Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:01:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716216.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_SRR9716216 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716216.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:01:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716216.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,140,310
Mapped reads	3,693,552 / 89.21%
Unmapped reads	446,758 / 10.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,995 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	190,888 / 4.61%
Duplication rate	3.58%
Clipped reads	3,705,880 / 89.51%

2.2. ACGT Content

Number/percentage of A's	55,498,464 / 25.81%
Number/percentage of C's	41,485,972 / 19.29%
Number/percentage of T's	67,511,177 / 31.39%
Number/percentage of G's	50,558,928 / 23.51%
Number/percentage of N's	2,769 / 0%
GC Percentage	42.8%

2.3. Coverage

Mean	0.0695

Standard Deviation	0.6128

2.4. Mapping Quality

Mean Mapping Quality	44.15

2.5. Mismatches and indels

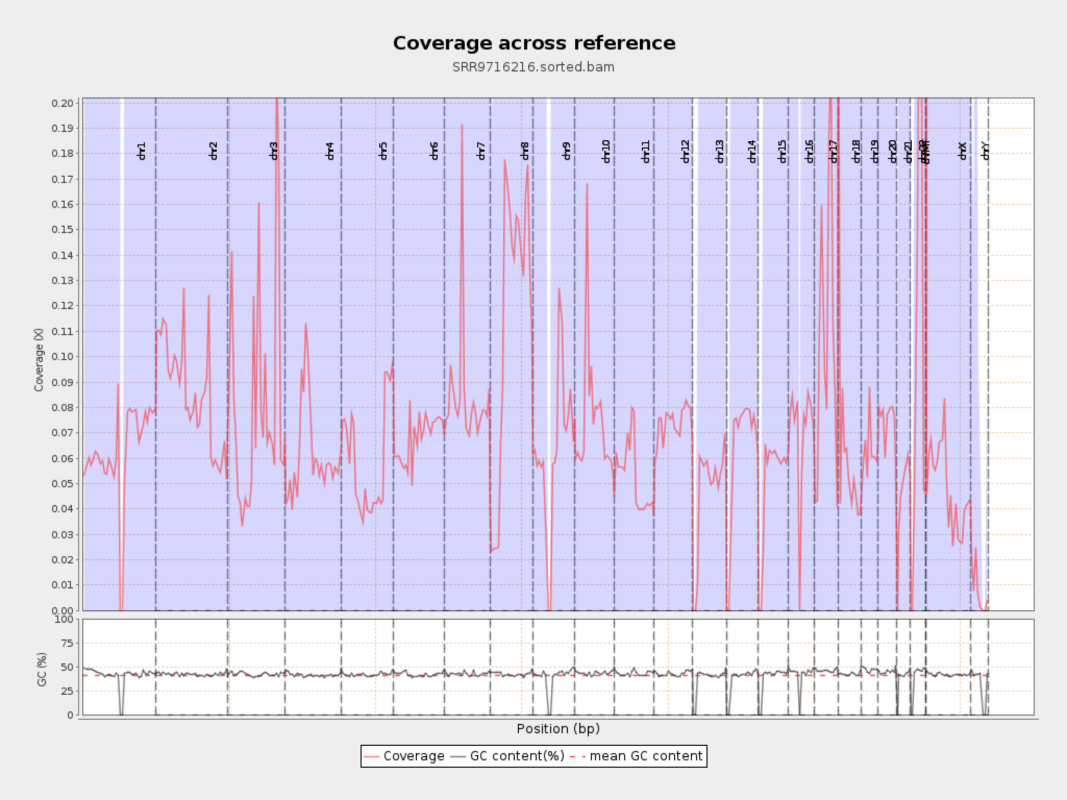
General error rate	0.52%
Mismatches	1,092,275
Insertions	14,215
Mapped reads with at least one insertion	0.38%
Deletions	39,822
Mapped reads with at least one deletion	1.07%
Homopolymer indels	40.35%

2.6. Chromosome stats

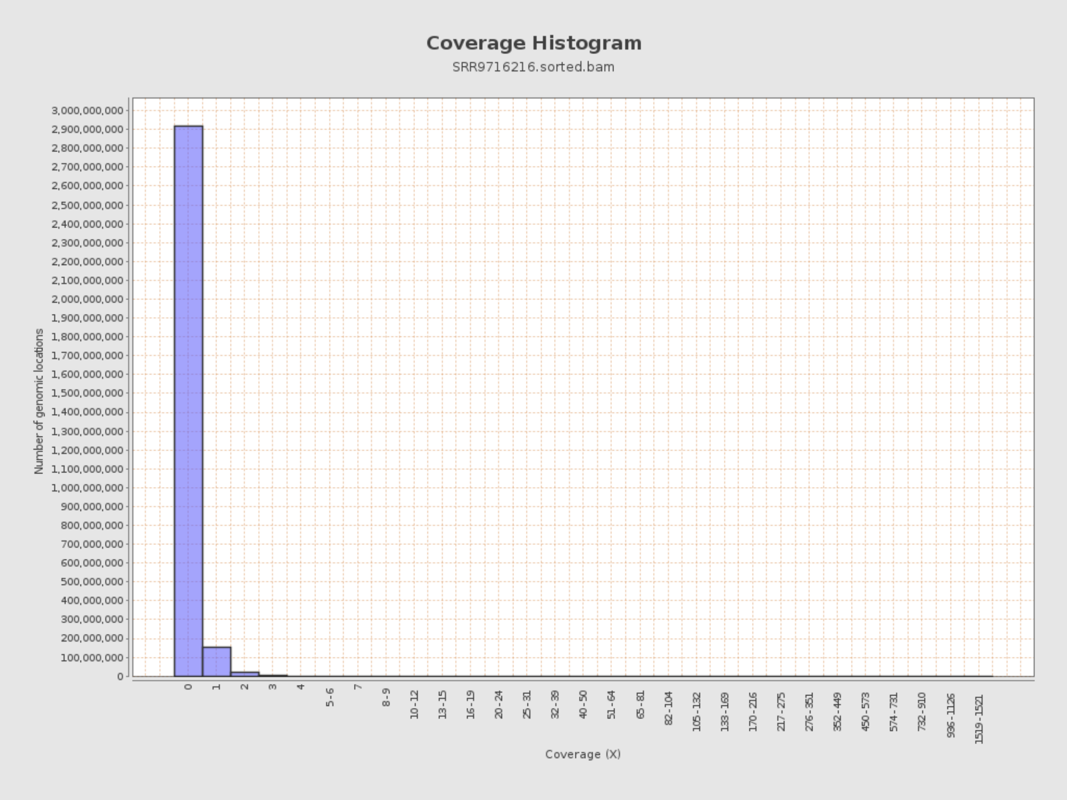
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15593478	0.0626	0.8188
chr2	243199373	20920575	0.086	0.7532
chr3	198022430	16089174	0.0812	0.3756
chr4	191154276	11818163	0.0618	0.3347
chr5	180915260	10699330	0.0591	0.2898
chr6	171115067	11622355	0.0679	0.357
chr7	159138663	13451751	0.0845	1.5283

chr8	146364022	16917620	0.1156	0.6297
chr9	141213431	8841675	0.0626	0.3969
chr10	135534747	10117418	0.0746	0.8124
chr11	135006516	7181190	0.0532	0.4523
chr12	133851895	9890569	0.0739	0.3793
chr13	115169878	5438628	0.0472	0.2544
chr14	107349540	6876403	0.0641	0.3105
chr15	102531392	5063914	0.0494	0.2822
chr16	90354753	6240593	0.0691	0.3402
chr17	81195210	8914908	0.1098	0.4296
chr18	78077248	4959653	0.0635	0.8235
chr19	59128983	3712913	0.0628	0.7495
chr20	63025520	4735403	0.0751	0.35
chr21	48129895	2188306	0.0455	0.2737
chr22	51304566	5698970	0.1111	0.4258
chrMT	16571	202691	12.2317	7.5142
chrX	155270560	7488166	0.0482	0.339
chrY	59373566	455861	0.0077	0.1871

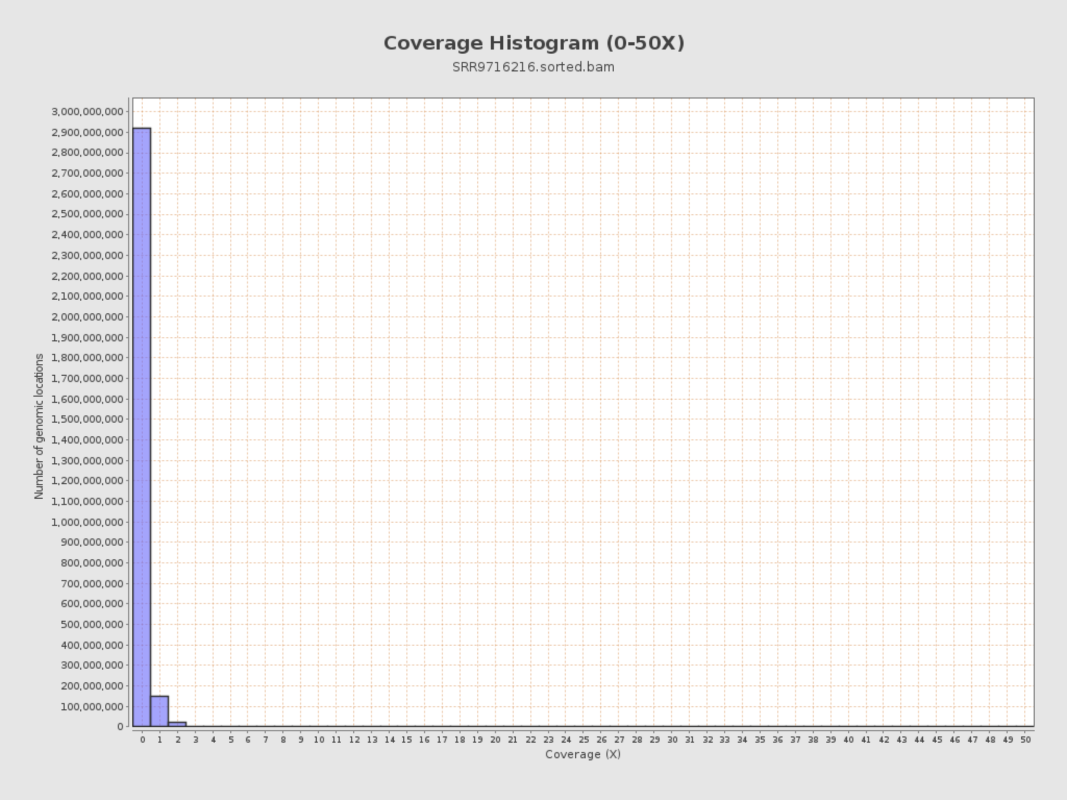
3. Results : Coverage across reference



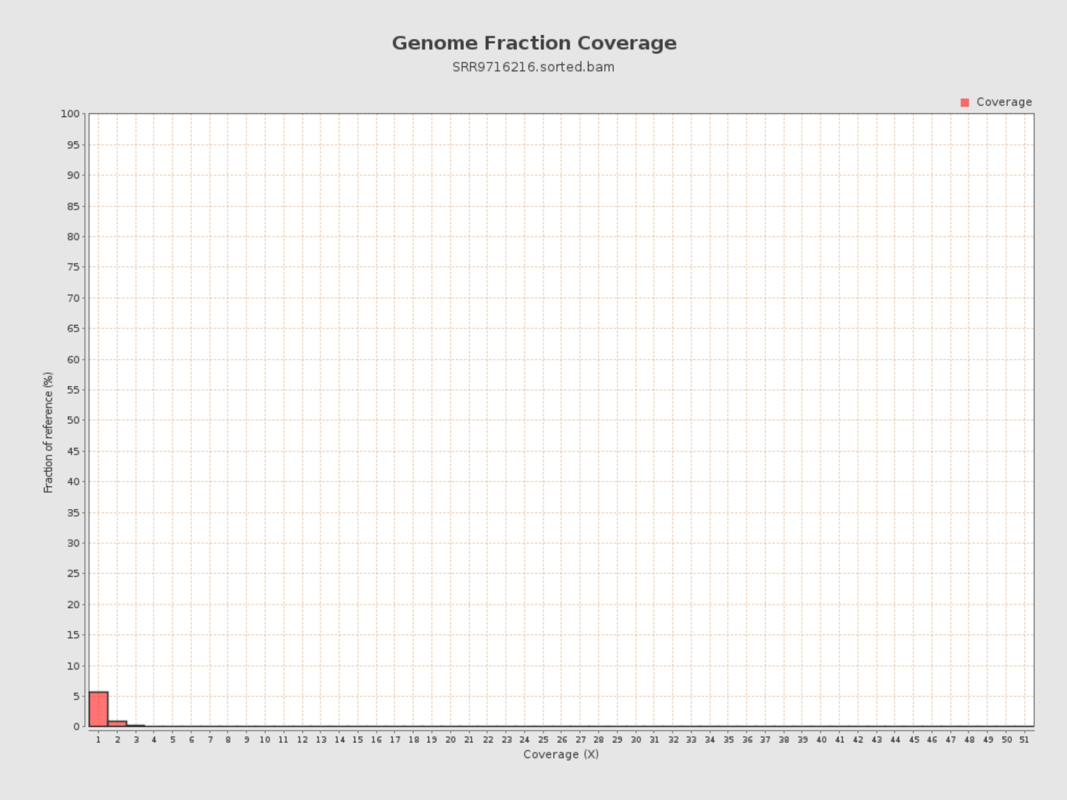
4. Results : Coverage Histogram



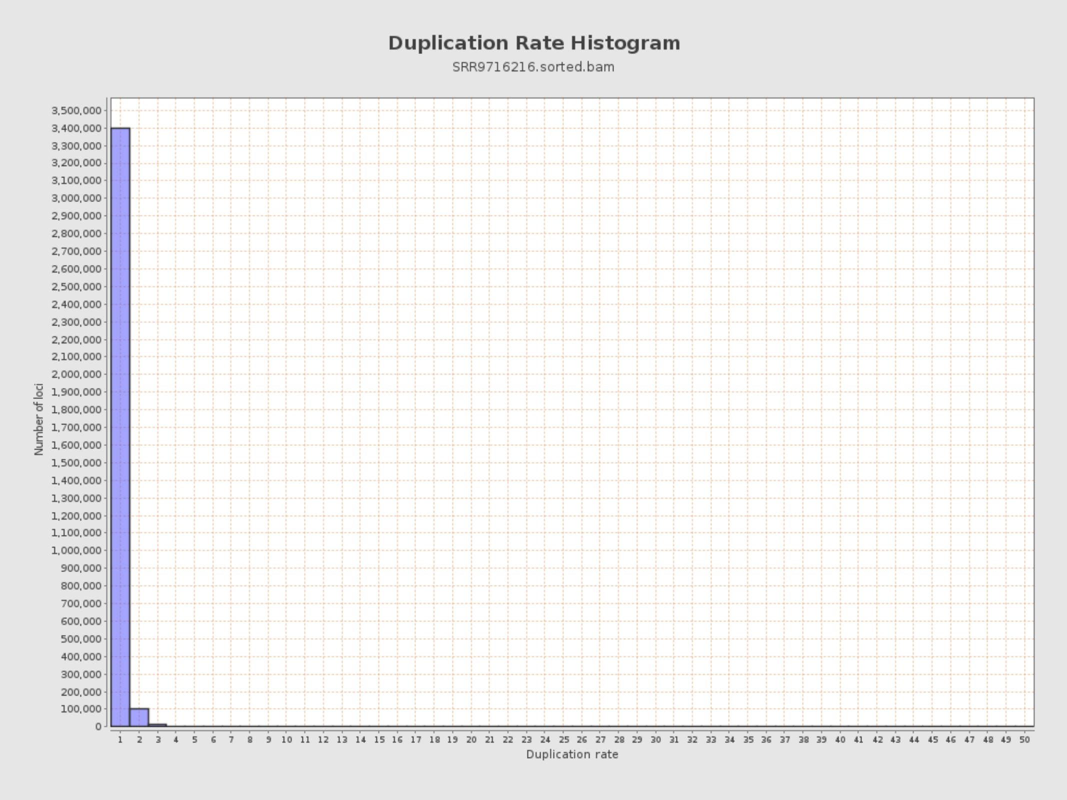
5. Results : Coverage Histogram (0-50X)



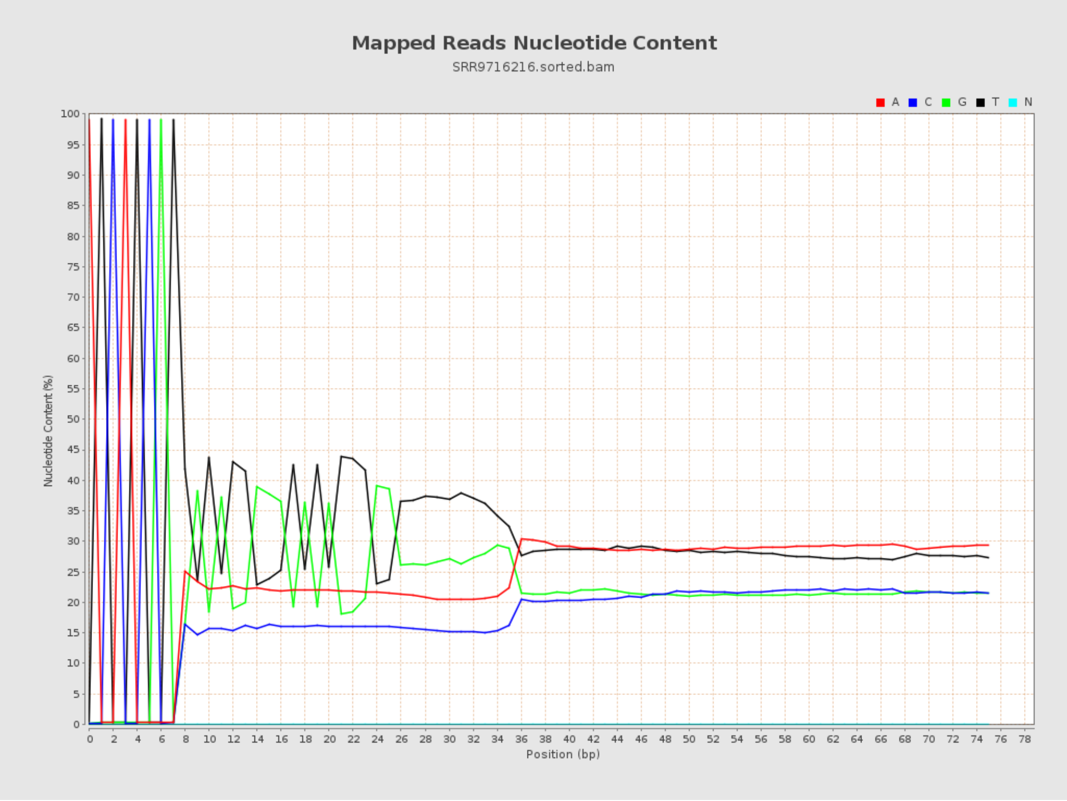
6. Results : Genome Fraction Coverage



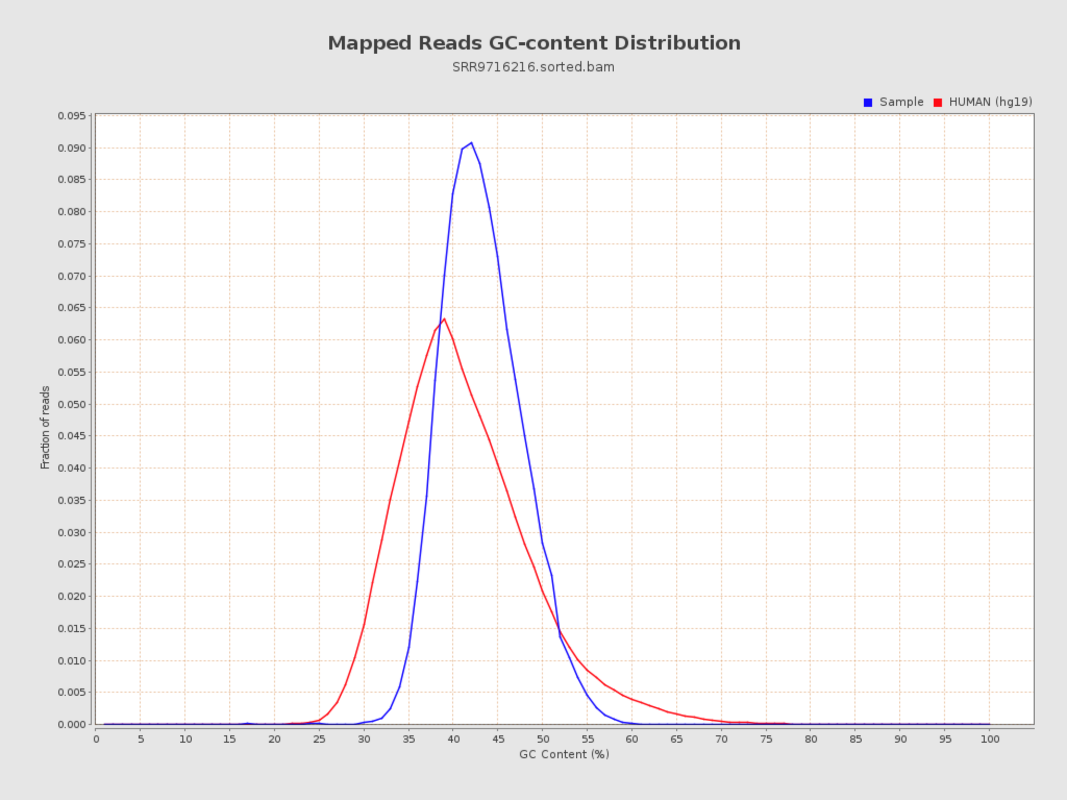
7. Results : Duplication Rate Histogram



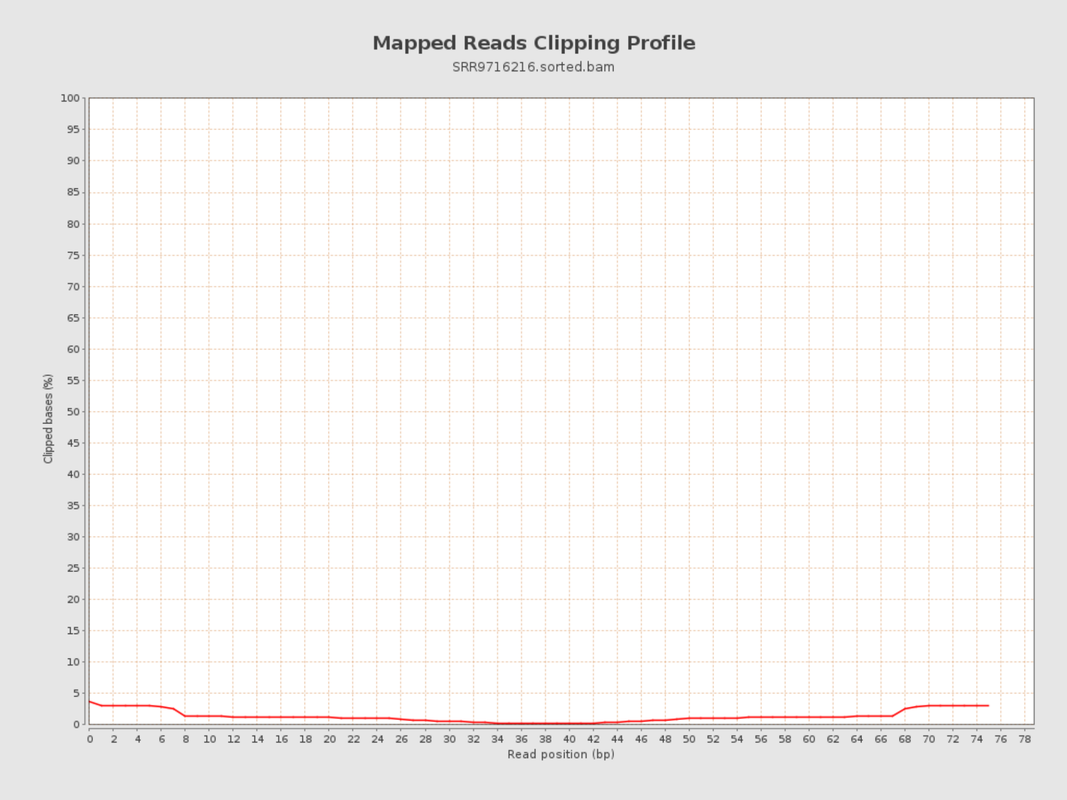
8. Results : Mapped Reads Nucleotide Content



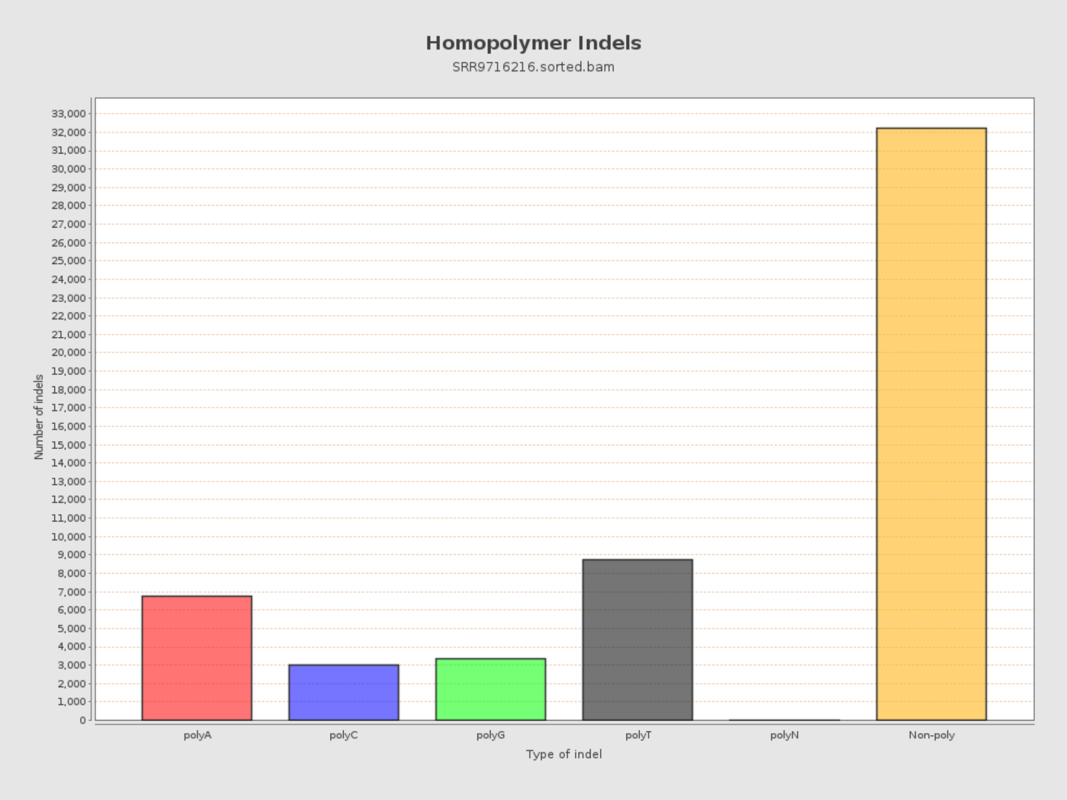
9. Results : Mapped Reads GC-content Distribution



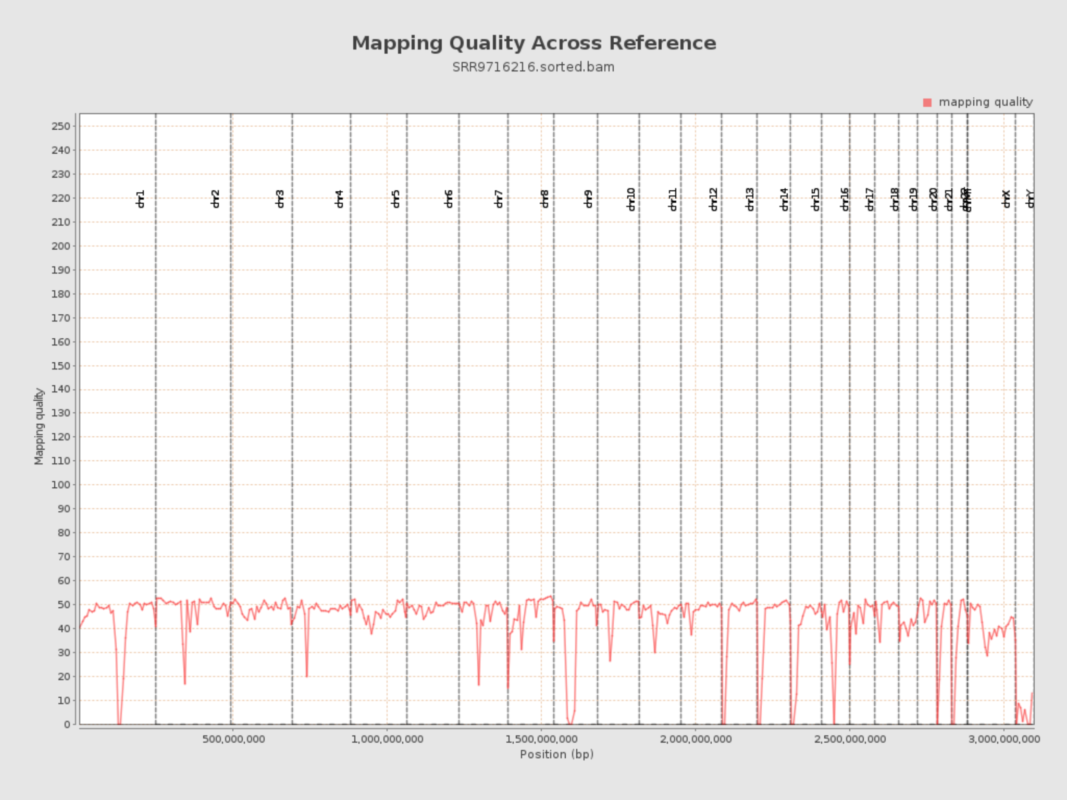
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram