Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 16:13:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716878.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_SRR9716878 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716878.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 16:13:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716878.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	411,108
Mapped reads	359,955 / 87.56%
Unmapped reads	51,153 / 12.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	940 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	5,655 / 1.38%
Duplication rate	1.21%
Clipped reads	360,501 / 87.69%

2.2. ACGT Content

Number/percentage of A's	4,982,414 / 24.15%
Number/percentage of C's	3,834,118 / 18.58%
Number/percentage of T's	6,657,716 / 32.27%
Number/percentage of G's	5,158,990 / 25%
Number/percentage of N's	210 / 0%
GC Percentage	43.59%

2.3. Coverage

Mean	0.0067

Standard Deviation	0.0937

2.4. Mapping Quality

Mean Mapping Quality	43.9

2.5. Mismatches and indels

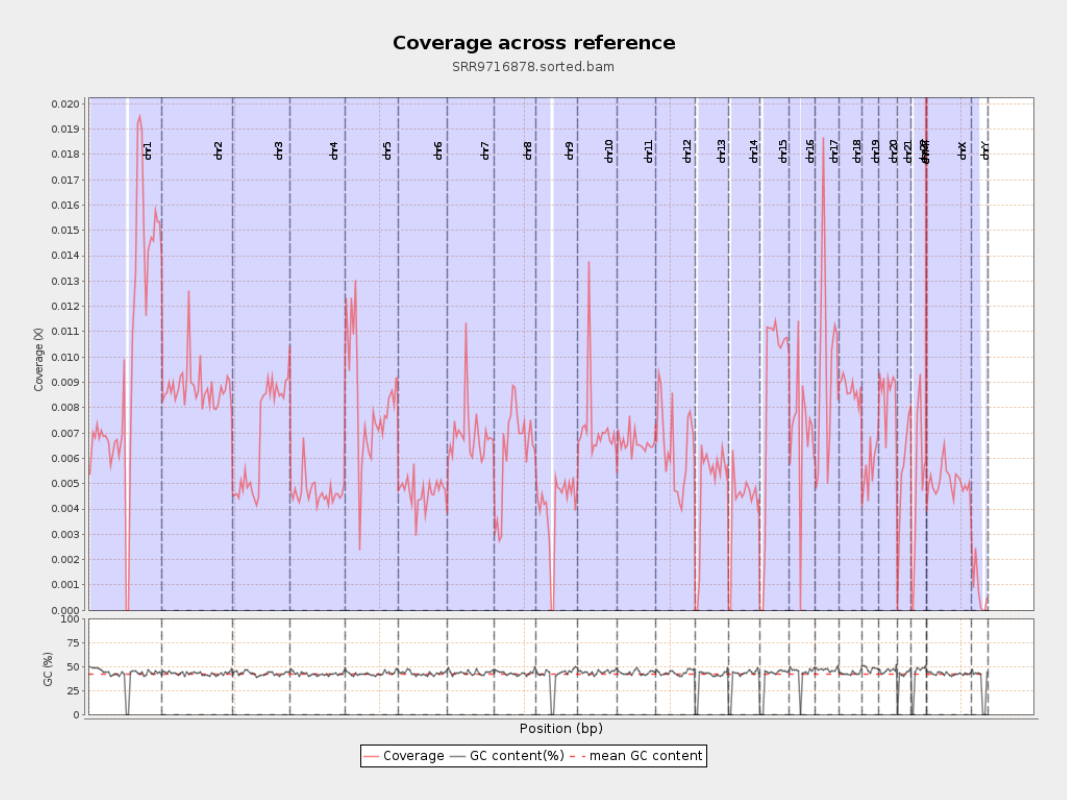
General error rate	0.5%
Mismatches	102,106
Insertions	1,017
Mapped reads with at least one insertion	0.28%
Deletions	3,616
Mapped reads with at least one deletion	1%
Homopolymer indels	44.33%

2.6. Chromosome stats

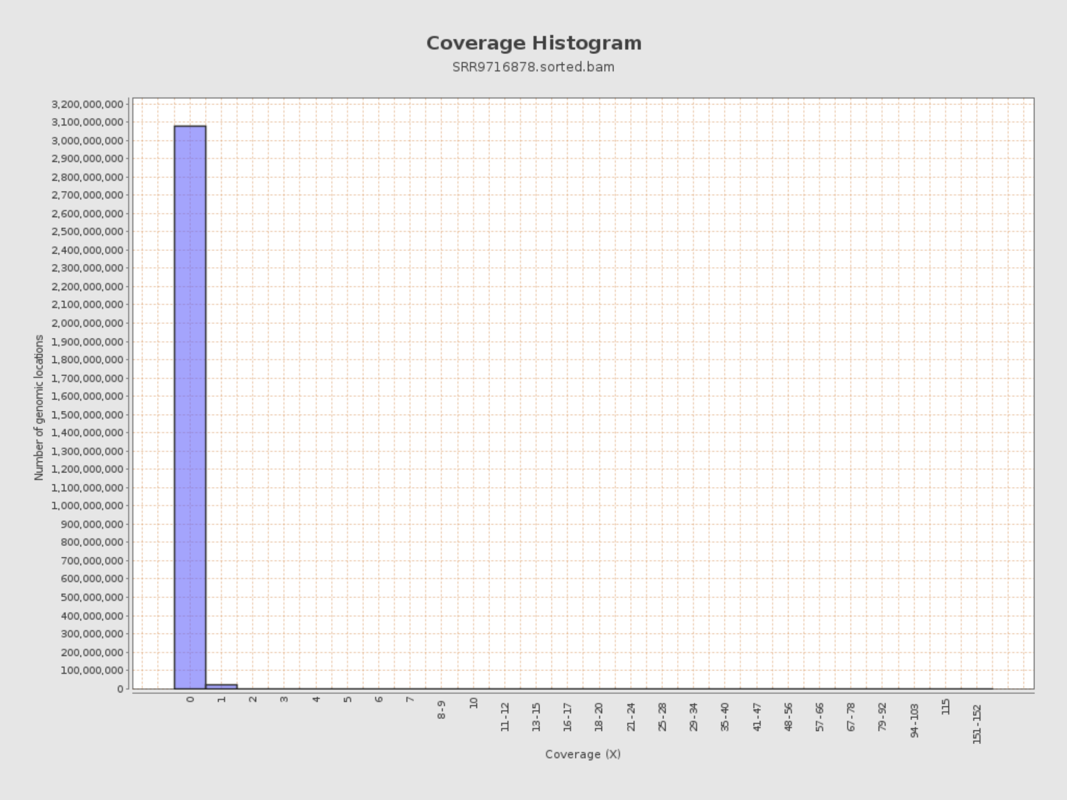
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2450829	0.0098	0.1274
chr2	243199373	2138797	0.0088	0.1207
chr3	198022430	1343054	0.0068	0.0849
chr4	191154276	891487	0.0047	0.071
chr5	180915260	1476758	0.0082	0.0924
chr6	171115067	796279	0.0047	0.073
chr7	159138663	1106863	0.007	0.1077

chr8	146364022	924552	0.0063	0.0853
chr9	141213431	566248	0.004	0.0719
chr10	135534747	977787	0.0072	0.1065
chr11	135006516	890966	0.0066	0.0916
chr12	133851895	849697	0.0063	0.0818
chr13	115169878	558084	0.0048	0.0712
chr14	107349540	442958	0.0041	0.0667
chr15	102531392	890620	0.0087	0.0959
chr16	90354753	634971	0.007	0.0894
chr17	81195210	791975	0.0098	0.1031
chr18	78077248	683419	0.0088	0.1269
chr19	59128983	336299	0.0057	0.1009
chr20	63025520	540447	0.0086	0.0951
chr21	48129895	264991	0.0055	0.0772
chr22	51304566	246817	0.0048	0.071
chrMT	16571	1164	0.0702	0.2556
chrX	155270560	787400	0.0051	0.0771
chrY	59373566	46778	0.0008	0.0312

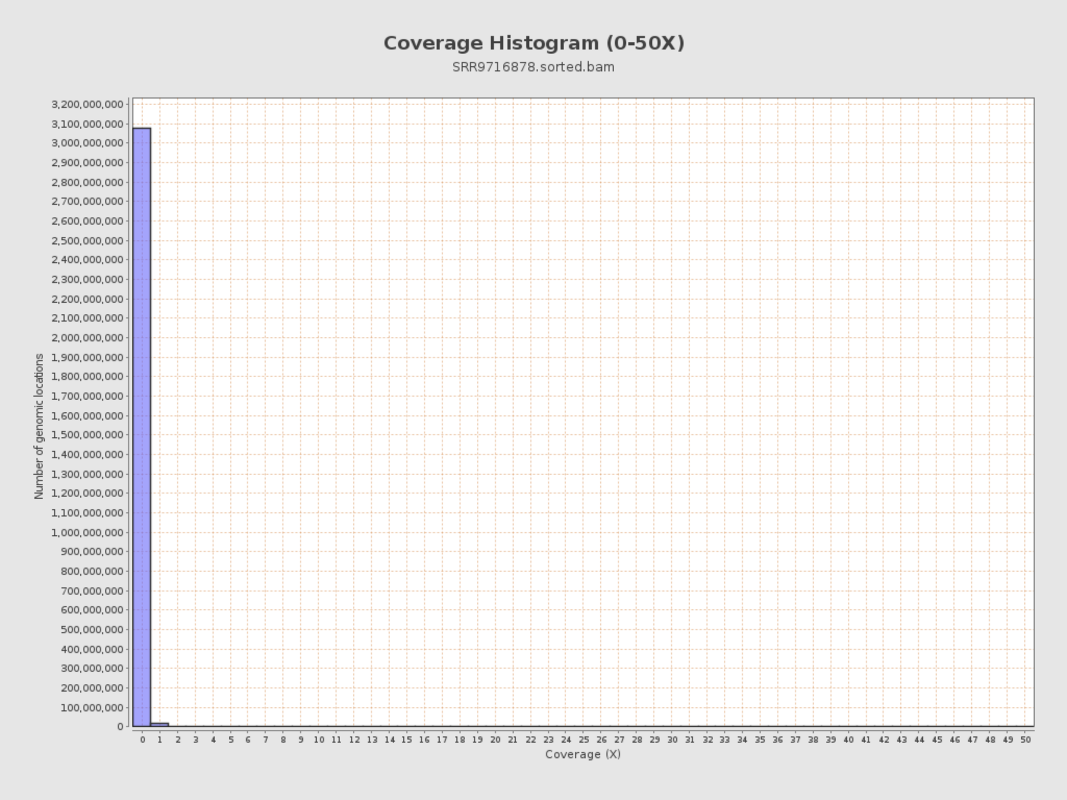
3. Results : Coverage across reference



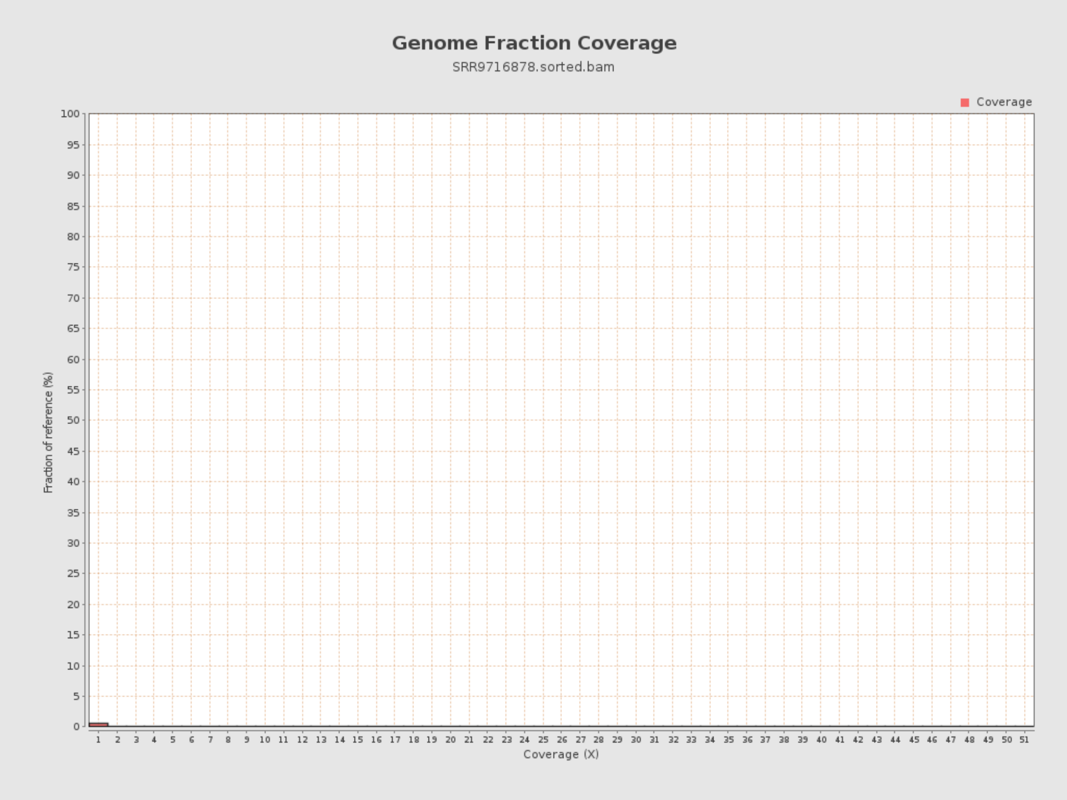
4. Results : Coverage Histogram



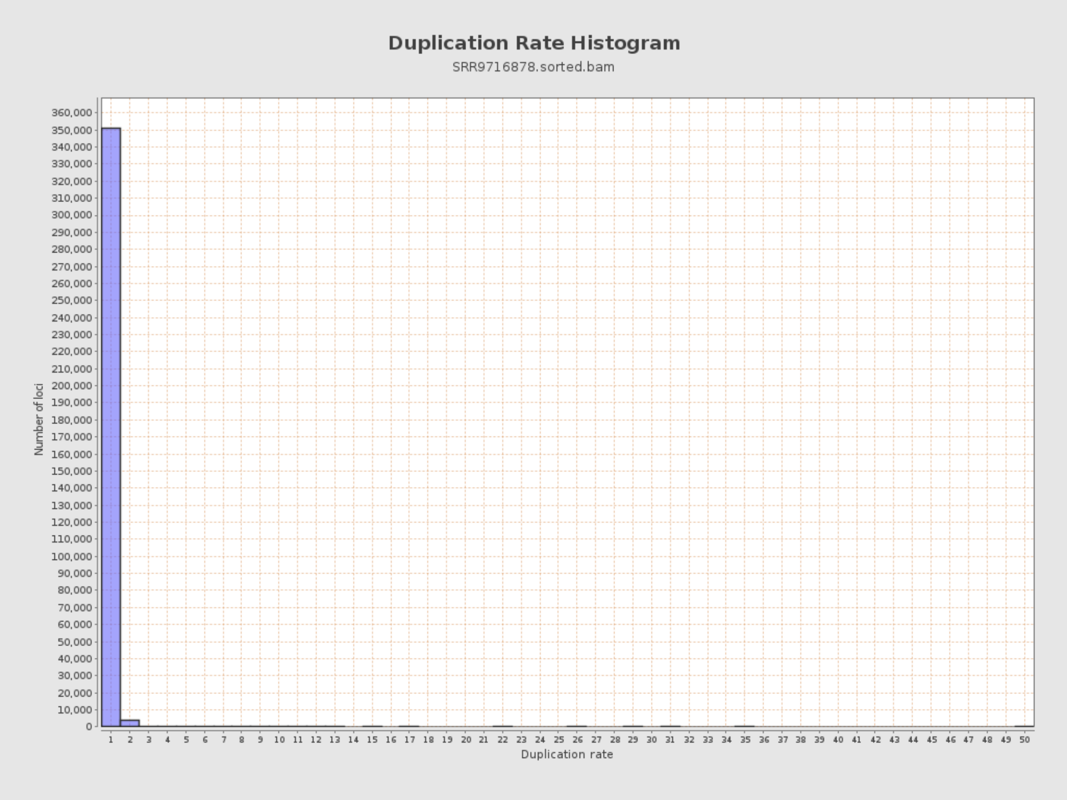
5. Results : Coverage Histogram (0-50X)



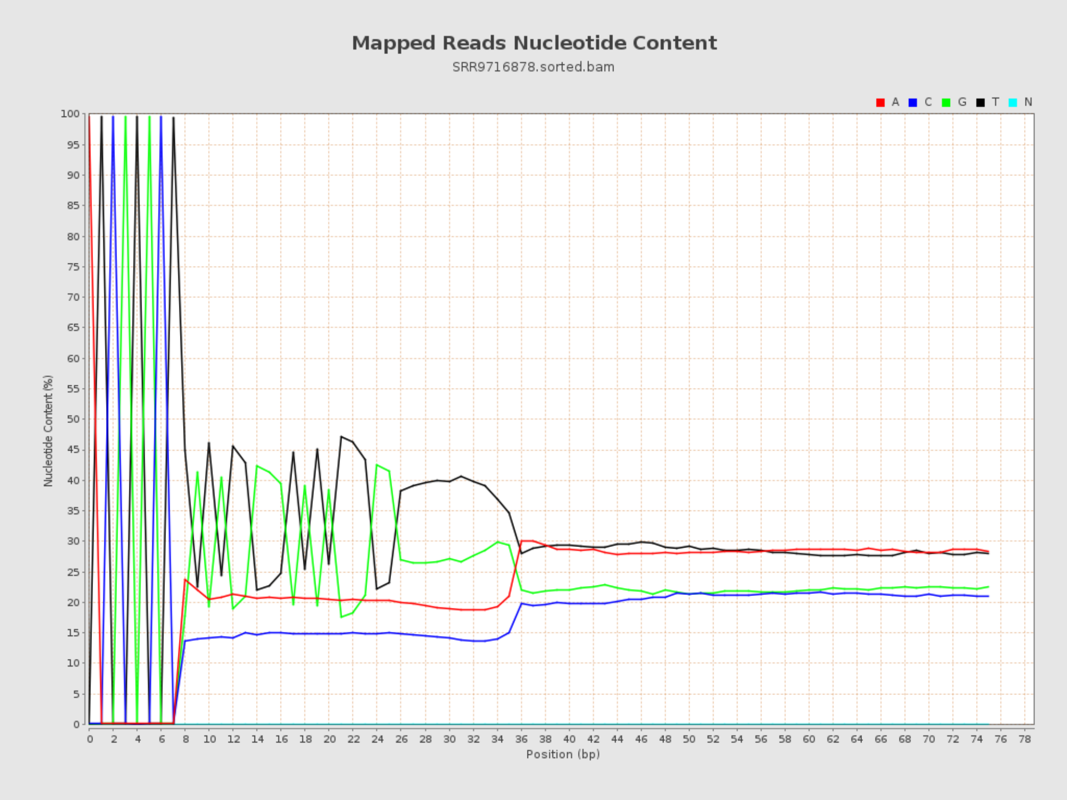
6. Results : Genome Fraction Coverage



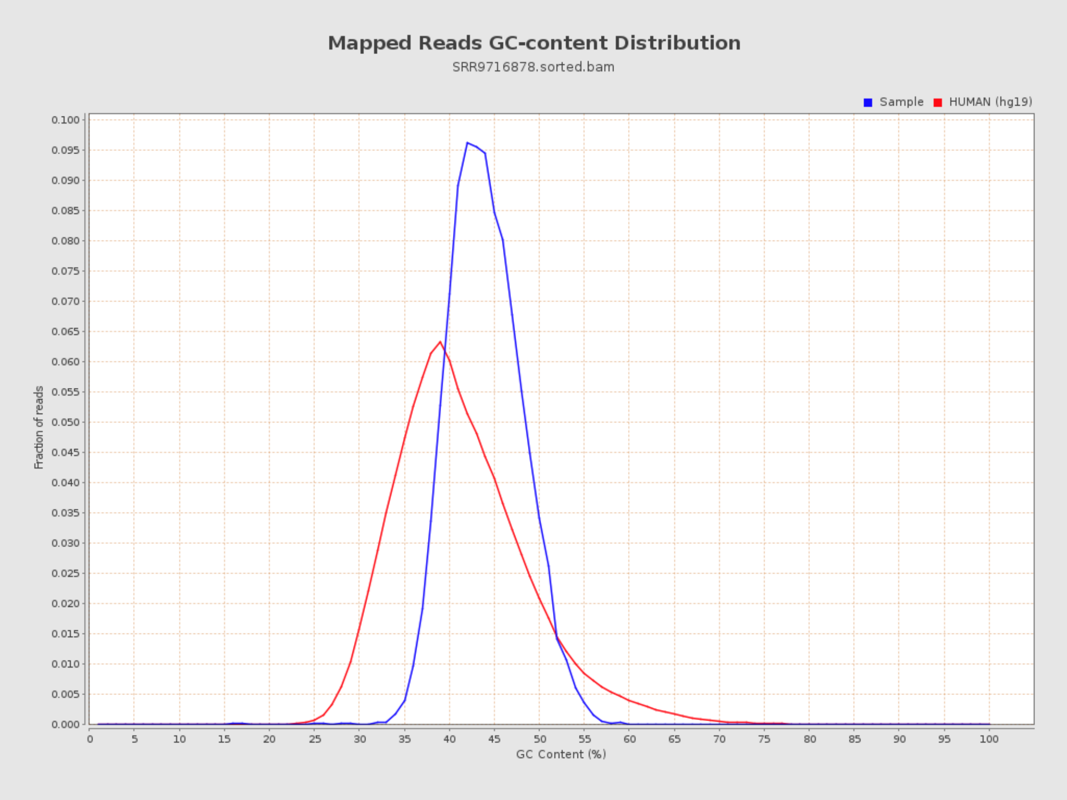
7. Results : Duplication Rate Histogram



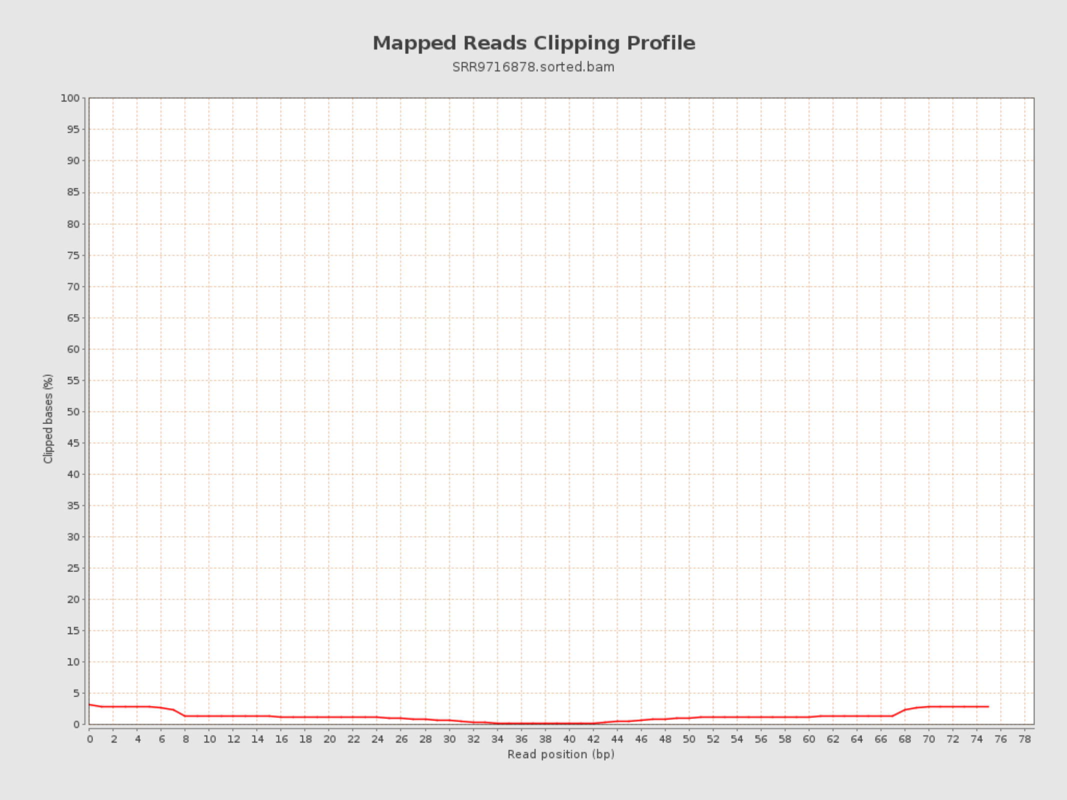
8. Results : Mapped Reads Nucleotide Content



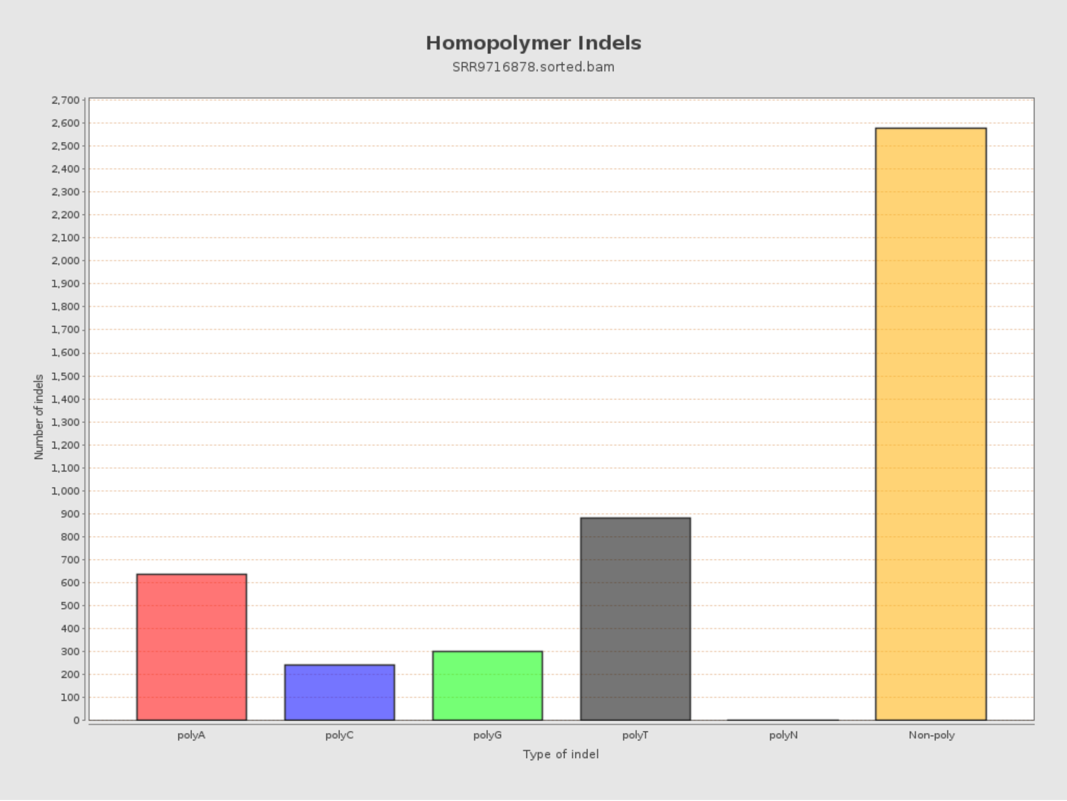
9. Results : Mapped Reads GC-content Distribution



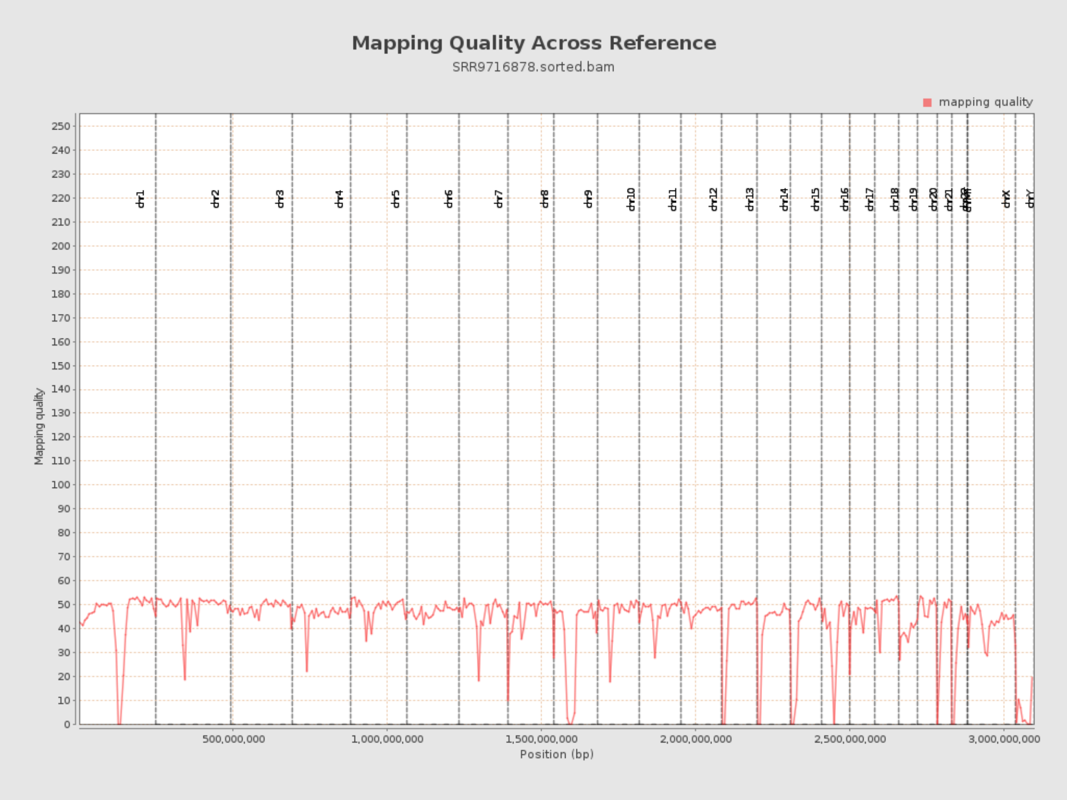
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram