Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:01:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238253.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_SRR6238253 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238253.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:01:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238253.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,283,770
Mapped reads	2,048,106 / 89.68%
Unmapped reads	235,664 / 10.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,840 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	63,622 / 2.79%
Duplication rate	1.96%
Clipped reads	1,065,343 / 46.65%

2.2. ACGT Content

Number/percentage of A's	37,550,596 / 28.11%
Number/percentage of C's	26,552,745 / 19.88%
Number/percentage of T's	39,124,467 / 29.29%
Number/percentage of G's	30,313,536 / 22.69%
Number/percentage of N's	31,563 / 0.02%
GC Percentage	42.57%

2.3. Coverage

Mean	0.0432

Standard Deviation	0.4133

2.4. Mapping Quality

Mean Mapping Quality	42.5

2.5. Mismatches and indels

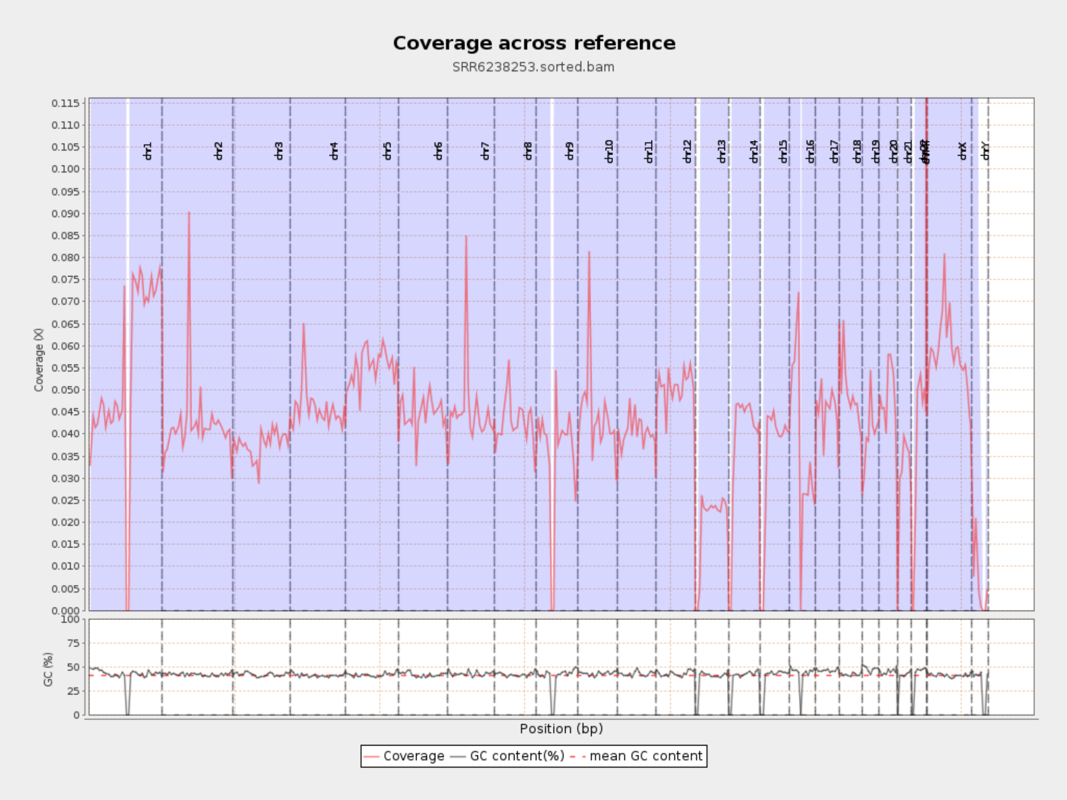
General error rate	0.9%
Mismatches	1,179,485
Insertions	11,532
Mapped reads with at least one insertion	0.56%
Deletions	37,754
Mapped reads with at least one deletion	1.82%
Homopolymer indels	44.03%

2.6. Chromosome stats

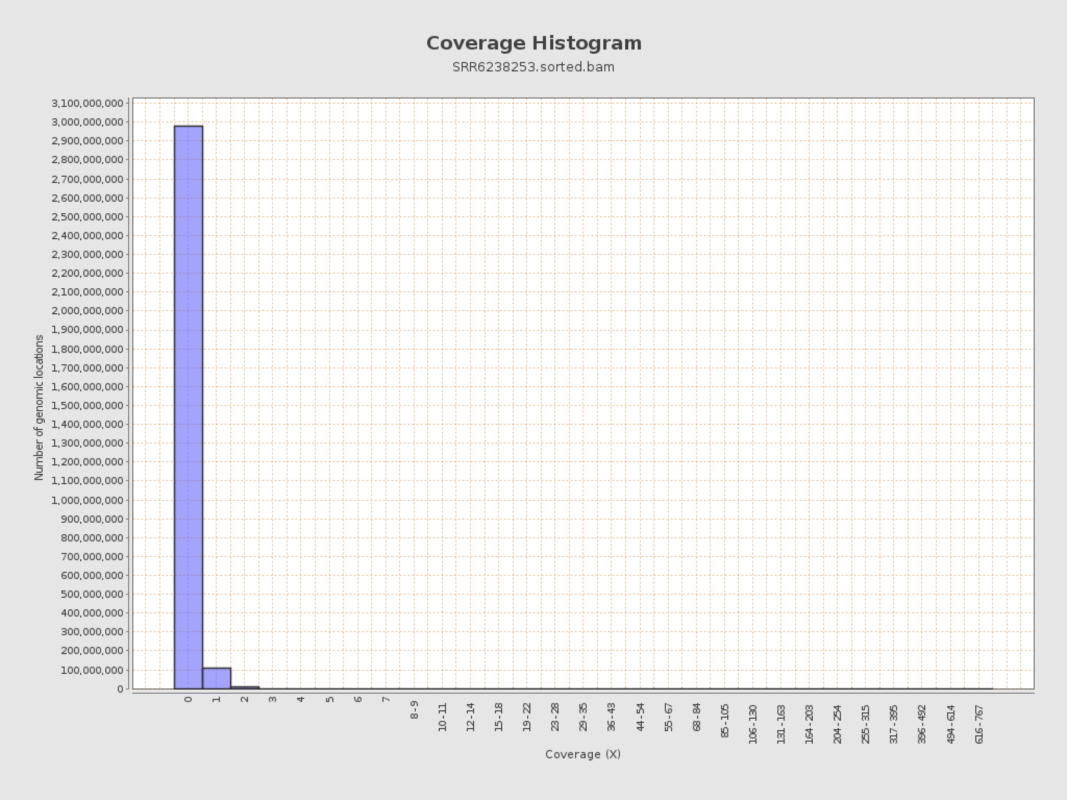
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13564268	0.0544	0.7086
chr2	243199373	10294225	0.0423	0.5335
chr3	198022430	7463498	0.0377	0.2133
chr4	191154276	8771460	0.0459	0.2586
chr5	180915260	10036143	0.0555	0.2607
chr6	171115067	7669653	0.0448	0.2911
chr7	159138663	7234083	0.0455	0.6125

chr8	146364022	6250073	0.0427	0.4702
chr9	141213431	4984093	0.0353	0.4126
chr10	135534747	6034924	0.0445	0.4238
chr11	135006516	5463475	0.0405	0.37
chr12	133851895	6768359	0.0506	0.2549
chr13	115169878	2274676	0.0198	0.1534
chr14	107349540	4073821	0.0379	0.2628
chr15	102531392	3521146	0.0343	0.2138
chr16	90354753	3443613	0.0381	0.2578
chr17	81195210	3674925	0.0453	0.2685
chr18	78077248	3893453	0.0499	0.7889
chr19	59128983	2388784	0.0404	0.5396
chr20	63025520	3044244	0.0483	0.2489
chr21	48129895	1475046	0.0306	0.2263
chr22	51304566	1808771	0.0353	0.2048
chrMT	16571	7594	0.4583	0.85
chrX	155270560	9077939	0.0585	0.3129
chrY	59373566	417405	0.007	0.1651

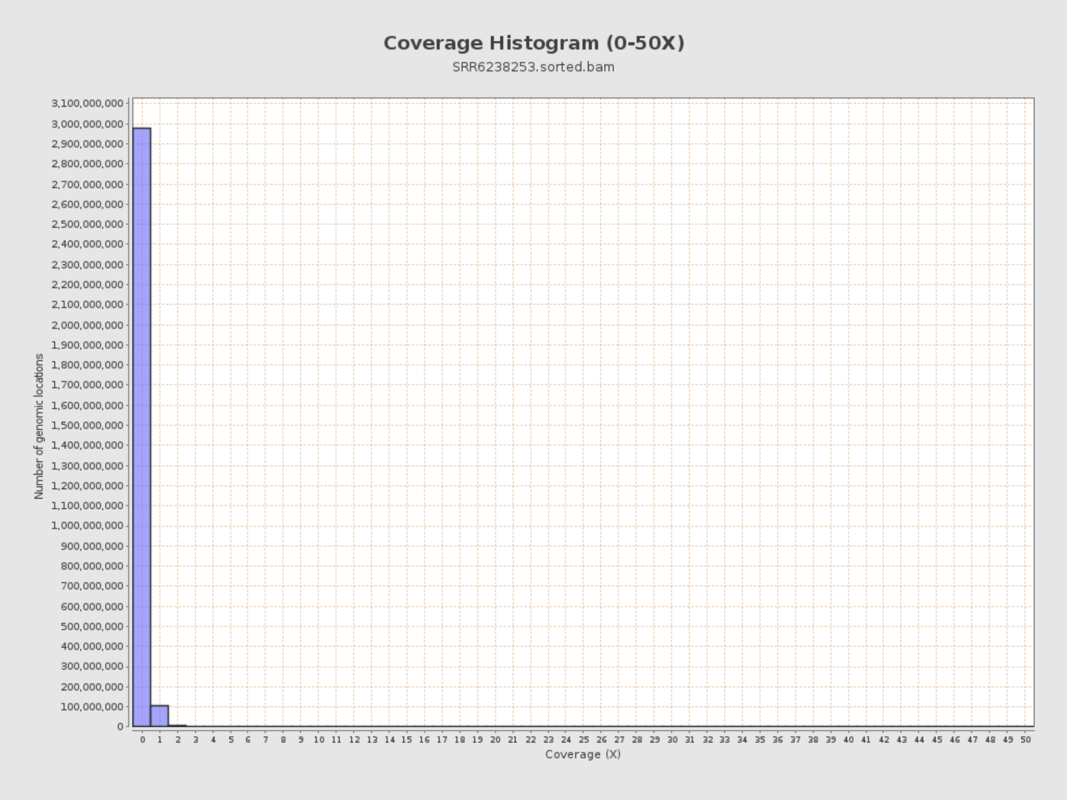
3. Results : Coverage across reference



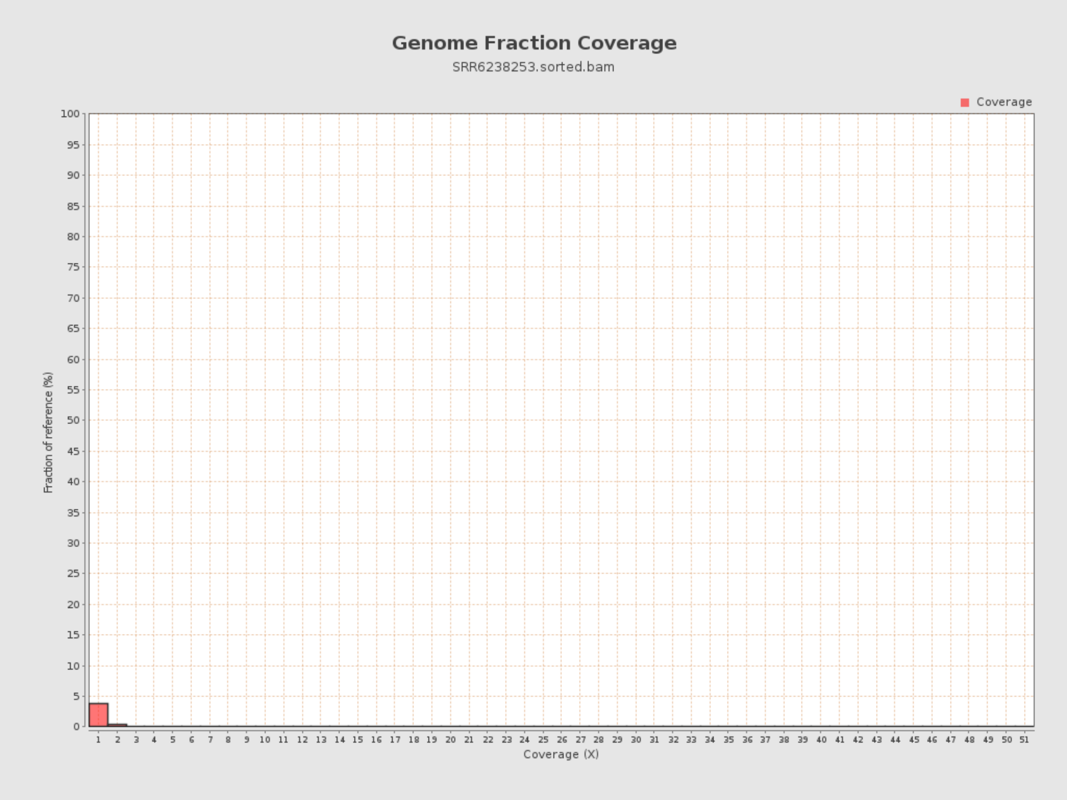
4. Results : Coverage Histogram



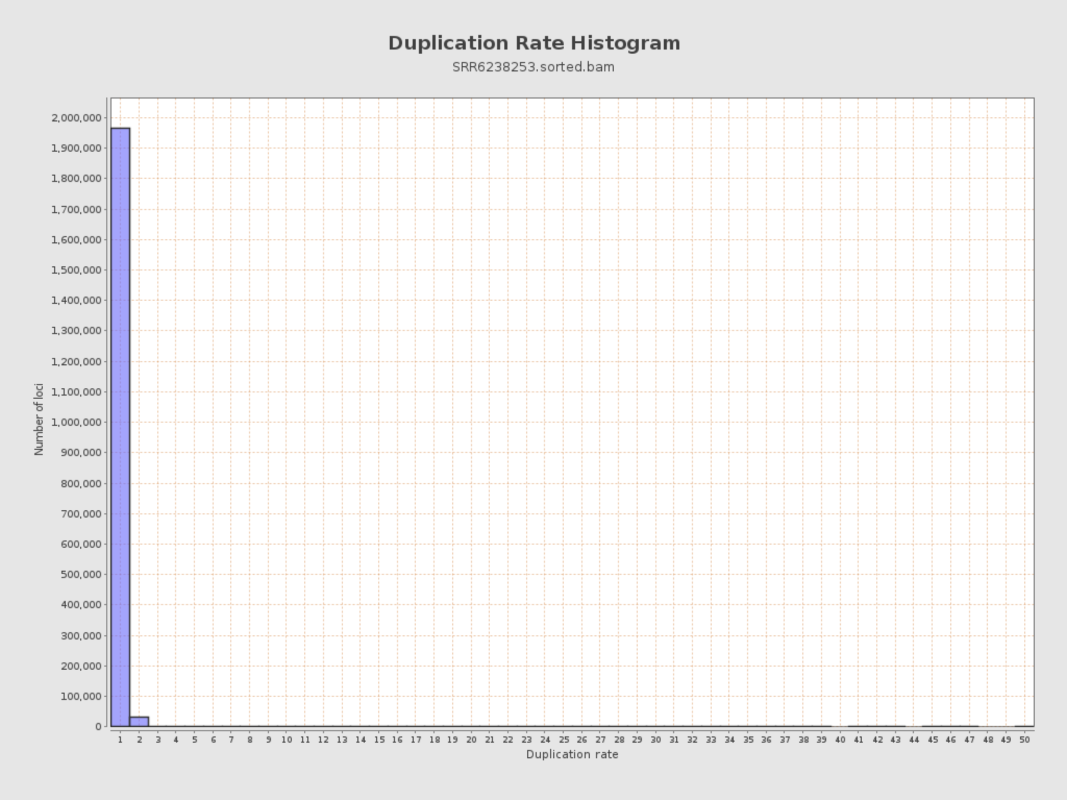
5. Results : Coverage Histogram (0-50X)



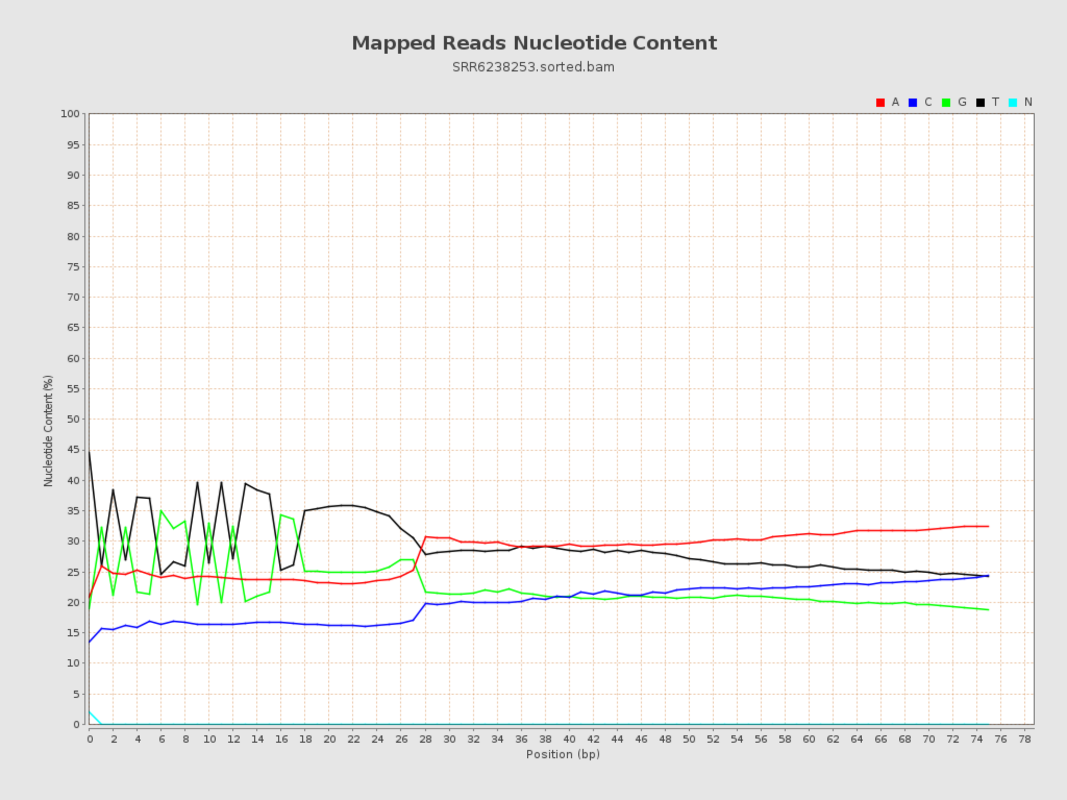
6. Results : Genome Fraction Coverage



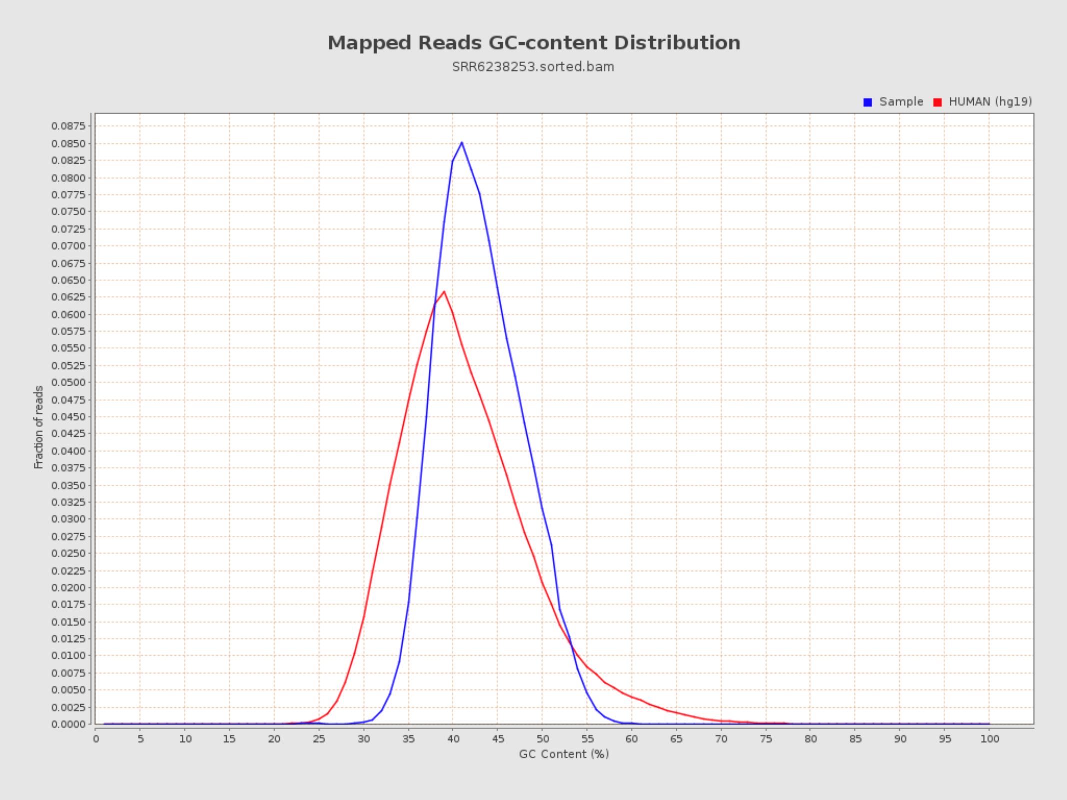
7. Results : Duplication Rate Histogram



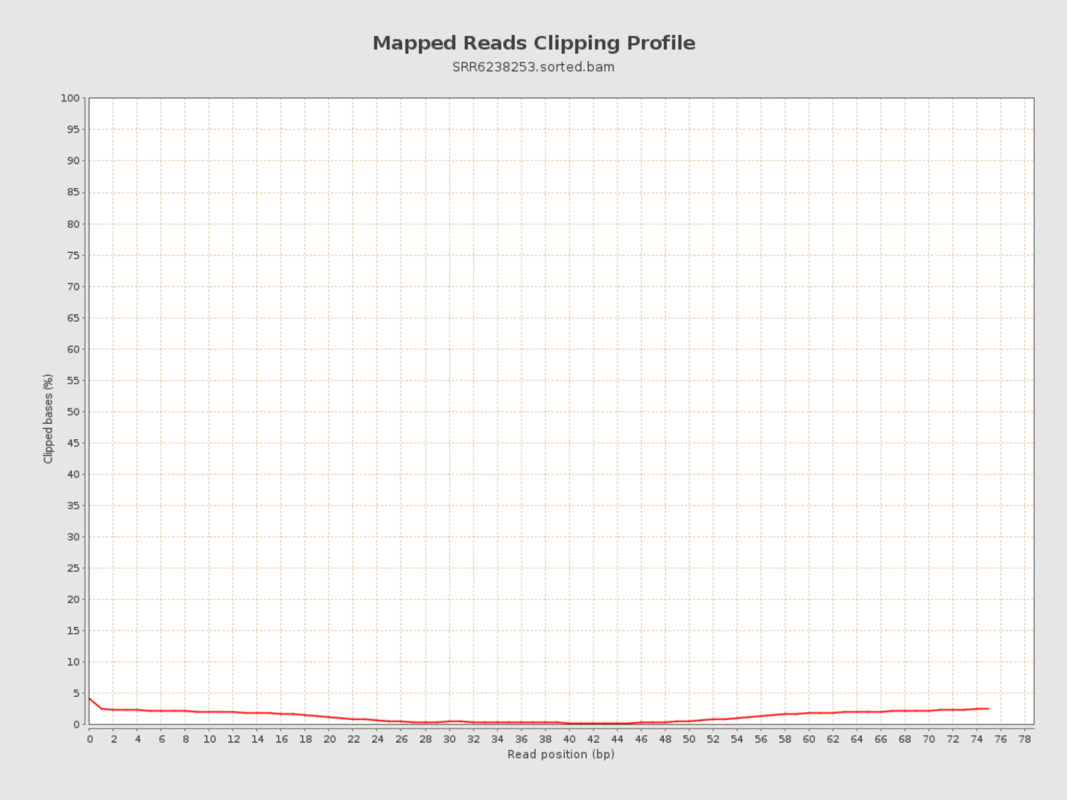
8. Results : Mapped Reads Nucleotide Content



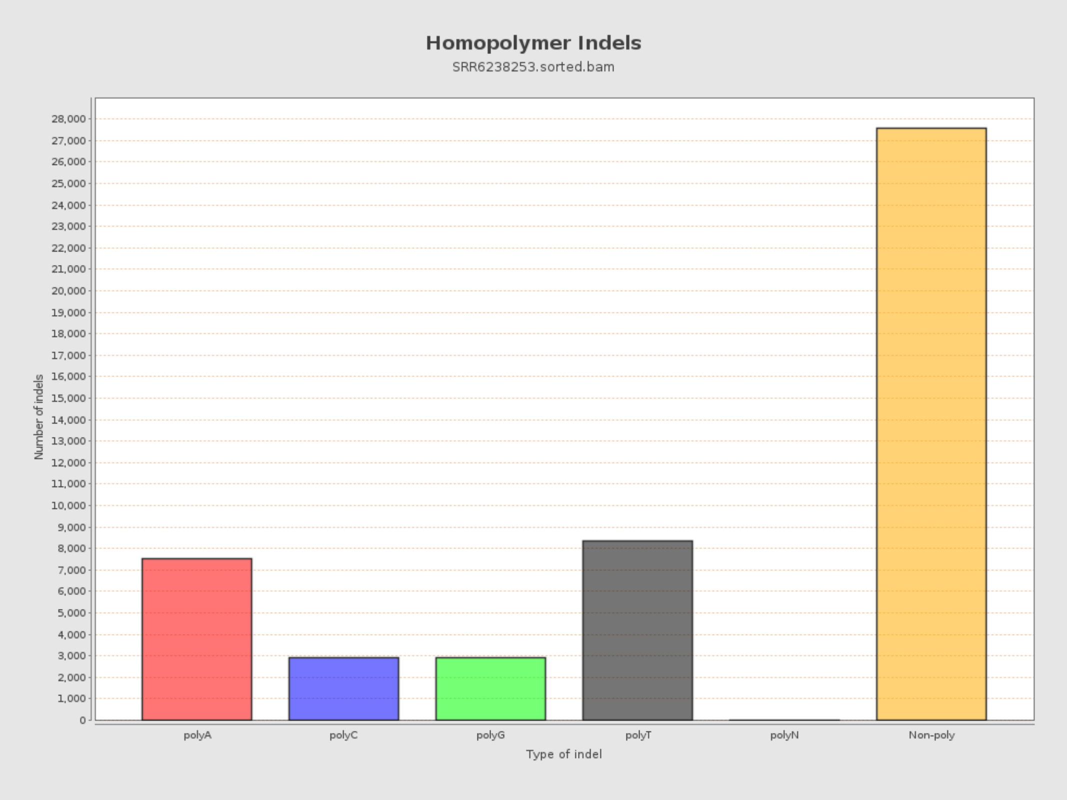
9. Results : Mapped Reads GC-content Distribution



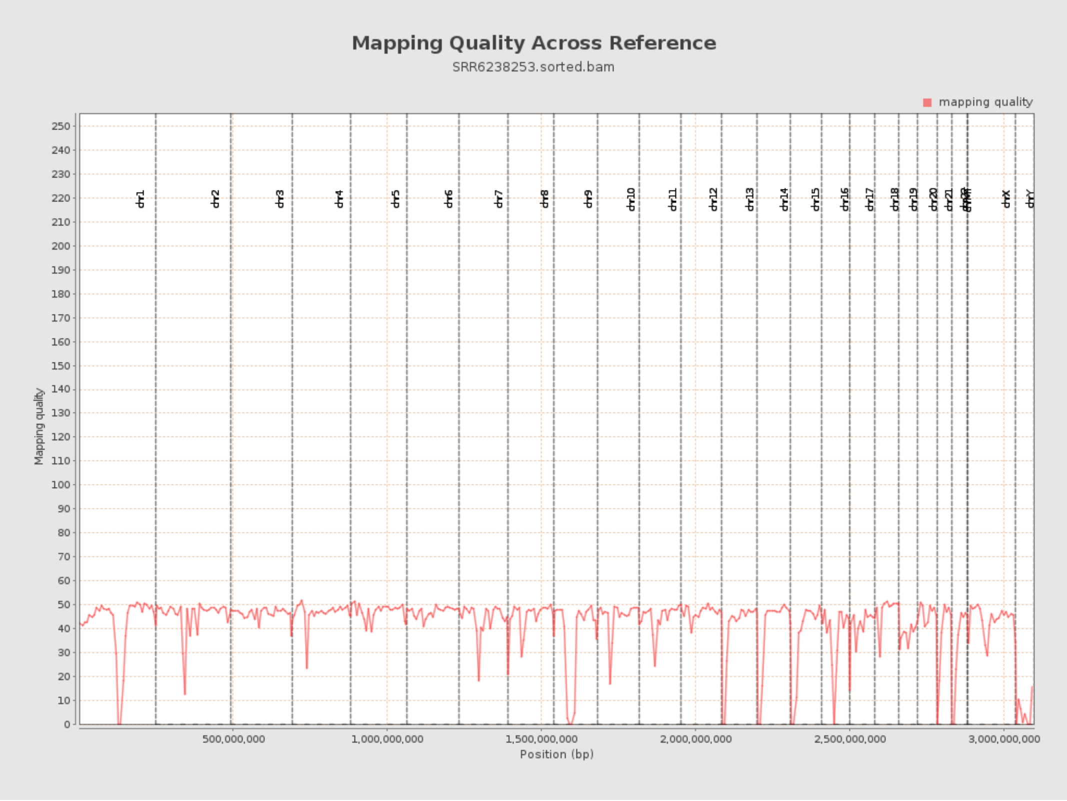
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram