Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 19:07:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238512.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_SRR6238512 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238512.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 19:07:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238512.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,713,584
Mapped reads	4,279,865 / 55.48%
Unmapped reads	3,433,719 / 44.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,779 / 0.45%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	1,362,181 / 17.66%
Duplication rate	21.87%
Clipped reads	2,780,275 / 36.04%

2.2. ACGT Content

Number/percentage of A's	64,170,923 / 24.51%
Number/percentage of C's	45,771,056 / 17.48%
Number/percentage of T's	87,762,429 / 33.52%
Number/percentage of G's	64,085,315 / 24.48%
Number/percentage of N's	17,254 / 0.01%
GC Percentage	41.96%

2.3. Coverage

Mean	0.0846

Standard Deviation	1.0425

2.4. Mapping Quality

Mean Mapping Quality	44.36

2.5. Mismatches and indels

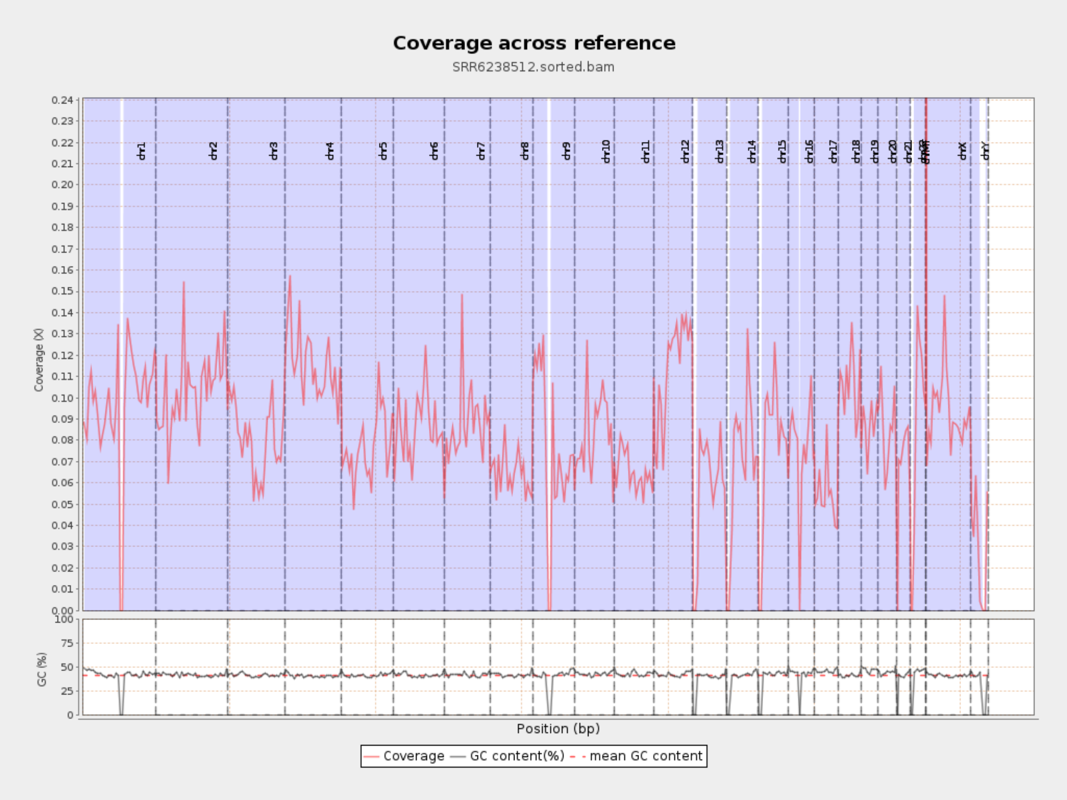
General error rate	0.58%
Mismatches	1,495,209
Insertions	17,125
Mapped reads with at least one insertion	0.4%
Deletions	65,045
Mapped reads with at least one deletion	1.5%
Homopolymer indels	42.51%

2.6. Chromosome stats

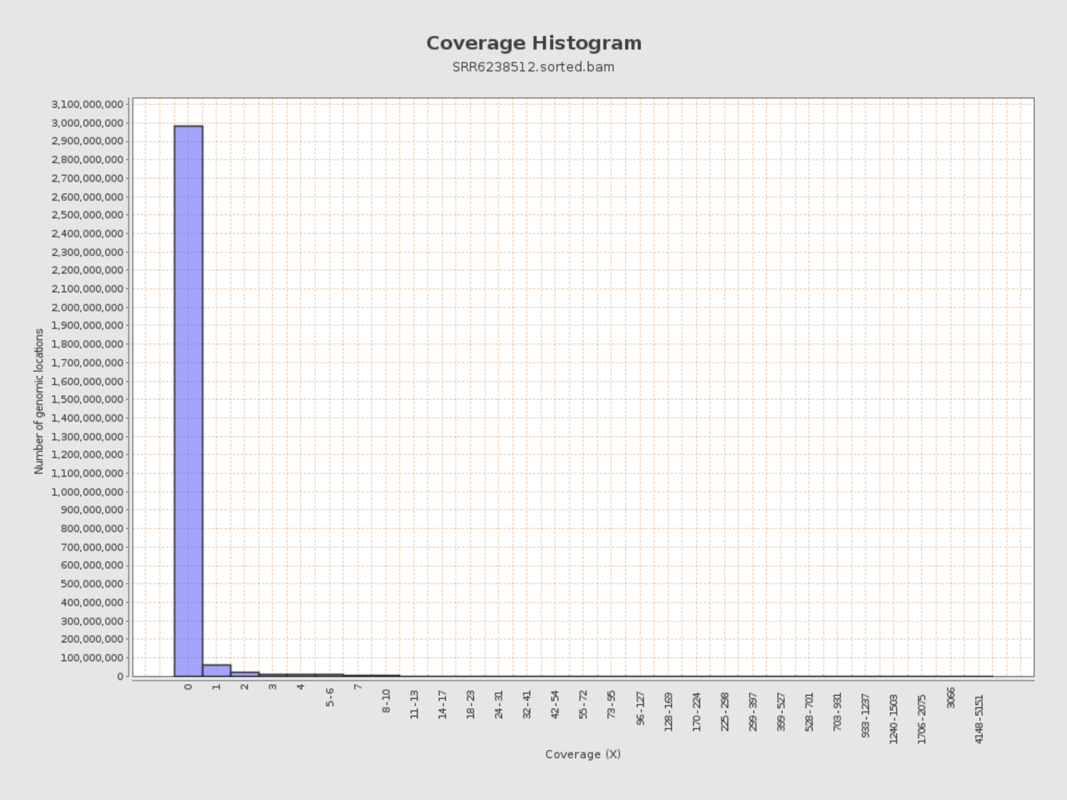
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24140604	0.0969	1.2969
chr2	243199373	25133542	0.1033	2.3699
chr3	198022430	15966985	0.0806	0.6912
chr4	191154276	22236495	0.1163	0.7147
chr5	180915260	13955808	0.0771	0.5814
chr6	171115067	14765925	0.0863	0.9445
chr7	159138663	14002886	0.088	1.1458

chr8	146364022	9383272	0.0641	0.8097
chr9	141213431	10676303	0.0756	0.7002
chr10	135534747	11383733	0.084	0.7509
chr11	135006516	8803337	0.0652	0.6099
chr12	133851895	15389439	0.115	0.7293
chr13	115169878	6586266	0.0572	0.6164
chr14	107349540	7656910	0.0713	0.5723
chr15	102531392	7798112	0.0761	0.6919
chr16	90354753	6710617	0.0743	0.6138
chr17	81195210	4438070	0.0547	0.5309
chr18	78077248	8273904	0.106	1.6445
chr19	59128983	5143120	0.087	0.9675
chr20	63025520	5449597	0.0865	0.6208
chr21	48129895	3274546	0.068	0.5775
chr22	51304566	4316416	0.0841	0.6344
chrMT	16571	134997	8.1466	6.7793
chrX	155270560	14563849	0.0938	0.6678
chrY	59373566	1734509	0.0292	0.532

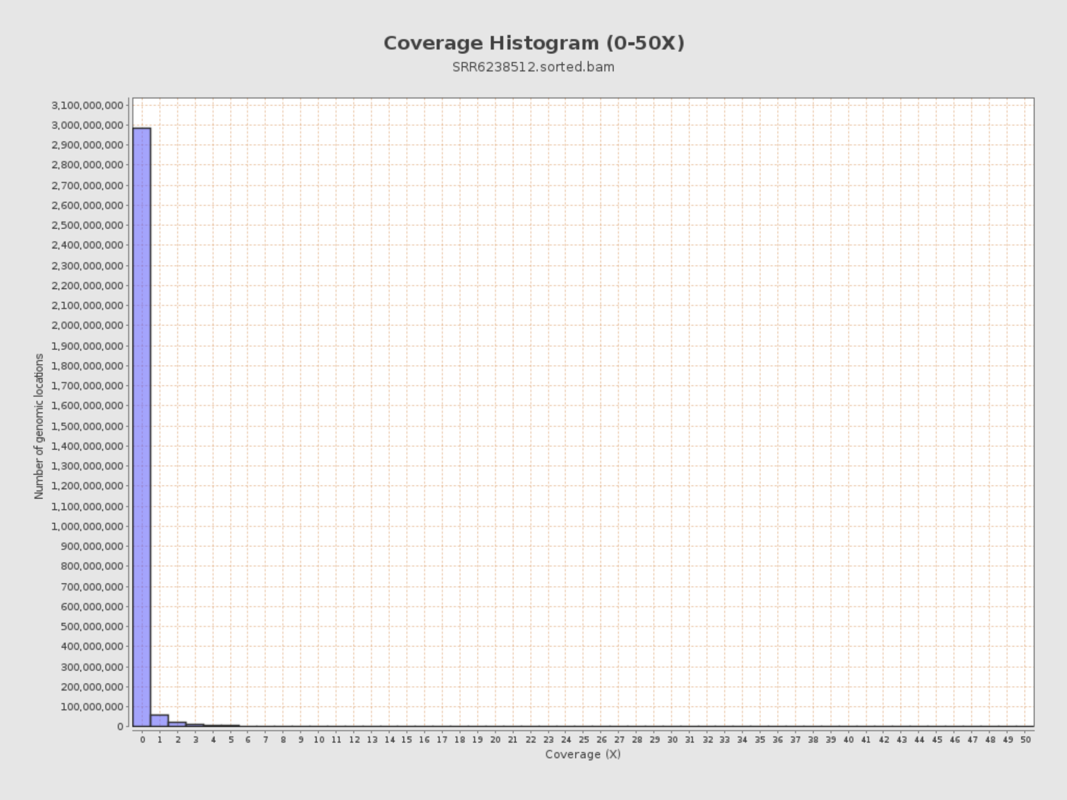
3. Results : Coverage across reference



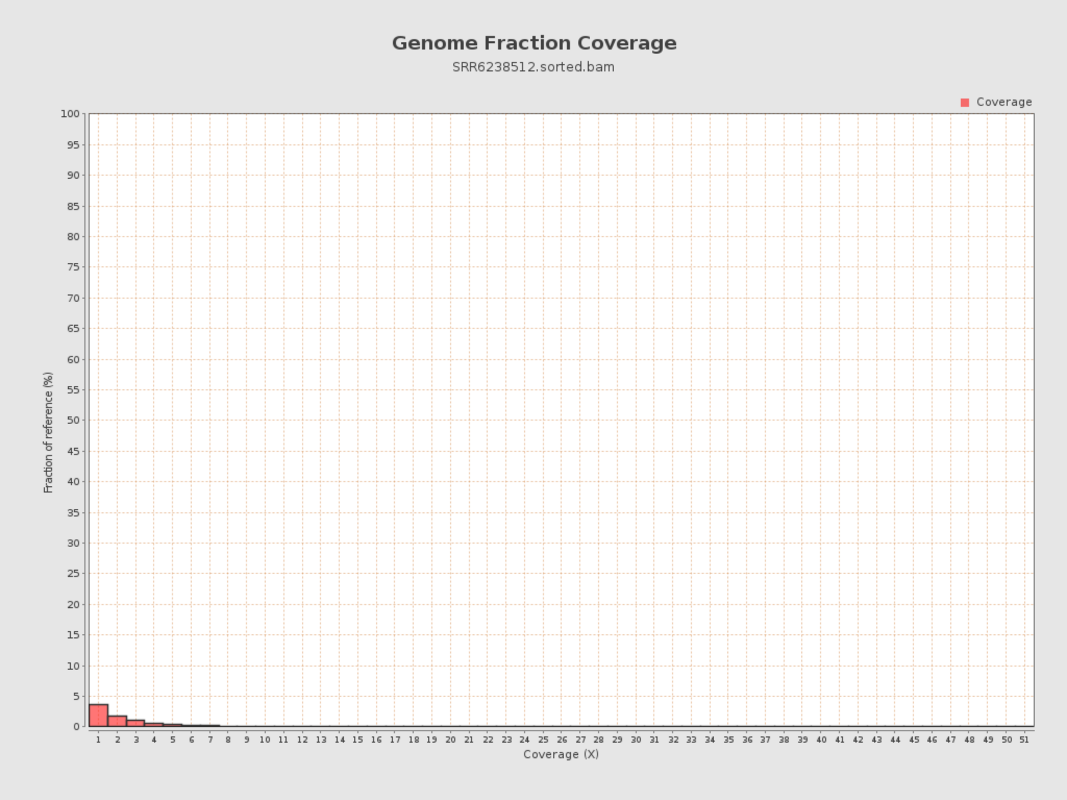
4. Results : Coverage Histogram



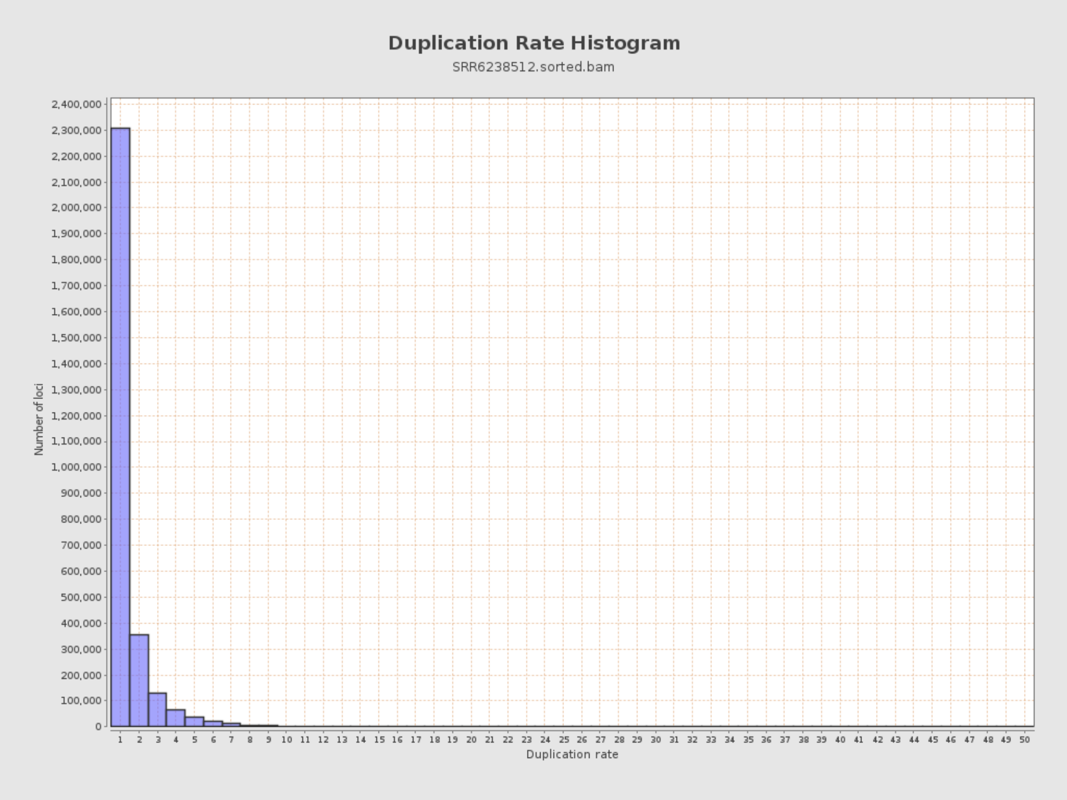
5. Results : Coverage Histogram (0-50X)



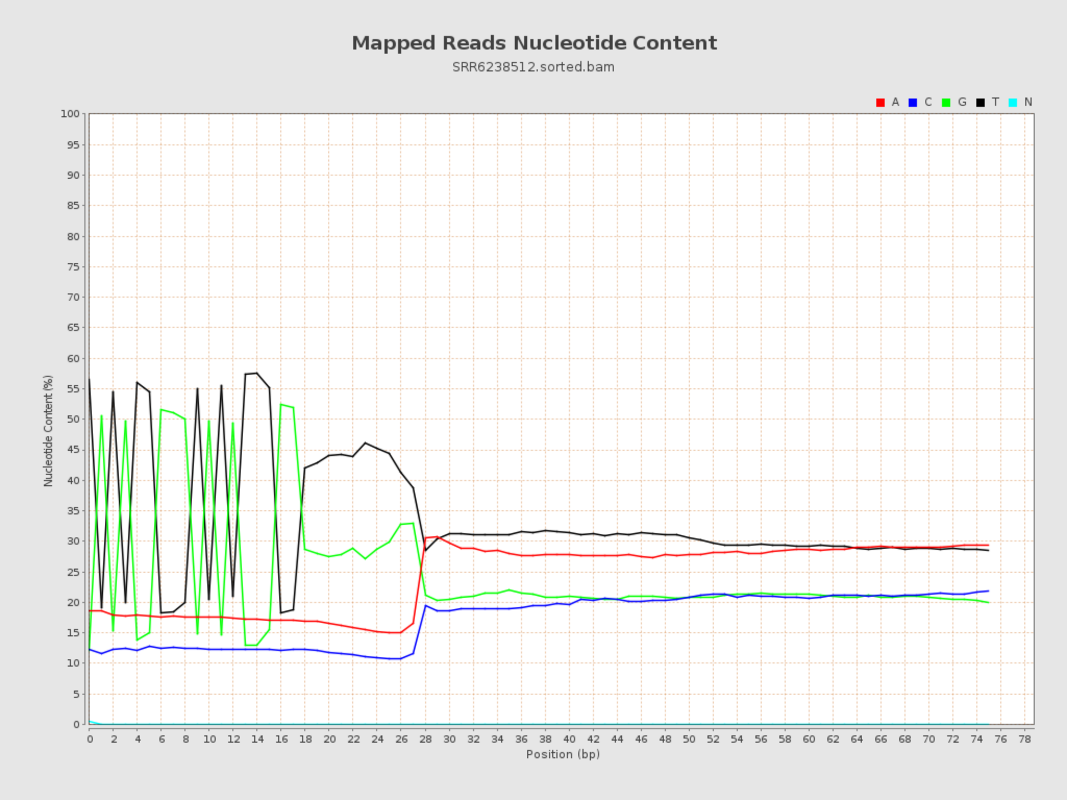
6. Results : Genome Fraction Coverage



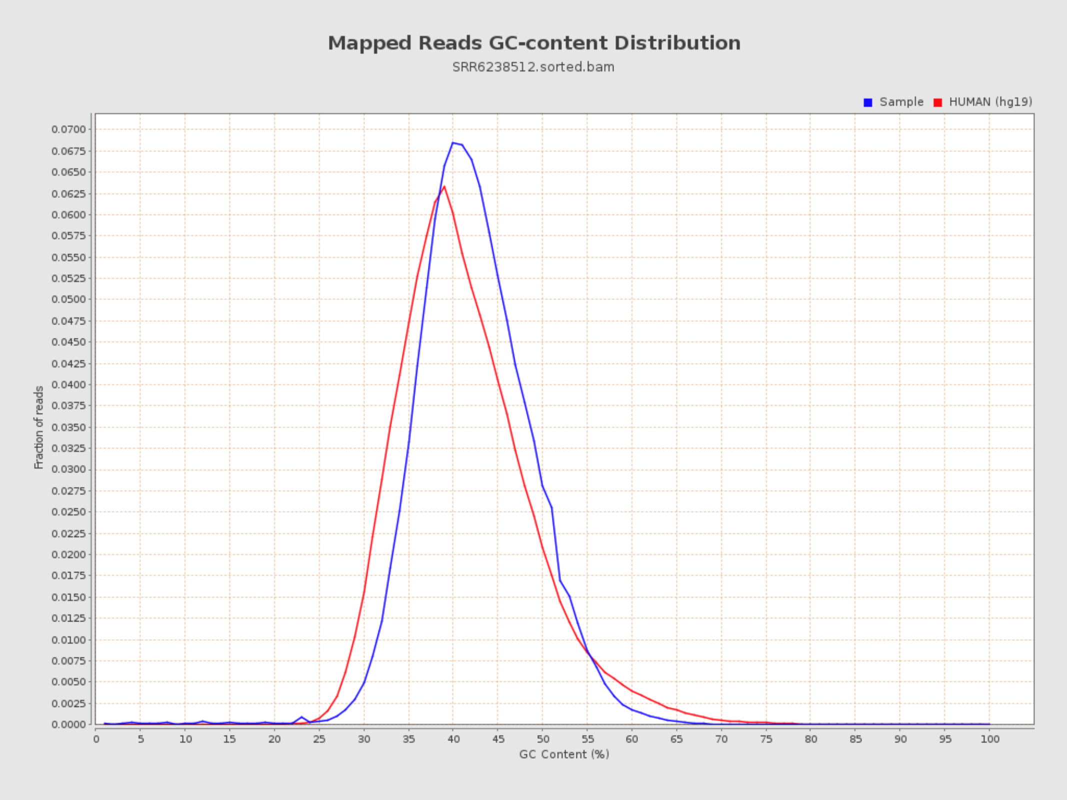
7. Results : Duplication Rate Histogram



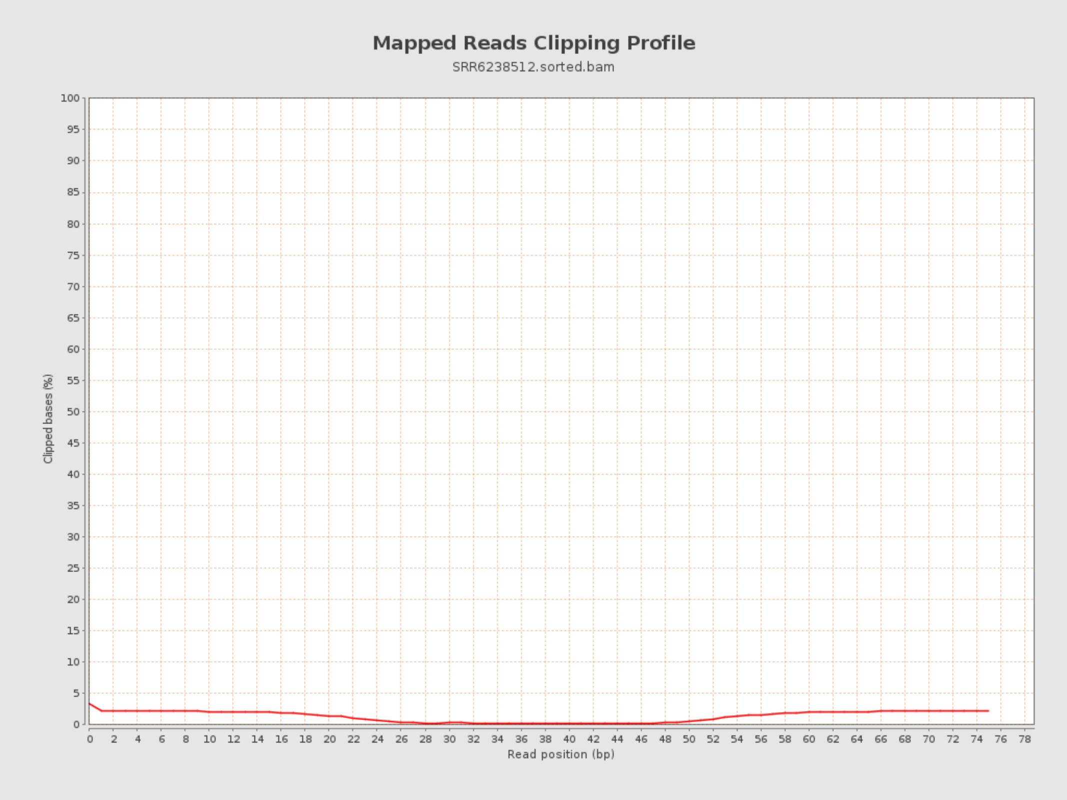
8. Results : Mapped Reads Nucleotide Content



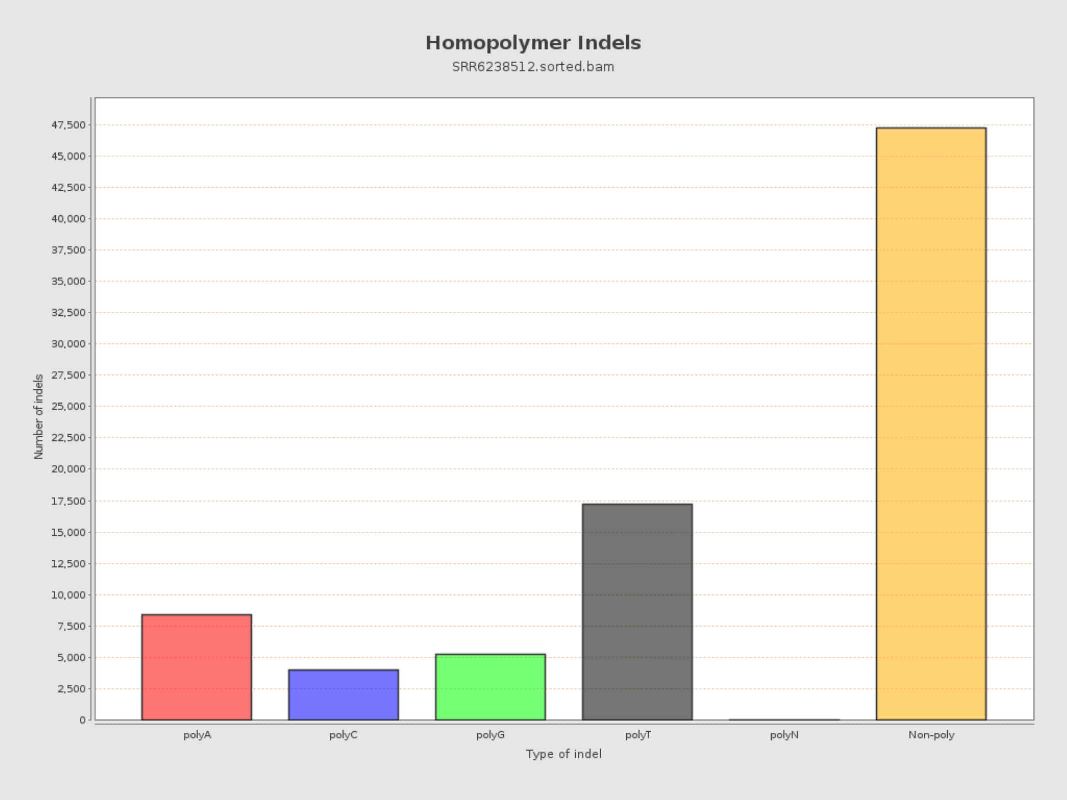
9. Results : Mapped Reads GC-content Distribution



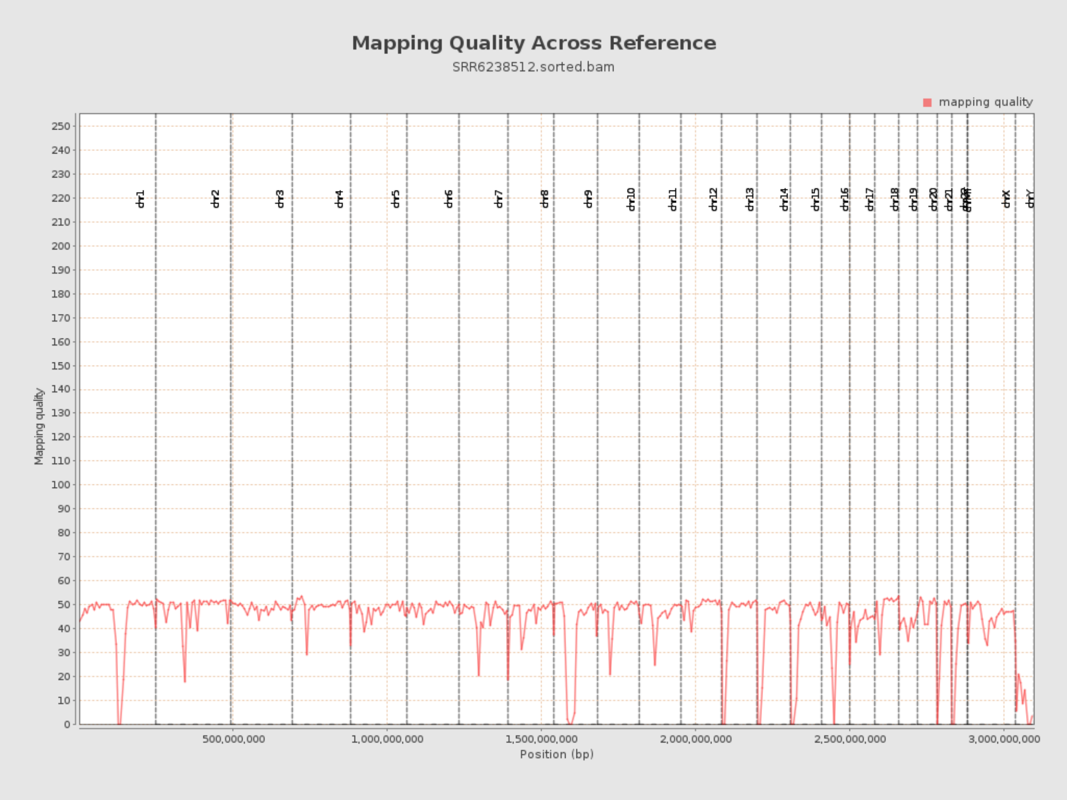
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram