Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 07:05:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716317.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_SRR9716317 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716317.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 07:05:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716317.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,896,383
Mapped reads	1,745,754 / 92.06%
Unmapped reads	150,629 / 7.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,078 / 1.74%
Read min/max/mean length	30 / 101 / 101.63
Duplicated reads (estimated)	70,714 / 3.73%
Duplication rate	3.02%
Clipped reads	1,776,051 / 93.65%

2.2. ACGT Content

Number/percentage of A's	35,976,860 / 26.14%
Number/percentage of C's	26,641,711 / 19.36%
Number/percentage of T's	42,579,927 / 30.94%
Number/percentage of G's	32,424,910 / 23.56%
Number/percentage of N's	9,359 / 0.01%
GC Percentage	42.92%

2.3. Coverage

Mean	0.0445

Standard Deviation	0.3715

2.4. Mapping Quality

Mean Mapping Quality	47.67

2.5. Mismatches and indels

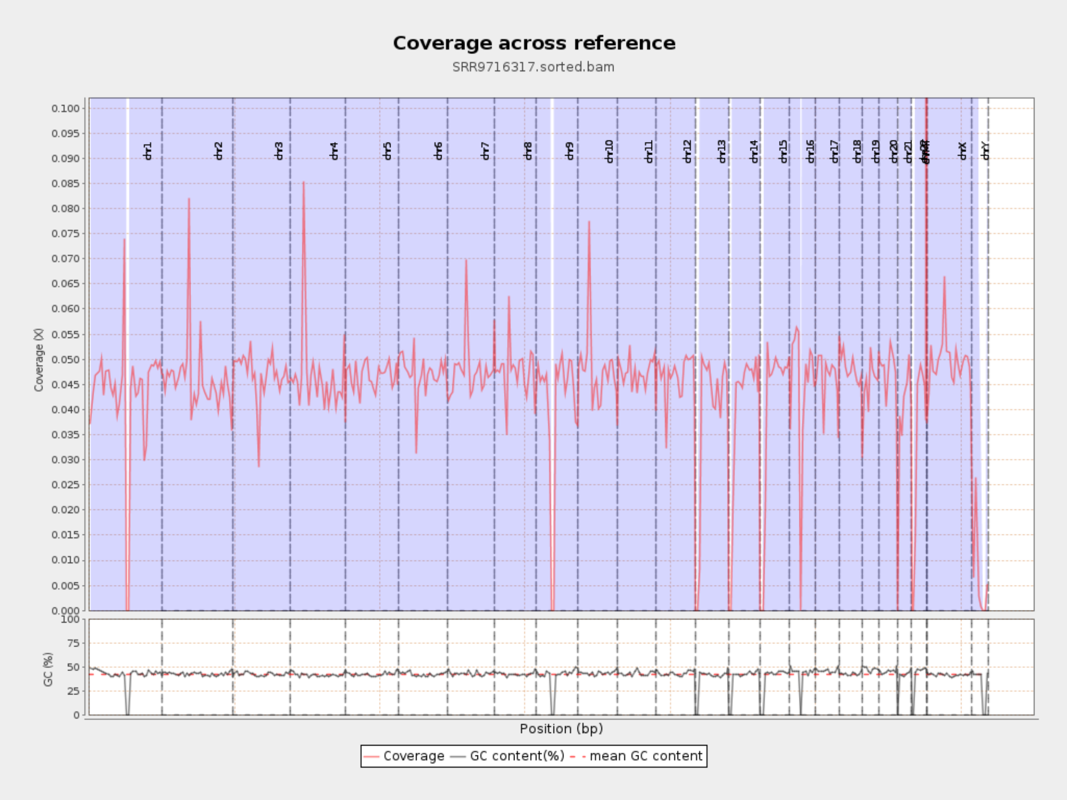
General error rate	0.7%
Mismatches	933,873
Insertions	11,768
Mapped reads with at least one insertion	0.66%
Deletions	33,090
Mapped reads with at least one deletion	1.87%
Homopolymer indels	42.26%

2.6. Chromosome stats

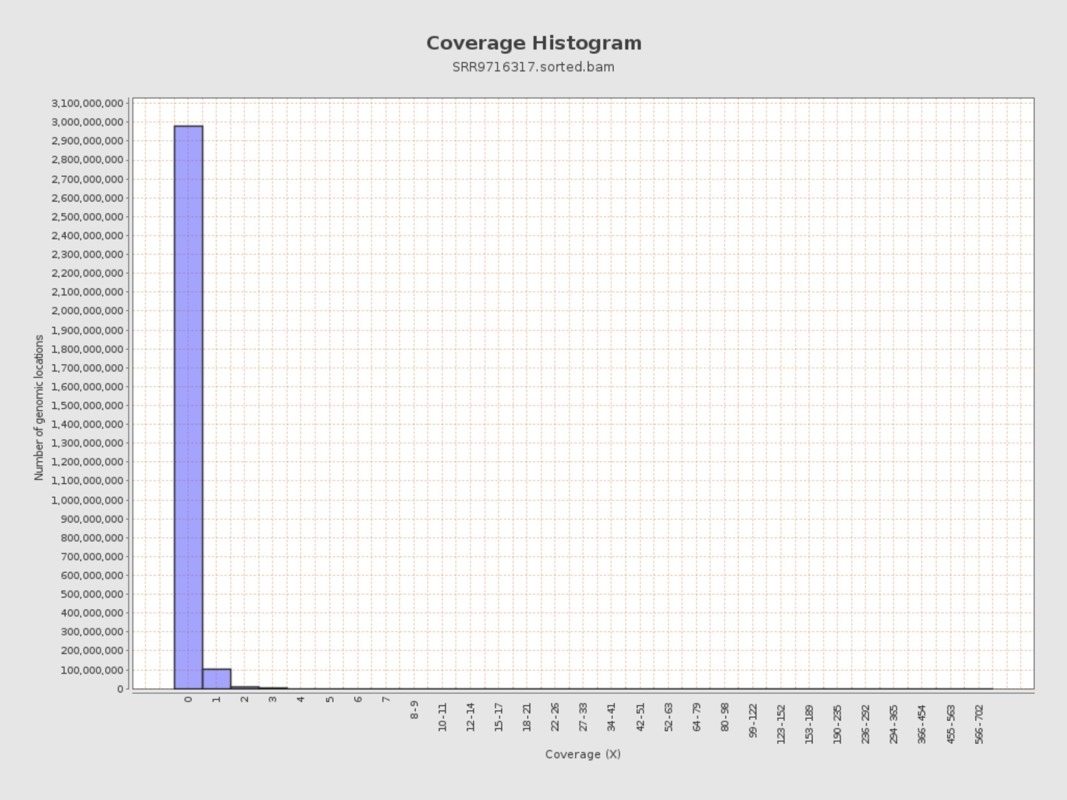
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10676363	0.0428	0.6361
chr2	243199373	11253713	0.0463	0.4503
chr3	198022430	9298600	0.047	0.2427
chr4	191154276	8911684	0.0466	0.3081
chr5	180915260	8453688	0.0467	0.2459
chr6	171115067	8071571	0.0472	0.2667
chr7	159138663	7613033	0.0478	0.5214

chr8	146364022	6979631	0.0477	0.4618
chr9	141213431	5759998	0.0408	0.3327
chr10	135534747	6541151	0.0483	0.387
chr11	135006516	6384302	0.0473	0.3516
chr12	133851895	6265084	0.0468	0.2446
chr13	115169878	4398559	0.0382	0.2188
chr14	107349540	4182064	0.039	0.2389
chr15	102531392	4060103	0.0396	0.2244
chr16	90354753	4036021	0.0447	0.257
chr17	81195210	3743776	0.0461	0.2761
chr18	78077248	3779813	0.0484	0.5253
chr19	59128983	2690650	0.0455	0.4529
chr20	63025520	3003301	0.0477	0.2595
chr21	48129895	1846581	0.0384	0.2541
chr22	51304566	1626881	0.0317	0.2012
chrMT	16571	12887	0.7777	1.249
chrX	155270560	7702425	0.0496	0.2969
chrY	59373566	404325	0.0068	0.2333

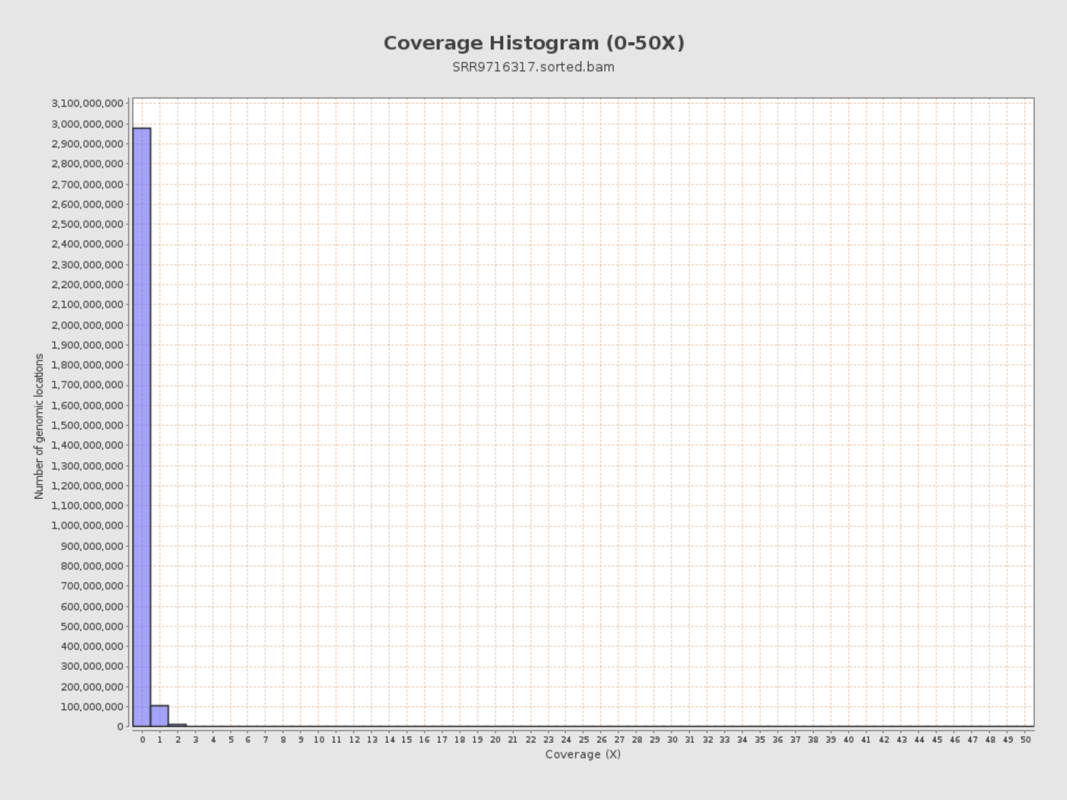
3. Results : Coverage across reference



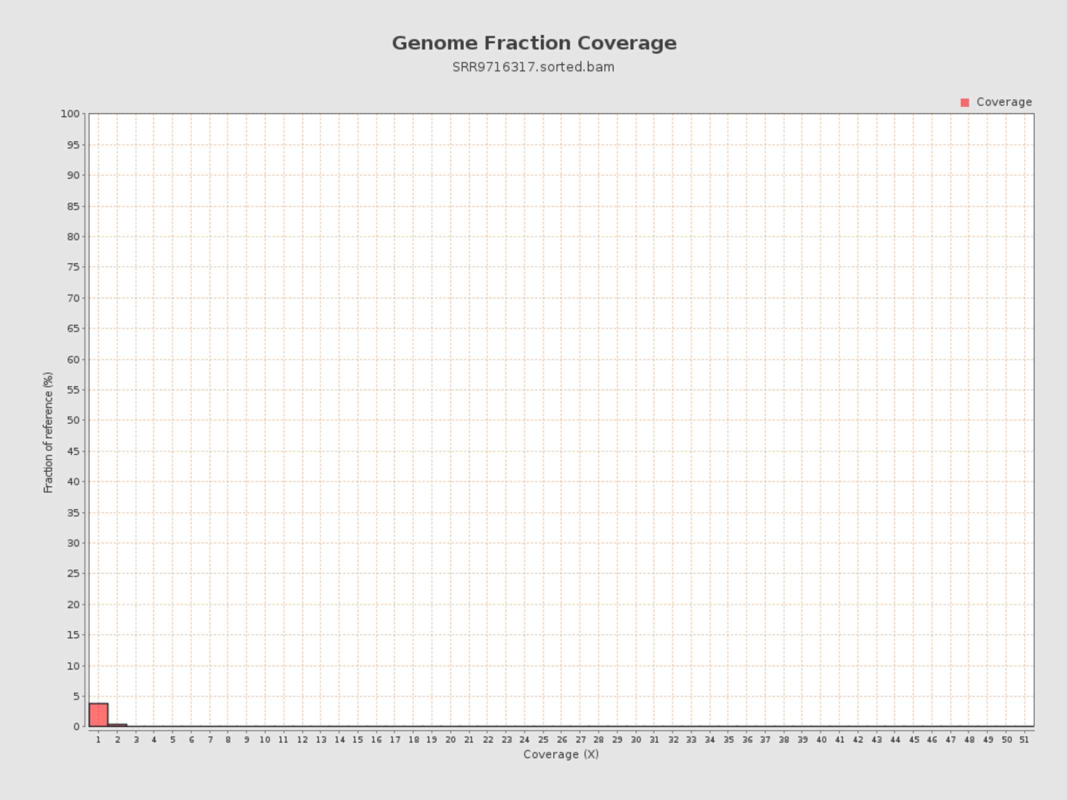
4. Results : Coverage Histogram



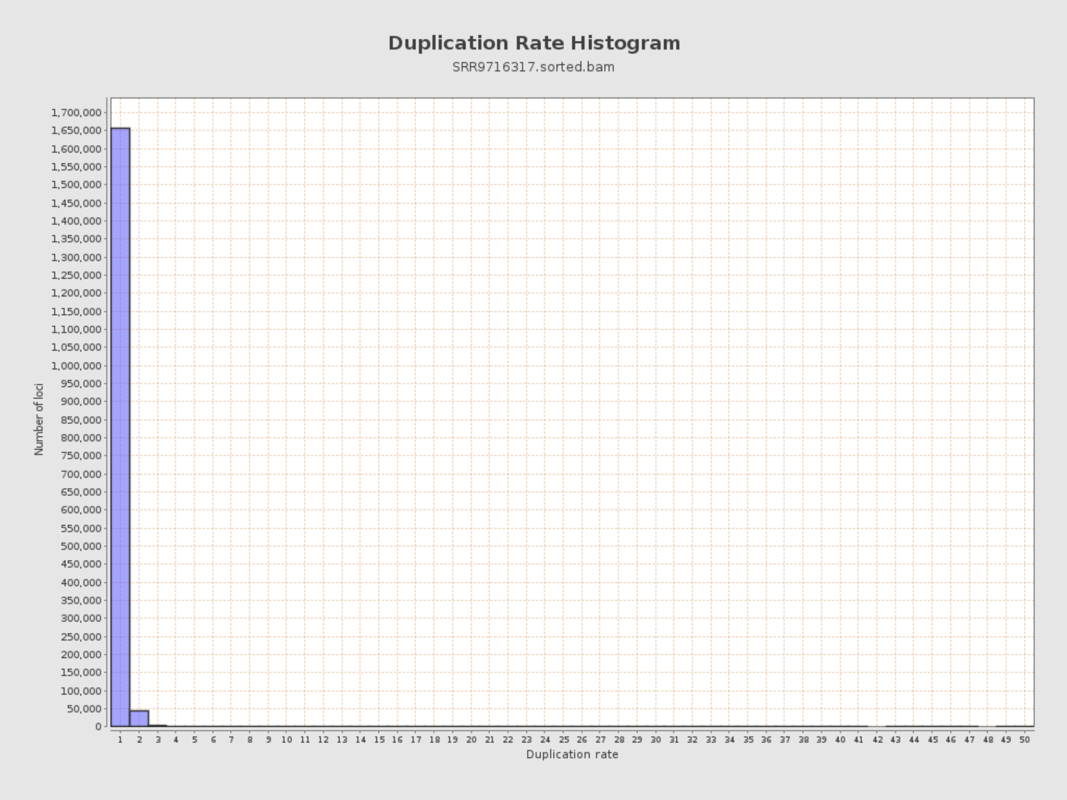
5. Results : Coverage Histogram (0-50X)



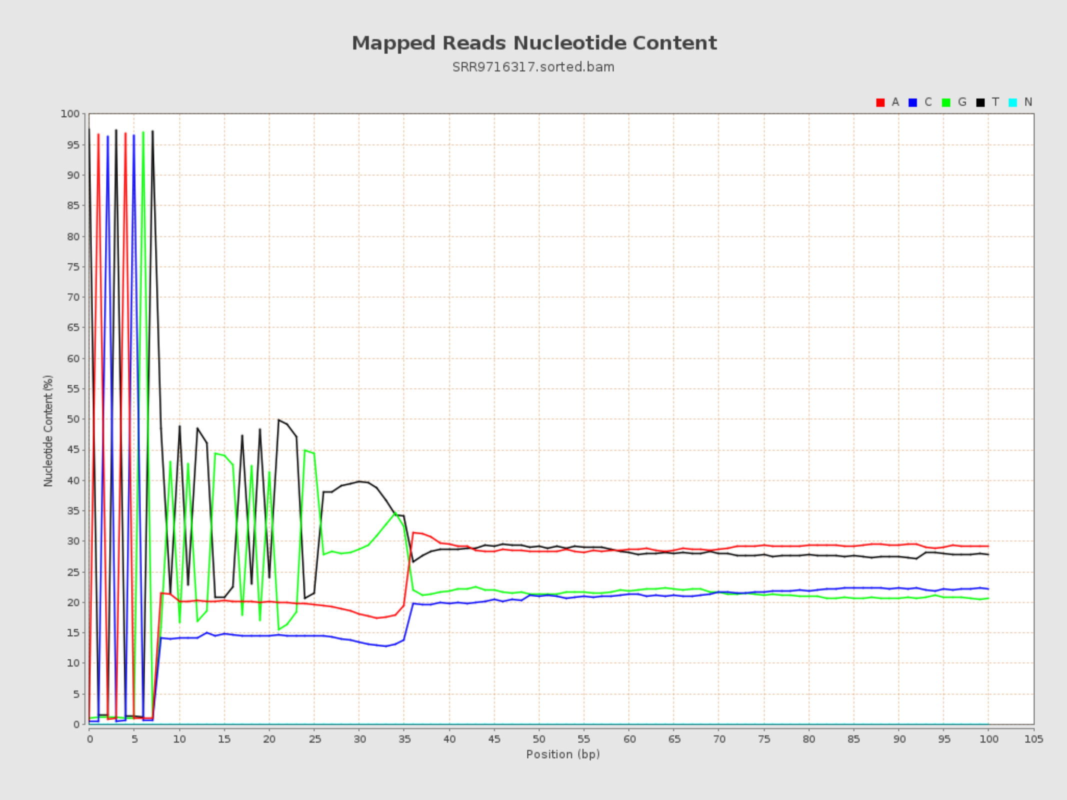
6. Results : Genome Fraction Coverage



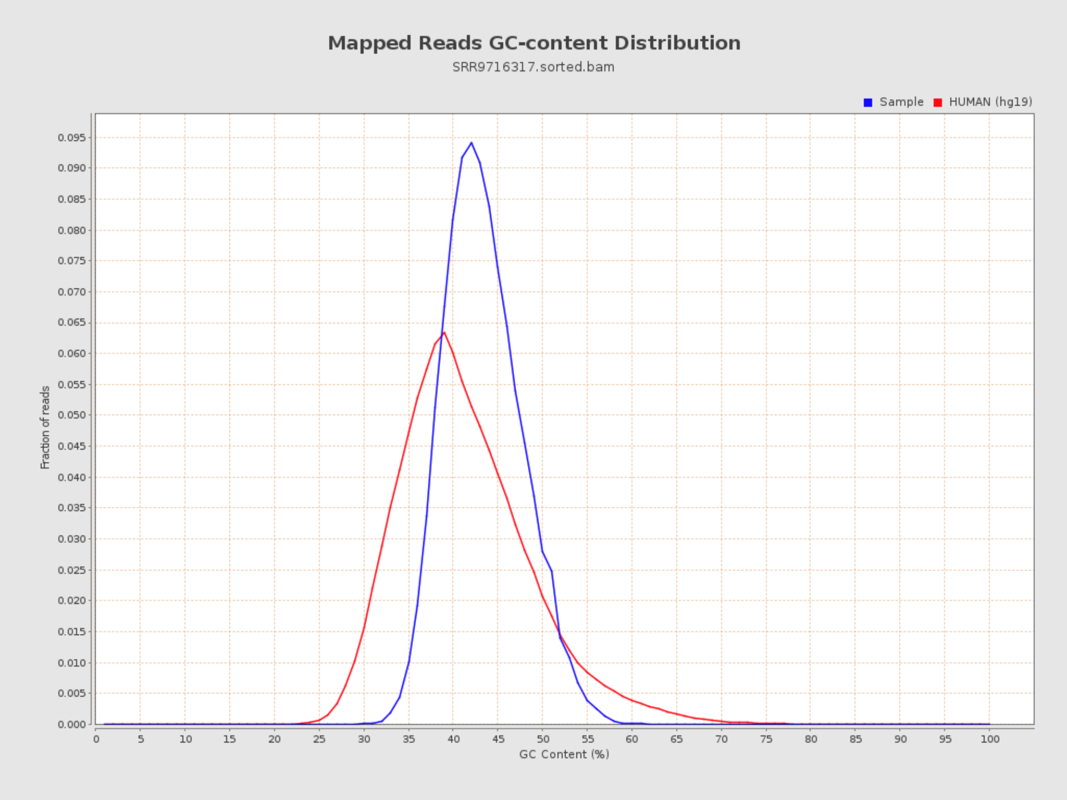
7. Results : Duplication Rate Histogram



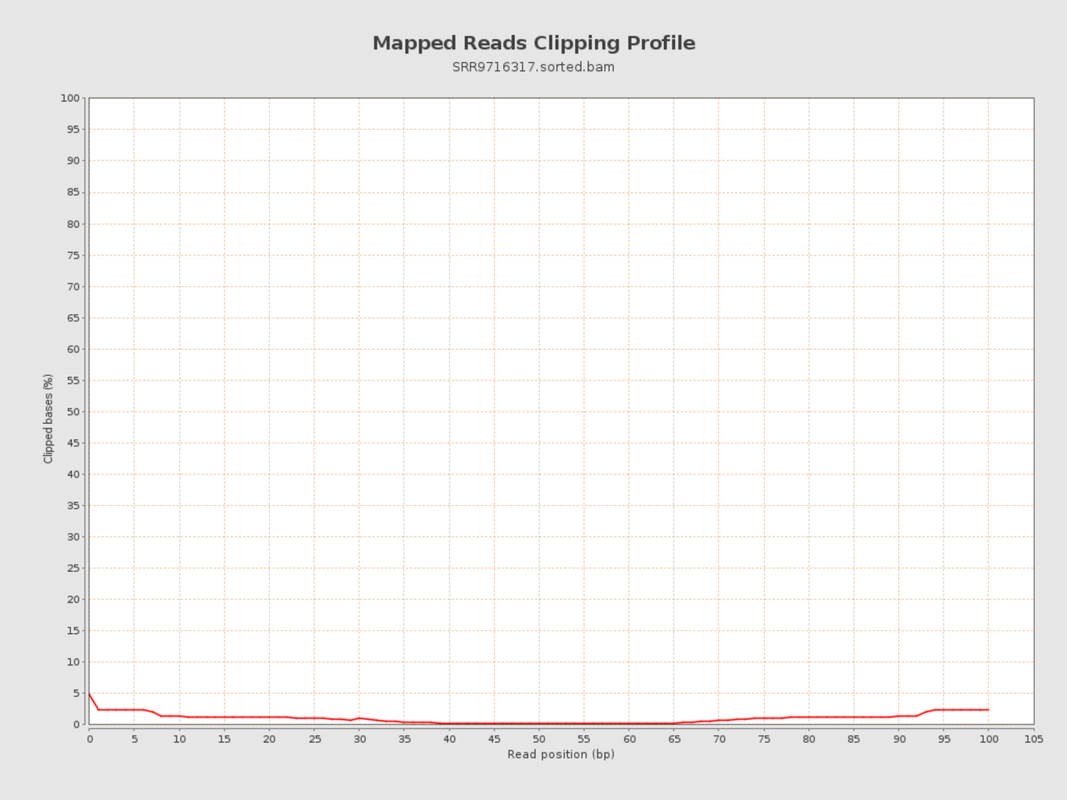
8. Results : Mapped Reads Nucleotide Content



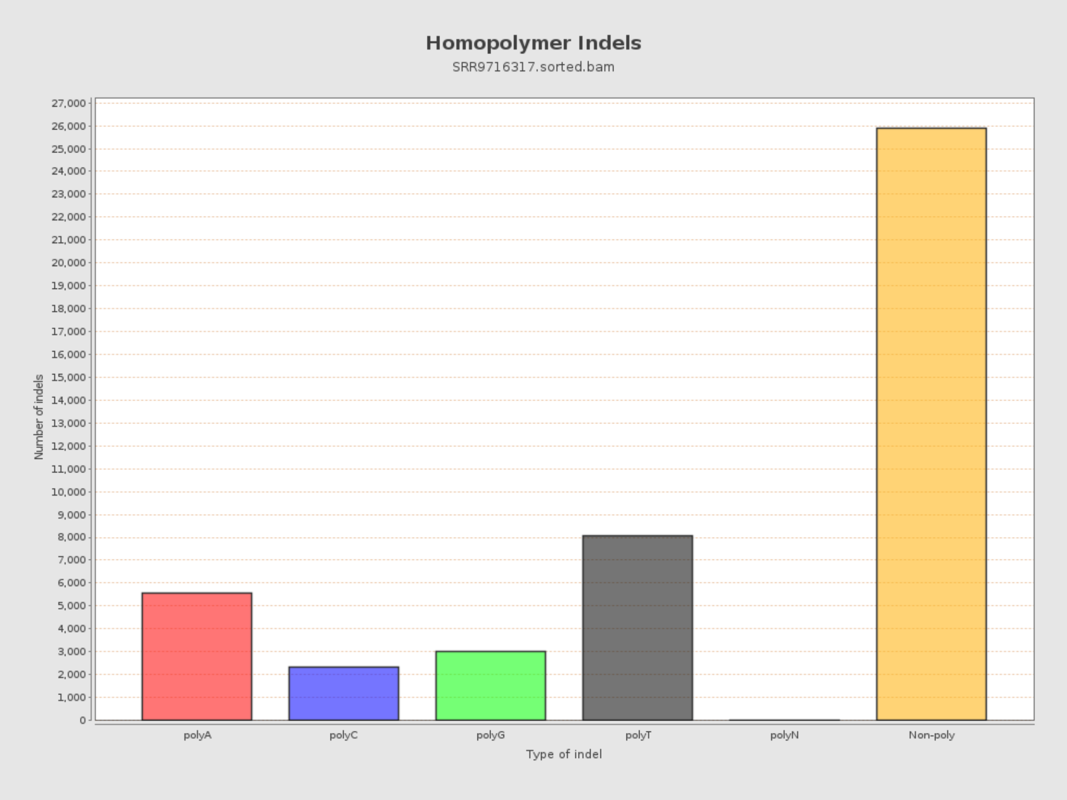
9. Results : Mapped Reads GC-content Distribution



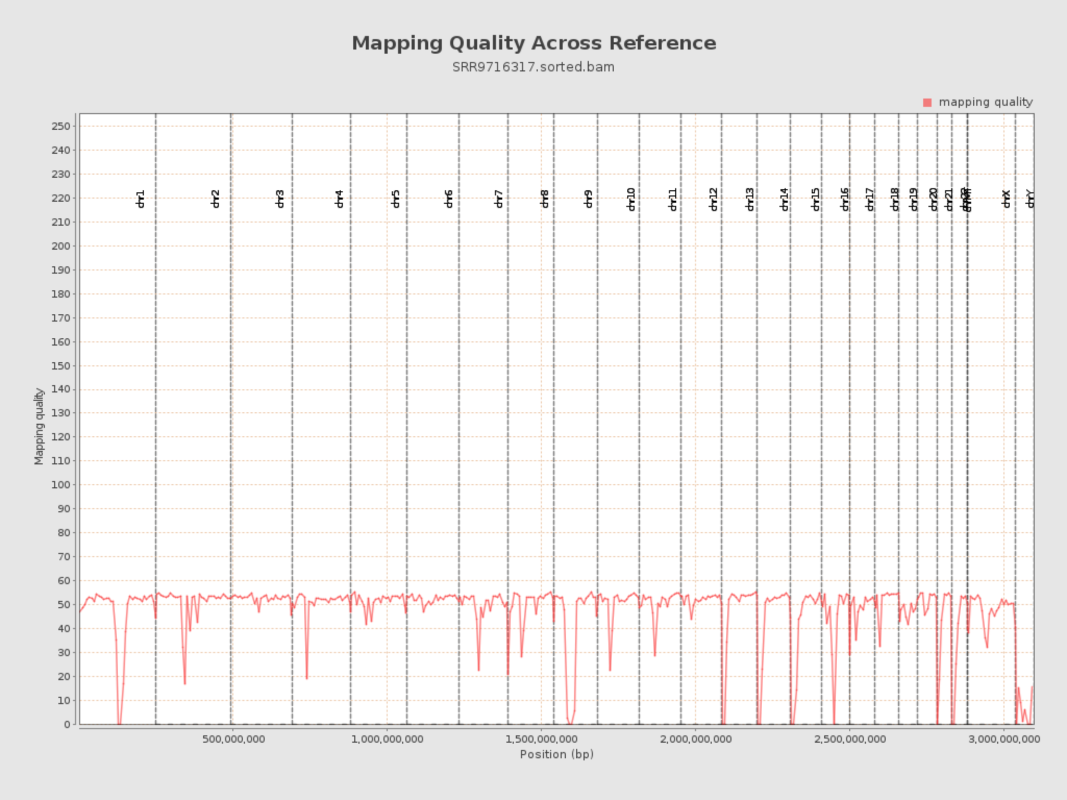
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram