Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:51:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716355.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_SRR9716355 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716355.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:51:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716355.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	429,653
Mapped reads	354,581 / 82.53%
Unmapped reads	75,072 / 17.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,232 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	5,865 / 1.37%
Duplication rate	1.18%
Clipped reads	354,824 / 82.58%

2.2. ACGT Content

Number/percentage of A's	5,233,084 / 25.49%
Number/percentage of C's	3,632,668 / 17.7%
Number/percentage of T's	6,465,815 / 31.5%
Number/percentage of G's	5,196,915 / 25.32%
Number/percentage of N's	356 / 0%
GC Percentage	43.01%

2.3. Coverage

Mean	0.0066

Standard Deviation	0.0959

2.4. Mapping Quality

Mean Mapping Quality	44.45

2.5. Mismatches and indels

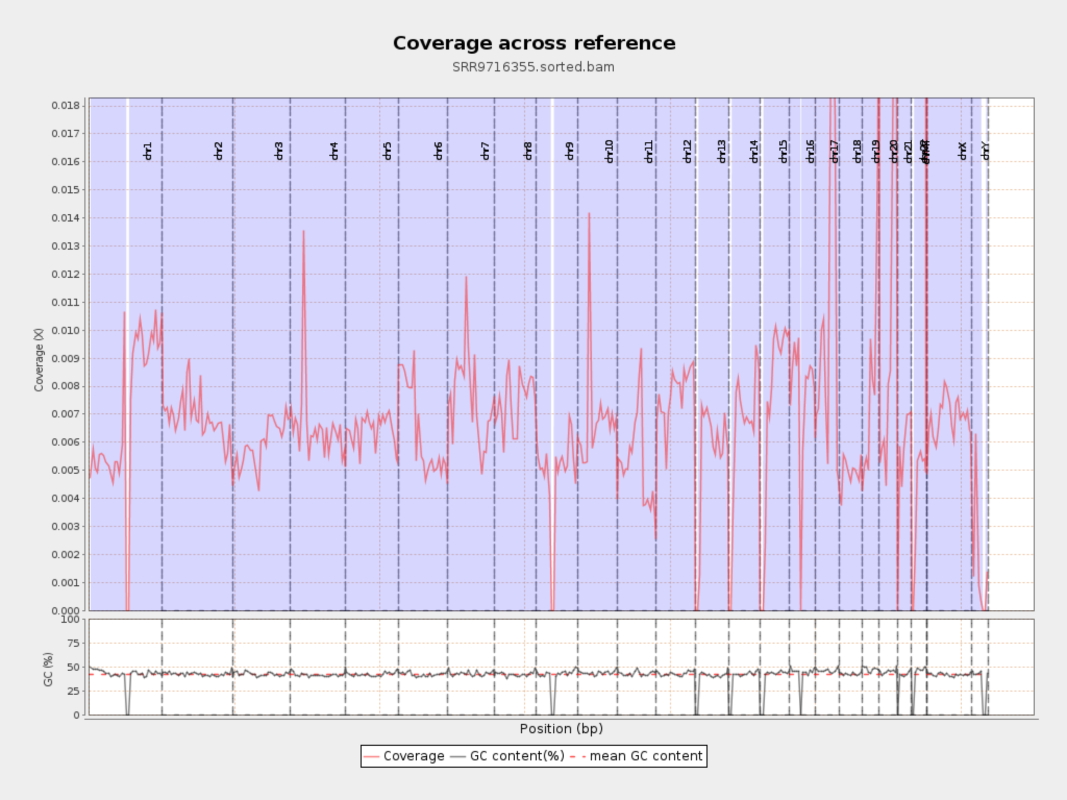
General error rate	0.54%
Mismatches	108,833
Insertions	1,399
Mapped reads with at least one insertion	0.39%
Deletions	4,223
Mapped reads with at least one deletion	1.18%
Homopolymer indels	42.85%

2.6. Chromosome stats

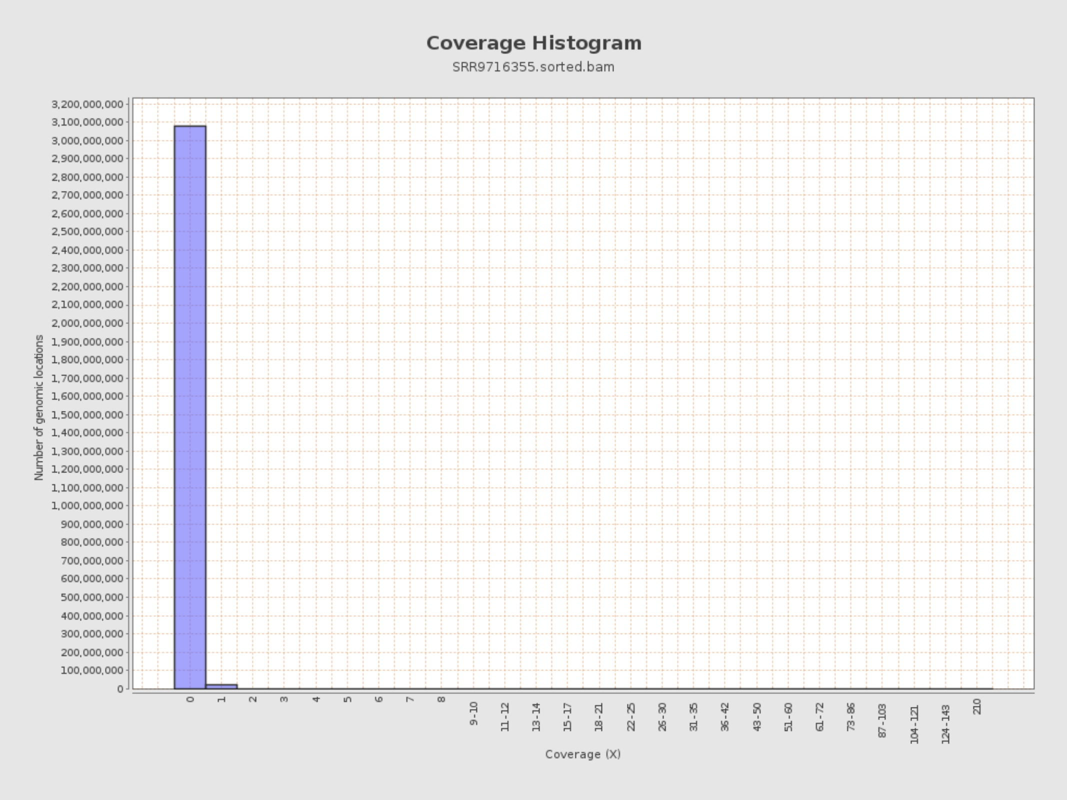
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1732067	0.0069	0.1216
chr2	243199373	1672005	0.0069	0.1198
chr3	198022430	1174565	0.0059	0.0789
chr4	191154276	1255416	0.0066	0.0891
chr5	180915260	1167389	0.0065	0.0823
chr6	171115067	1095863	0.0064	0.0857
chr7	159138663	1204850	0.0076	0.1091

chr8	146364022	1091758	0.0075	0.1196
chr9	141213431	669164	0.0047	0.0749
chr10	135534747	923308	0.0068	0.1028
chr11	135006516	719447	0.0053	0.08
chr12	133851895	1032837	0.0077	0.09
chr13	115169878	617368	0.0054	0.0749
chr14	107349540	673847	0.0063	0.0815
chr15	102531392	745409	0.0073	0.087
chr16	90354753	690263	0.0076	0.0909
chr17	81195210	863814	0.0106	0.1065
chr18	78077248	382451	0.0049	0.0944
chr19	59128983	513093	0.0087	0.1098
chr20	63025520	685809	0.0109	0.108
chr21	48129895	267828	0.0056	0.0822
chr22	51304566	195174	0.0038	0.0631
chrMT	16571	3349	0.2021	0.478
chrX	155270560	1066065	0.0069	0.0863
chrY	59373566	92582	0.0016	0.069

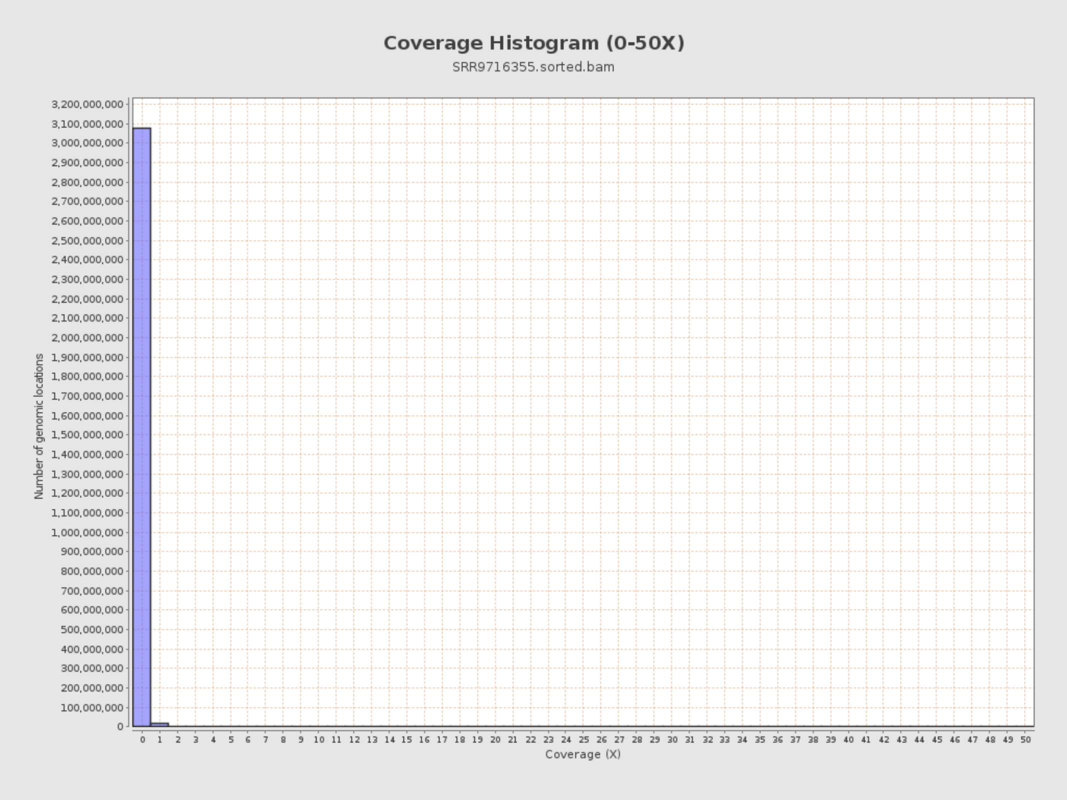
3. Results : Coverage across reference



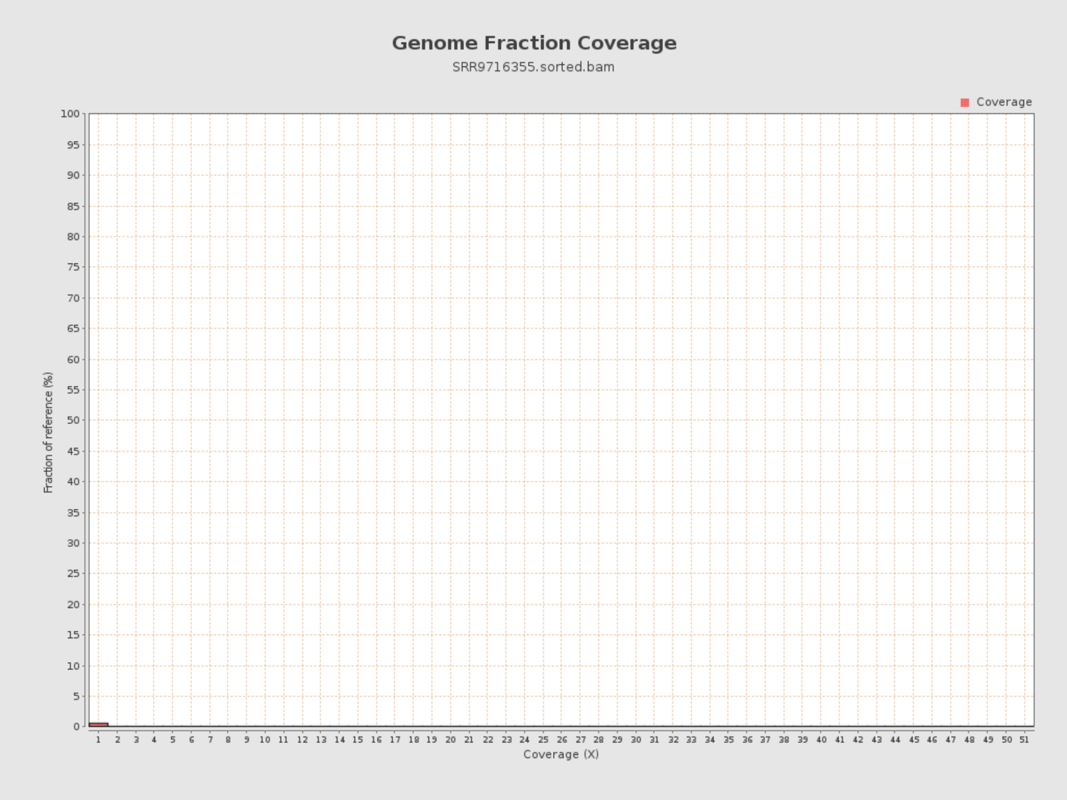
4. Results : Coverage Histogram



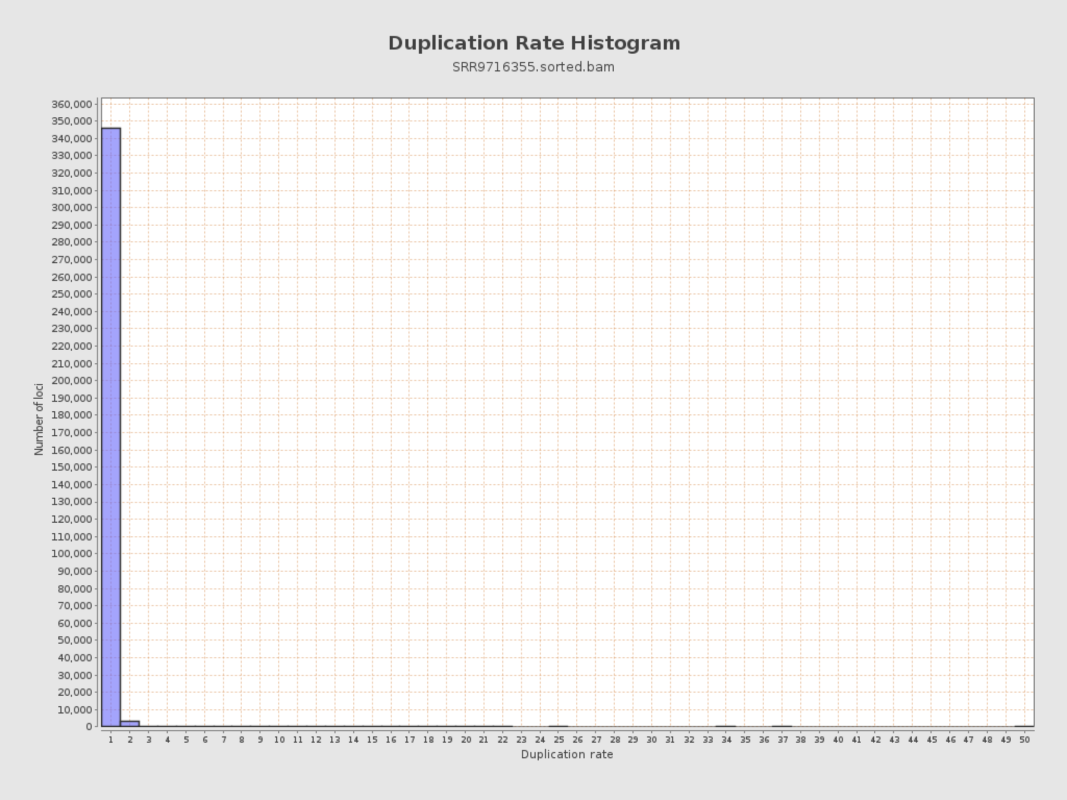
5. Results : Coverage Histogram (0-50X)



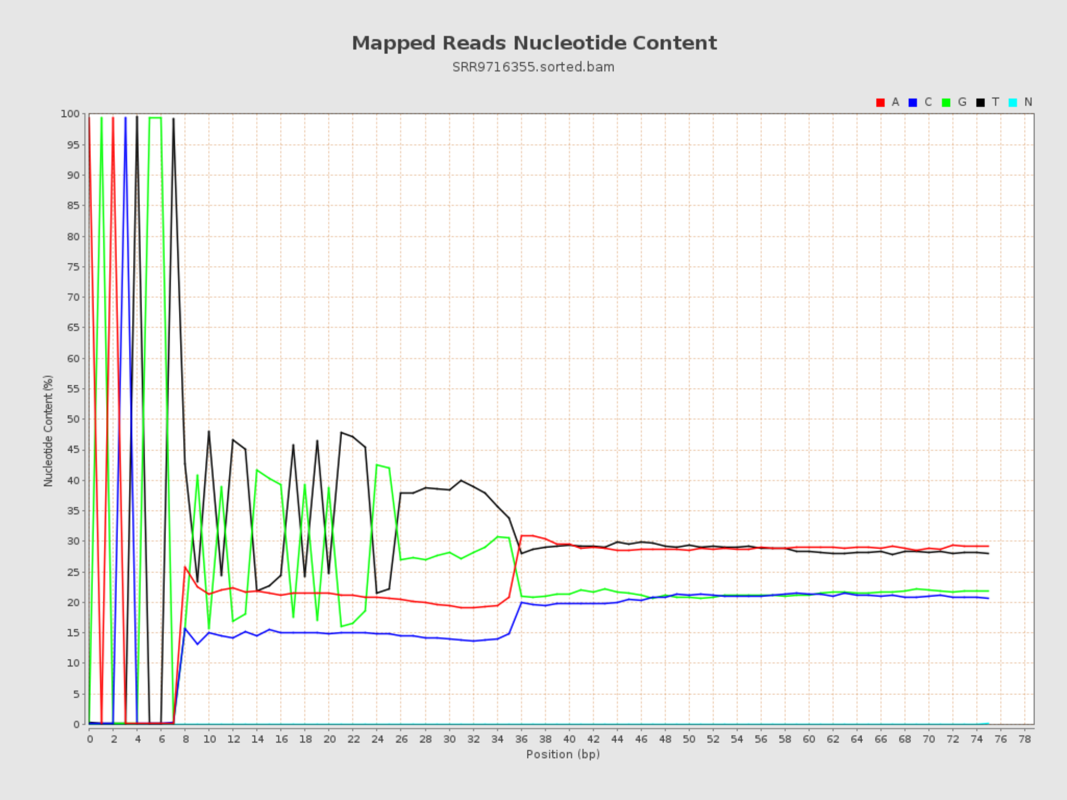
6. Results : Genome Fraction Coverage



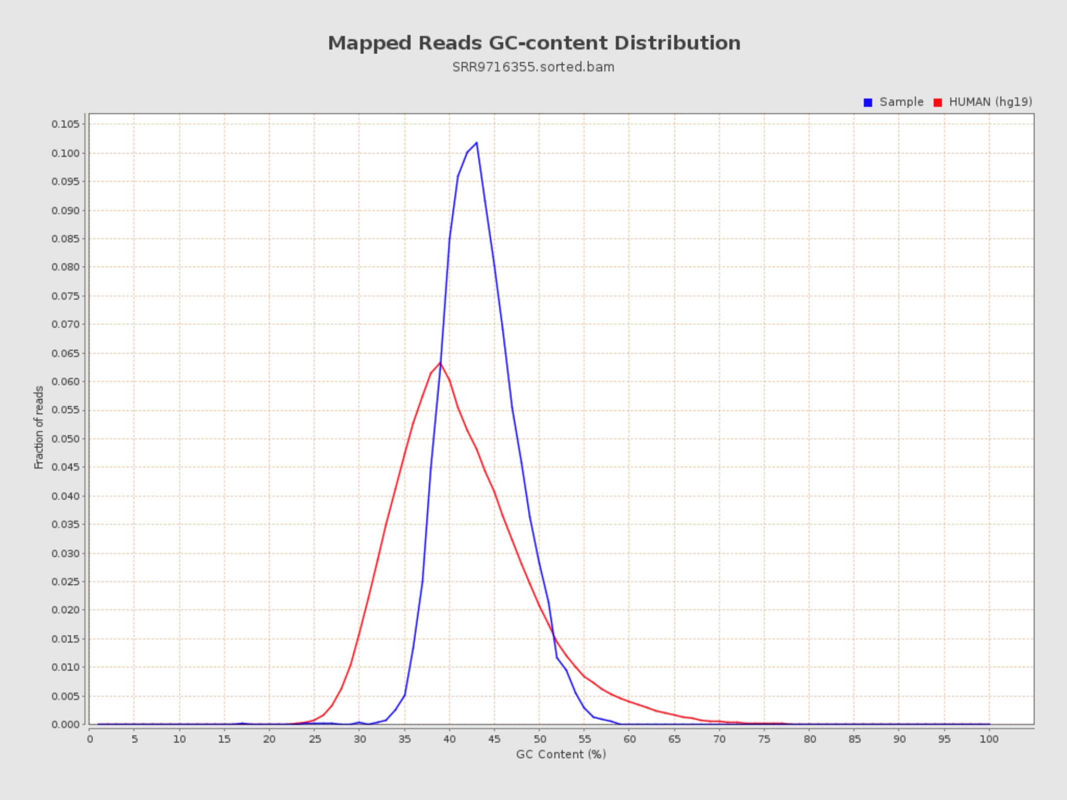
7. Results : Duplication Rate Histogram



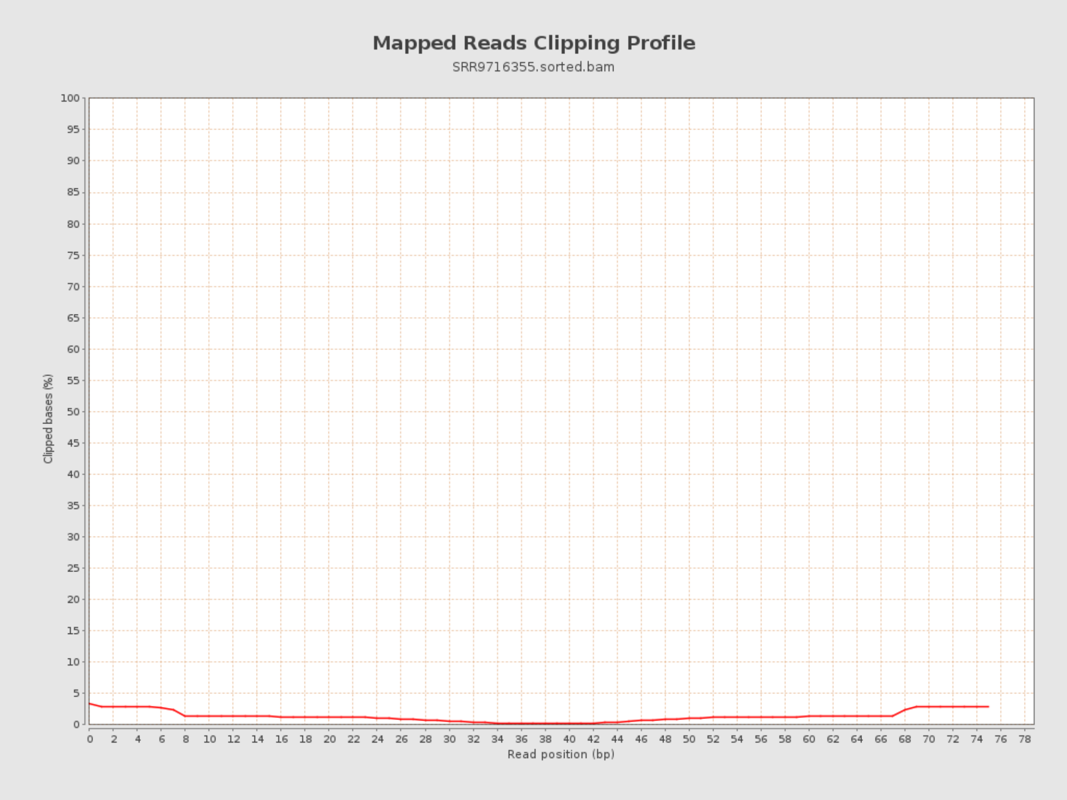
8. Results : Mapped Reads Nucleotide Content



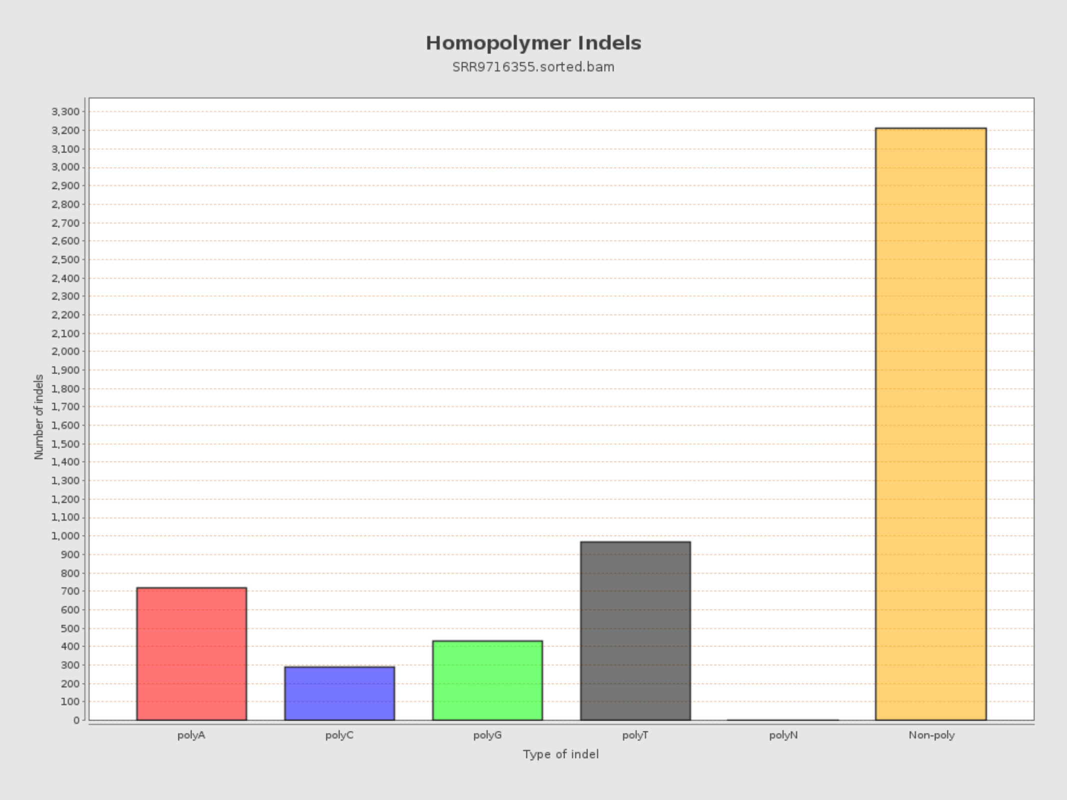
9. Results : Mapped Reads GC-content Distribution



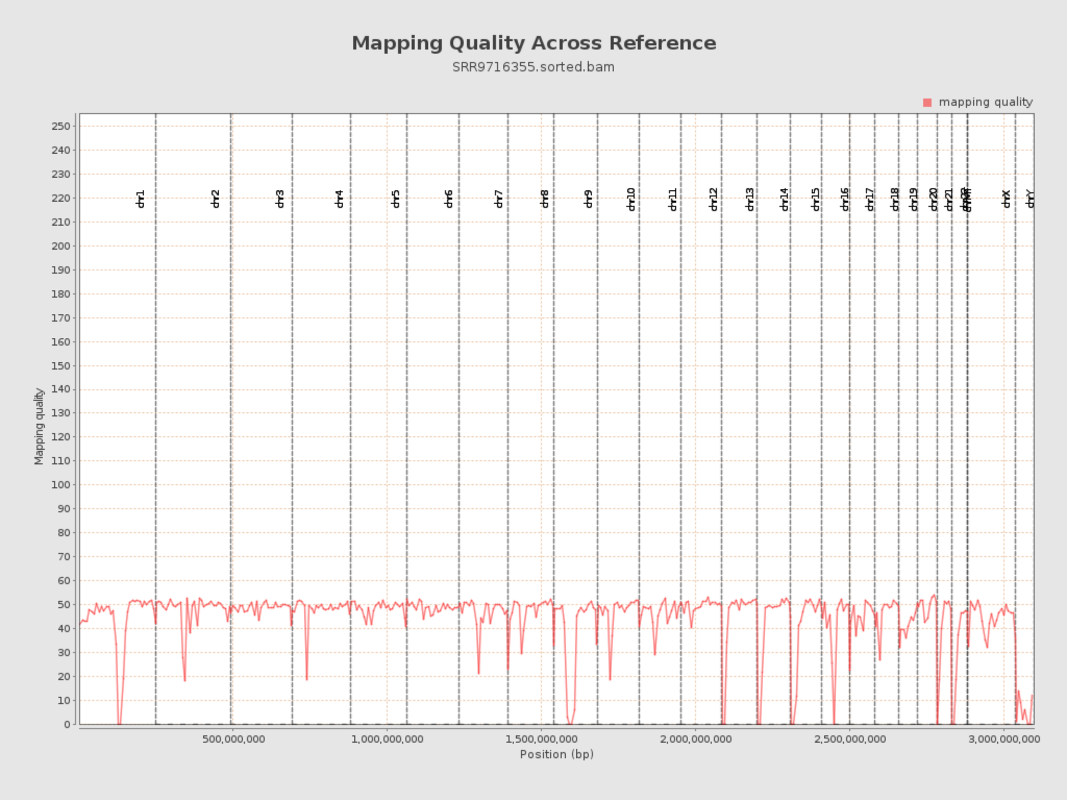
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram