Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 14:02:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716833.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_SRR9716833 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716833.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 14:02:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716833.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	630,374
Mapped reads	485,668 / 77.04%
Unmapped reads	144,706 / 22.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,008 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	13,739 / 2.18%
Duplication rate	2.33%
Clipped reads	487,449 / 77.33%

2.2. ACGT Content

Number/percentage of A's	7,321,768 / 25.38%
Number/percentage of C's	5,399,930 / 18.72%
Number/percentage of T's	9,211,332 / 31.93%
Number/percentage of G's	6,916,772 / 23.97%
Number/percentage of N's	216 / 0%
GC Percentage	42.69%

2.3. Coverage

Mean	0.0093

Standard Deviation	0.1179

2.4. Mapping Quality

Mean Mapping Quality	45.56

2.5. Mismatches and indels

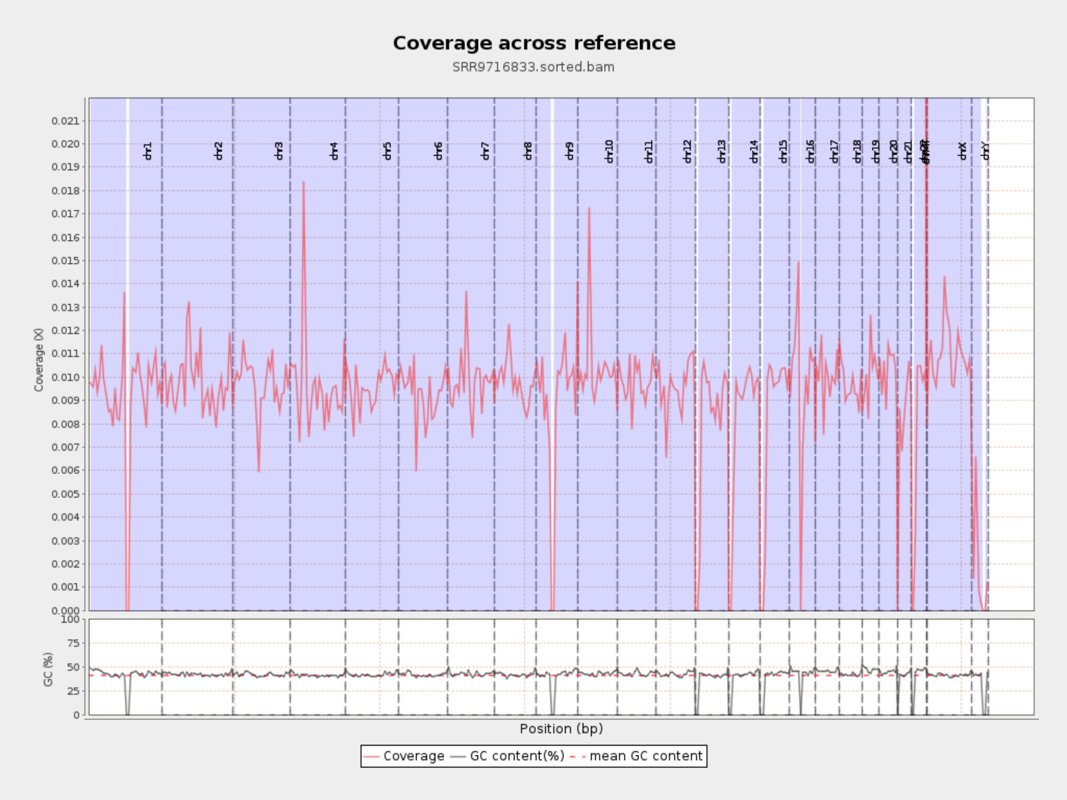
General error rate	0.51%
Mismatches	142,216
Insertions	1,986
Mapped reads with at least one insertion	0.41%
Deletions	5,153
Mapped reads with at least one deletion	1.05%
Homopolymer indels	42.3%

2.6. Chromosome stats

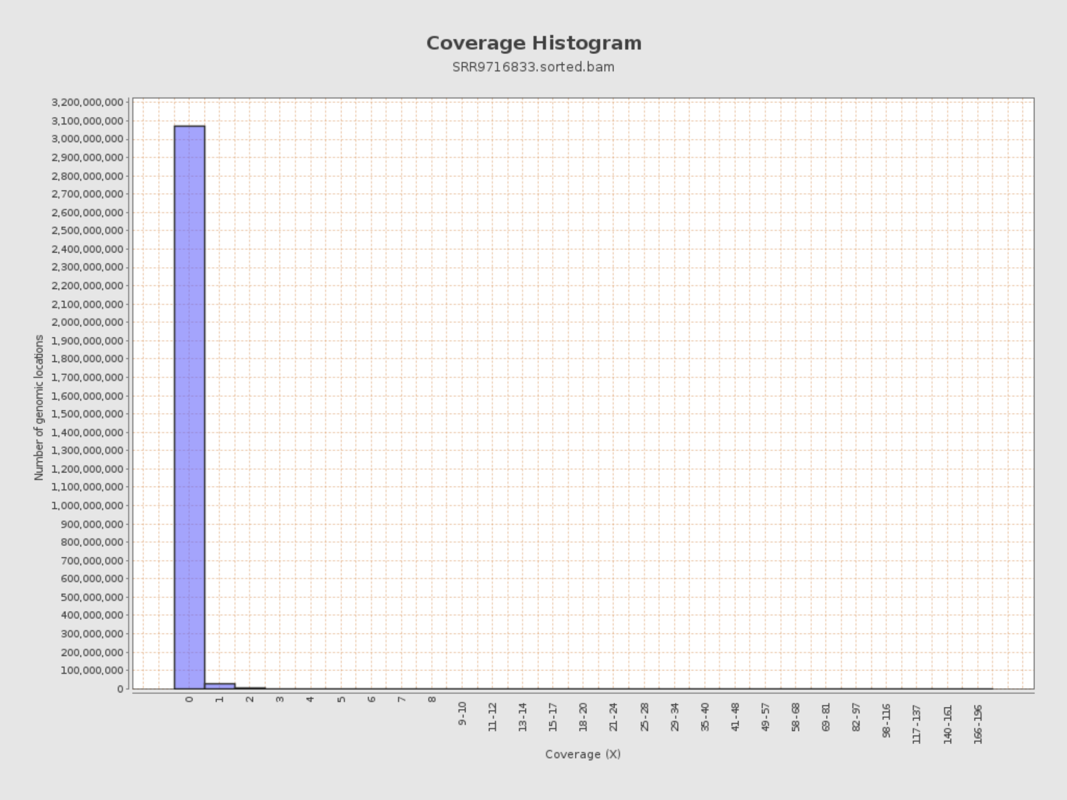
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2275464	0.0091	0.1435
chr2	243199373	2395872	0.0099	0.14
chr3	198022430	1923585	0.0097	0.1049
chr4	191154276	1831907	0.0096	0.1129
chr5	180915260	1732780	0.0096	0.1044
chr6	171115067	1588354	0.0093	0.1067
chr7	159138663	1564722	0.0098	0.1282

chr8	146364022	1439828	0.0098	0.1475
chr9	141213431	1220151	0.0086	0.1053
chr10	135534747	1407648	0.0104	0.1301
chr11	135006516	1326054	0.0098	0.1139
chr12	133851895	1283202	0.0096	0.1046
chr13	115169878	902851	0.0078	0.0944
chr14	107349540	862422	0.008	0.0956
chr15	102531392	828299	0.0081	0.0953
chr16	90354753	887460	0.0098	0.1083
chr17	81195210	815558	0.01	0.11
chr18	78077248	755239	0.0097	0.1472
chr19	59128983	599139	0.0101	0.1302
chr20	63025520	648636	0.0103	0.1104
chr21	48129895	386223	0.008	0.1029
chr22	51304566	361372	0.007	0.0897
chrMT	16571	27919	1.6848	1.5443
chrX	155270560	1693094	0.0109	0.1136
chrY	59373566	100483	0.0017	0.066

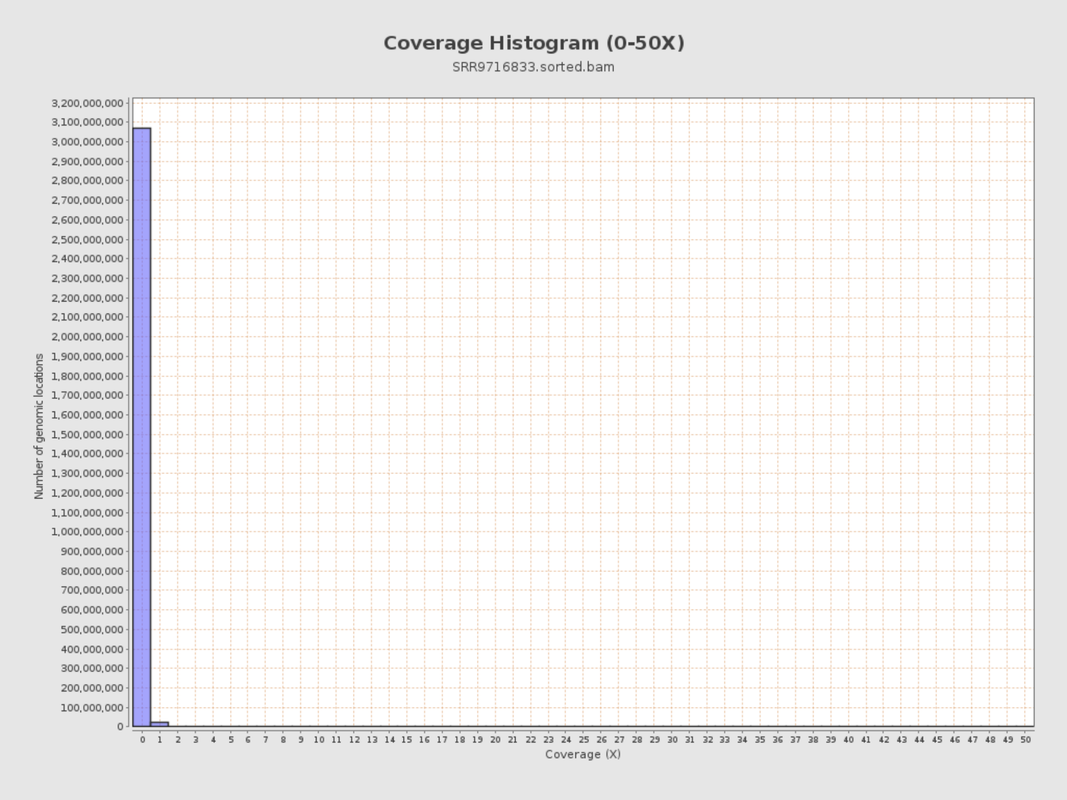
3. Results : Coverage across reference



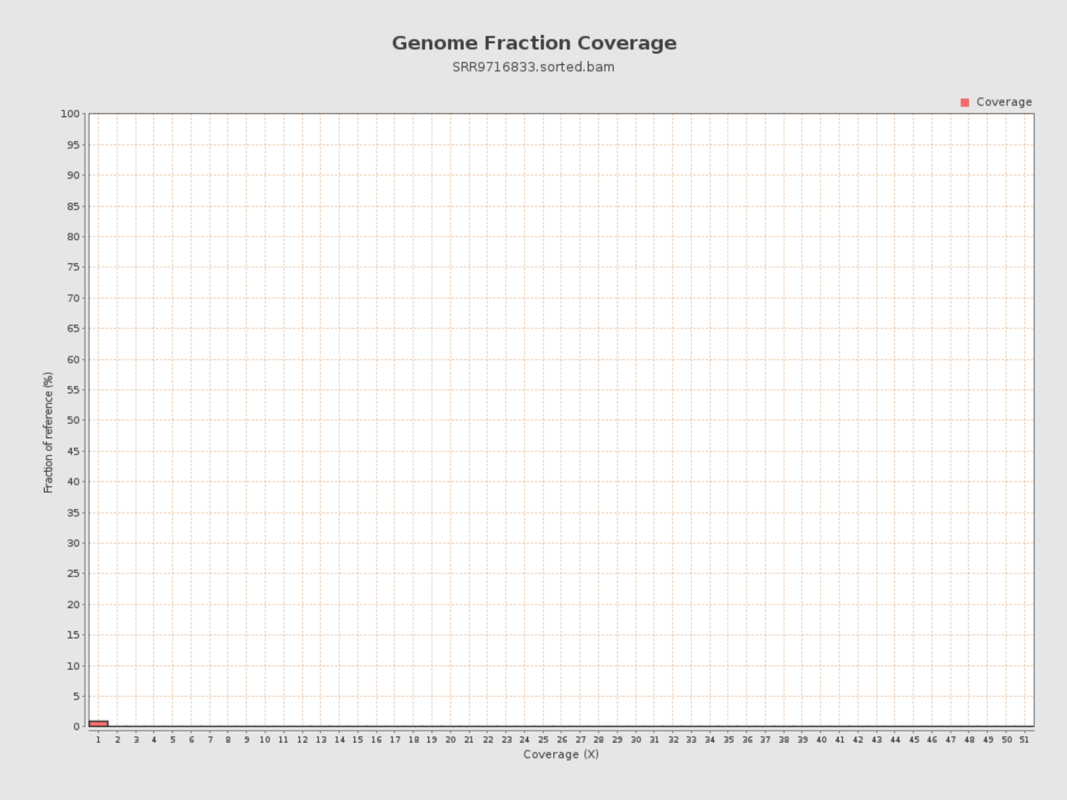
4. Results : Coverage Histogram



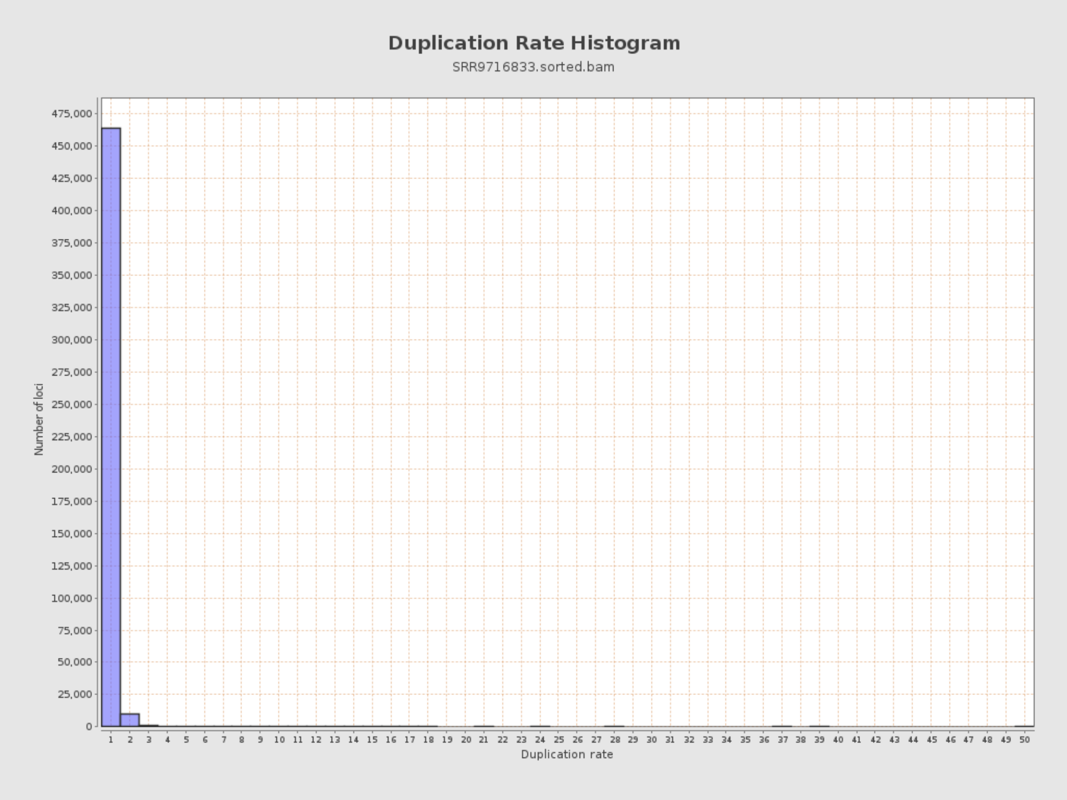
5. Results : Coverage Histogram (0-50X)



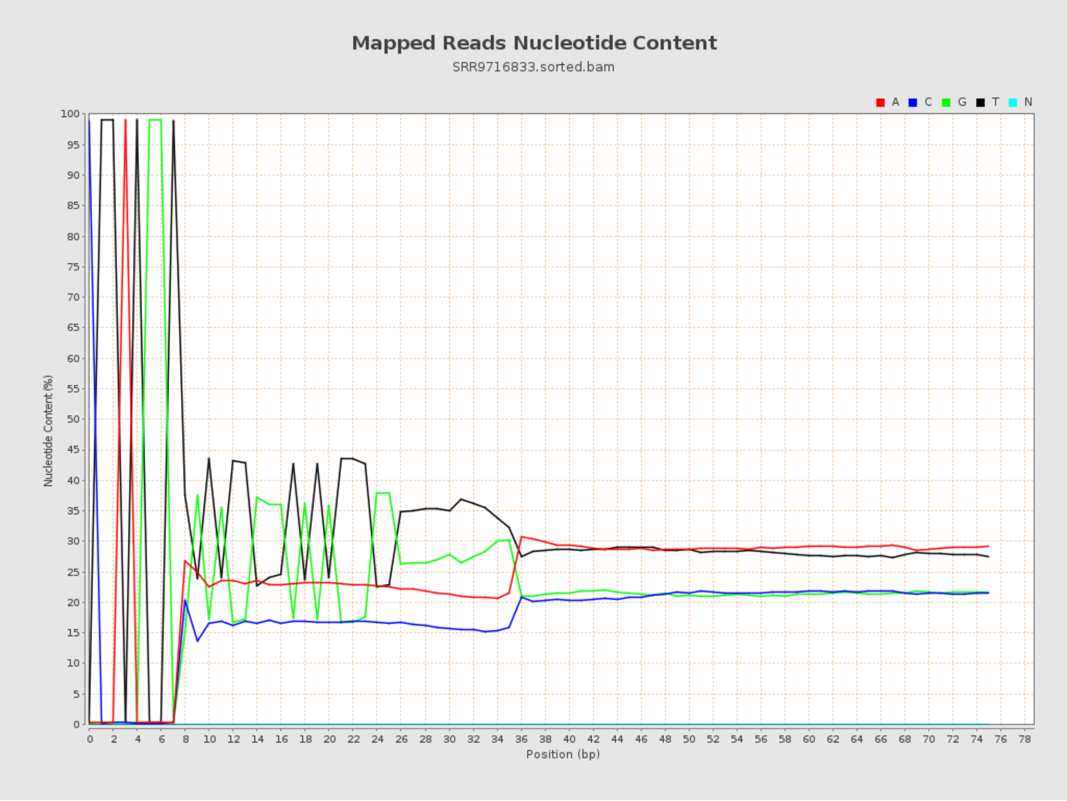
6. Results : Genome Fraction Coverage



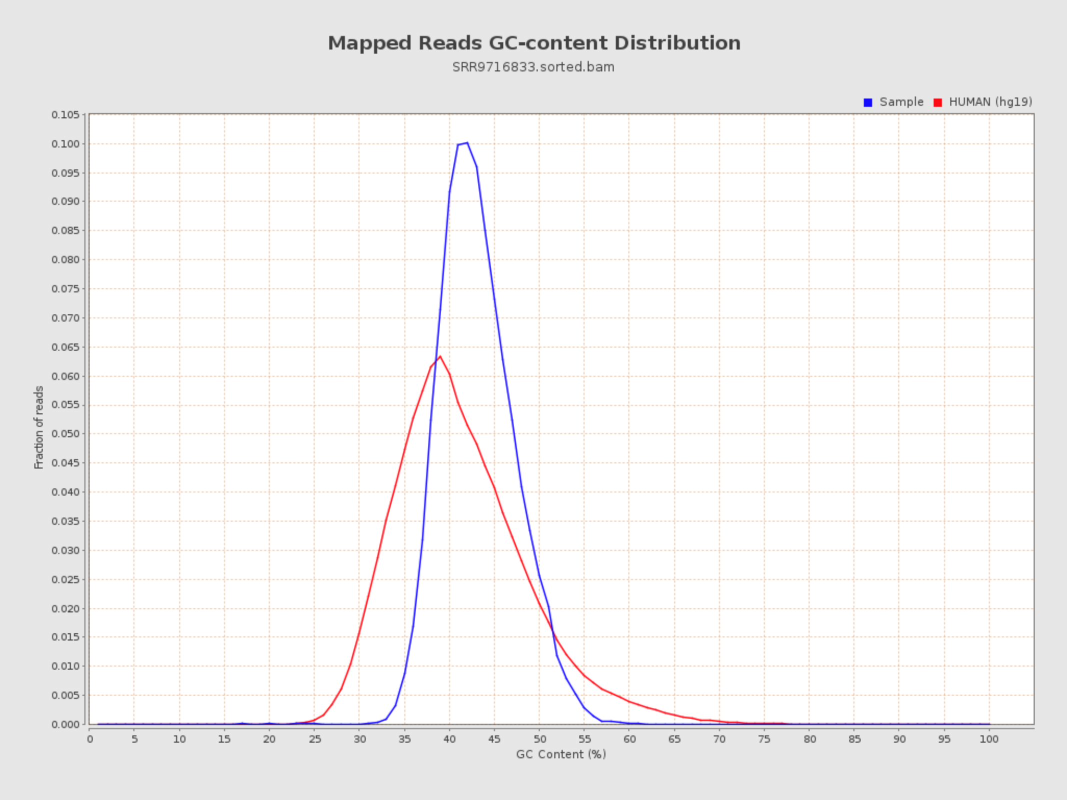
7. Results : Duplication Rate Histogram



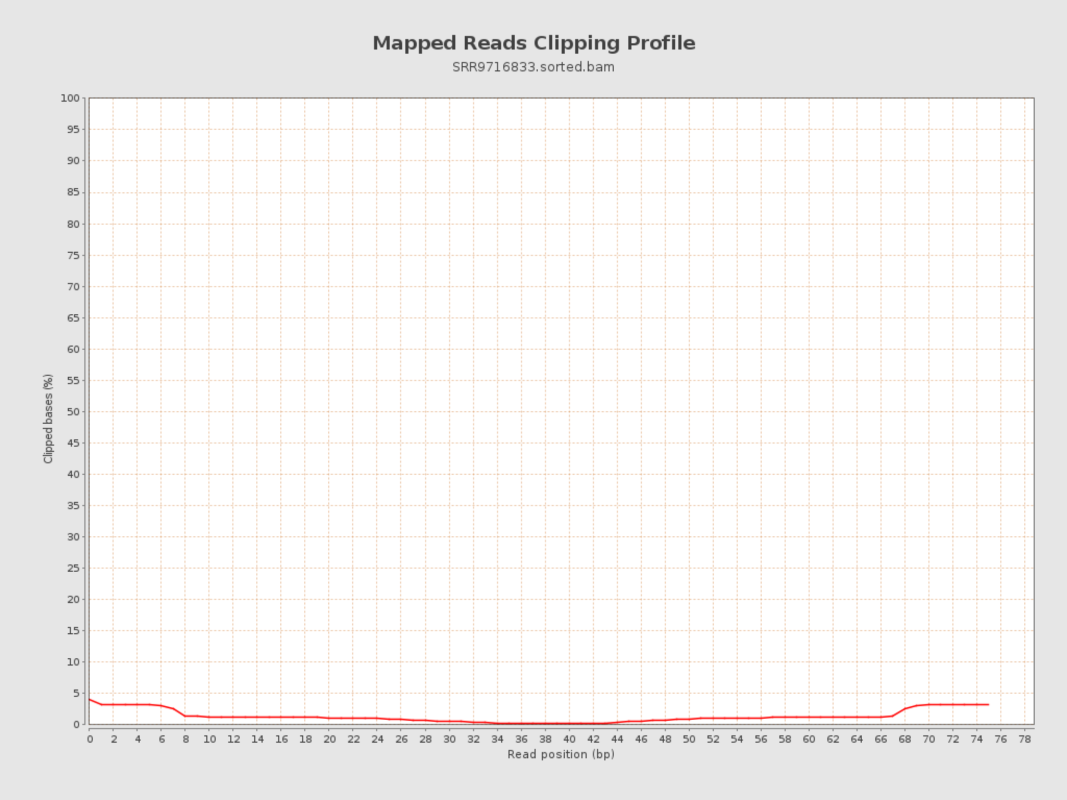
8. Results : Mapped Reads Nucleotide Content



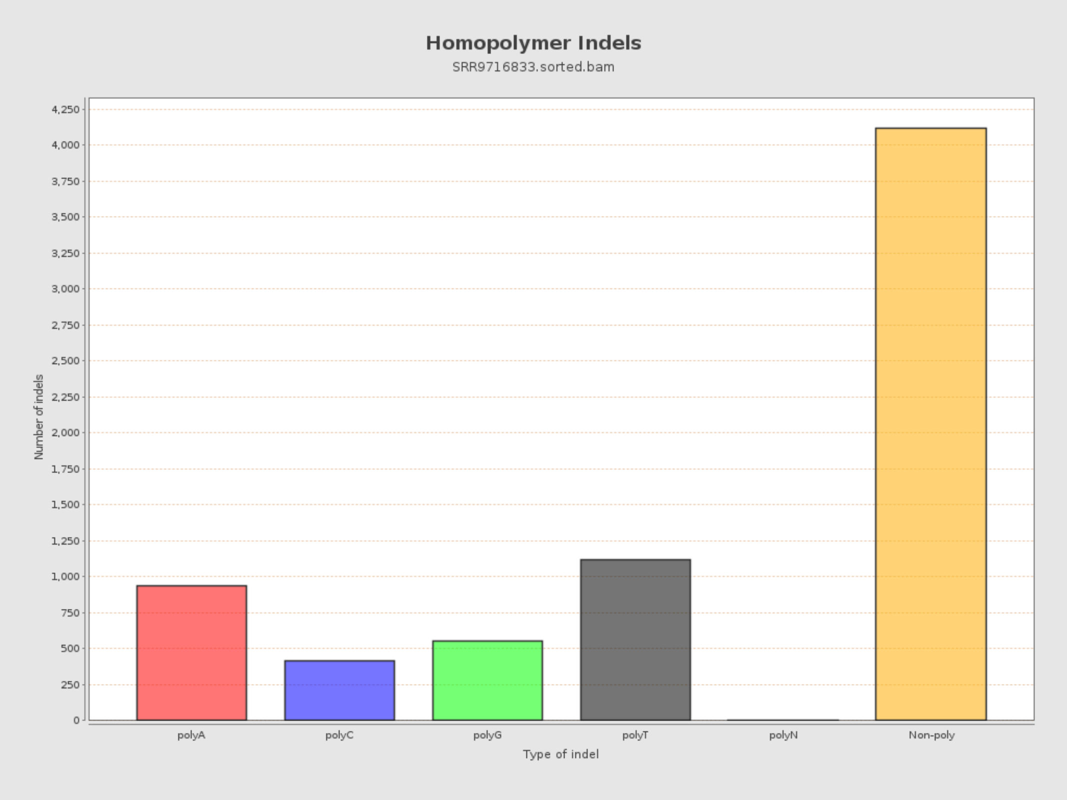
9. Results : Mapped Reads GC-content Distribution



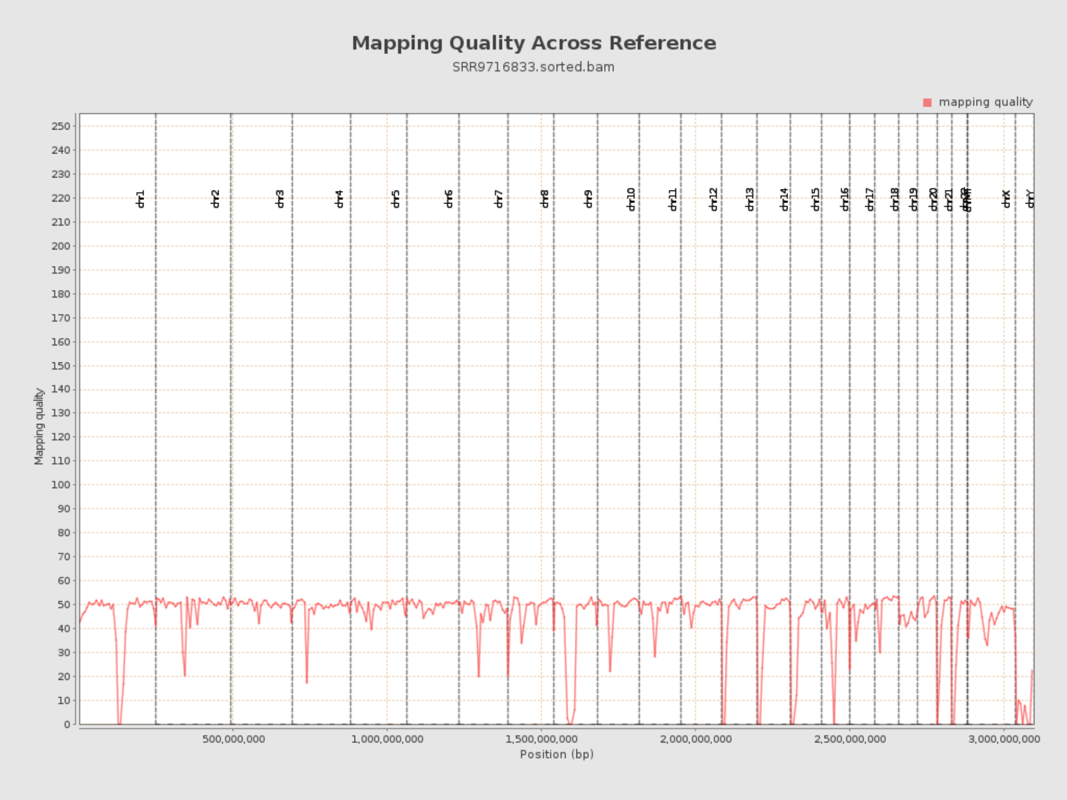
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram