Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 15:24:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238301.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_SRR6238301 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238301.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 15:24:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238301.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,192,908
Mapped reads	1,048,038 / 87.86%
Unmapped reads	144,870 / 12.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,999 / 1.01%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	54,956 / 4.61%
Duplication rate	4.24%
Clipped reads	514,553 / 43.13%

2.2. ACGT Content

Number/percentage of A's	18,736,837 / 27.34%
Number/percentage of C's	12,214,576 / 17.82%
Number/percentage of T's	22,159,264 / 32.33%
Number/percentage of G's	15,369,723 / 22.43%
Number/percentage of N's	56,983 / 0.08%
GC Percentage	40.25%

2.3. Coverage

Mean	0.0222

Standard Deviation	0.2489

2.4. Mapping Quality

Mean Mapping Quality	44.09

2.5. Mismatches and indels

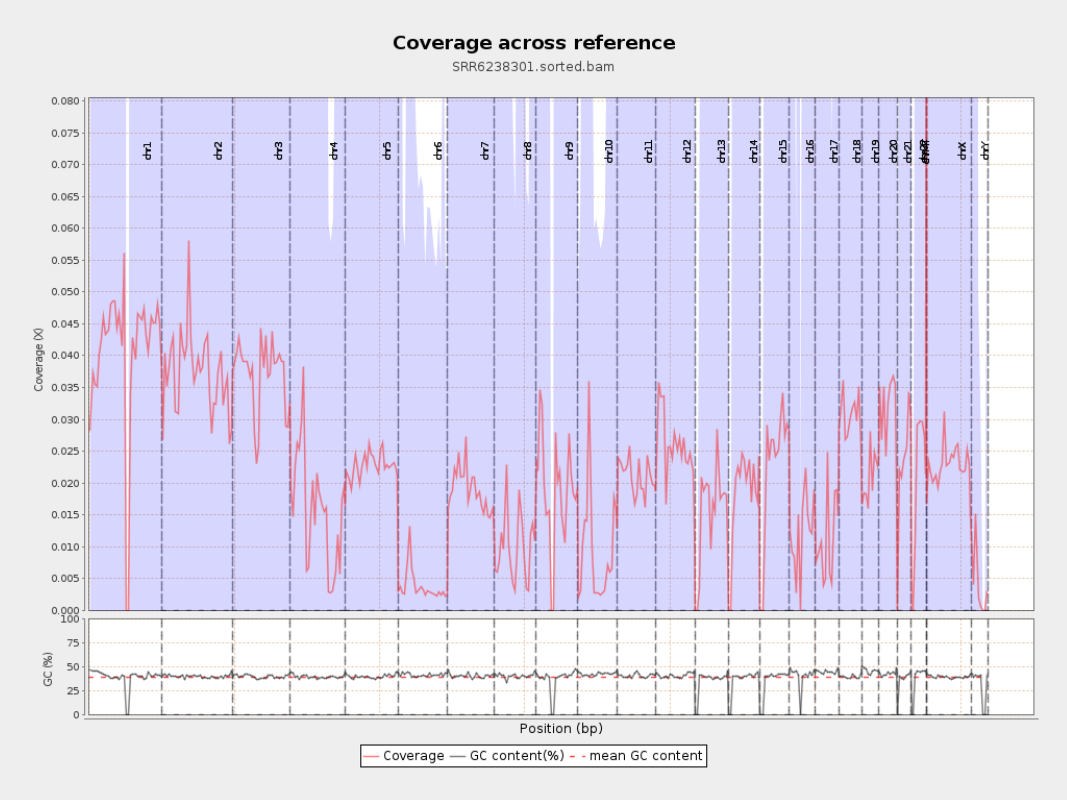
General error rate	0.85%
Mismatches	574,152
Insertions	5,414
Mapped reads with at least one insertion	0.51%
Deletions	20,214
Mapped reads with at least one deletion	1.9%
Homopolymer indels	46.62%

2.6. Chromosome stats

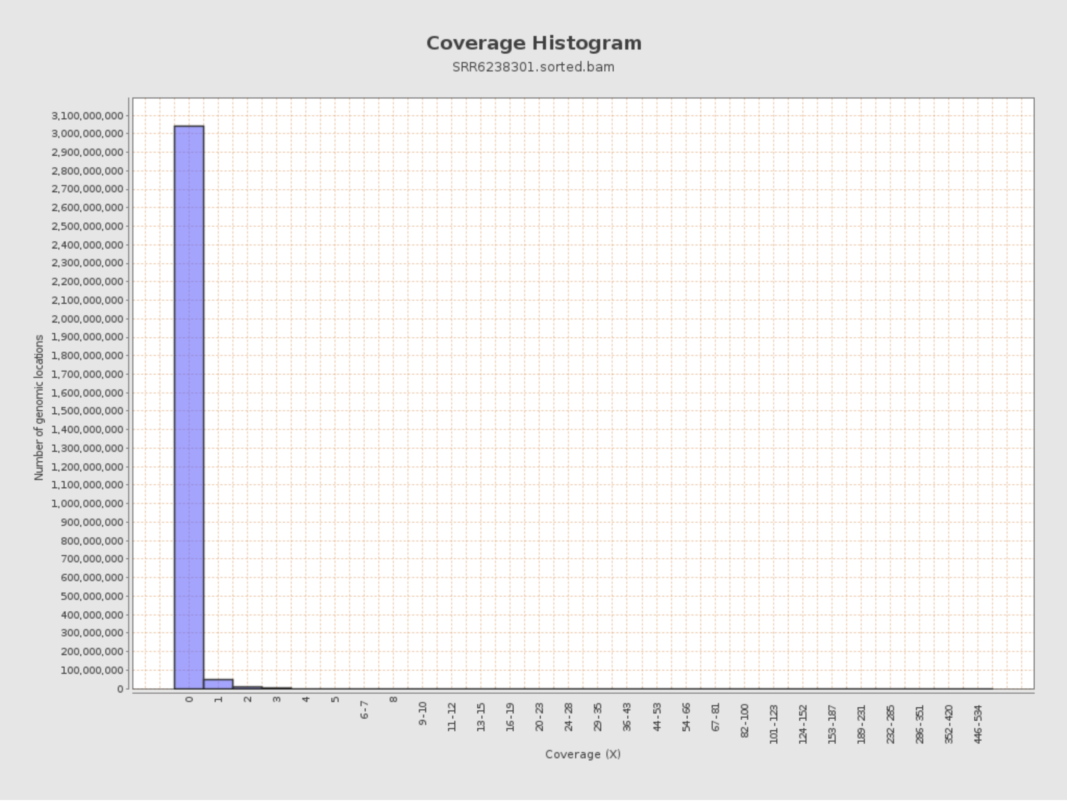
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10140384	0.0407	0.4703
chr2	243199373	9098660	0.0374	0.3187
chr3	198022430	7345859	0.0371	0.2256
chr4	191154276	3012119	0.0158	0.1782
chr5	180915260	4132186	0.0228	0.177
chr6	171115067	655468	0.0038	0.0827
chr7	159138663	3030848	0.019	0.2003

chr8	146364022	1404529	0.0096	0.3404
chr9	141213431	2658274	0.0188	0.2192
chr10	135534747	1188769	0.0088	0.2297
chr11	135006516	2816502	0.0209	0.1923
chr12	133851895	3463047	0.0259	0.1883
chr13	115169878	1764597	0.0153	0.1436
chr14	107349540	1926839	0.0179	0.1583
chr15	102531392	2329307	0.0227	0.177
chr16	90354753	1089837	0.0121	0.1457
chr17	81195210	899405	0.0111	0.1288
chr18	78077248	2415781	0.0309	0.395
chr19	59128983	1236238	0.0209	0.2926
chr20	63025520	2020955	0.0321	0.214
chr21	48129895	1131482	0.0235	0.1987
chr22	51304566	1022586	0.0199	0.1627
chrMT	16571	2190	0.1322	0.3946
chrX	155270560	3553672	0.0229	0.1872
chrY	59373566	233548	0.0039	0.1414

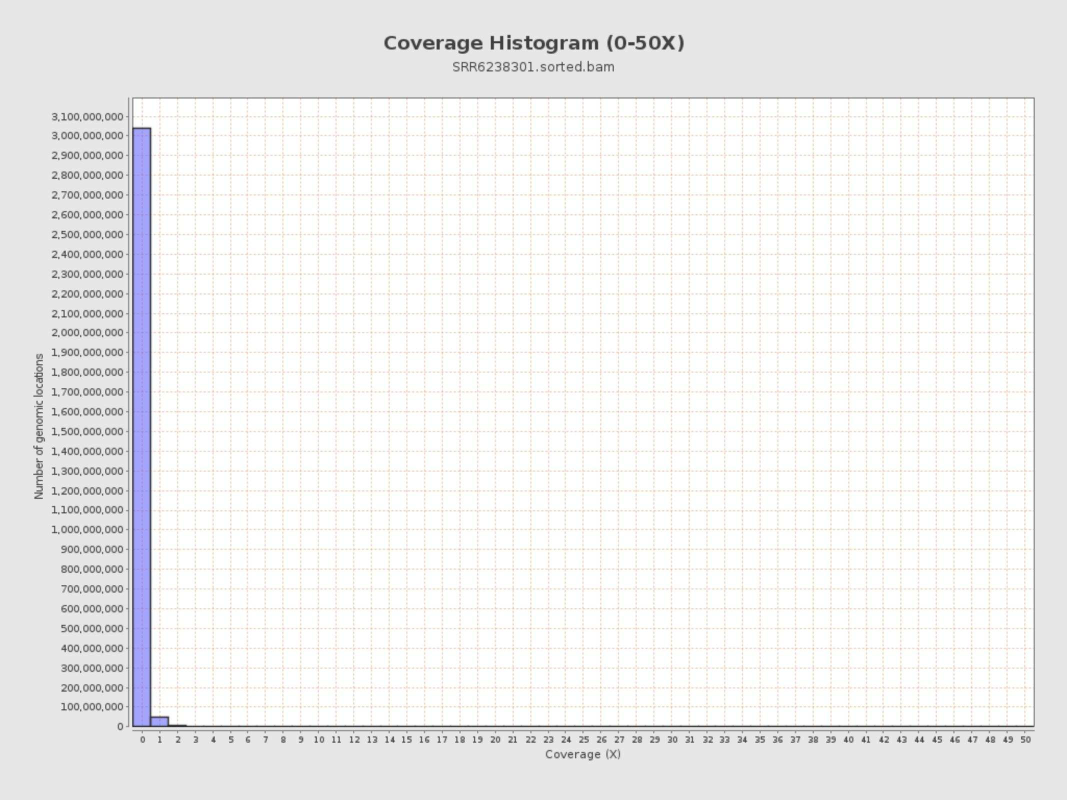
3. Results : Coverage across reference



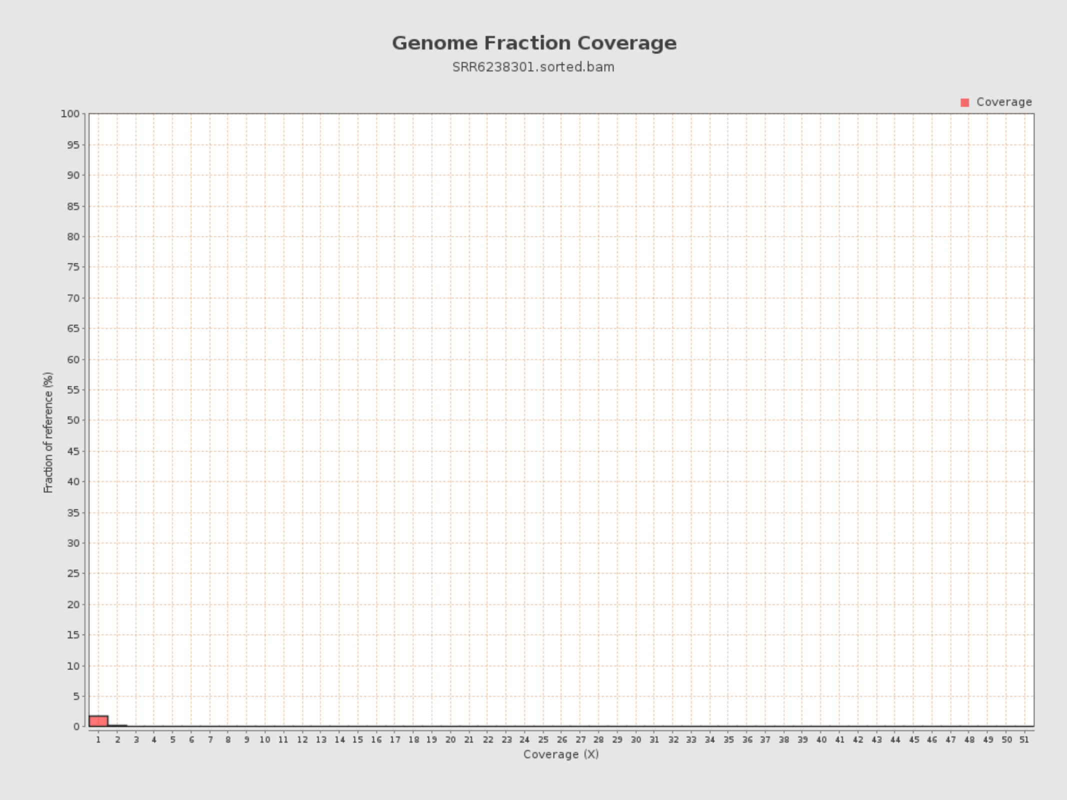
4. Results : Coverage Histogram



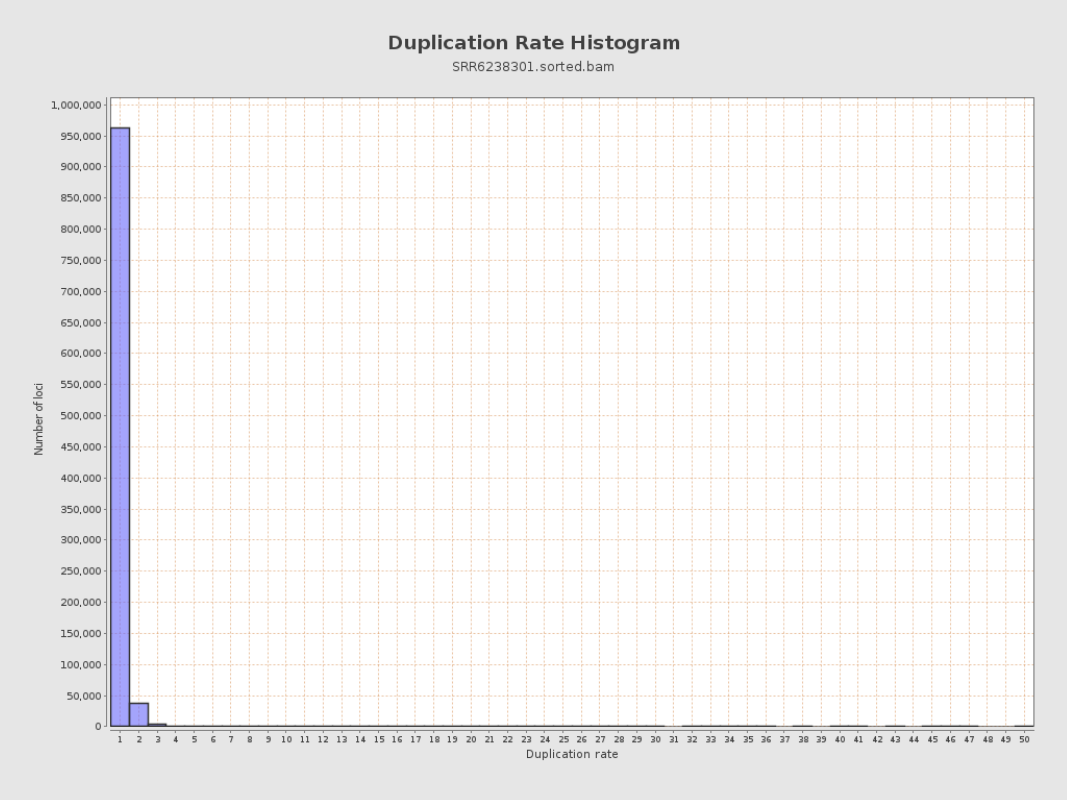
5. Results : Coverage Histogram (0-50X)



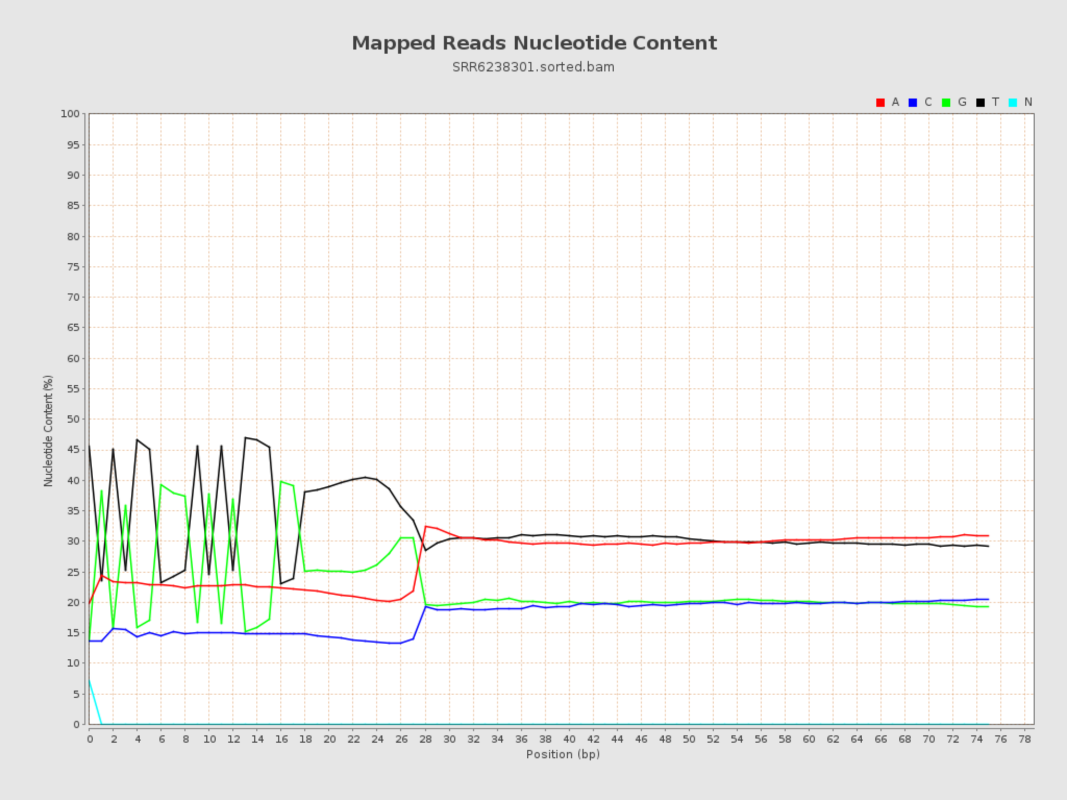
6. Results : Genome Fraction Coverage



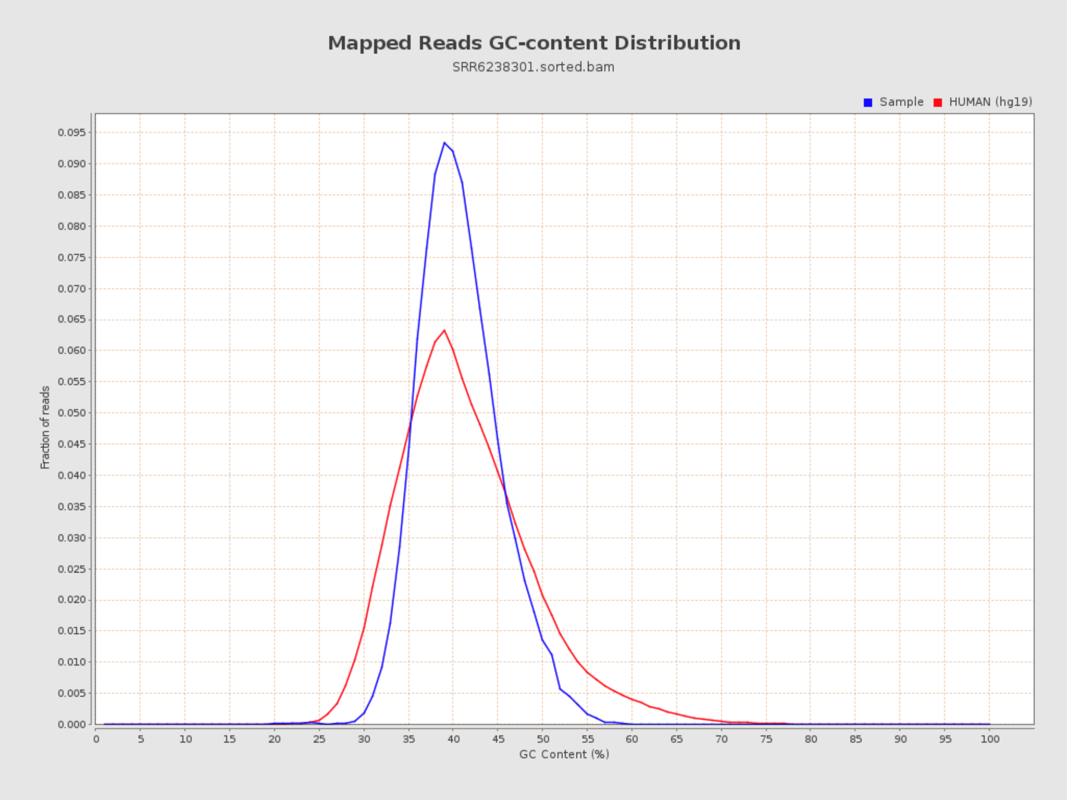
7. Results : Duplication Rate Histogram



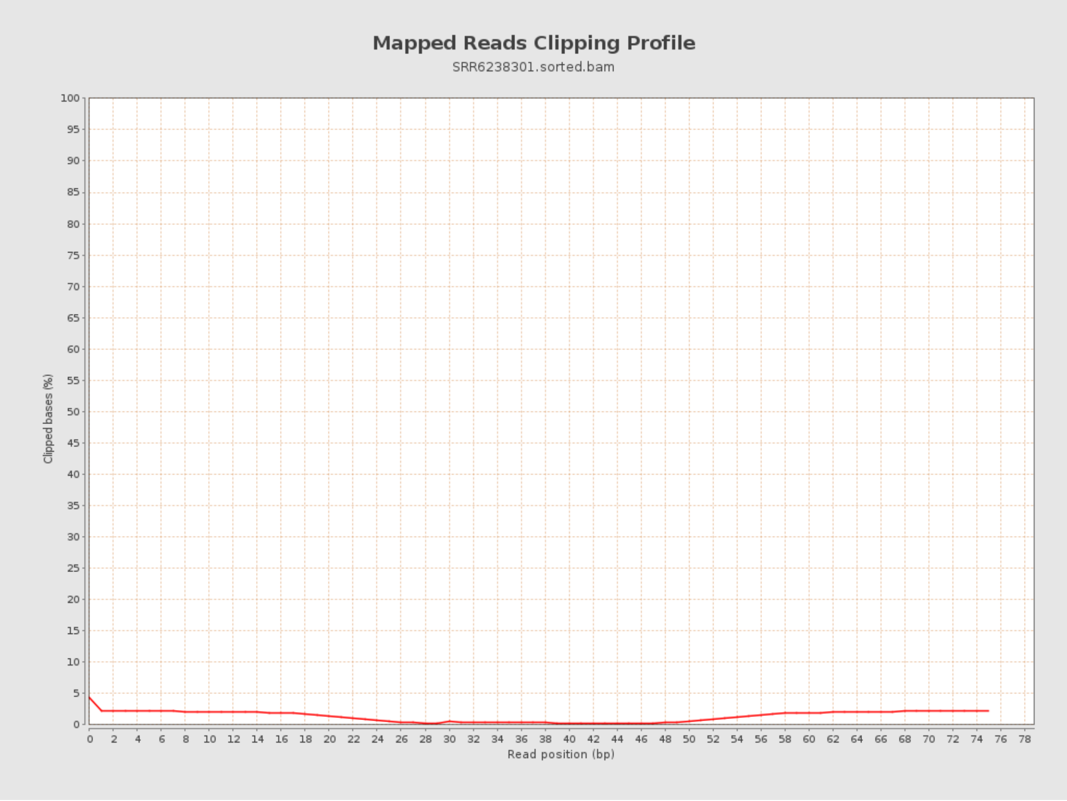
8. Results : Mapped Reads Nucleotide Content



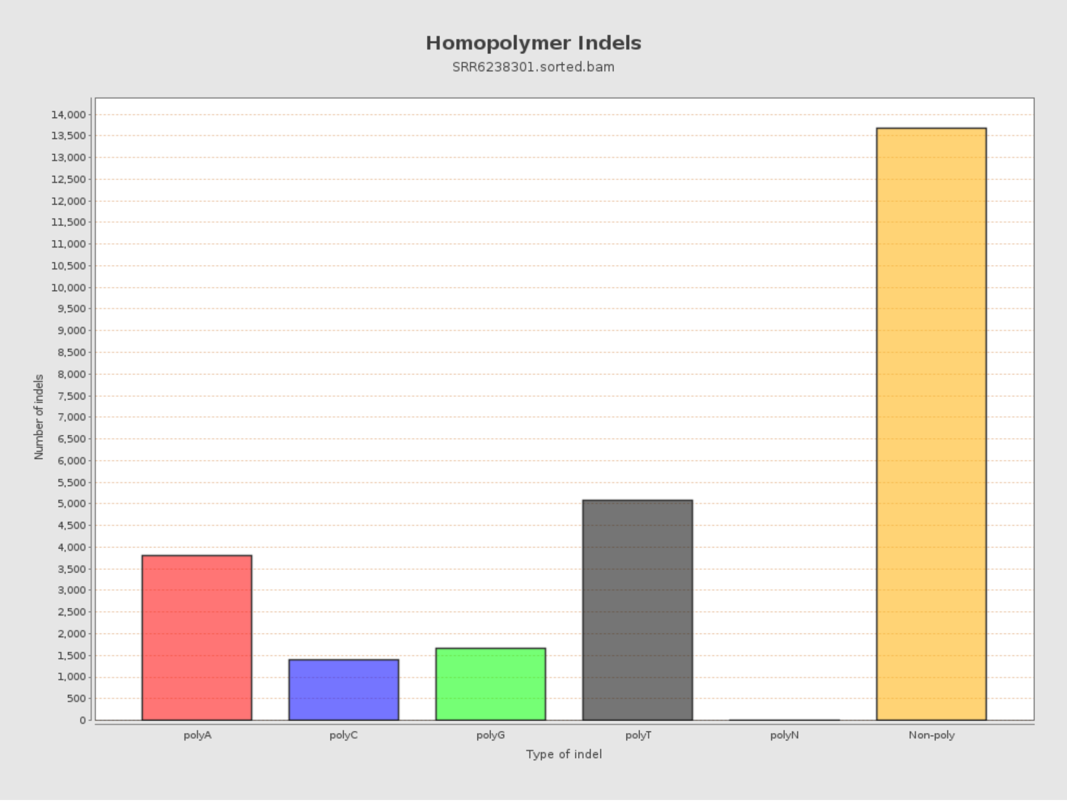
9. Results : Mapped Reads GC-content Distribution



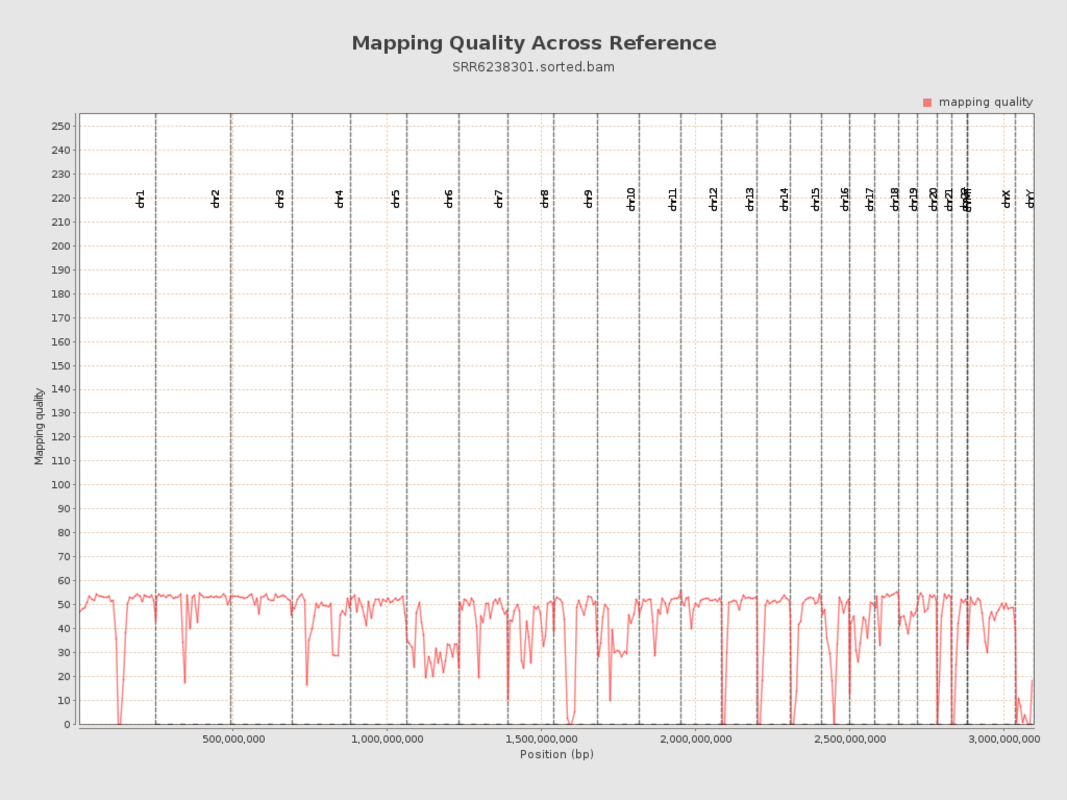
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram