Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 18:54:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238509.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_SRR6238509 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238509.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 18:54:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238509.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,716,340
Mapped reads	3,297,419 / 88.73%
Unmapped reads	418,921 / 11.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,674 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	945,688 / 25.45%
Duplication rate	19.03%
Clipped reads	2,122,726 / 57.12%

2.2. ACGT Content

Number/percentage of A's	50,081,407 / 24.79%
Number/percentage of C's	35,813,793 / 17.73%
Number/percentage of T's	67,427,644 / 33.38%
Number/percentage of G's	48,663,612 / 24.09%
Number/percentage of N's	13,995 / 0.01%
GC Percentage	41.82%

2.3. Coverage

Mean	0.0653

Standard Deviation	1.0659

2.4. Mapping Quality

Mean Mapping Quality	41.28

2.5. Mismatches and indels

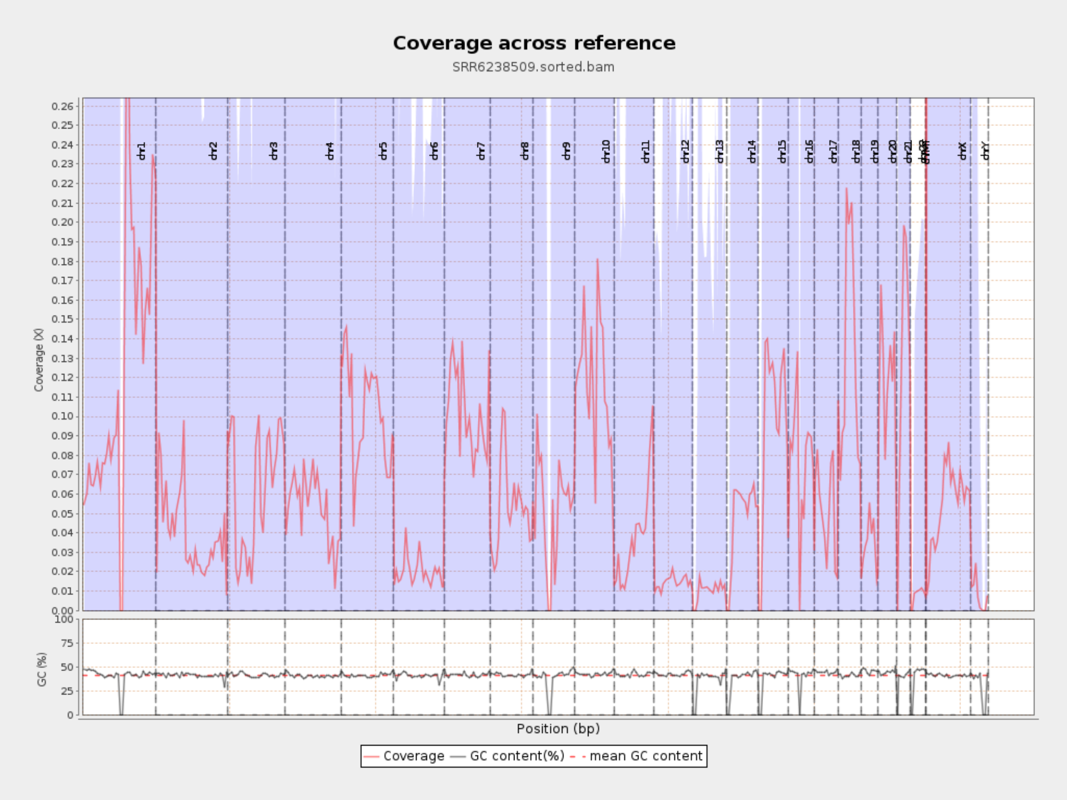
General error rate	0.66%
Mismatches	1,317,541
Insertions	12,247
Mapped reads with at least one insertion	0.37%
Deletions	79,204
Mapped reads with at least one deletion	2.37%
Homopolymer indels	39.81%

2.6. Chromosome stats

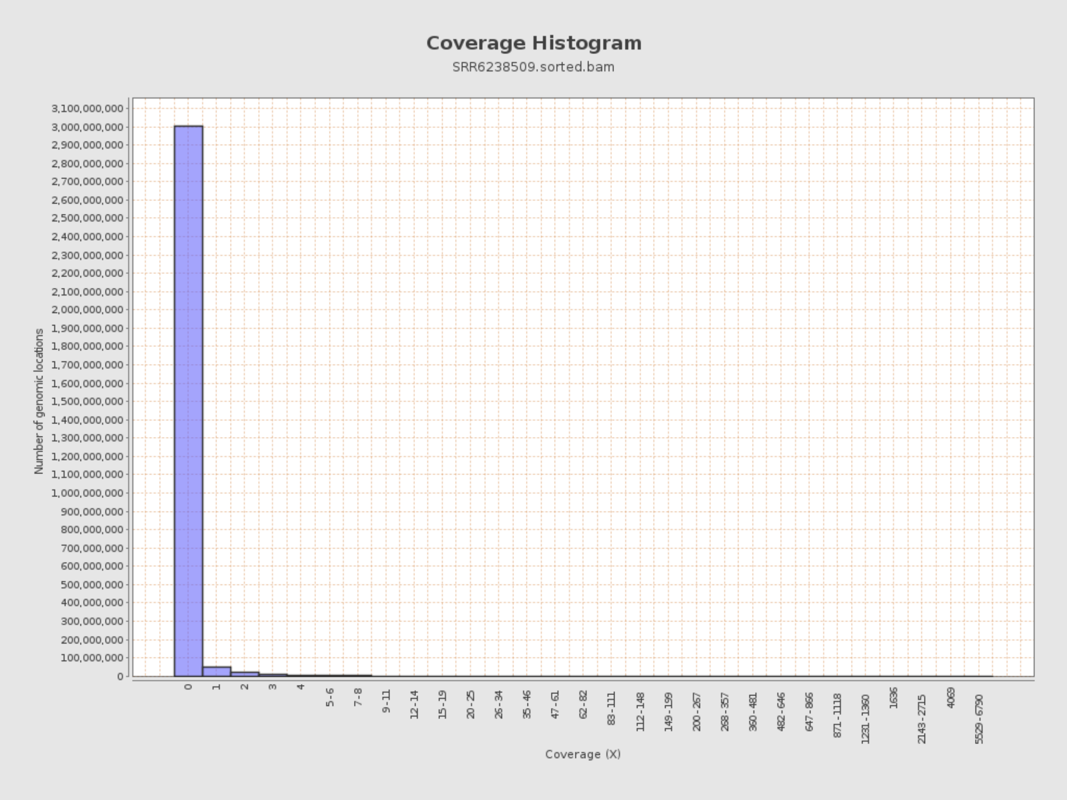
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30854285	0.1238	1.0288
chr2	243199373	9759673	0.0401	2.9581
chr3	198022430	12183597	0.0615	0.5037
chr4	191154276	10197647	0.0533	0.4424
chr5	180915260	18498185	0.1022	0.6284
chr6	171115067	3472885	0.0203	0.8198
chr7	159138663	16152078	0.1015	0.9701

chr8	146364022	7824738	0.0535	0.6797
chr9	141213431	7250834	0.0513	0.5631
chr10	135534747	15934528	0.1176	0.7137
chr11	135006516	5120956	0.0379	0.3913
chr12	133851895	1962505	0.0147	0.245
chr13	115169878	1184203	0.0103	0.5084
chr14	107349540	5255637	0.049	0.4438
chr15	102531392	9897729	0.0965	0.8827
chr16	90354753	6752249	0.0747	0.5838
chr17	81195210	4288684	0.0528	0.4668
chr18	78077248	10302026	0.1319	1.534
chr19	59128983	2058201	0.0348	0.6702
chr20	63025520	7737918	0.1228	0.7248
chr21	48129895	6022376	0.1251	0.7075
chr22	51304566	408247	0.008	0.1519
chrMT	16571	93510	5.643	5.7277
chrX	155270560	8443450	0.0544	0.4686
chrY	59373566	478846	0.0081	0.2577

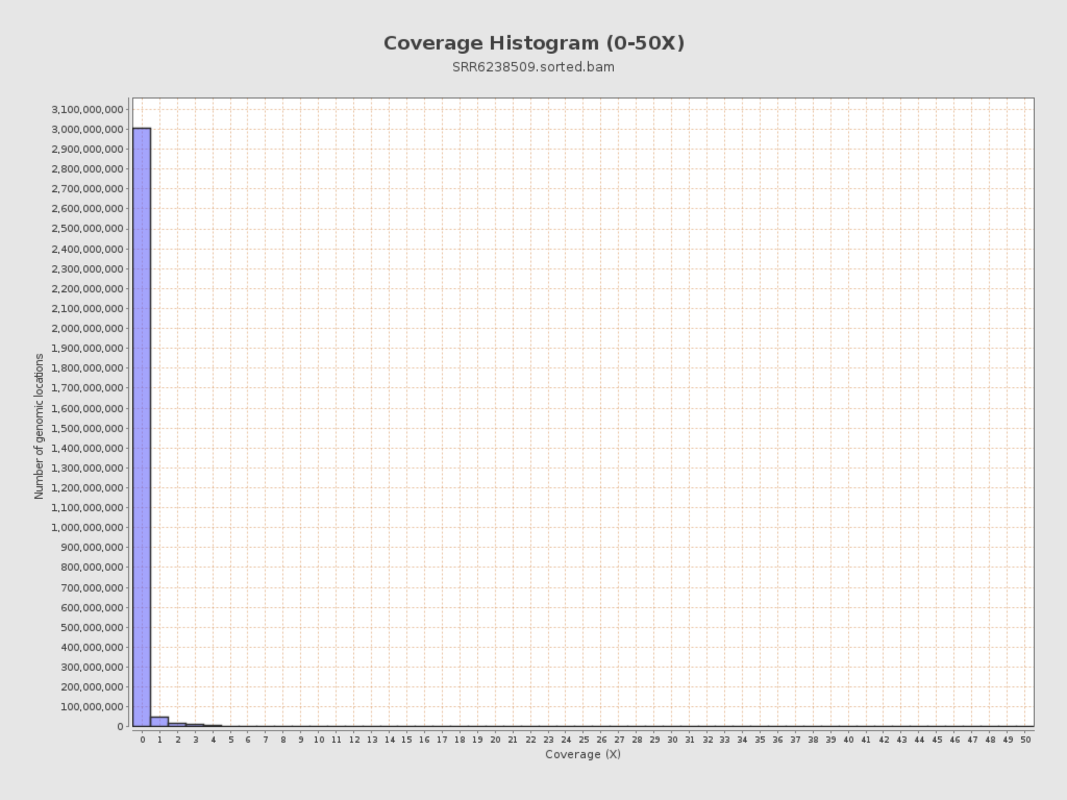
3. Results : Coverage across reference



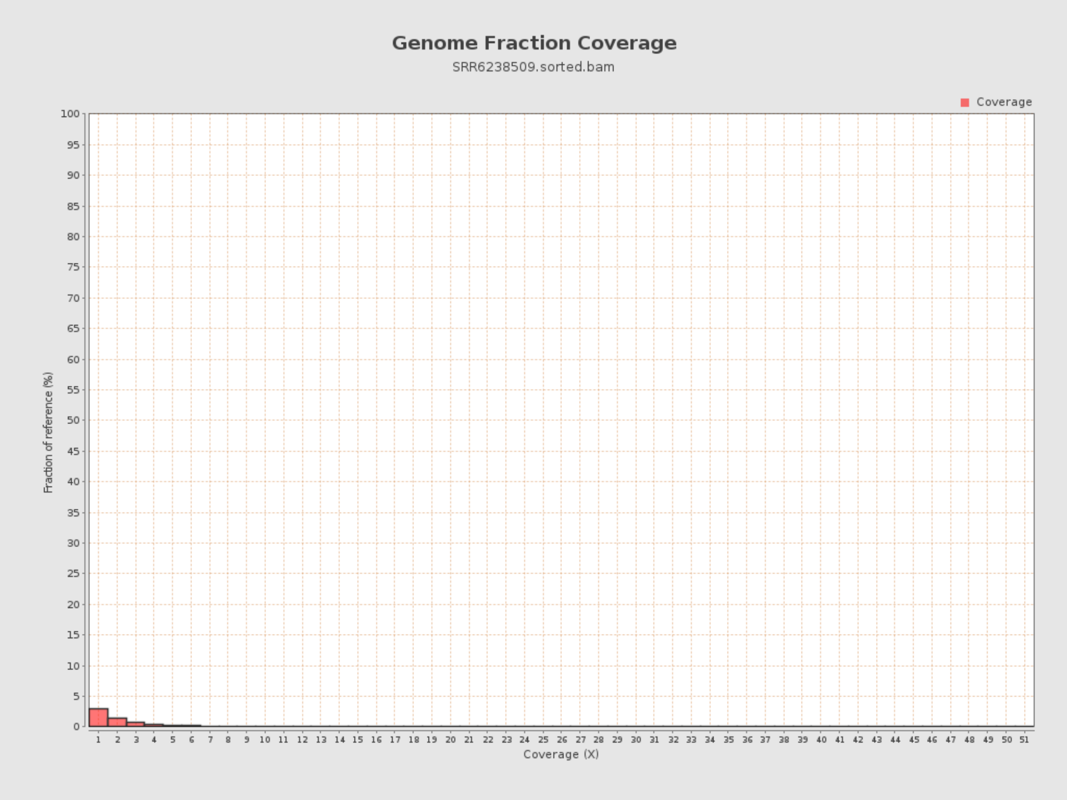
4. Results : Coverage Histogram



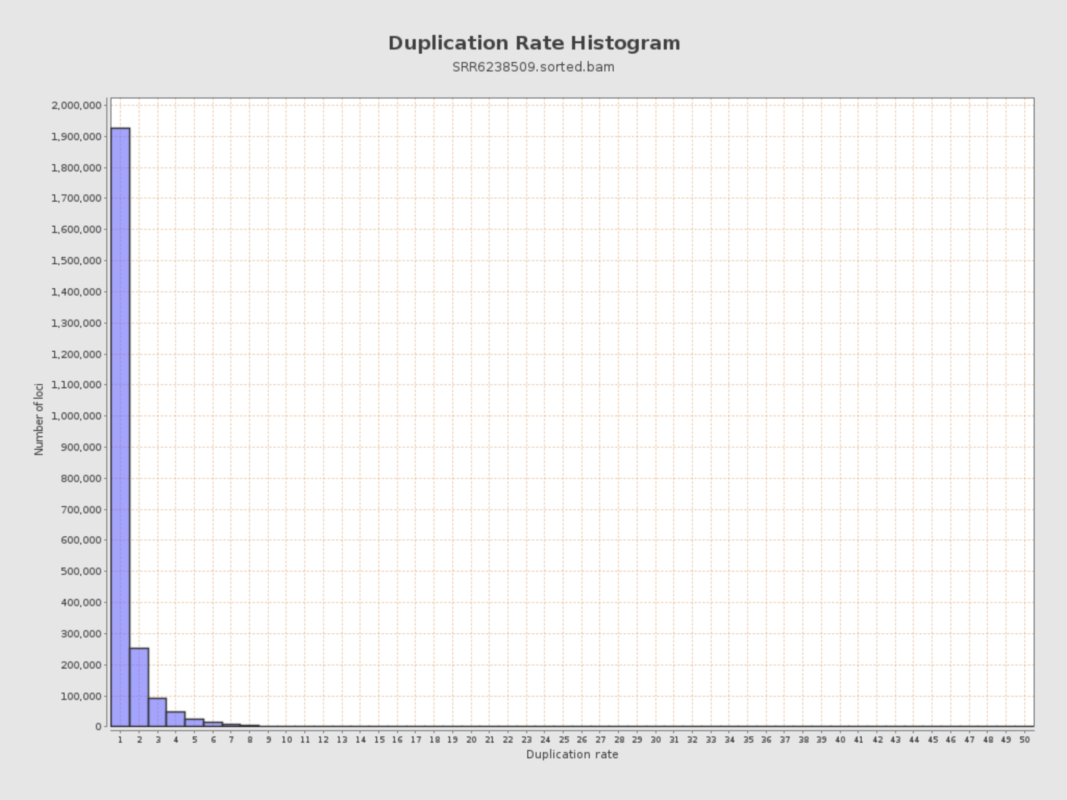
5. Results : Coverage Histogram (0-50X)



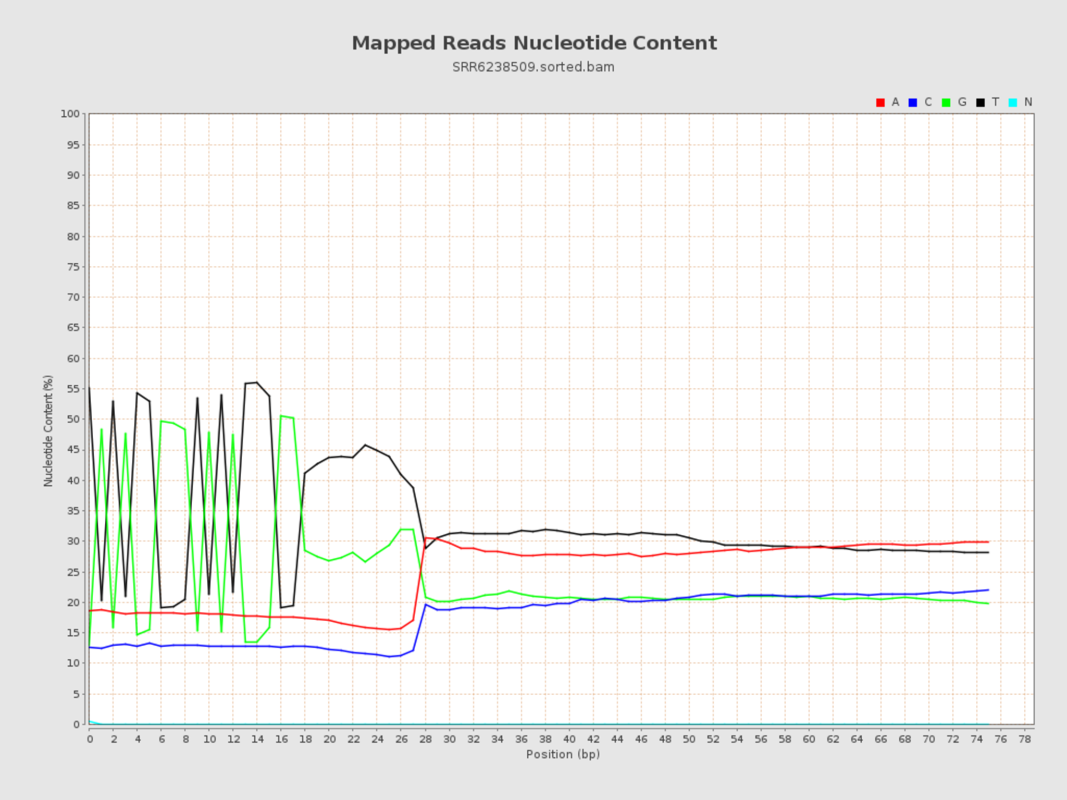
6. Results : Genome Fraction Coverage



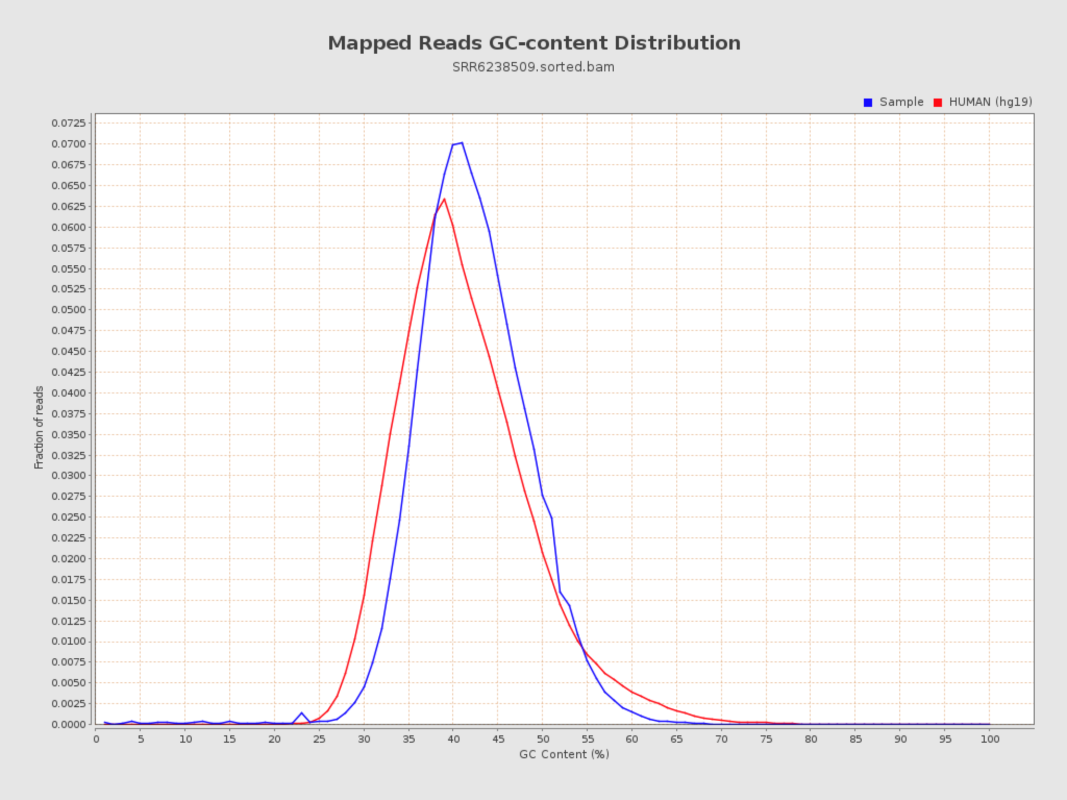
7. Results : Duplication Rate Histogram



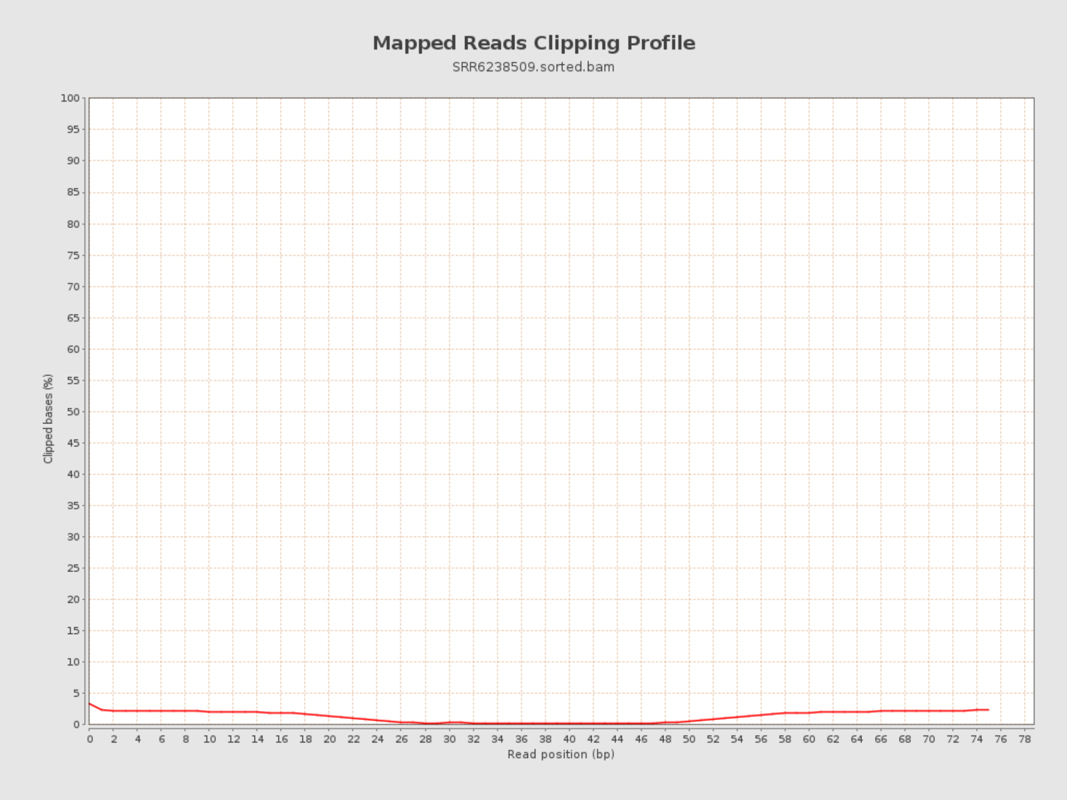
8. Results : Mapped Reads Nucleotide Content



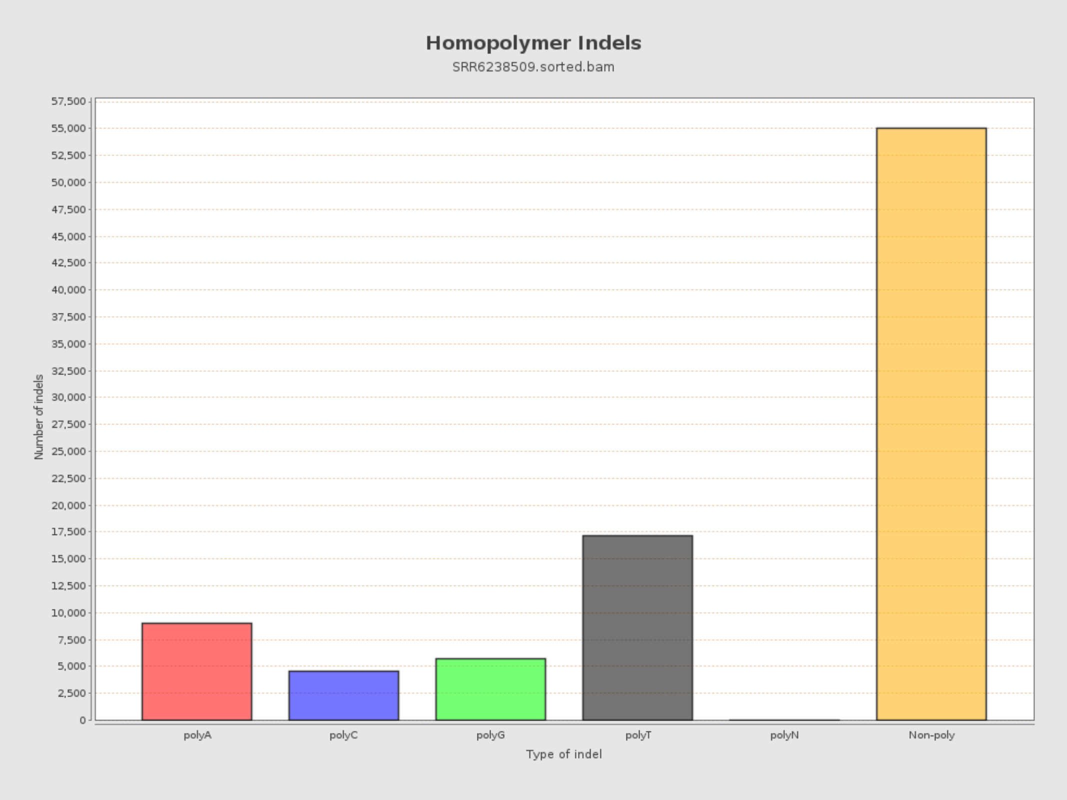
9. Results : Mapped Reads GC-content Distribution



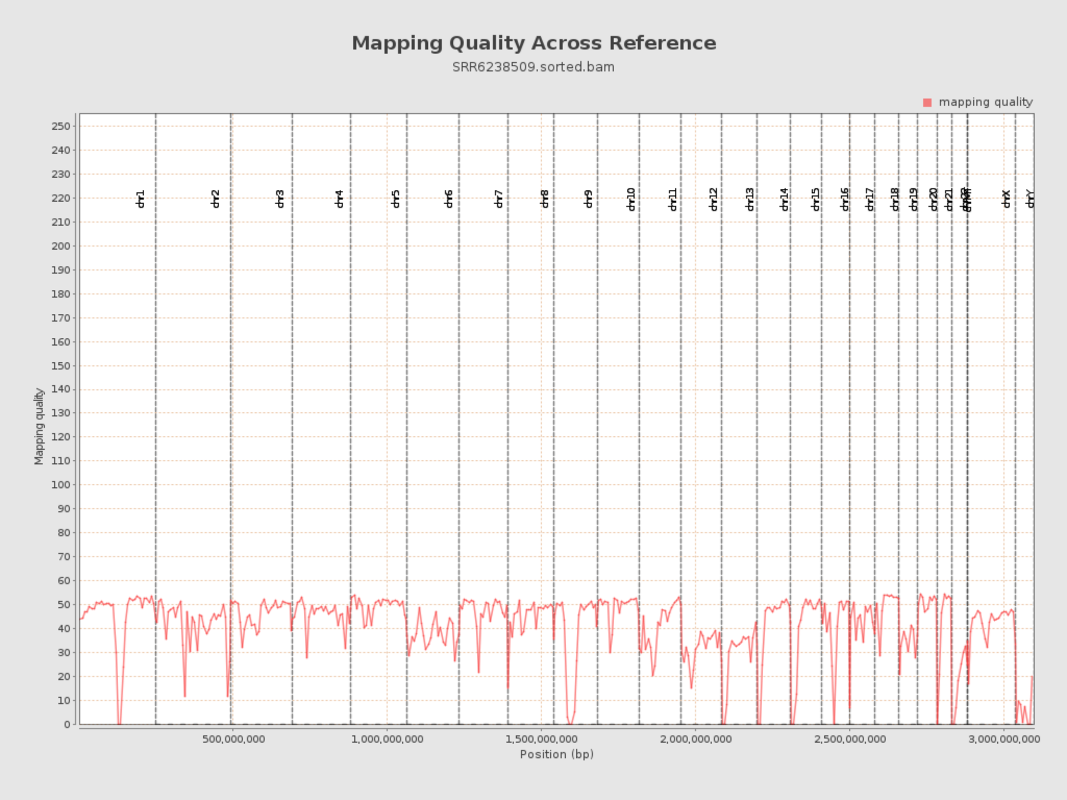
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram