Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:31:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716345.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_SRR9716345 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716345.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:31:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716345.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	976,535
Mapped reads	897,528 / 91.91%
Unmapped reads	79,007 / 8.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,830 / 2.03%
Read min/max/mean length	30 / 101 / 101.73
Duplicated reads (estimated)	23,536 / 2.41%
Duplication rate	1.75%
Clipped reads	915,169 / 93.72%

2.2. ACGT Content

Number/percentage of A's	18,358,605 / 25.93%
Number/percentage of C's	13,696,943 / 19.35%
Number/percentage of T's	21,924,702 / 30.97%
Number/percentage of G's	16,805,216 / 23.74%
Number/percentage of N's	5,035 / 0.01%
GC Percentage	43.09%

2.3. Coverage

Mean	0.0229

Standard Deviation	0.2539

2.4. Mapping Quality

Mean Mapping Quality	47.09

2.5. Mismatches and indels

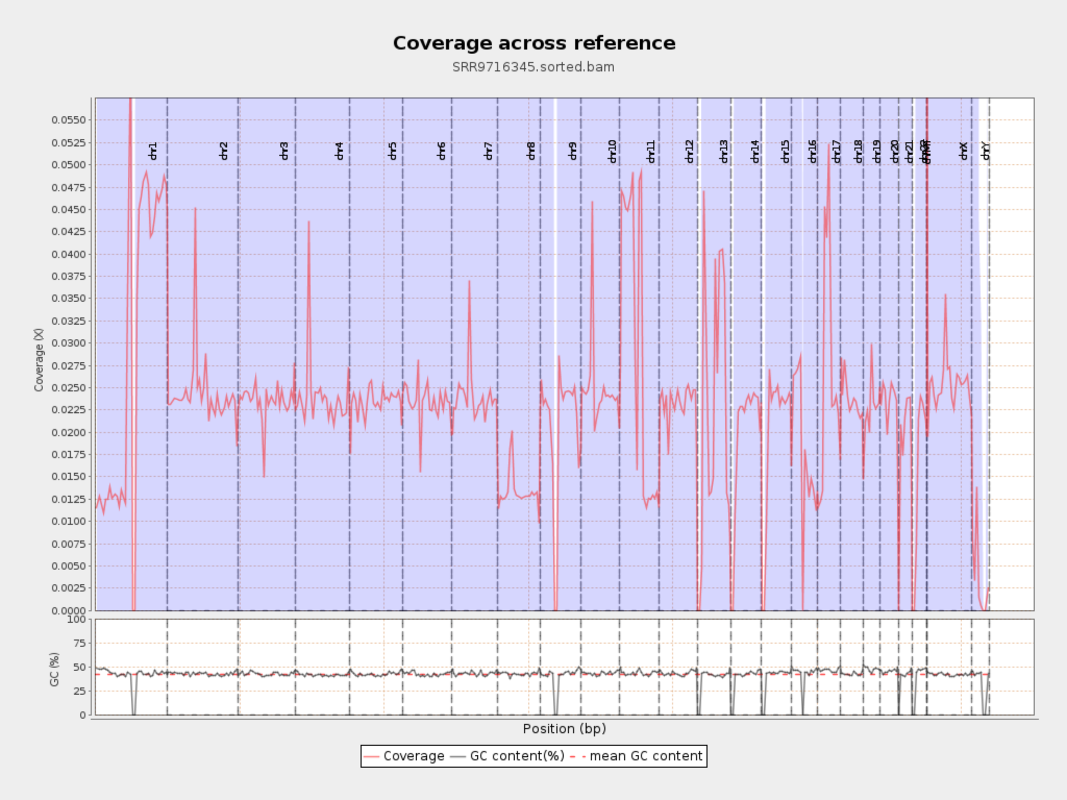
General error rate	0.67%
Mismatches	458,860
Insertions	6,141
Mapped reads with at least one insertion	0.67%
Deletions	17,989
Mapped reads with at least one deletion	1.97%
Homopolymer indels	42.78%

2.6. Chromosome stats

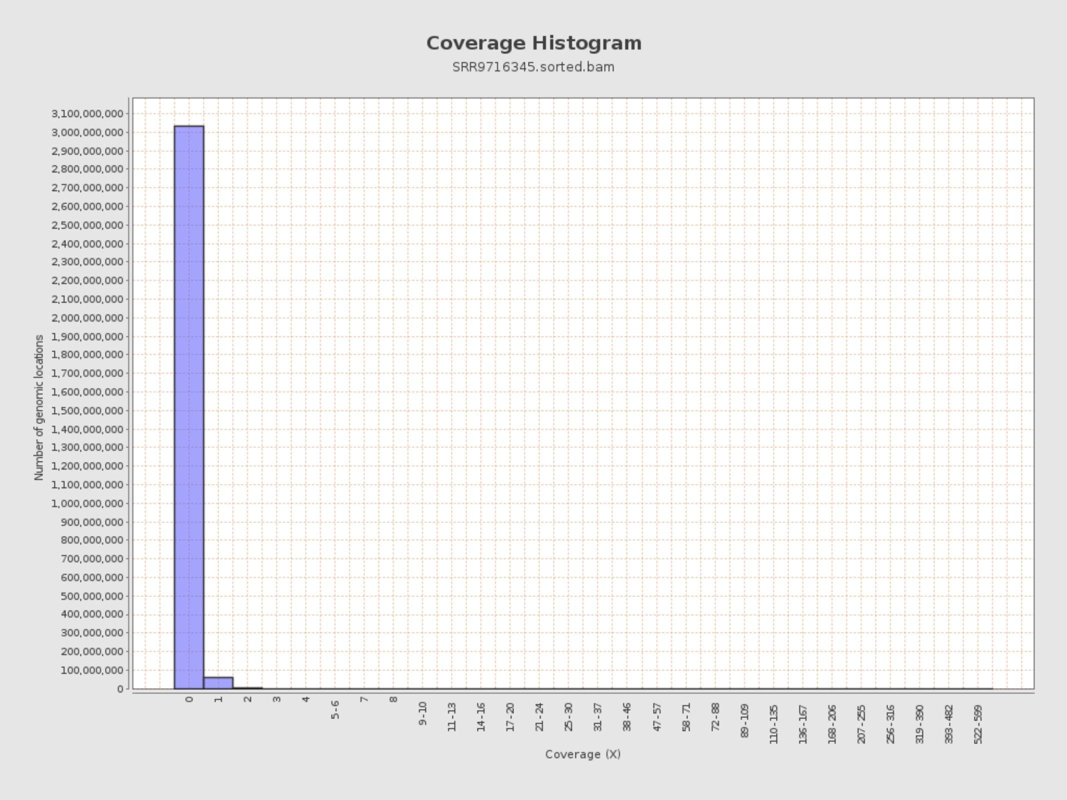
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7120372	0.0286	0.5337
chr2	243199373	5936112	0.0244	0.25
chr3	198022430	4649399	0.0235	0.1628
chr4	191154276	4602542	0.0241	0.1858
chr5	180915260	4269232	0.0236	0.1635
chr6	171115067	4003353	0.0234	0.1721
chr7	159138663	3830826	0.0241	0.2883

chr8	146364022	1959093	0.0134	0.2478
chr9	141213431	2928108	0.0207	0.2114
chr10	135534747	3392046	0.025	0.2466
chr11	135006516	4033549	0.0299	0.2664
chr12	133851895	3126487	0.0234	0.1622
chr13	115169878	2559271	0.0222	0.1587
chr14	107349540	2073671	0.0193	0.1544
chr15	102531392	2023726	0.0197	0.1484
chr16	90354753	1591654	0.0176	0.1522
chr17	81195210	2149015	0.0265	0.192
chr18	78077248	1857338	0.0238	0.3347
chr19	59128983	1354065	0.0229	0.4021
chr20	63025520	1475242	0.0234	0.1659
chr21	48129895	924087	0.0192	0.1636
chr22	51304566	794860	0.0155	0.1318
chrMT	16571	1795	0.1083	0.3683
chrX	155270560	3959270	0.0255	0.1932
chrY	59373566	209605	0.0035	0.1246

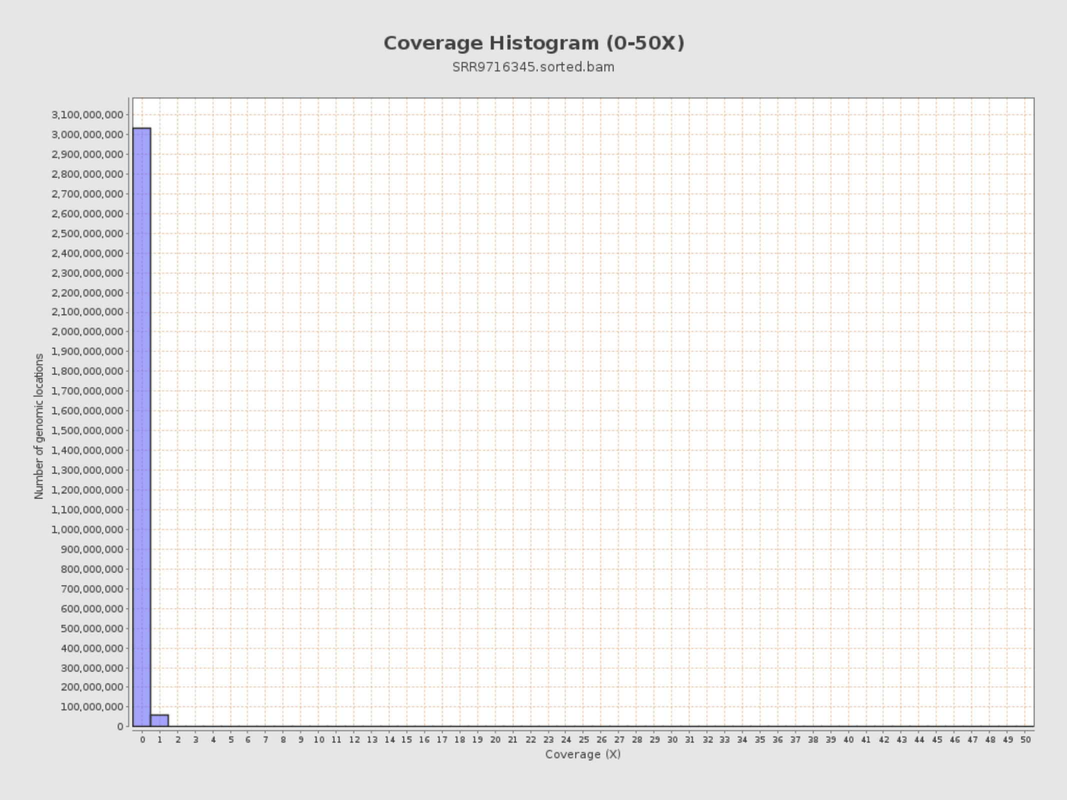
3. Results : Coverage across reference



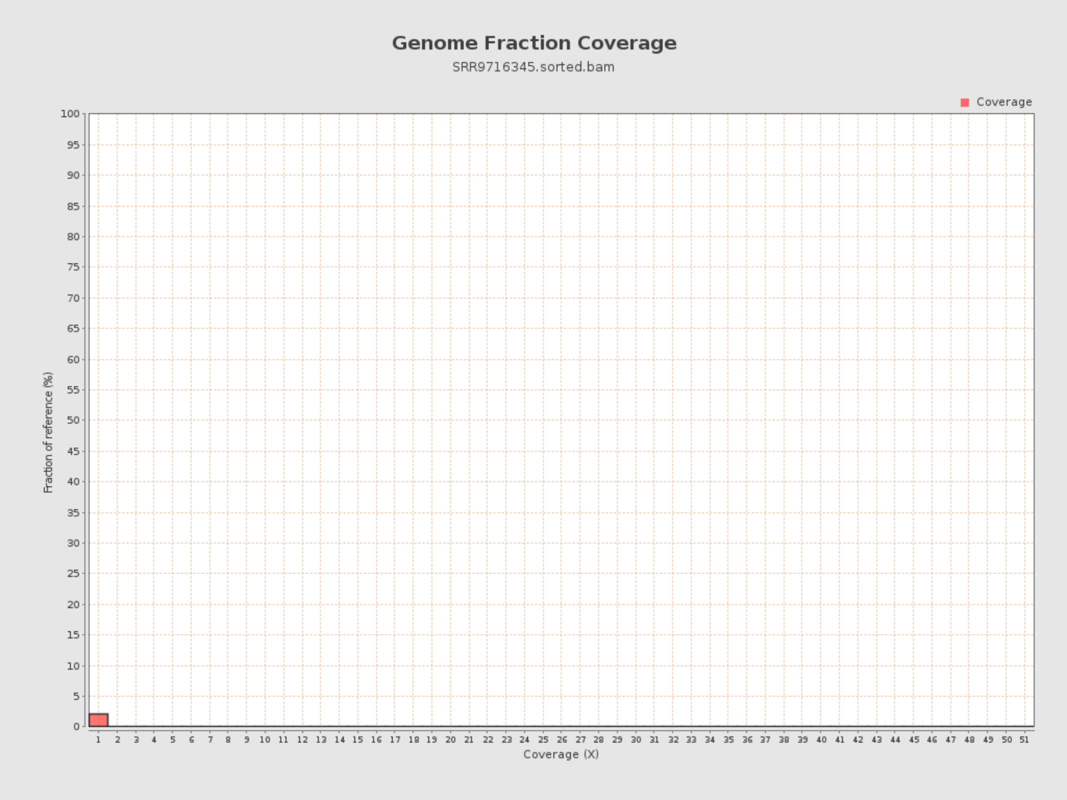
4. Results : Coverage Histogram



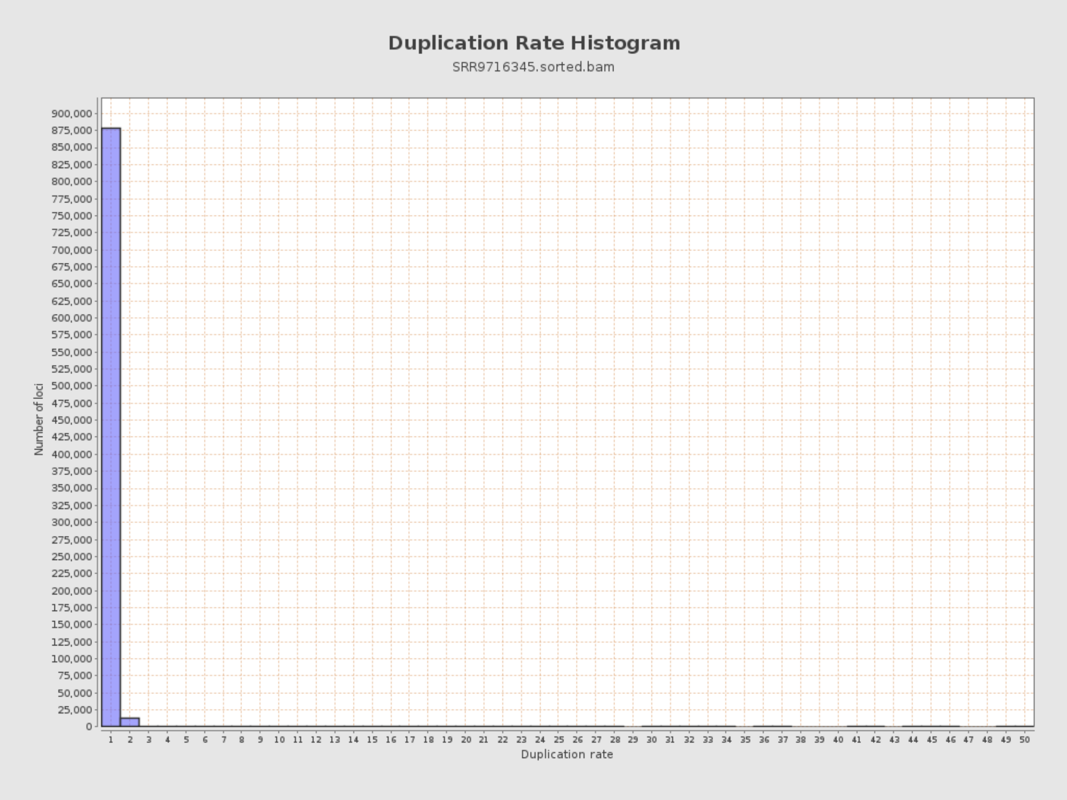
5. Results : Coverage Histogram (0-50X)



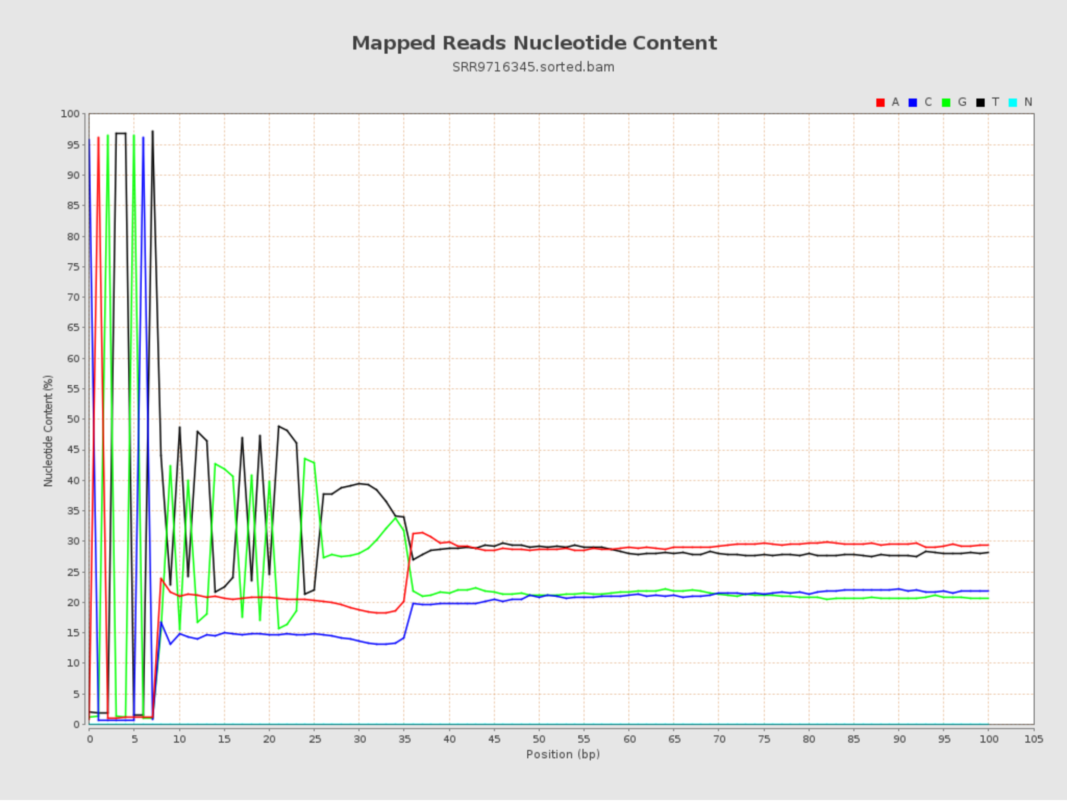
6. Results : Genome Fraction Coverage



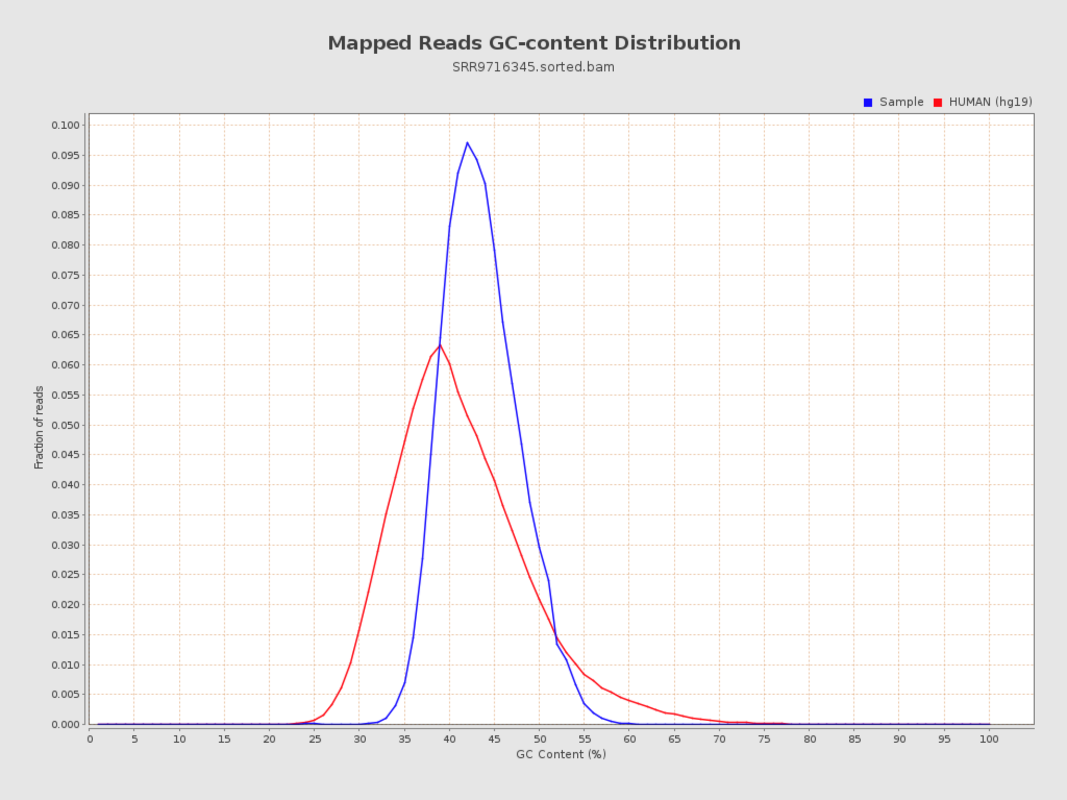
7. Results : Duplication Rate Histogram



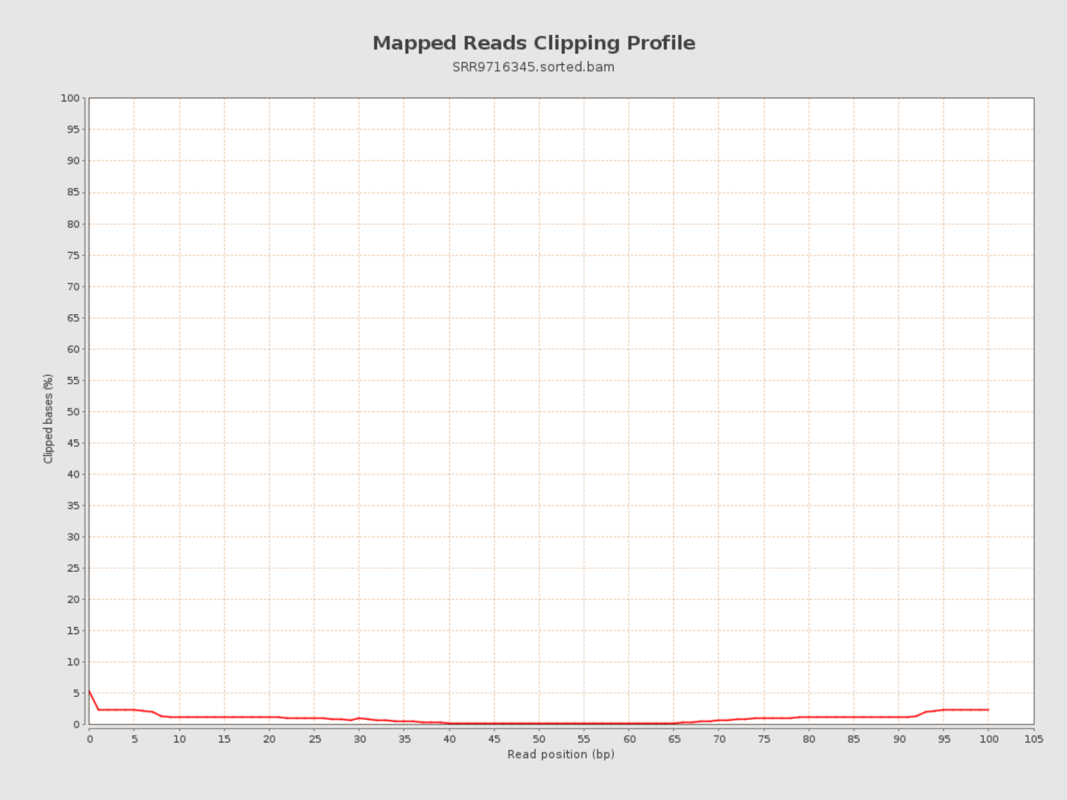
8. Results : Mapped Reads Nucleotide Content



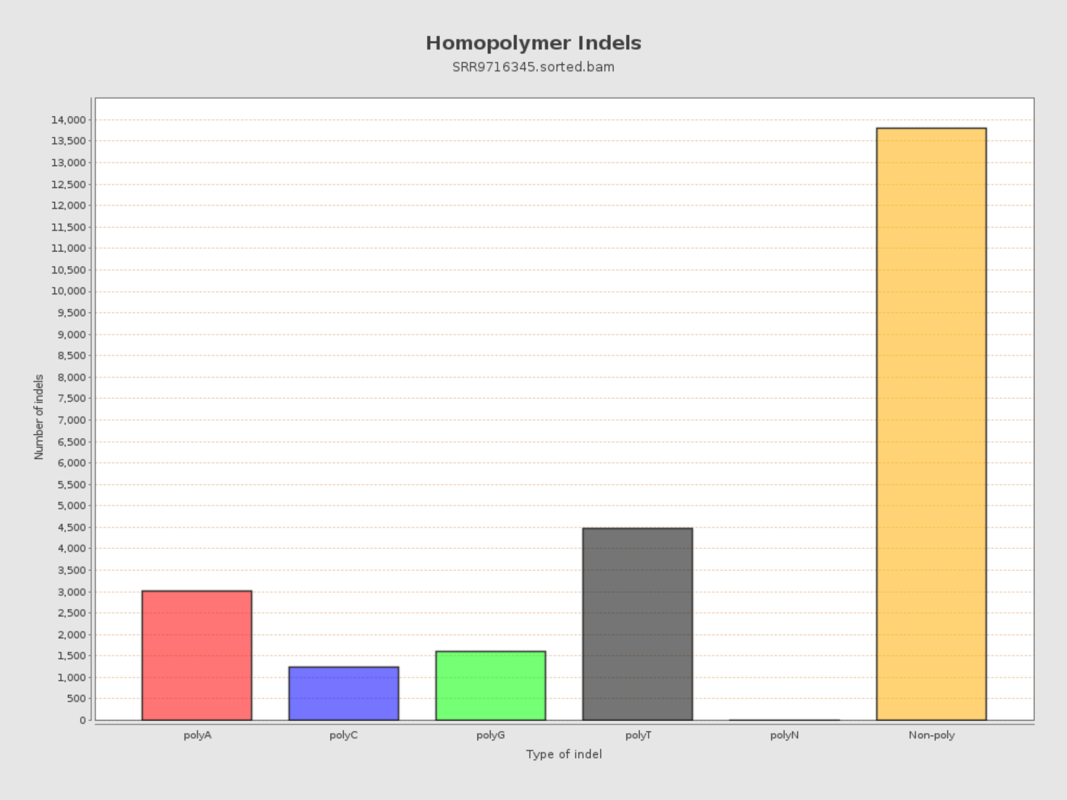
9. Results : Mapped Reads GC-content Distribution



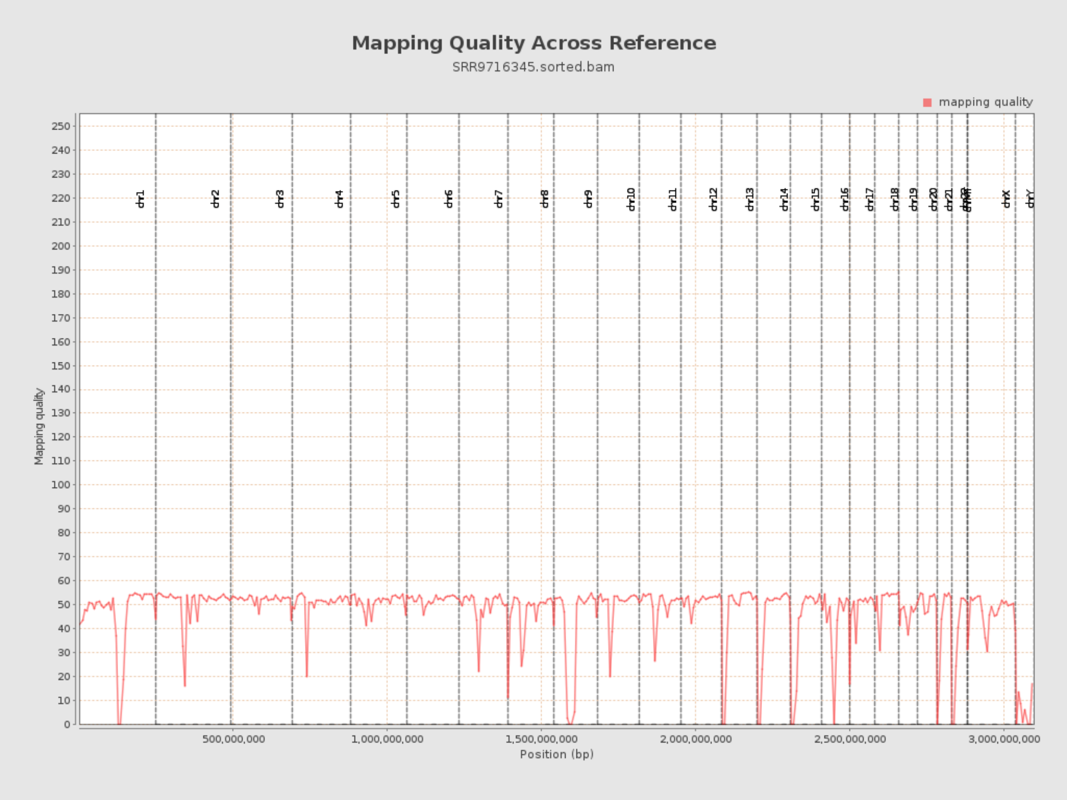
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram