Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:09:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716219.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_SRR9716219 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716219.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:09:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716219.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	866,127
Mapped reads	750,914 / 86.7%
Unmapped reads	115,213 / 13.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,721 / 0.55%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	22,384 / 2.58%
Duplication rate	2.36%
Clipped reads	752,871 / 86.92%

2.2. ACGT Content

Number/percentage of A's	11,747,711 / 26.7%
Number/percentage of C's	8,197,798 / 18.63%
Number/percentage of T's	13,431,693 / 30.52%
Number/percentage of G's	10,627,975 / 24.15%
Number/percentage of N's	446 / 0%
GC Percentage	42.78%

2.3. Coverage

Mean	0.0142

Standard Deviation	0.1544

2.4. Mapping Quality

Mean Mapping Quality	45.21

2.5. Mismatches and indels

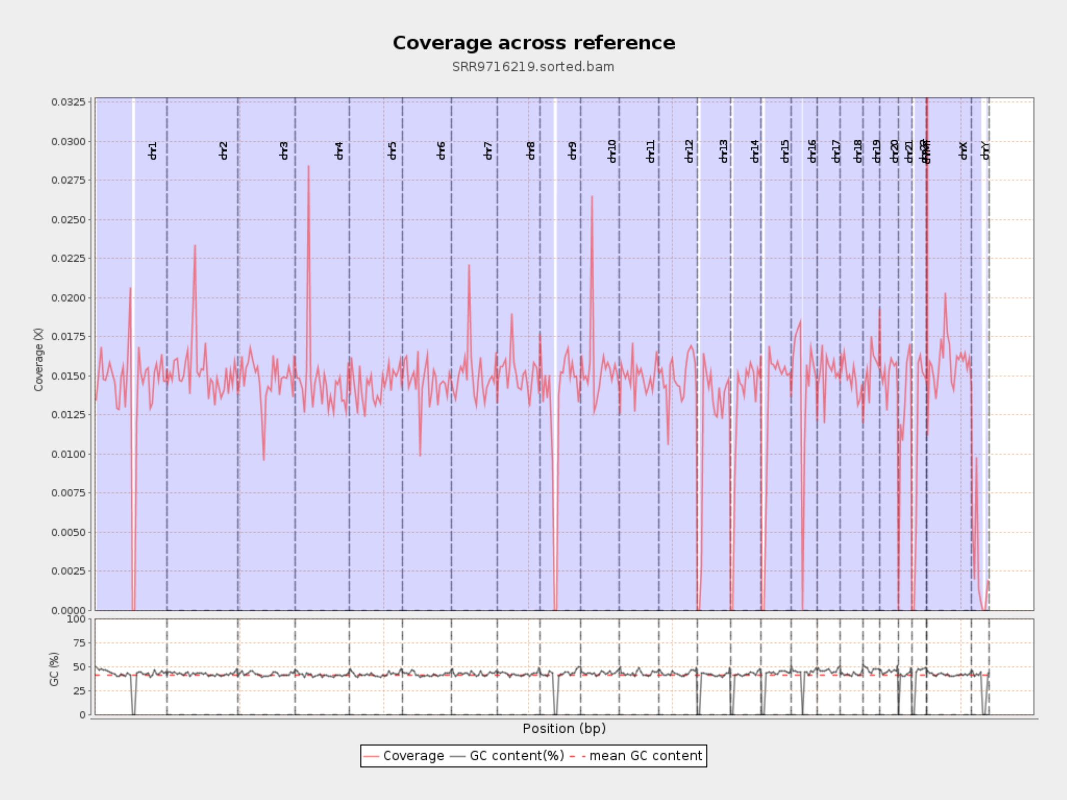
General error rate	0.52%
Mismatches	221,470
Insertions	3,794
Mapped reads with at least one insertion	0.5%
Deletions	8,150
Mapped reads with at least one deletion	1.08%
Homopolymer indels	40.2%

2.6. Chromosome stats

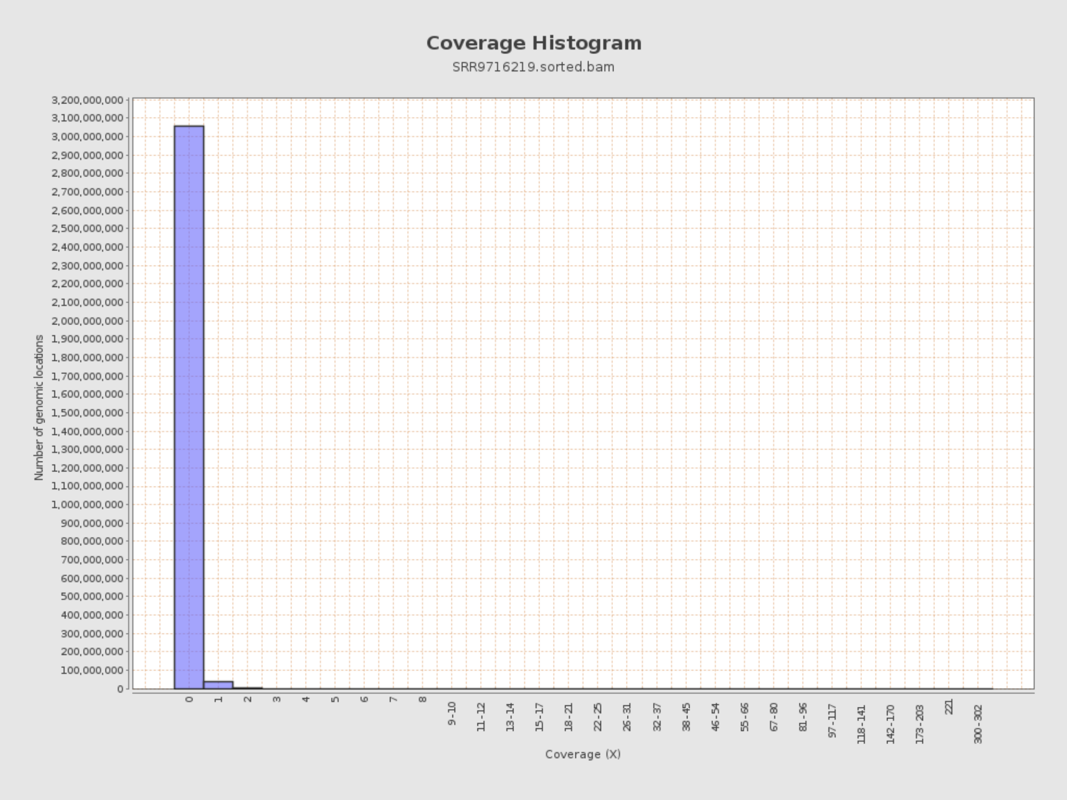
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3496849	0.014	0.2076
chr2	243199373	3734052	0.0154	0.1957
chr3	198022430	2923707	0.0148	0.1294
chr4	191154276	2823797	0.0148	0.1465
chr5	180915260	2619470	0.0145	0.1287
chr6	171115067	2491758	0.0146	0.133
chr7	159138663	2407286	0.0151	0.1804

chr8	146364022	2215934	0.0151	0.17
chr9	141213431	1843429	0.0131	0.1321
chr10	135534747	2121914	0.0157	0.1781
chr11	135006516	2019560	0.015	0.146
chr12	133851895	1992931	0.0149	0.1311
chr13	115169878	1353939	0.0118	0.1157
chr14	107349540	1341912	0.0125	0.1197
chr15	102531392	1302304	0.0127	0.1212
chr16	90354753	1294837	0.0143	0.1318
chr17	81195210	1232518	0.0152	0.1364
chr18	78077248	1158864	0.0148	0.2062
chr19	59128983	914419	0.0155	0.1716
chr20	63025520	949390	0.0151	0.1331
chr21	48129895	604242	0.0126	0.1334
chr22	51304566	552560	0.0108	0.1107
chrMT	16571	14997	0.905	1.1213
chrX	155270560	2457871	0.0158	0.1387
chrY	59373566	150362	0.0025	0.0974

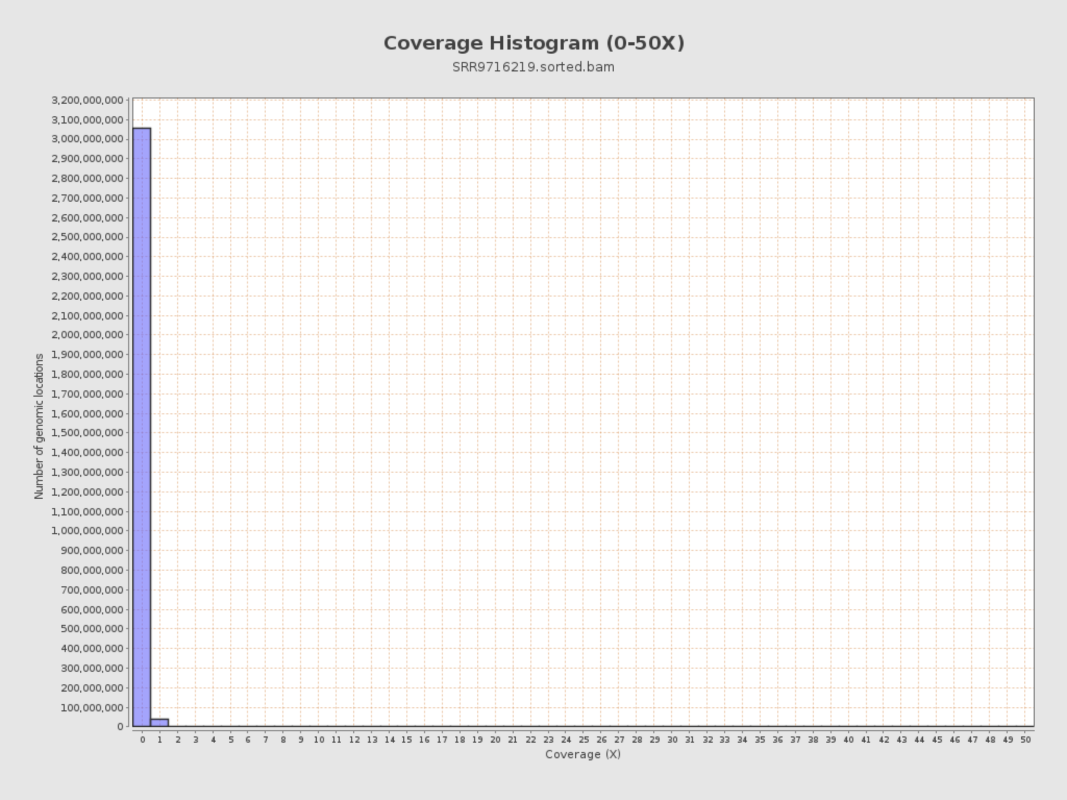
3. Results : Coverage across reference



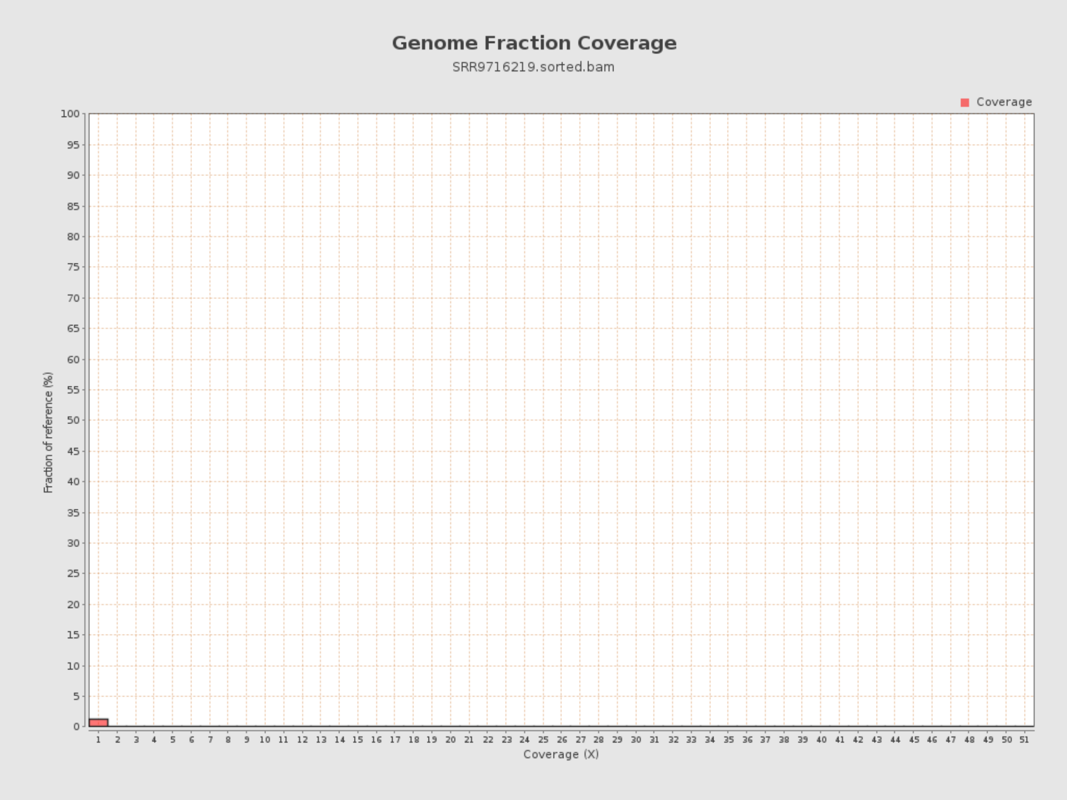
4. Results : Coverage Histogram



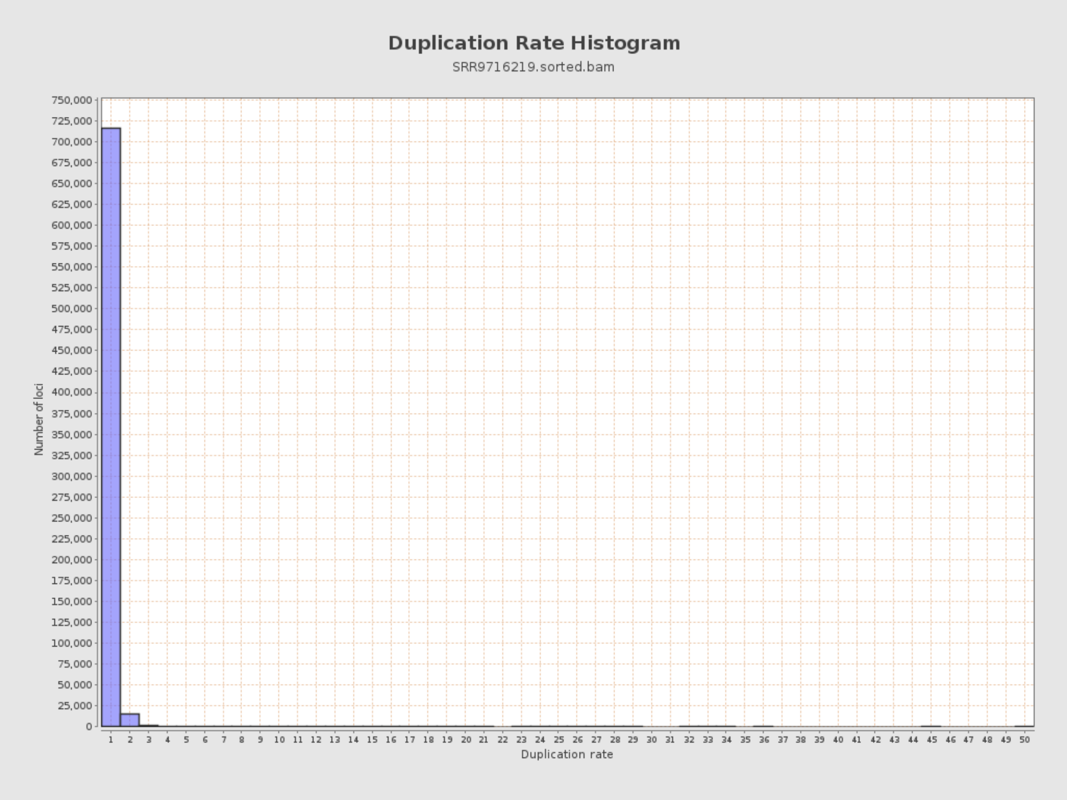
5. Results : Coverage Histogram (0-50X)



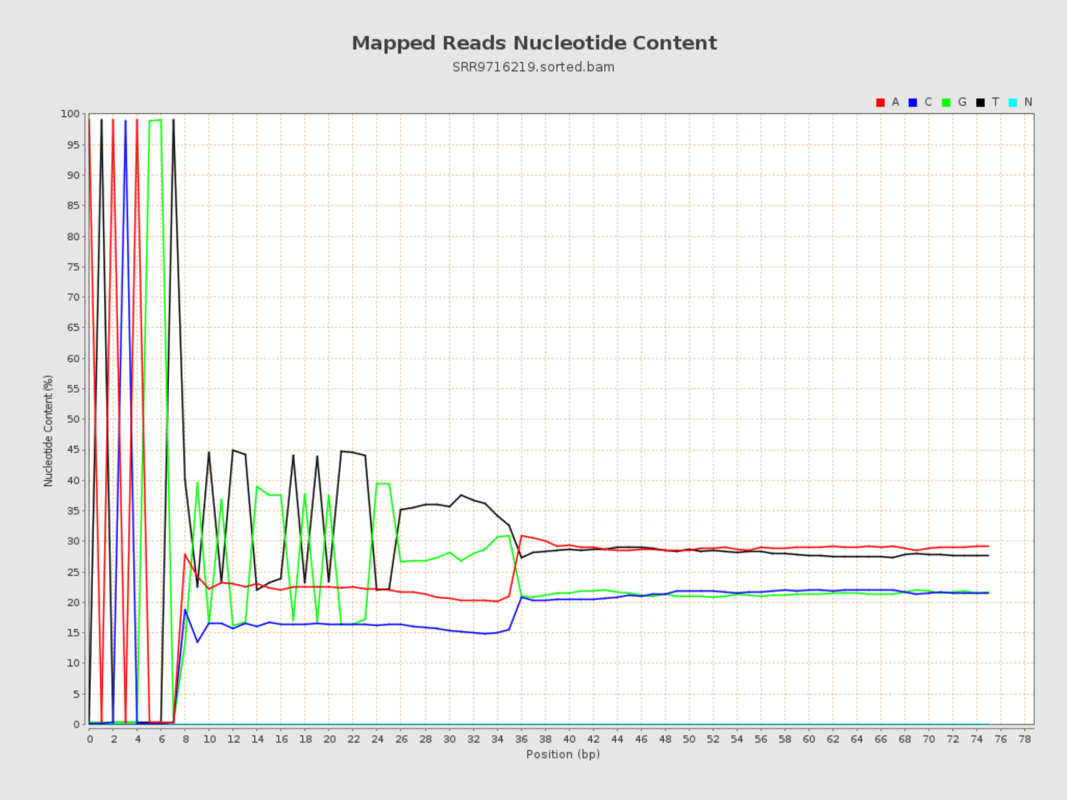
6. Results : Genome Fraction Coverage



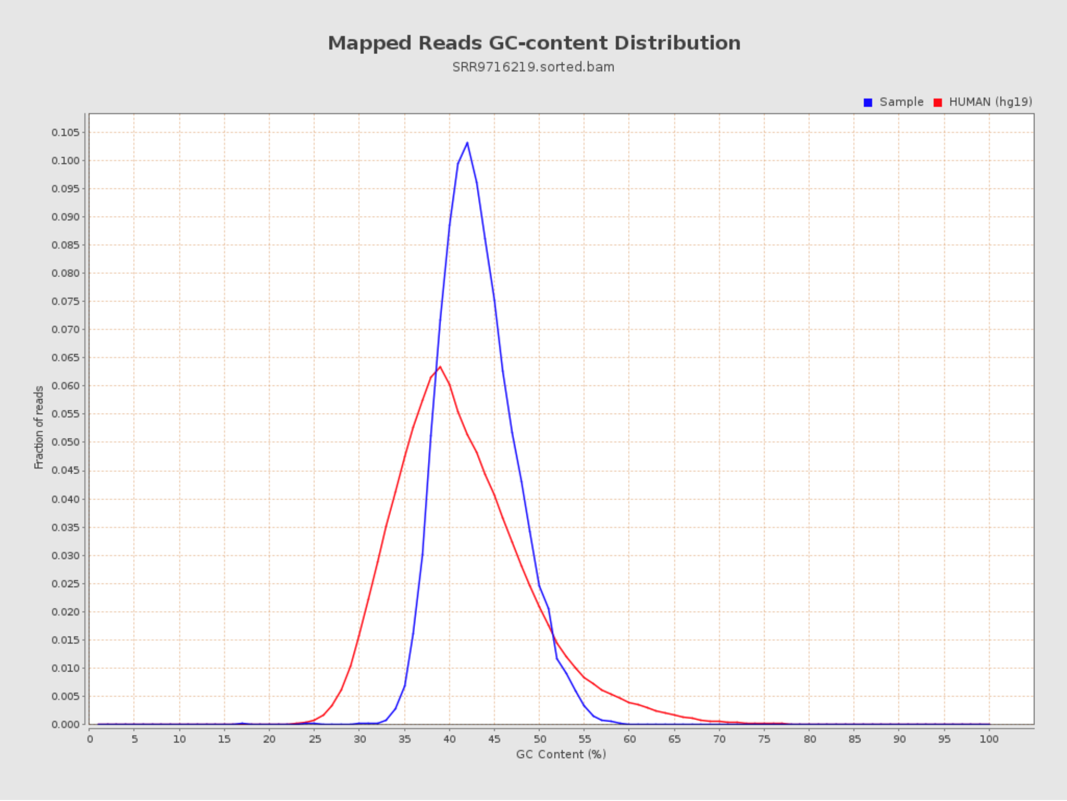
7. Results : Duplication Rate Histogram



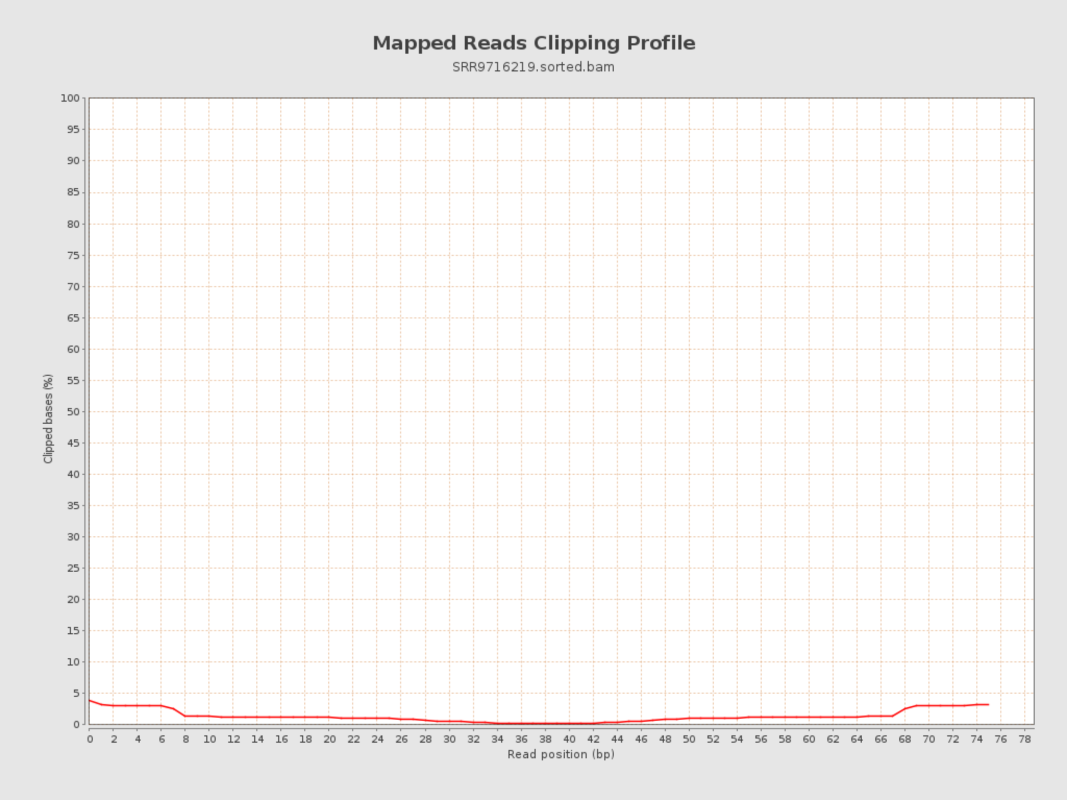
8. Results : Mapped Reads Nucleotide Content



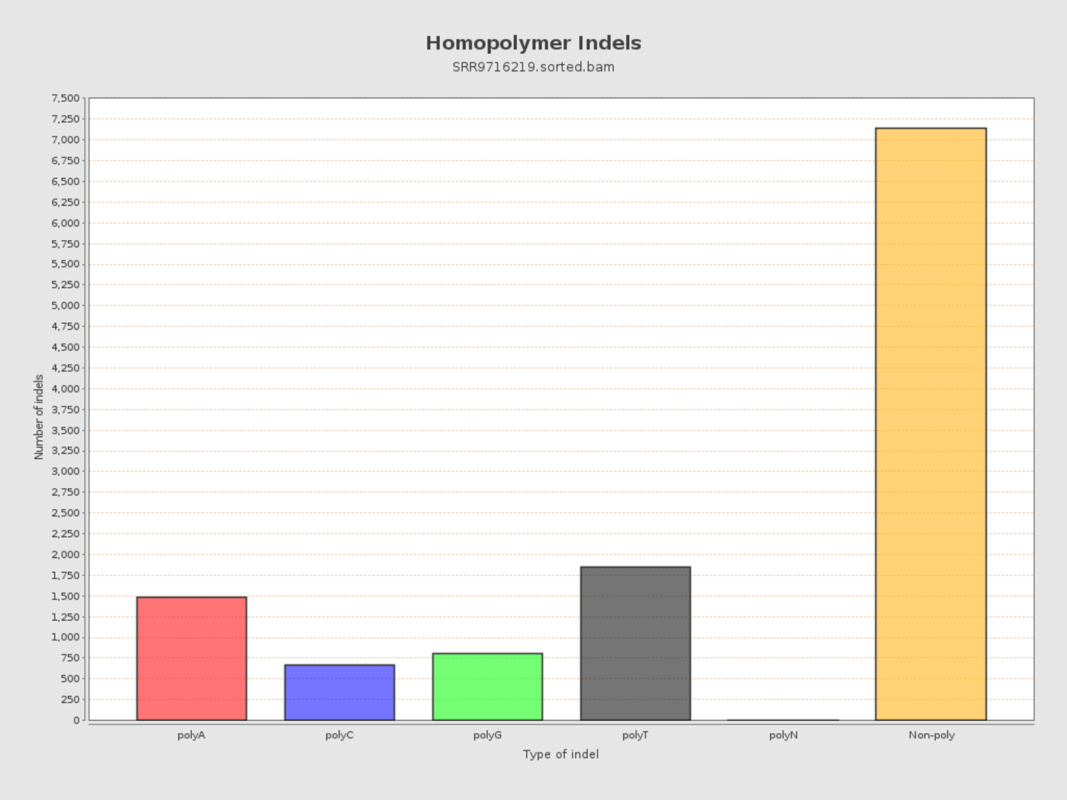
9. Results : Mapped Reads GC-content Distribution



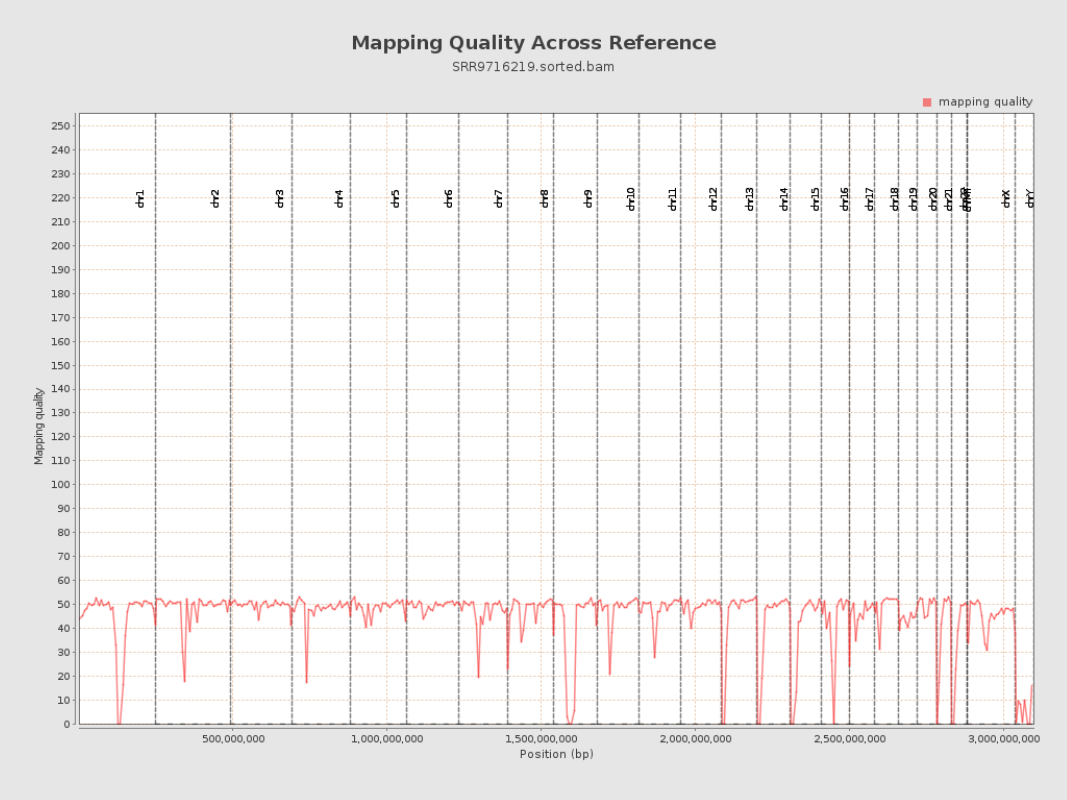
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram