Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 20:19:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238532.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_SRR6238532 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238532.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 20:19:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238532.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,160,206
Mapped reads	3,179,434 / 76.42%
Unmapped reads	980,772 / 23.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,870 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	1,417,579 / 34.07%
Duplication rate	22.33%
Clipped reads	2,178,609 / 52.37%

2.2. ACGT Content

Number/percentage of A's	47,441,967 / 24.73%
Number/percentage of C's	32,656,051 / 17.02%
Number/percentage of T's	65,796,158 / 34.29%
Number/percentage of G's	45,959,595 / 23.96%
Number/percentage of N's	4,231 / 0%
GC Percentage	40.98%

2.3. Coverage

Mean	0.062

Standard Deviation	1.245

2.4. Mapping Quality

Mean Mapping Quality	43.92

2.5. Mismatches and indels

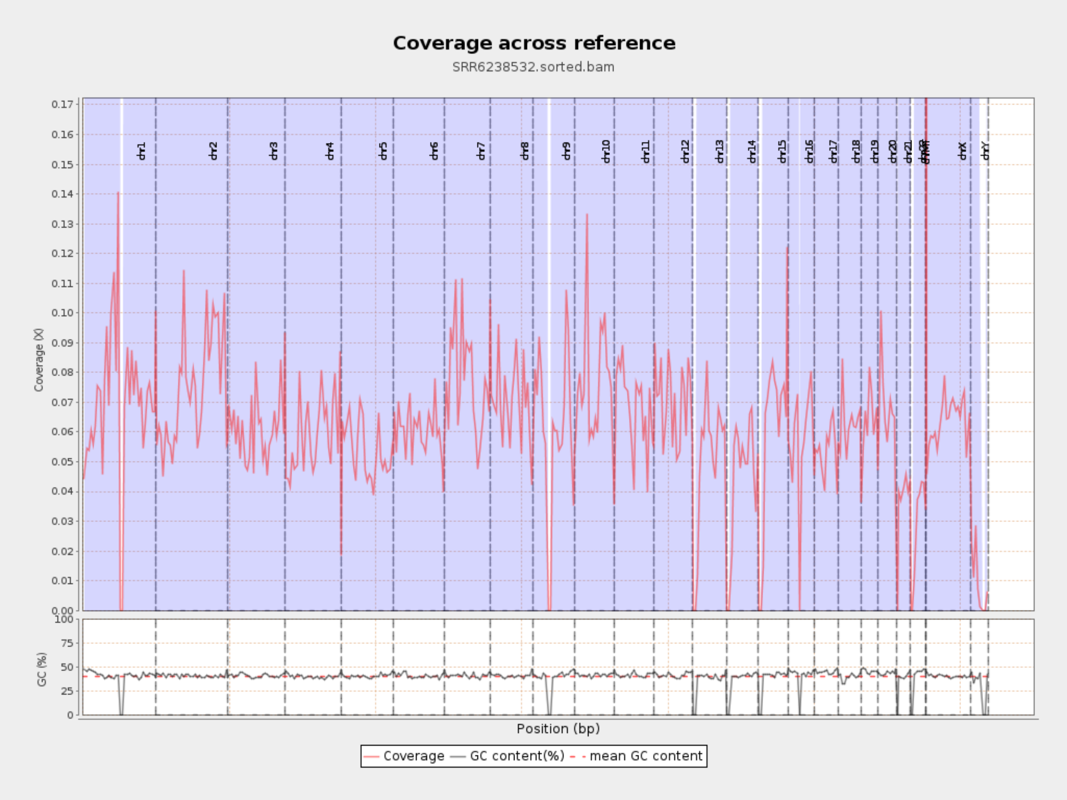
General error rate	0.62%
Mismatches	1,155,047
Insertions	13,264
Mapped reads with at least one insertion	0.41%
Deletions	58,623
Mapped reads with at least one deletion	1.82%
Homopolymer indels	41.99%

2.6. Chromosome stats

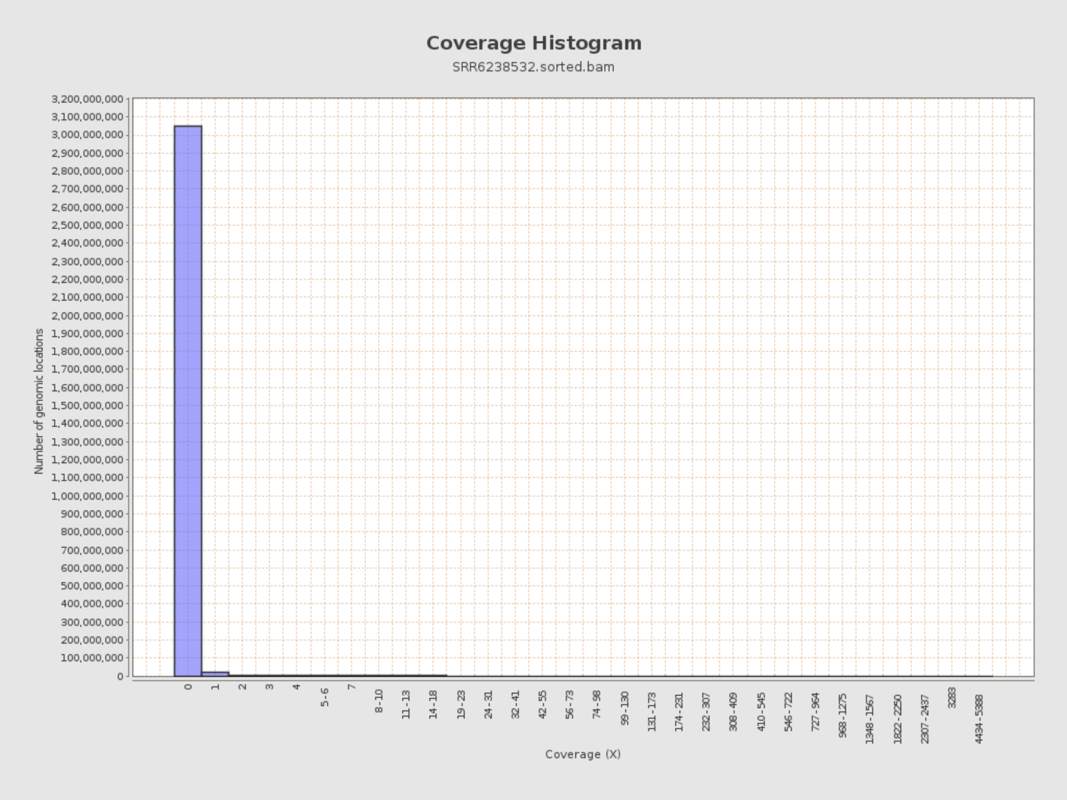
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17337994	0.0696	1.474
chr2	243199373	18289535	0.0752	2.51
chr3	198022430	12006579	0.0606	0.8051
chr4	191154276	11376936	0.0595	0.7764
chr5	180915260	9704293	0.0536	0.7334
chr6	171115067	10389638	0.0607	1.0953
chr7	159138663	12128126	0.0762	1.1675

chr8	146364022	10283865	0.0703	0.9886
chr9	141213431	8667611	0.0614	0.8818
chr10	135534747	10365329	0.0765	1.0616
chr11	135006516	9135864	0.0677	0.8466
chr12	133851895	9542267	0.0713	0.8645
chr13	115169878	5705680	0.0495	0.9246
chr14	107349540	4769388	0.0444	0.7062
chr15	102531392	6052742	0.059	0.936
chr16	90354753	5028683	0.0557	0.7819
chr17	81195210	4436949	0.0546	0.7502
chr18	78077248	4910923	0.0629	3.1085
chr19	59128983	3792234	0.0641	1.0774
chr20	63025520	4320625	0.0686	0.8647
chr21	48129895	1796877	0.0373	0.5851
chr22	51304566	1416766	0.0276	0.5248
chrMT	16571	89197	5.3827	8.3525
chrX	155270560	9870770	0.0636	0.8109
chrY	59373566	537274	0.009	0.4347

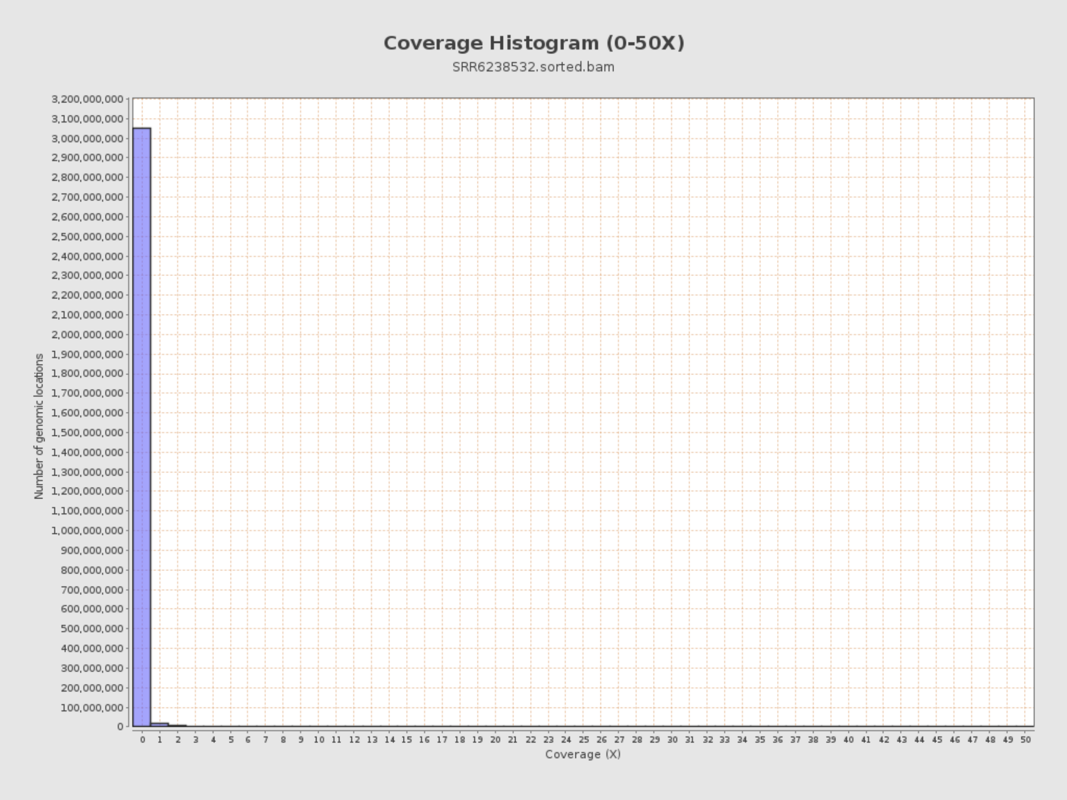
3. Results : Coverage across reference



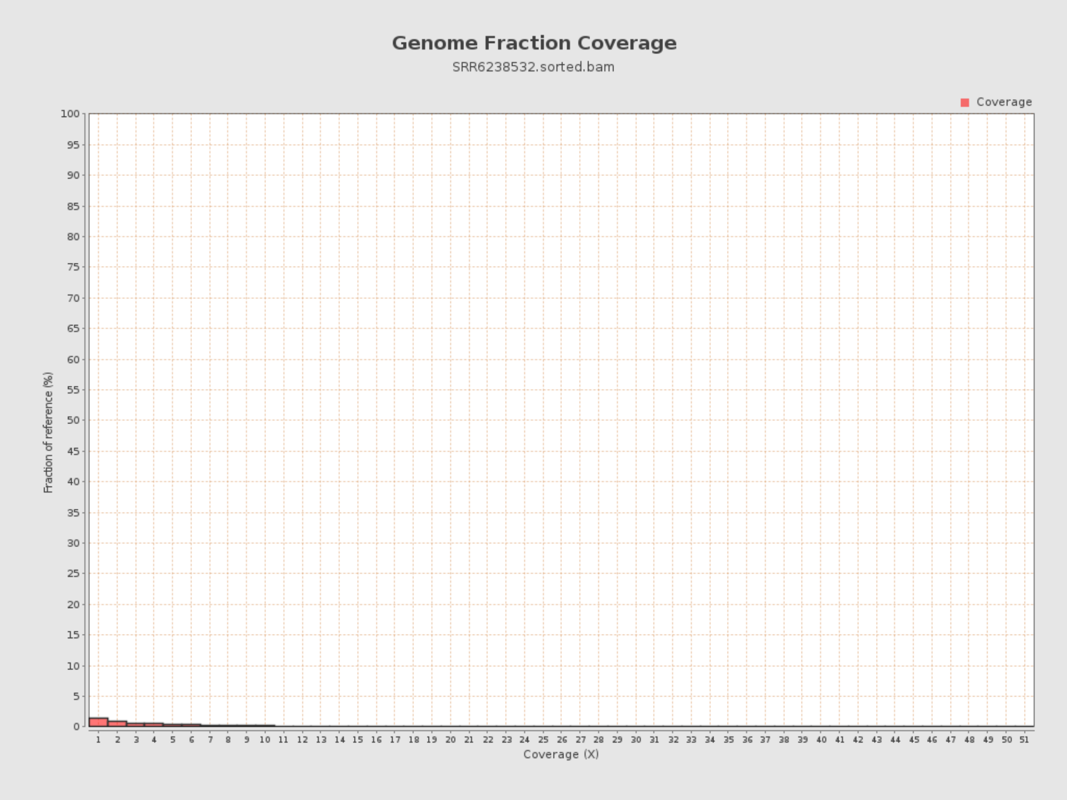
4. Results : Coverage Histogram



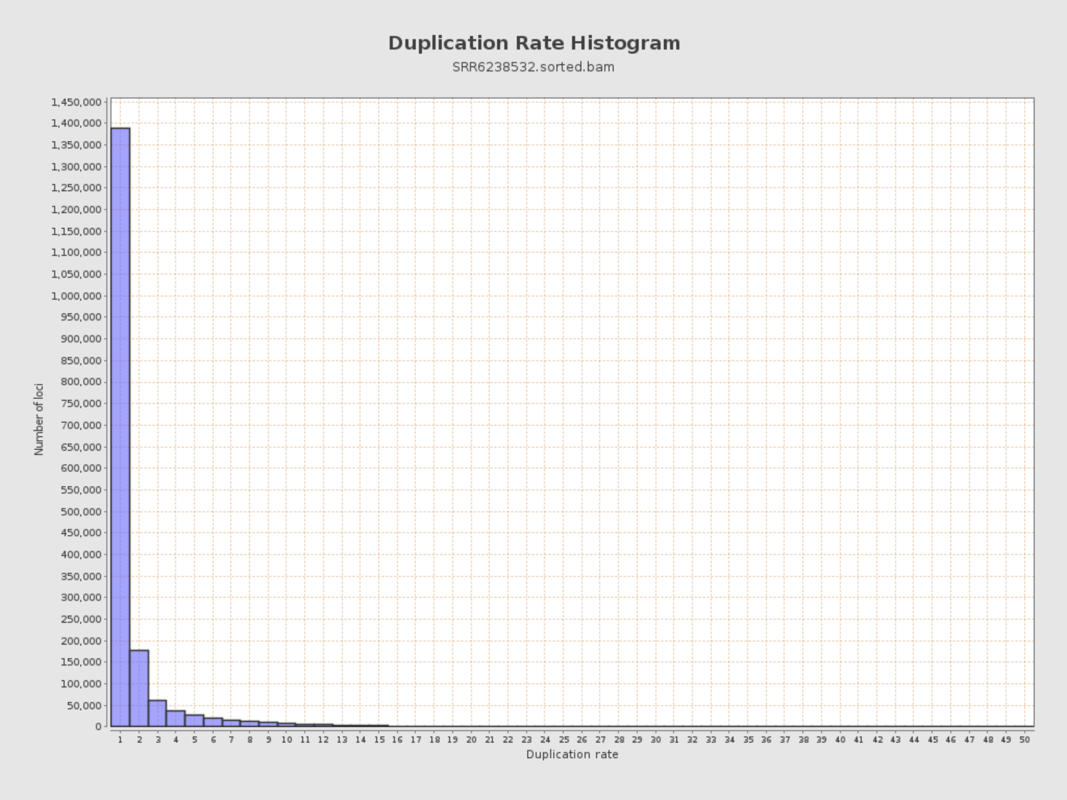
5. Results : Coverage Histogram (0-50X)



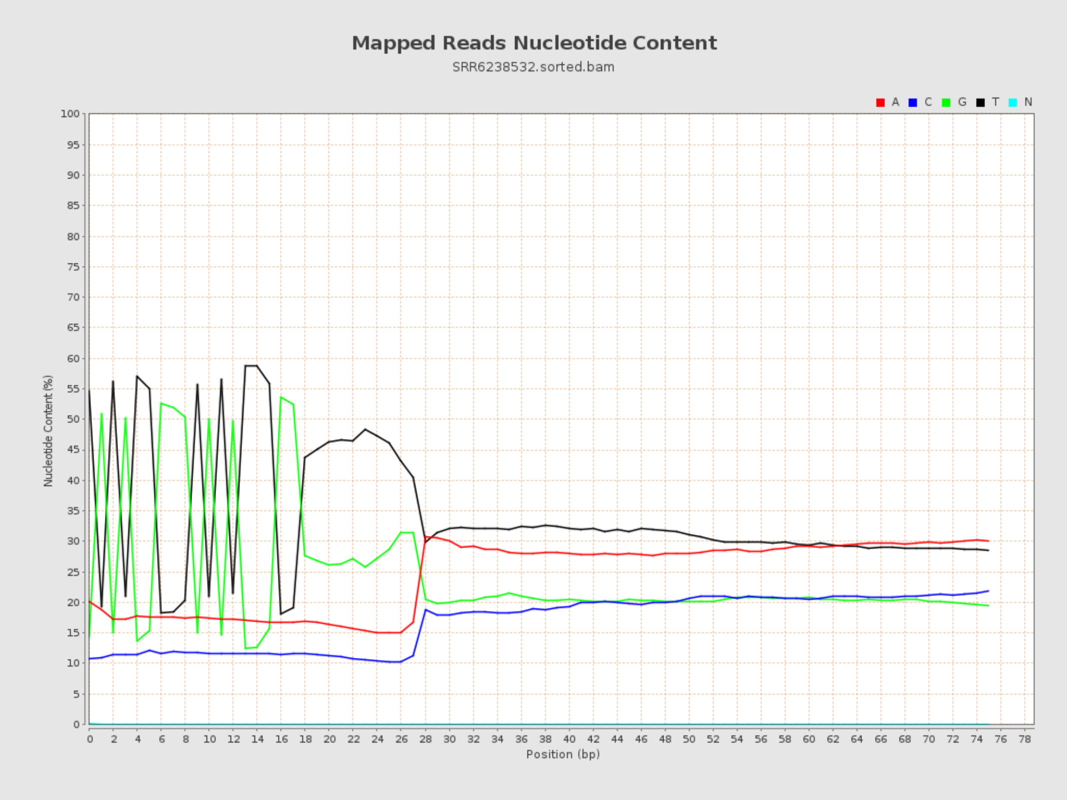
6. Results : Genome Fraction Coverage



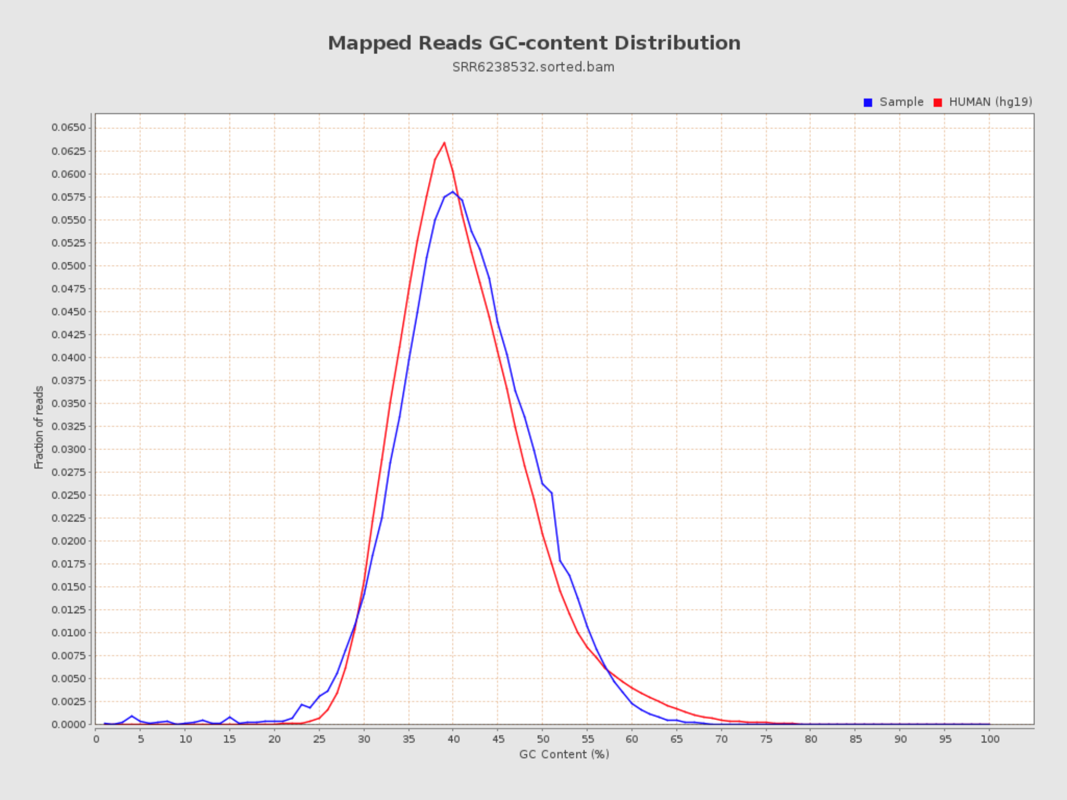
7. Results : Duplication Rate Histogram



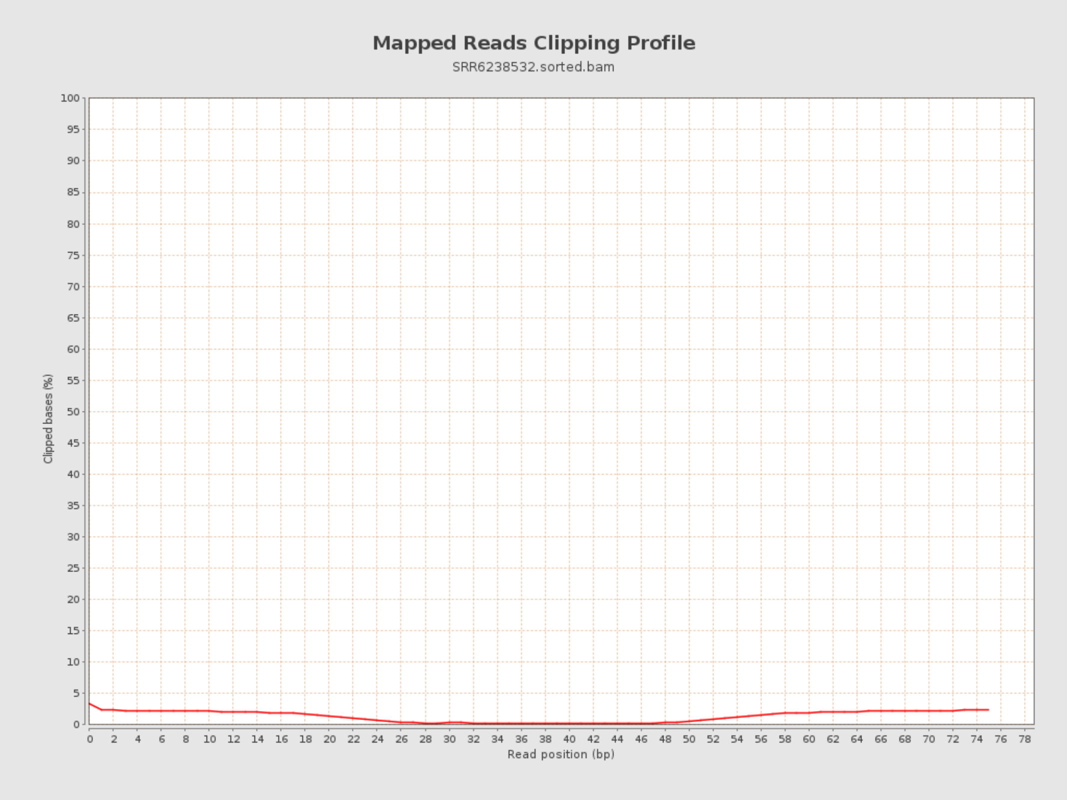
8. Results : Mapped Reads Nucleotide Content



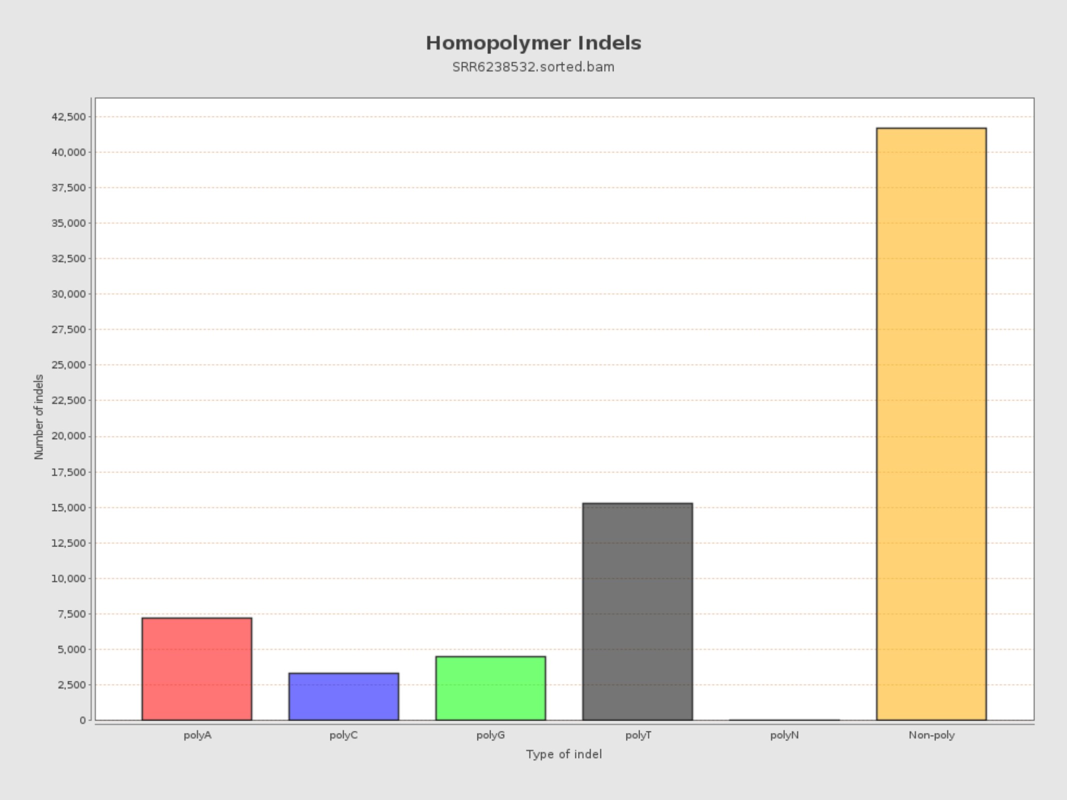
9. Results : Mapped Reads GC-content Distribution



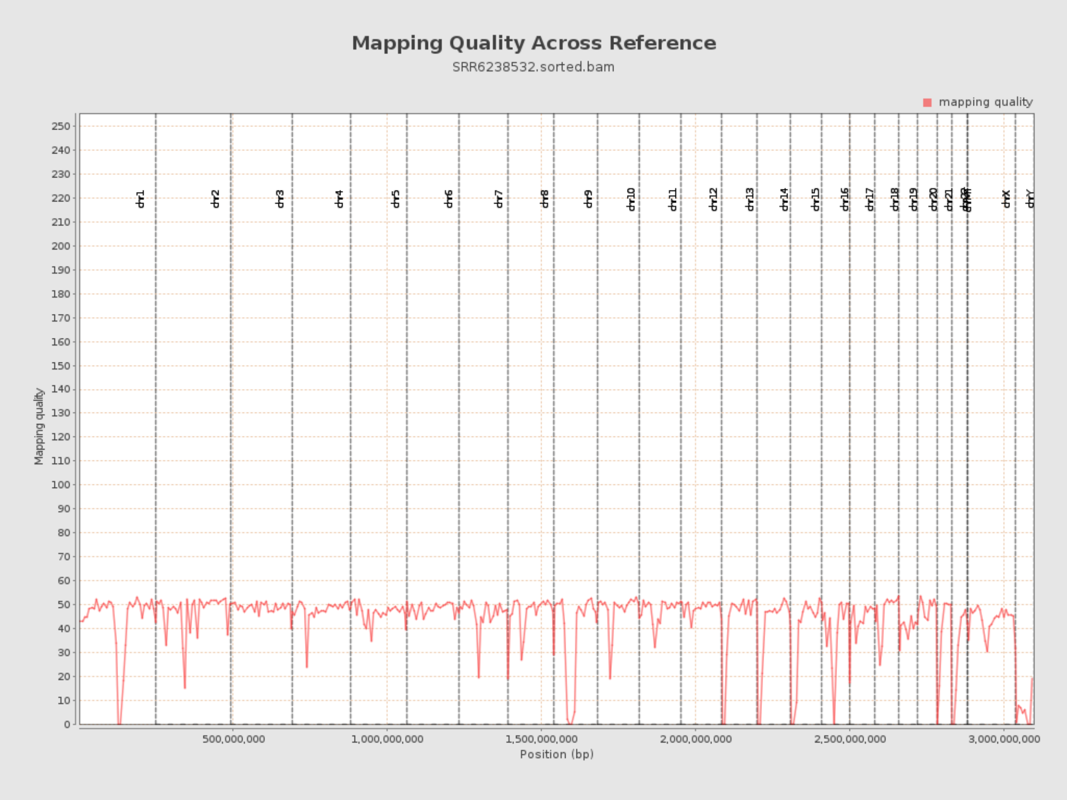
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram