Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 17:45:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238492.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_SRR6238492 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238492.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 17:45:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238492.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,298,820
Mapped reads	1,929,097 / 83.92%
Unmapped reads	369,723 / 16.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,053 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	827,813 / 36.01%
Duplication rate	23.68%
Clipped reads	1,322,089 / 57.51%

2.2. ACGT Content

Number/percentage of A's	29,524,793 / 25.36%
Number/percentage of C's	18,992,898 / 16.31%
Number/percentage of T's	41,169,125 / 35.36%
Number/percentage of G's	26,731,043 / 22.96%
Number/percentage of N's	2,500 / 0%
GC Percentage	39.27%

2.3. Coverage

Mean	0.0376

Standard Deviation	0.8913

2.4. Mapping Quality

Mean Mapping Quality	39.16

2.5. Mismatches and indels

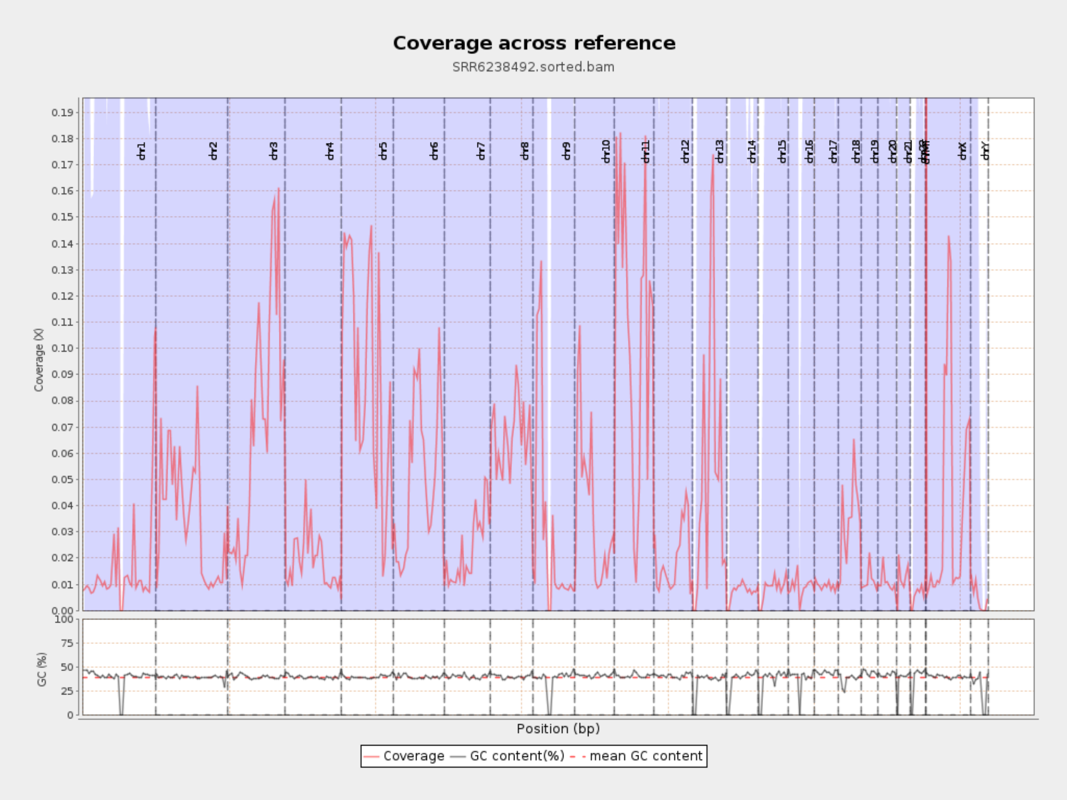
General error rate	0.61%
Mismatches	699,177
Insertions	7,437
Mapped reads with at least one insertion	0.38%
Deletions	32,859
Mapped reads with at least one deletion	1.69%
Homopolymer indels	41.47%

2.6. Chromosome stats

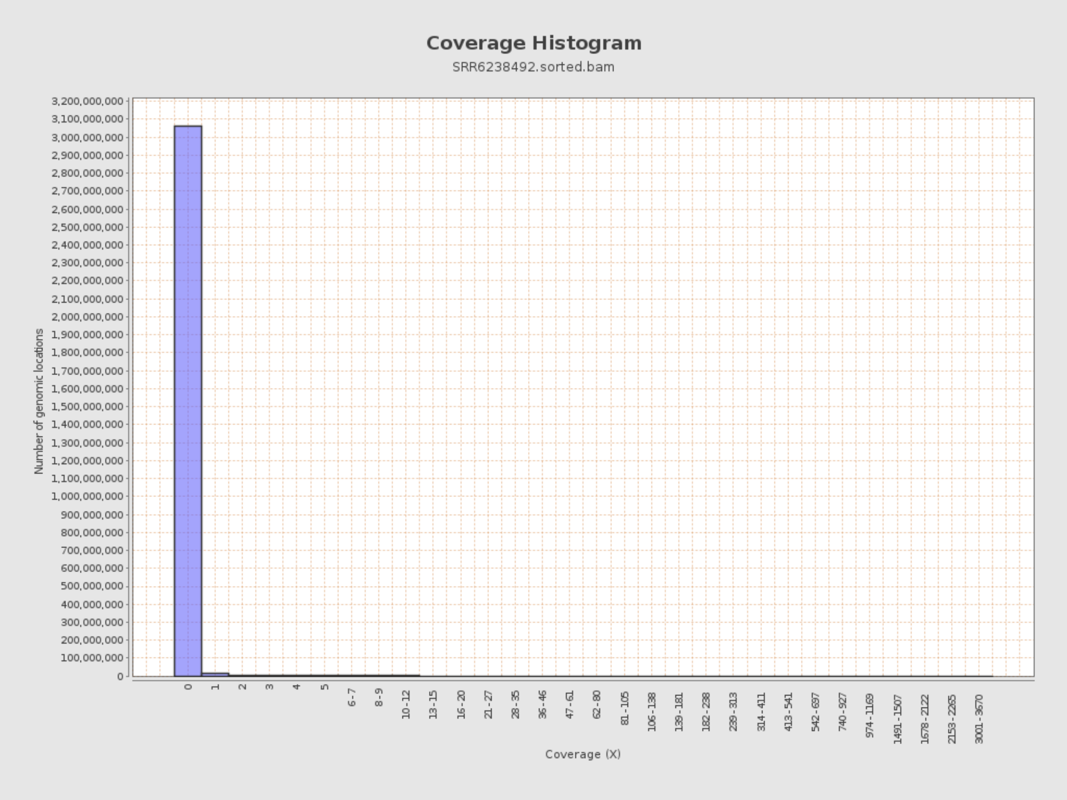
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4049951	0.0162	0.5208
chr2	243199373	8578451	0.0353	1.7111
chr3	198022430	13730796	0.0693	0.756
chr4	191154276	3608844	0.0189	0.3798
chr5	180915260	16168448	0.0894	0.8581
chr6	171115067	8770445	0.0513	0.9279
chr7	159138663	3710783	0.0233	0.5451

chr8	146364022	9626734	0.0658	0.8818
chr9	141213431	4327020	0.0306	0.4891
chr10	135534747	5199660	0.0384	0.5778
chr11	135006516	14736603	0.1092	1.0273
chr12	133851895	2644900	0.0198	0.3893
chr13	115169878	6415203	0.0557	0.8366
chr14	107349540	776673	0.0072	0.2518
chr15	102531392	877651	0.0086	0.4741
chr16	90354753	803822	0.0089	0.3663
chr17	81195210	771845	0.0095	0.2792
chr18	78077248	2747148	0.0352	2.8699
chr19	59128983	683959	0.0116	0.4465
chr20	63025520	674199	0.0107	0.3096
chr21	48129895	596122	0.0124	0.2951
chr22	51304566	304770	0.0059	0.1757
chrMT	16571	18912	1.1413	2.8458
chrX	155270560	6371518	0.041	0.5769
chrY	59373566	279002	0.0047	0.3108

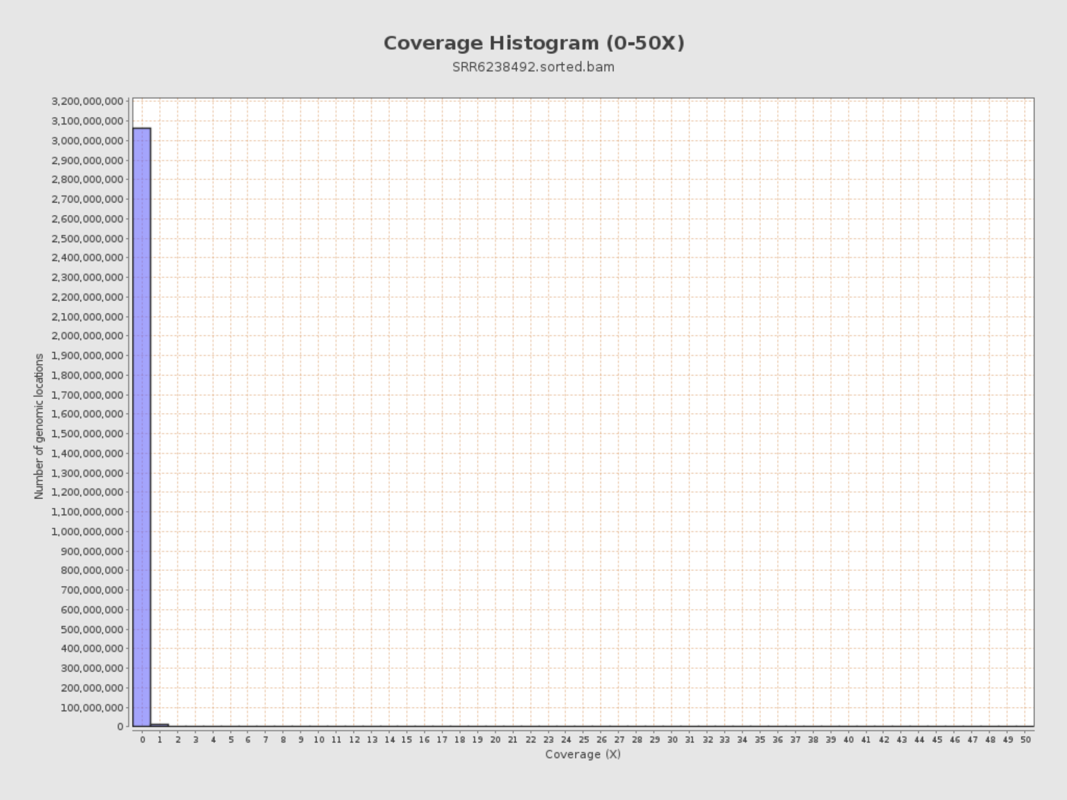
3. Results : Coverage across reference



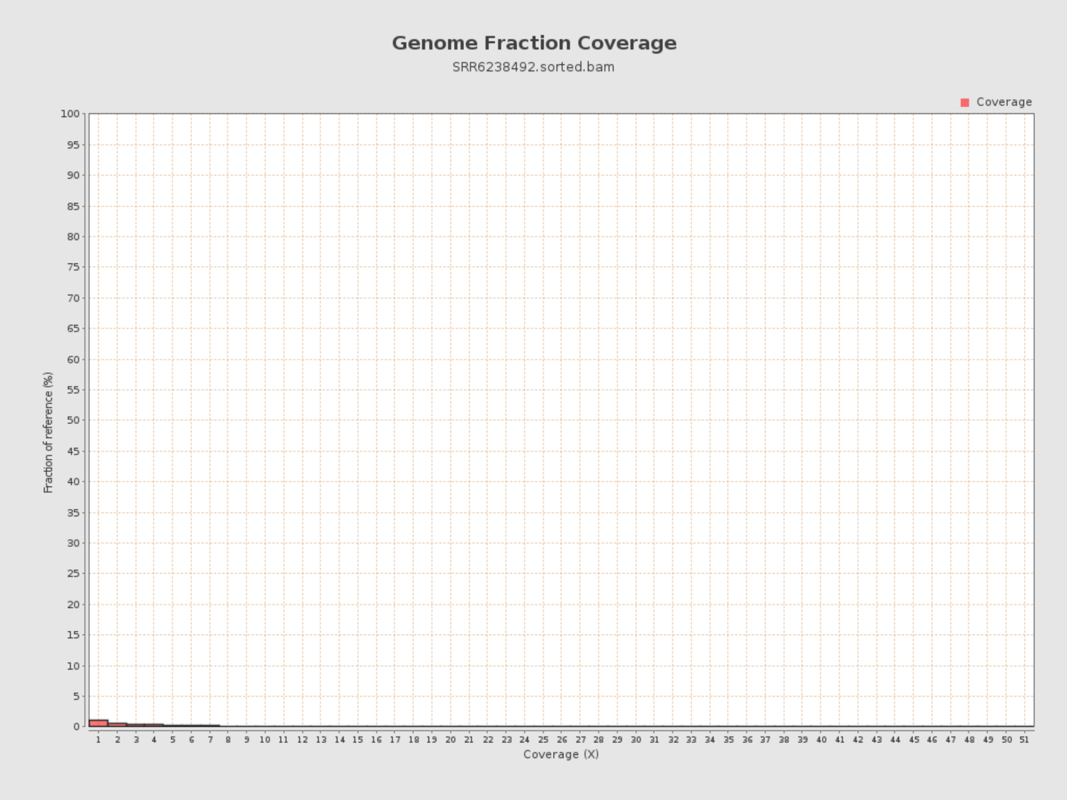
4. Results : Coverage Histogram



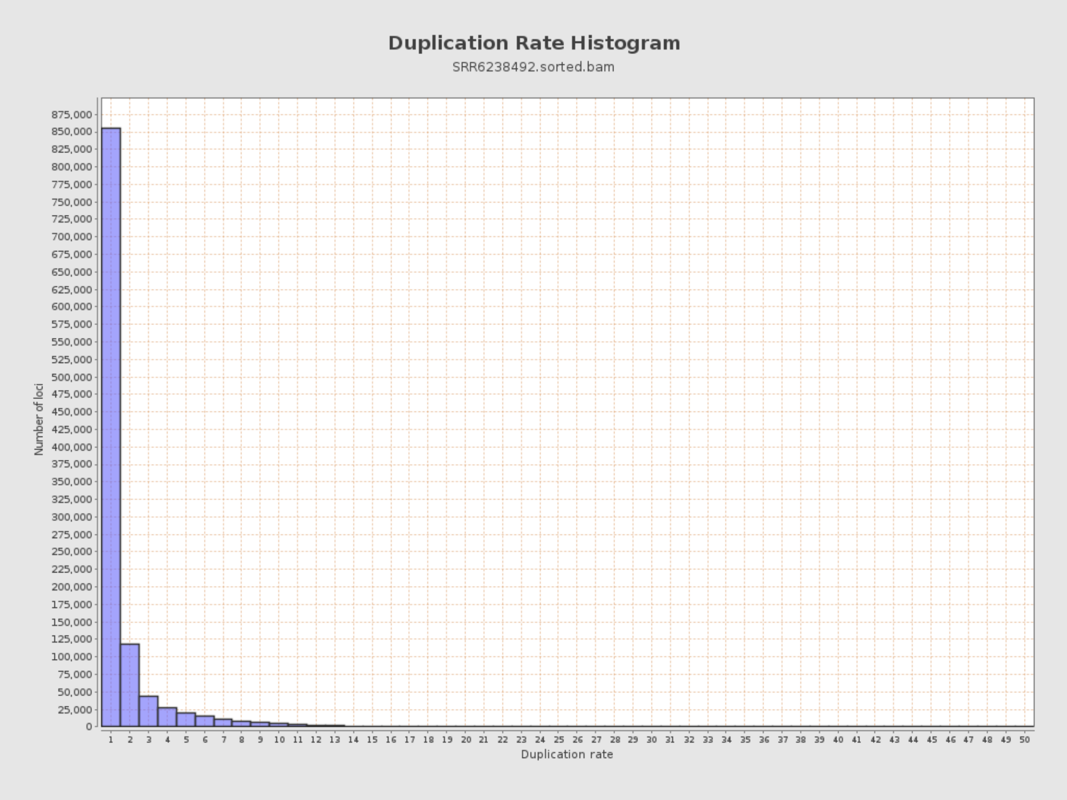
5. Results : Coverage Histogram (0-50X)



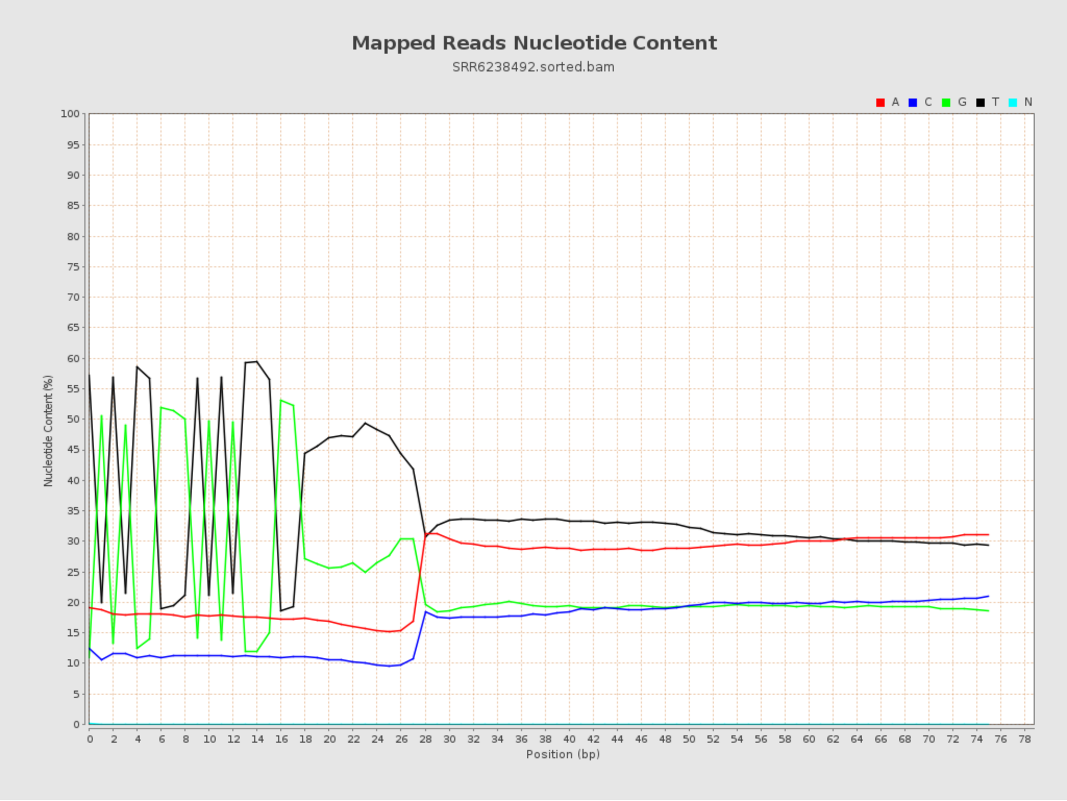
6. Results : Genome Fraction Coverage



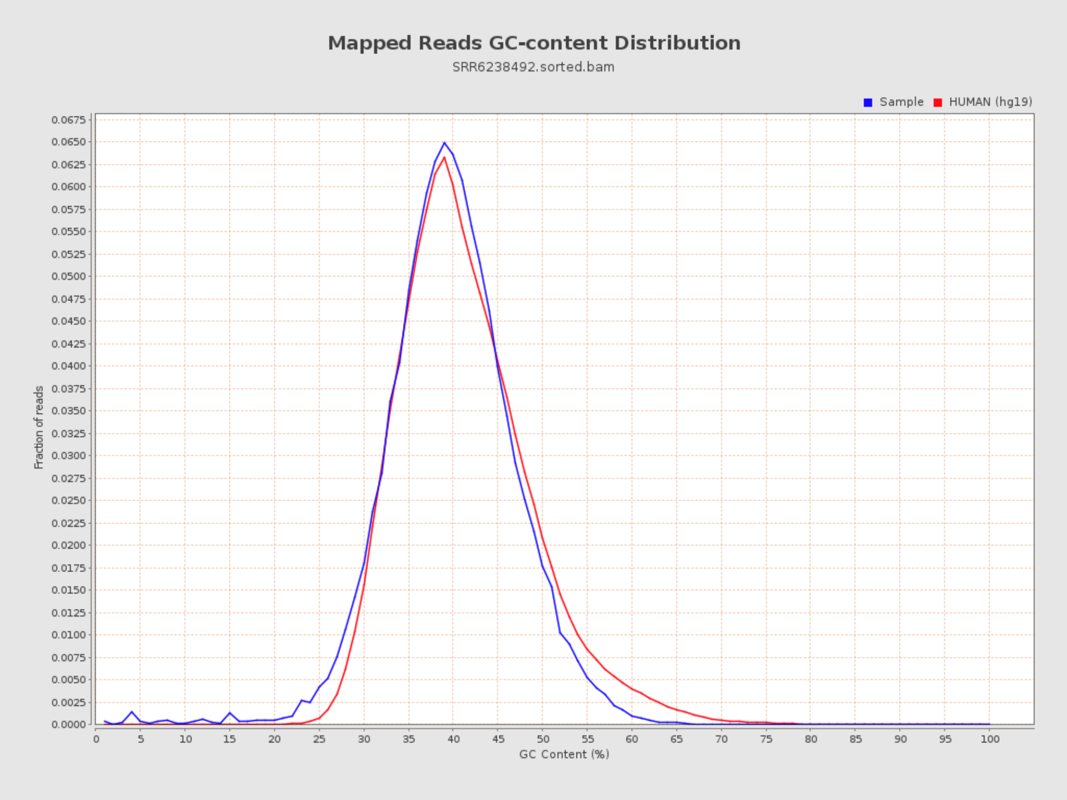
7. Results : Duplication Rate Histogram



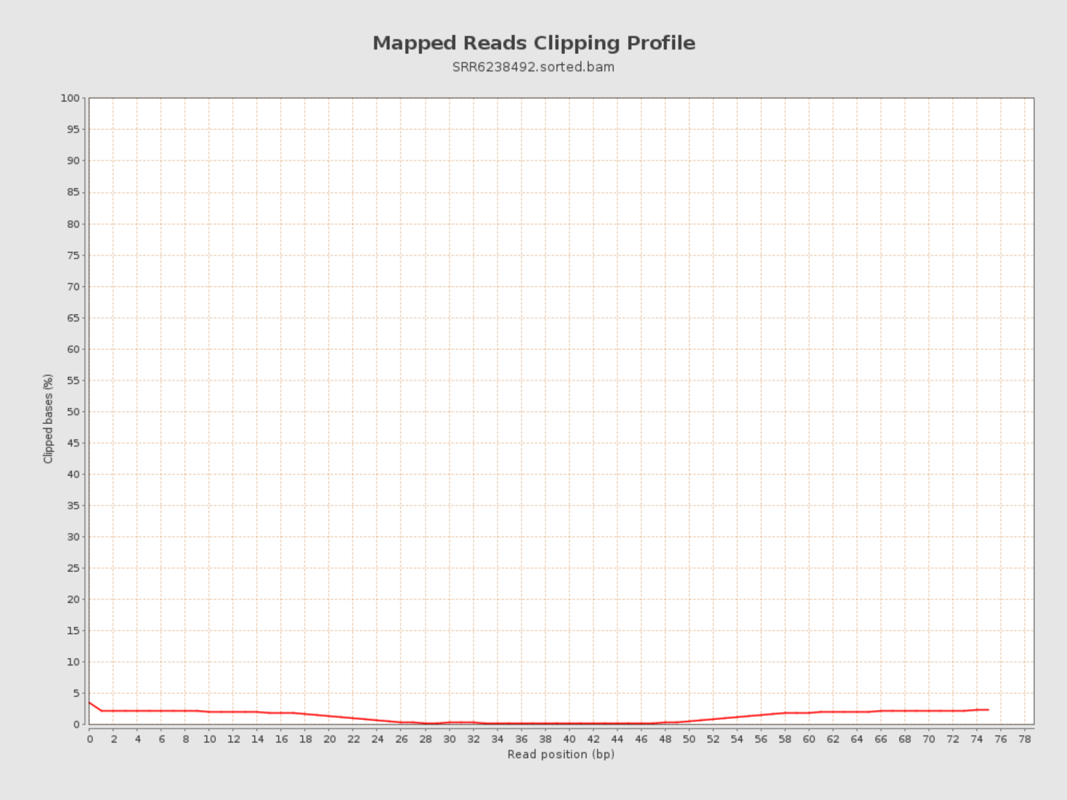
8. Results : Mapped Reads Nucleotide Content



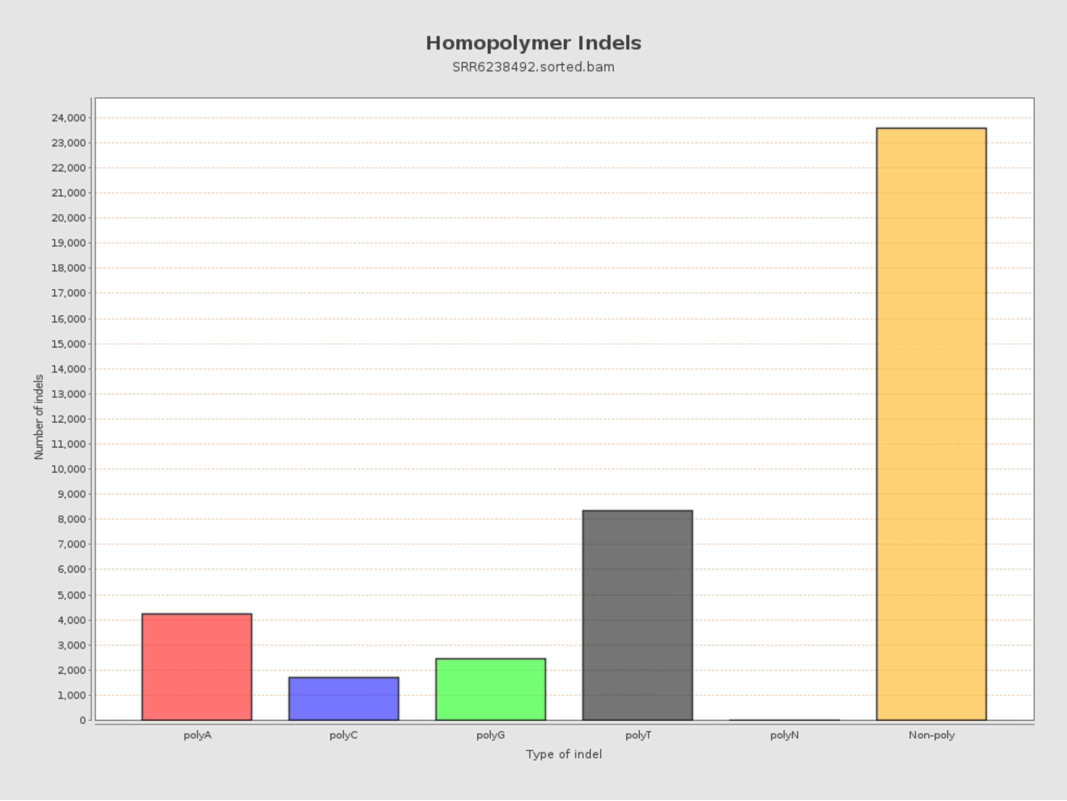
9. Results : Mapped Reads GC-content Distribution



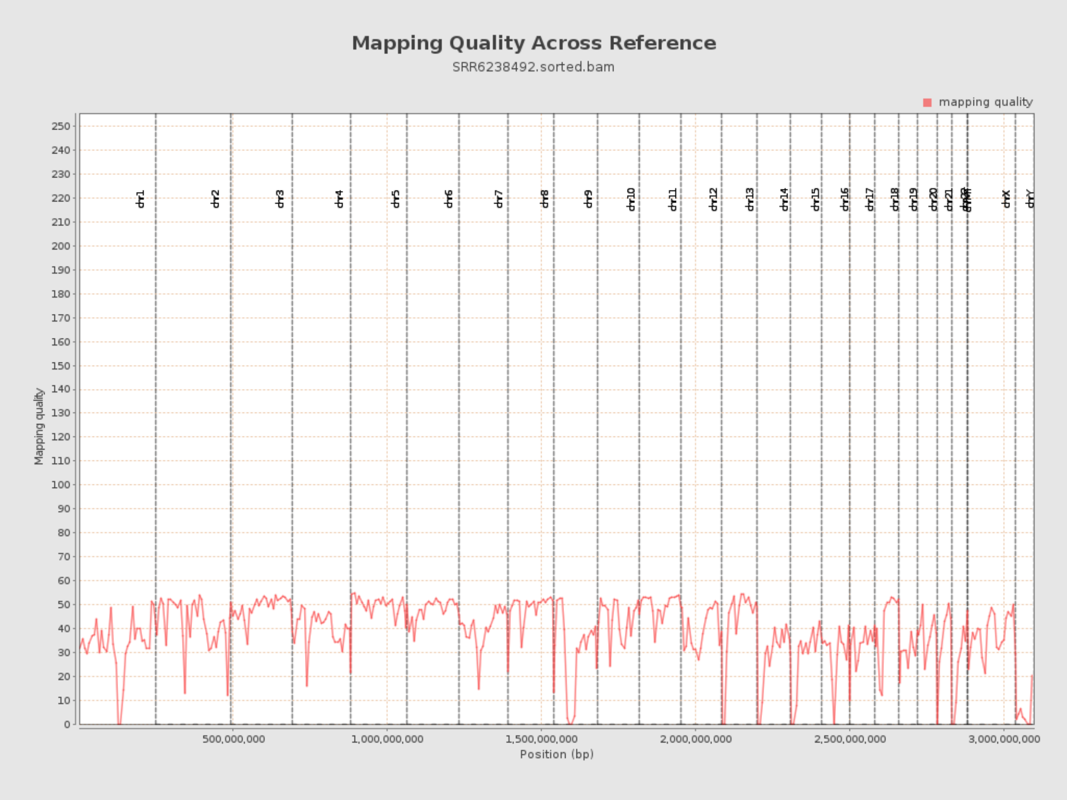
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram