Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 15:16:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238298.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_SRR6238298 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238298.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 15:16:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238298.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,724,085
Mapped reads	3,323,002 / 89.23%
Unmapped reads	401,083 / 10.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,535 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	168,430 / 4.52%
Duplication rate	3.87%
Clipped reads	1,712,148 / 45.97%

2.2. ACGT Content

Number/percentage of A's	59,044,618 / 27.17%
Number/percentage of C's	41,682,568 / 19.18%
Number/percentage of T's	66,504,540 / 30.61%
Number/percentage of G's	50,006,042 / 23.01%
Number/percentage of N's	58,277 / 0.03%
GC Percentage	42.2%

2.3. Coverage

Mean	0.0702

Standard Deviation	0.5526

2.4. Mapping Quality

Mean Mapping Quality	45.12

2.5. Mismatches and indels

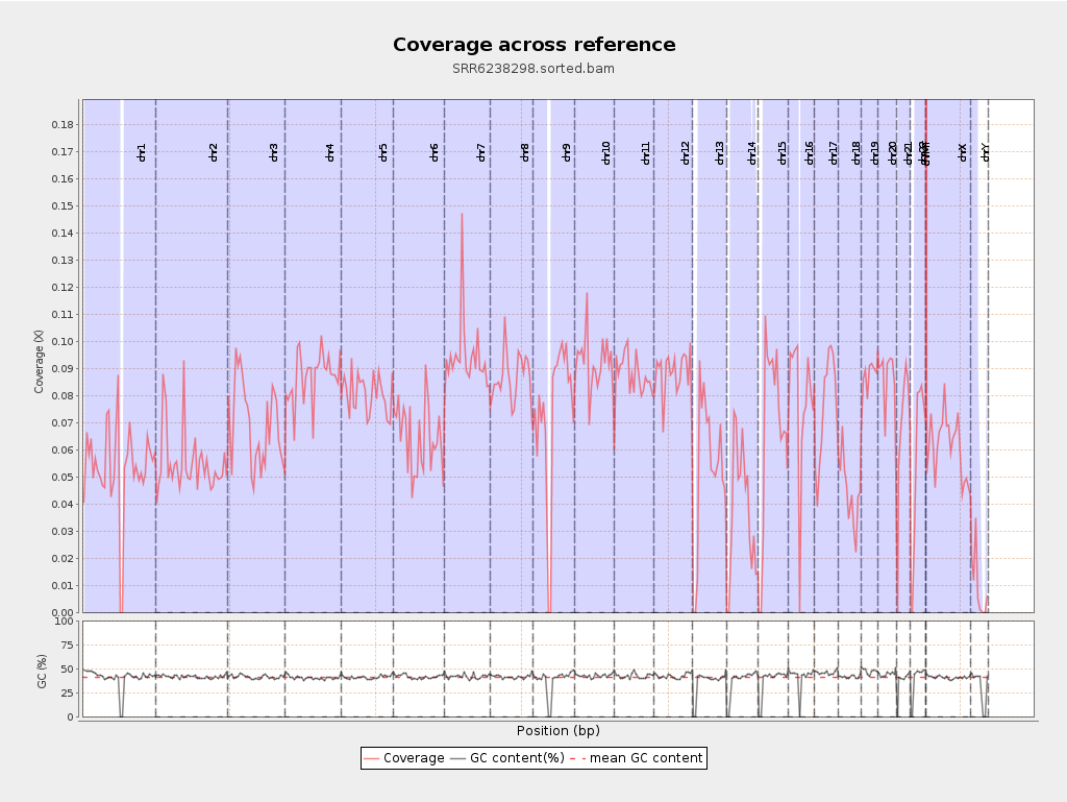
General error rate	0.84%
Mismatches	1,793,033
Insertions	16,626
Mapped reads with at least one insertion	0.5%
Deletions	56,833
Mapped reads with at least one deletion	1.69%
Homopolymer indels	46.06%

2.6. Chromosome stats

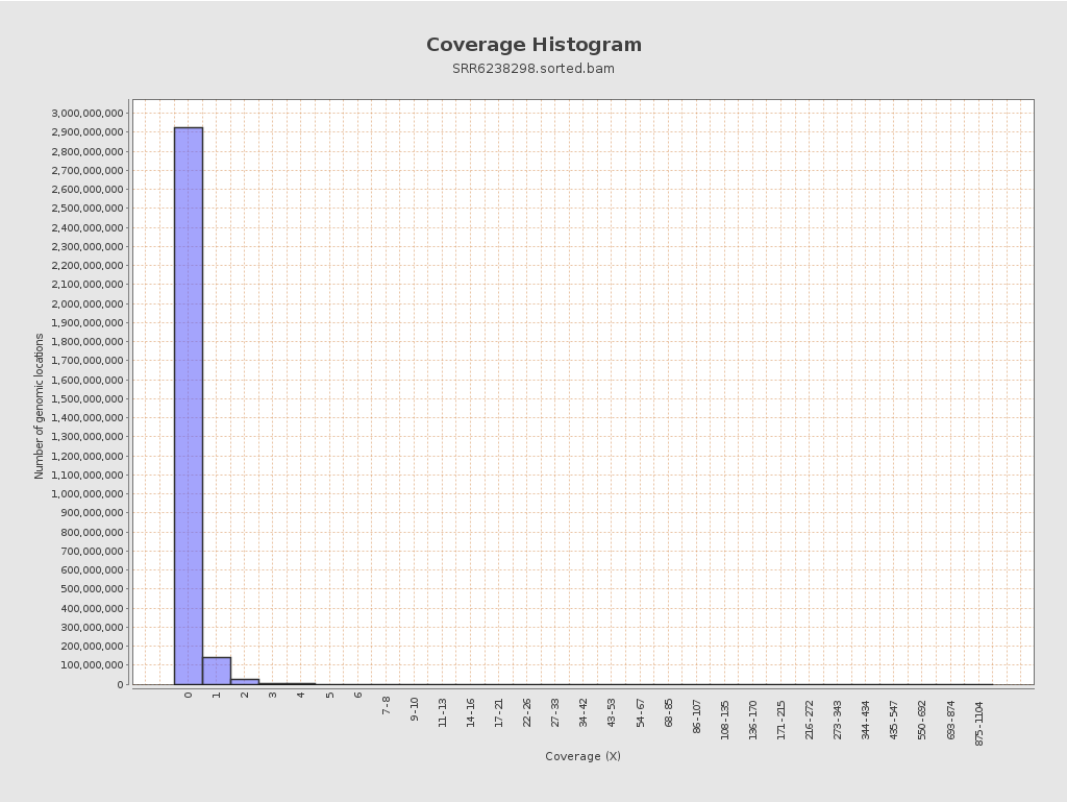
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13365004	0.0536	0.9197
chr2	243199373	13380125	0.055	0.6383
chr3	198022430	13720511	0.0693	0.3179
chr4	191154276	16653020	0.0871	0.388
chr5	180915260	14617499	0.0808	0.348
chr6	171115067	10959537	0.064	0.3681
chr7	159138663	15025310	0.0944	0.991

chr8	146364022	12643071	0.0864	0.7276
chr9	141213431	10411377	0.0737	0.4805
chr10	135534747	12491679	0.0922	0.5536
chr11	135006516	11797282	0.0874	0.5461
chr12	133851895	11831730	0.0884	0.3678
chr13	115169878	6143626	0.0533	0.2794
chr14	107349540	4106029	0.0382	0.272
chr15	102531392	6886551	0.0672	0.3284
chr16	90354753	6916858	0.0766	0.3732
chr17	81195210	6173894	0.076	0.4315
chr18	78077248	3473098	0.0445	0.7898
chr19	59128983	5159599	0.0873	0.6473
chr20	63025520	5443666	0.0864	0.3672
chr21	48129895	3286808	0.0683	0.3485
chr22	51304566	2852450	0.0556	0.2904
chrMT	16571	16244	0.9803	1.2603
chrX	155270560	9470377	0.061	0.3604
chrY	59373566	564907	0.0095	0.3238

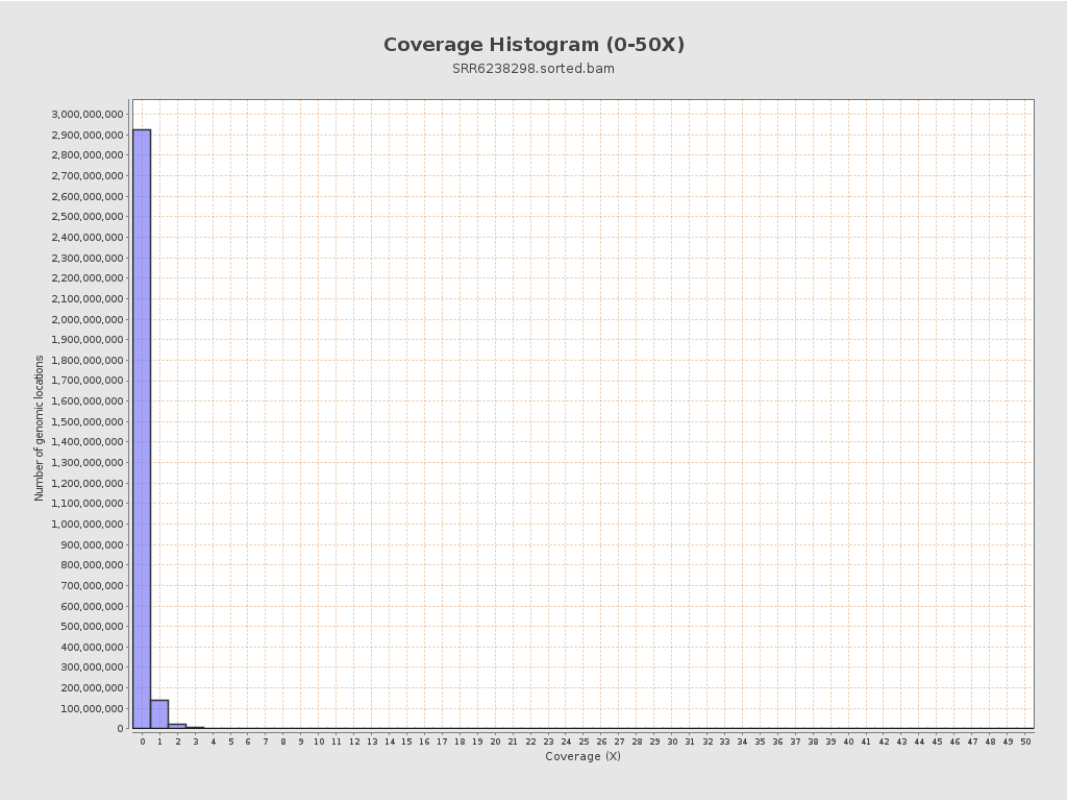
3. Results : Coverage across reference



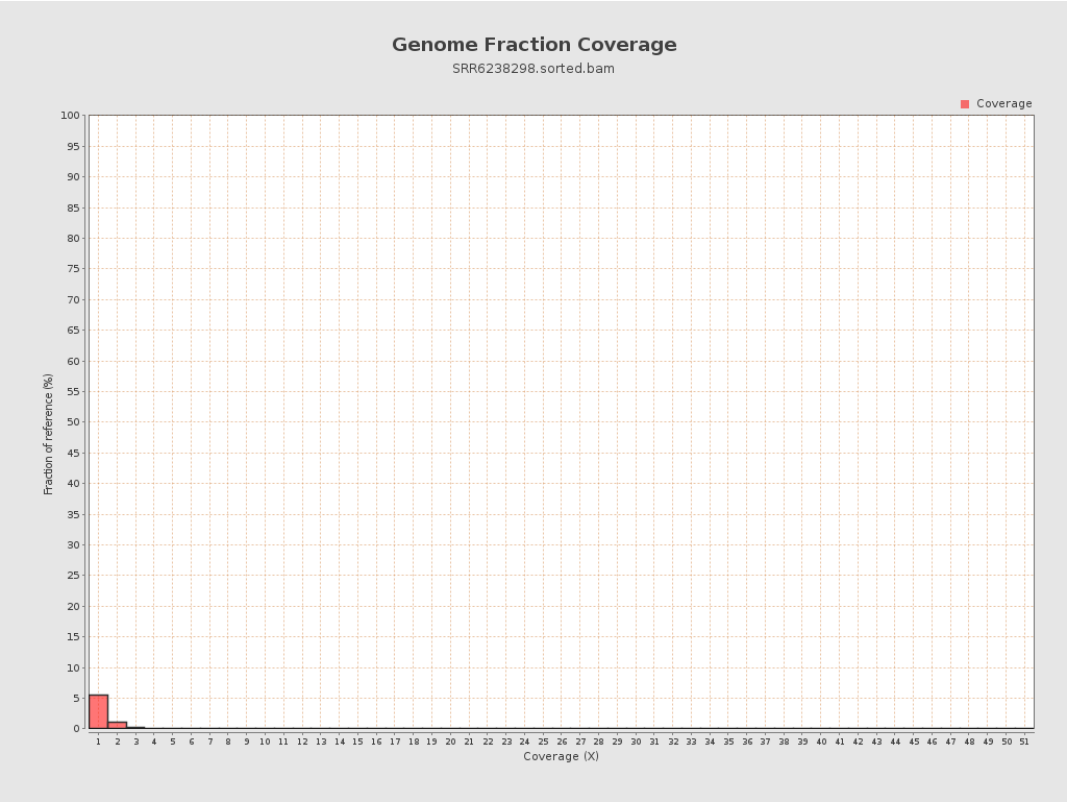
4. Results : Coverage Histogram



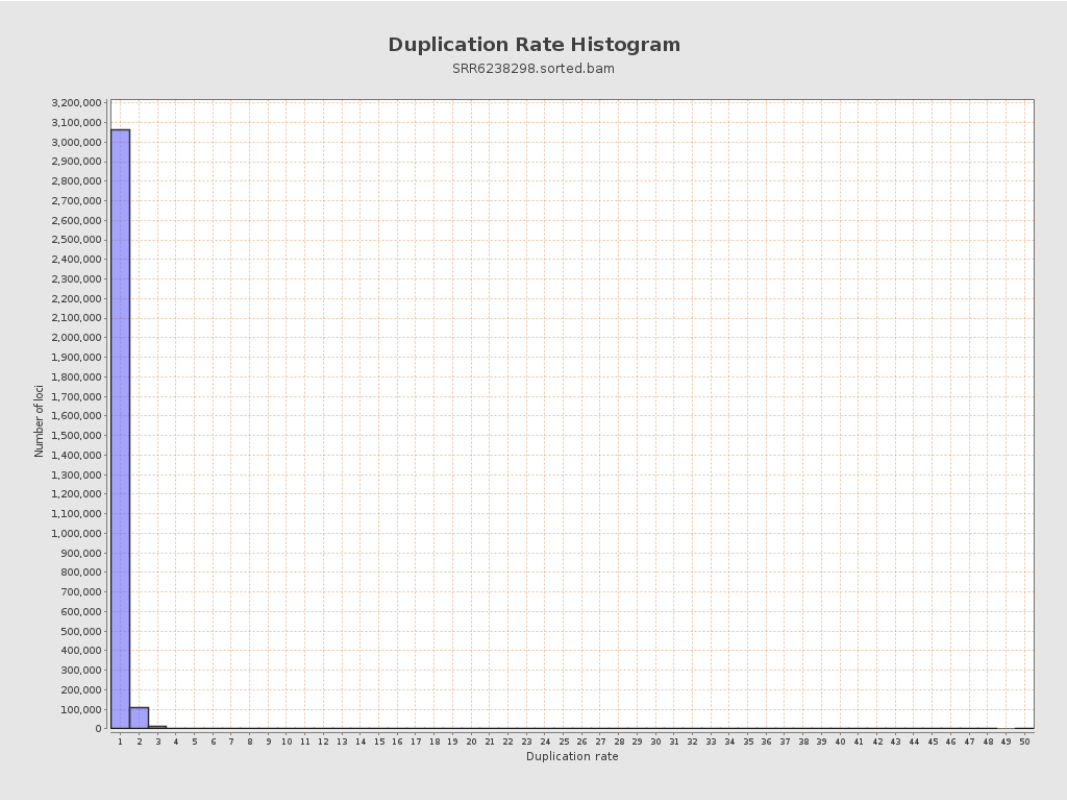
5. Results : Coverage Histogram (0-50X)



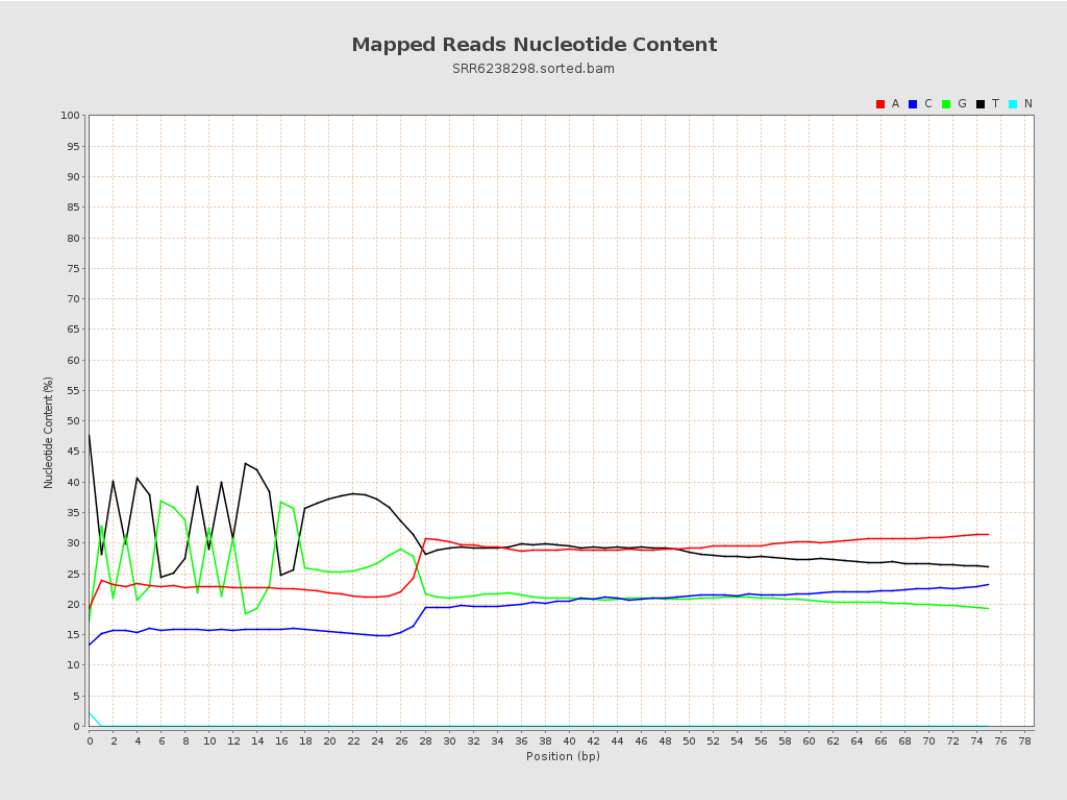
6. Results : Genome Fraction Coverage



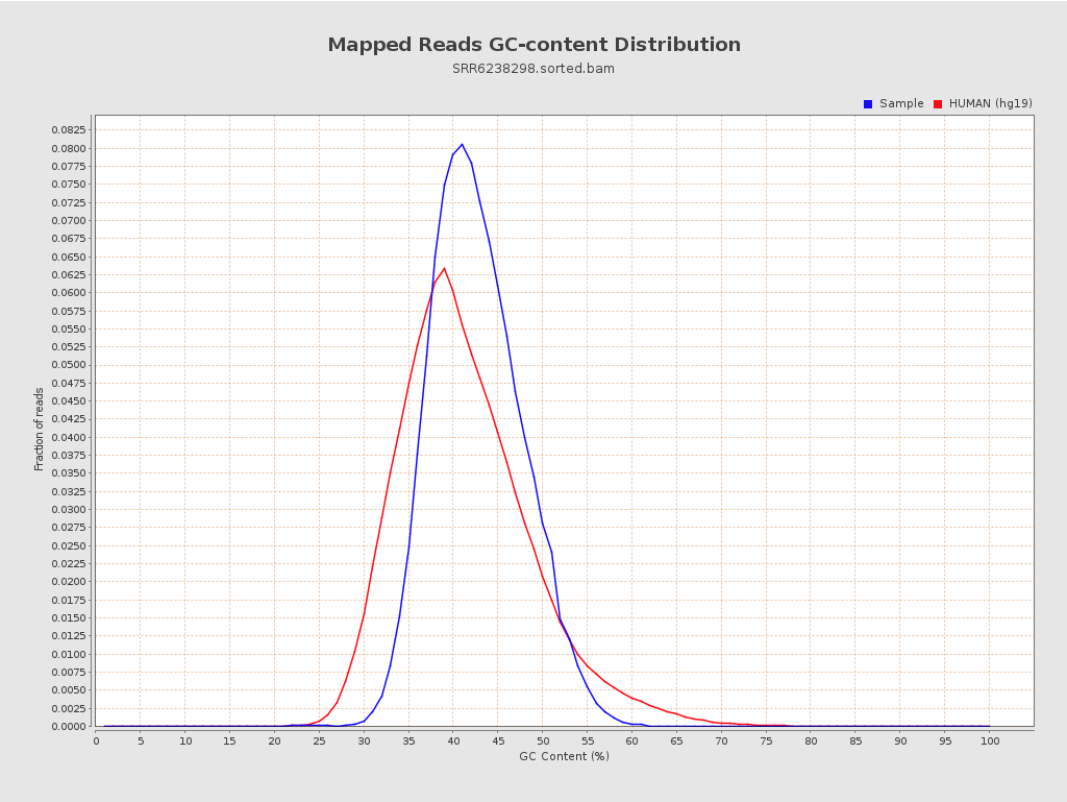
7. Results : Duplication Rate Histogram



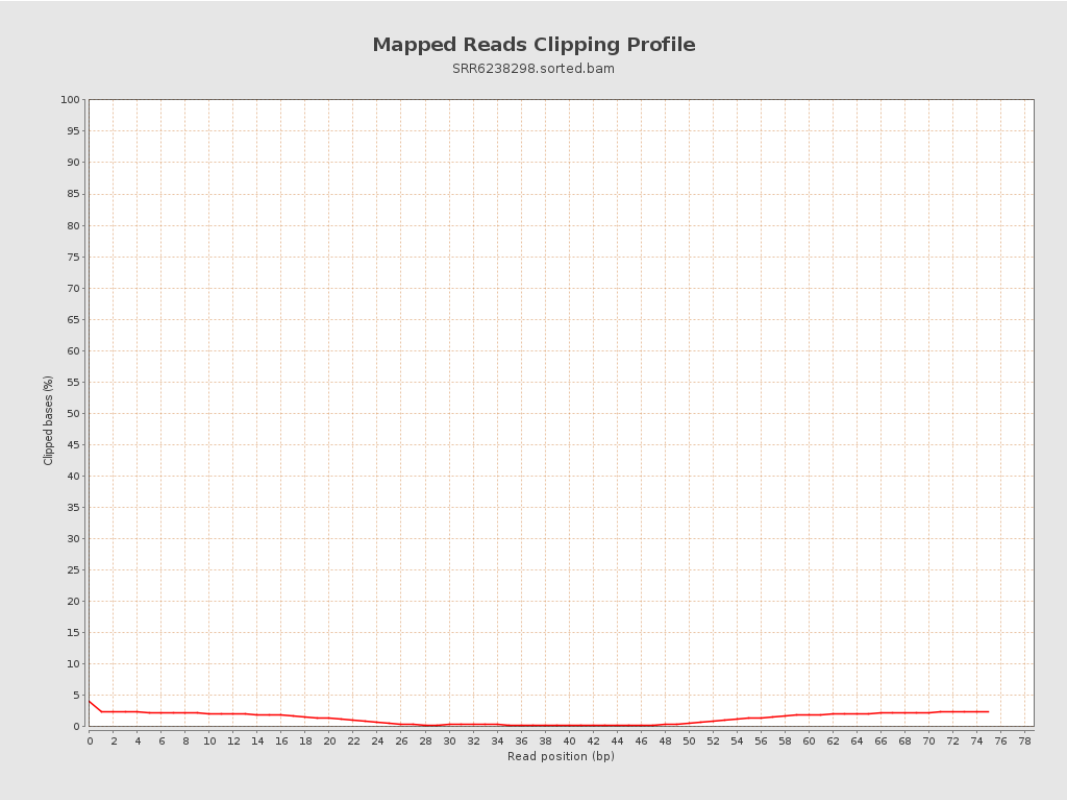
8. Results : Mapped Reads Nucleotide Content



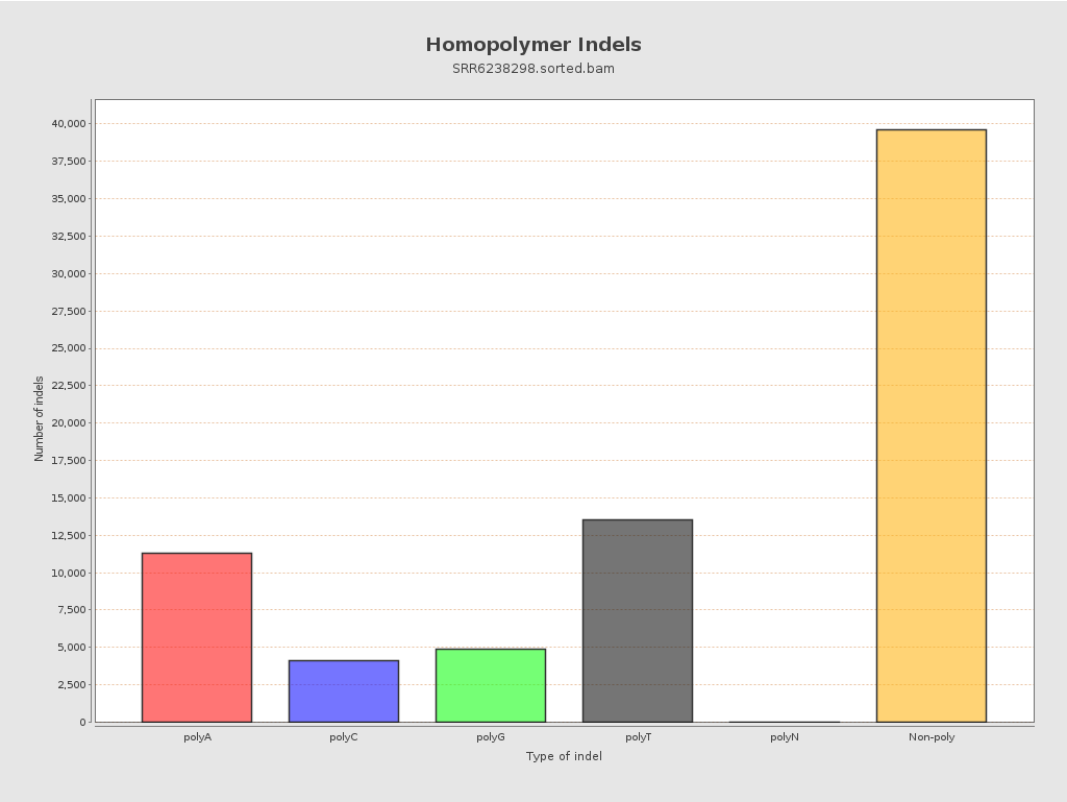
9. Results : Mapped Reads GC-content Distribution



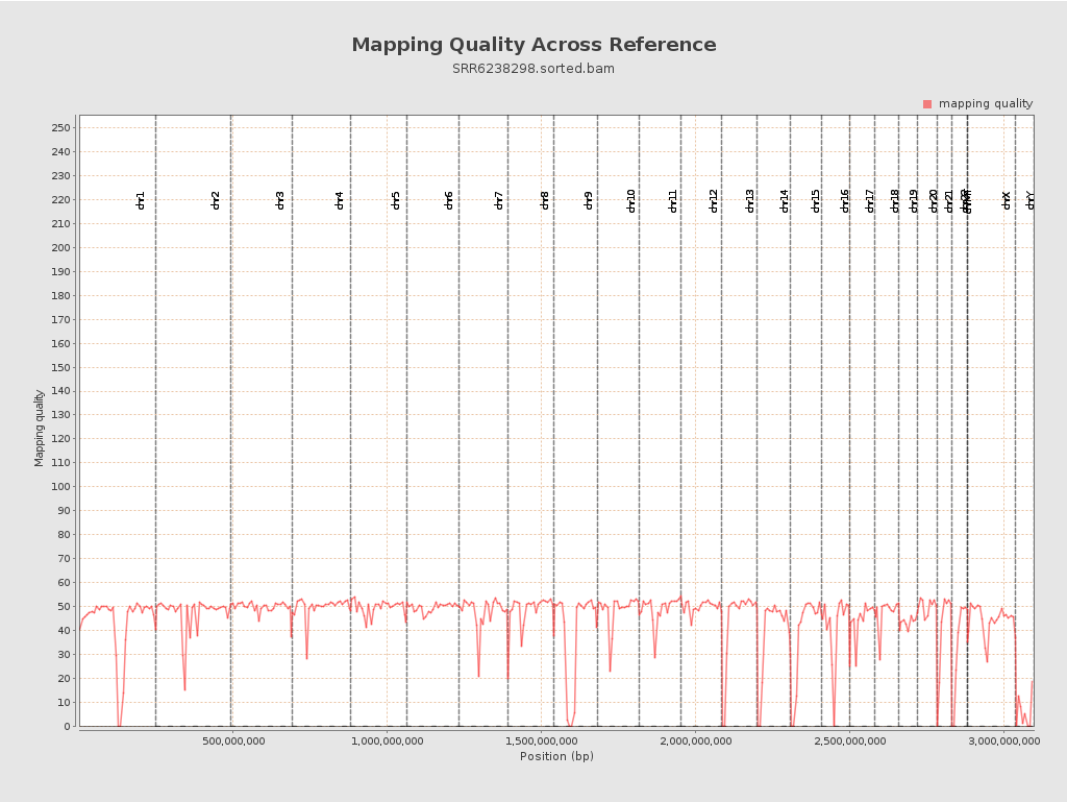
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram