Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 05:28:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716279.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_SRR9716279 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716279.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 05:28:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716279.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	644,866
Mapped reads	542,990 / 84.2%
Unmapped reads	101,876 / 15.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,654 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	8,507 / 1.32%
Duplication rate	1.1%
Clipped reads	543,337 / 84.26%

2.2. ACGT Content

Number/percentage of A's	7,075,959 / 23.56%
Number/percentage of C's	6,318,667 / 21.04%
Number/percentage of T's	8,988,767 / 29.93%
Number/percentage of G's	7,646,076 / 25.46%
Number/percentage of N's	874 / 0%
GC Percentage	46.5%

2.3. Coverage

Mean	0.0097

Standard Deviation	0.1139

2.4. Mapping Quality

Mean Mapping Quality	39.3

2.5. Mismatches and indels

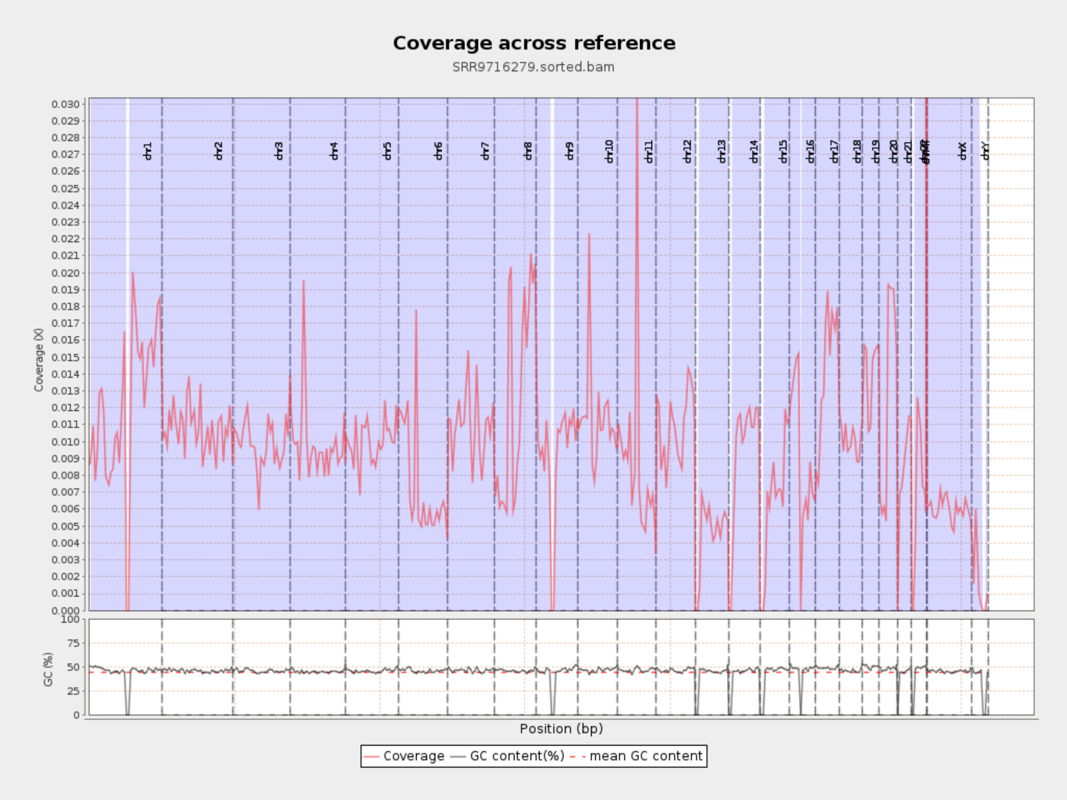
General error rate	0.54%
Mismatches	158,304
Insertions	2,647
Mapped reads with at least one insertion	0.48%
Deletions	4,994
Mapped reads with at least one deletion	0.91%
Homopolymer indels	36.38%

2.6. Chromosome stats

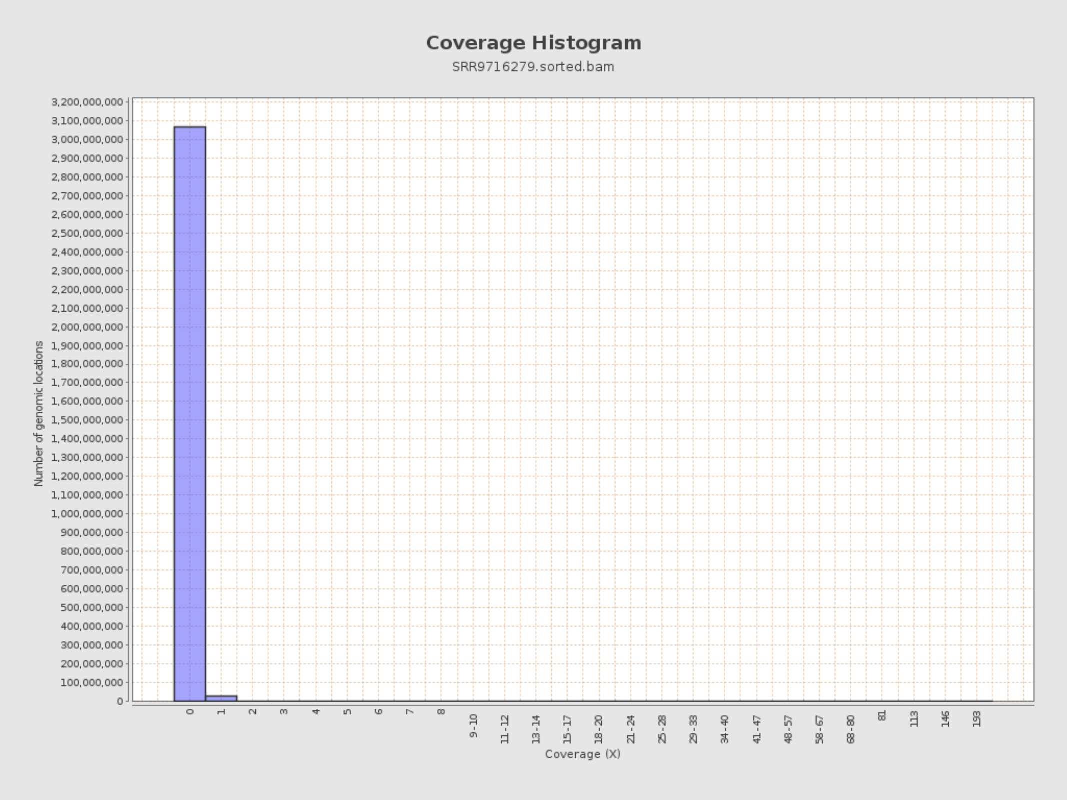
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3009709	0.0121	0.1307
chr2	243199373	2627056	0.0108	0.1396
chr3	198022430	1951660	0.0099	0.1072
chr4	191154276	1885257	0.0099	0.1115
chr5	180915260	1810722	0.01	0.1043
chr6	171115067	1282254	0.0075	0.0923
chr7	159138663	1749489	0.011	0.1239

chr8	146364022	1845914	0.0126	0.1217
chr9	141213431	1278351	0.0091	0.104
chr10	135534747	1541652	0.0114	0.1517
chr11	135006516	1221235	0.009	0.1171
chr12	133851895	1462592	0.0109	0.1097
chr13	115169878	522763	0.0045	0.0708
chr14	107349540	991005	0.0092	0.1025
chr15	102531392	661485	0.0065	0.0845
chr16	90354753	816617	0.009	0.1039
chr17	81195210	1178238	0.0145	0.1293
chr18	78077248	785653	0.0101	0.1216
chr19	59128983	827212	0.014	0.141
chr20	63025520	796151	0.0126	0.1202
chr21	48129895	401734	0.0083	0.1004
chr22	51304566	336327	0.0066	0.0858
chrMT	16571	19829	1.1966	1.4427
chrX	155270560	939401	0.0061	0.0875
chrY	59373566	96402	0.0016	0.0593

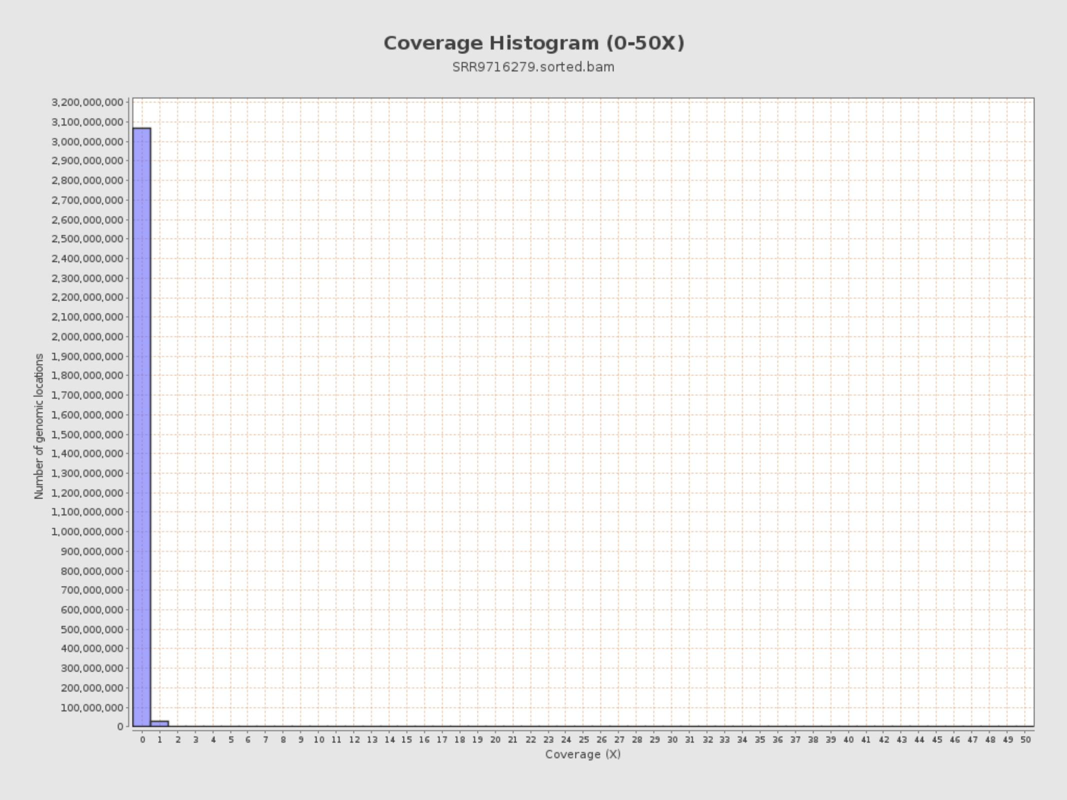
3. Results : Coverage across reference



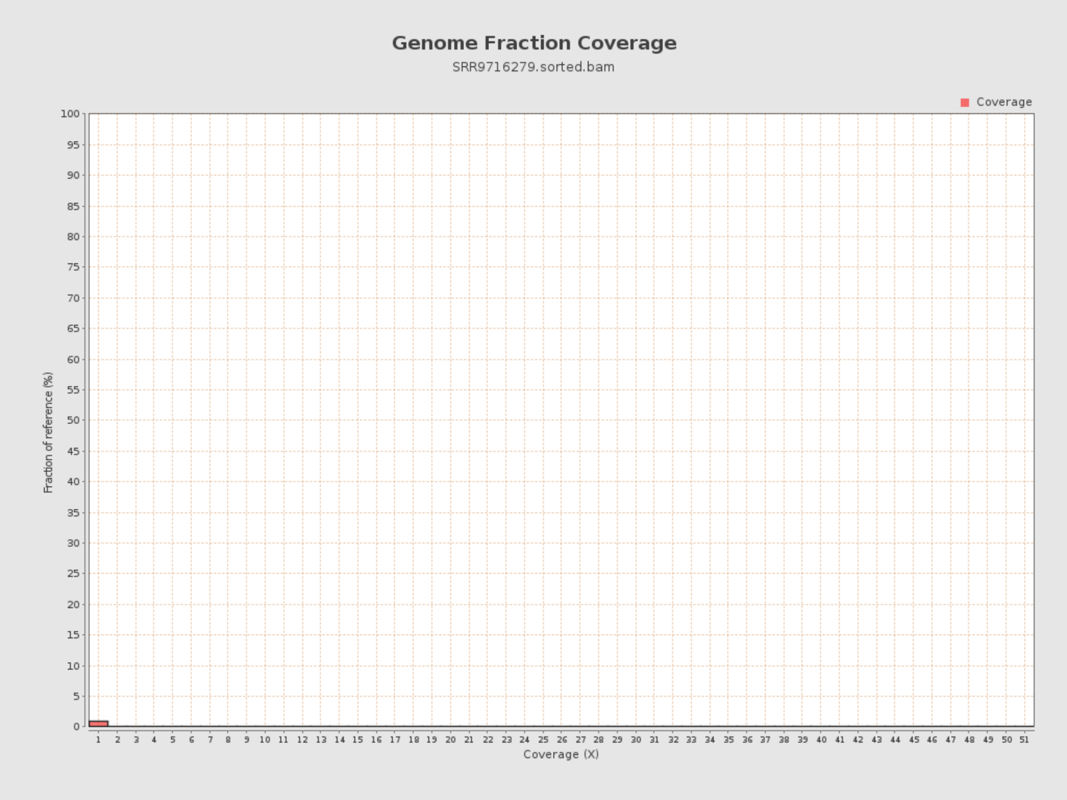
4. Results : Coverage Histogram



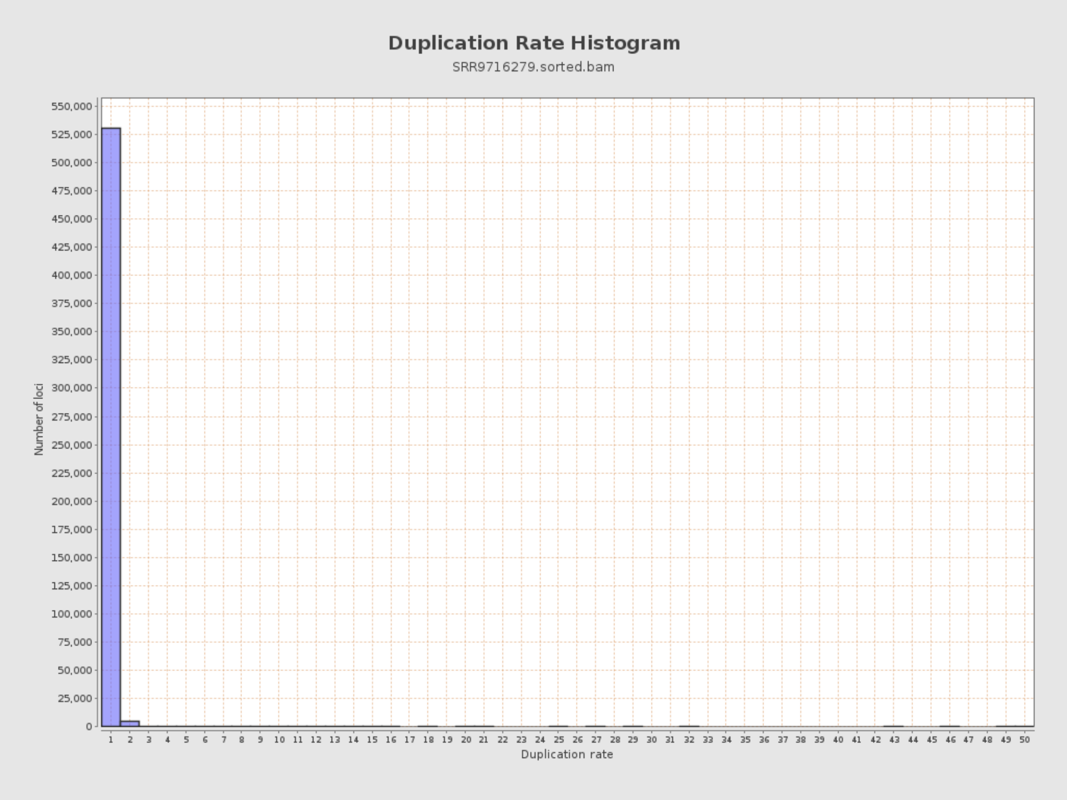
5. Results : Coverage Histogram (0-50X)



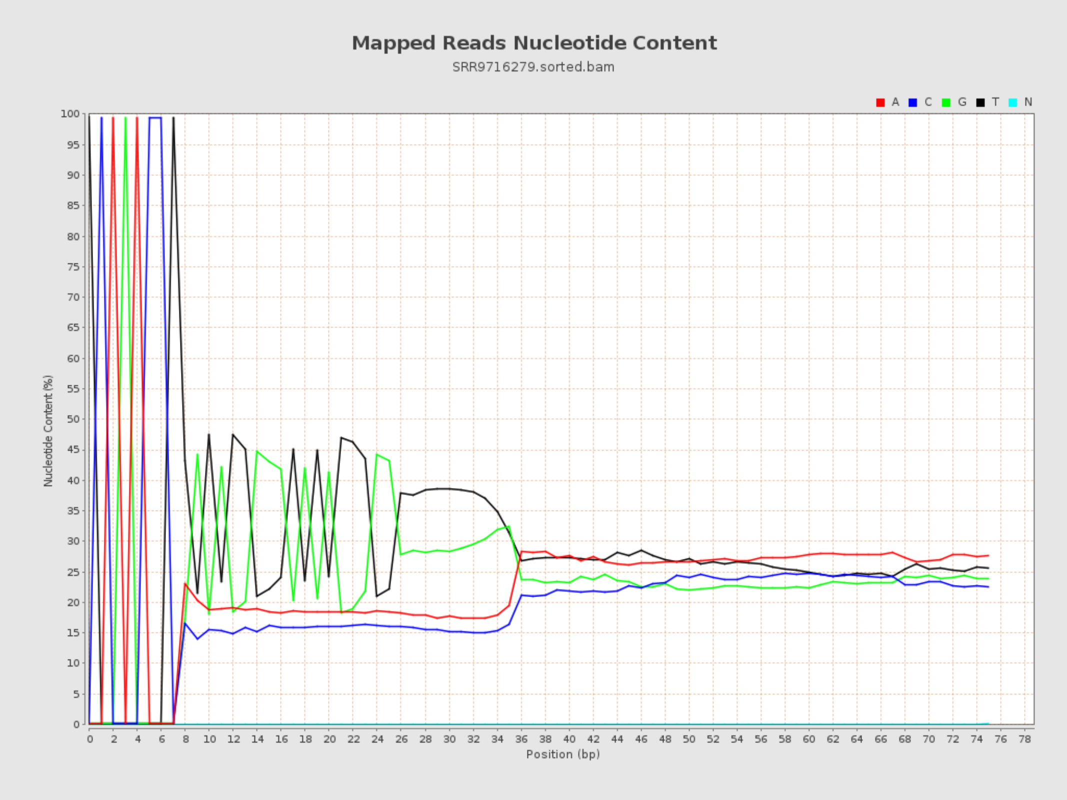
6. Results : Genome Fraction Coverage



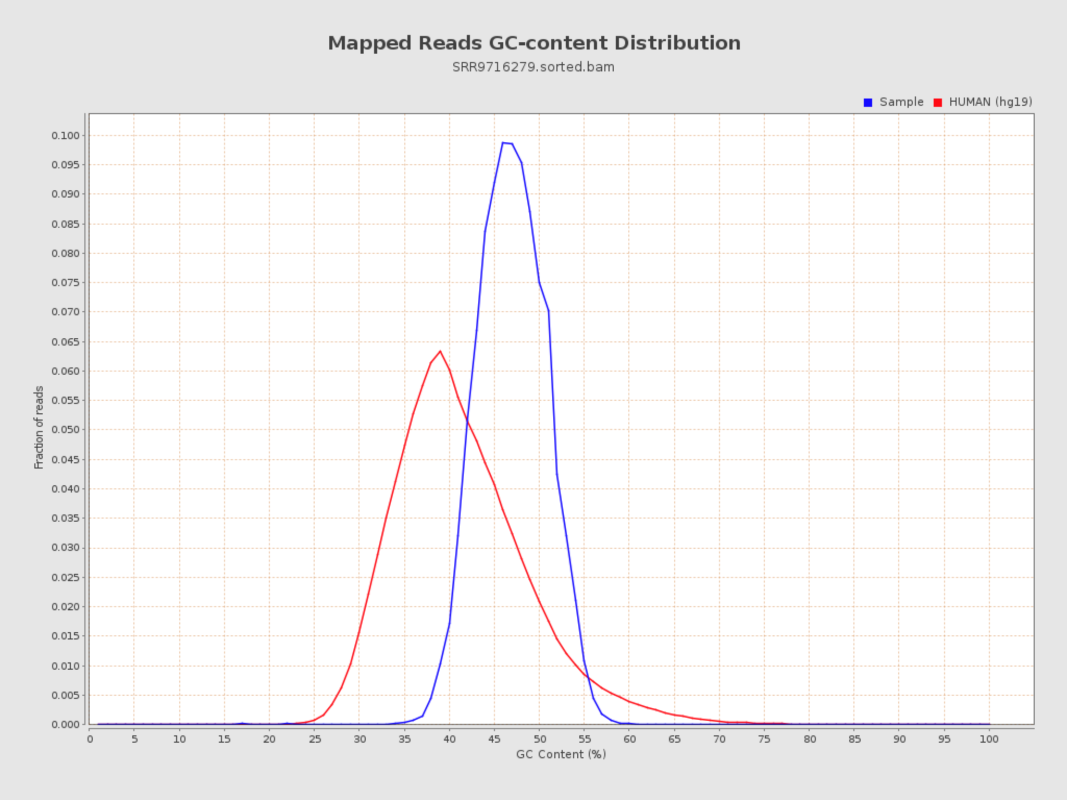
7. Results : Duplication Rate Histogram



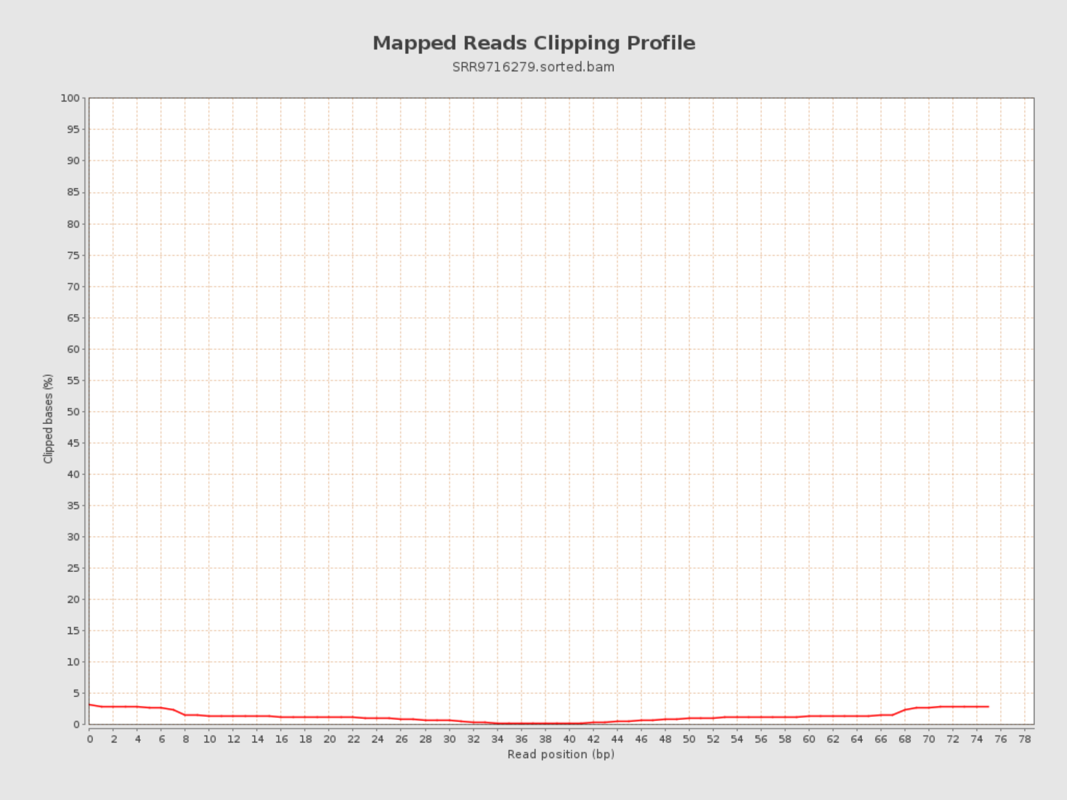
8. Results : Mapped Reads Nucleotide Content



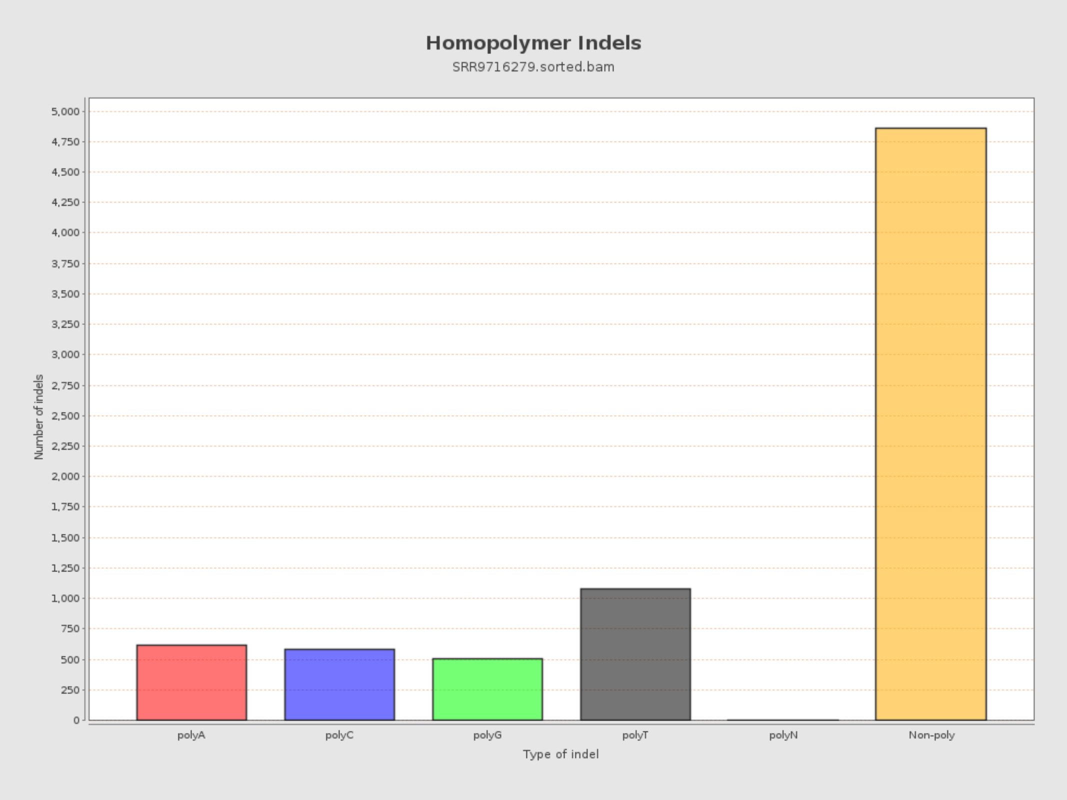
9. Results : Mapped Reads GC-content Distribution



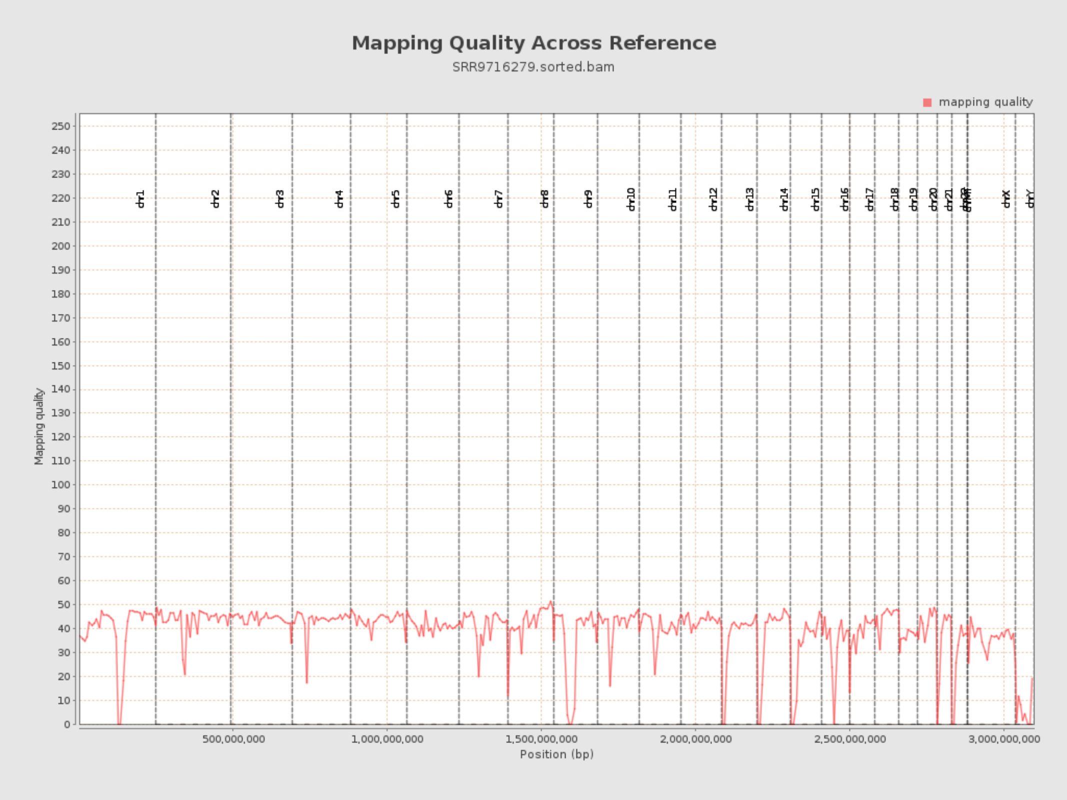
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram