Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:54:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238271.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_SRR6238271 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238271.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:54:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238271.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,710,823
Mapped reads	2,486,576 / 91.73%
Unmapped reads	224,247 / 8.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,513 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	100,310 / 3.7%
Duplication rate	3%
Clipped reads	1,257,117 / 46.37%

2.2. ACGT Content

Number/percentage of A's	44,761,317 / 27.48%
Number/percentage of C's	30,706,034 / 18.85%
Number/percentage of T's	50,075,000 / 30.75%
Number/percentage of G's	37,272,714 / 22.89%
Number/percentage of N's	44,957 / 0.03%
GC Percentage	41.74%

2.3. Coverage

Mean	0.0526

Standard Deviation	0.4507

2.4. Mapping Quality

Mean Mapping Quality	43.92

2.5. Mismatches and indels

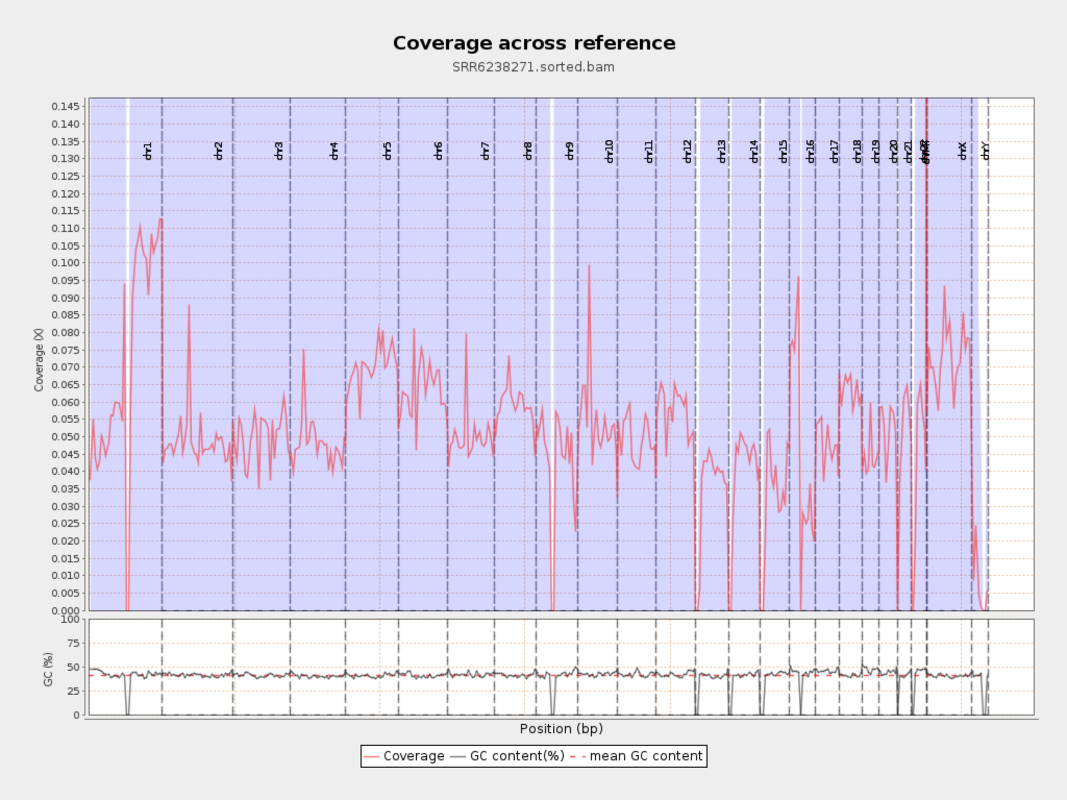
General error rate	0.89%
Mismatches	1,431,698
Insertions	13,157
Mapped reads with at least one insertion	0.52%
Deletions	54,176
Mapped reads with at least one deletion	2.15%
Homopolymer indels	44.39%

2.6. Chromosome stats

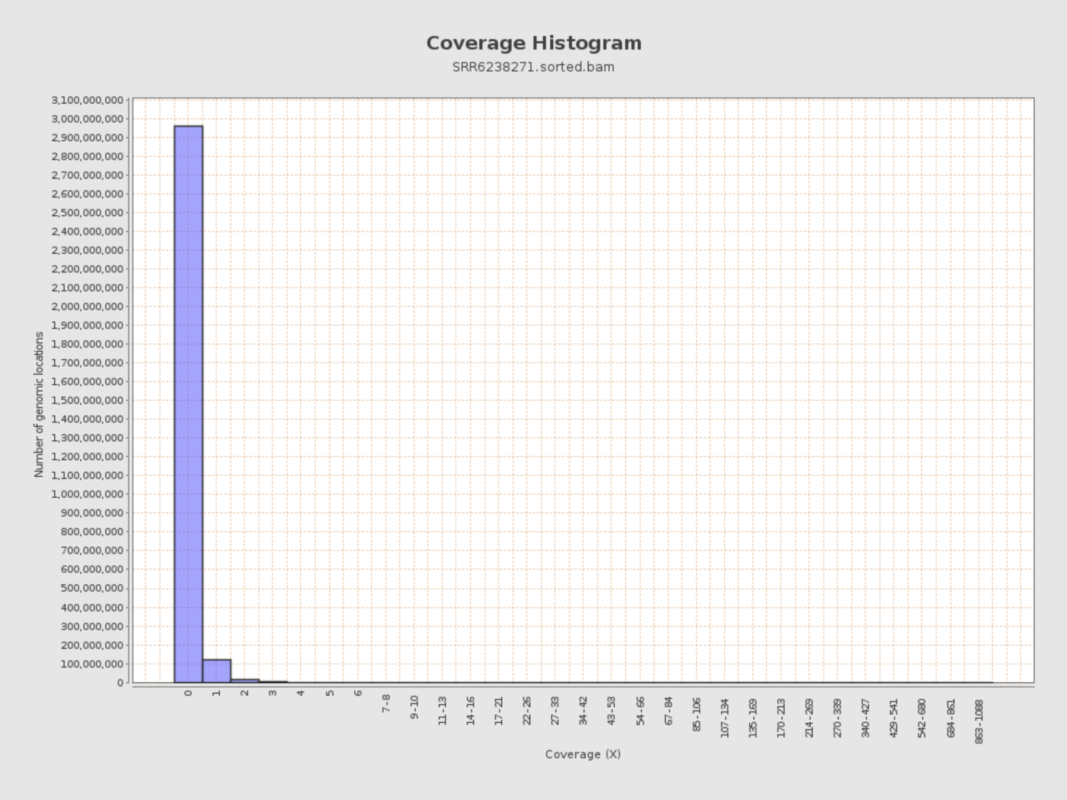
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17678028	0.0709	0.8971
chr2	243199373	11849116	0.0487	0.5273
chr3	198022430	9910094	0.05	0.2584
chr4	191154276	9197102	0.0481	0.2855
chr5	180915260	12722216	0.0703	0.3057
chr6	171115067	10866119	0.0635	0.3557
chr7	159138663	7940480	0.0499	0.5804

chr8	146364022	8639554	0.059	0.5188
chr9	141213431	5923566	0.0419	0.3625
chr10	135534747	7518362	0.0555	0.4973
chr11	135006516	6643253	0.0492	0.3282
chr12	133851895	7644364	0.0571	0.2816
chr13	115169878	3875726	0.0337	0.2104
chr14	107349540	4182424	0.039	0.2718
chr15	102531392	3300955	0.0322	0.2134
chr16	90354753	4203807	0.0465	0.2925
chr17	81195210	3896037	0.048	0.2866
chr18	78077248	4947580	0.0634	0.6749
chr19	59128983	2633661	0.0445	0.6174
chr20	63025520	3246137	0.0515	0.2694
chr21	48129895	2326942	0.0483	0.28
chr22	51304566	2037463	0.0397	0.2287
chrMT	16571	5520	0.3331	0.7314
chrX	155270560	11275322	0.0726	0.3495
chrY	59373566	485621	0.0082	0.1958

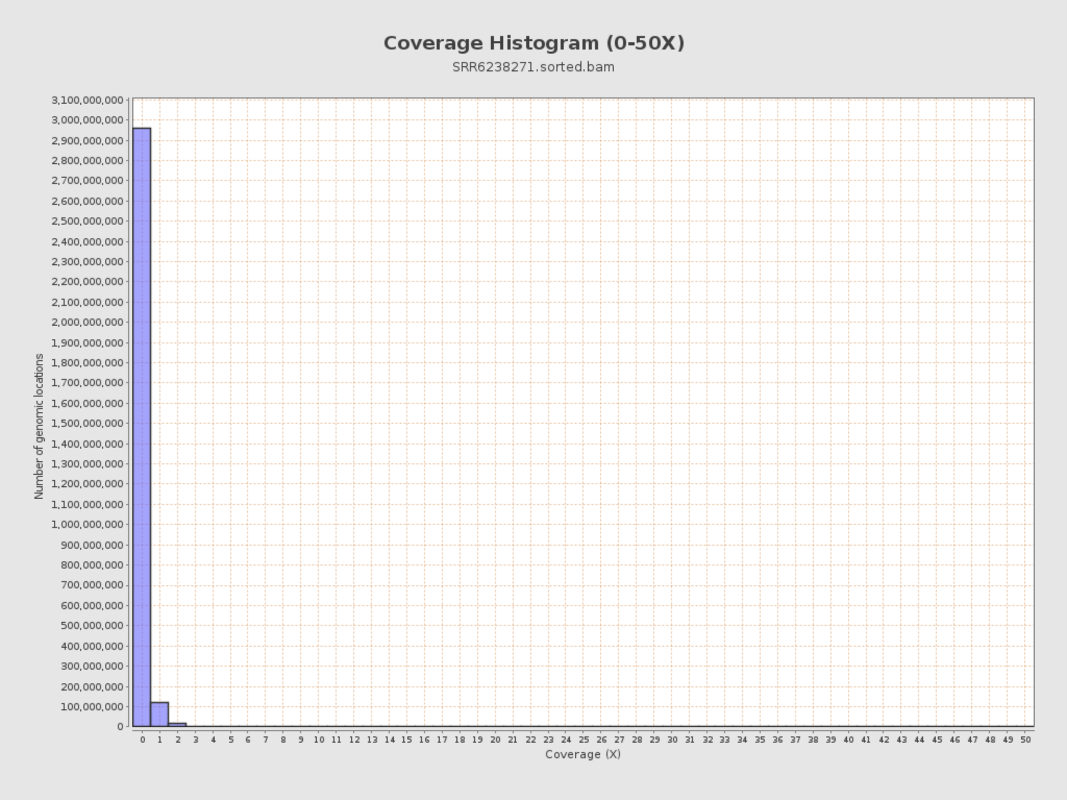
3. Results : Coverage across reference



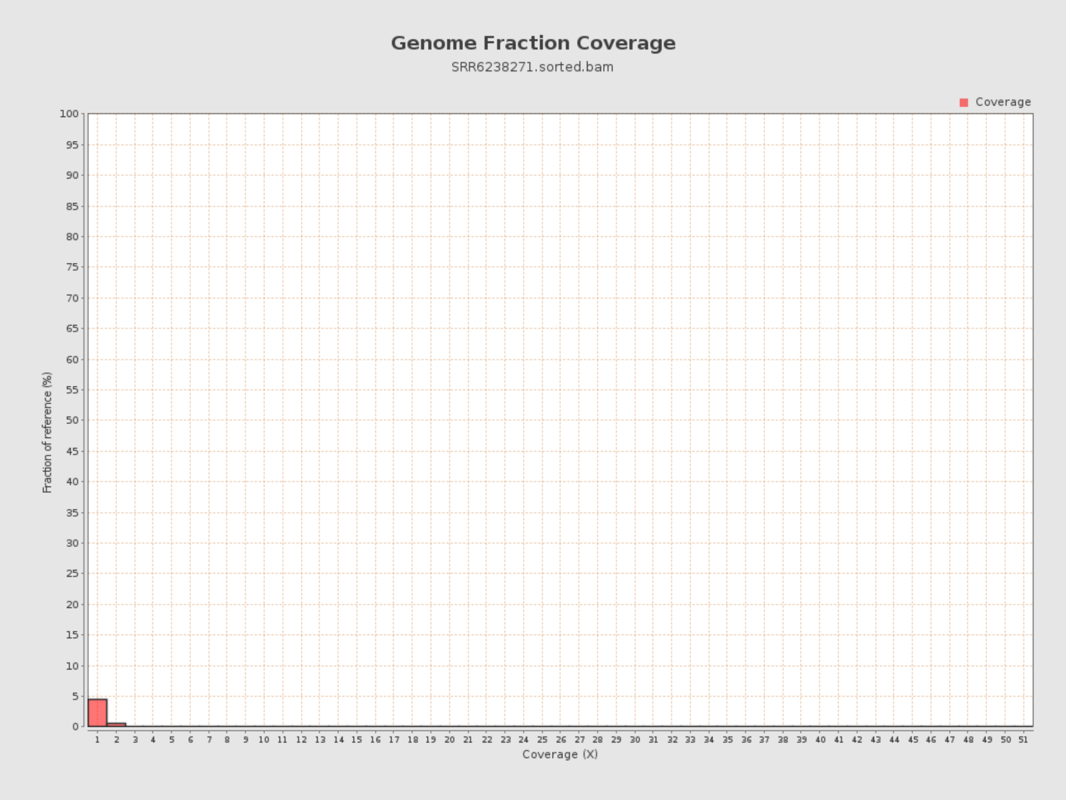
4. Results : Coverage Histogram



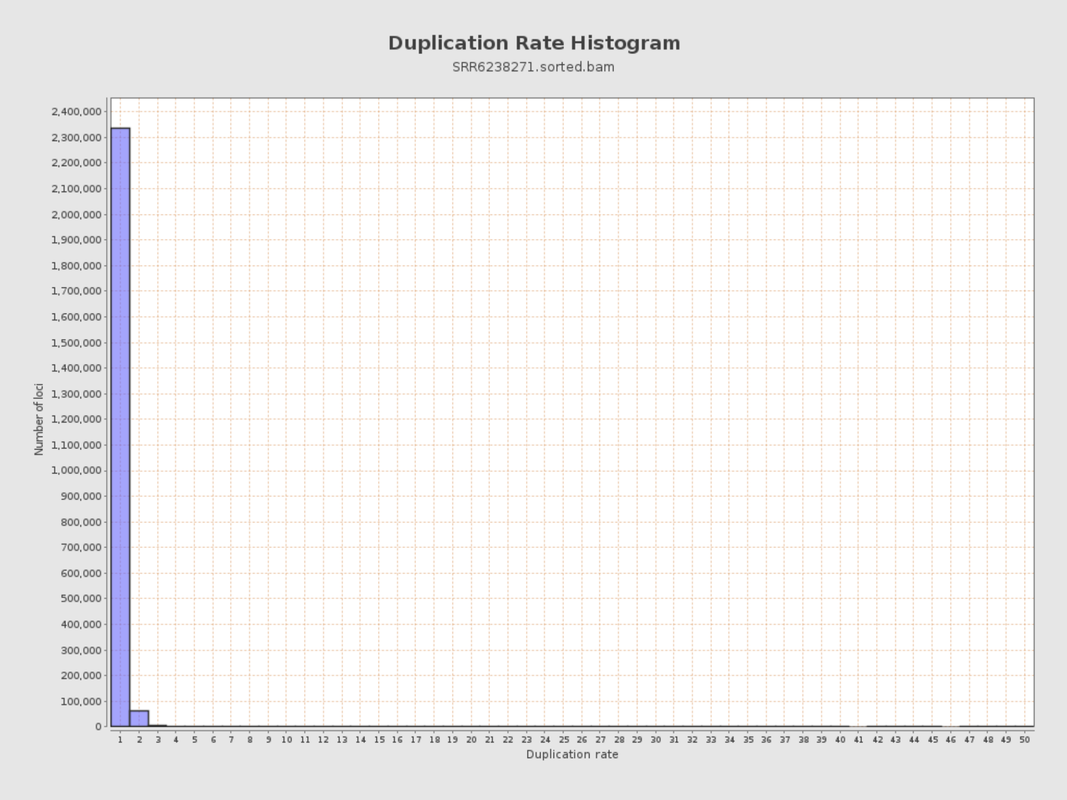
5. Results : Coverage Histogram (0-50X)



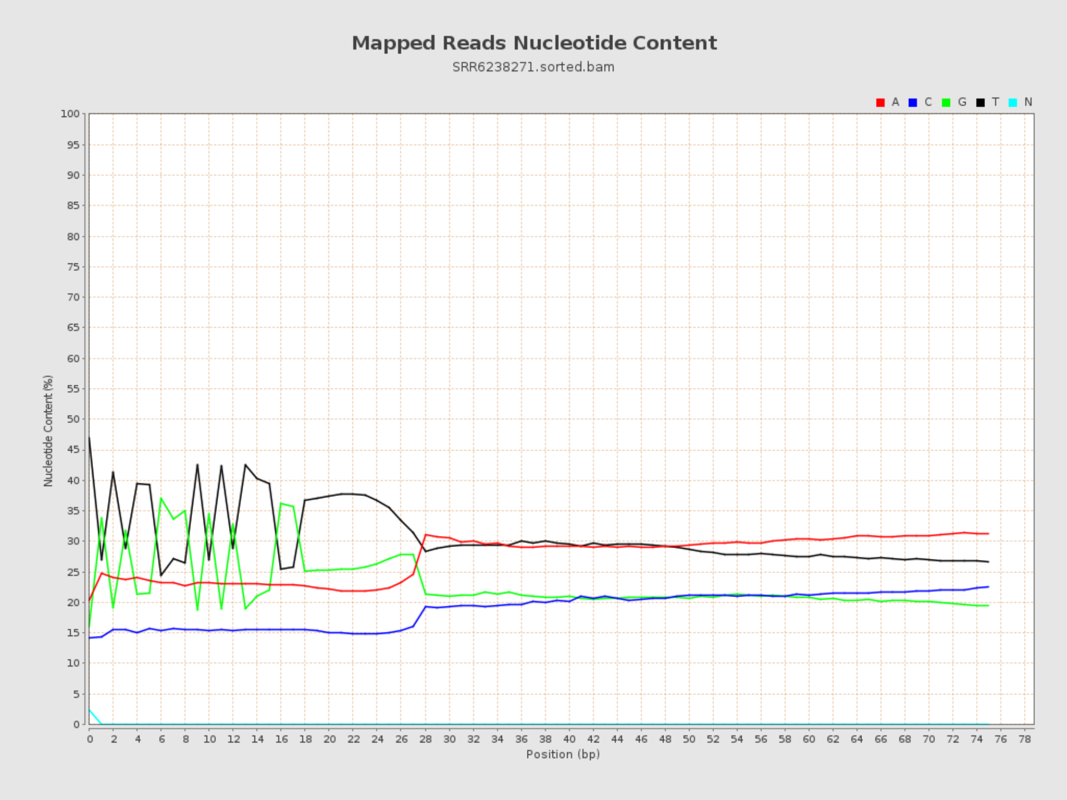
6. Results : Genome Fraction Coverage



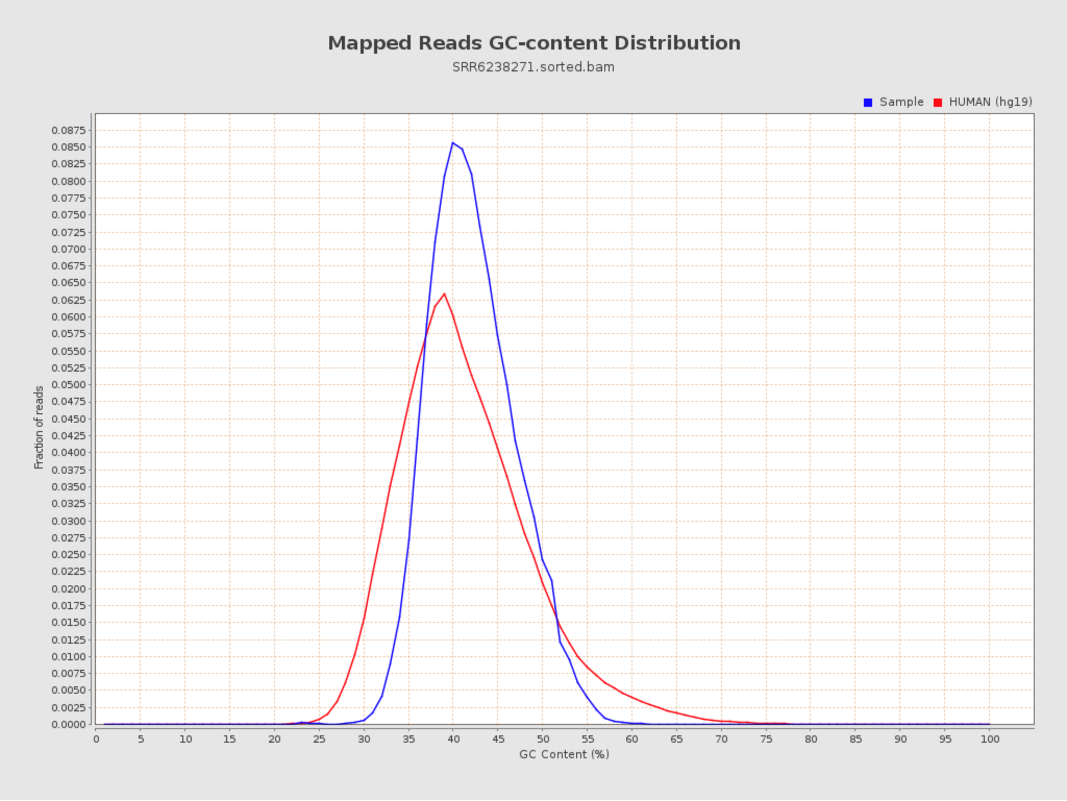
7. Results : Duplication Rate Histogram



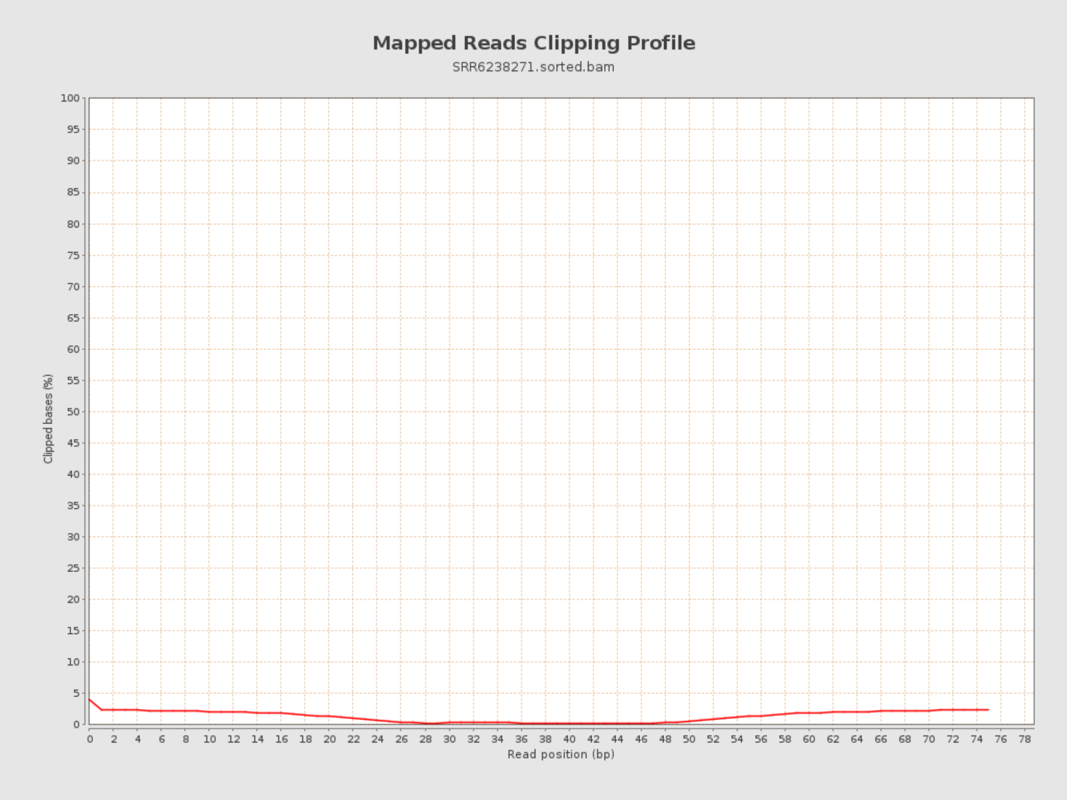
8. Results : Mapped Reads Nucleotide Content



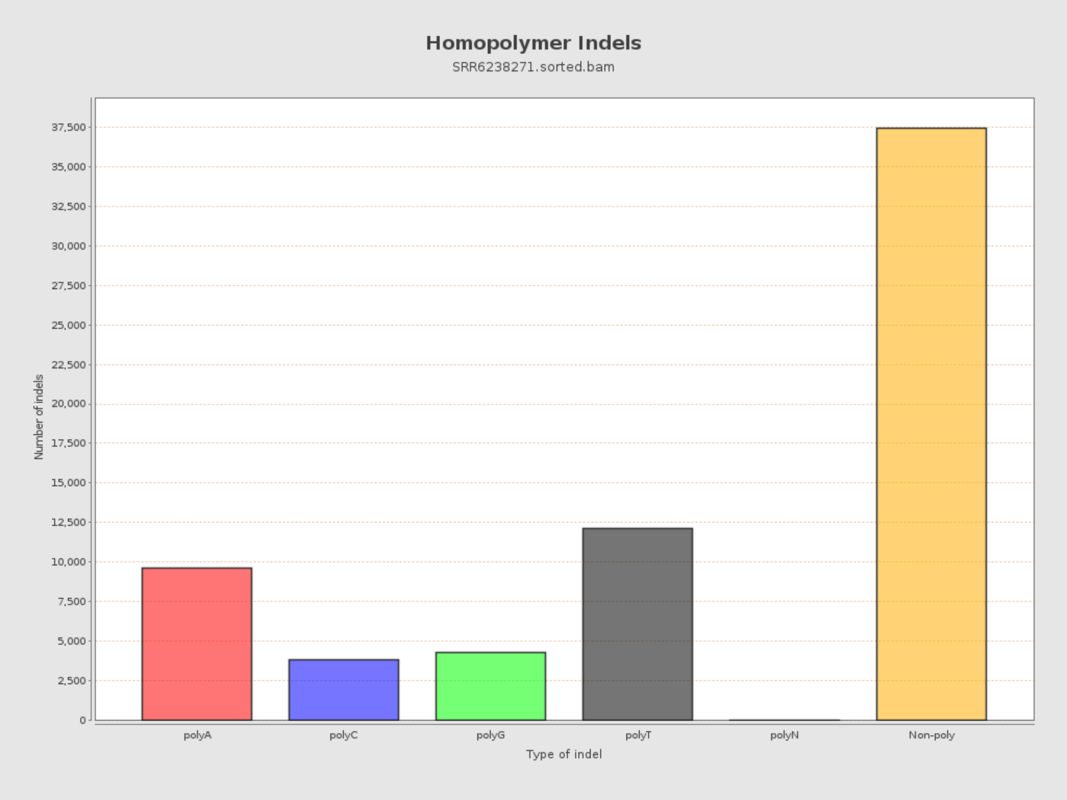
9. Results : Mapped Reads GC-content Distribution



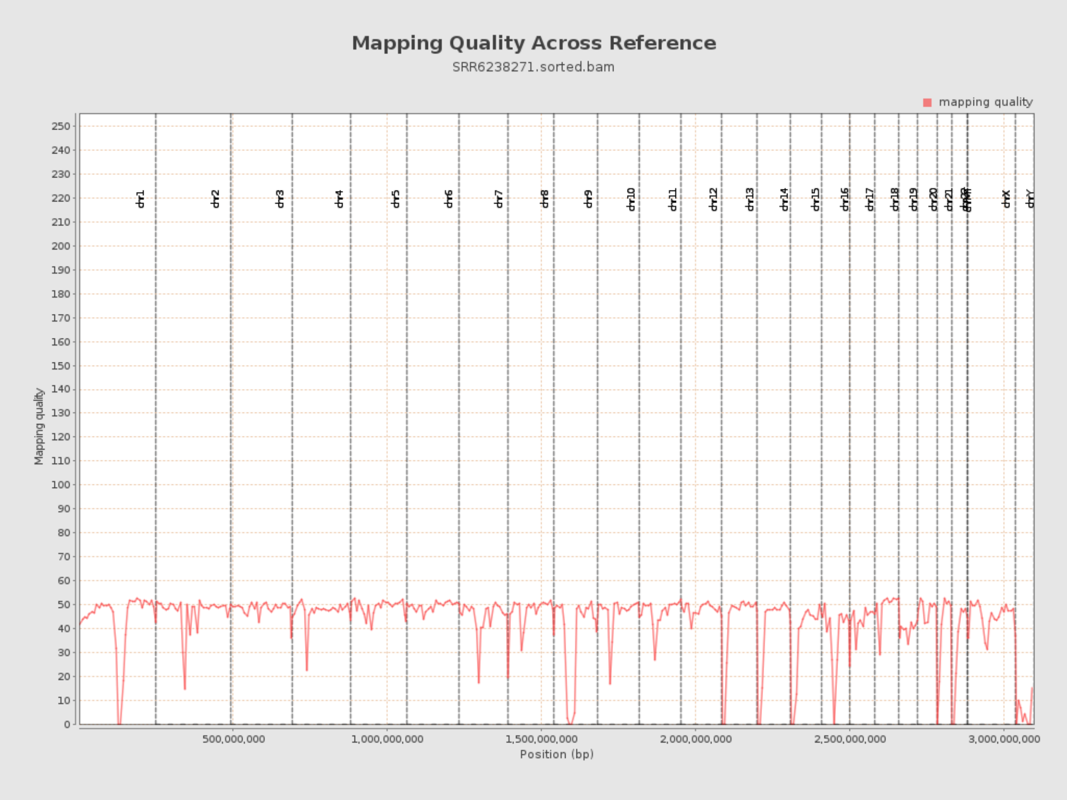
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram