Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:08:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716335.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_SRR9716335 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716335.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:08:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716335.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	985,562
Mapped reads	866,926 / 87.96%
Unmapped reads	118,636 / 12.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,229 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	24,728 / 2.51%
Duplication rate	2.18%
Clipped reads	867,652 / 88.04%

2.2. ACGT Content

Number/percentage of A's	12,191,633 / 24.94%
Number/percentage of C's	9,374,788 / 19.18%
Number/percentage of T's	16,095,610 / 32.93%
Number/percentage of G's	11,214,056 / 22.94%
Number/percentage of N's	788 / 0%
GC Percentage	42.12%

2.3. Coverage

Mean	0.0158

Standard Deviation	0.1719

2.4. Mapping Quality

Mean Mapping Quality	44.41

2.5. Mismatches and indels

General error rate	0.57%
Mismatches	272,155
Insertions	3,040
Mapped reads with at least one insertion	0.35%
Deletions	8,725
Mapped reads with at least one deletion	1%
Homopolymer indels	43.69%

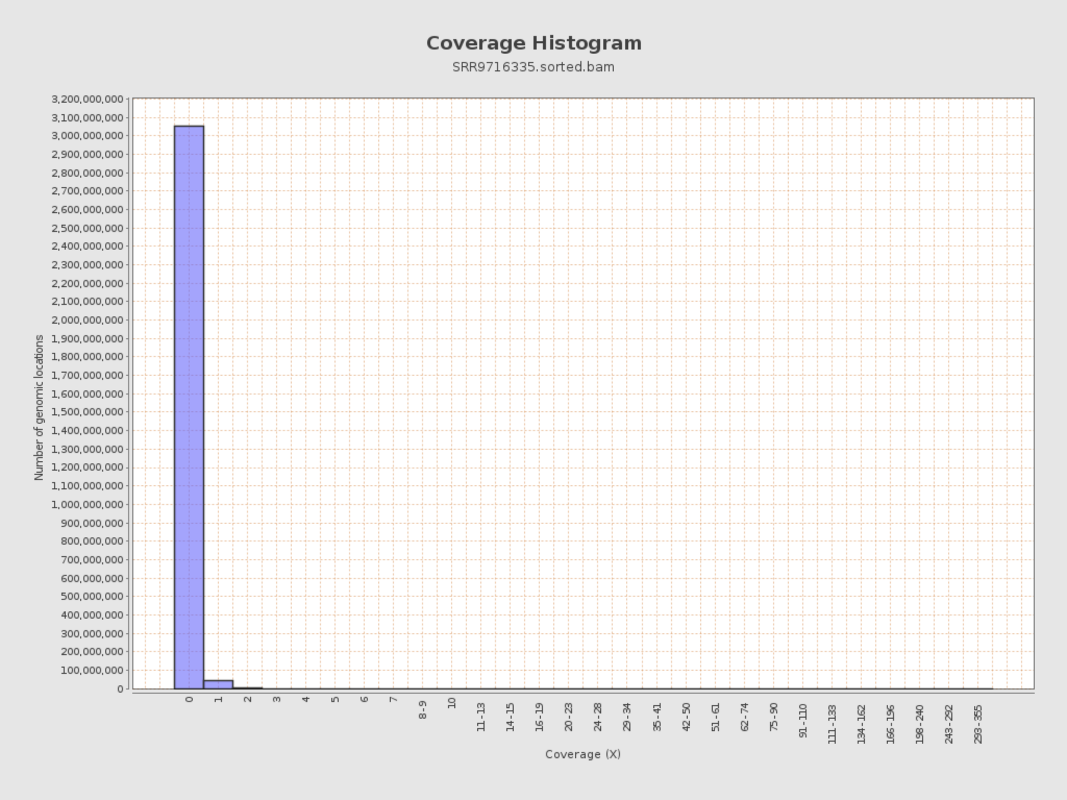
2.6. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3890742	0.0156	0.2832
chr2	243199373	4113945	0.0169	0.1816
chr3	198022430	3273570	0.0165	0.1351
chr4	191154276	3221299	0.0169	0.1466
chr5	180915260	2968406	0.0164	0.1356
chr6	171115067	2843641	0.0166	0.1446
chr7	159138663	2661744	0.0167	0.1936

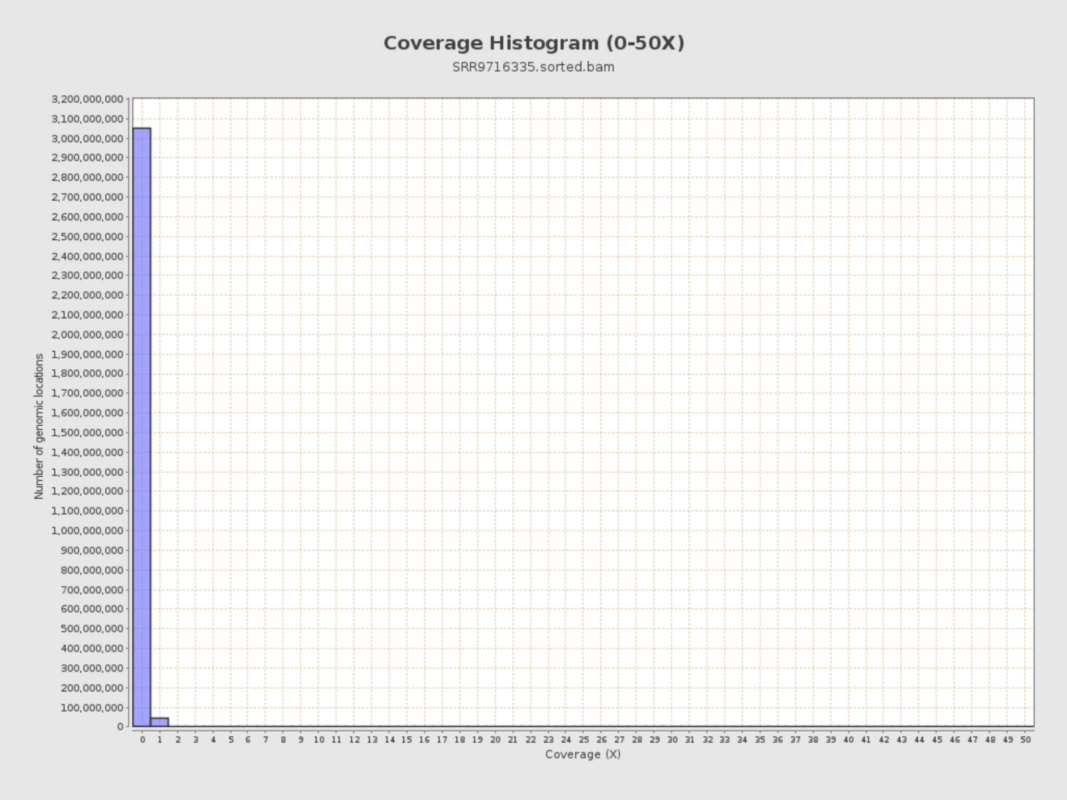
chr8	146364022	2491079	0.017	0.1835
chr9	141213431	2064871	0.0146	0.1698
chr10	135534747	2309136	0.017	0.179
chr11	135006516	2229004	0.0165	0.1598
chr12	133851895	2229325	0.0167	0.1393
chr13	115169878	1560758	0.0136	0.1216
chr14	107349540	1501265	0.014	0.1324
chr15	102531392	1362567	0.0133	0.1212
chr16	90354753	1412927	0.0156	0.1409
chr17	81195210	1280875	0.0158	0.1357
chr18	78077248	1315837	0.0169	0.2641
chr19	59128983	969212	0.0164	0.2206
chr20	63025520	1018754	0.0162	0.1377
chr21	48129895	651603	0.0135	0.1309
chr22	51304566	556413	0.0108	0.1091
chrMT	16571	3295	0.1988	0.4634
chrX	155270560	2808180	0.0181	0.1561
chrY	59373566	153153	0.0026	0.0769

3. Results : Coverage across reference

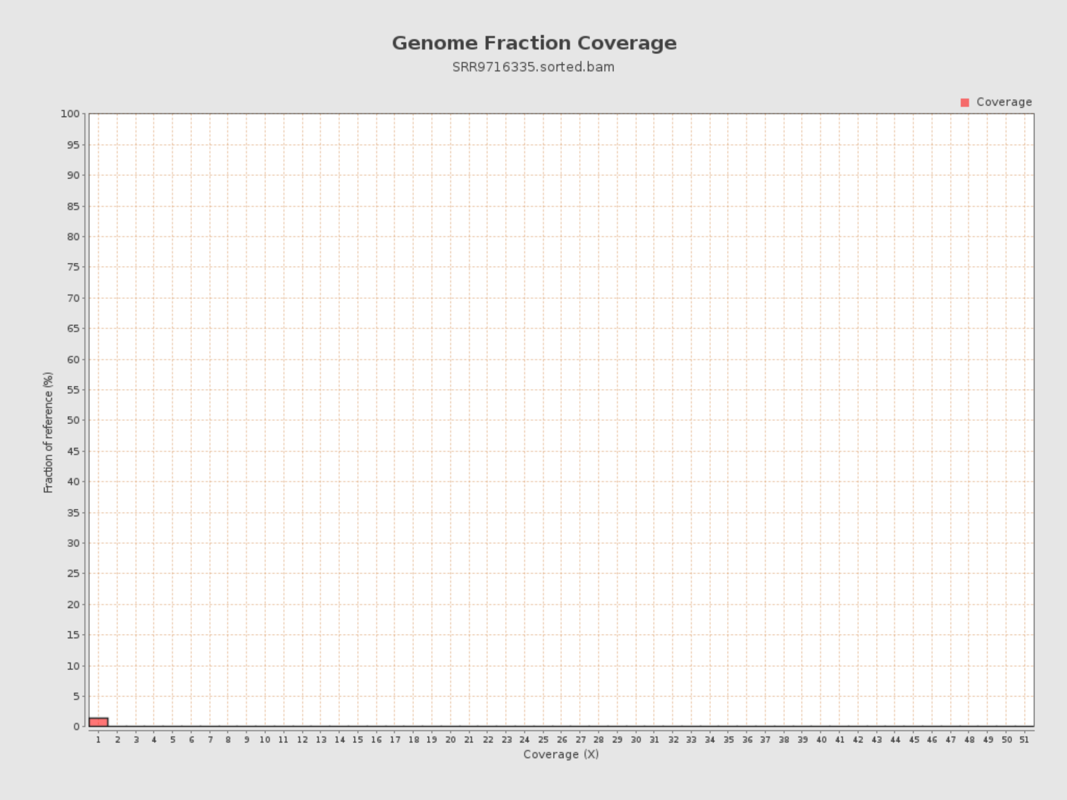
4. Results : Coverage Histogram



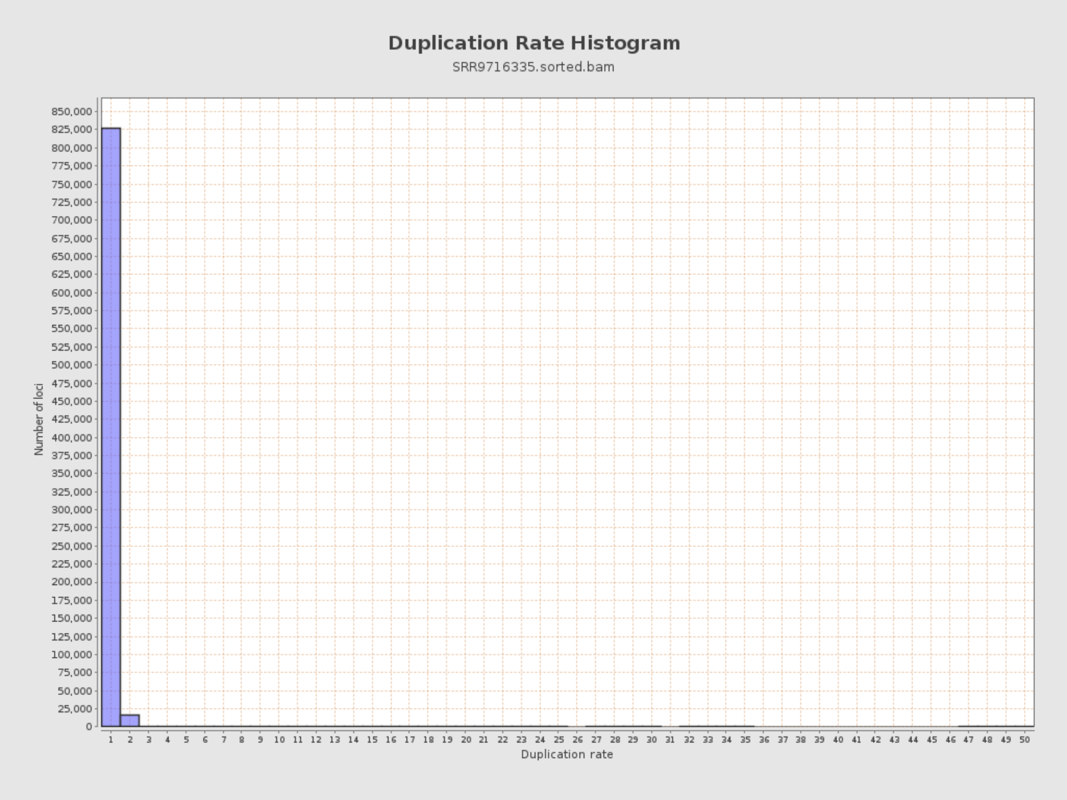
5. Results : Coverage Histogram (0-50X)



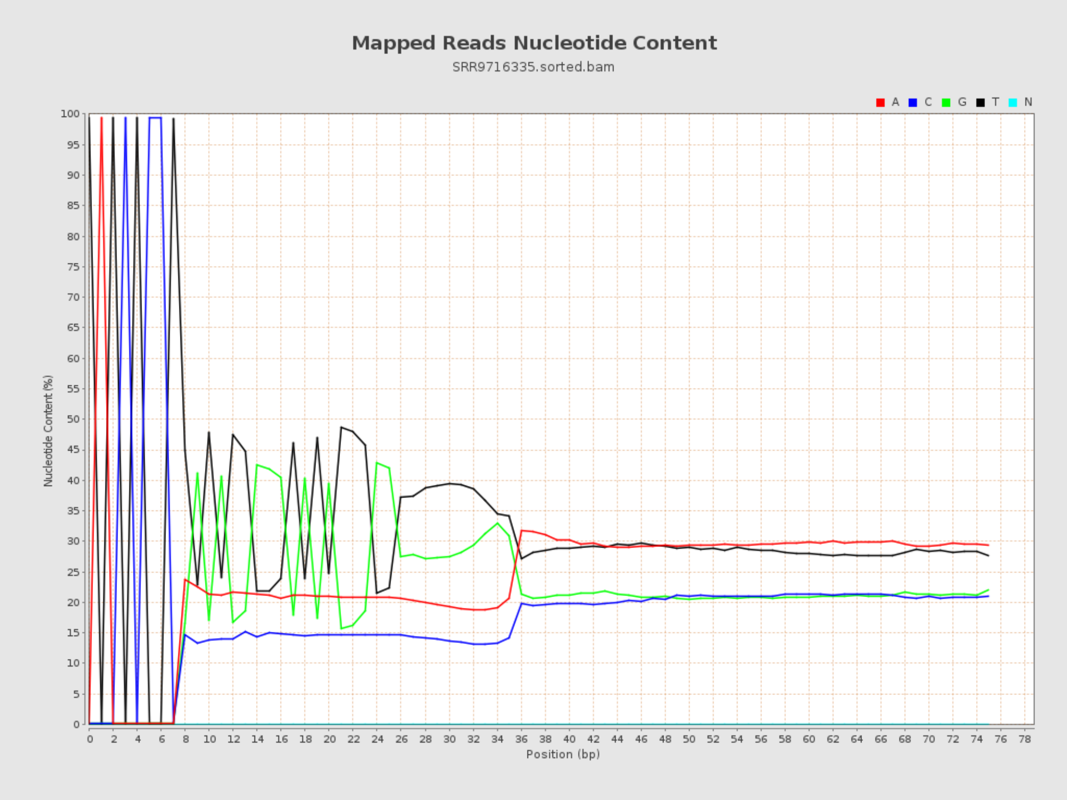
6. Results : Genome Fraction Coverage



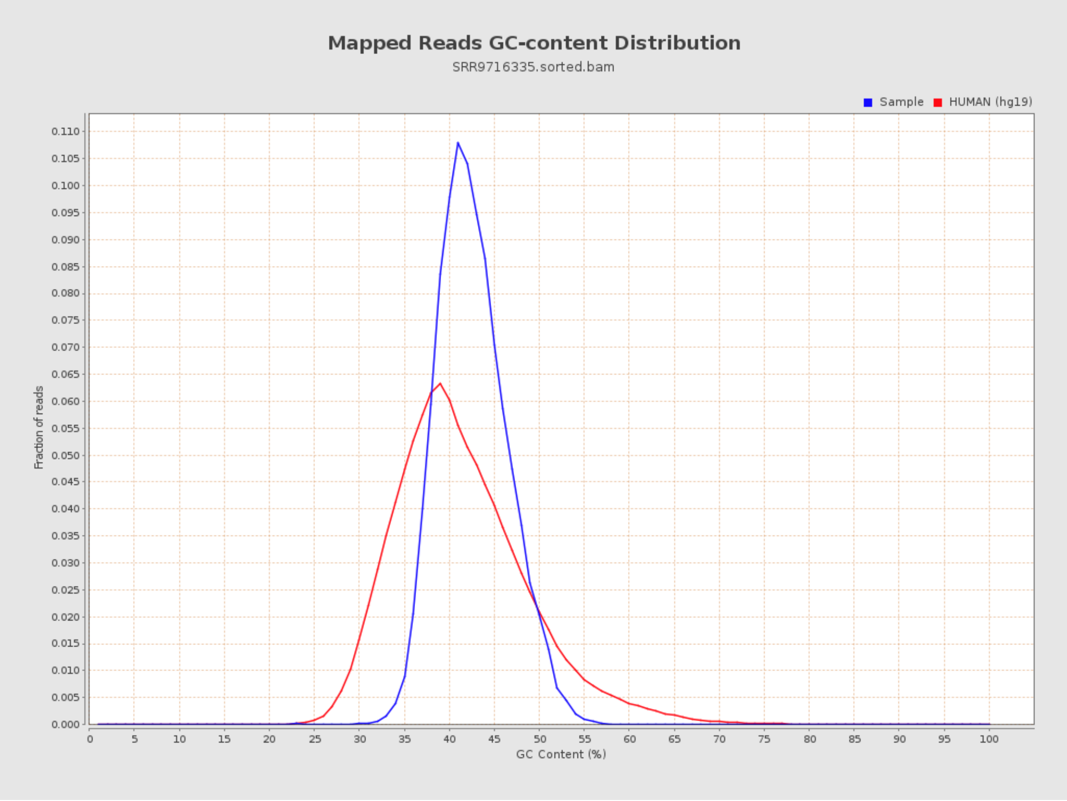
7. Results : Duplication Rate Histogram



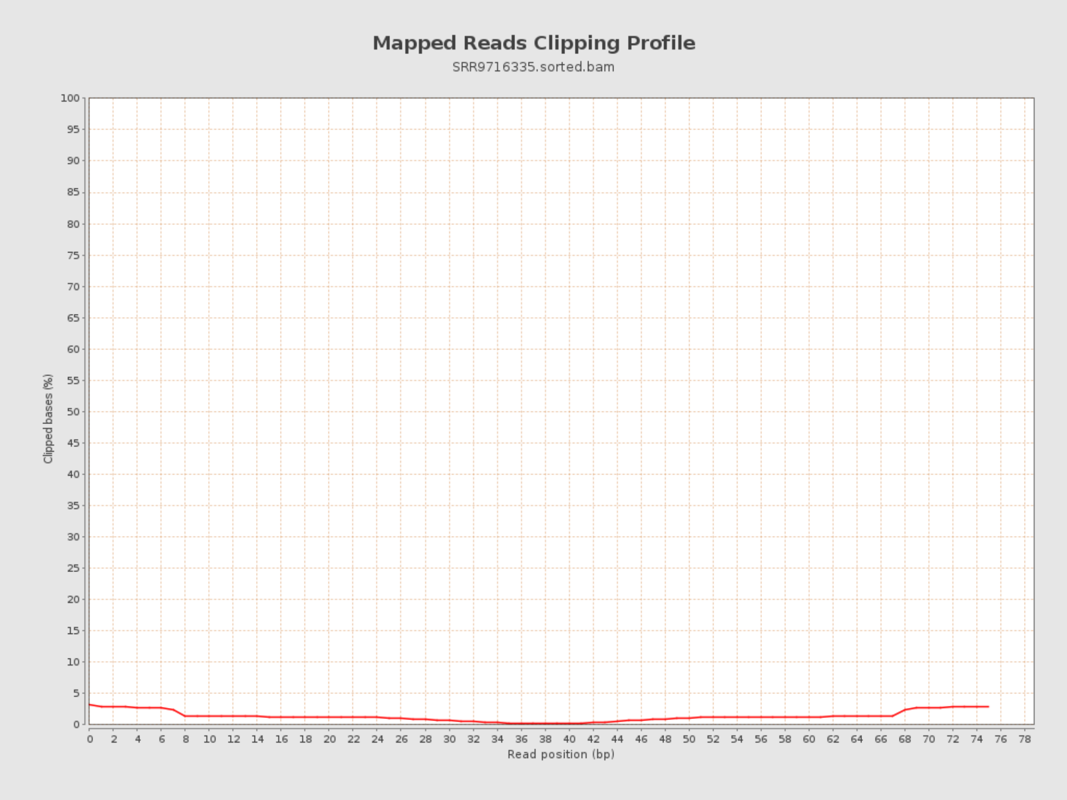
8. Results : Mapped Reads Nucleotide Content



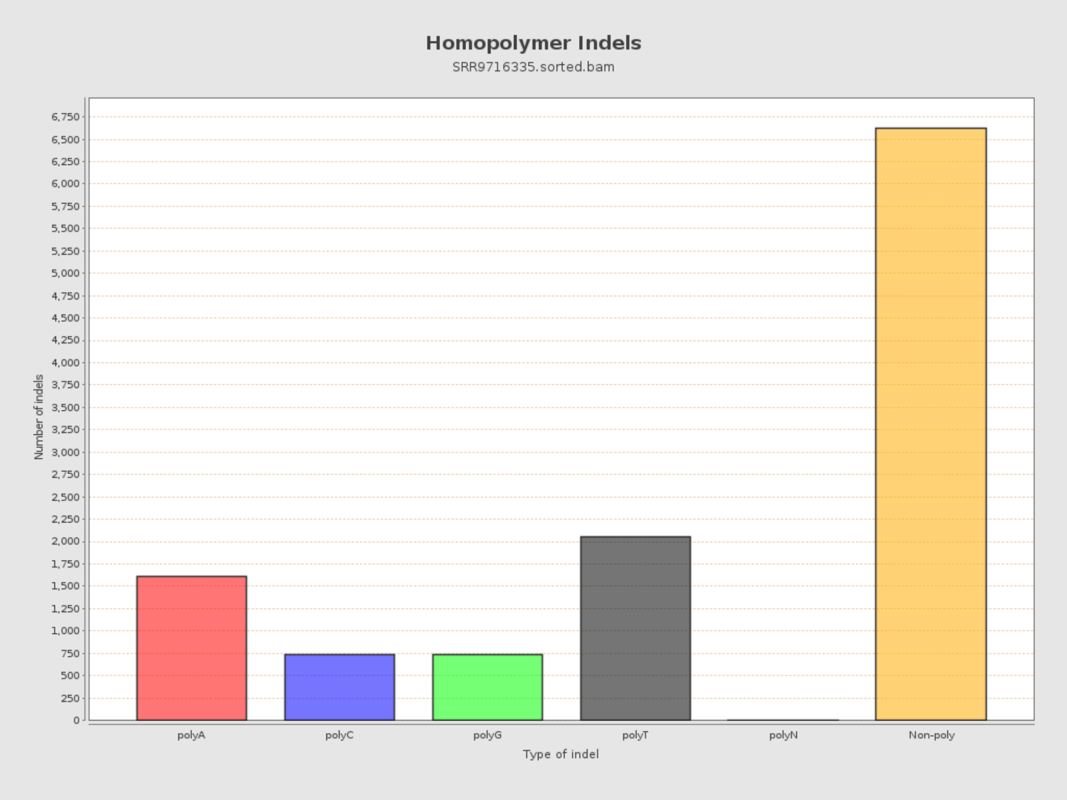
9. Results : Mapped Reads GC-content Distribution



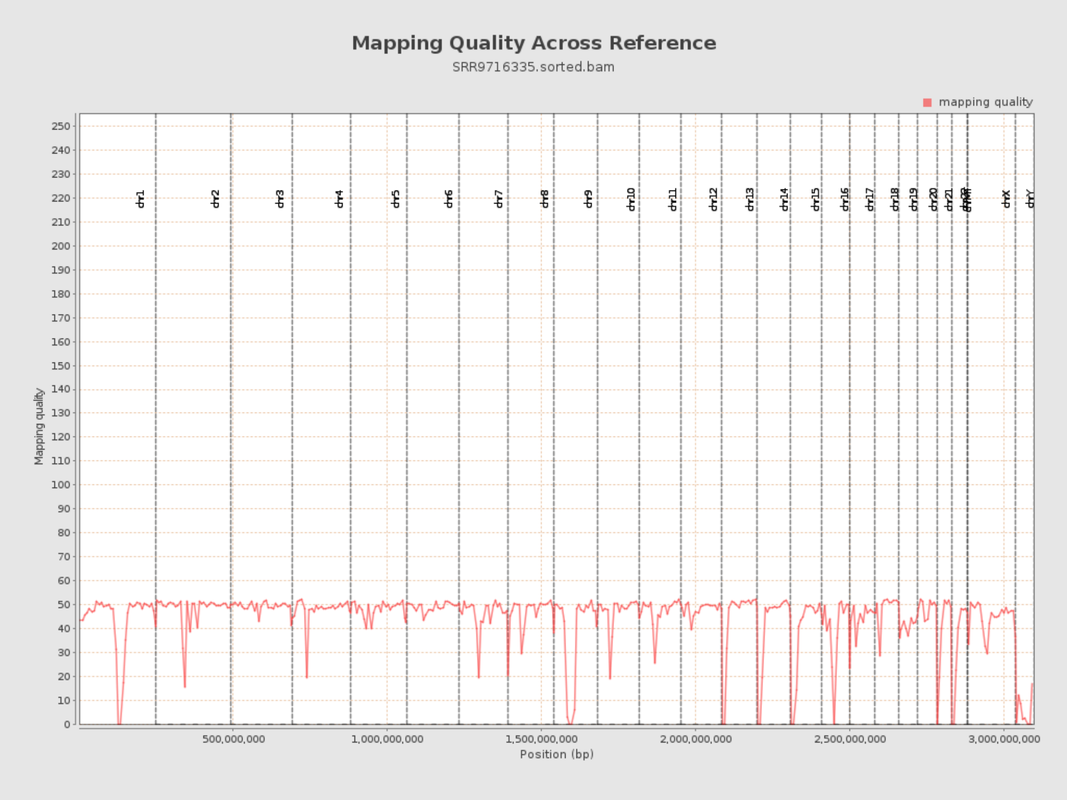
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram