Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:55:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238052.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_SRR6238052 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238052.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:55:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238052.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,129,798
Mapped reads	1,889,518 / 88.72%
Unmapped reads	240,280 / 11.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,877 / 1.17%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	135,213 / 6.35%
Duplication rate	5.71%
Clipped reads	831,461 / 39.04%

2.2. ACGT Content

Number/percentage of A's	34,561,676 / 27.38%
Number/percentage of C's	24,234,122 / 19.2%
Number/percentage of T's	39,129,478 / 31%
Number/percentage of G's	28,300,263 / 22.42%
Number/percentage of N's	7,711 / 0.01%
GC Percentage	41.62%

2.3. Coverage

Mean	0.0408

Standard Deviation	0.3874

2.4. Mapping Quality

Mean Mapping Quality	42.5

2.5. Mismatches and indels

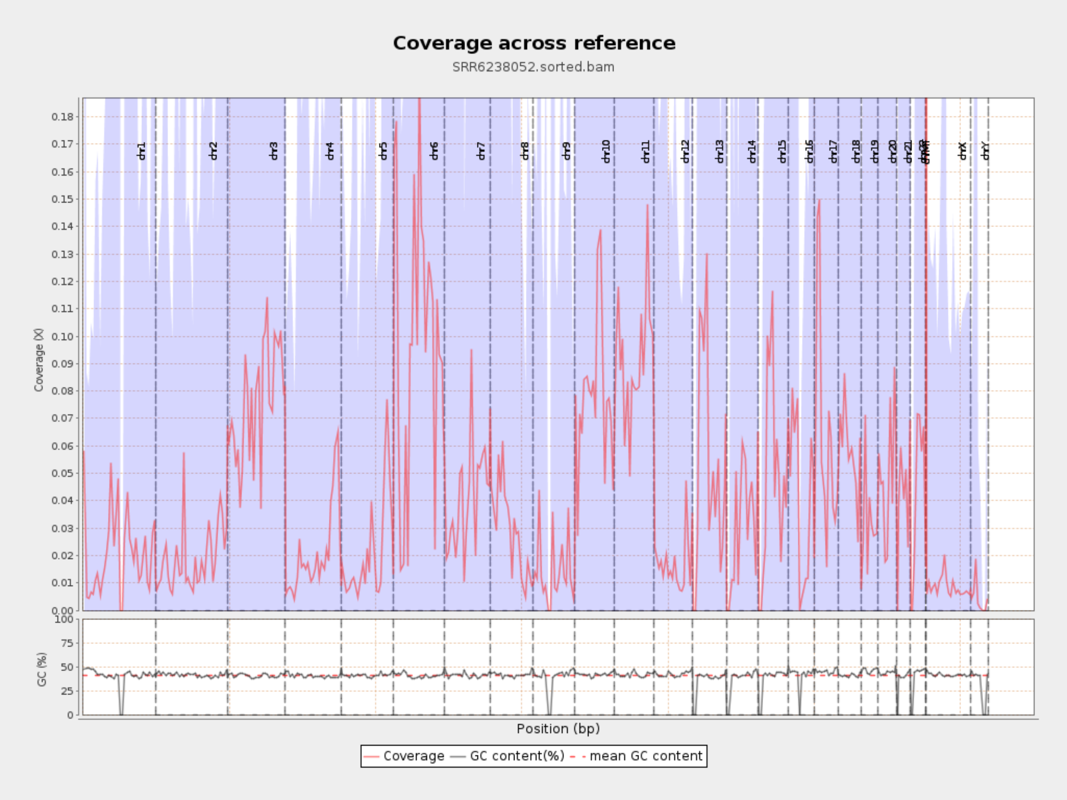
General error rate	0.76%
Mismatches	944,440
Insertions	8,609
Mapped reads with at least one insertion	0.45%
Deletions	32,068
Mapped reads with at least one deletion	1.68%
Homopolymer indels	45.39%

2.6. Chromosome stats

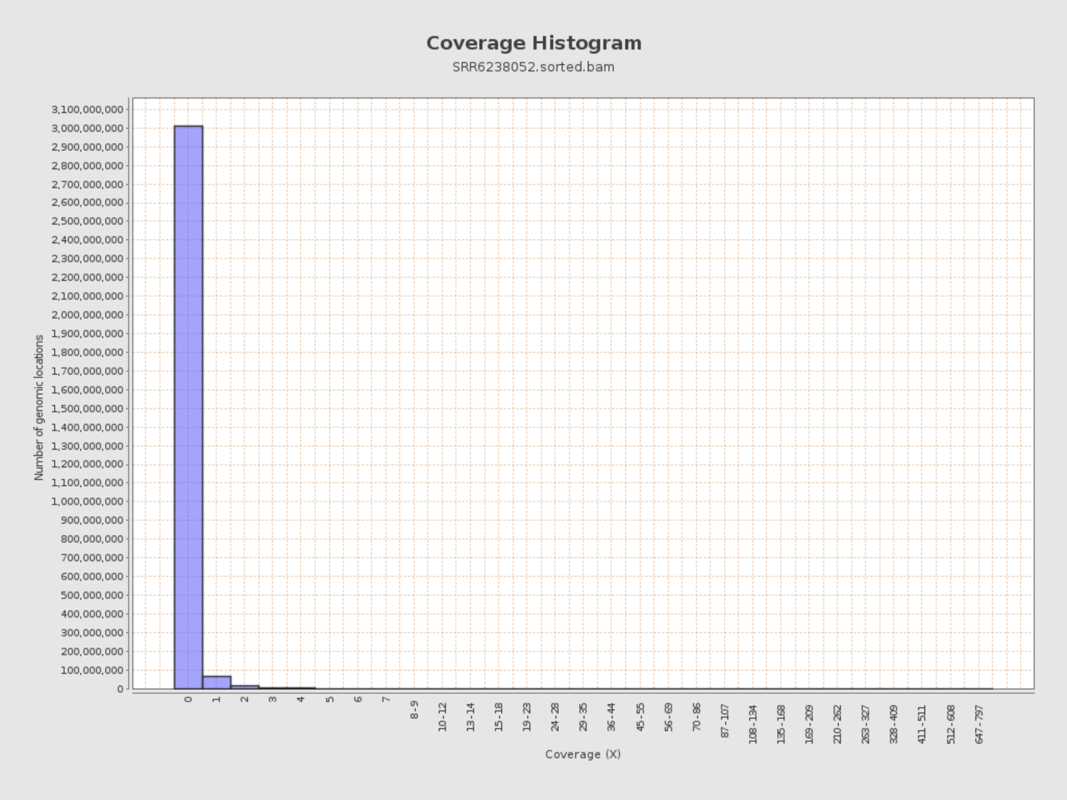
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5134868	0.0206	0.5737
chr2	243199373	4566044	0.0188	0.4156
chr3	198022430	15012259	0.0758	0.3729
chr4	191154276	3967167	0.0208	0.1968
chr5	180915260	3802488	0.021	0.2015
chr6	171115067	17067191	0.0997	0.4914
chr7	159138663	6550820	0.0412	0.367

chr8	146364022	4261589	0.0291	0.5463
chr9	141213431	2031681	0.0144	0.2893
chr10	135534747	10642753	0.0785	0.4537
chr11	135006516	12441729	0.0922	0.4987
chr12	133851895	2285174	0.0171	0.1846
chr13	115169878	6013423	0.0522	0.3132
chr14	107349540	3152257	0.0294	0.2376
chr15	102531392	4803307	0.0468	0.2932
chr16	90354753	3620362	0.0401	0.2941
chr17	81195210	5291401	0.0652	0.3812
chr18	78077248	4544530	0.0582	0.6735
chr19	59128983	1945266	0.0329	0.3679
chr20	63025520	3156010	0.0501	0.3187
chr21	48129895	1984953	0.0412	0.29
chr22	51304566	2247883	0.0438	0.2862
chrMT	16571	165051	9.9602	6.2528
chrX	155270560	1322507	0.0085	0.1581
chrY	59373566	279669	0.0047	0.1669

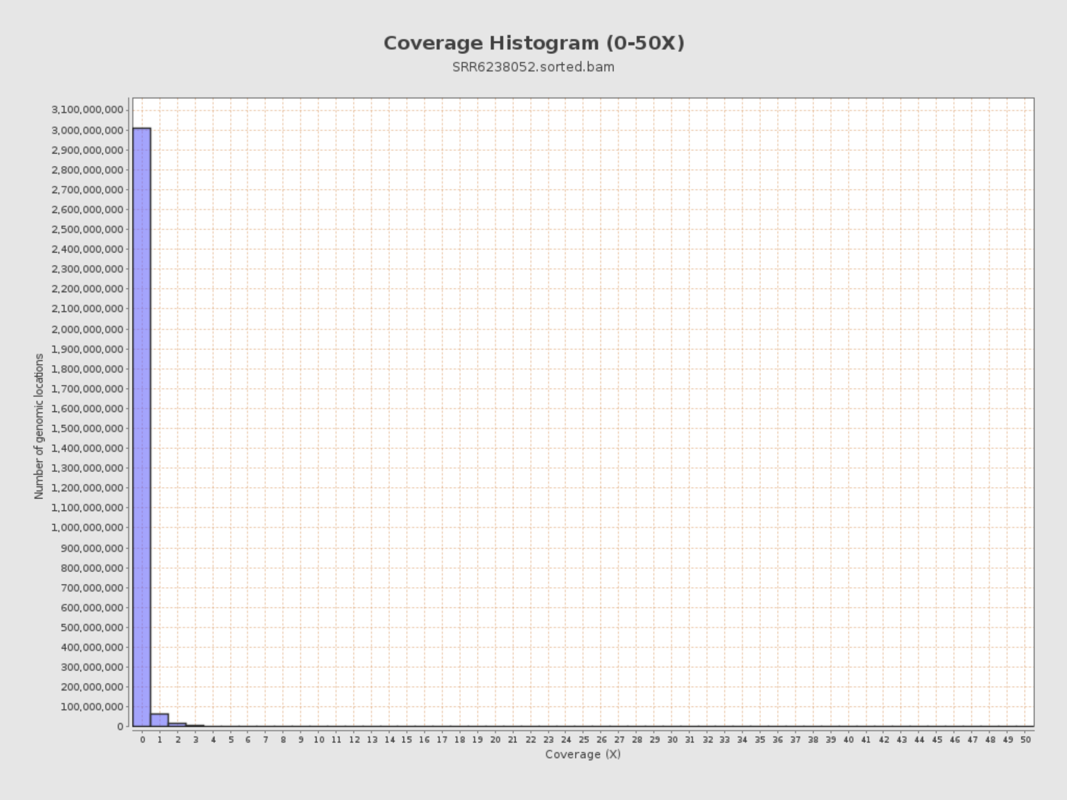
3. Results : Coverage across reference



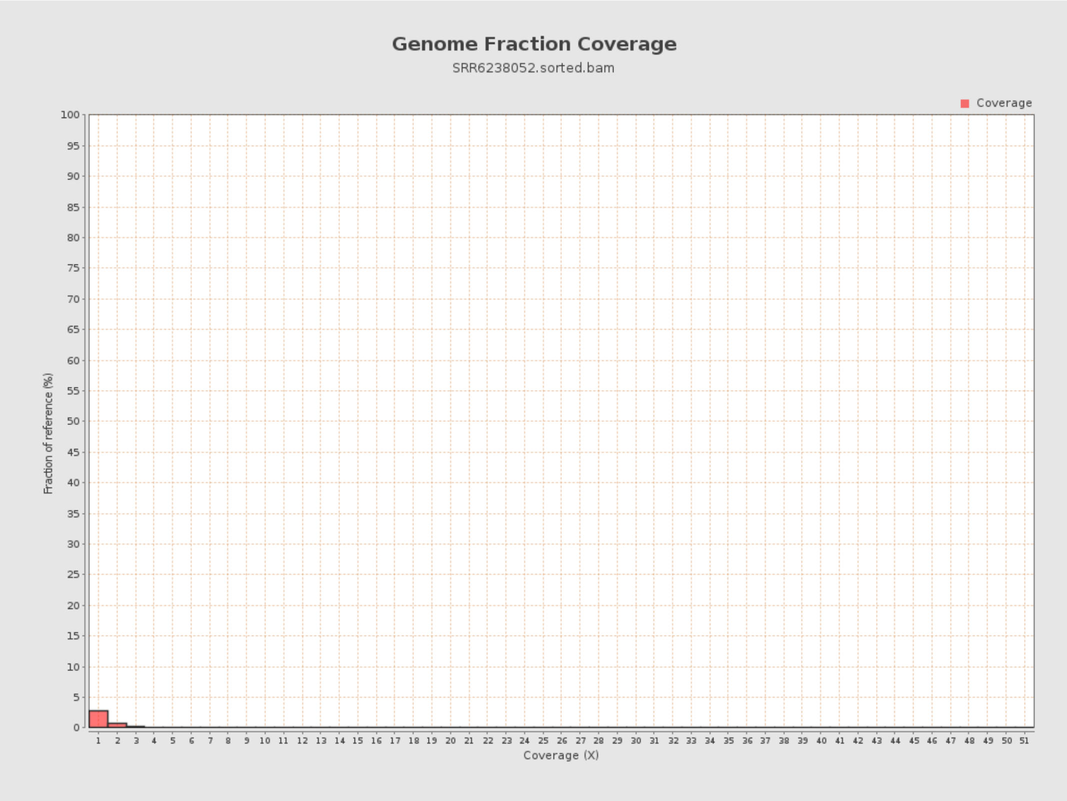
4. Results : Coverage Histogram



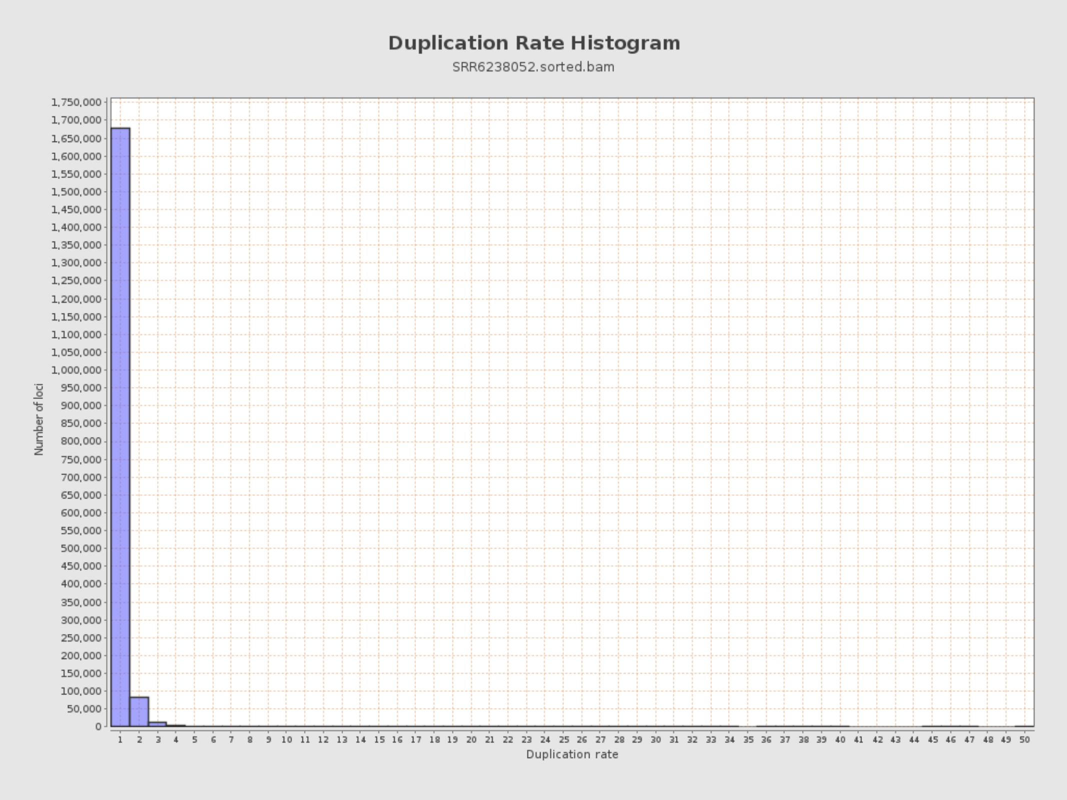
5. Results : Coverage Histogram (0-50X)



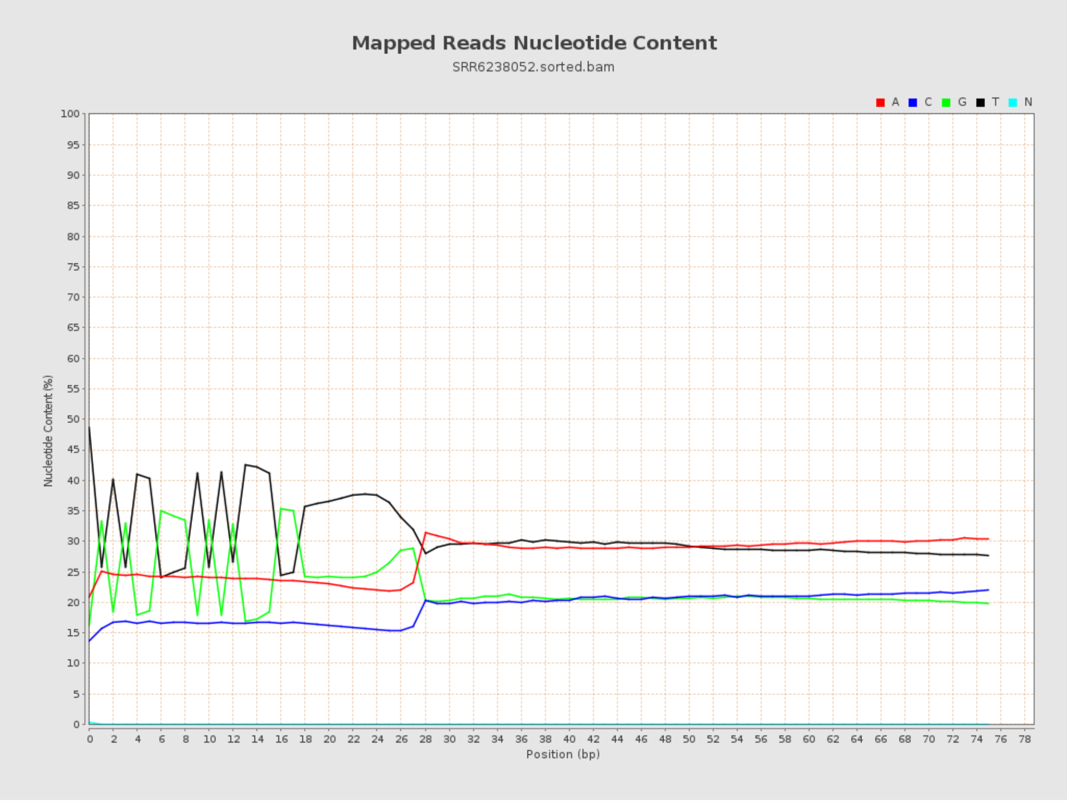
6. Results : Genome Fraction Coverage



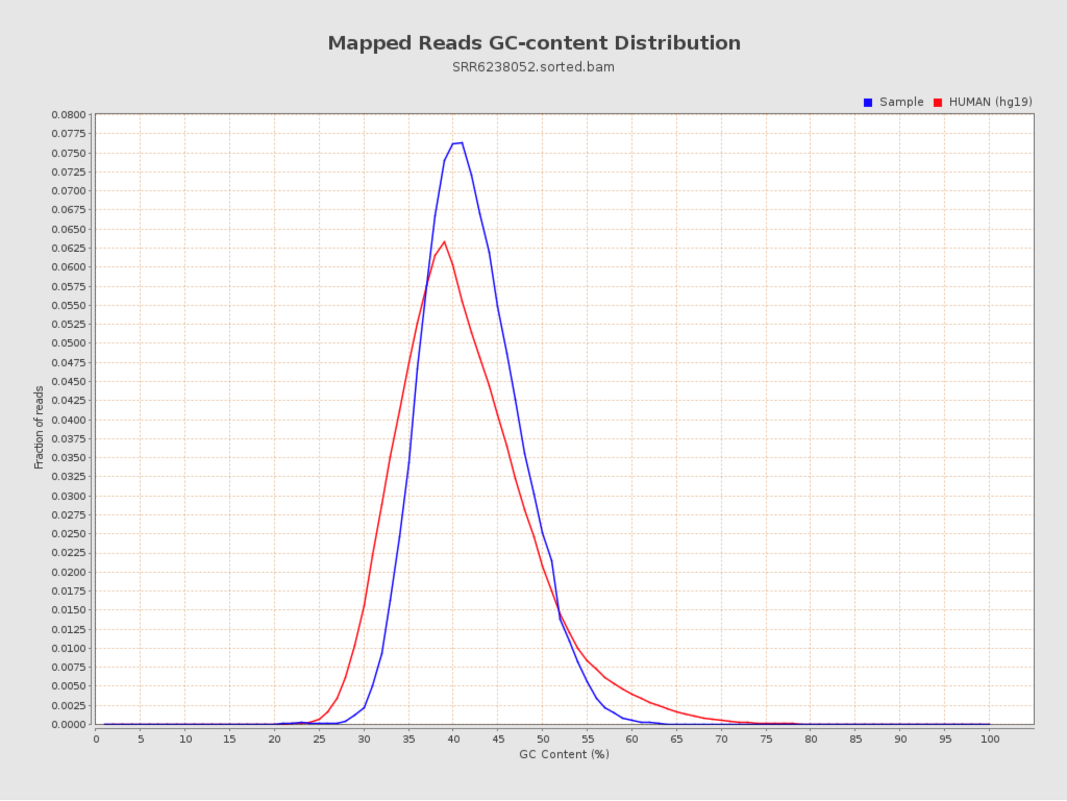
7. Results : Duplication Rate Histogram



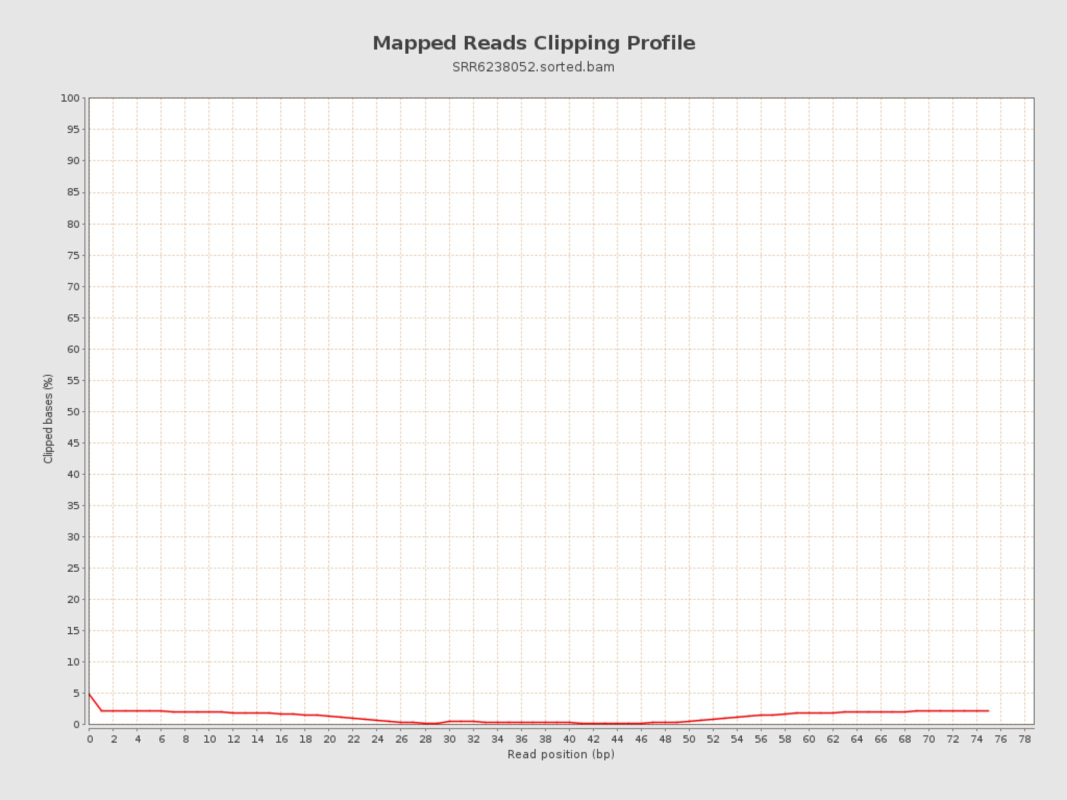
8. Results : Mapped Reads Nucleotide Content



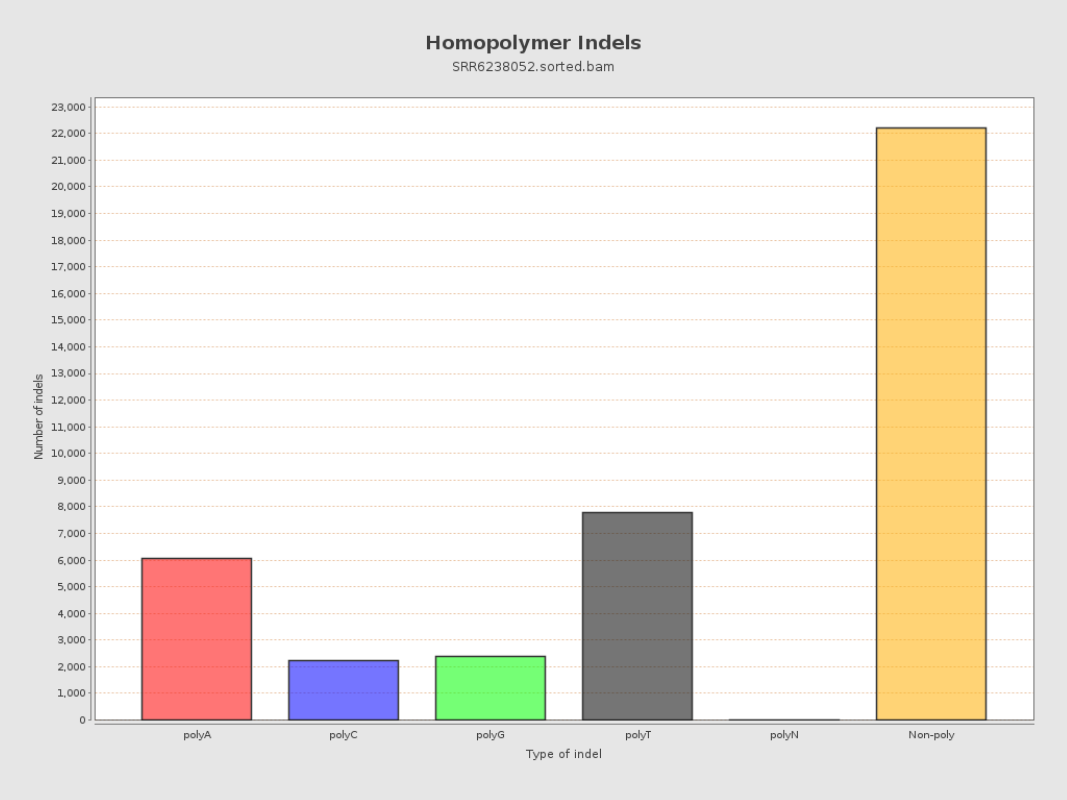
9. Results : Mapped Reads GC-content Distribution



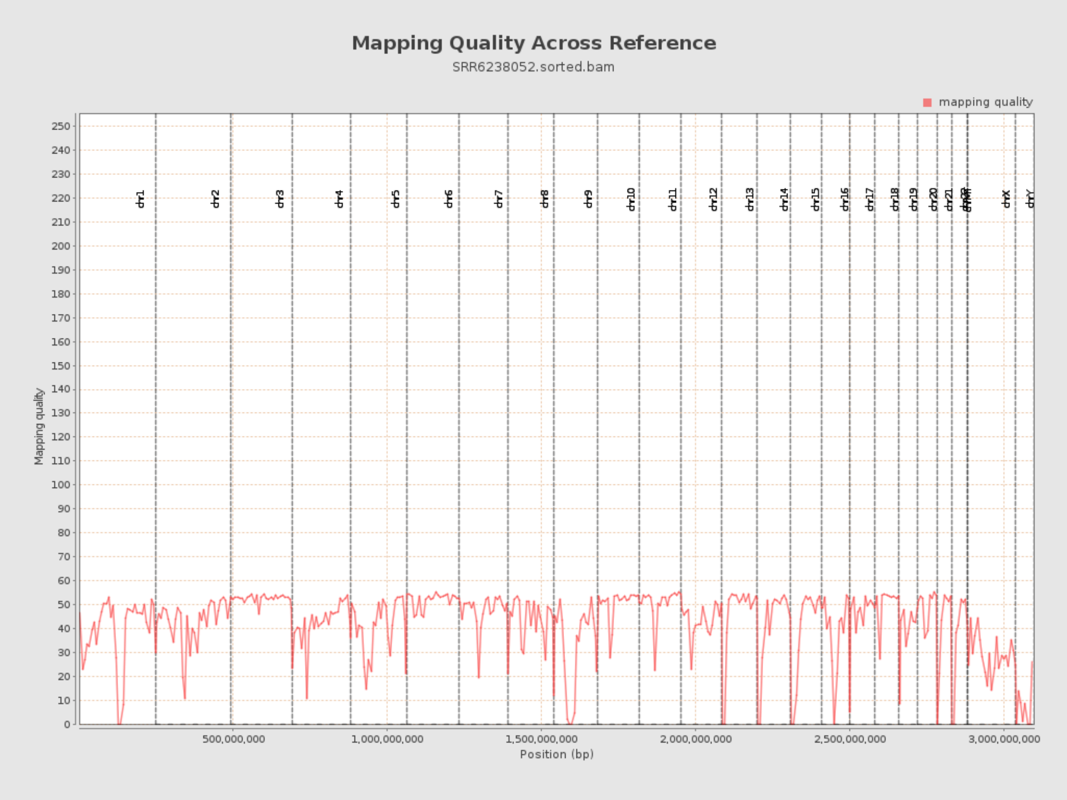
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram