Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 14:06:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716835.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_SRR9716835 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716835.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 14:06:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716835.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	877,451
Mapped reads	780,743 / 88.98%
Unmapped reads	96,708 / 11.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,166 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	16,245 / 1.85%
Duplication rate	1.49%
Clipped reads	782,557 / 89.19%

2.2. ACGT Content

Number/percentage of A's	11,429,940 / 25.1%
Number/percentage of C's	8,039,280 / 17.65%
Number/percentage of T's	14,352,210 / 31.52%
Number/percentage of G's	11,714,777 / 25.73%
Number/percentage of N's	478 / 0%
GC Percentage	43.38%

2.3. Coverage

Mean	0.0147

Standard Deviation	0.1582

2.4. Mapping Quality

Mean Mapping Quality	44.7

2.5. Mismatches and indels

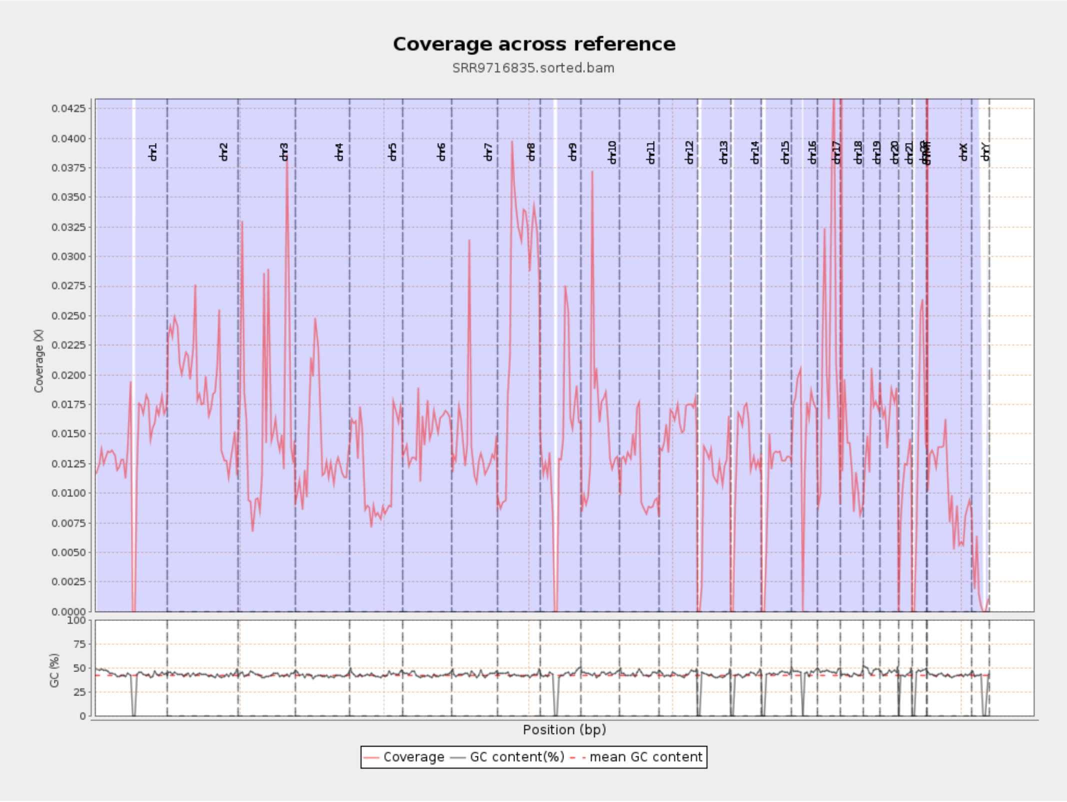
General error rate	0.51%
Mismatches	226,612
Insertions	3,154
Mapped reads with at least one insertion	0.4%
Deletions	8,393
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.05%

2.6. Chromosome stats

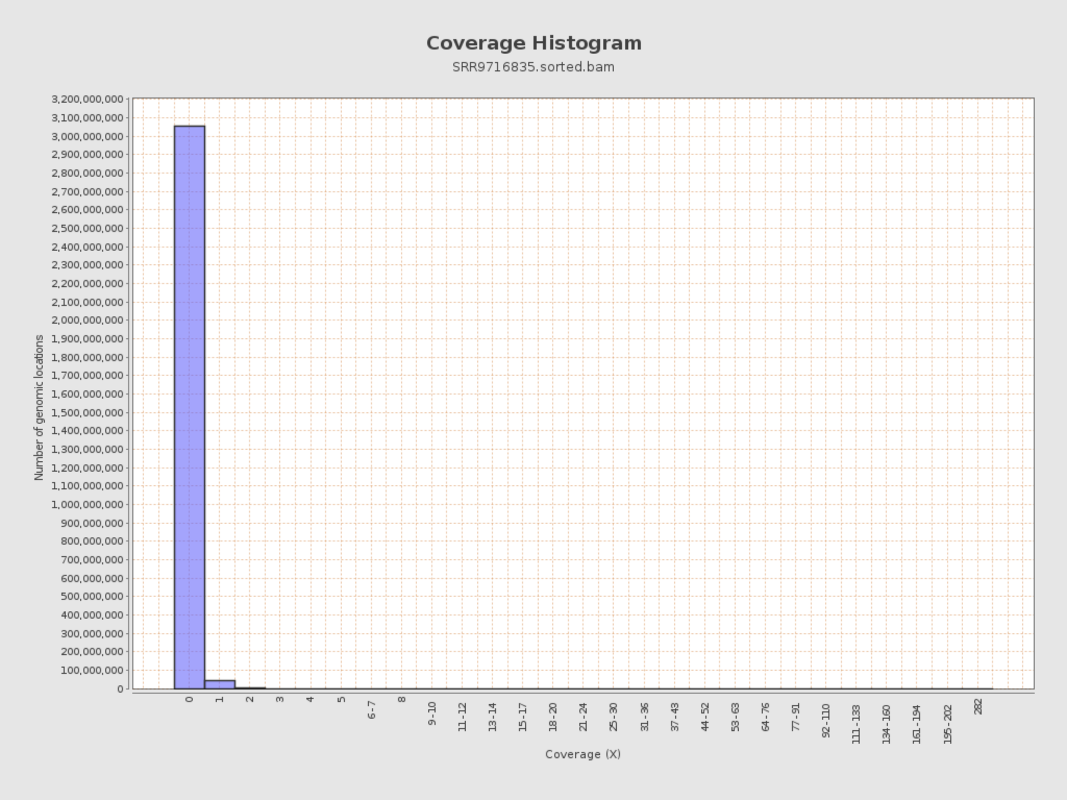
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3455782	0.0139	0.2037
chr2	243199373	4625614	0.019	0.1938
chr3	198022430	3277354	0.0166	0.1369
chr4	191154276	2594186	0.0136	0.1287
chr5	180915260	2155335	0.0119	0.1141
chr6	171115067	2583640	0.0151	0.1338
chr7	159138663	2246429	0.0141	0.2457

chr8	146364022	3893258	0.0266	0.2028
chr9	141213431	1954414	0.0138	0.1352
chr10	135534747	2086246	0.0154	0.1973
chr11	135006516	1579483	0.0117	0.1296
chr12	133851895	2146032	0.016	0.1365
chr13	115169878	1225165	0.0106	0.1072
chr14	107349540	1335257	0.0124	0.1177
chr15	102531392	1102409	0.0108	0.1111
chr16	90354753	1424395	0.0158	0.1342
chr17	81195210	1825760	0.0225	0.1606
chr18	78077248	1100807	0.0141	0.185
chr19	59128983	933025	0.0158	0.1894
chr20	63025520	1070294	0.017	0.1393
chr21	48129895	509469	0.0106	0.1109
chr22	51304566	704645	0.0137	0.1218
chrMT	16571	3904	0.2356	0.5337
chrX	155270560	1603288	0.0103	0.1126
chrY	59373566	113600	0.0019	0.0614

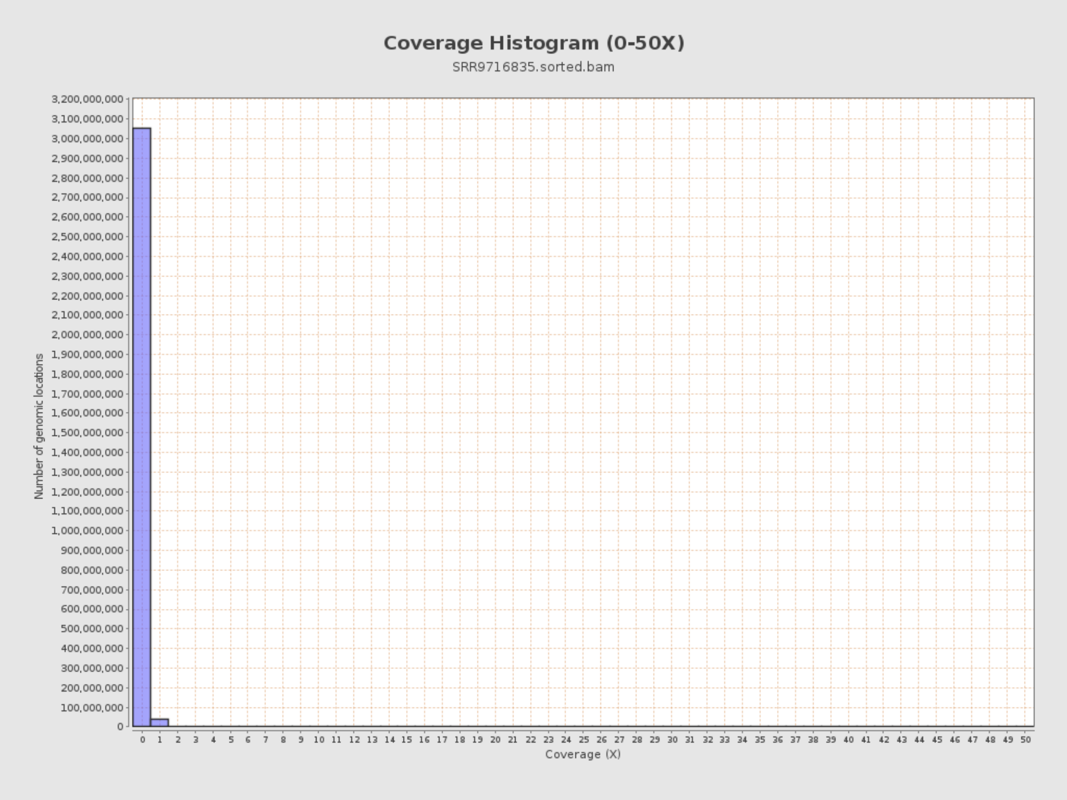
3. Results : Coverage across reference



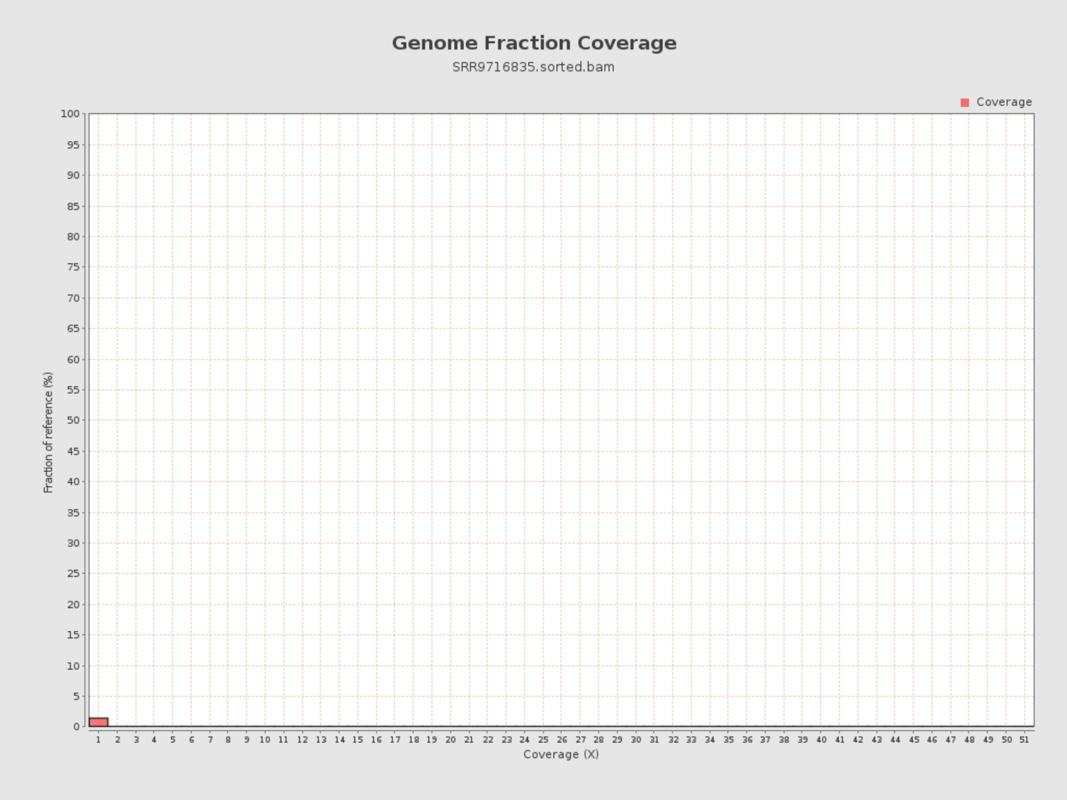
4. Results : Coverage Histogram



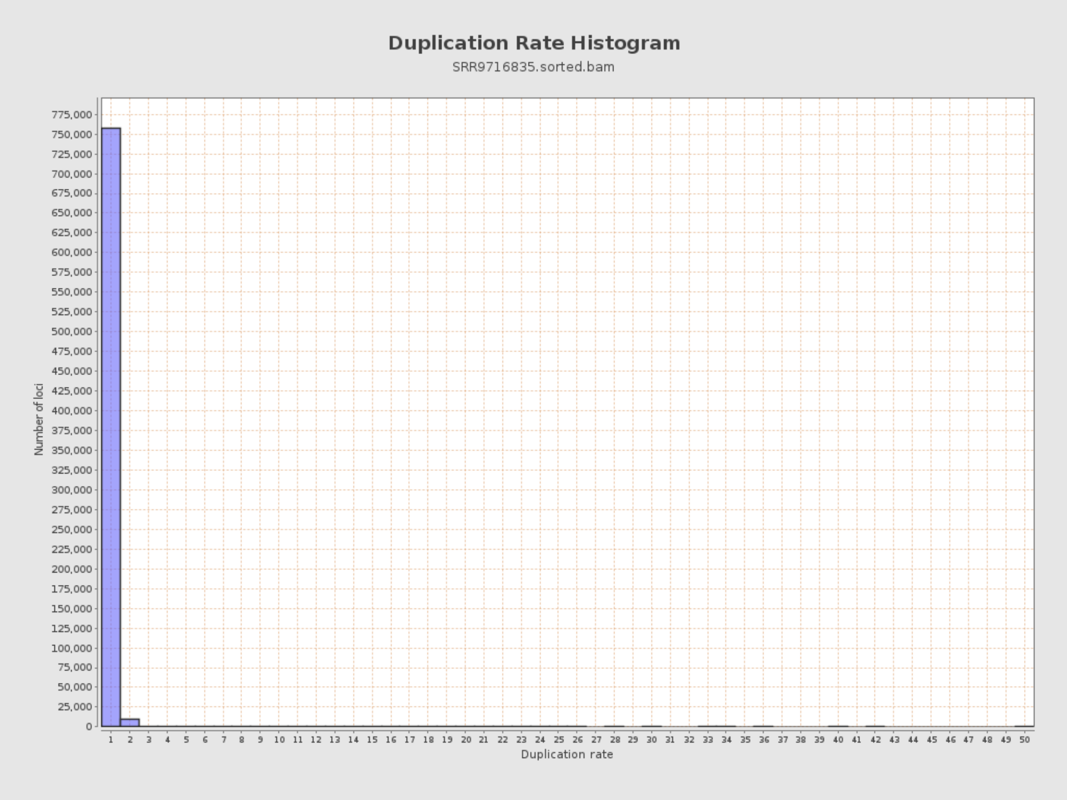
5. Results : Coverage Histogram (0-50X)



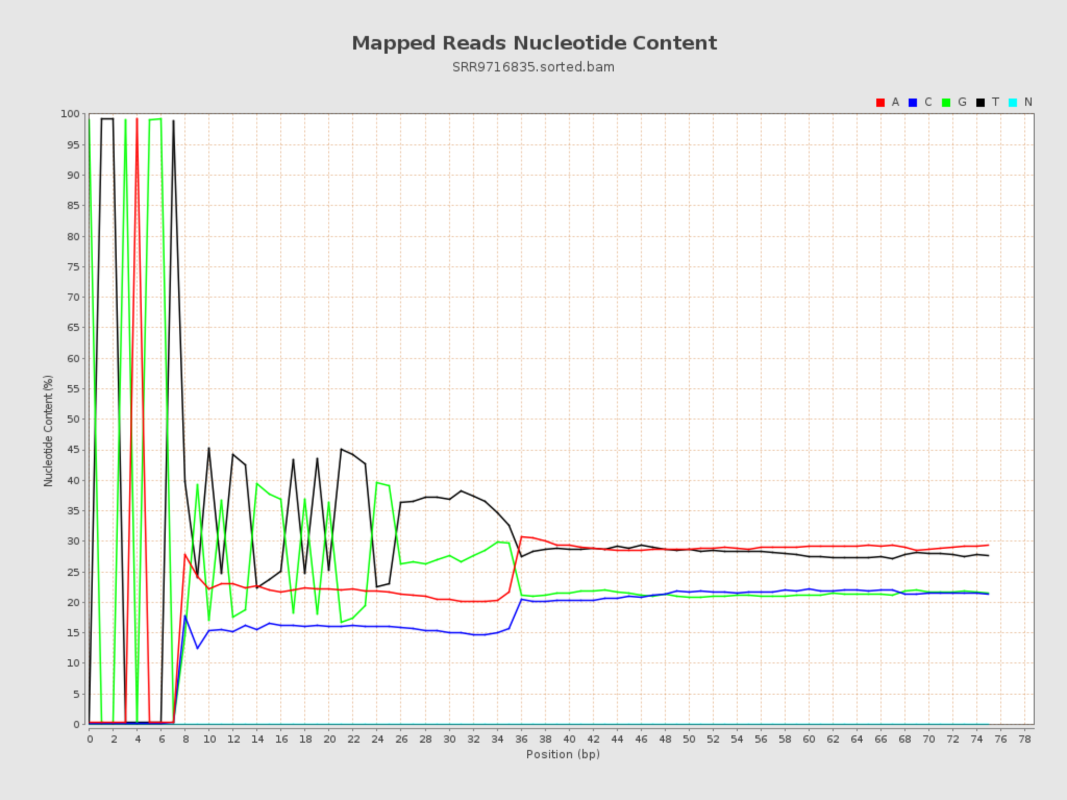
6. Results : Genome Fraction Coverage



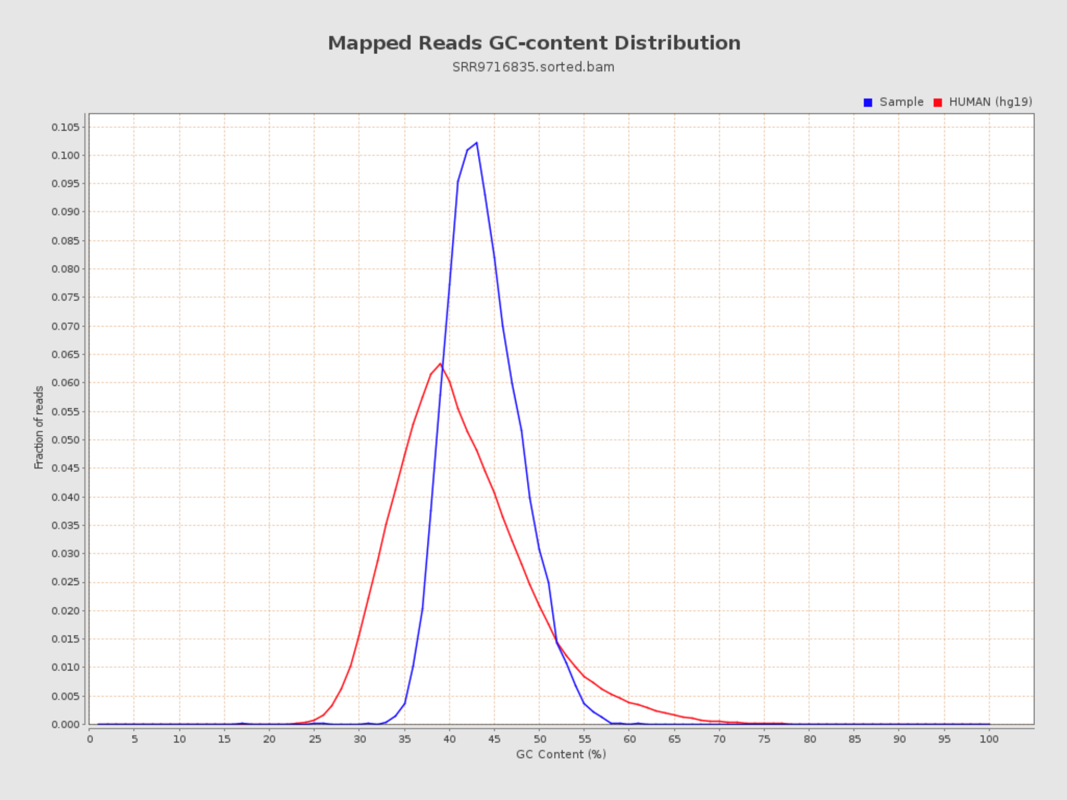
7. Results : Duplication Rate Histogram



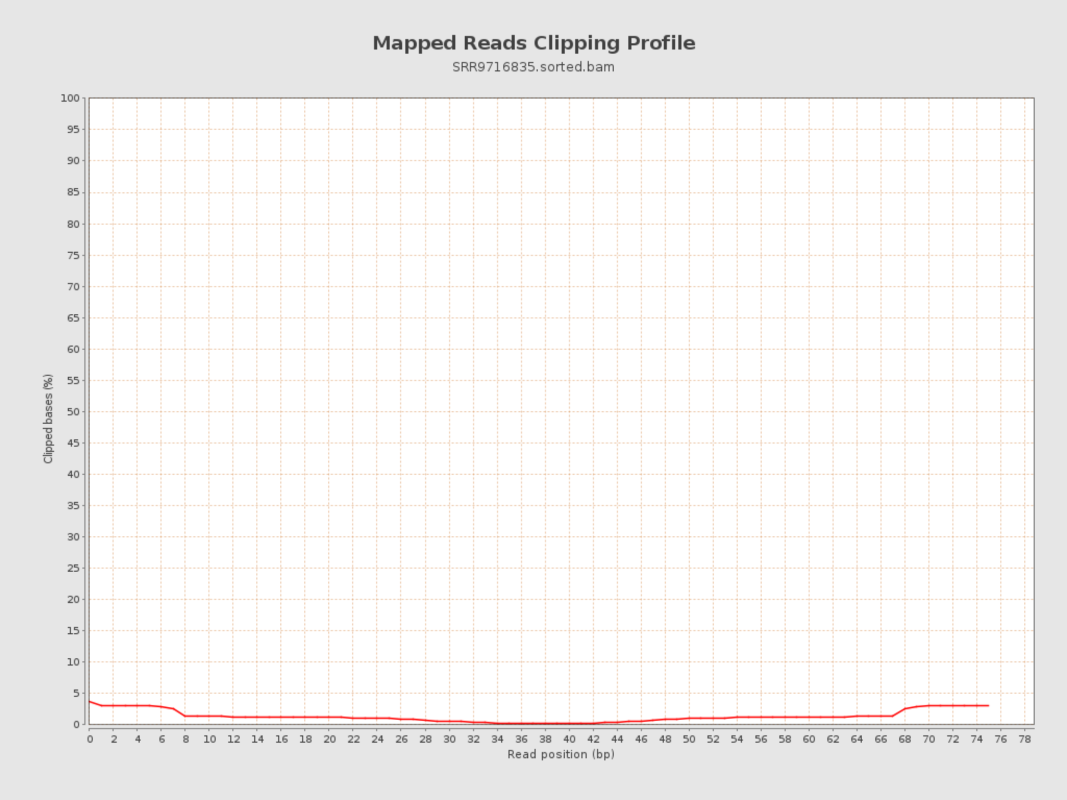
8. Results : Mapped Reads Nucleotide Content



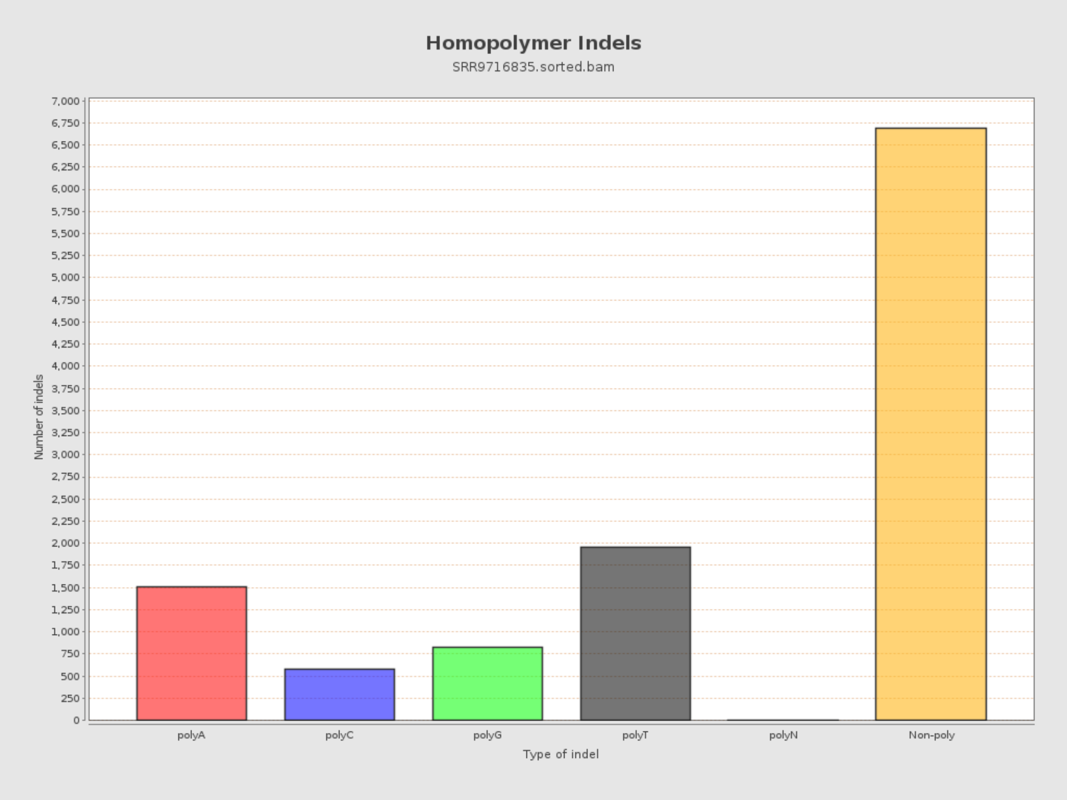
9. Results : Mapped Reads GC-content Distribution



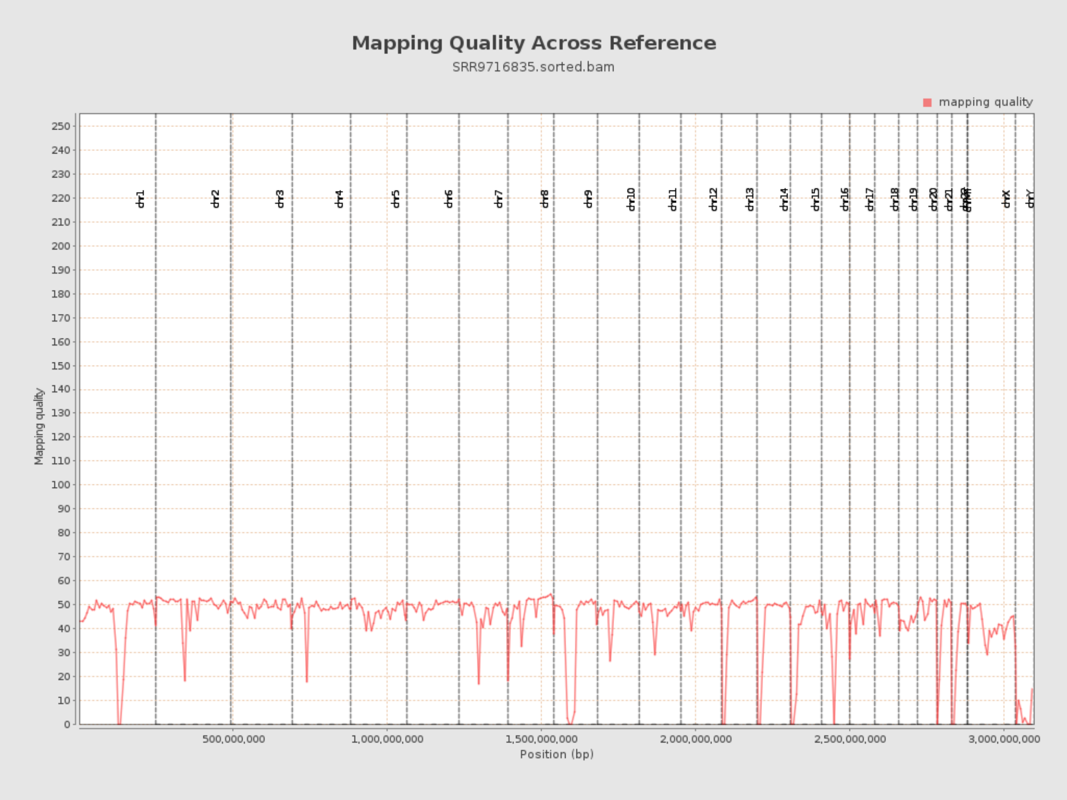
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram