Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 16:01:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238313.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_SRR6238313 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238313.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 16:01:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238313.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,483,314
Mapped reads	2,250,655 / 90.63%
Unmapped reads	232,659 / 9.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,494 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	98,054 / 3.95%
Duplication rate	3.24%
Clipped reads	1,149,173 / 46.28%

2.2. ACGT Content

Number/percentage of A's	40,377,537 / 27.4%
Number/percentage of C's	28,049,676 / 19.04%
Number/percentage of T's	45,304,532 / 30.75%
Number/percentage of G's	33,571,524 / 22.79%
Number/percentage of N's	34,441 / 0.02%
GC Percentage	41.82%

2.3. Coverage

Mean	0.0476

Standard Deviation	0.4239

2.4. Mapping Quality

Mean Mapping Quality	45.27

2.5. Mismatches and indels

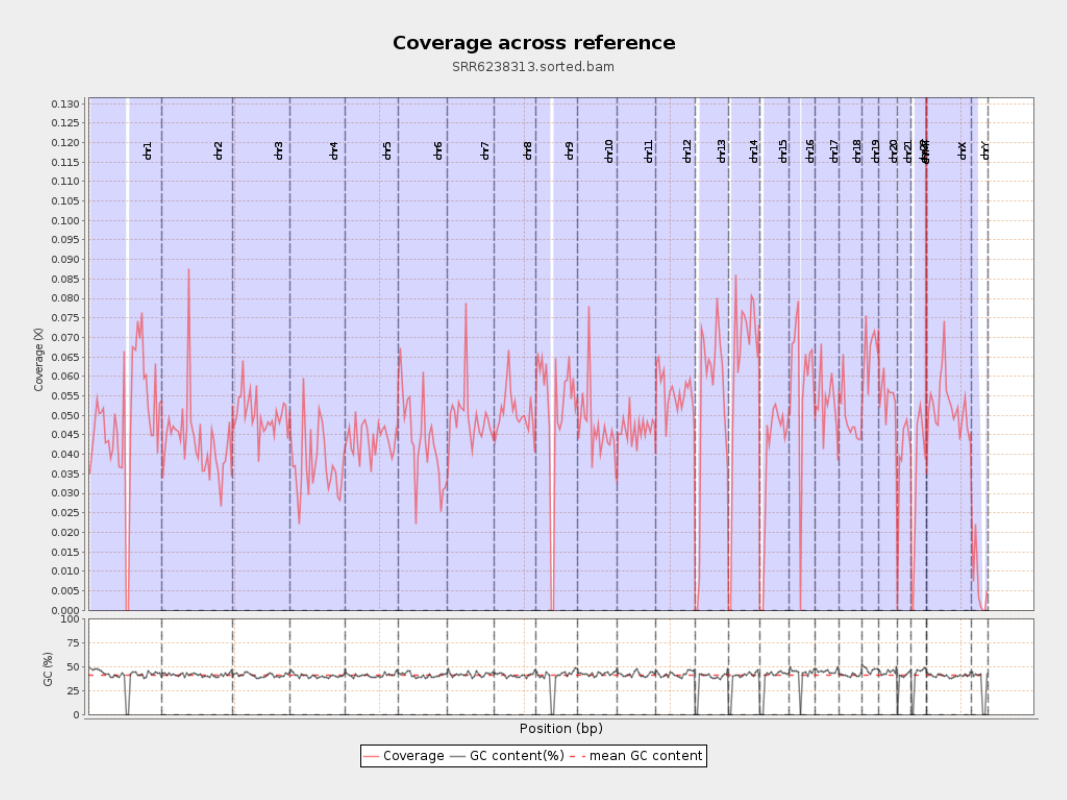
General error rate	0.86%
Mismatches	1,248,147
Insertions	11,645
Mapped reads with at least one insertion	0.51%
Deletions	43,567
Mapped reads with at least one deletion	1.91%
Homopolymer indels	45.15%

2.6. Chromosome stats

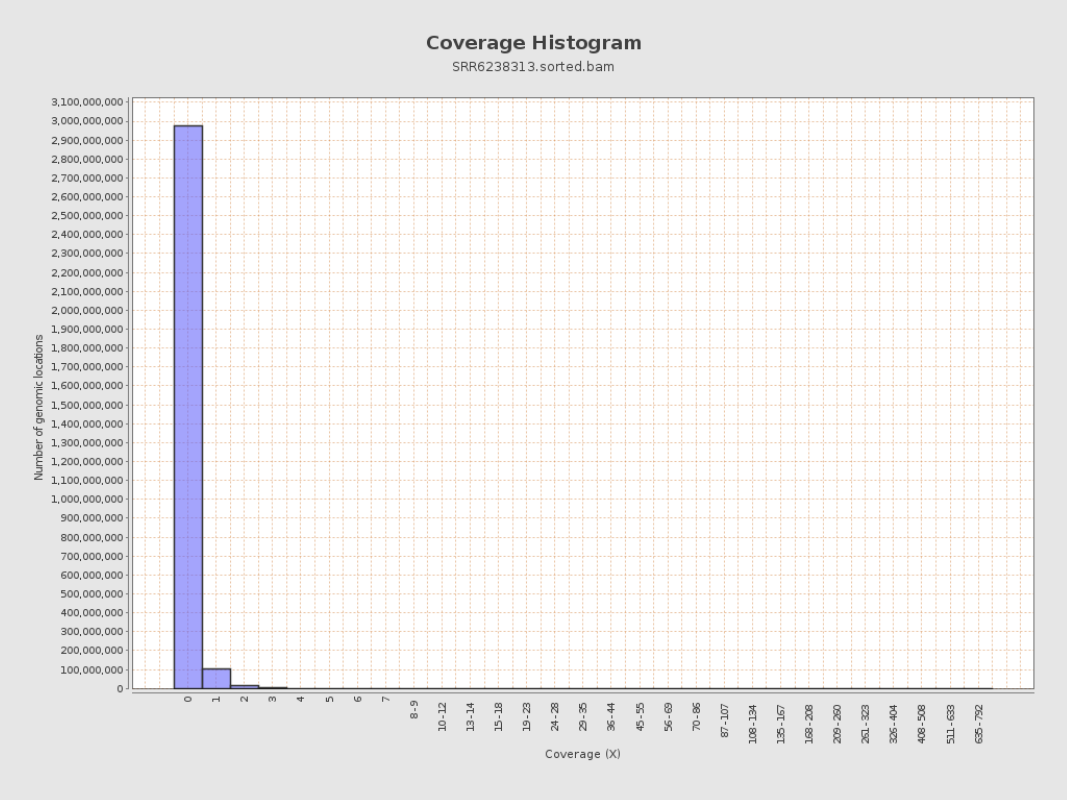
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12115169	0.0486	0.7199
chr2	243199373	10520647	0.0433	0.5326
chr3	198022430	9933851	0.0502	0.259
chr4	191154276	7118716	0.0372	0.253
chr5	180915260	7935217	0.0439	0.2444
chr6	171115067	7520448	0.0439	0.2862
chr7	159138663	7880613	0.0495	0.5547

chr8	146364022	7422616	0.0507	0.5458
chr9	141213431	7202817	0.051	0.4292
chr10	135534747	6364436	0.047	0.4068
chr11	135006516	6256583	0.0463	0.3556
chr12	133851895	7500510	0.056	0.2865
chr13	115169878	6005525	0.0521	0.2657
chr14	107349540	6652267	0.062	0.3322
chr15	102531392	4025231	0.0393	0.2331
chr16	90354753	5368413	0.0594	0.3221
chr17	81195210	4285086	0.0528	0.3193
chr18	78077248	3847658	0.0493	0.8203
chr19	59128983	3937546	0.0666	0.5202
chr20	63025520	3413396	0.0542	0.2836
chr21	48129895	1894065	0.0394	0.2653
chr22	51304566	1709260	0.0333	0.2107
chrMT	16571	5441	0.3283	0.6895
chrX	155270560	8101653	0.0522	0.3039
chrY	59373566	393487	0.0066	0.1712

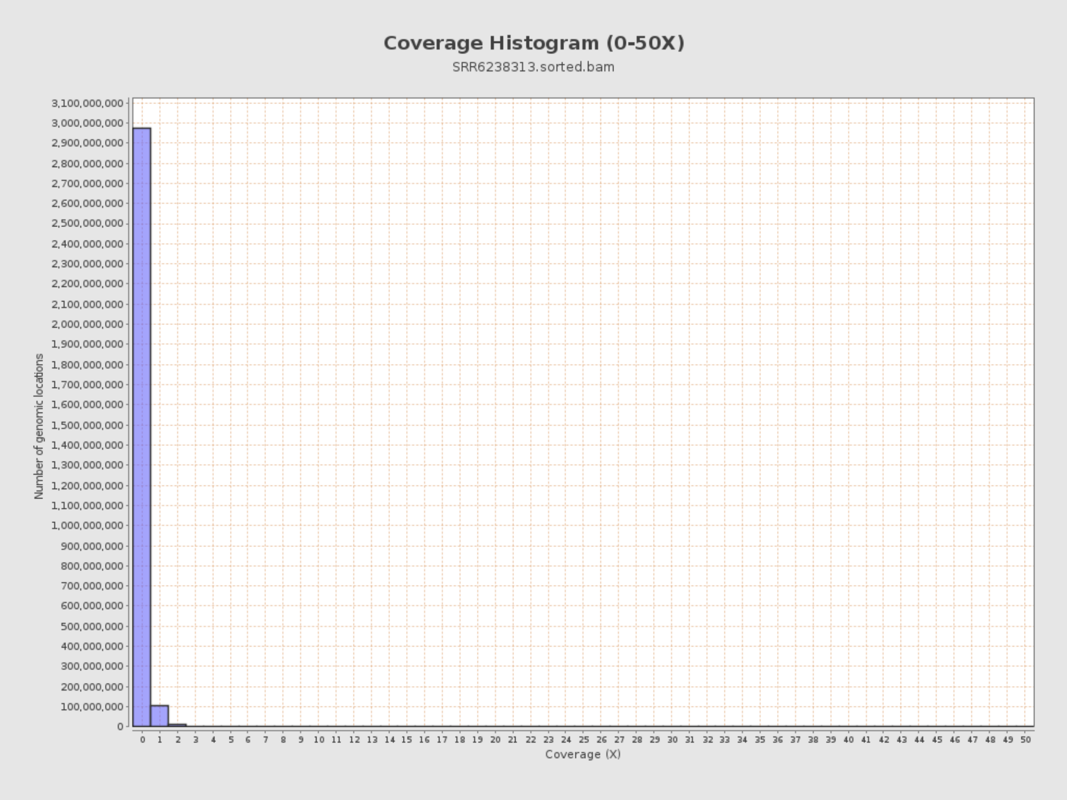
3. Results : Coverage across reference



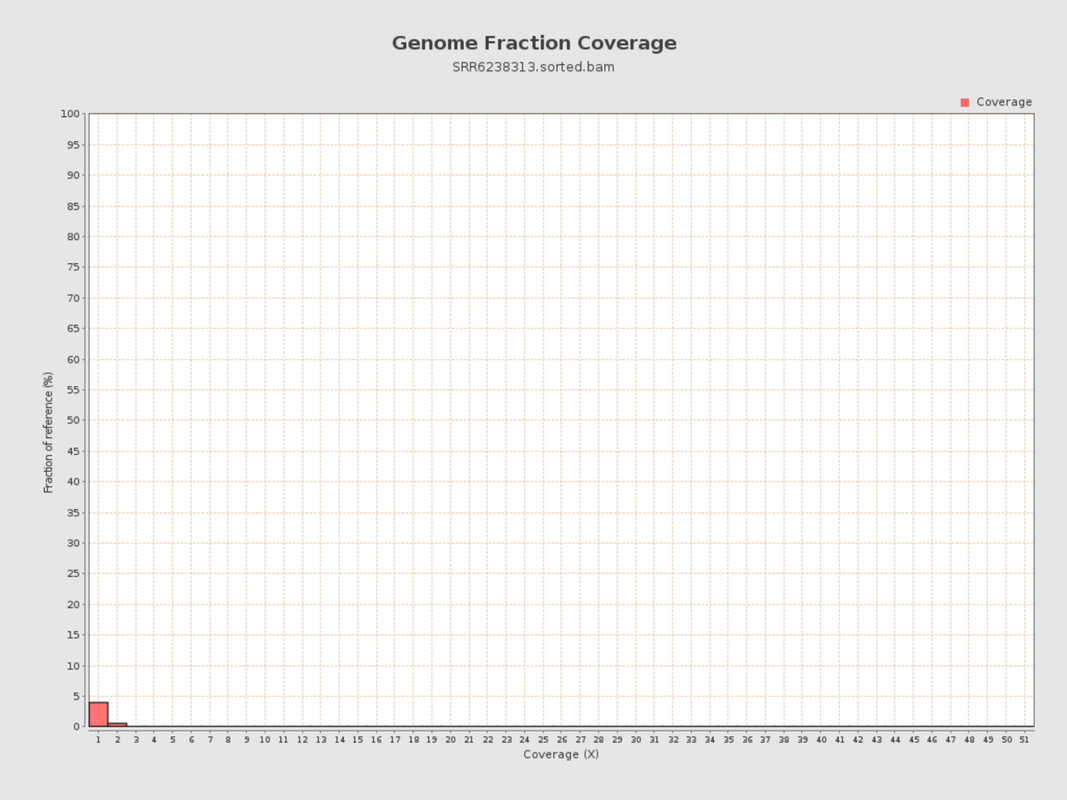
4. Results : Coverage Histogram



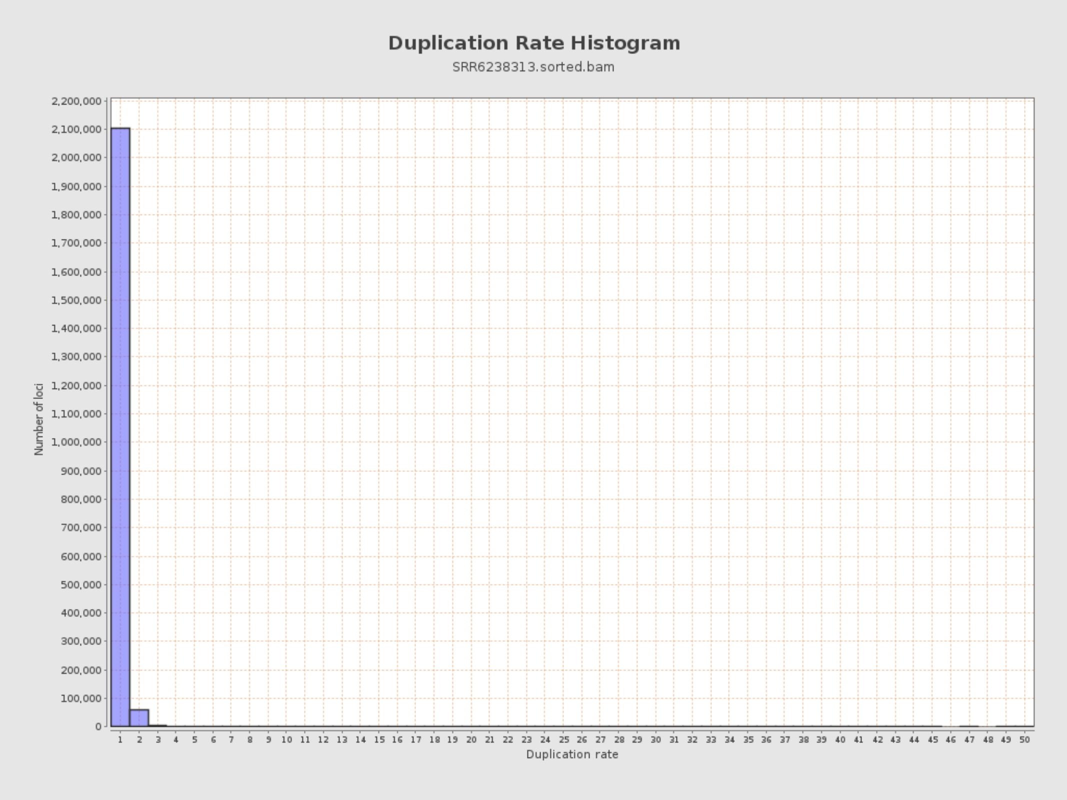
5. Results : Coverage Histogram (0-50X)



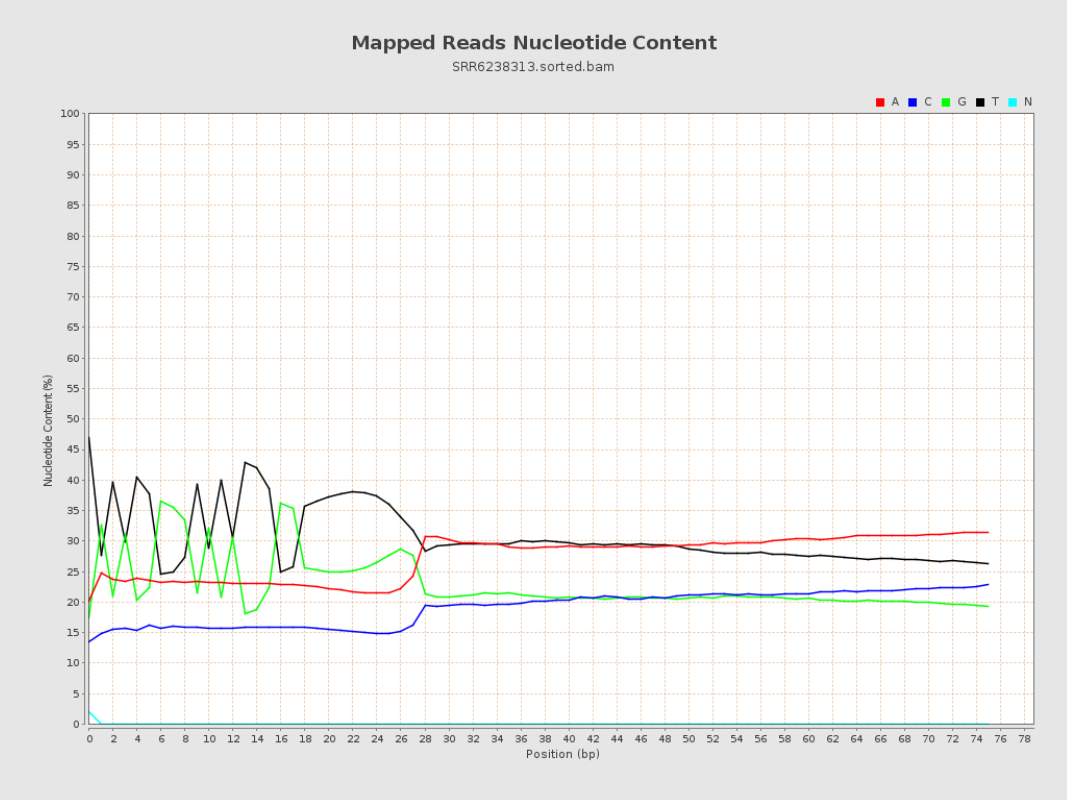
6. Results : Genome Fraction Coverage



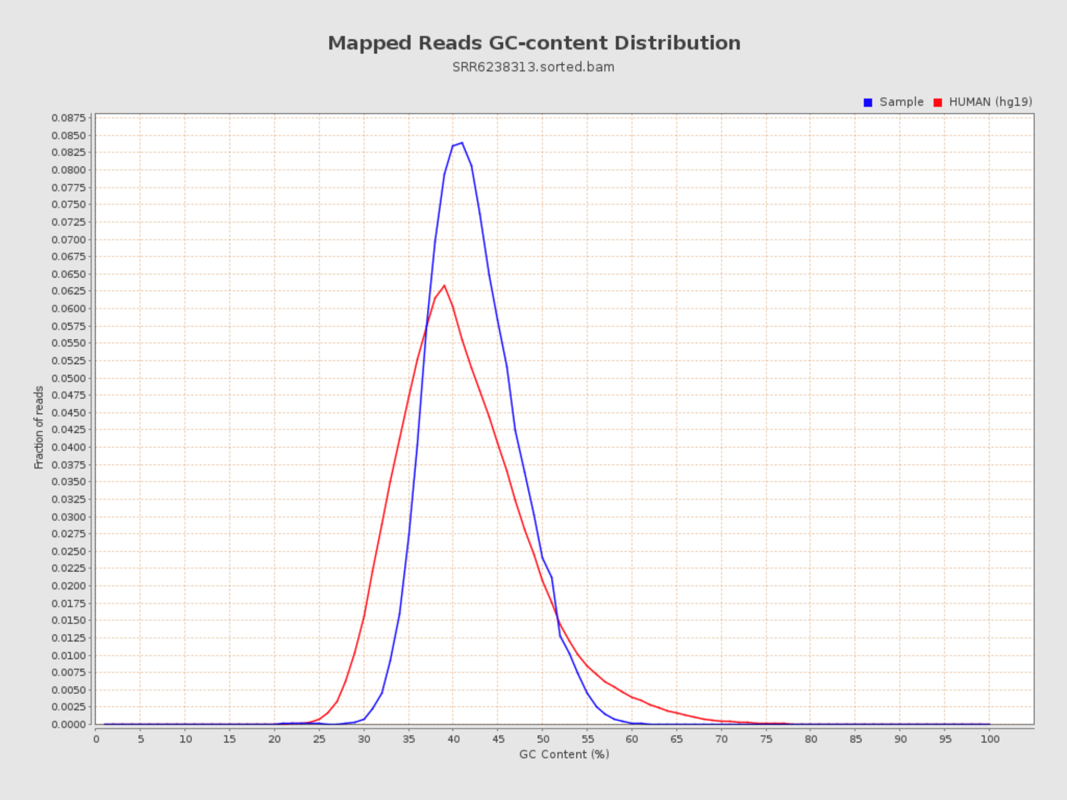
7. Results : Duplication Rate Histogram



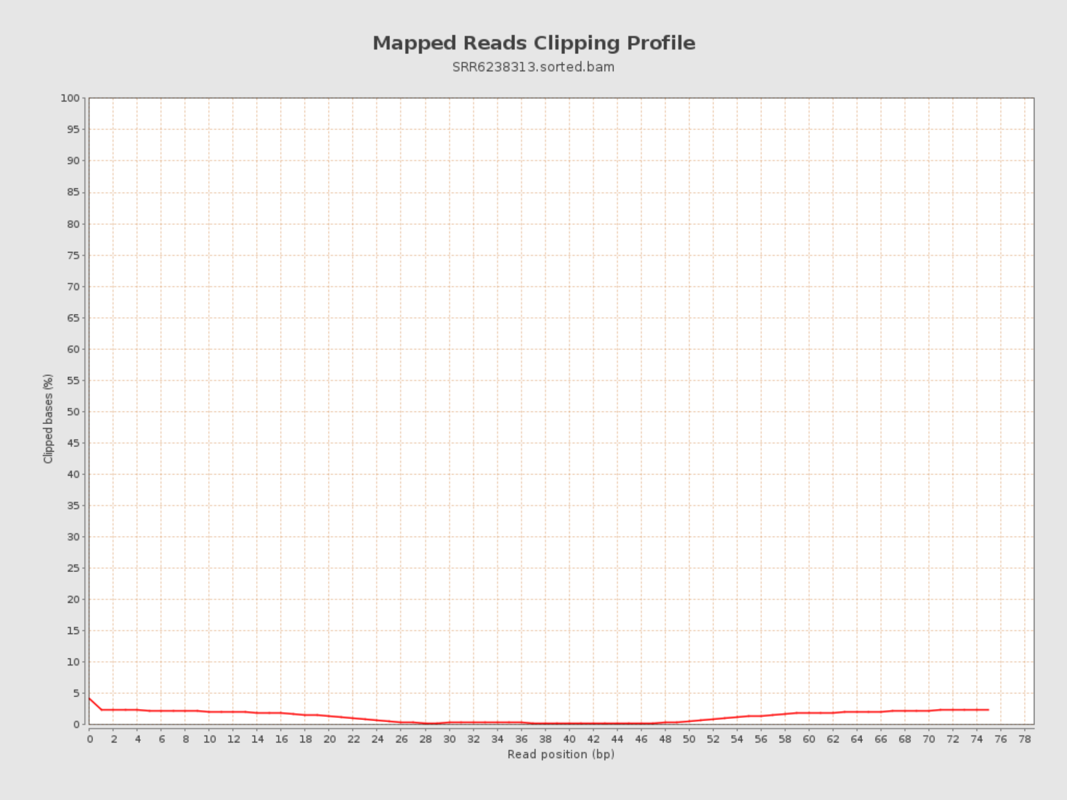
8. Results : Mapped Reads Nucleotide Content



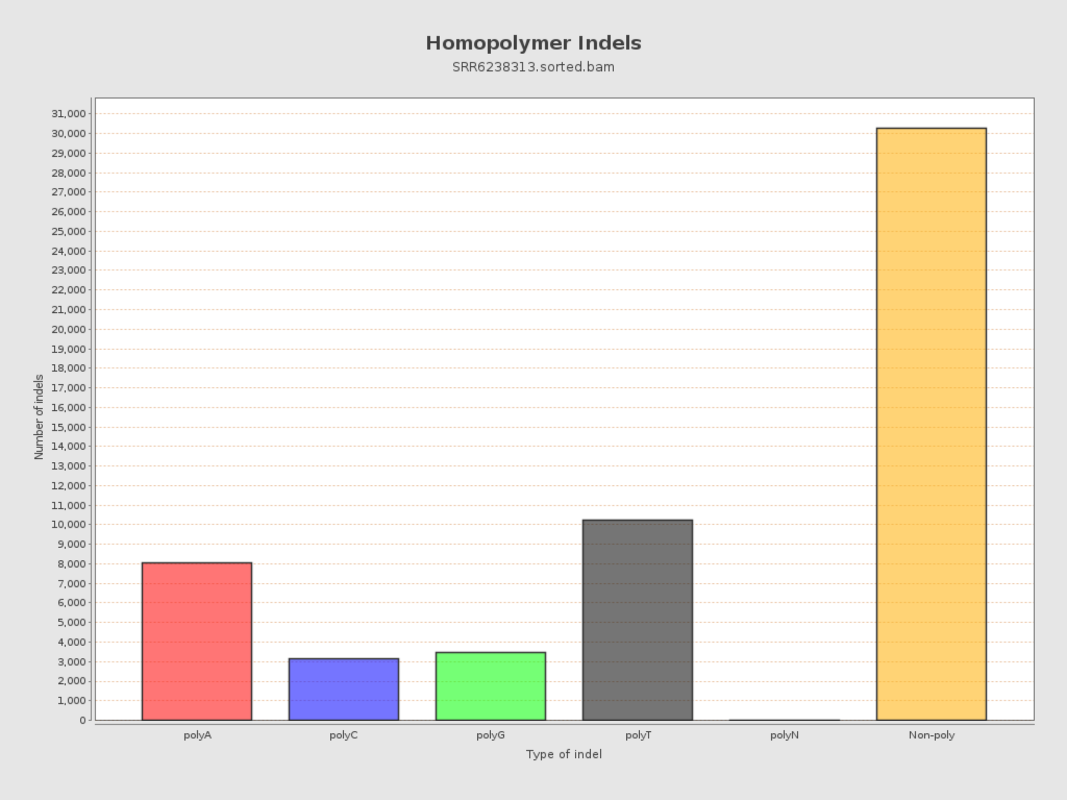
9. Results : Mapped Reads GC-content Distribution



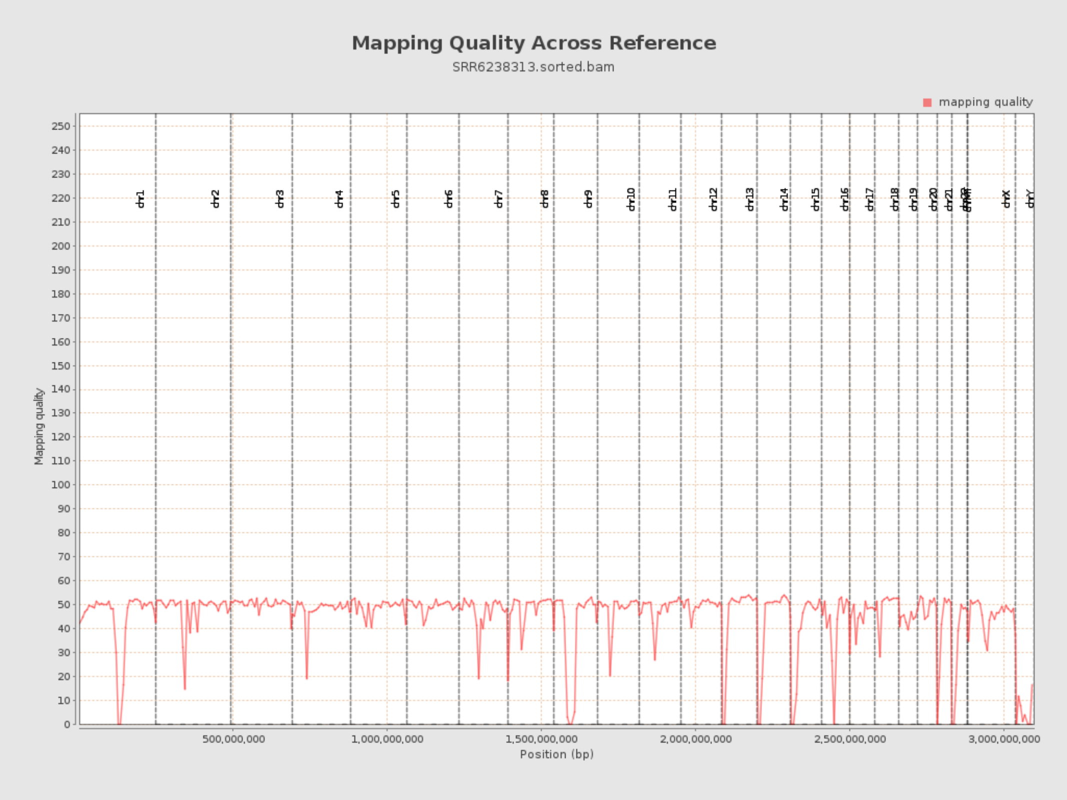
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram