Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 00:37:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717013.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_SRR9717013 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717013.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 00:37:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717013.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	40,342,045
Mapped reads	39,329,554 / 97.49%
Unmapped reads	1,012,491 / 2.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,571 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	2,556,495 / 6.34%
Duplication rate	1.88%
Clipped reads	39,159,727 / 97.07%

2.2. ACGT Content

Number/percentage of A's	746,921,001 / 28.05%
Number/percentage of C's	562,742,646 / 21.13%
Number/percentage of T's	788,147,465 / 29.6%
Number/percentage of G's	564,385,589 / 21.2%
Number/percentage of N's	442,958 / 0.02%
GC Percentage	42.33%

2.3. Coverage

Mean	0.8603

Standard Deviation	12.7626

2.4. Mapping Quality

Mean Mapping Quality	48.83

2.5. Mismatches and indels

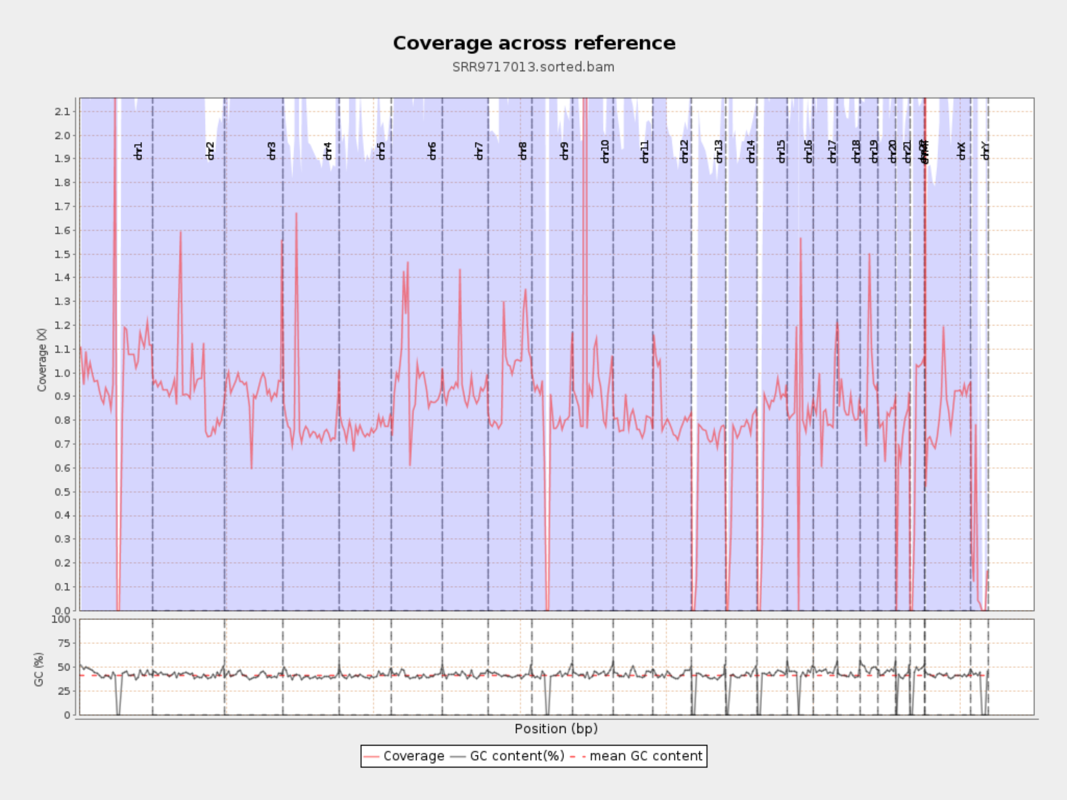
General error rate	0.39%
Mismatches	9,772,996
Insertions	229,833
Mapped reads with at least one insertion	0.58%
Deletions	242,234
Mapped reads with at least one deletion	0.61%
Homopolymer indels	37.47%

2.6. Chromosome stats

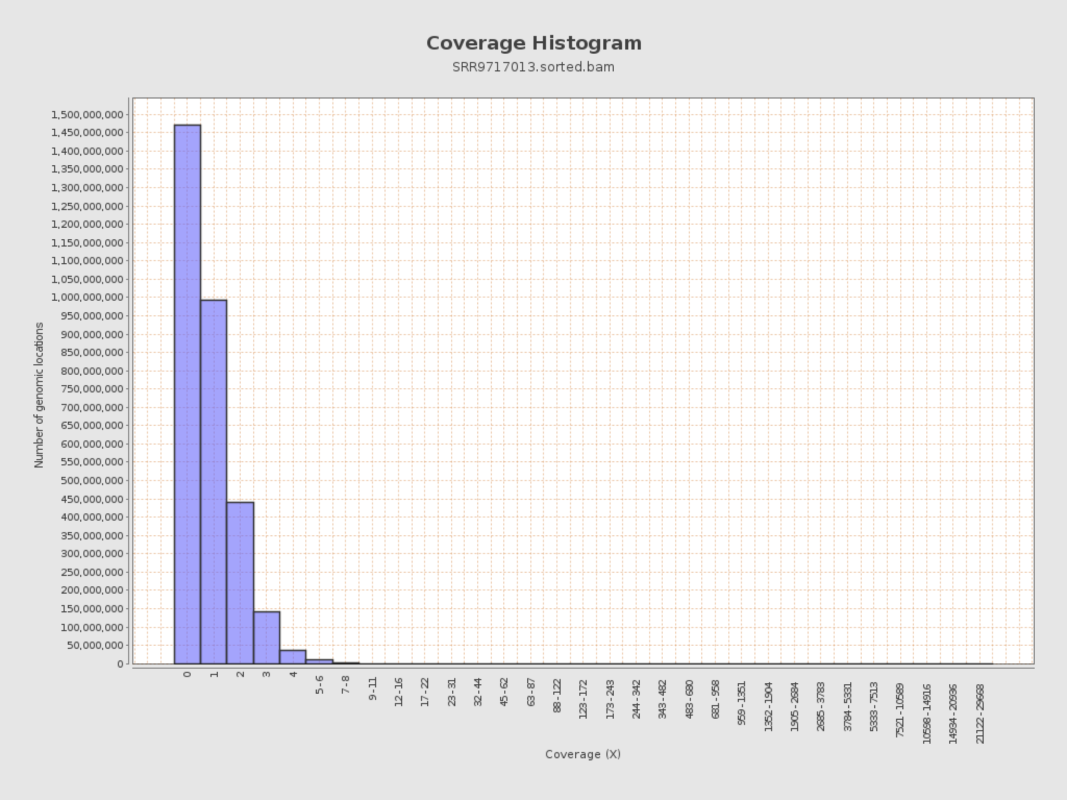
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	249235103	0.9999	25.6192
chr2	243199373	227208323	0.9342	6.1518
chr3	198022430	184899993	0.9337	7.209
chr4	191154276	151506760	0.7926	4.6205
chr5	180915260	138832315	0.7674	1.5417
chr6	171115067	167065570	0.9763	5.8684
chr7	159138663	151107669	0.9495	8.1279

chr8	146364022	147141793	1.0053	4.0187
chr9	141213431	108023336	0.765	4.5426
chr10	135534747	163325326	1.205	43.1035
chr11	135006516	107334313	0.795	4.0114
chr12	133851895	113049427	0.8446	1.6438
chr13	115169878	72050280	0.6256	0.922
chr14	107349540	69477545	0.6472	2.2316
chr15	102531392	74576839	0.7274	1.0093
chr16	90354753	76224353	0.8436	8.1509
chr17	81195210	69687313	0.8583	2.9425
chr18	78077248	67848654	0.869	10.5234
chr19	59128983	57393130	0.9706	17.1783
chr20	63025520	50303457	0.7981	1.9129
chr21	48129895	33354602	0.693	4.4825
chr22	51304566	36642318	0.7142	1.8879
chrMT	16571	5216683	314.808	82.4904
chrX	155270560	131385521	0.8462	2.8786
chrY	59373566	10209008	0.1719	6.5955

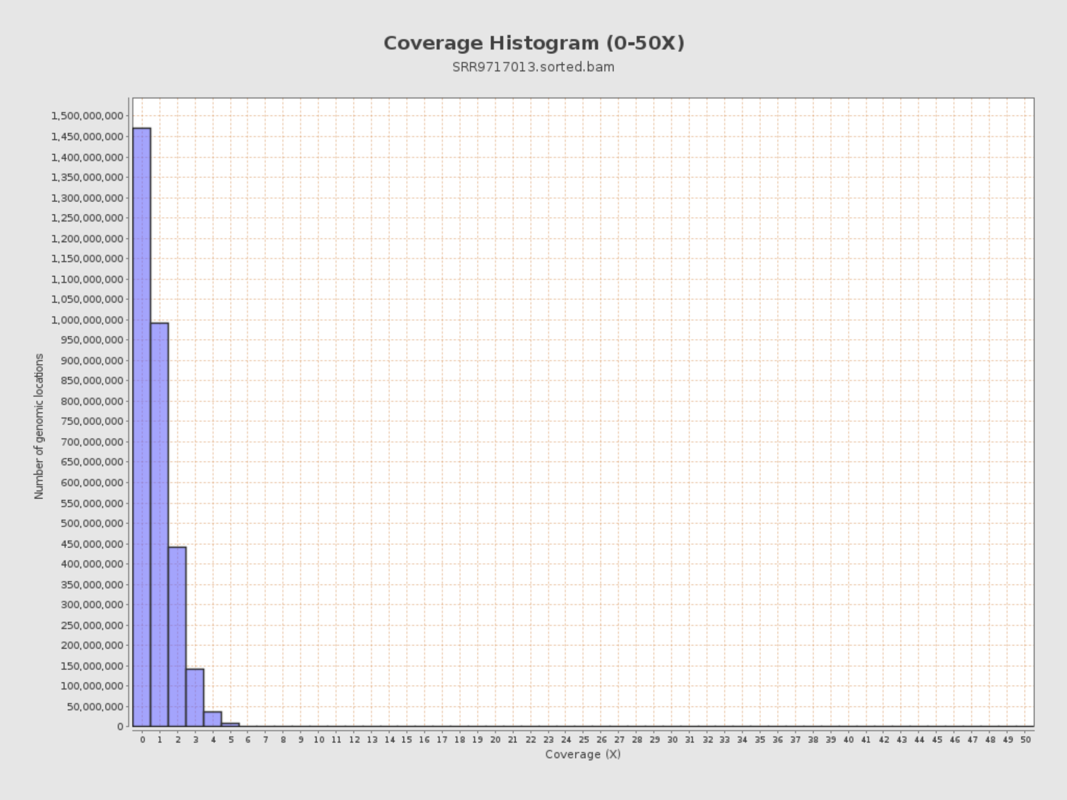
3. Results : Coverage across reference



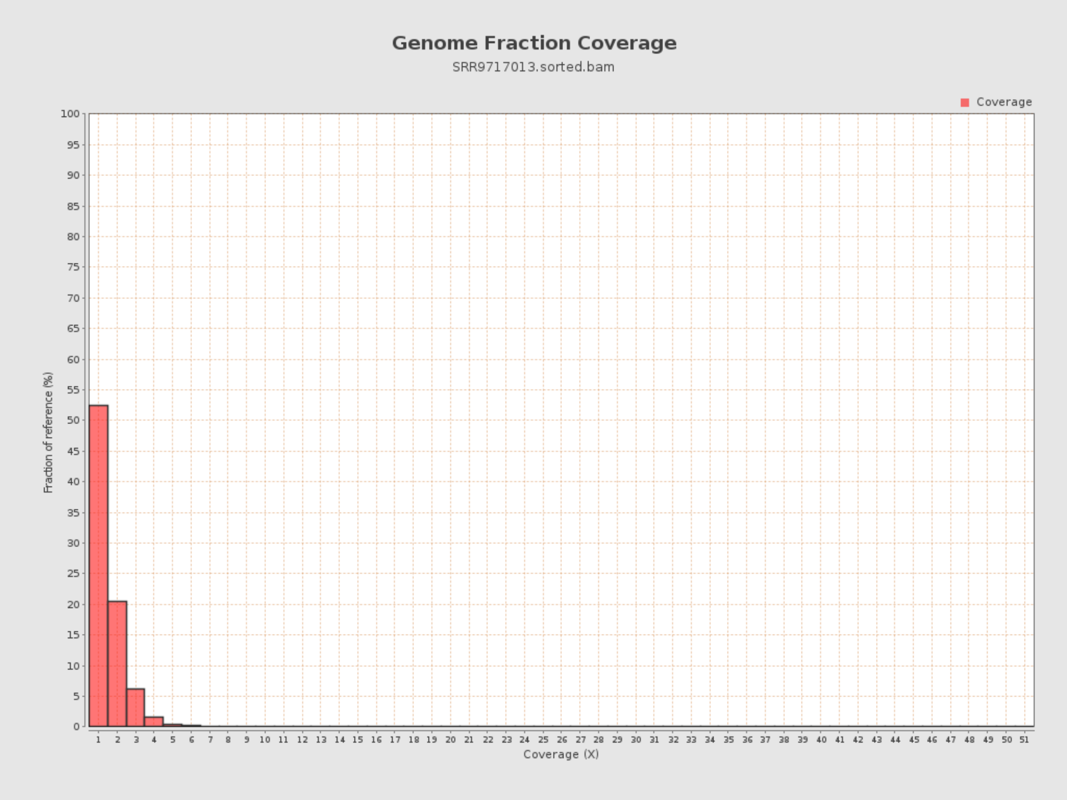
4. Results : Coverage Histogram



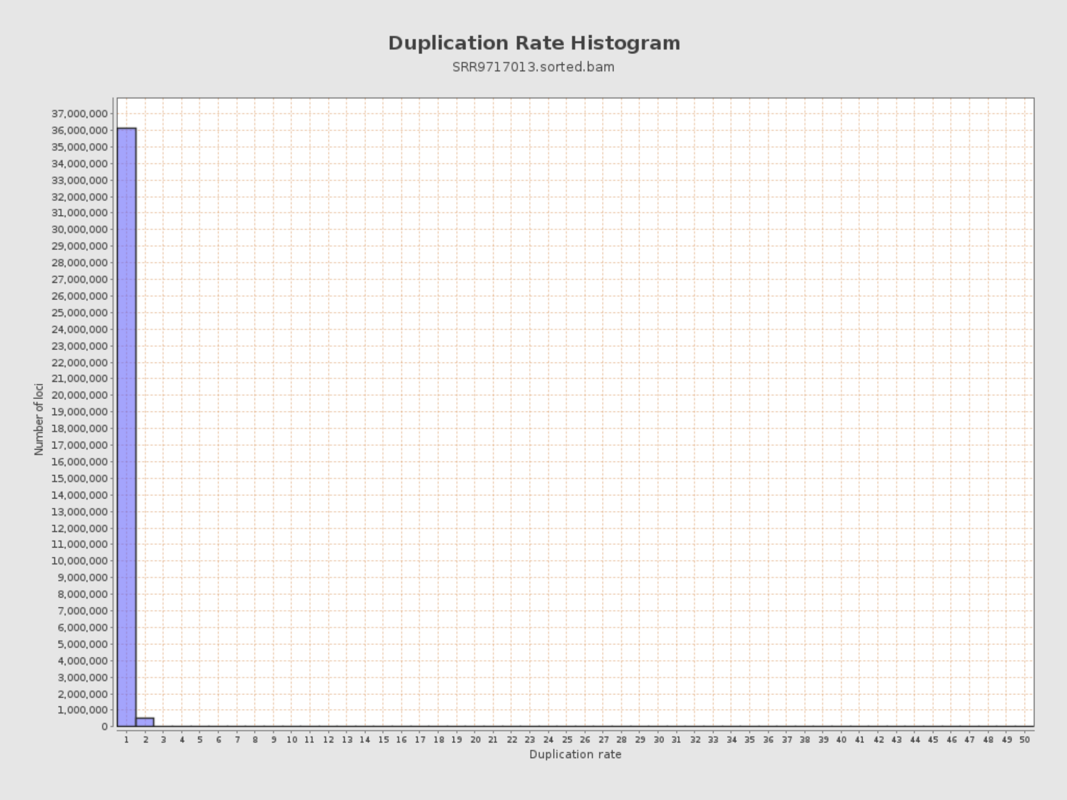
5. Results : Coverage Histogram (0-50X)



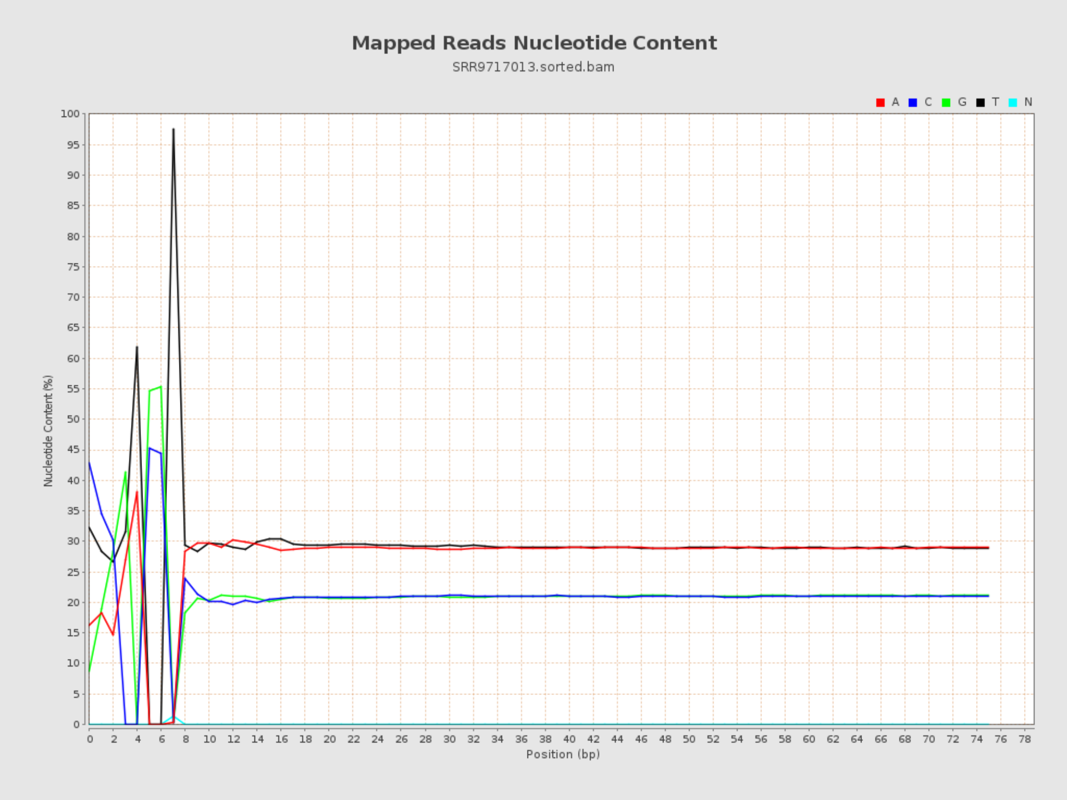
6. Results : Genome Fraction Coverage



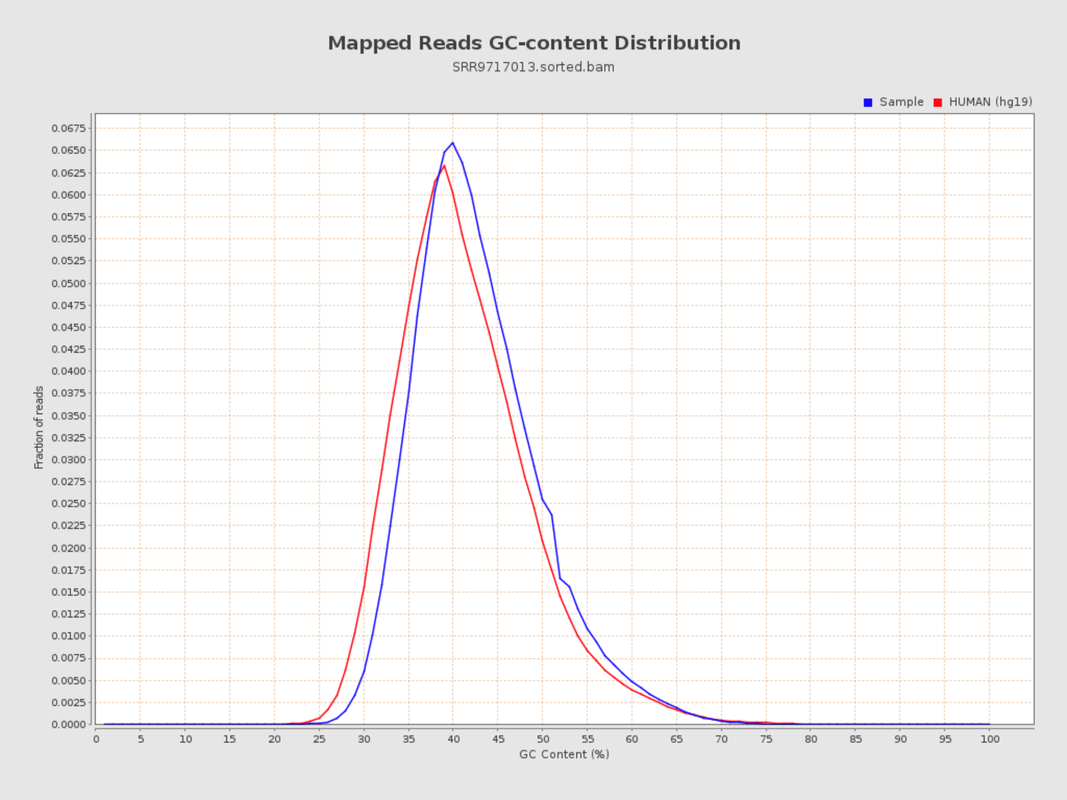
7. Results : Duplication Rate Histogram



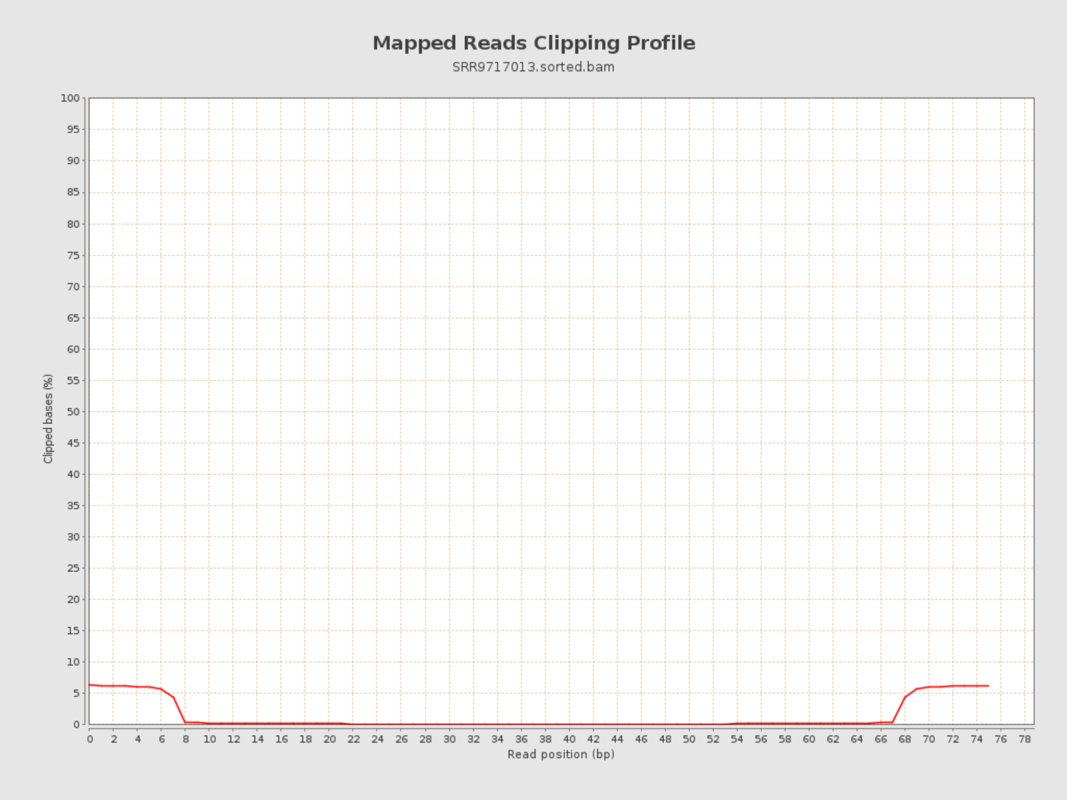
8. Results : Mapped Reads Nucleotide Content



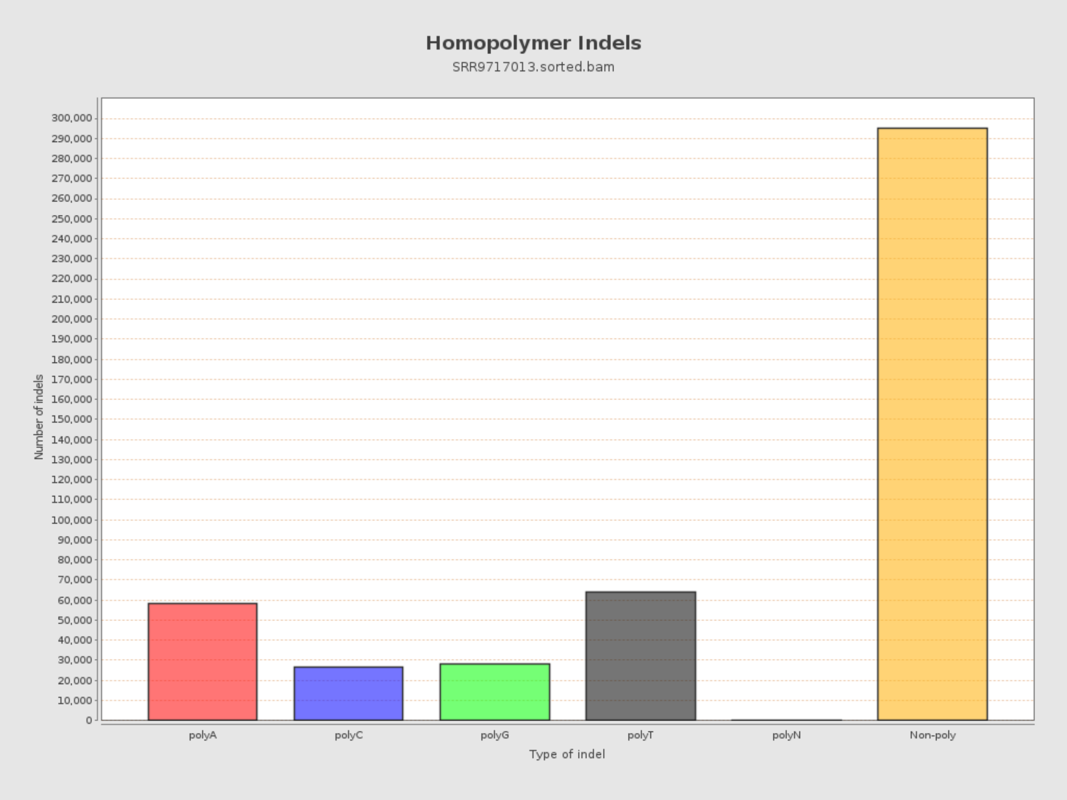
9. Results : Mapped Reads GC-content Distribution



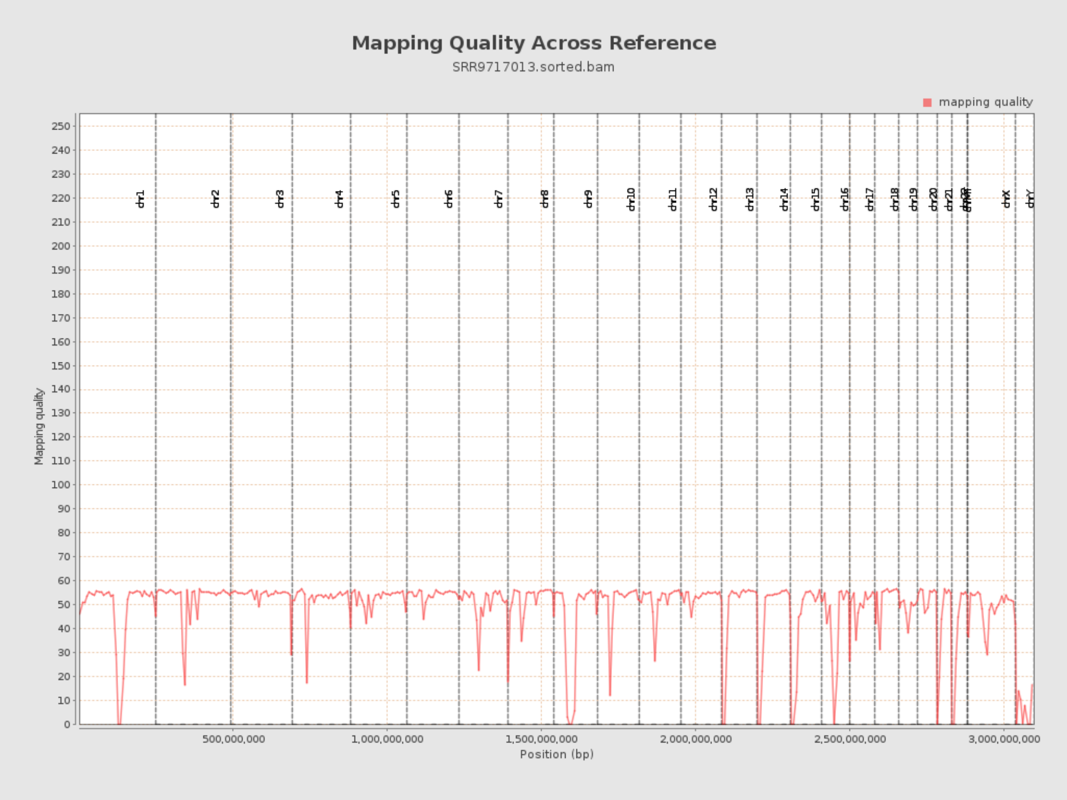
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram