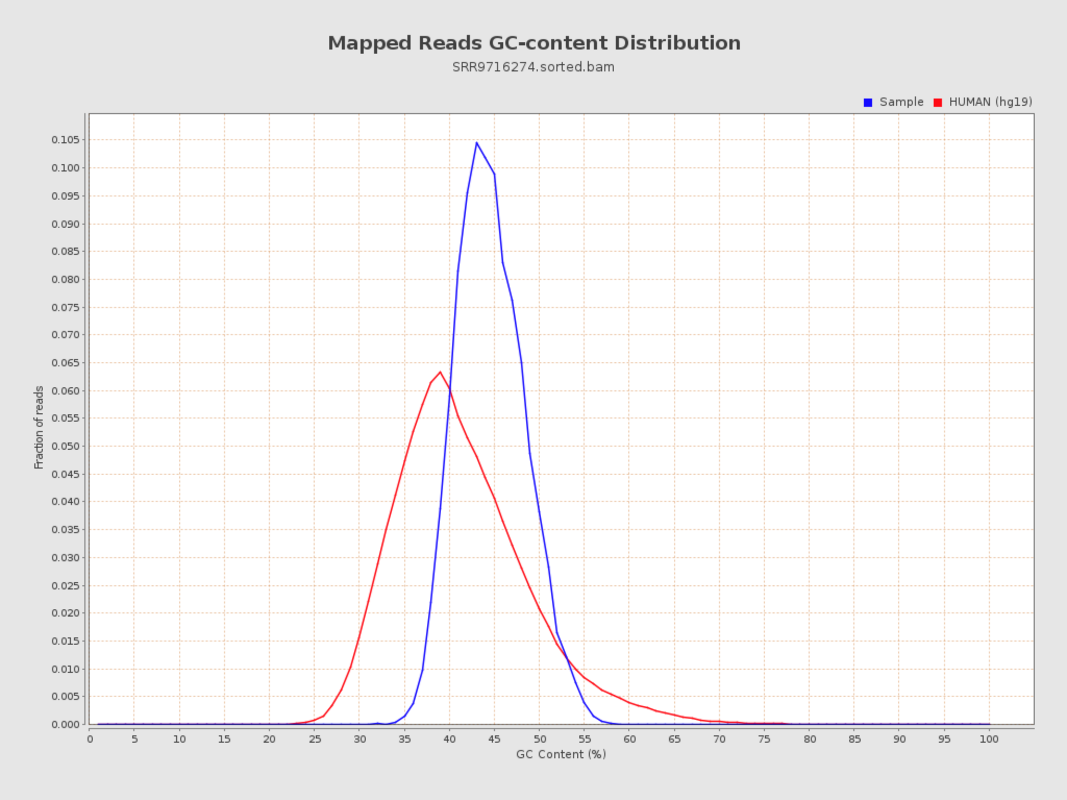
7. Results : Duplication Rate Histogram



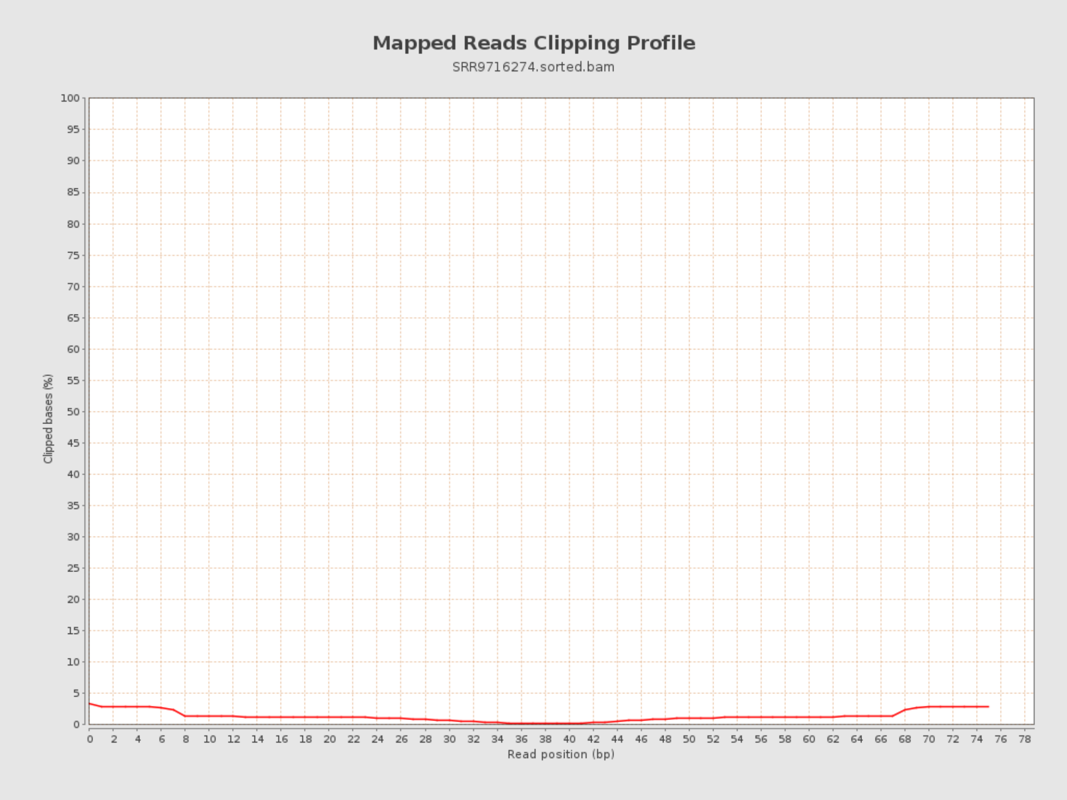
8. Results : Mapped Reads Nucleotide Content



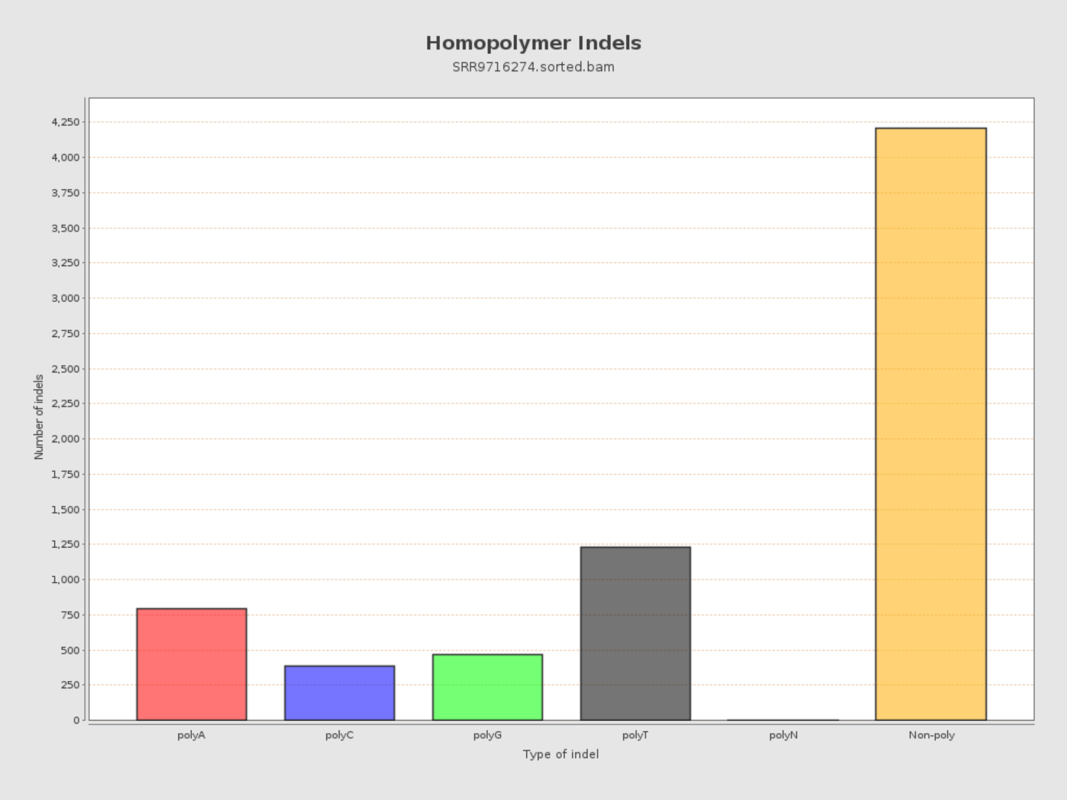
9. Results : Mapped Reads GC-content Distribution



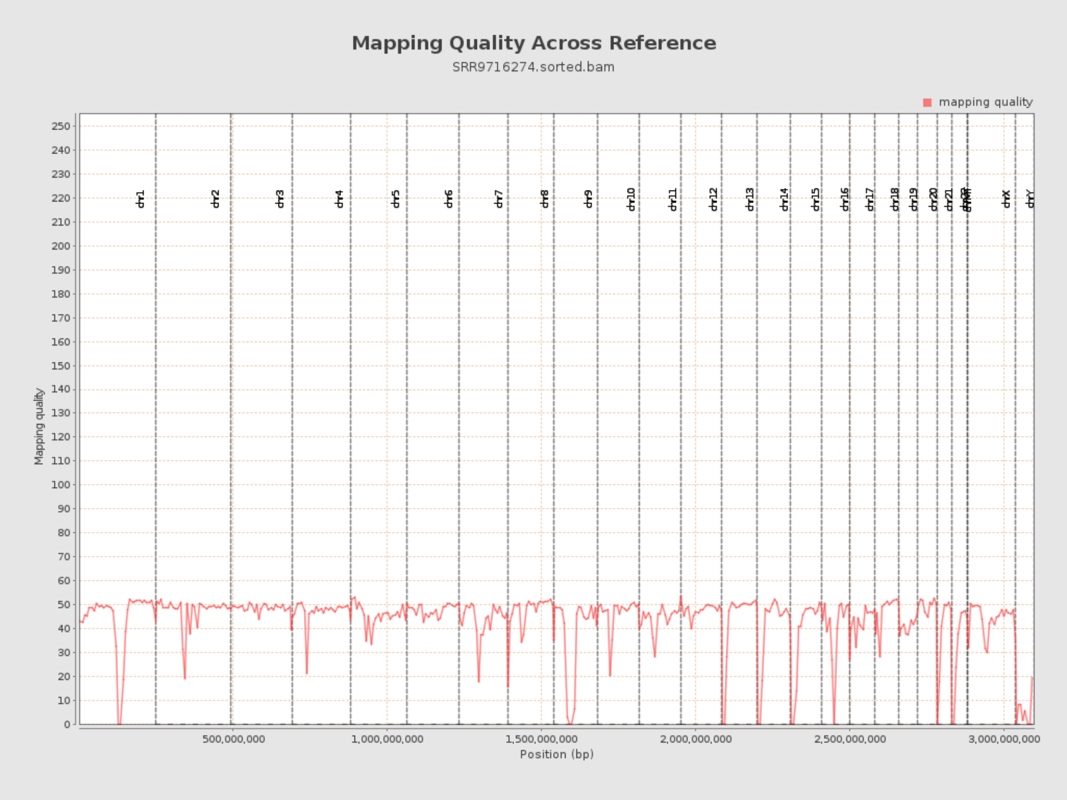
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram