Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:31:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716178.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_SRR9716178 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716178.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:31:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716178.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	973,626
Mapped reads	885,942 / 90.99%
Unmapped reads	87,684 / 9.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,417 / 1.79%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	23,248 / 2.39%
Duplication rate	1.89%
Clipped reads	901,633 / 92.61%

2.2. ACGT Content

Number/percentage of A's	18,642,819 / 26.69%
Number/percentage of C's	13,163,369 / 18.84%
Number/percentage of T's	21,192,848 / 30.34%
Number/percentage of G's	16,848,325 / 24.12%
Number/percentage of N's	4,703 / 0.01%
GC Percentage	42.96%

2.3. Coverage

Mean	0.0226

Standard Deviation	0.2179

2.4. Mapping Quality

Mean Mapping Quality	47.64

2.5. Mismatches and indels

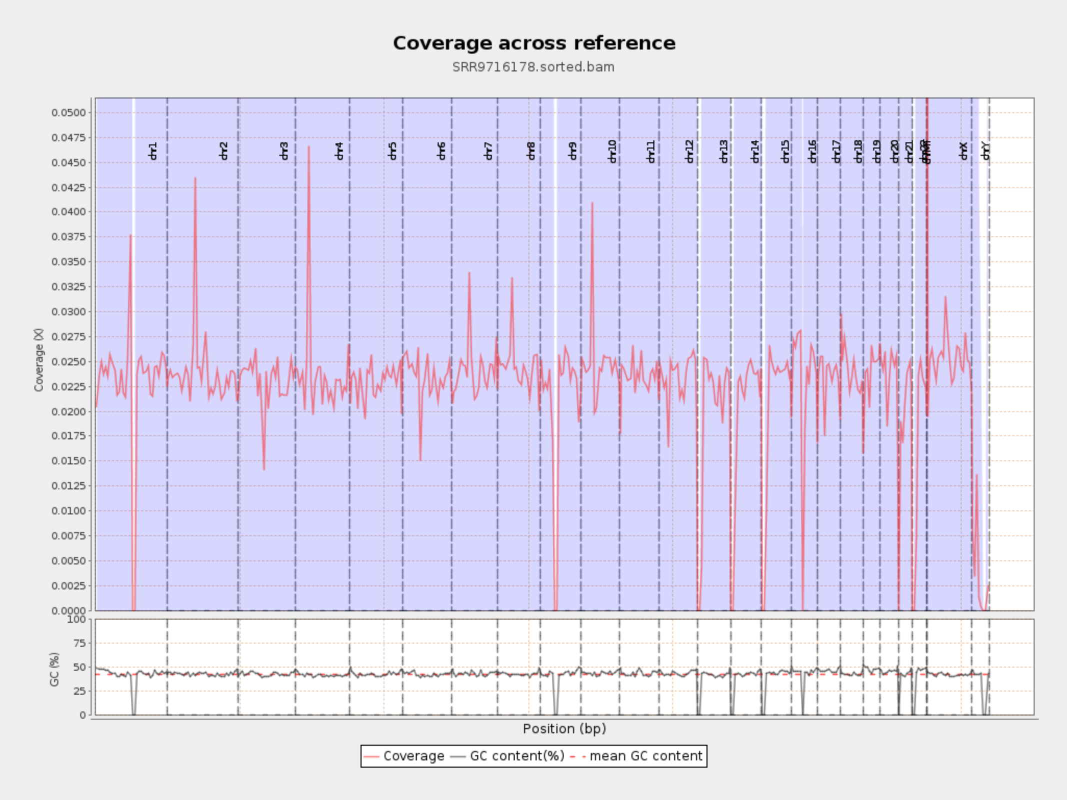
General error rate	0.67%
Mismatches	454,532
Insertions	6,065
Mapped reads with at least one insertion	0.67%
Deletions	16,760
Mapped reads with at least one deletion	1.86%
Homopolymer indels	42.17%

2.6. Chromosome stats

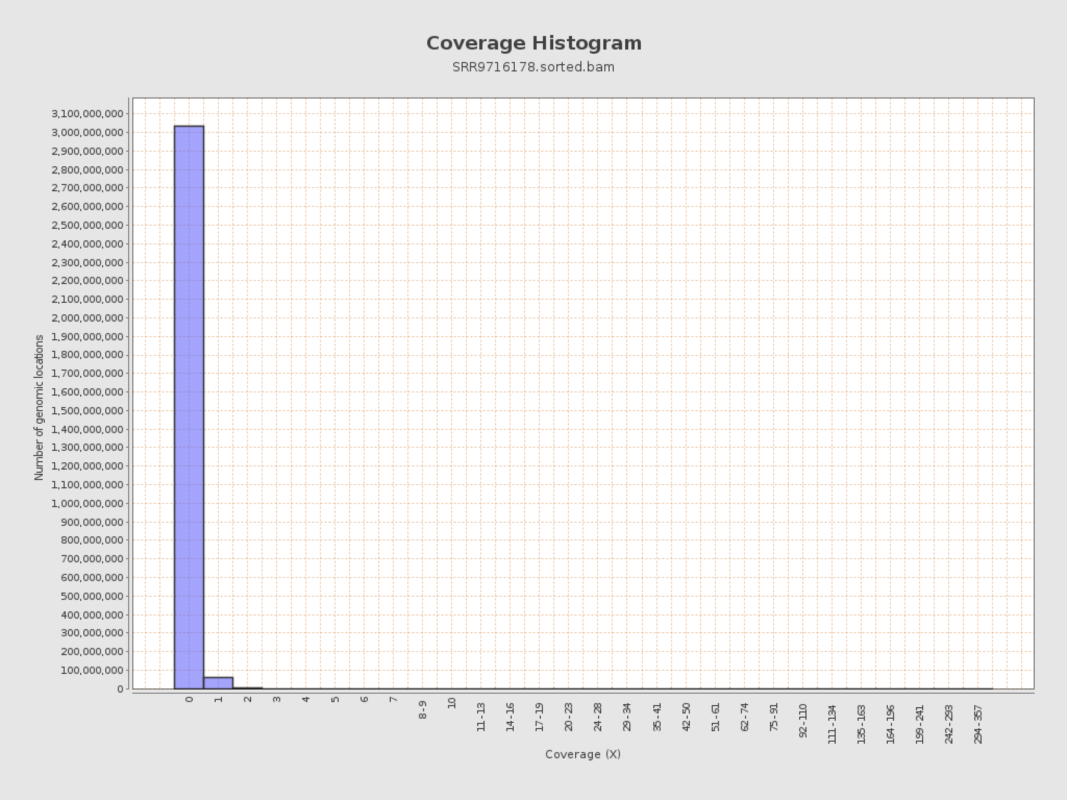
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5674823	0.0228	0.351
chr2	243199373	5852756	0.0241	0.2571
chr3	198022430	4549162	0.023	0.161
chr4	191154276	4545732	0.0238	0.1948
chr5	180915260	4182799	0.0231	0.1626
chr6	171115067	4004341	0.0234	0.1716
chr7	159138663	3851712	0.0242	0.2714

chr8	146364022	3594347	0.0246	0.2618
chr9	141213431	2926010	0.0207	0.1983
chr10	135534747	3392758	0.025	0.2337
chr11	135006516	3197204	0.0237	0.2166
chr12	133851895	3130611	0.0234	0.1636
chr13	115169878	2208284	0.0192	0.147
chr14	107349540	2088050	0.0195	0.154
chr15	102531392	2038956	0.0199	0.15
chr16	90354753	2046919	0.0227	0.1683
chr17	81195210	1902595	0.0234	0.1752
chr18	78077248	1882764	0.0241	0.293
chr19	59128983	1420668	0.024	0.2612
chr20	63025520	1498074	0.0238	0.1703
chr21	48129895	927371	0.0193	0.1641
chr22	51304566	827430	0.0161	0.1354
chrMT	16571	5870	0.3542	0.6158
chrX	155270560	3928649	0.0253	0.1832
chrY	59373566	206046	0.0035	0.129

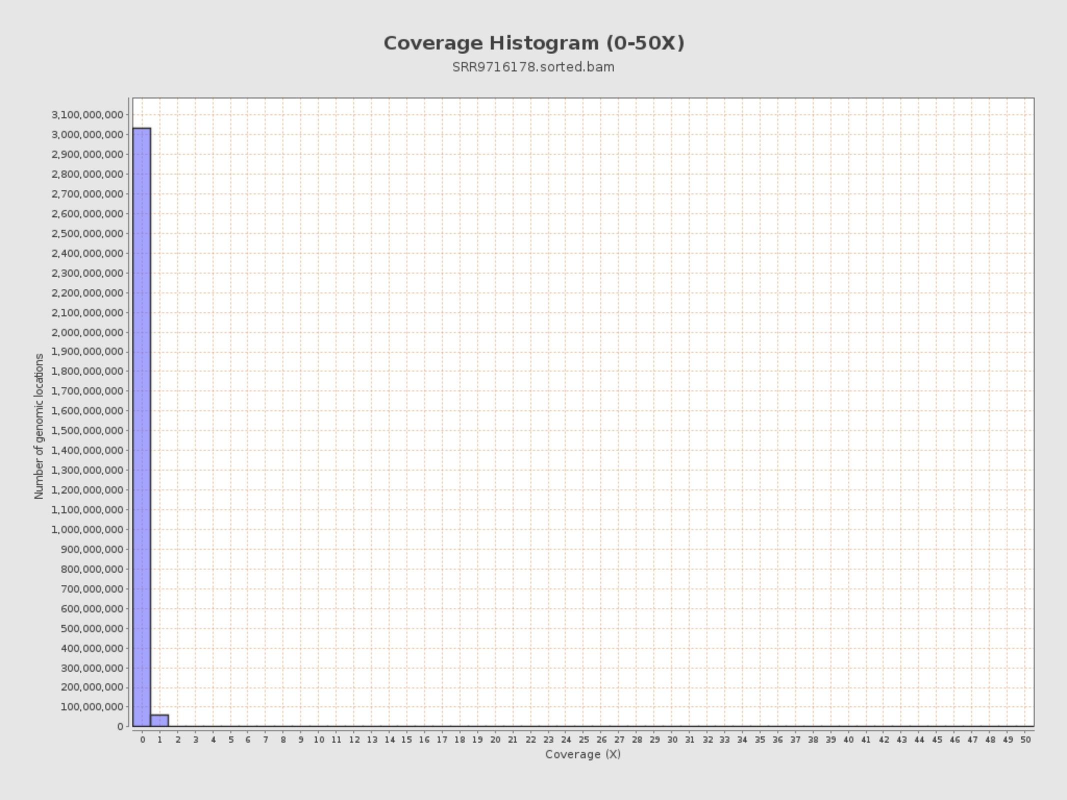
3. Results : Coverage across reference



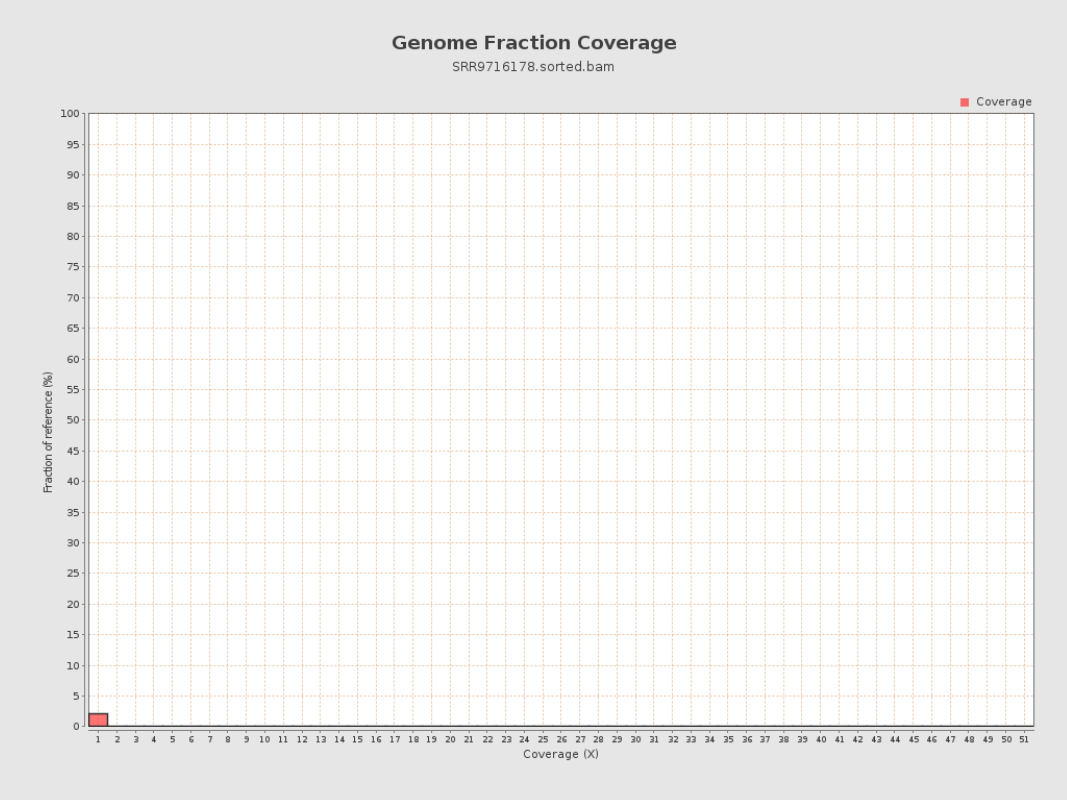
4. Results : Coverage Histogram



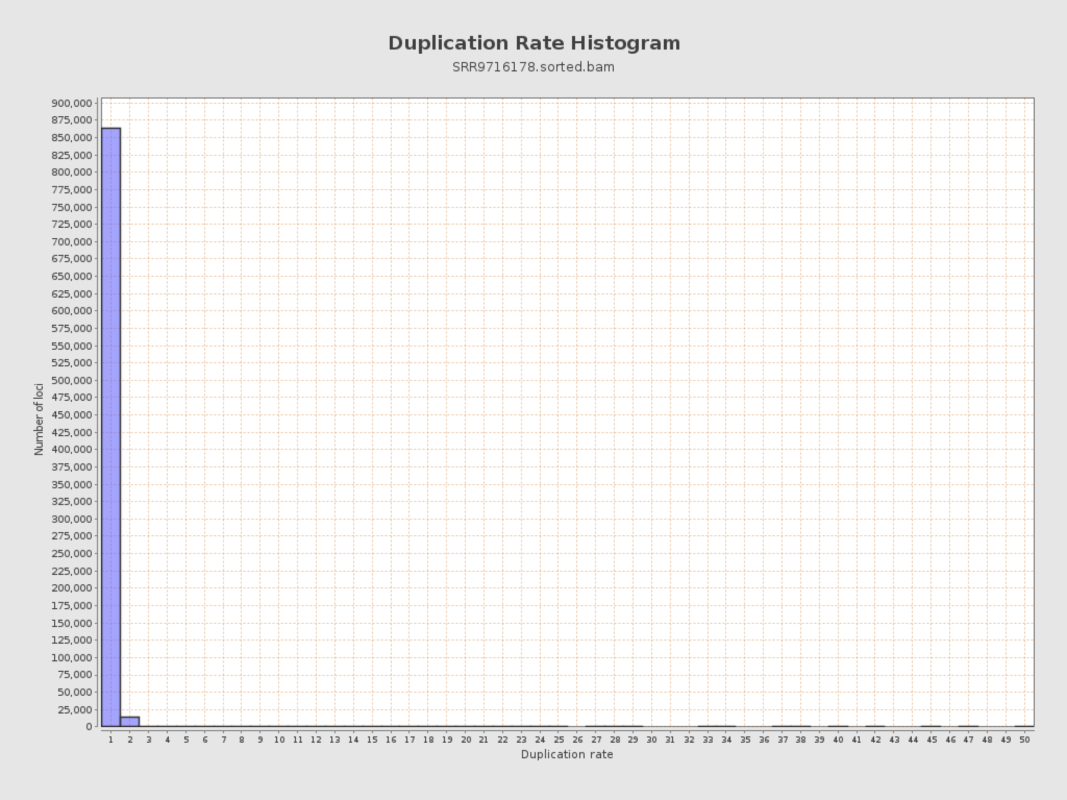
5. Results : Coverage Histogram (0-50X)



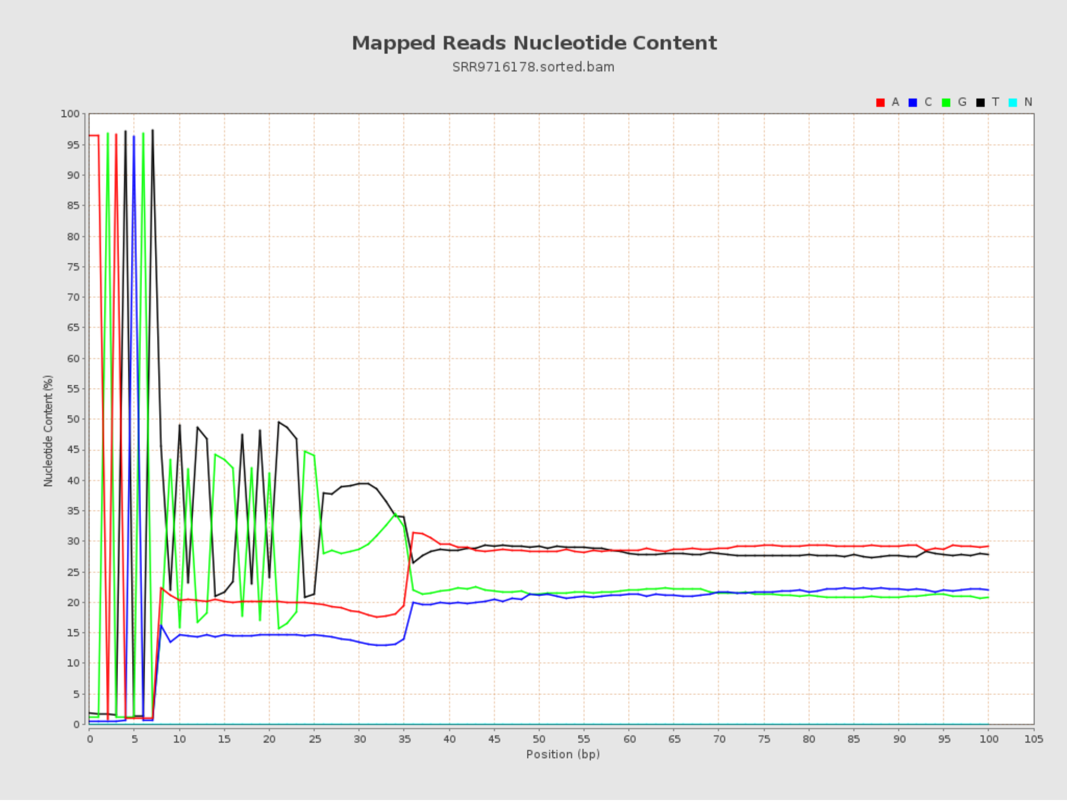
6. Results : Genome Fraction Coverage



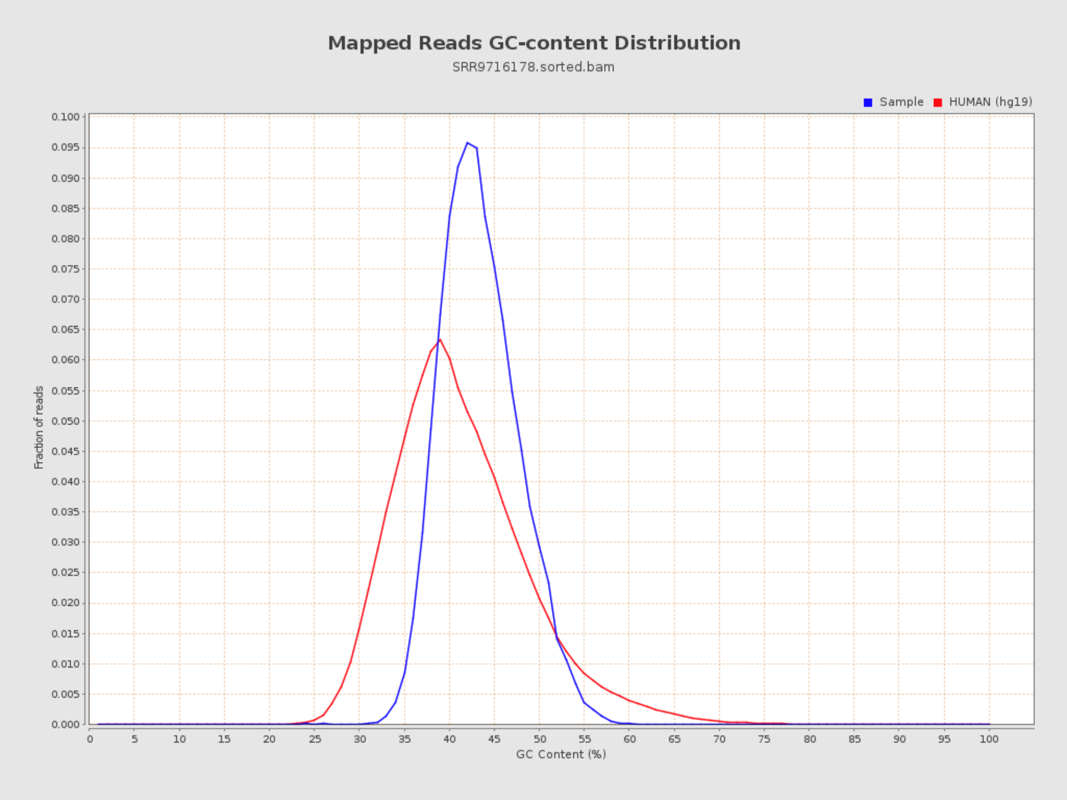
7. Results : Duplication Rate Histogram



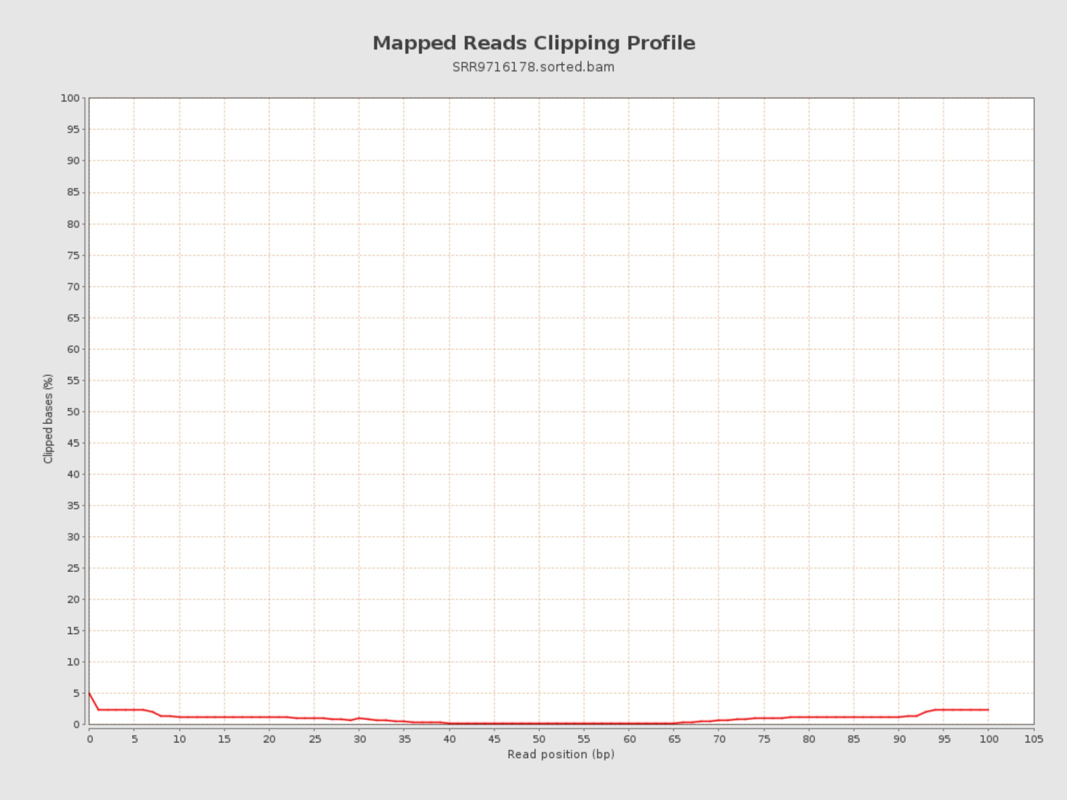
8. Results : Mapped Reads Nucleotide Content



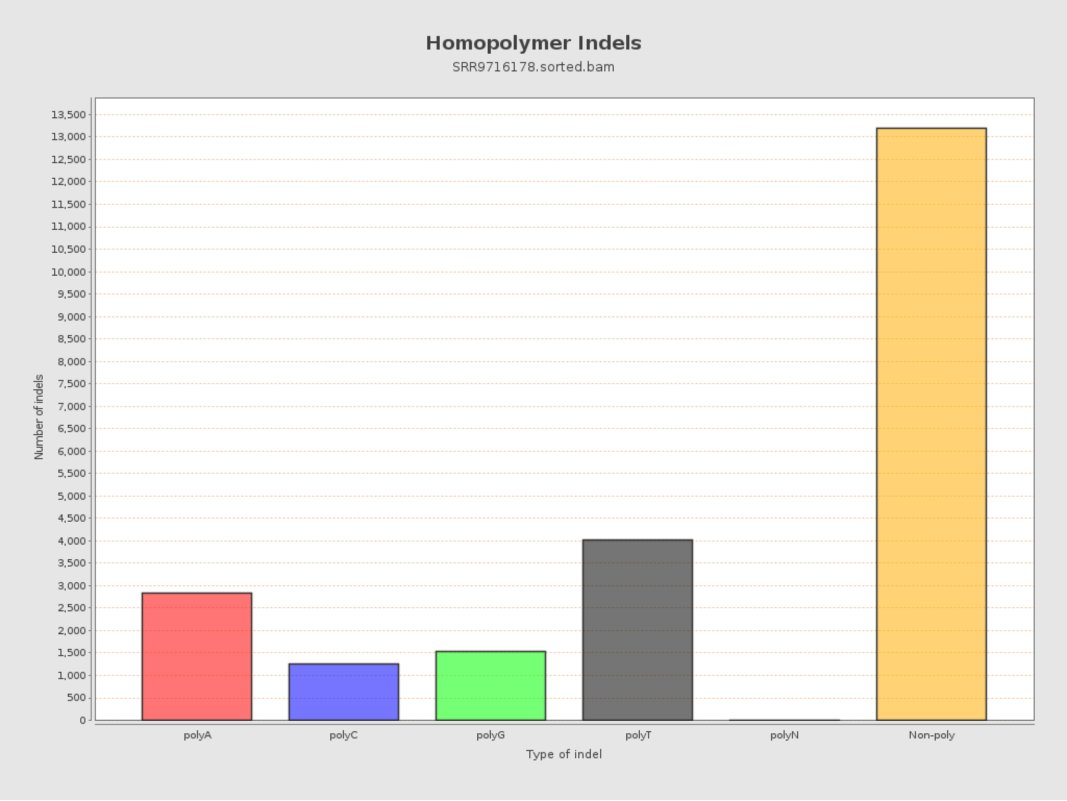
9. Results : Mapped Reads GC-content Distribution



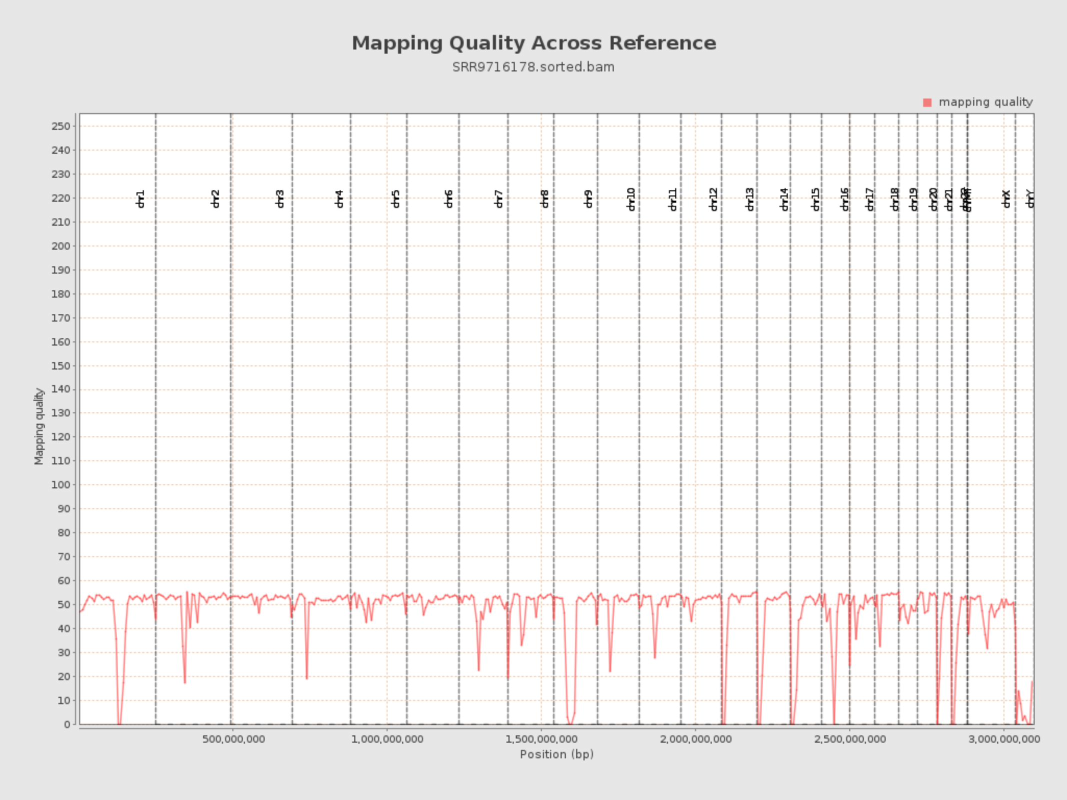
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram