Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 17:37:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238490.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_SRR6238490 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238490.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 17:37:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238490.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,312,476
Mapped reads	3,056,271 / 92.27%
Unmapped reads	256,205 / 7.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,105 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	1,092,406 / 32.98%
Duplication rate	22.52%
Clipped reads	1,994,166 / 60.2%

2.2. ACGT Content

Number/percentage of A's	45,207,142 / 24.13%
Number/percentage of C's	32,237,598 / 17.21%
Number/percentage of T's	63,768,050 / 34.04%
Number/percentage of G's	46,097,004 / 24.61%
Number/percentage of N's	12,419 / 0.01%
GC Percentage	41.82%

2.3. Coverage

Mean	0.0605

Standard Deviation	0.9105

2.4. Mapping Quality

Mean Mapping Quality	36.17

2.5. Mismatches and indels

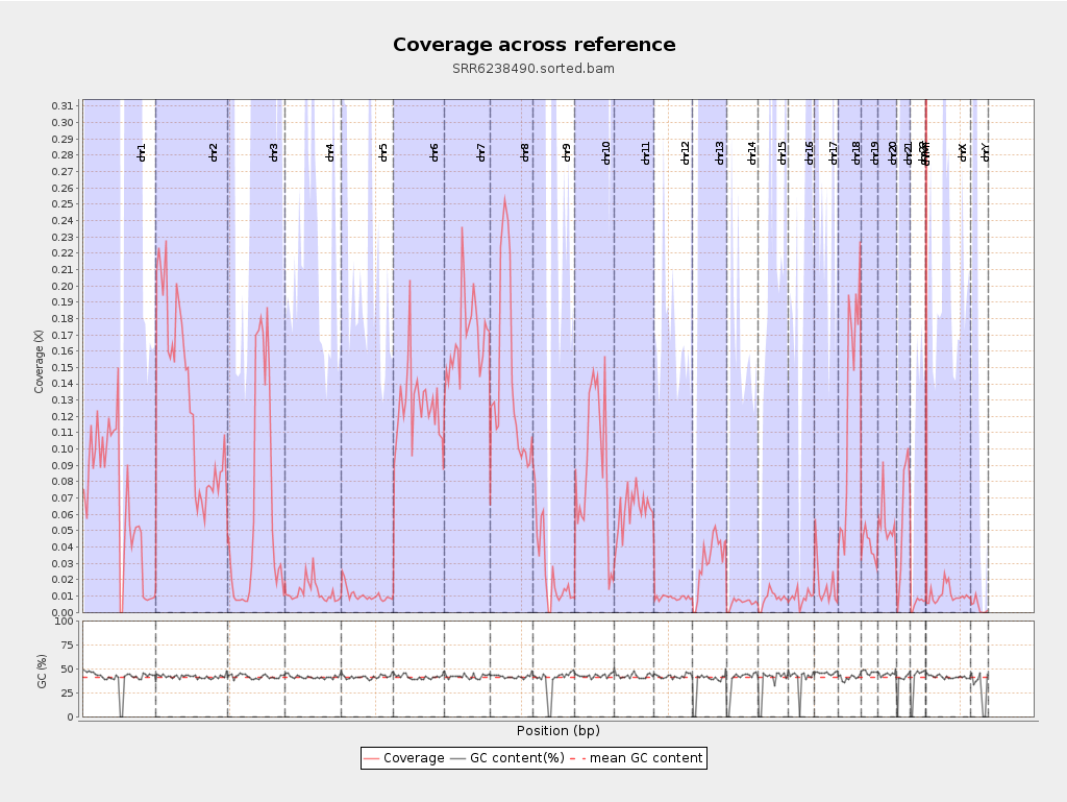
General error rate	0.53%
Mismatches	972,842
Insertions	11,061
Mapped reads with at least one insertion	0.36%
Deletions	46,813
Mapped reads with at least one deletion	1.52%
Homopolymer indels	42.56%

2.6. Chromosome stats

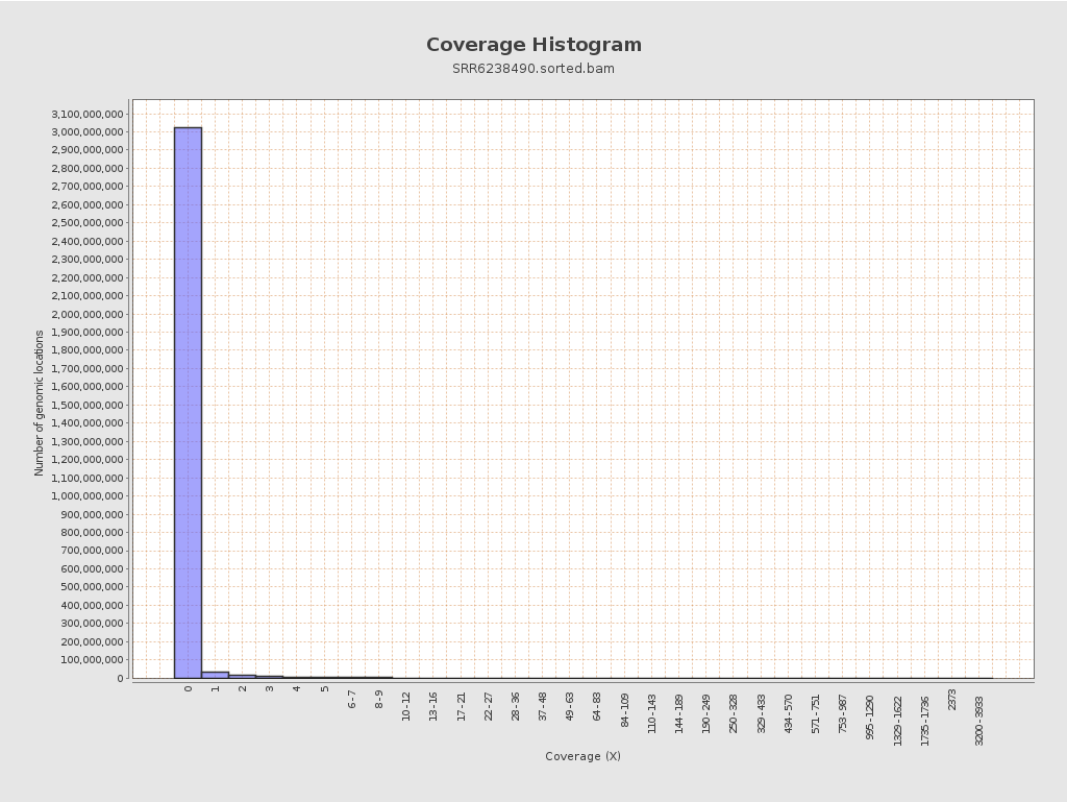
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	16409831	0.0658	0.9037
chr2	243199373	31355515	0.1289	1.8972
chr3	198022430	12121155	0.0612	0.5534
chr4	191154276	2412255	0.0126	0.2184
chr5	180915260	1954055	0.0108	0.2104
chr6	171115067	21726523	0.127	1.2397
chr7	159138663	27005181	0.1697	1.8943

chr8	146364022	20957884	0.1432	0.9688
chr9	141213431	3513889	0.0249	0.3762
chr10	135534747	12285576	0.0906	0.6861
chr11	135006516	8417369	0.0623	0.5854
chr12	133851895	1205239	0.009	0.1756
chr13	115169878	3620742	0.0314	0.5292
chr14	107349540	642517	0.006	0.1578
chr15	102531392	855578	0.0083	0.3891
chr16	90354753	812663	0.009	0.228
chr17	81195210	1475774	0.0182	0.2801
chr18	78077248	9714428	0.1244	1.4749
chr19	59128983	2446231	0.0414	0.6087
chr20	63025520	3483104	0.0553	0.5221
chr21	48129895	2794958	0.0581	0.5279
chr22	51304566	287390	0.0056	0.1251
chrMT	16571	36047	2.1753	3.4622
chrX	155270560	1662250	0.0107	0.2118
chrY	59373566	204728	0.0034	0.2406

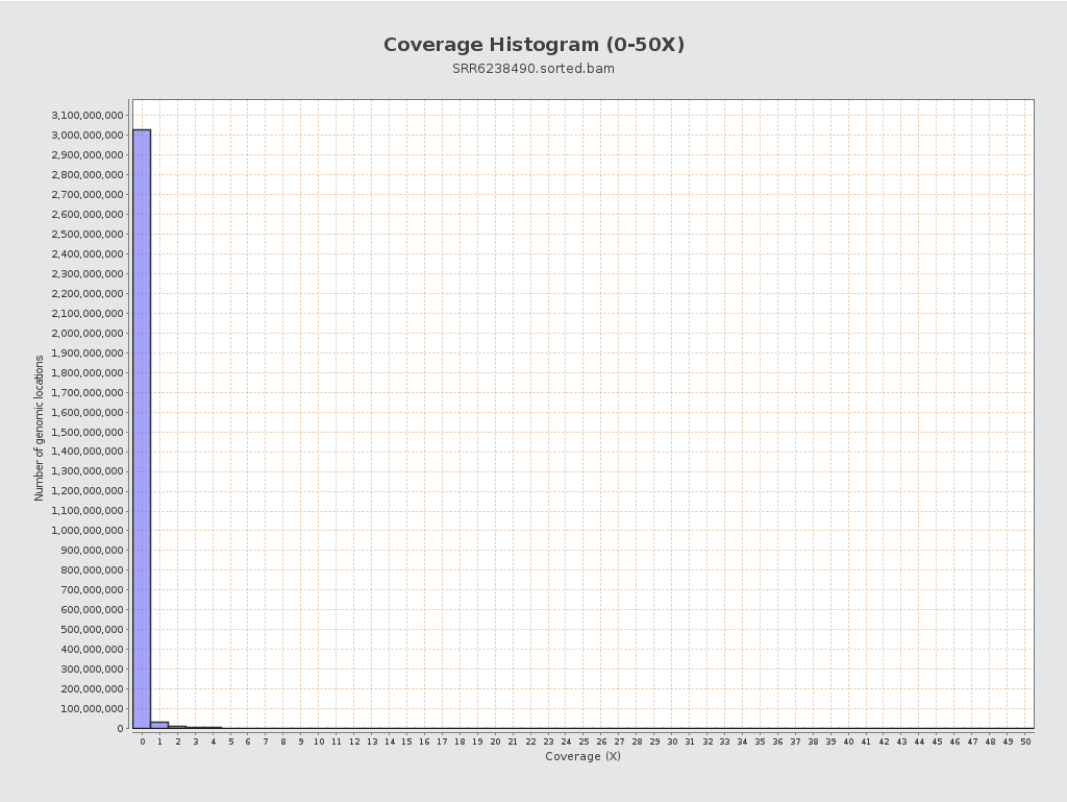
3. Results : Coverage across reference



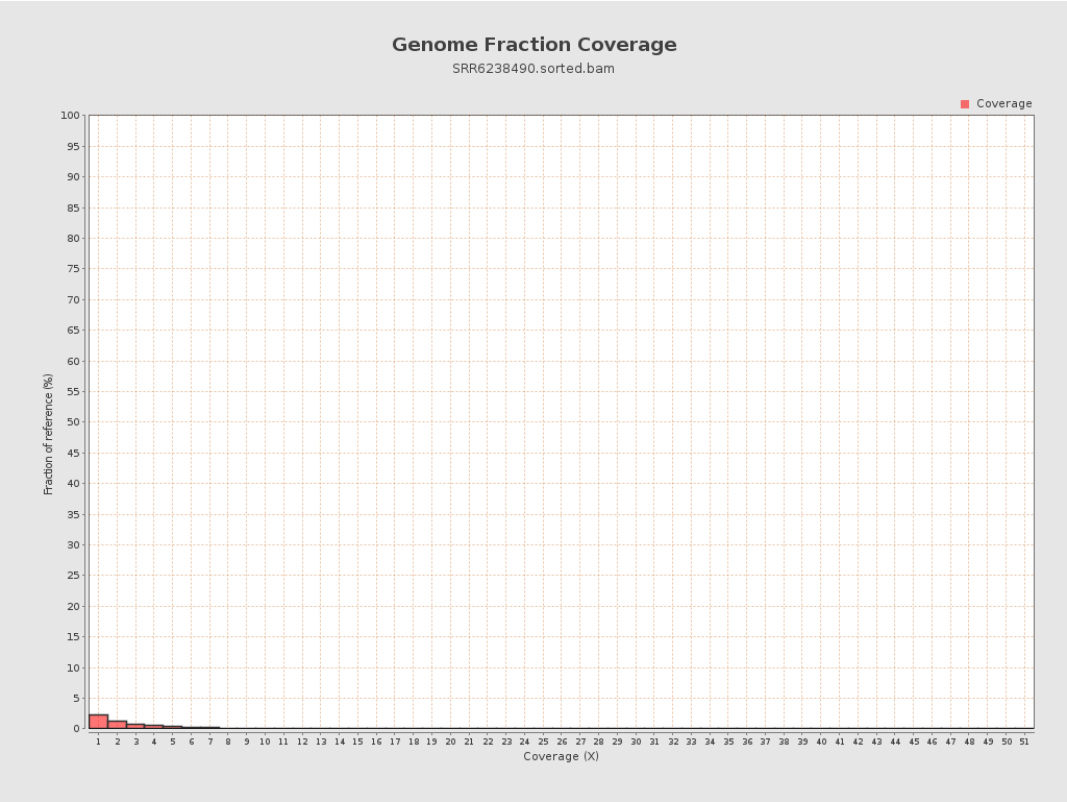
4. Results : Coverage Histogram



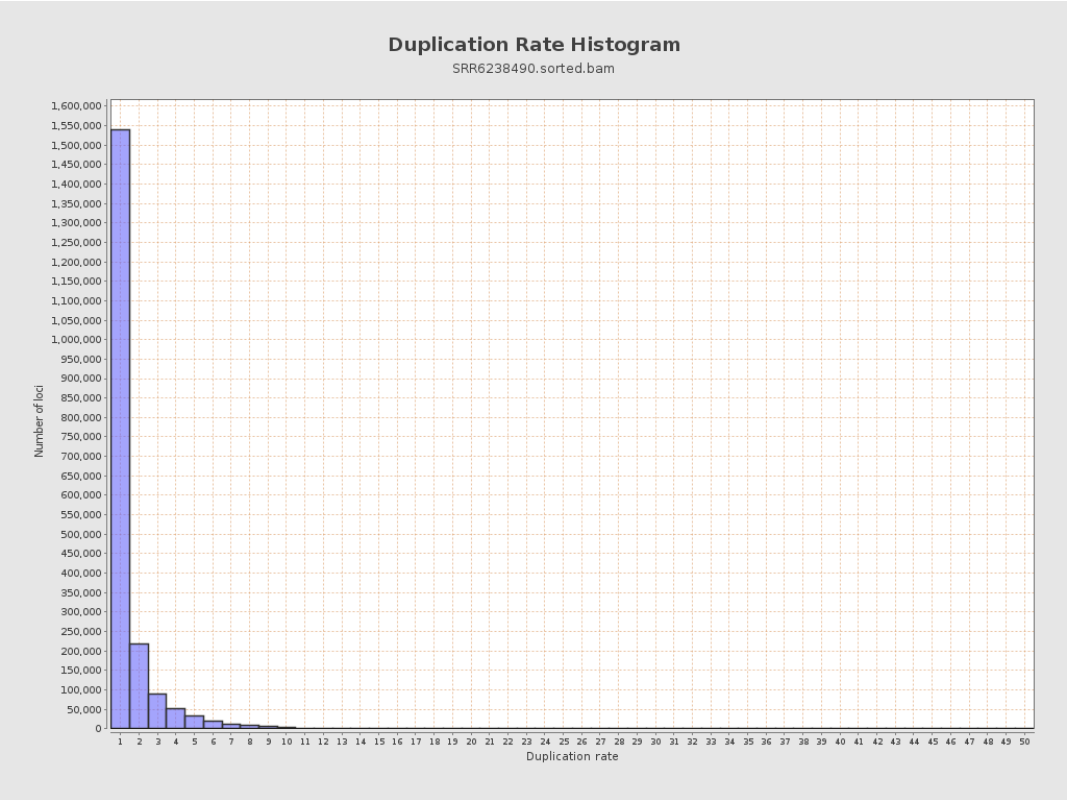
5. Results : Coverage Histogram (0-50X)



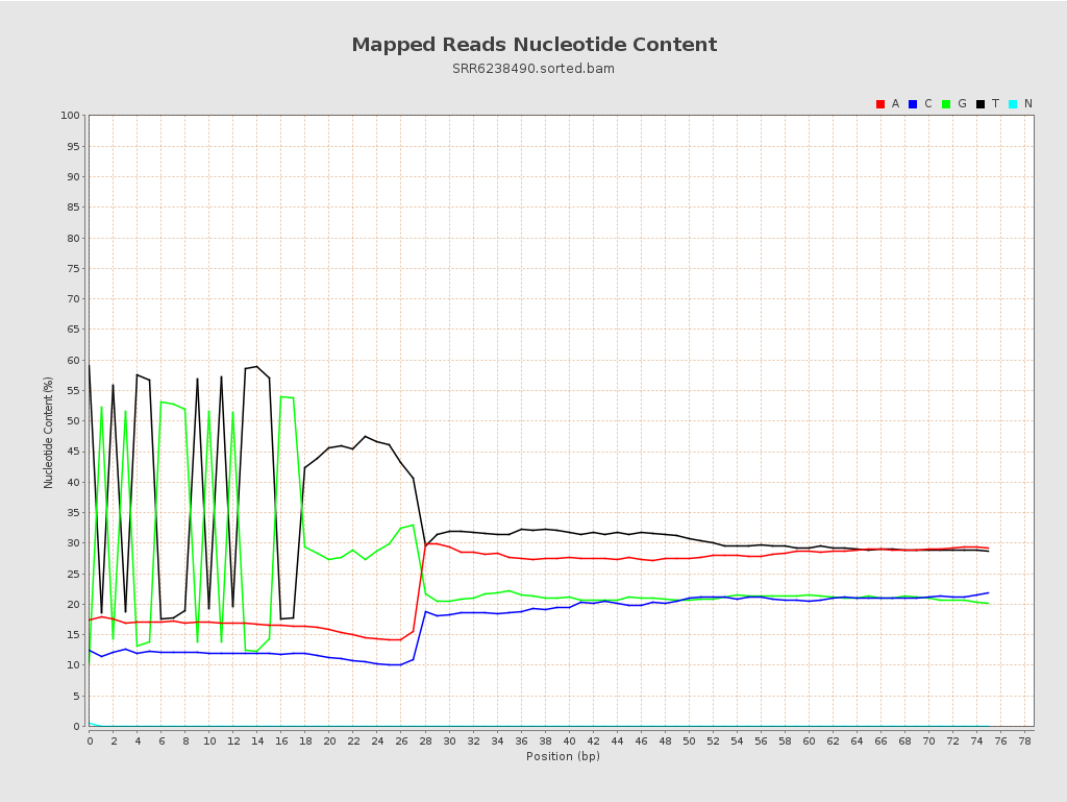
6. Results : Genome Fraction Coverage



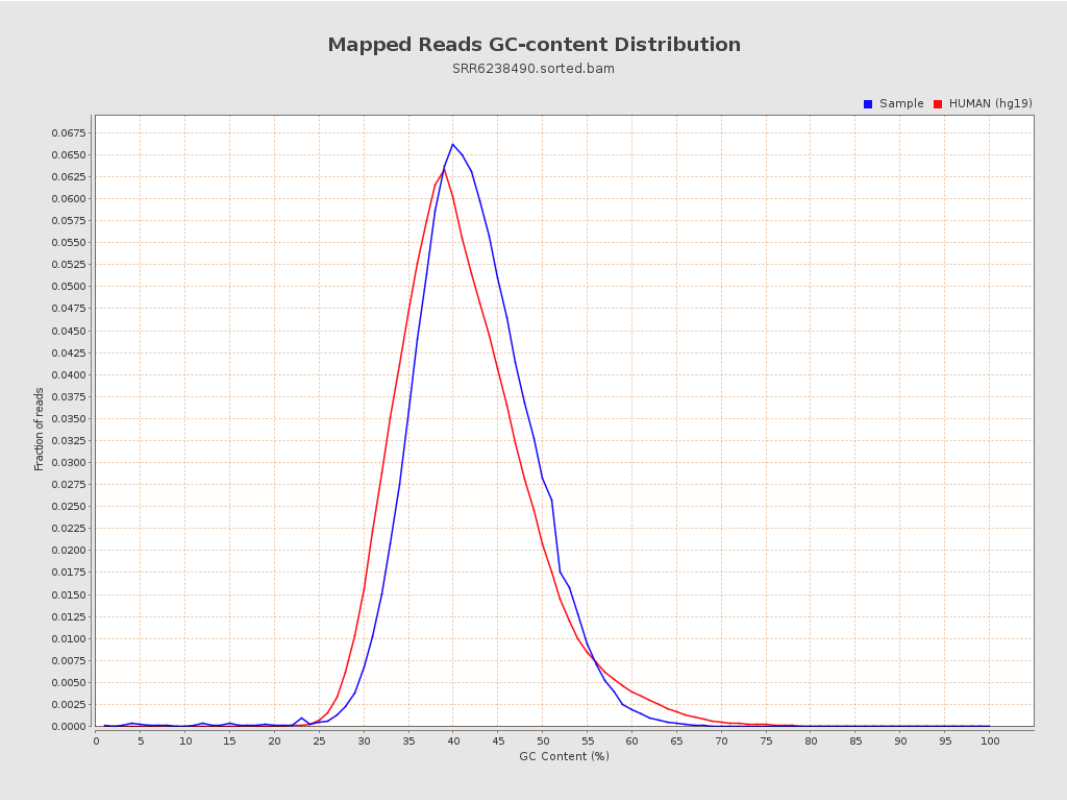
7. Results : Duplication Rate Histogram



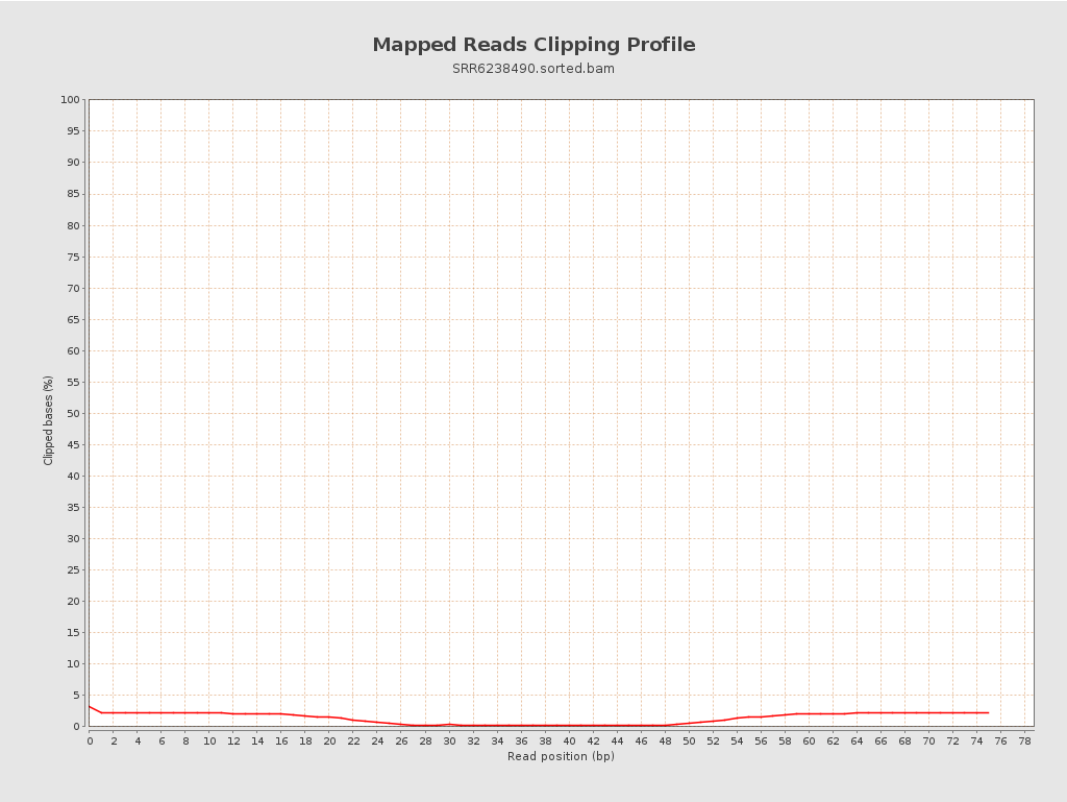
8. Results : Mapped Reads Nucleotide Content



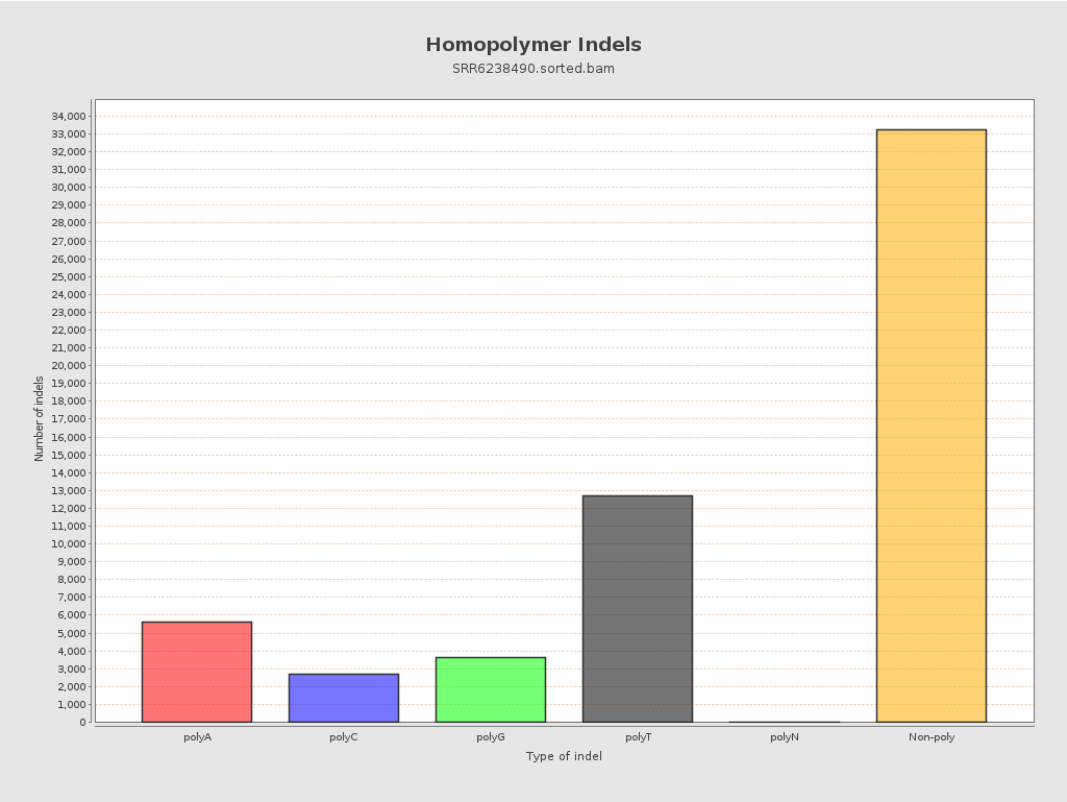
9. Results : Mapped Reads GC-content Distribution



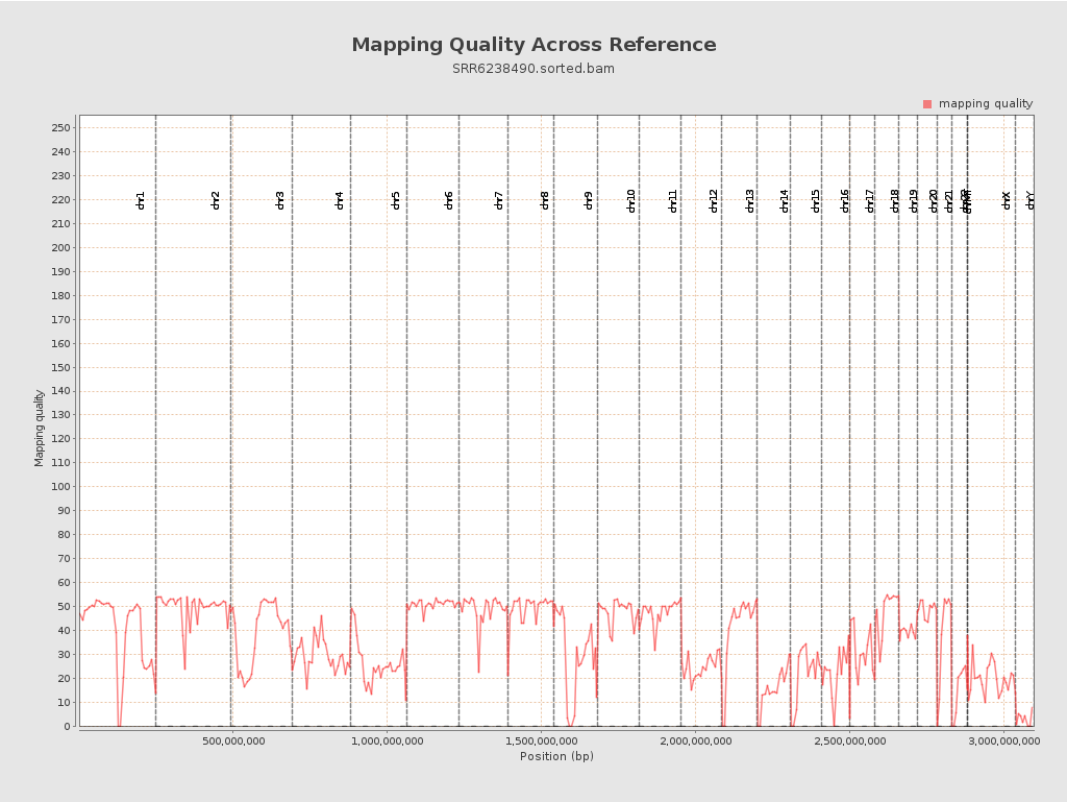
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram