Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 22:48:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716578.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_SRR9716578 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716578.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 22:48:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716578.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,877,551
Mapped reads	1,709,669 / 91.06%
Unmapped reads	167,882 / 8.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,397 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	57,798 / 3.08%
Duplication rate	2.33%
Clipped reads	1,717,212 / 91.46%

2.2. ACGT Content

Number/percentage of A's	25,991,290 / 26%
Number/percentage of C's	19,395,250 / 19.4%
Number/percentage of T's	31,328,483 / 31.34%
Number/percentage of G's	23,255,671 / 23.26%
Number/percentage of N's	1,289 / 0%
GC Percentage	42.66%

2.3. Coverage

Mean	0.0323

Standard Deviation	0.3166

2.4. Mapping Quality

Mean Mapping Quality	44.49

2.5. Mismatches and indels

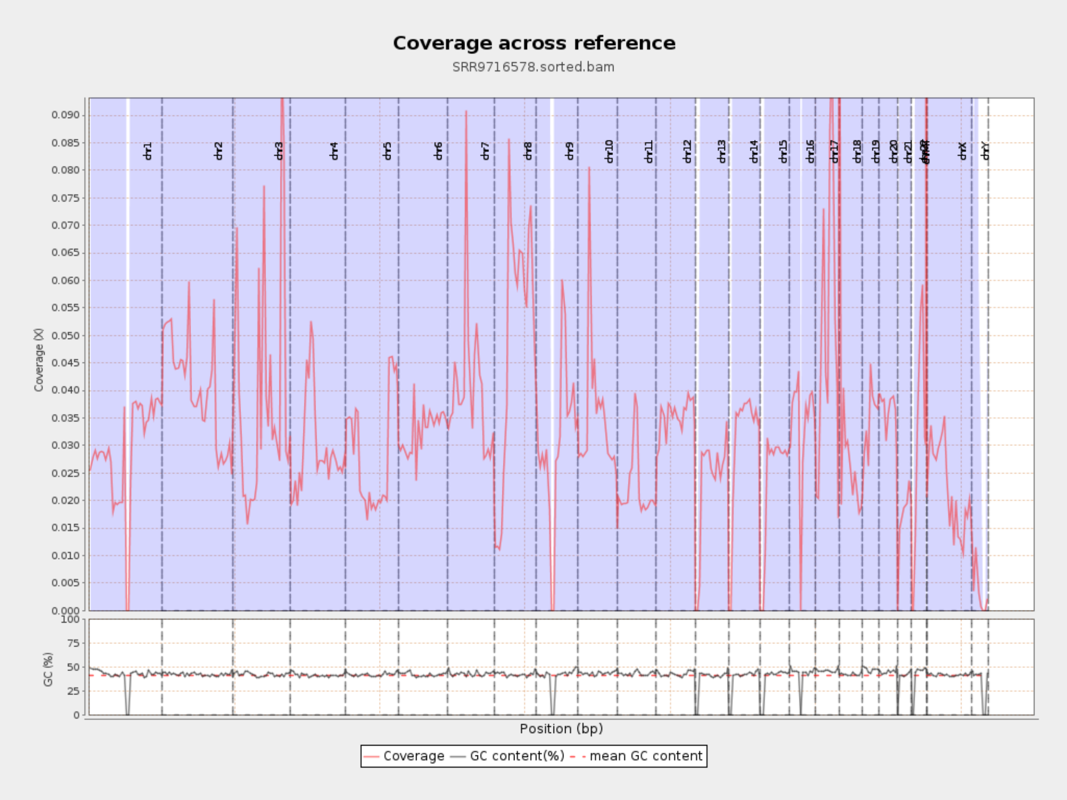
General error rate	0.51%
Mismatches	498,490
Insertions	6,289
Mapped reads with at least one insertion	0.37%
Deletions	17,988
Mapped reads with at least one deletion	1.04%
Homopolymer indels	40.86%

2.6. Chromosome stats

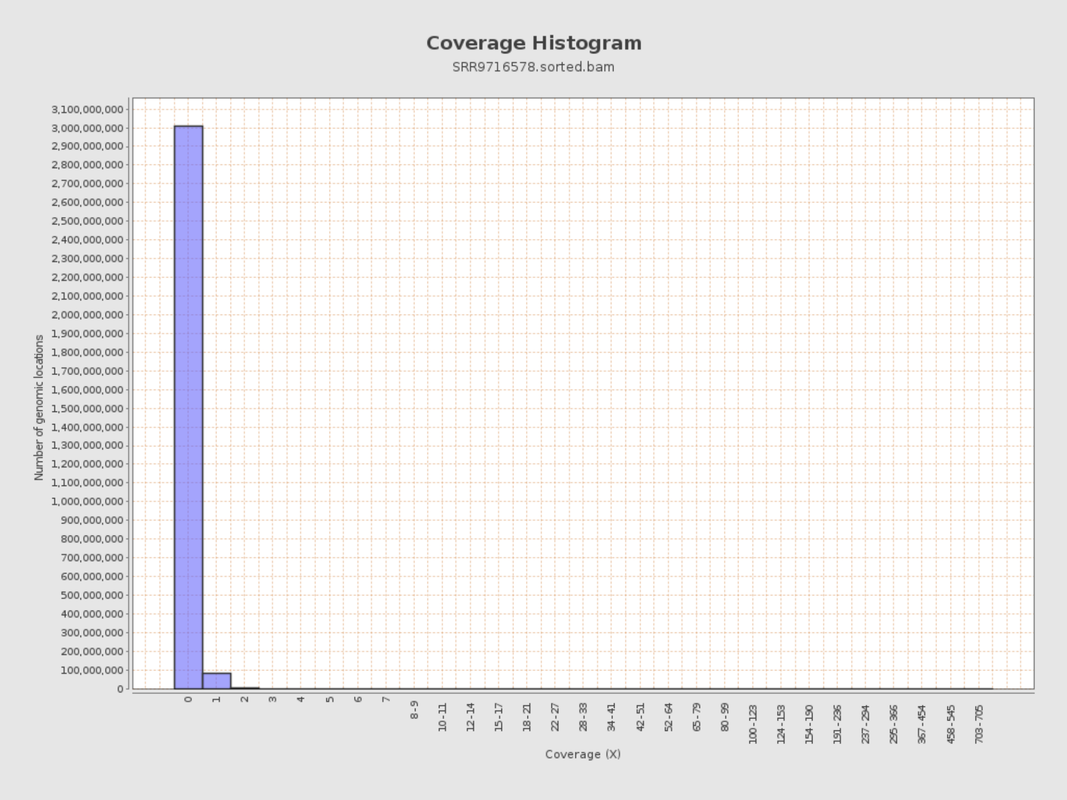
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7132910	0.0286	0.4042
chr2	243199373	9880371	0.0406	0.3786
chr3	198022430	7697499	0.0389	0.2292
chr4	191154276	5629650	0.0295	0.2039
chr5	180915260	5095598	0.0282	0.1837
chr6	171115067	5595524	0.0327	0.213
chr7	159138663	6442291	0.0405	0.7519

chr8	146364022	7267587	0.0497	0.3338
chr9	141213431	4261767	0.0302	0.2271
chr10	135534747	4775932	0.0352	0.4165
chr11	135006516	2991092	0.0222	0.2092
chr12	133851895	4710380	0.0352	0.2305
chr13	115169878	2651991	0.023	0.1652
chr14	107349540	3277574	0.0305	0.1956
chr15	102531392	2424324	0.0236	0.1699
chr16	90354753	3055960	0.0338	0.2125
chr17	81195210	4166446	0.0513	0.2588
chr18	78077248	2372846	0.0304	0.3641
chr19	59128983	2040019	0.0345	0.376
chr20	63025520	2300969	0.0365	0.2205
chr21	48129895	822230	0.0171	0.1526
chr22	51304566	1546975	0.0302	0.1889
chrMT	16571	140829	8.4985	5.5759
chrX	155270560	3502781	0.0226	0.1863
chrY	59373566	217012	0.0037	0.0965

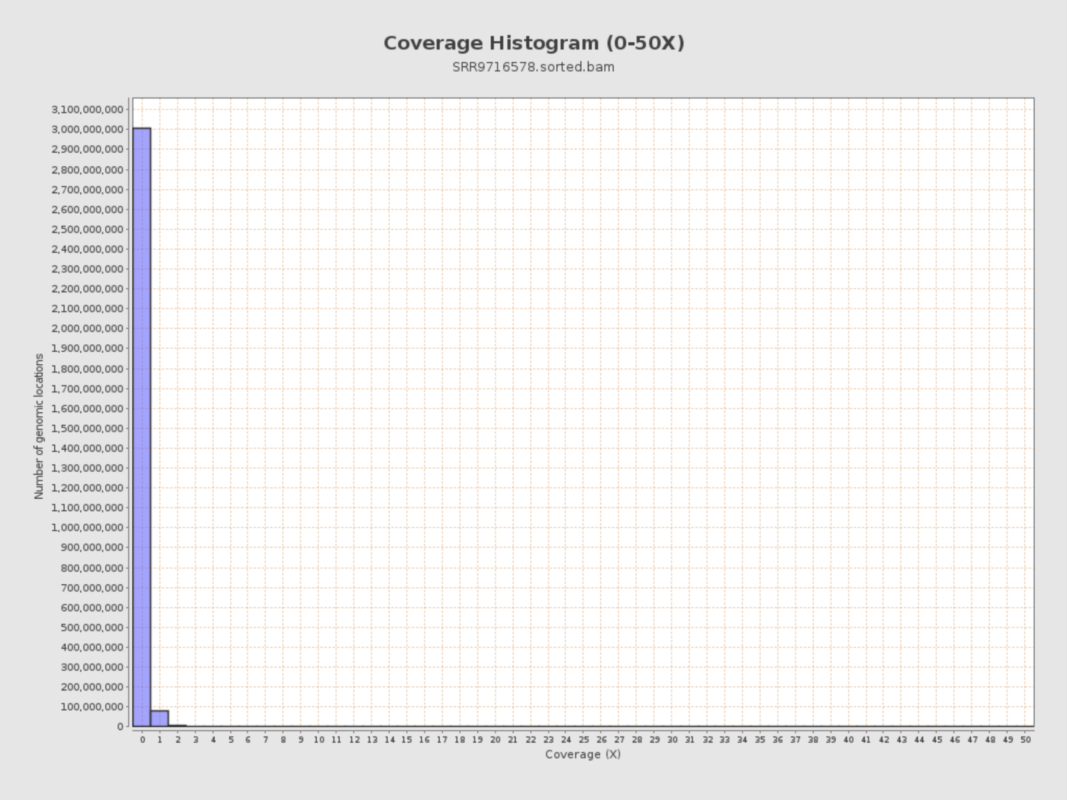
3. Results : Coverage across reference



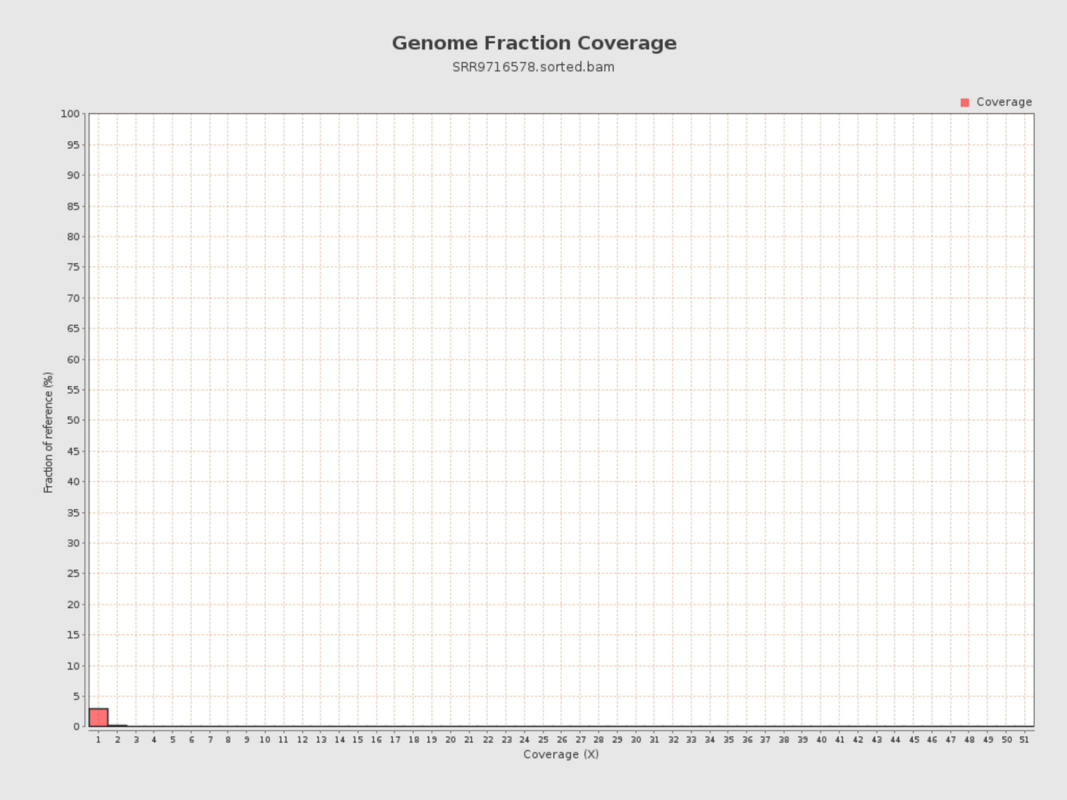
4. Results : Coverage Histogram



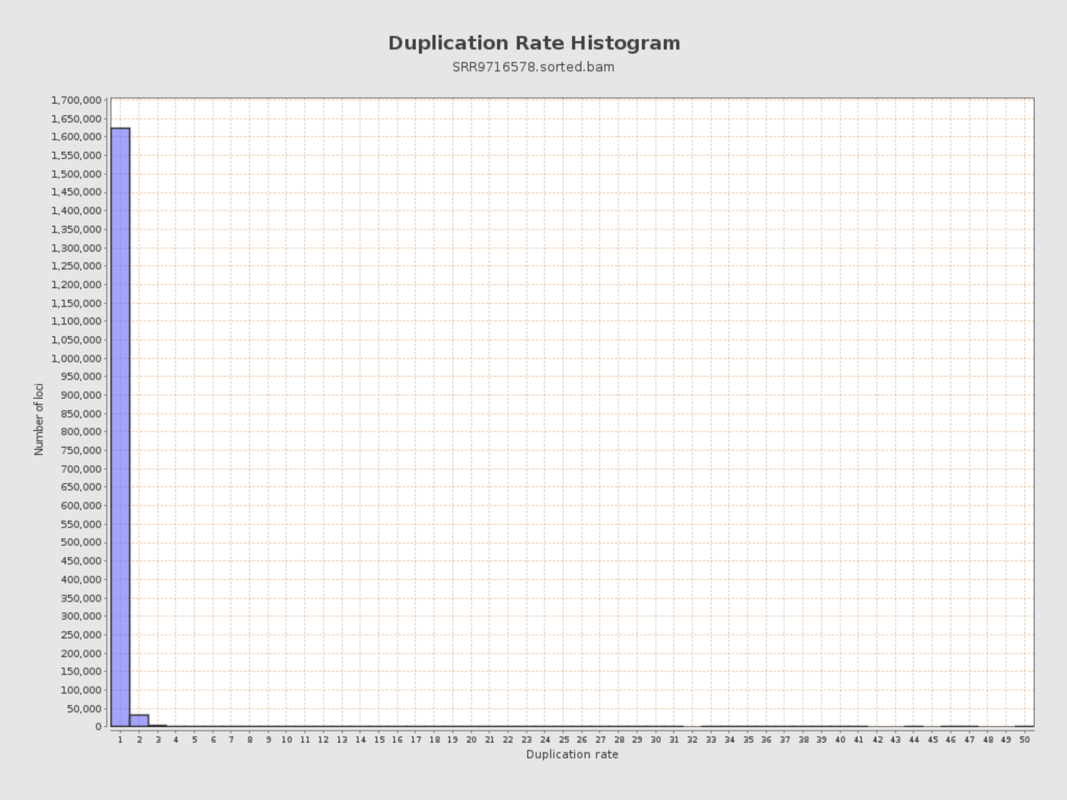
5. Results : Coverage Histogram (0-50X)



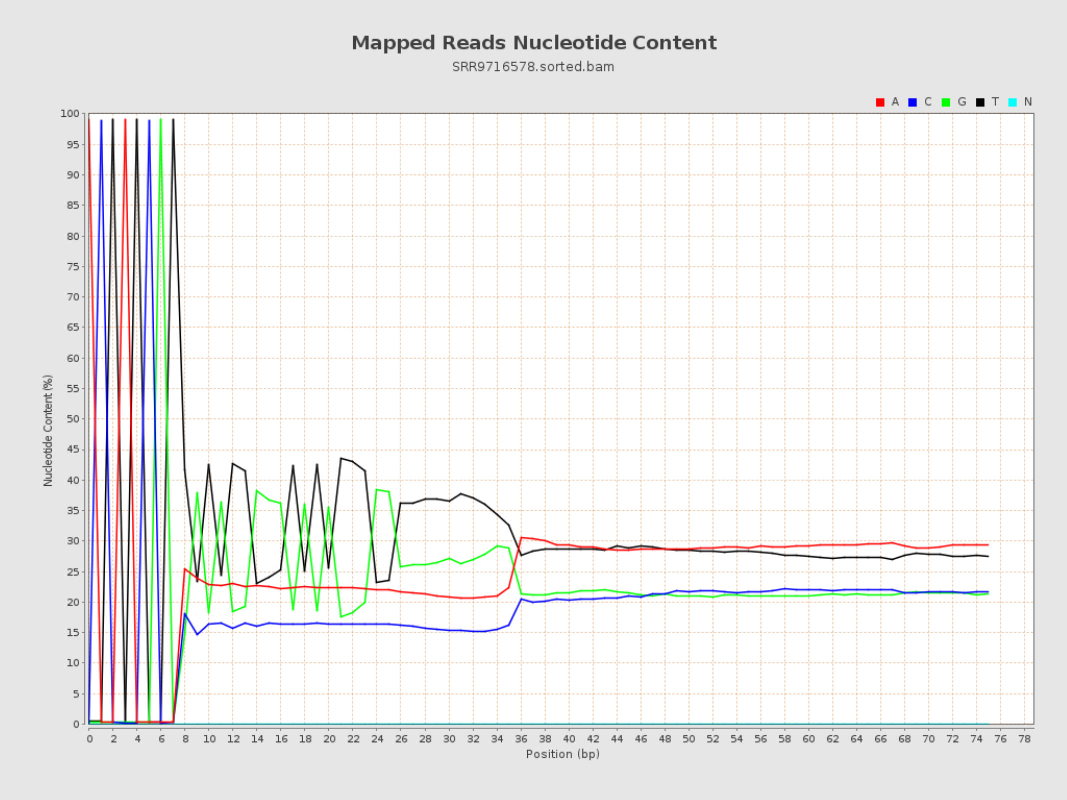
6. Results : Genome Fraction Coverage



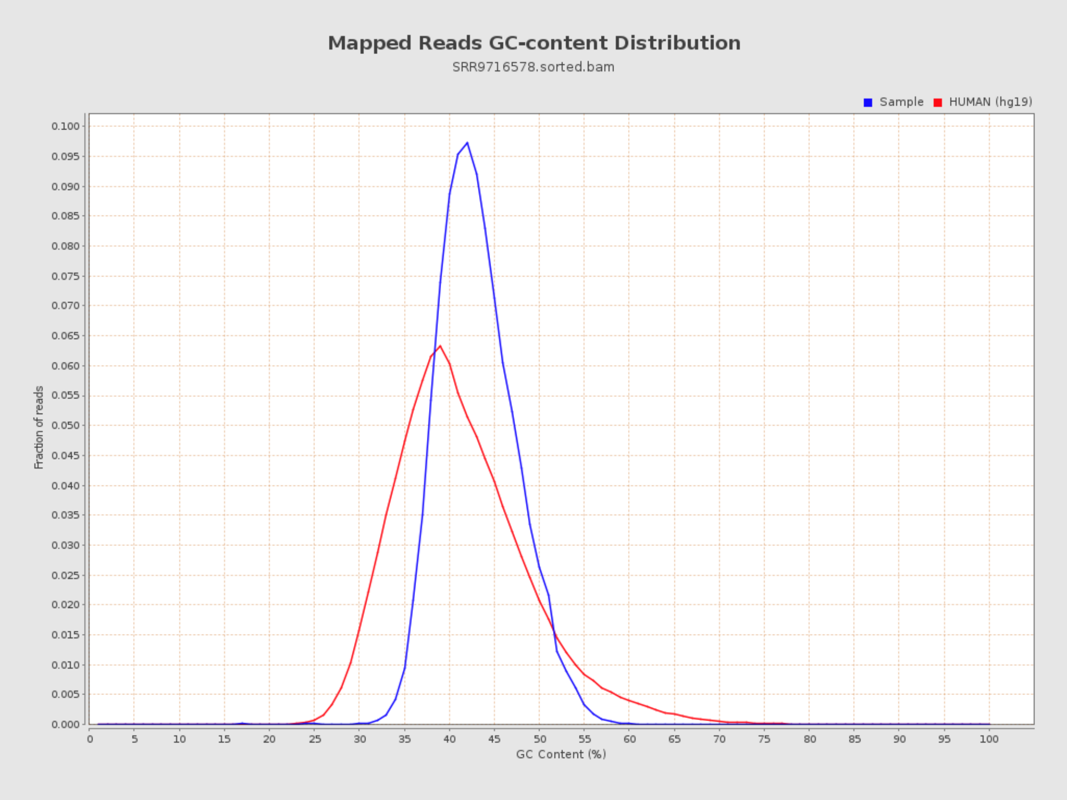
7. Results : Duplication Rate Histogram



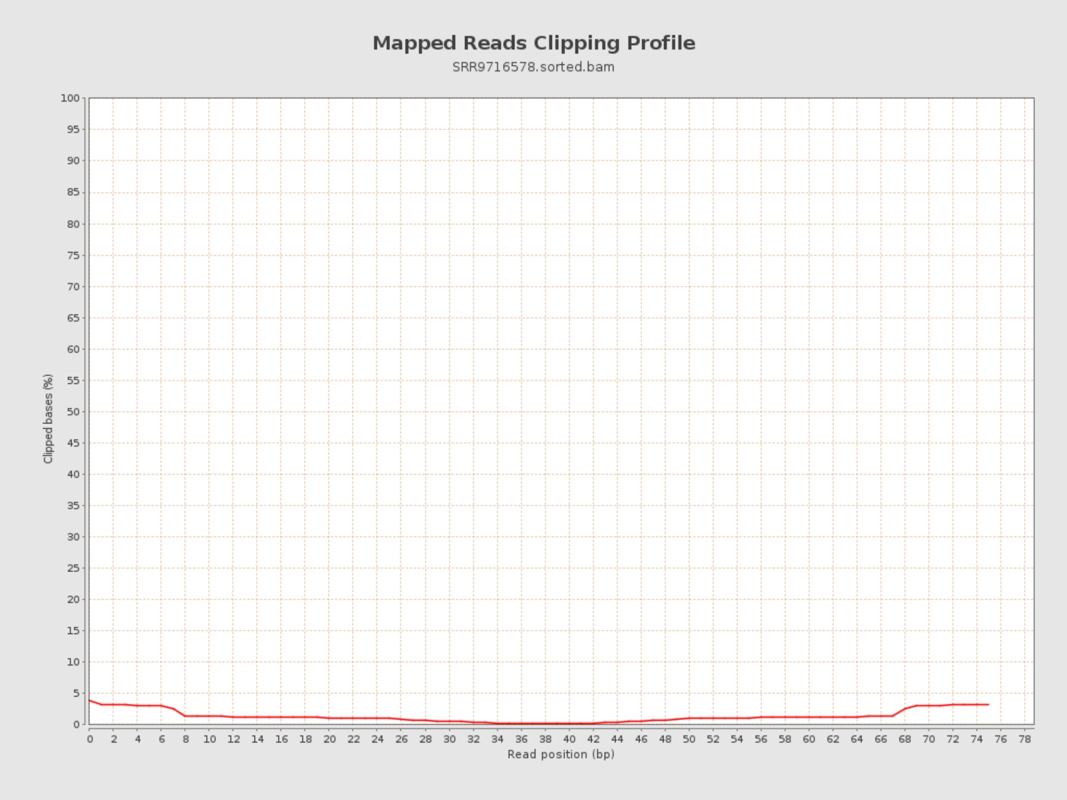
8. Results : Mapped Reads Nucleotide Content



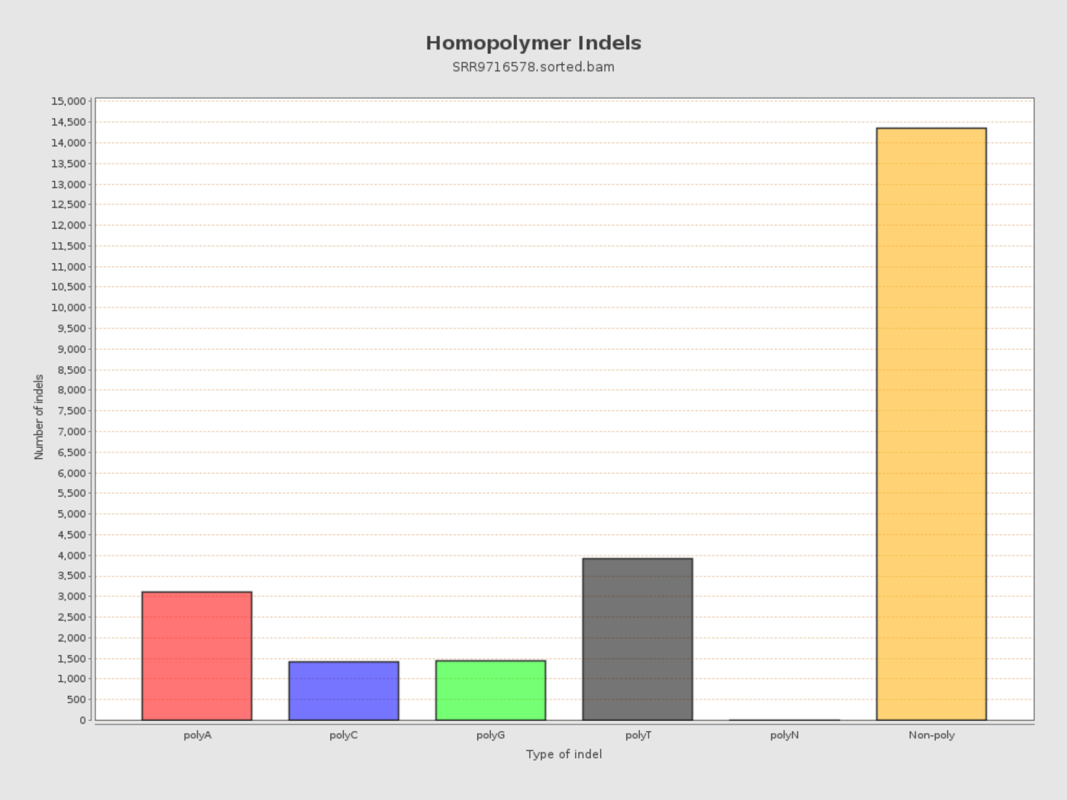
9. Results : Mapped Reads GC-content Distribution



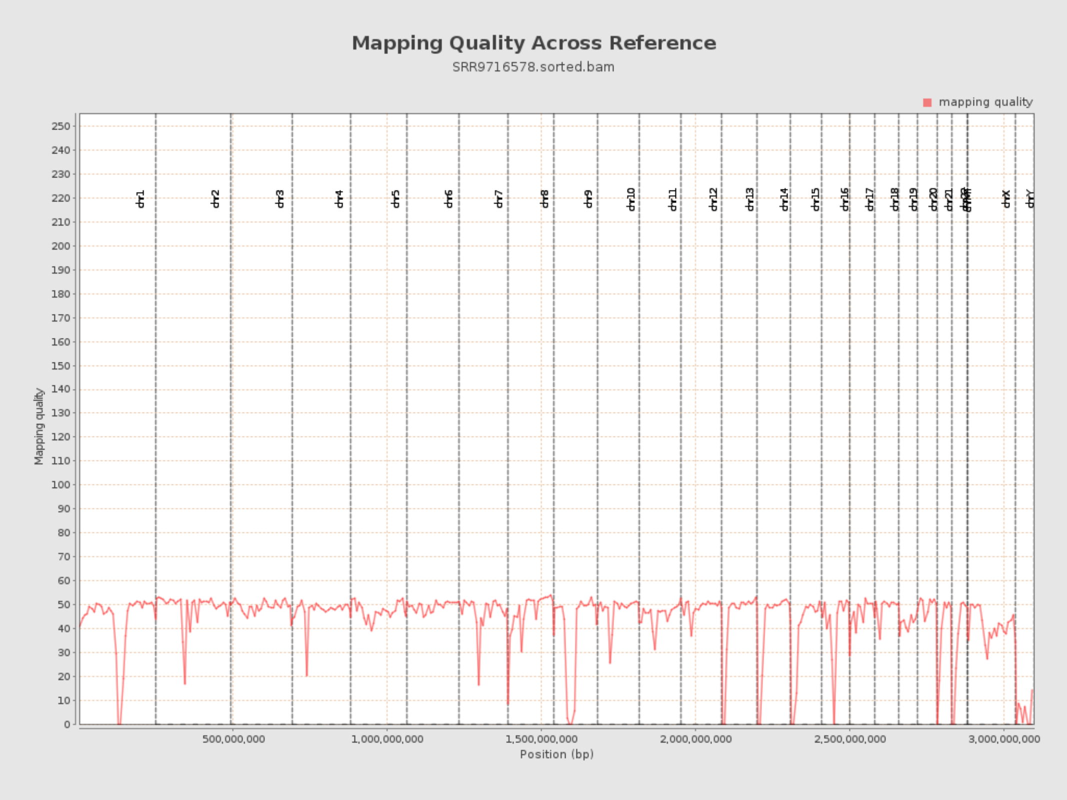
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram