Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 00:42:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238650.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_SRR6238650 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238650.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 00:42:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238650.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,974,303
Mapped reads	2,490,304 / 83.73%
Unmapped reads	483,999 / 16.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,220 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	1,102,195 / 37.06%
Duplication rate	20.75%
Clipped reads	1,634,041 / 54.94%

2.2. ACGT Content

Number/percentage of A's	37,949,775 / 25.02%
Number/percentage of C's	26,541,409 / 17.5%
Number/percentage of T's	51,456,074 / 33.92%
Number/percentage of G's	35,740,457 / 23.56%
Number/percentage of N's	3,472 / 0%
GC Percentage	41.06%

2.3. Coverage

Mean	0.049

Standard Deviation	1.0457

2.4. Mapping Quality

Mean Mapping Quality	41.02

2.5. Mismatches and indels

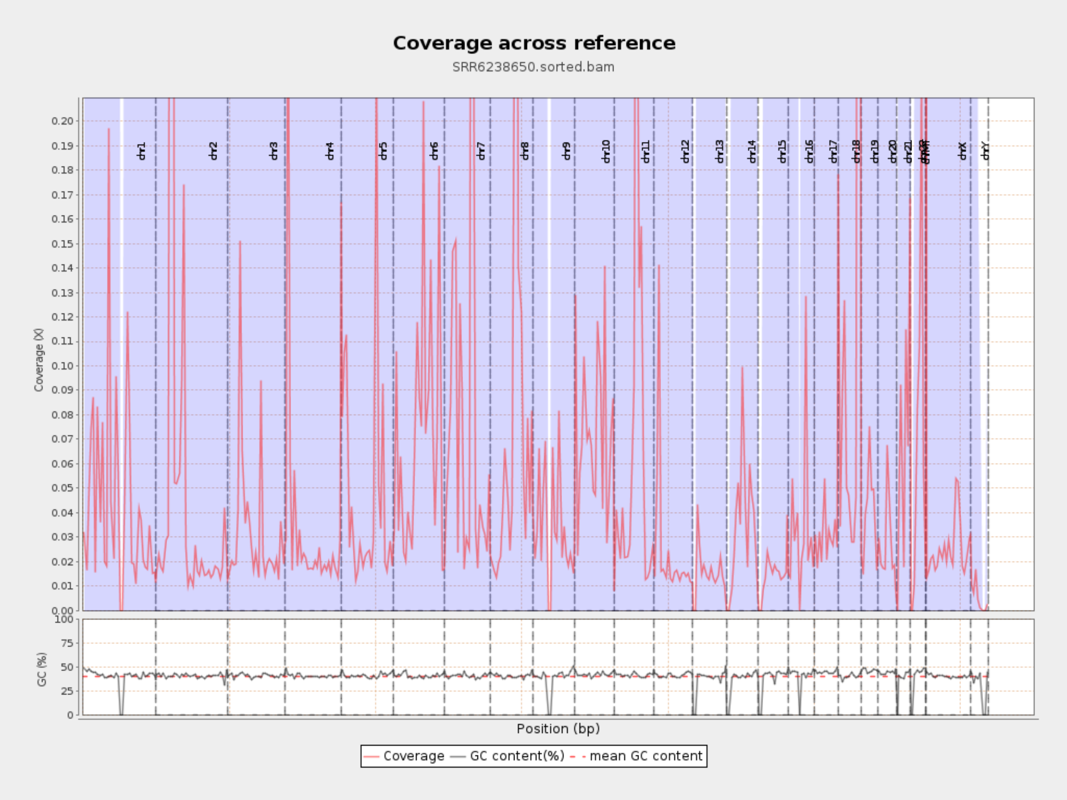
General error rate	0.59%
Mismatches	880,216
Insertions	9,190
Mapped reads with at least one insertion	0.37%
Deletions	37,040
Mapped reads with at least one deletion	1.47%
Homopolymer indels	40.72%

2.6. Chromosome stats

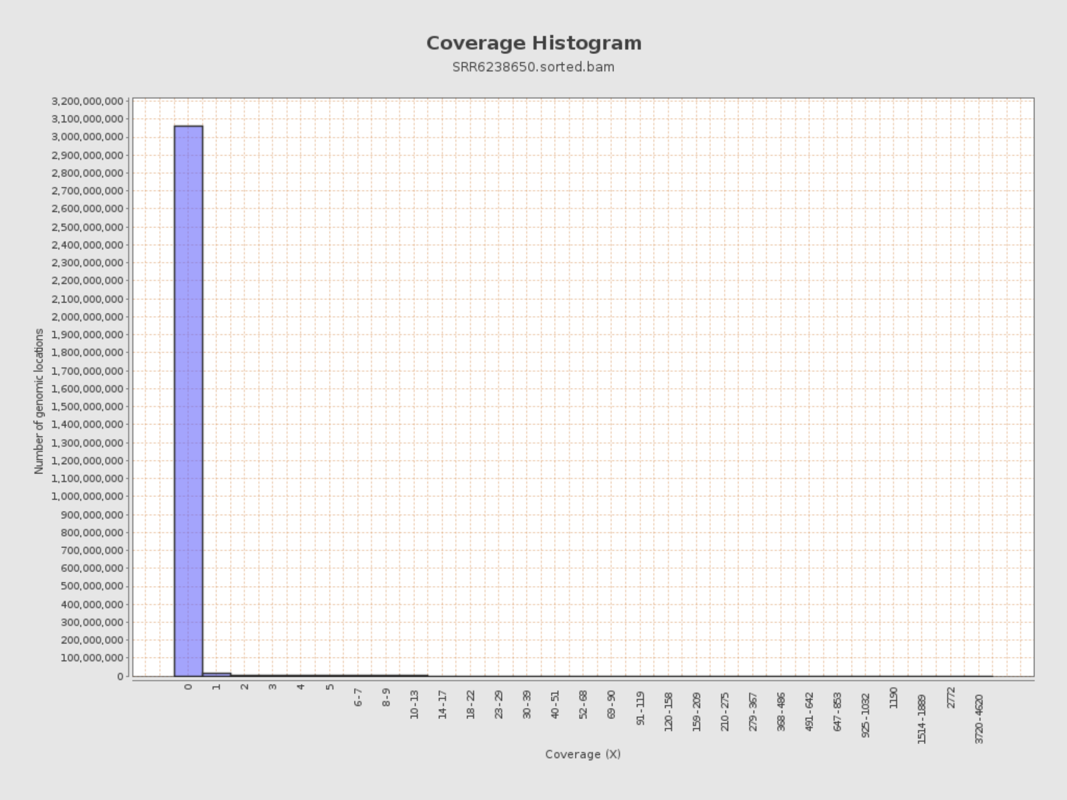
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10958884	0.044	0.7561
chr2	243199373	16166864	0.0665	2.2042
chr3	198022430	6434441	0.0325	0.6041
chr4	191154276	6442239	0.0337	0.6109
chr5	180915260	8429633	0.0466	0.7305
chr6	171115067	12397416	0.0725	1.1243
chr7	159138663	13348660	0.0839	1.1044

chr8	146364022	12039388	0.0823	1.0815
chr9	141213431	4734345	0.0335	0.6248
chr10	135534747	9824845	0.0725	0.9361
chr11	135006516	8821945	0.0653	0.9089
chr12	133851895	3268601	0.0244	0.5202
chr13	115169878	1812685	0.0157	0.6156
chr14	107349540	3804253	0.0354	0.6432
chr15	102531392	1468177	0.0143	0.5553
chr16	90354753	3029343	0.0335	0.6265
chr17	81195210	2427121	0.0299	0.5616
chr18	78077248	10985602	0.1407	2.6636
chr19	59128983	2365758	0.04	0.7137
chr20	63025520	1690380	0.0268	0.5419
chr21	48129895	3348909	0.0696	0.8935
chr22	51304566	3720611	0.0725	0.9649
chrMT	16571	18387	1.1096	3.367
chrX	155270560	3909507	0.0252	0.5135
chrY	59373566	305712	0.0051	0.2889

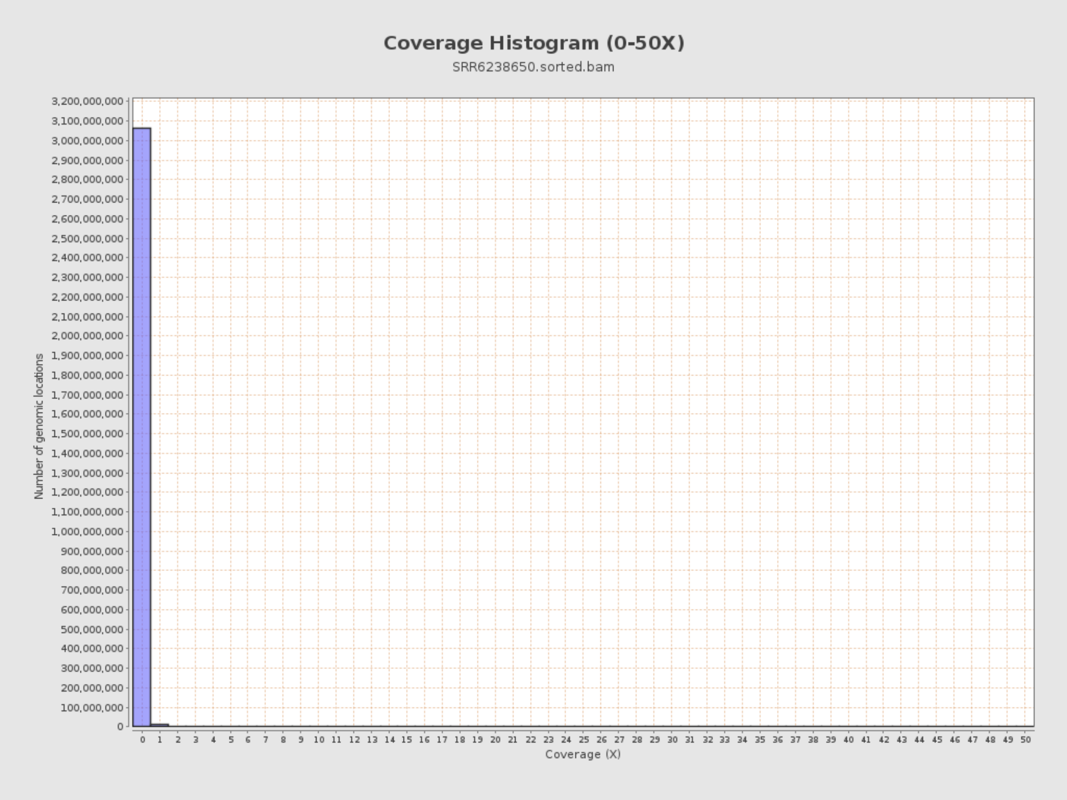
3. Results : Coverage across reference



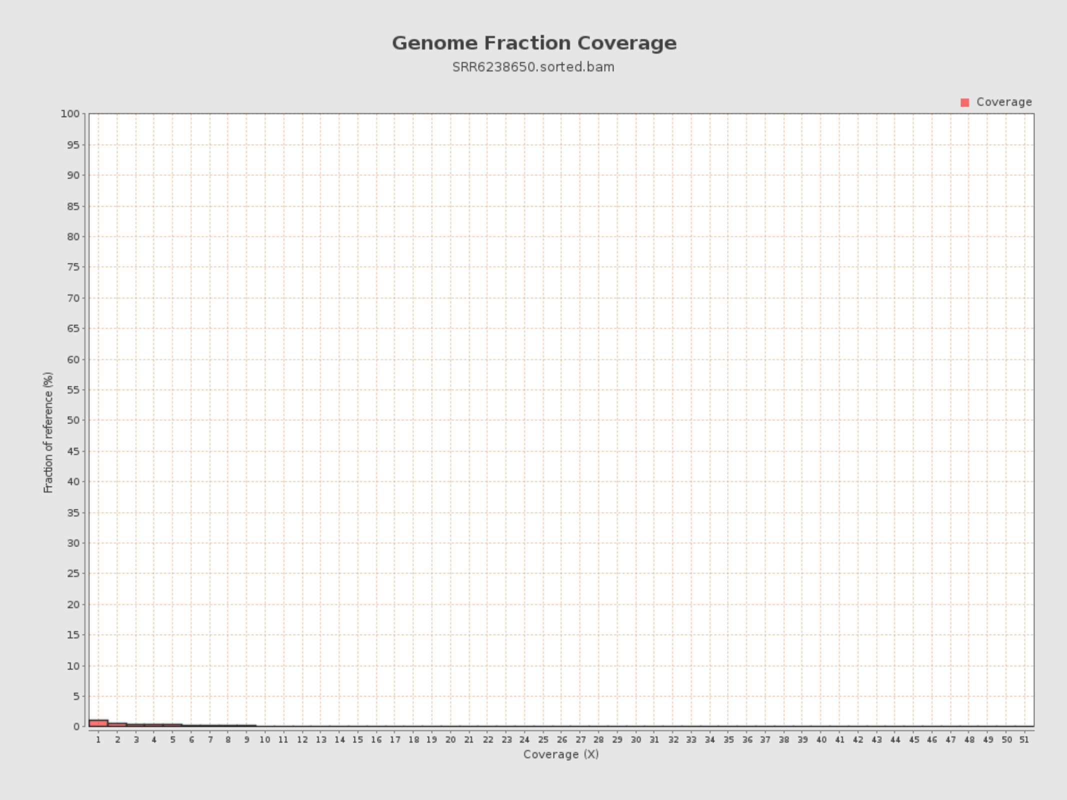
4. Results : Coverage Histogram



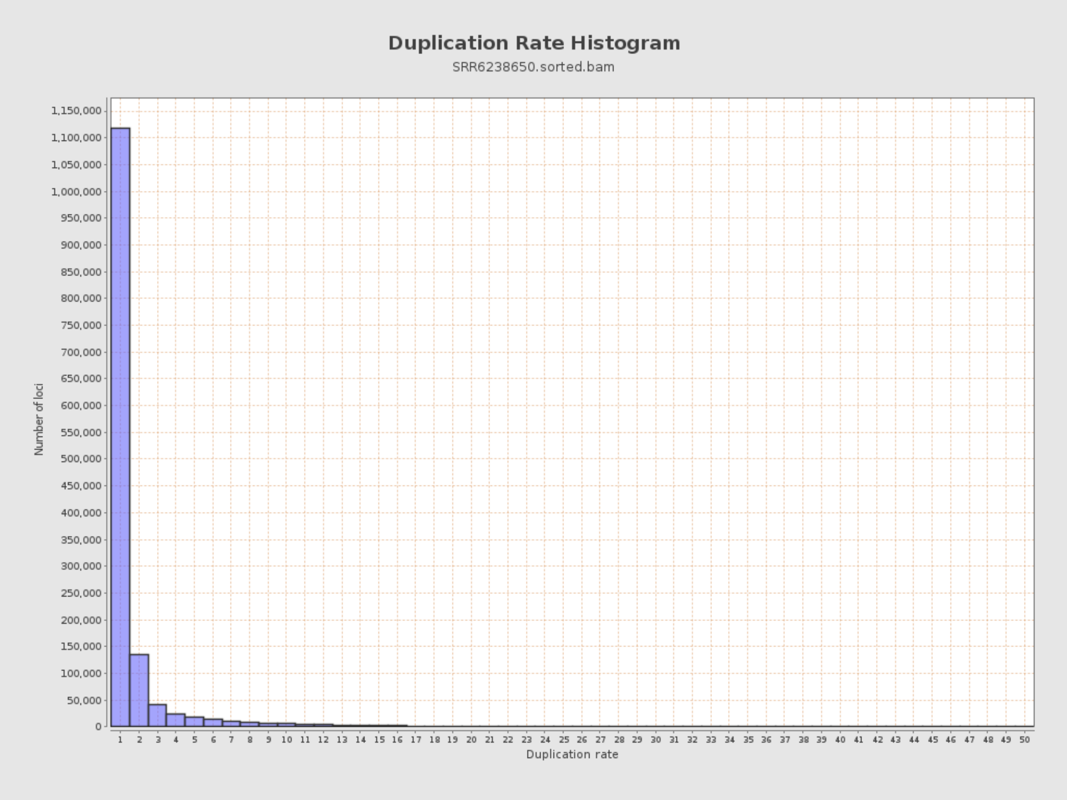
5. Results : Coverage Histogram (0-50X)



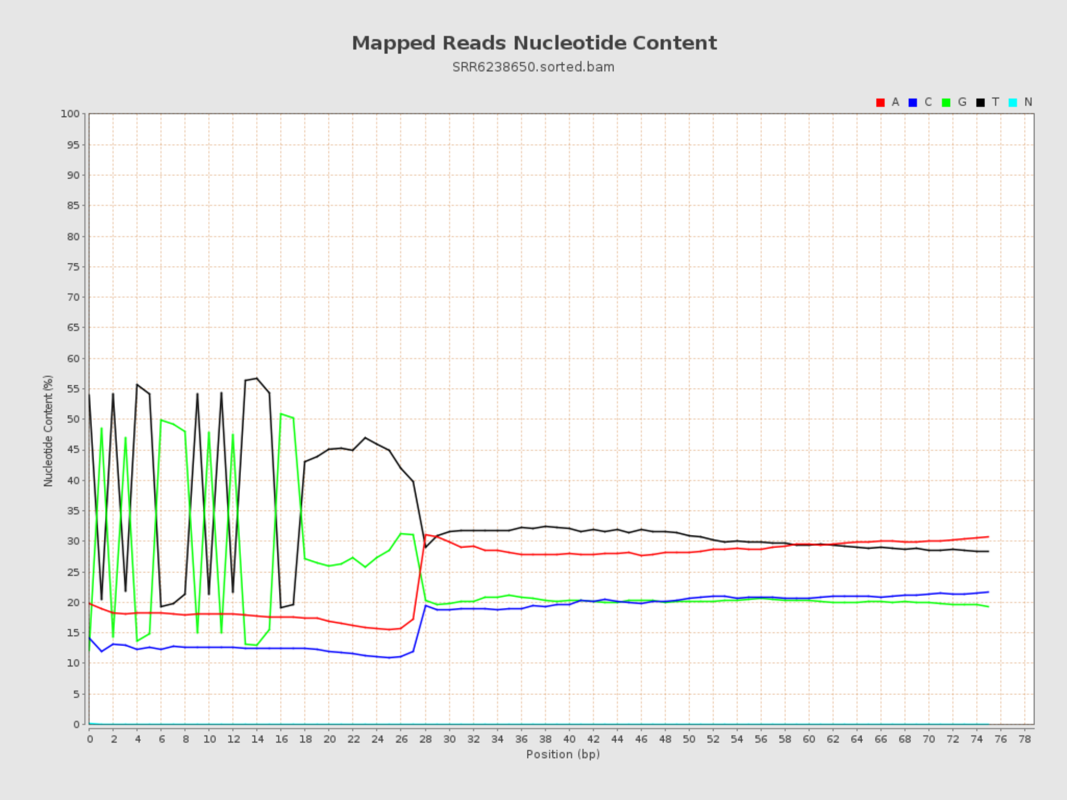
6. Results : Genome Fraction Coverage



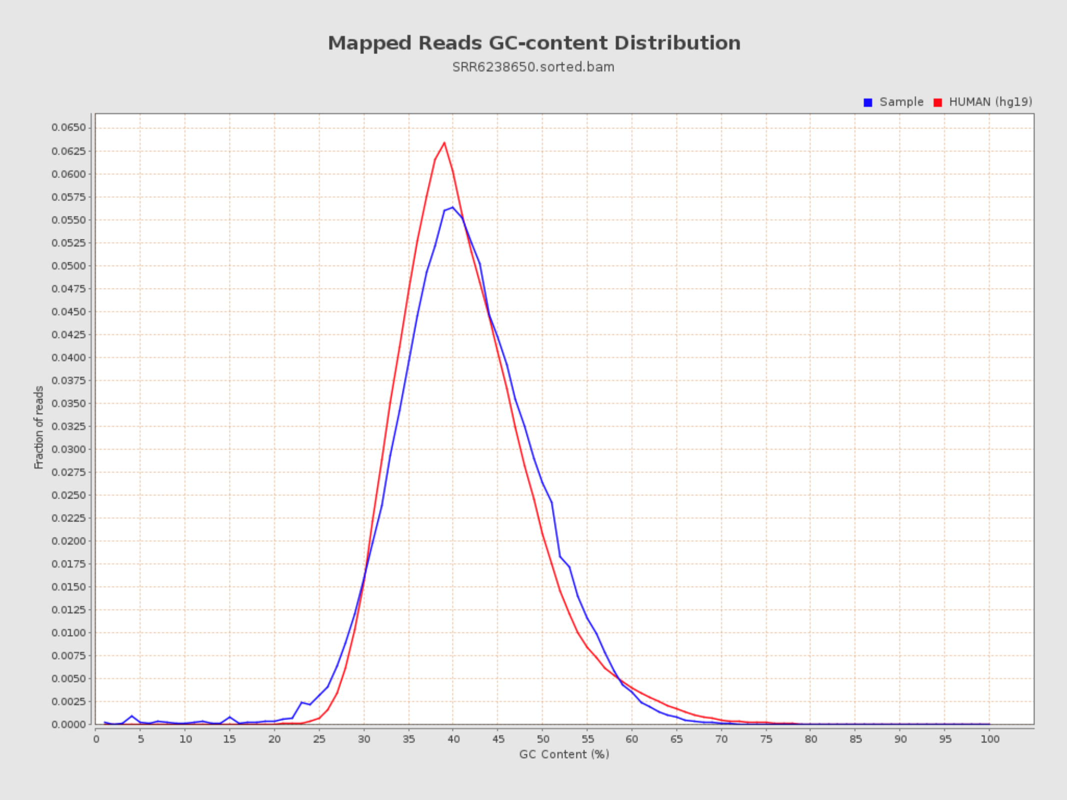
7. Results : Duplication Rate Histogram



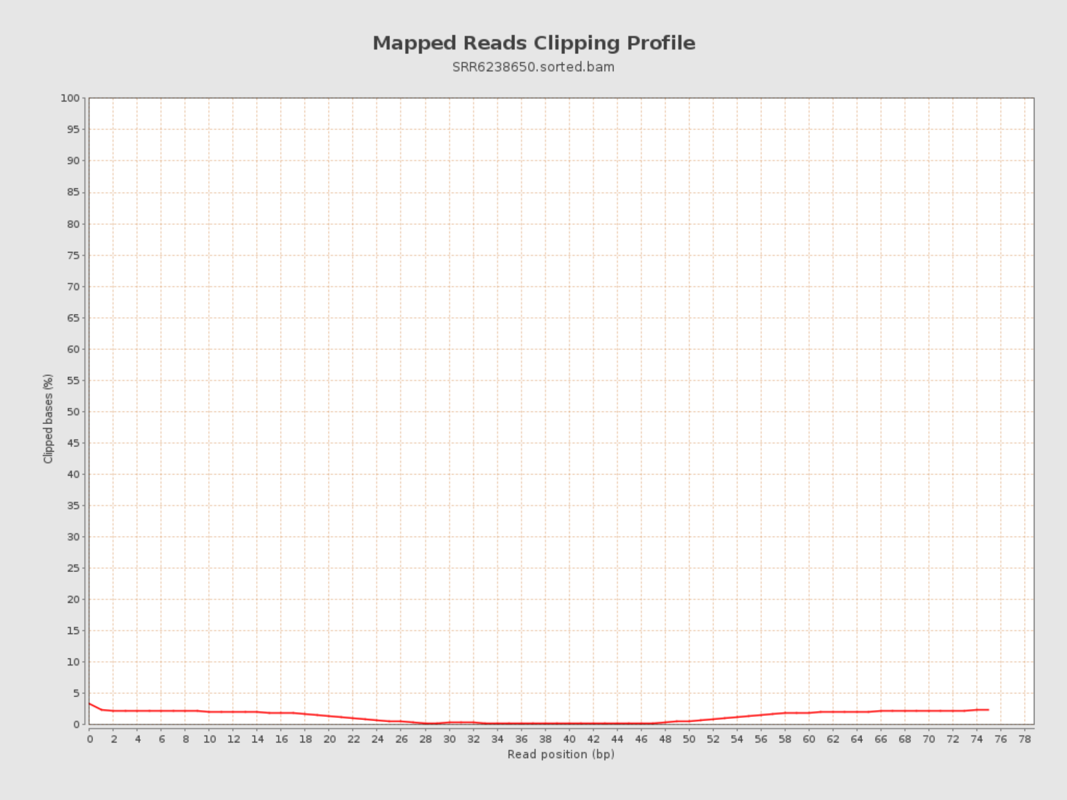
8. Results : Mapped Reads Nucleotide Content



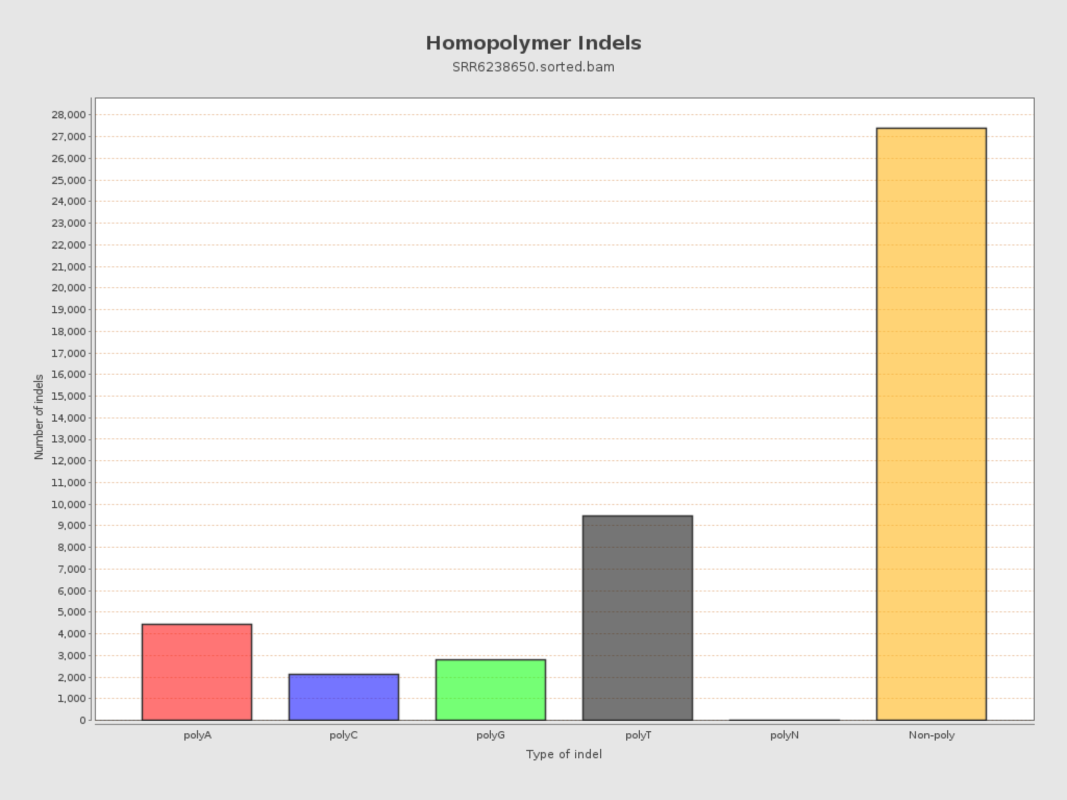
9. Results : Mapped Reads GC-content Distribution



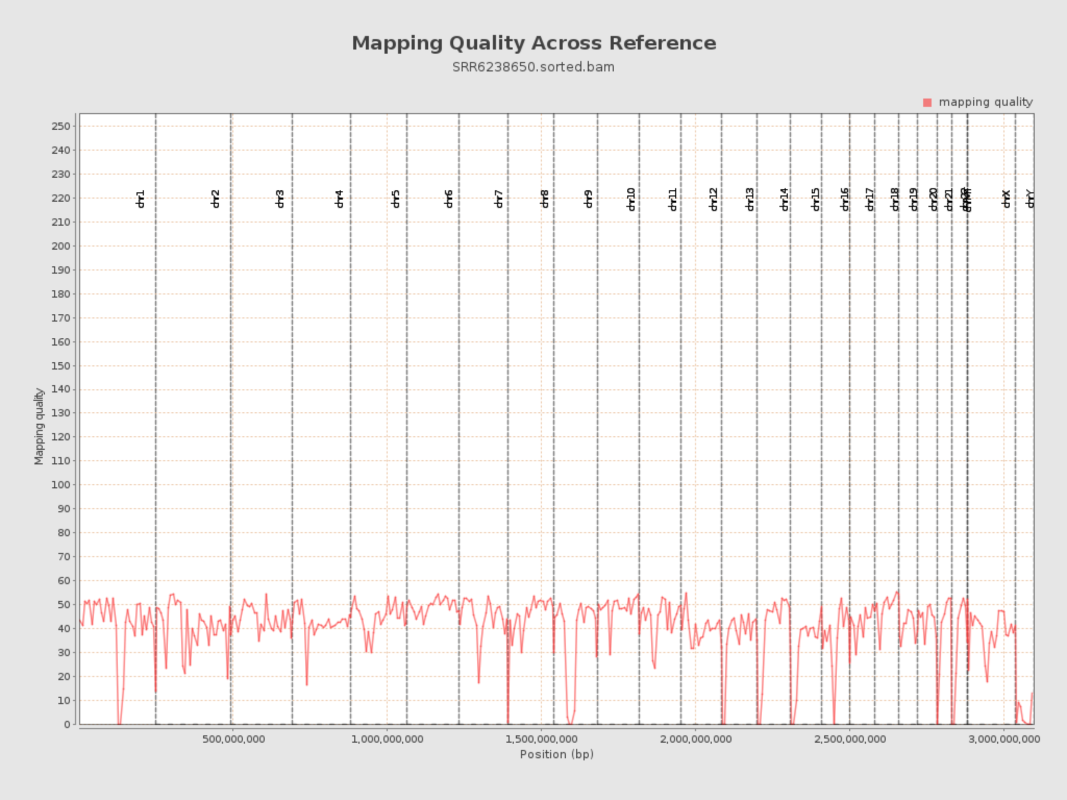
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram