Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 14:17:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238279.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_SRR6238279 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238279.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 14:17:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238279.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,517,401
Mapped reads	1,356,244 / 89.38%
Unmapped reads	161,157 / 10.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,848 / 1.11%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	80,328 / 5.29%
Duplication rate	5.07%
Clipped reads	648,686 / 42.75%

2.2. ACGT Content

Number/percentage of A's	24,269,981 / 27.27%
Number/percentage of C's	15,938,714 / 17.91%
Number/percentage of T's	28,791,751 / 32.35%
Number/percentage of G's	19,943,491 / 22.41%
Number/percentage of N's	69,173 / 0.08%
GC Percentage	40.31%

2.3. Coverage

Mean	0.0288

Standard Deviation	0.252

2.4. Mapping Quality

Mean Mapping Quality	44.05

2.5. Mismatches and indels

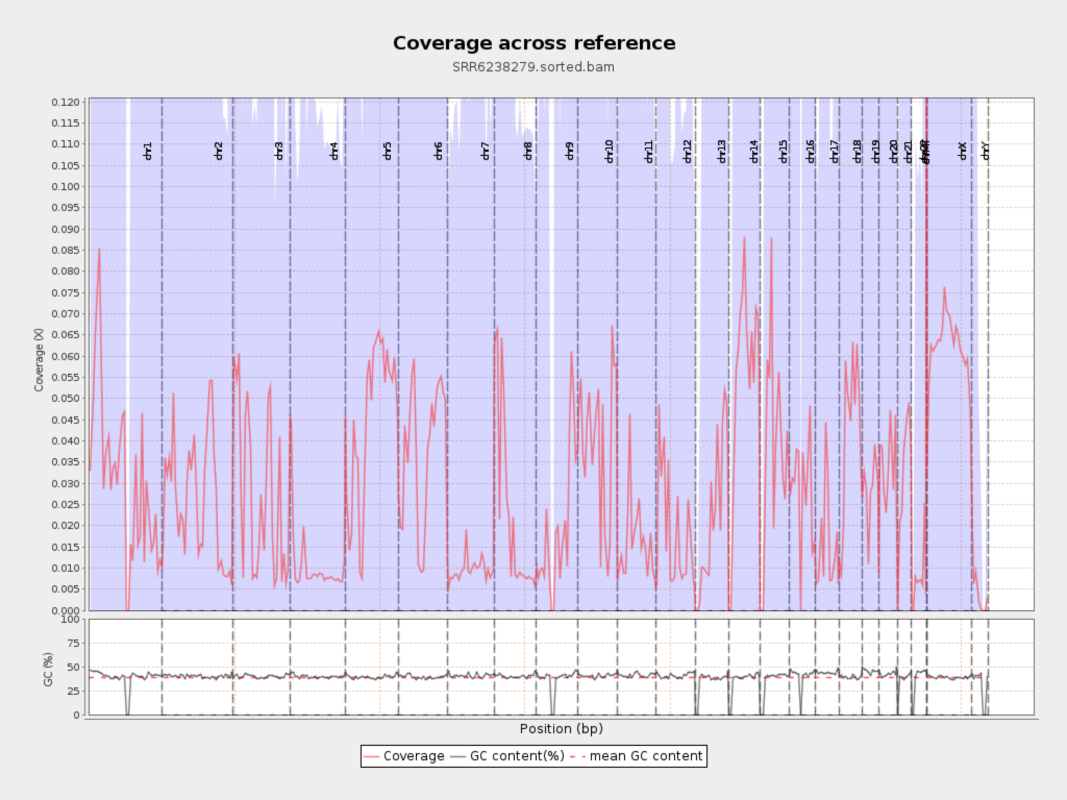
General error rate	0.84%
Mismatches	735,605
Insertions	6,650
Mapped reads with at least one insertion	0.49%
Deletions	27,421
Mapped reads with at least one deletion	2%
Homopolymer indels	47.14%

2.6. Chromosome stats

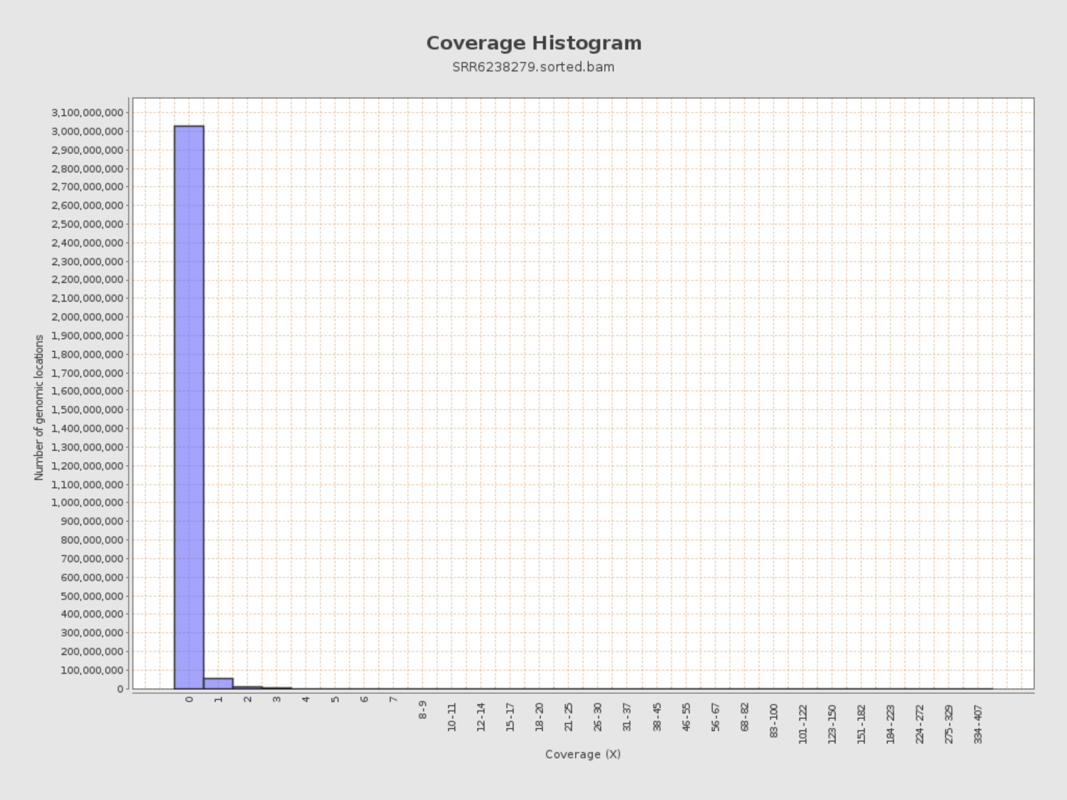
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7847953	0.0315	0.3761
chr2	243199373	6422621	0.0264	0.2774
chr3	198022430	5347082	0.027	0.2018
chr4	191154276	1906361	0.01	0.1257
chr5	180915260	8282198	0.0458	0.2609
chr6	171115067	6411924	0.0375	0.2768
chr7	159138663	1546520	0.0097	0.1682

chr8	146364022	3300360	0.0225	0.2301
chr9	141213431	2748620	0.0195	0.2051
chr10	135534747	5420220	0.04	0.2947
chr11	135006516	2200510	0.0163	0.1927
chr12	133851895	2435780	0.0182	0.1658
chr13	115169878	2544780	0.0221	0.1837
chr14	107349540	5899207	0.055	0.2893
chr15	102531392	3872714	0.0378	0.2395
chr16	90354753	2559312	0.0283	0.2178
chr17	81195210	1309180	0.0161	0.1555
chr18	78077248	3371292	0.0432	0.4344
chr19	59128983	1638605	0.0277	0.2689
chr20	63025520	2180377	0.0346	0.2273
chr21	48129895	1553849	0.0323	0.2216
chr22	51304566	420094	0.0082	0.1071
chrMT	16571	4722	0.285	0.6632
chrX	155270560	9586174	0.0617	0.3226
chrY	59373566	248339	0.0042	0.085

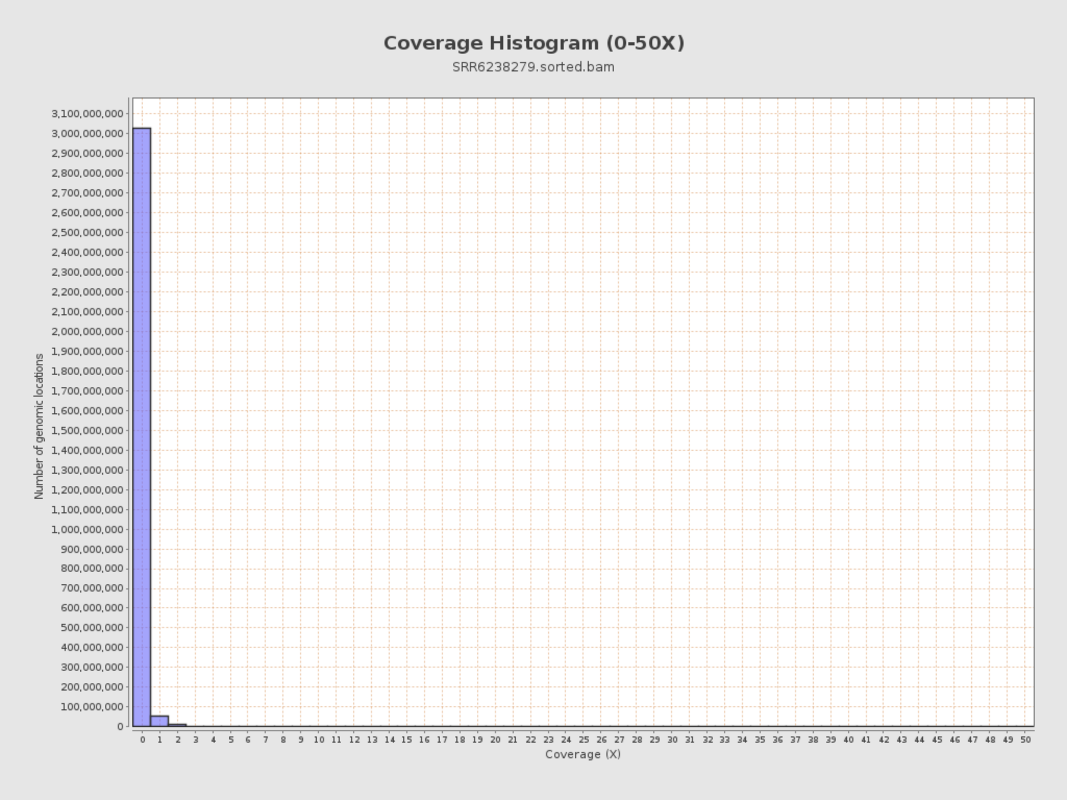
3. Results : Coverage across reference



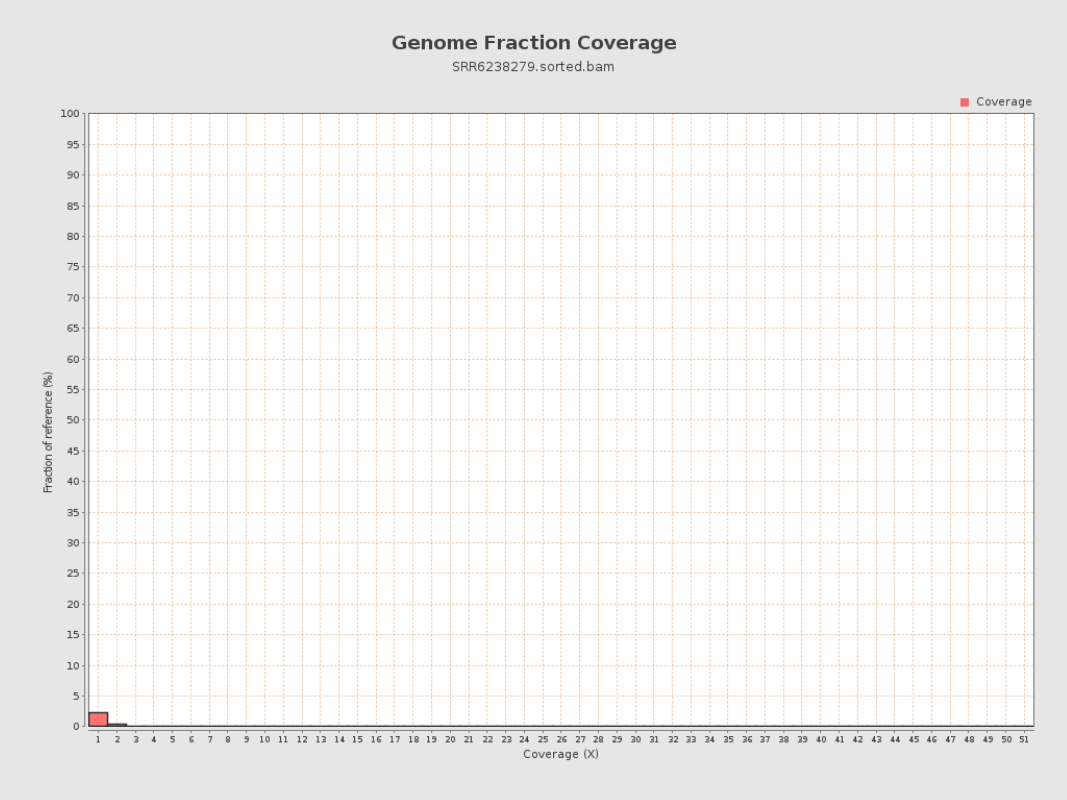
4. Results : Coverage Histogram



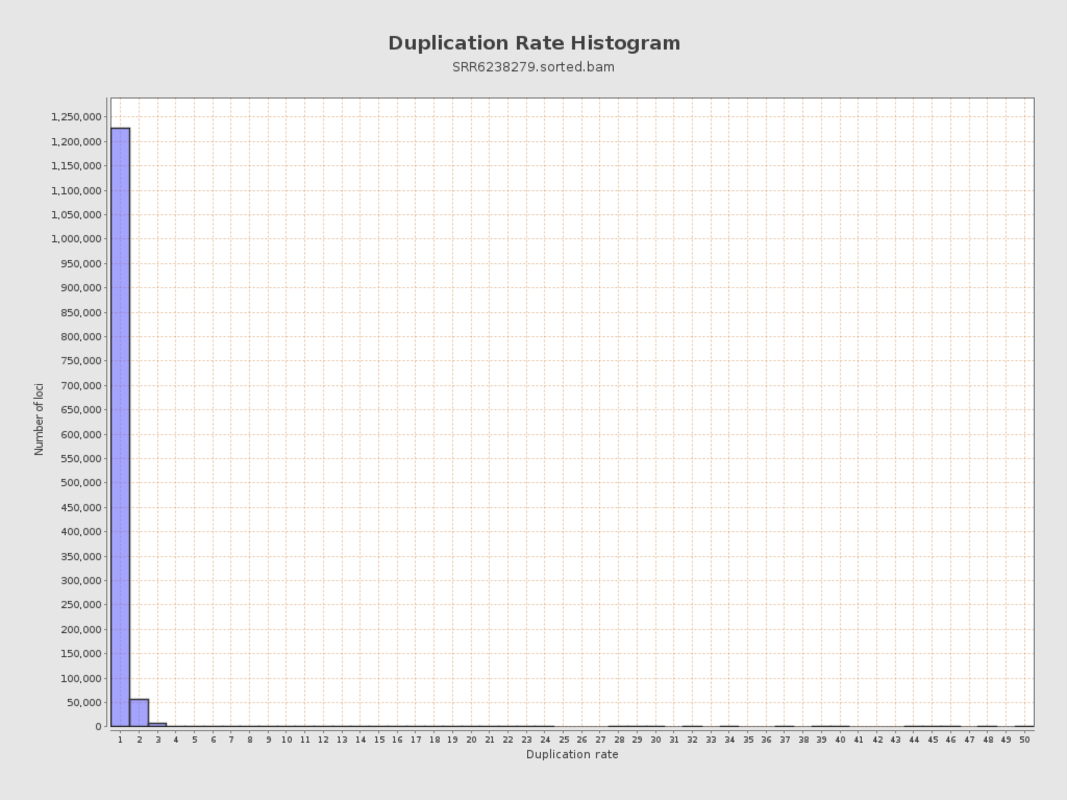
5. Results : Coverage Histogram (0-50X)



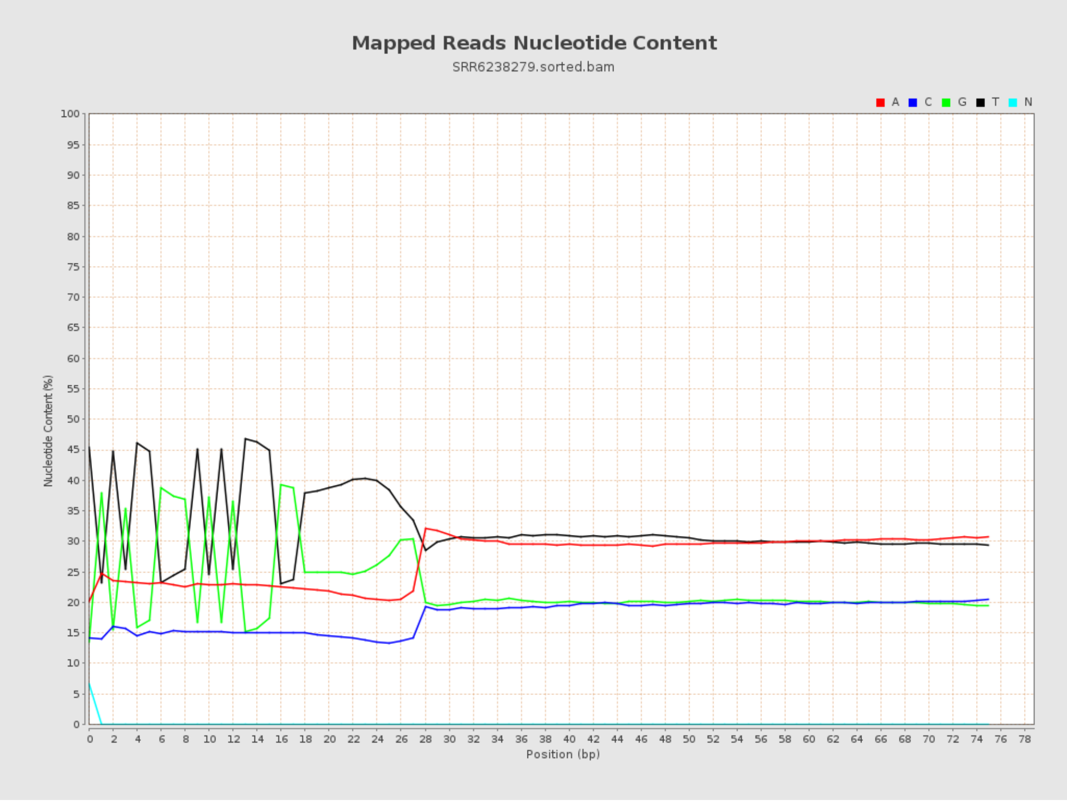
6. Results : Genome Fraction Coverage



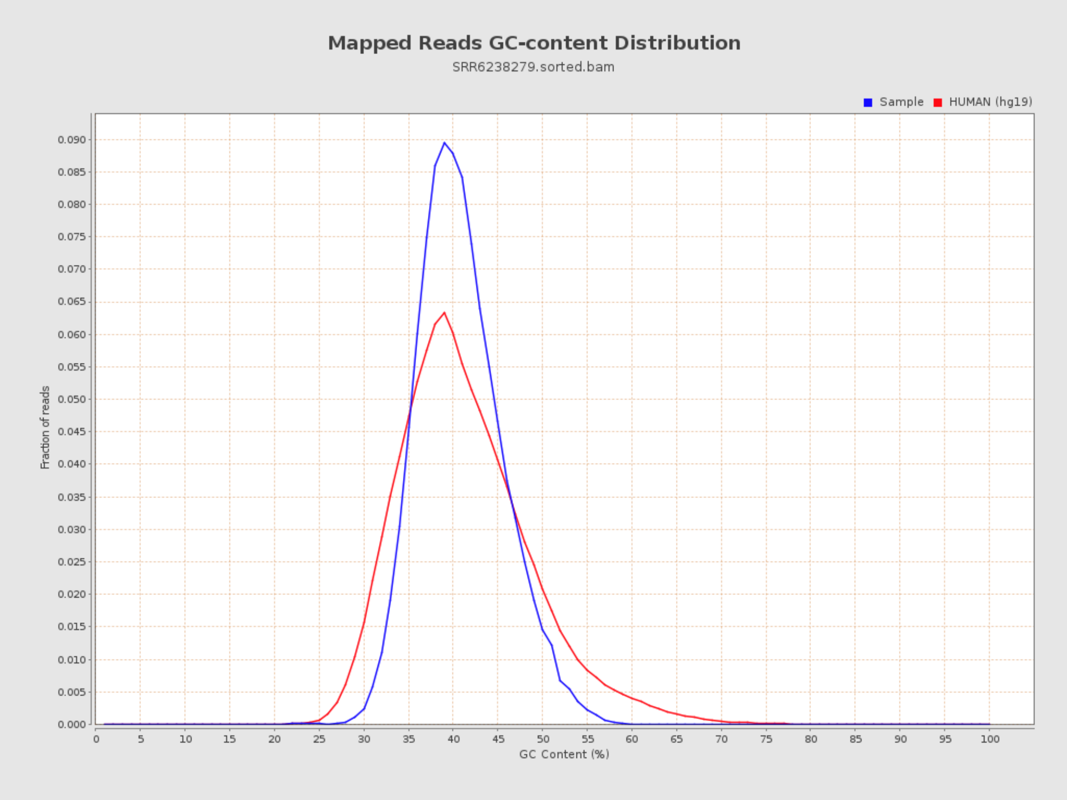
7. Results : Duplication Rate Histogram



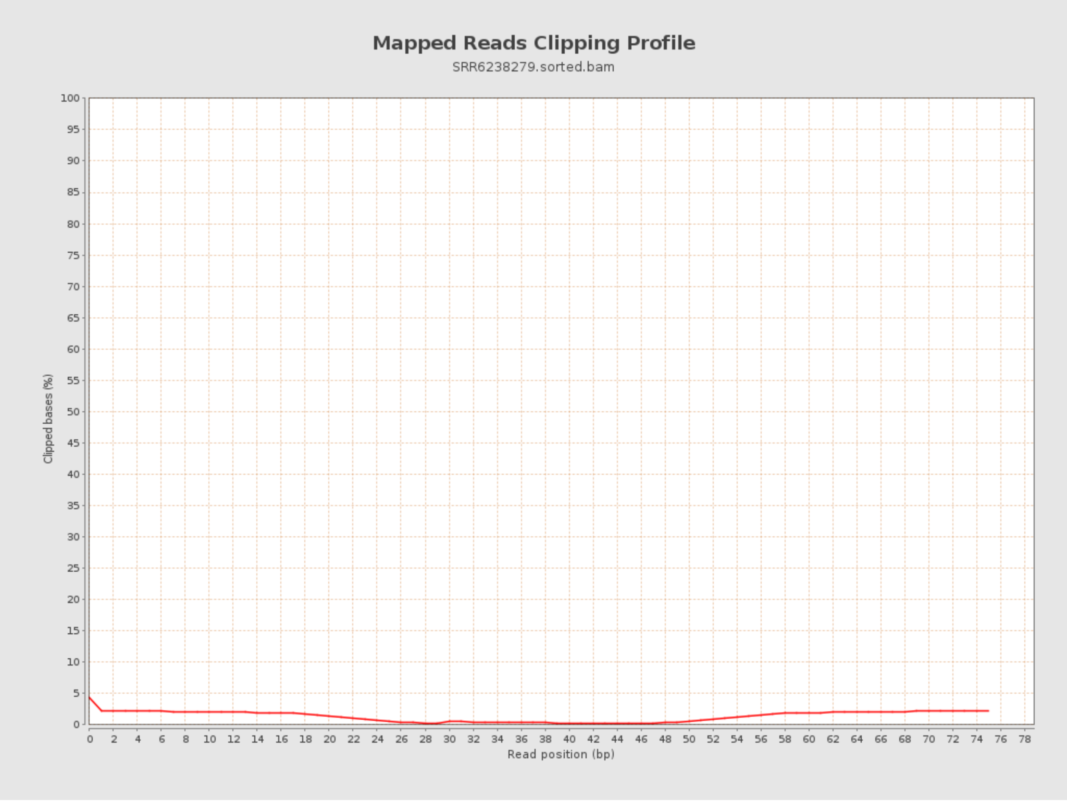
8. Results : Mapped Reads Nucleotide Content



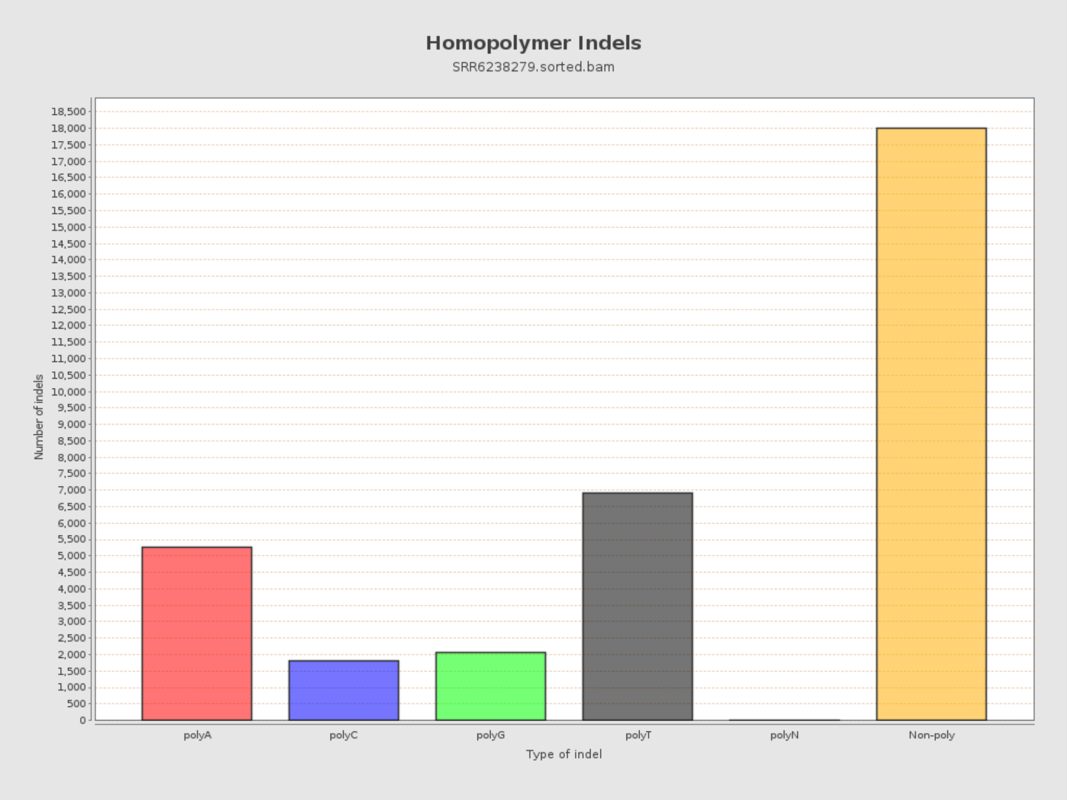
9. Results : Mapped Reads GC-content Distribution



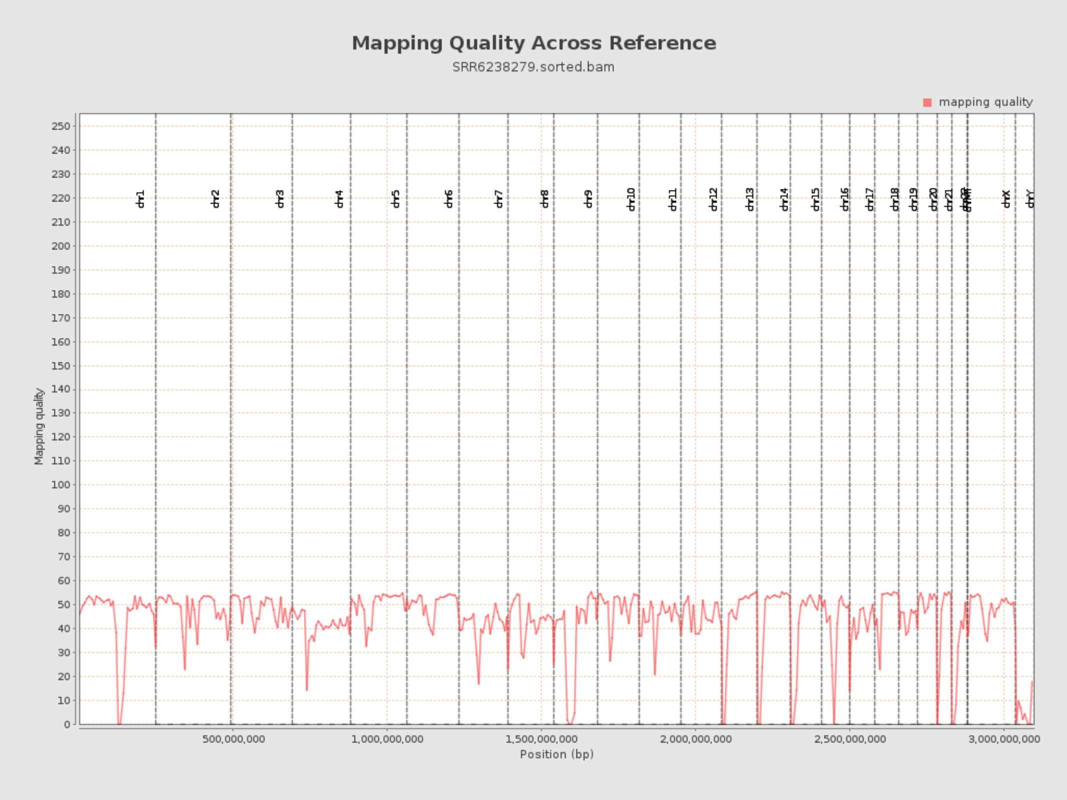
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram