Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 00:59:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717016.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_SRR9717016 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717016.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 00:59:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717016.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,882,242
Mapped reads	1,757,708 / 93.38%
Unmapped reads	124,534 / 6.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,088 / 1.81%
Read min/max/mean length	30 / 101 / 101.66
Duplicated reads (estimated)	91,703 / 4.87%
Duplication rate	4.1%
Clipped reads	1,788,855 / 95.04%

2.2. ACGT Content

Number/percentage of A's	34,088,901 / 25%
Number/percentage of C's	28,304,814 / 20.76%
Number/percentage of T's	40,544,378 / 29.74%
Number/percentage of G's	33,389,973 / 24.49%
Number/percentage of N's	5,037 / 0%
GC Percentage	45.25%

2.3. Coverage

Mean	0.0441

Standard Deviation	0.3681

2.4. Mapping Quality

Mean Mapping Quality	46.37

2.5. Mismatches and indels

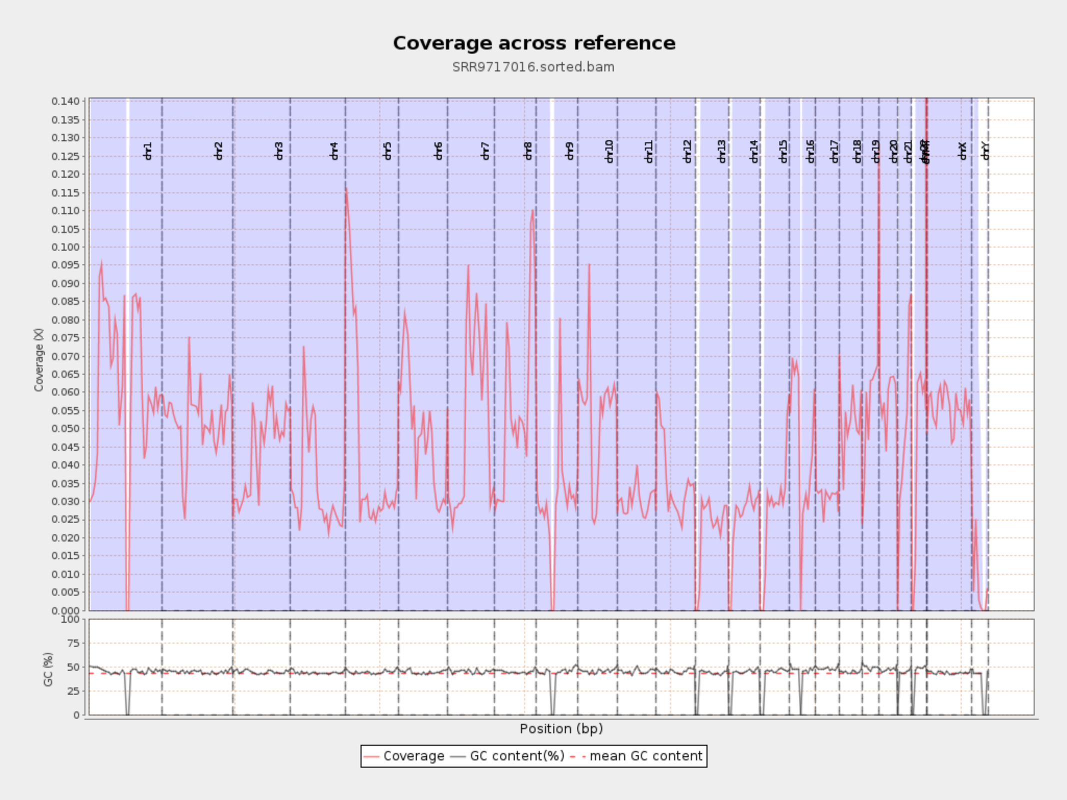
General error rate	0.69%
Mismatches	908,583
Insertions	10,931
Mapped reads with at least one insertion	0.61%
Deletions	26,263
Mapped reads with at least one deletion	1.47%
Homopolymer indels	39.36%

2.6. Chromosome stats

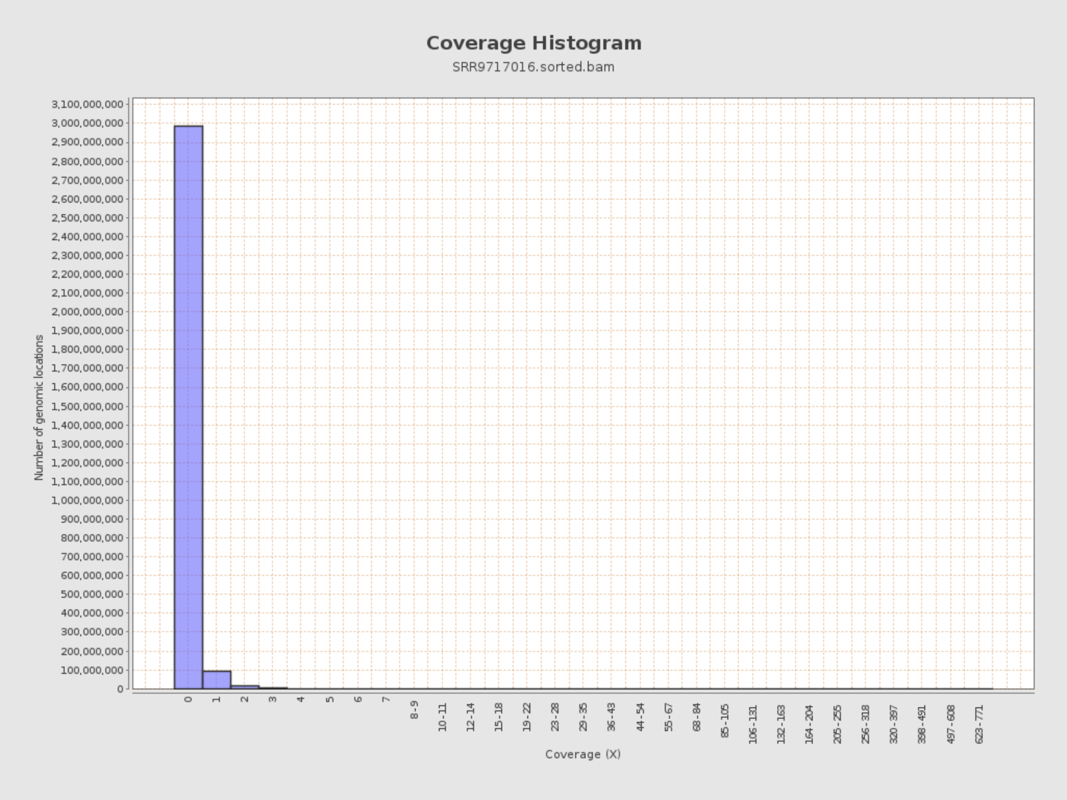
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15297500	0.0614	0.7312
chr2	243199373	12664595	0.0521	0.3757
chr3	198022430	8747699	0.0442	0.2484
chr4	191154276	6522928	0.0341	0.2992
chr5	180915260	8136254	0.045	0.2554
chr6	171115067	8360934	0.0489	0.2777
chr7	159138663	8502942	0.0534	0.4743

chr8	146364022	8240075	0.0563	0.3794
chr9	141213431	4156766	0.0294	0.2501
chr10	135534747	7340193	0.0542	0.4807
chr11	135006516	4091749	0.0303	0.2949
chr12	133851895	4831917	0.0361	0.2231
chr13	115169878	2568384	0.0223	0.1734
chr14	107349540	2665771	0.0248	0.1998
chr15	102531392	2815325	0.0275	0.1936
chr16	90354753	4105469	0.0454	0.2641
chr17	81195210	2537819	0.0313	0.2305
chr18	78077248	4066335	0.0521	0.3705
chr19	59128983	3442544	0.0582	0.5539
chr20	63025520	3658053	0.058	0.2997
chr21	48129895	2338393	0.0486	0.3081
chr22	51304566	2156272	0.042	0.2527
chrMT	16571	45889	2.7692	2.4757
chrX	155270560	8669072	0.0558	0.2945
chrY	59373566	423812	0.0071	0.2354

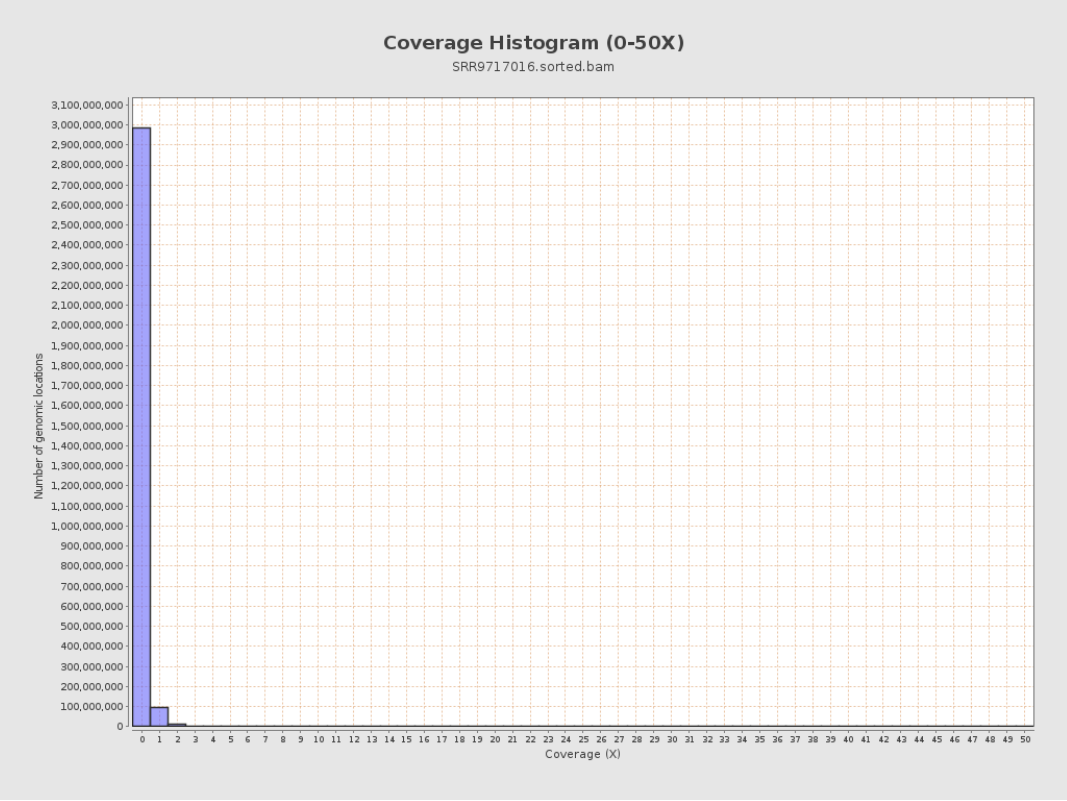
3. Results : Coverage across reference



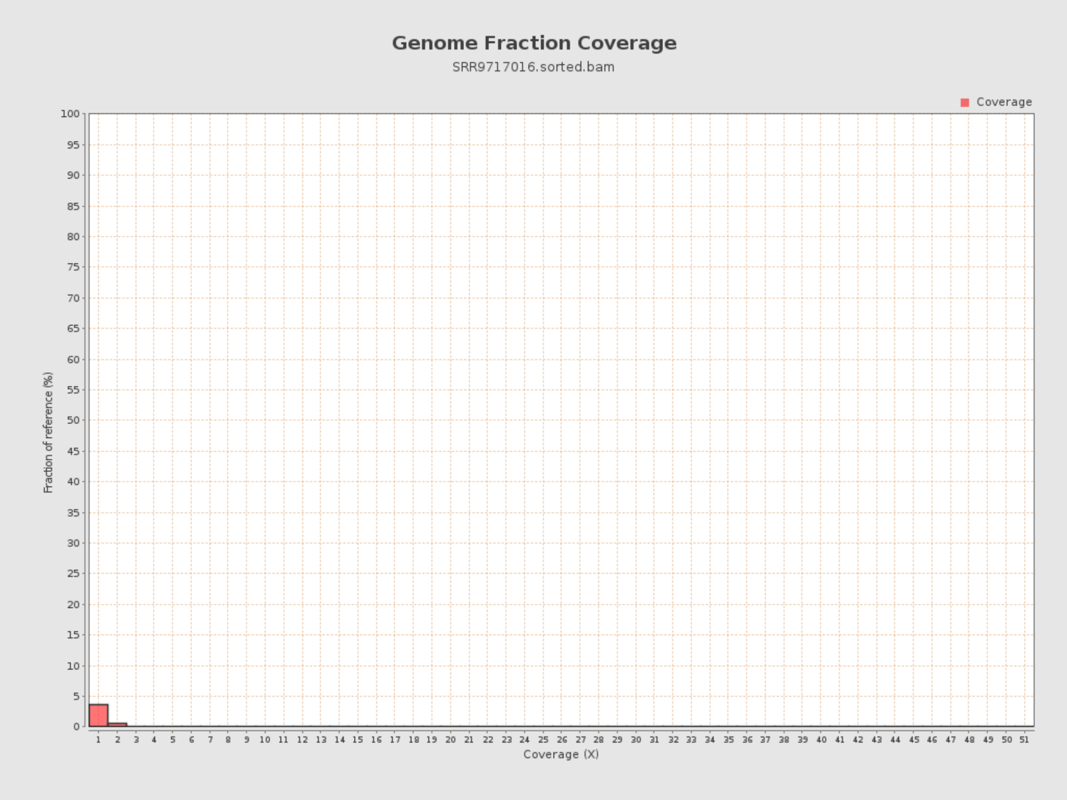
4. Results : Coverage Histogram



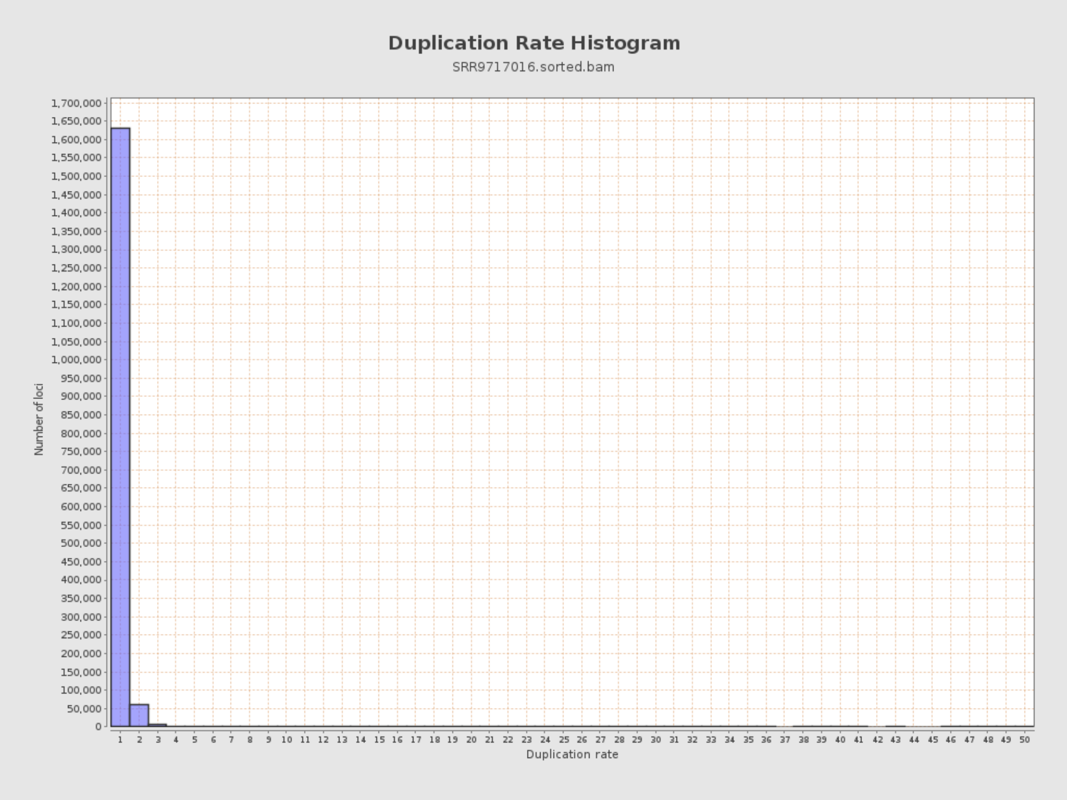
5. Results : Coverage Histogram (0-50X)



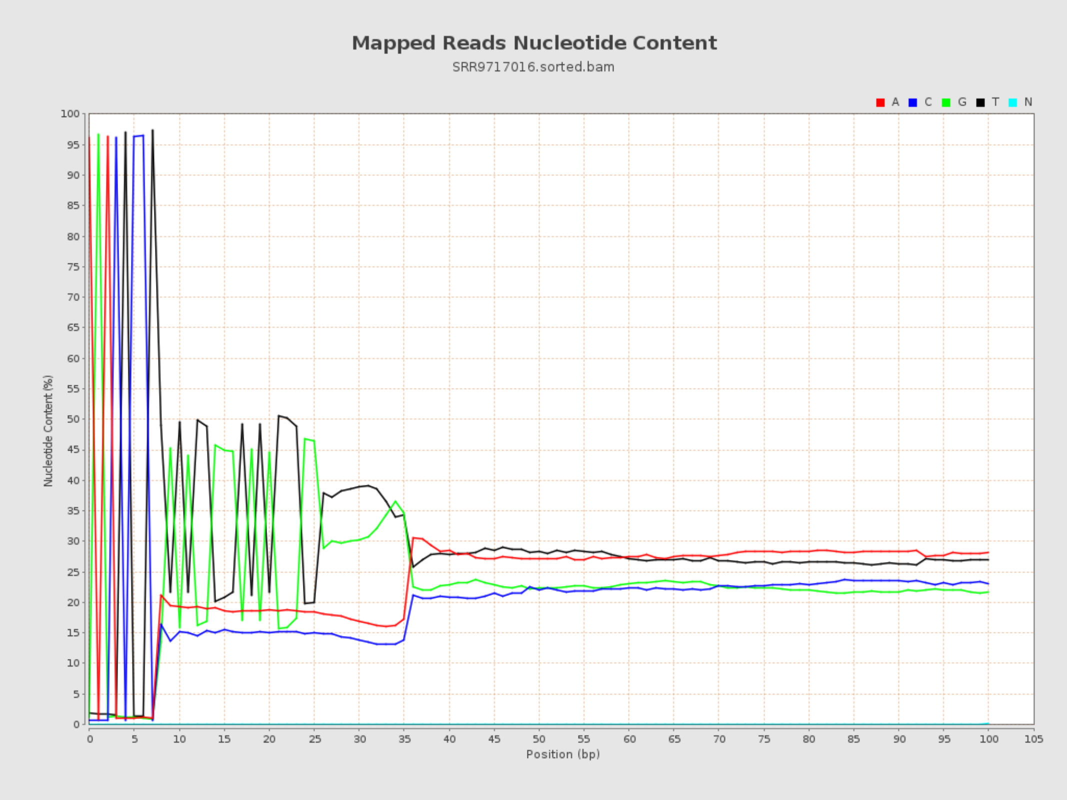
6. Results : Genome Fraction Coverage



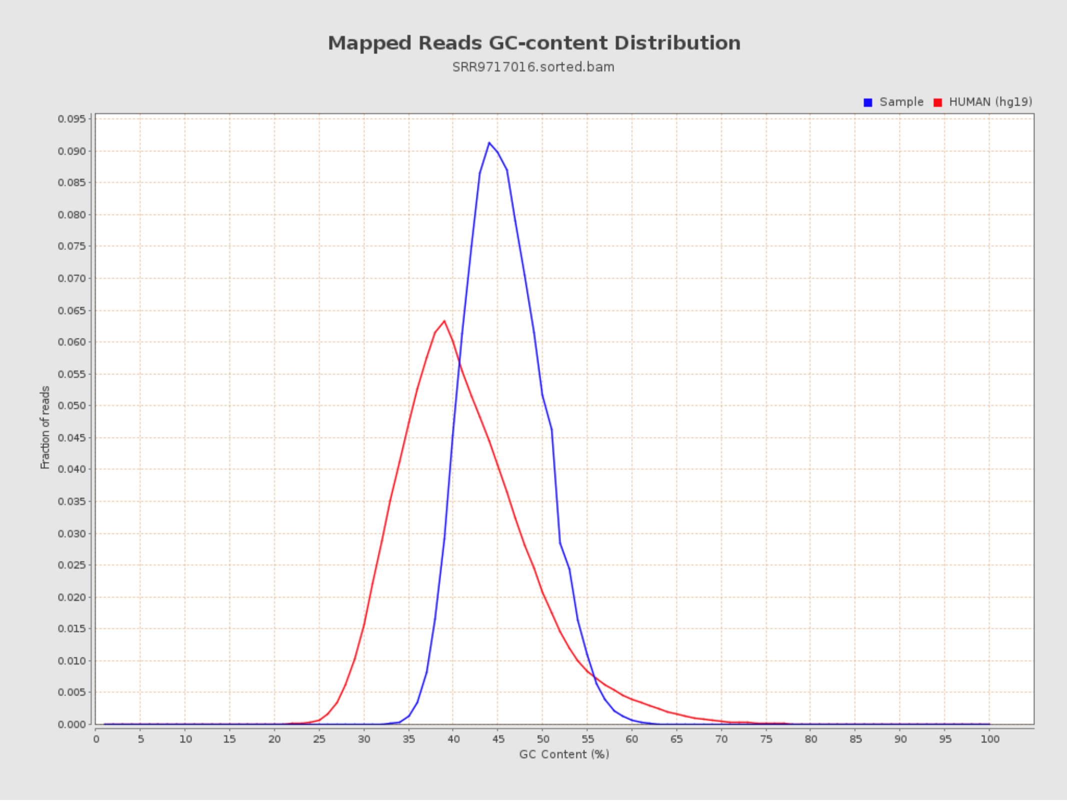
7. Results : Duplication Rate Histogram



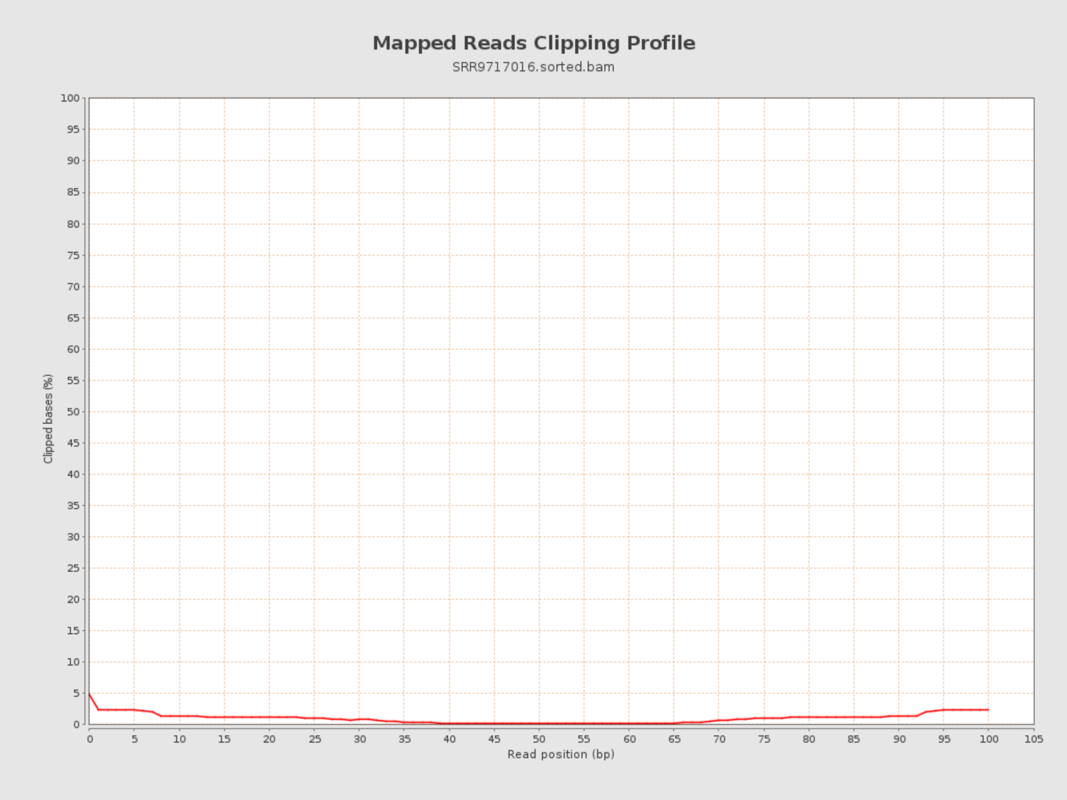
8. Results : Mapped Reads Nucleotide Content



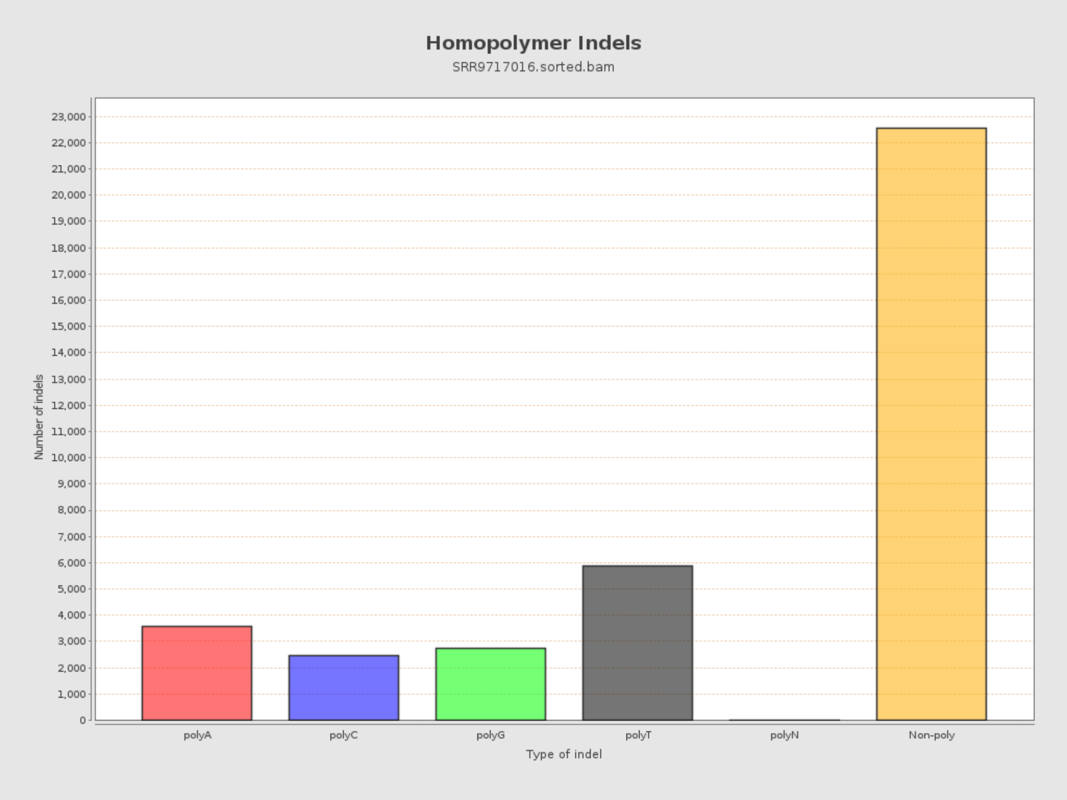
9. Results : Mapped Reads GC-content Distribution



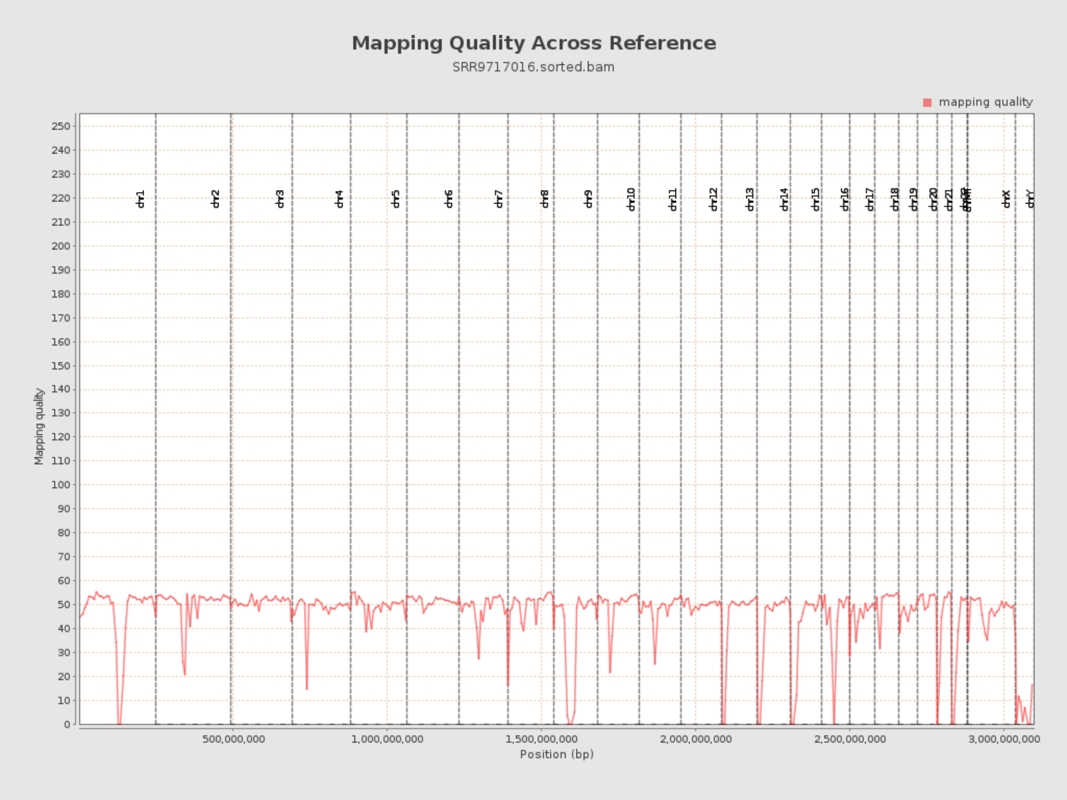
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram