Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 18:05:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238497.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_SRR6238497 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238497.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 18:05:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238497.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,631,495
Mapped reads	2,821,536 / 77.7%
Unmapped reads	809,959 / 22.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,743 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	1,020,279 / 28.1%
Duplication rate	20.38%
Clipped reads	1,792,528 / 49.36%

2.2. ACGT Content

Number/percentage of A's	42,660,948 / 24.59%
Number/percentage of C's	30,897,145 / 17.81%
Number/percentage of T's	57,978,634 / 33.42%
Number/percentage of G's	41,953,542 / 24.18%
Number/percentage of N's	11,569 / 0.01%
GC Percentage	41.99%

2.3. Coverage

Mean	0.0561

Standard Deviation	1.005

2.4. Mapping Quality

Mean Mapping Quality	43.61

2.5. Mismatches and indels

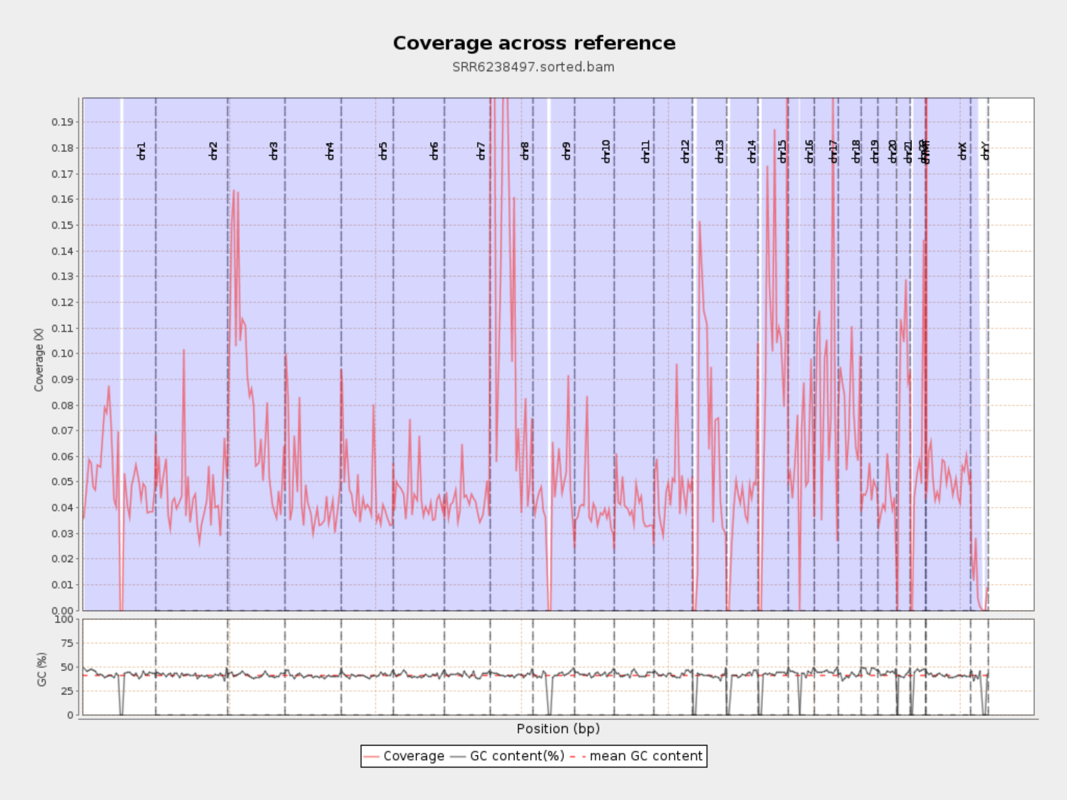
General error rate	0.61%
Mismatches	1,038,302
Insertions	12,593
Mapped reads with at least one insertion	0.44%
Deletions	43,214
Mapped reads with at least one deletion	1.52%
Homopolymer indels	41.49%

2.6. Chromosome stats

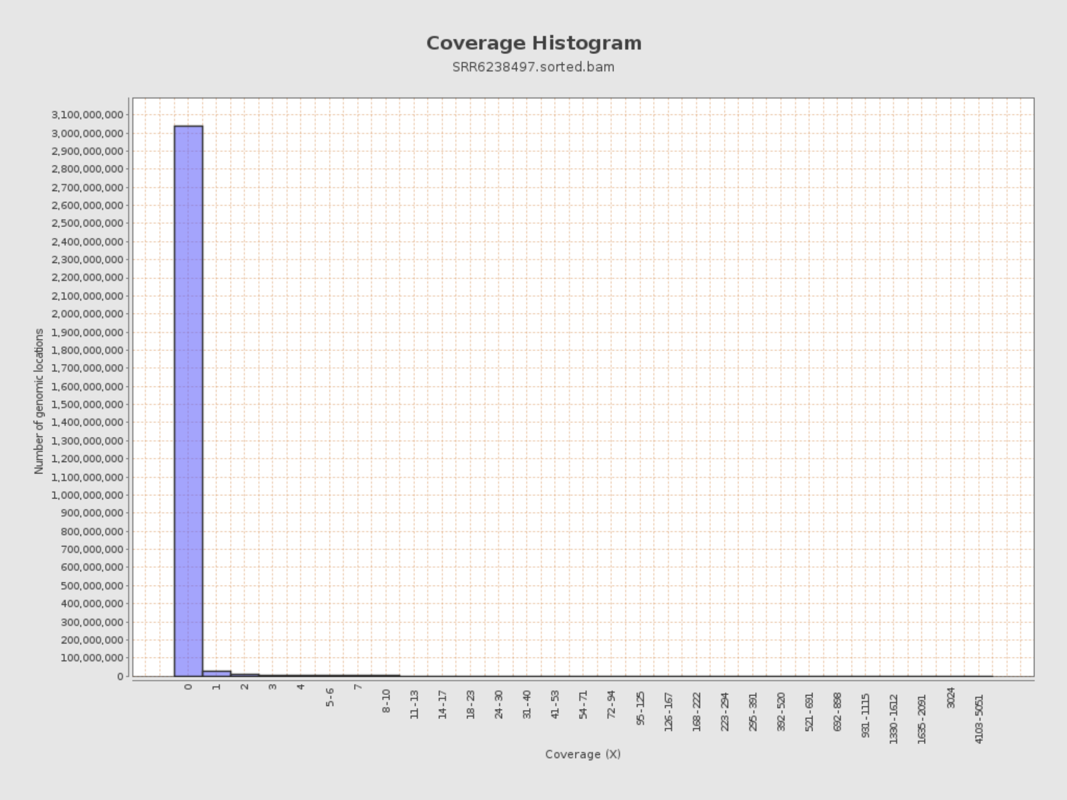
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12414487	0.0498	0.8118
chr2	243199373	11006926	0.0453	2.3017
chr3	198022430	15928828	0.0804	0.7452
chr4	191154276	8658702	0.0453	0.548
chr5	180915260	8177978	0.0452	0.5459
chr6	171115067	7615147	0.0445	0.8804
chr7	159138663	6760260	0.0425	0.6846

chr8	146364022	17657709	0.1206	1.1987
chr9	141213431	6210964	0.044	0.6542
chr10	135534747	5414938	0.04	0.5735
chr11	135006516	5421551	0.0402	0.5529
chr12	133851895	6465140	0.0483	0.5749
chr13	115169878	7605246	0.066	0.8091
chr14	107349540	4114792	0.0383	0.506
chr15	102531392	10177069	0.0993	0.8903
chr16	90354753	5245530	0.0581	0.6681
chr17	81195210	7405008	0.0912	0.8352
chr18	78077248	6163864	0.0789	2.2687
chr19	59128983	2795186	0.0473	0.7052
chr20	63025520	2662050	0.0422	0.5475
chr21	48129895	4262460	0.0886	0.7869
chr22	51304566	2801718	0.0546	0.6063
chrMT	16571	46874	2.8287	4.3616
chrX	155270560	8022817	0.0517	0.5897
chrY	59373566	540001	0.0091	0.3777

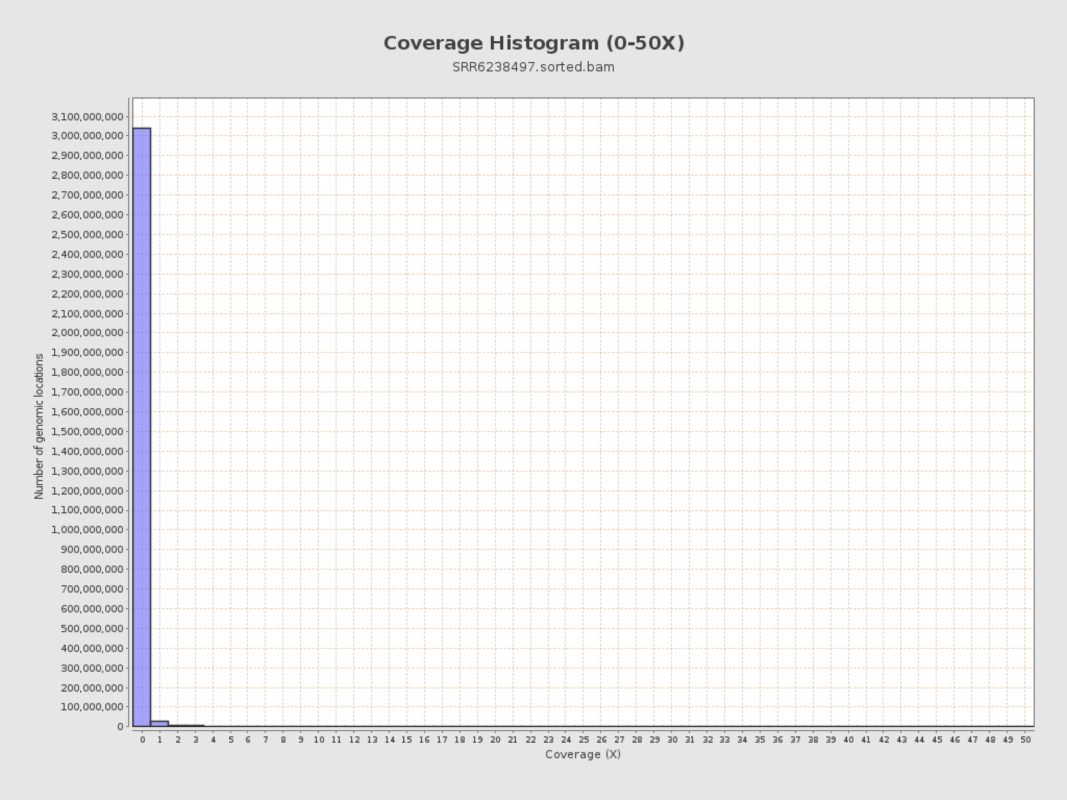
3. Results : Coverage across reference



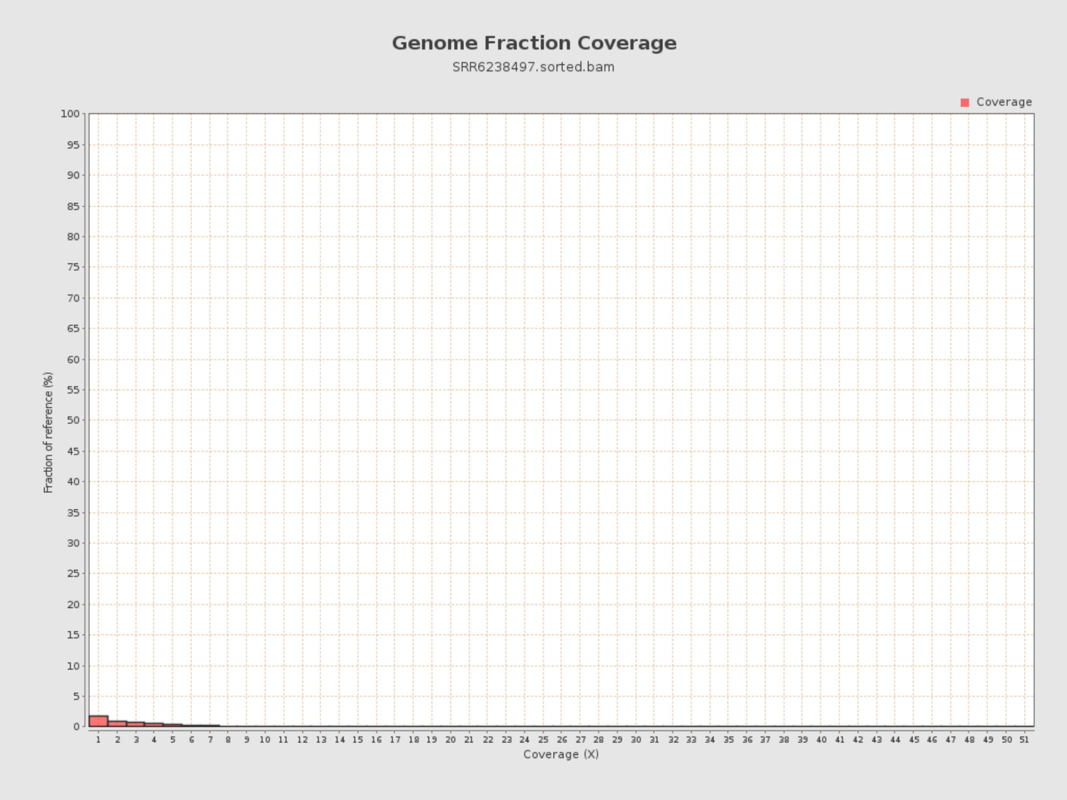
4. Results : Coverage Histogram



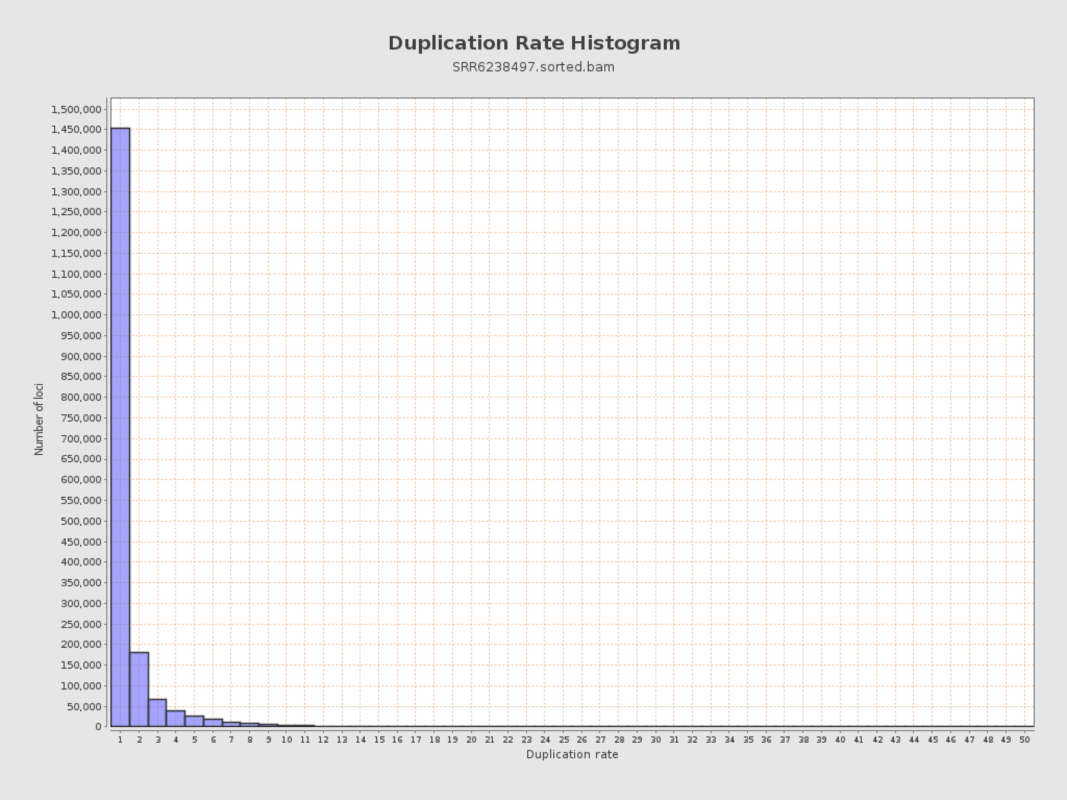
5. Results : Coverage Histogram (0-50X)



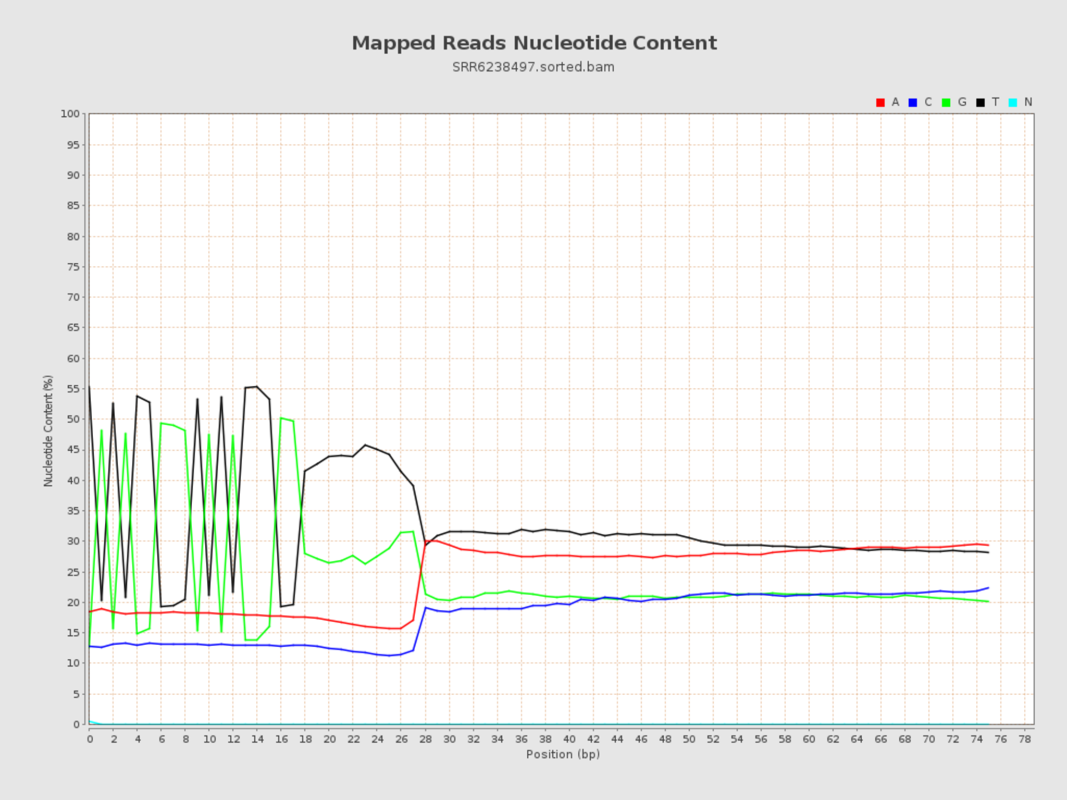
6. Results : Genome Fraction Coverage



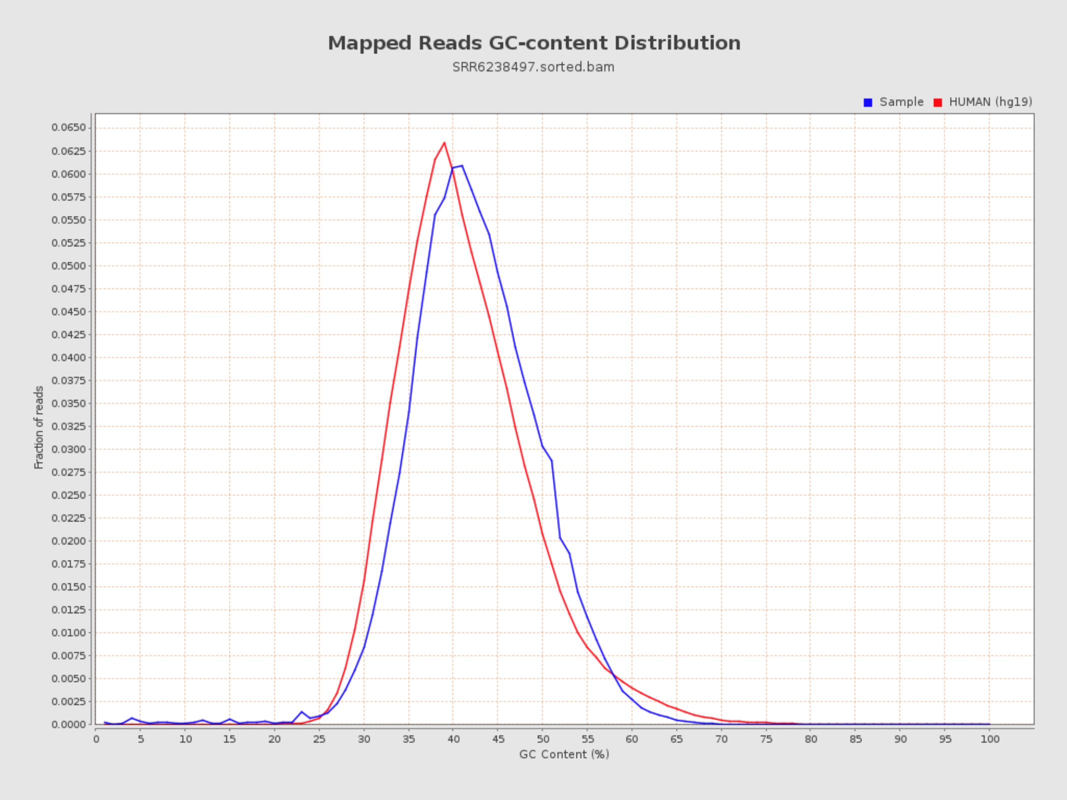
7. Results : Duplication Rate Histogram



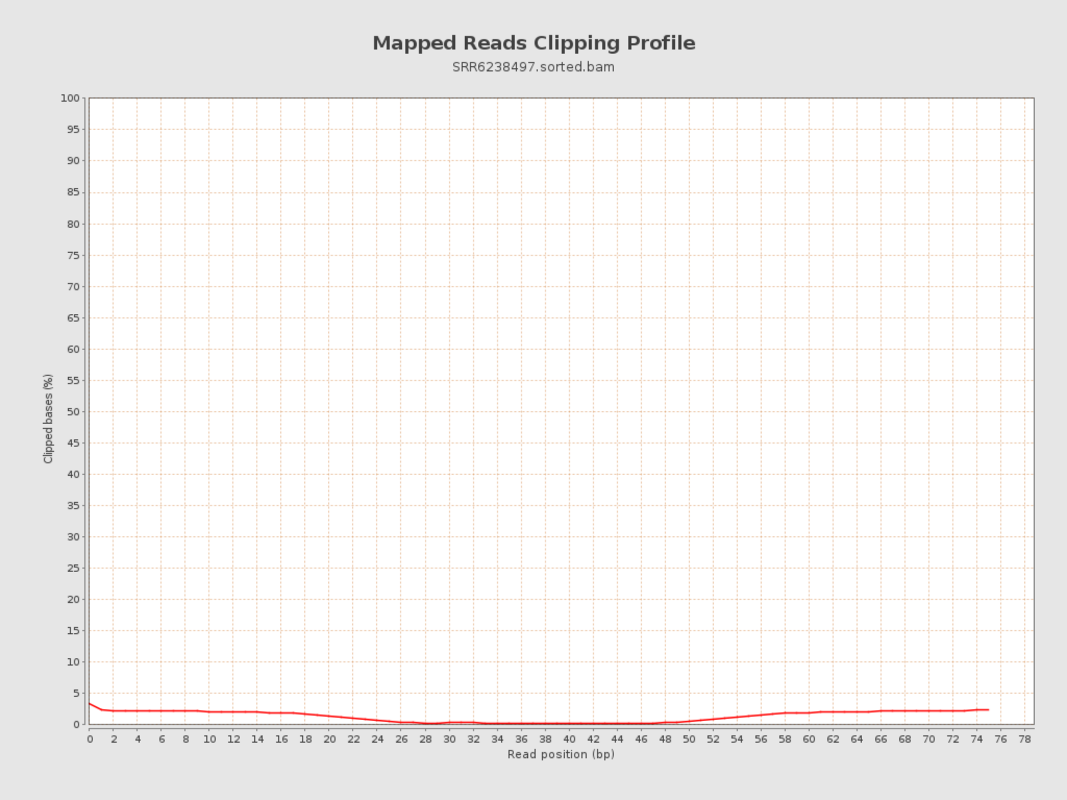
8. Results : Mapped Reads Nucleotide Content



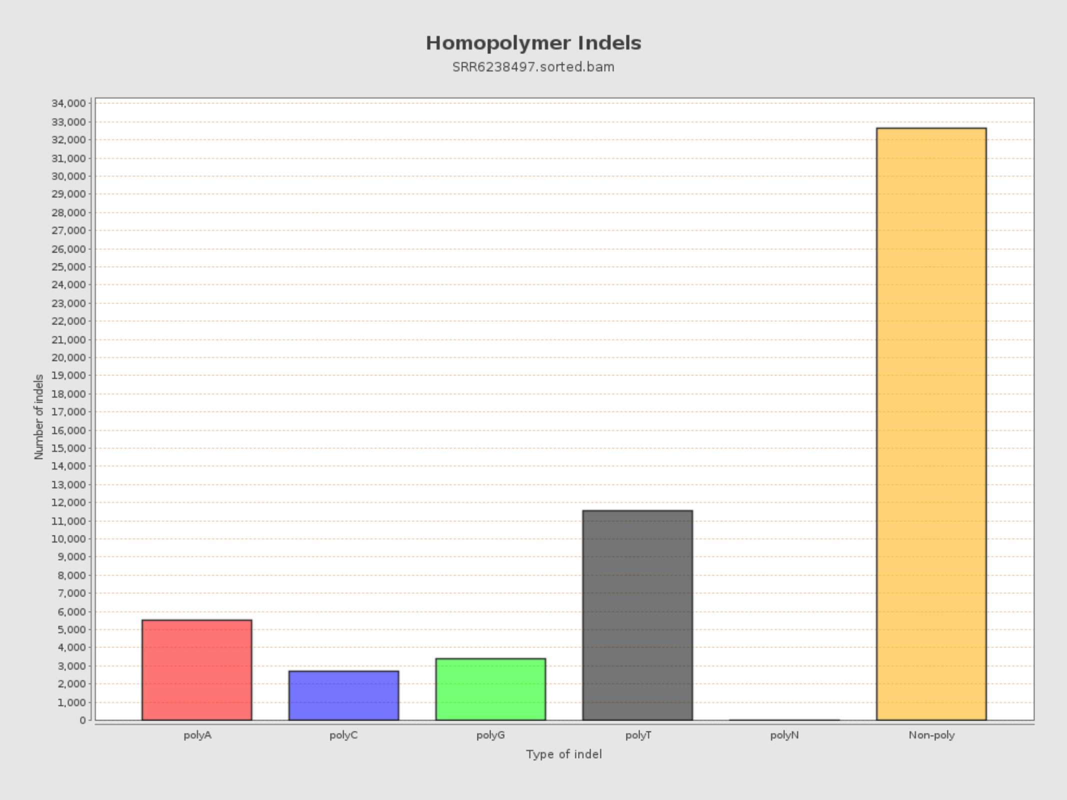
9. Results : Mapped Reads GC-content Distribution



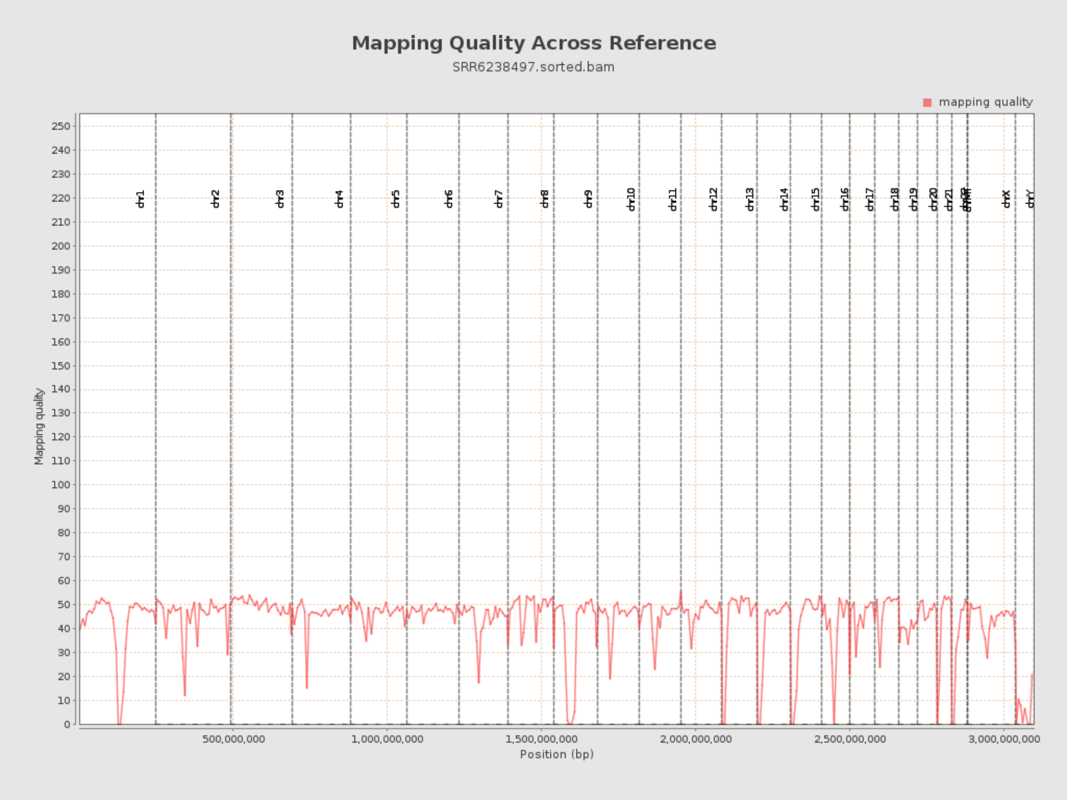
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram