Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 00:46:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238651.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_SRR6238651 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238651.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 00:46:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238651.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,096,524
Mapped reads	2,511,252 / 81.1%
Unmapped reads	585,272 / 18.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,973 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	1,182,725 / 38.2%
Duplication rate	24.95%
Clipped reads	1,810,486 / 58.47%

2.2. ACGT Content

Number/percentage of A's	36,452,166 / 24.44%
Number/percentage of C's	24,337,424 / 16.32%
Number/percentage of T's	52,665,246 / 35.31%
Number/percentage of G's	35,703,418 / 23.94%
Number/percentage of N's	3,163 / 0%
GC Percentage	40.25%

2.3. Coverage

Mean	0.0482

Standard Deviation	1.0486

2.4. Mapping Quality

Mean Mapping Quality	42.25

2.5. Mismatches and indels

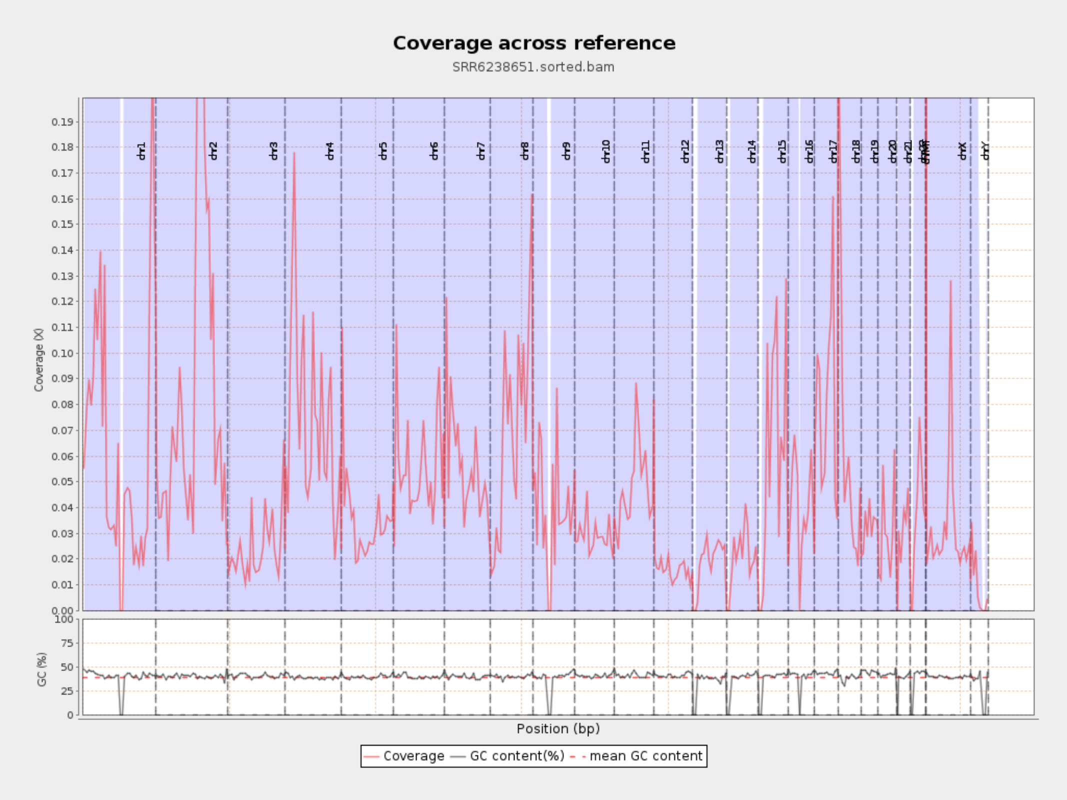
General error rate	0.7%
Mismatches	1,026,240
Insertions	9,839
Mapped reads with at least one insertion	0.39%
Deletions	56,212
Mapped reads with at least one deletion	2.21%
Homopolymer indels	41.04%

2.6. Chromosome stats

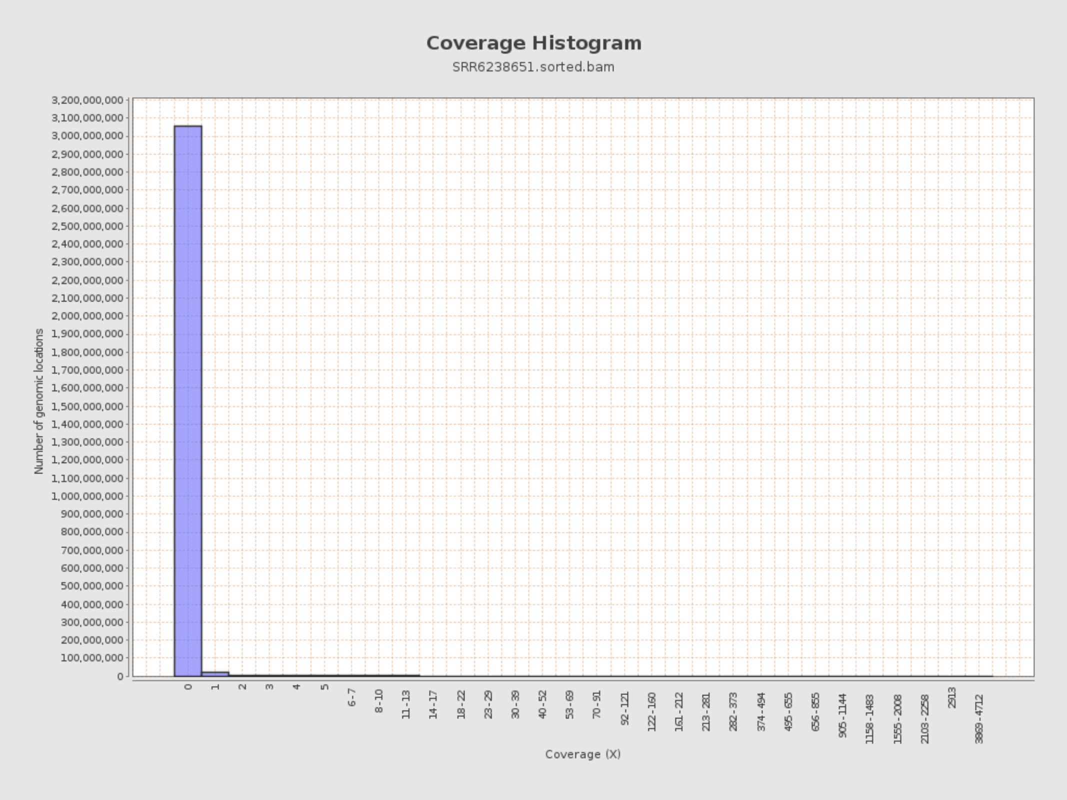
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15838412	0.0635	0.881
chr2	243199373	22117916	0.0909	2.2832
chr3	198022430	4786615	0.0242	0.4814
chr4	191154276	14372520	0.0752	0.8493
chr5	180915260	6422714	0.0355	0.5497
chr6	171115067	9561012	0.0559	1.0328
chr7	159138663	8940591	0.0562	0.8729

chr8	146364022	10379315	0.0709	1.5135
chr9	141213431	5536445	0.0392	0.6203
chr10	135534747	3915277	0.0289	0.4911
chr11	135006516	6469485	0.0479	0.6682
chr12	133851895	2099925	0.0157	0.3434
chr13	115169878	2171611	0.0189	0.623
chr14	107349540	2234820	0.0208	0.4584
chr15	102531392	6310477	0.0615	0.9234
chr16	90354753	3527269	0.039	0.6117
chr17	81195210	6848892	0.0844	0.9373
chr18	78077248	4956120	0.0635	2.5874
chr19	59128983	1929200	0.0326	0.592
chr20	63025520	1953760	0.031	0.5273
chr21	48129895	1399590	0.0291	0.4929
chr22	51304566	1942494	0.0379	0.5813
chrMT	16571	11773	0.7105	2.4444
chrX	155270560	4981811	0.0321	0.5187
chrY	59373566	546847	0.0092	0.3847

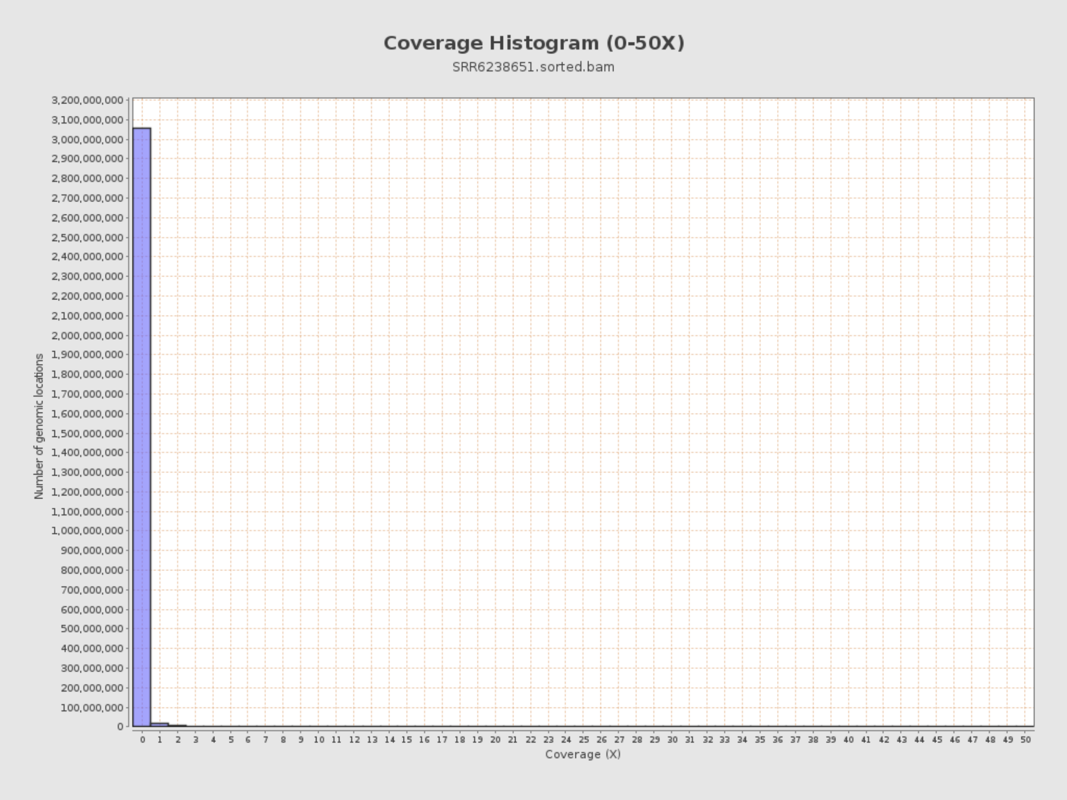
3. Results : Coverage across reference



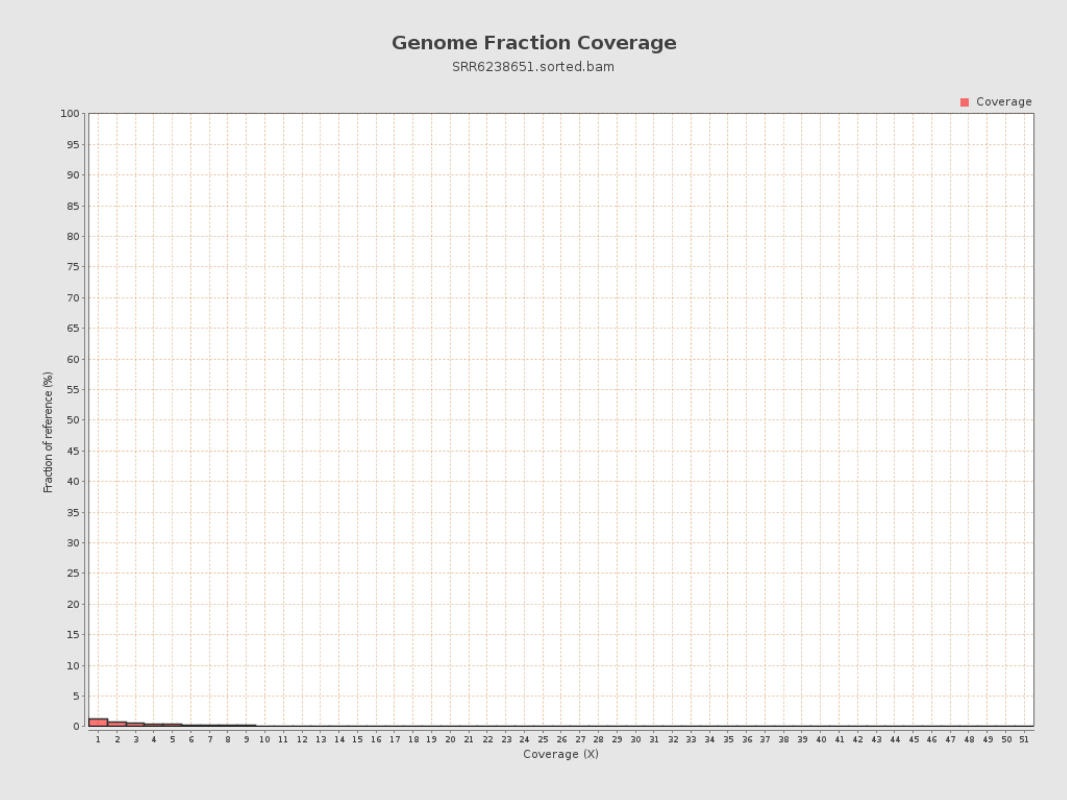
4. Results : Coverage Histogram



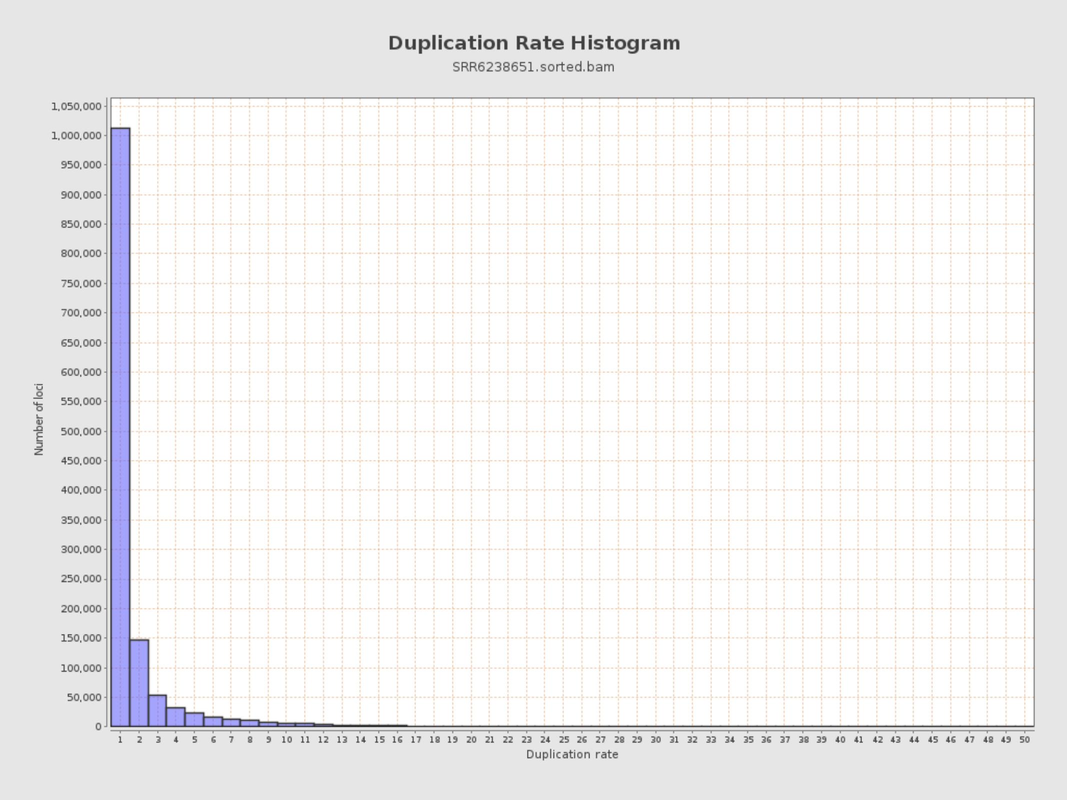
5. Results : Coverage Histogram (0-50X)



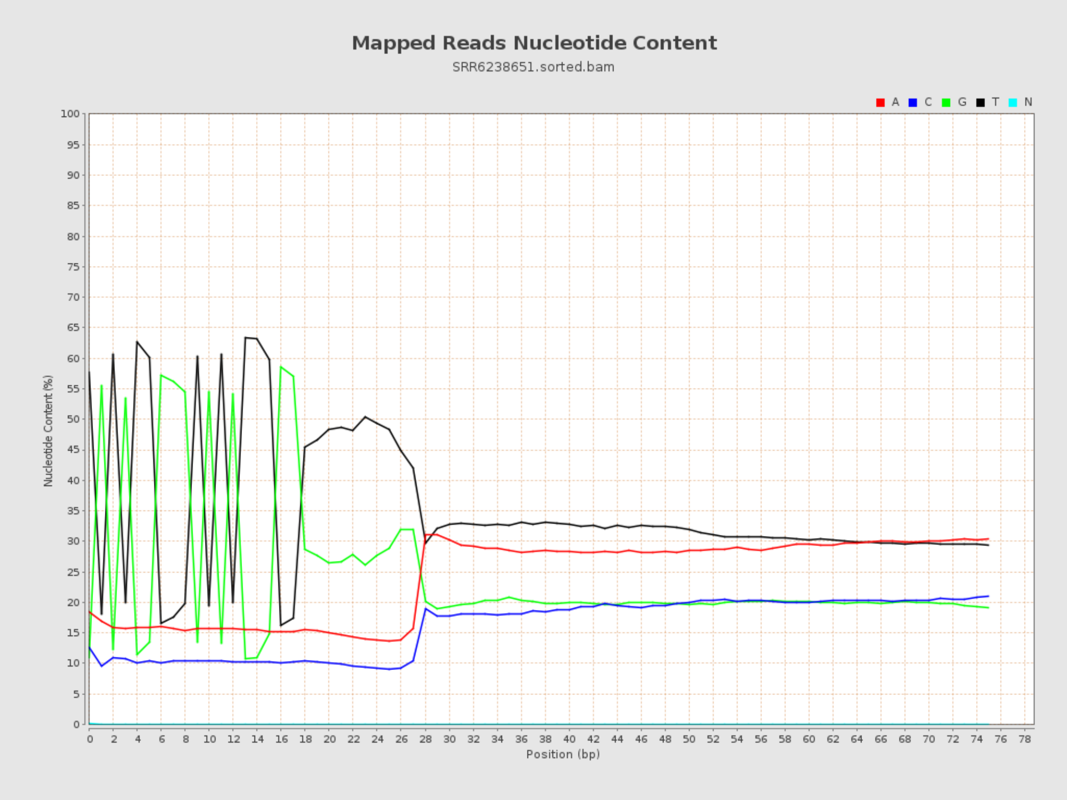
6. Results : Genome Fraction Coverage



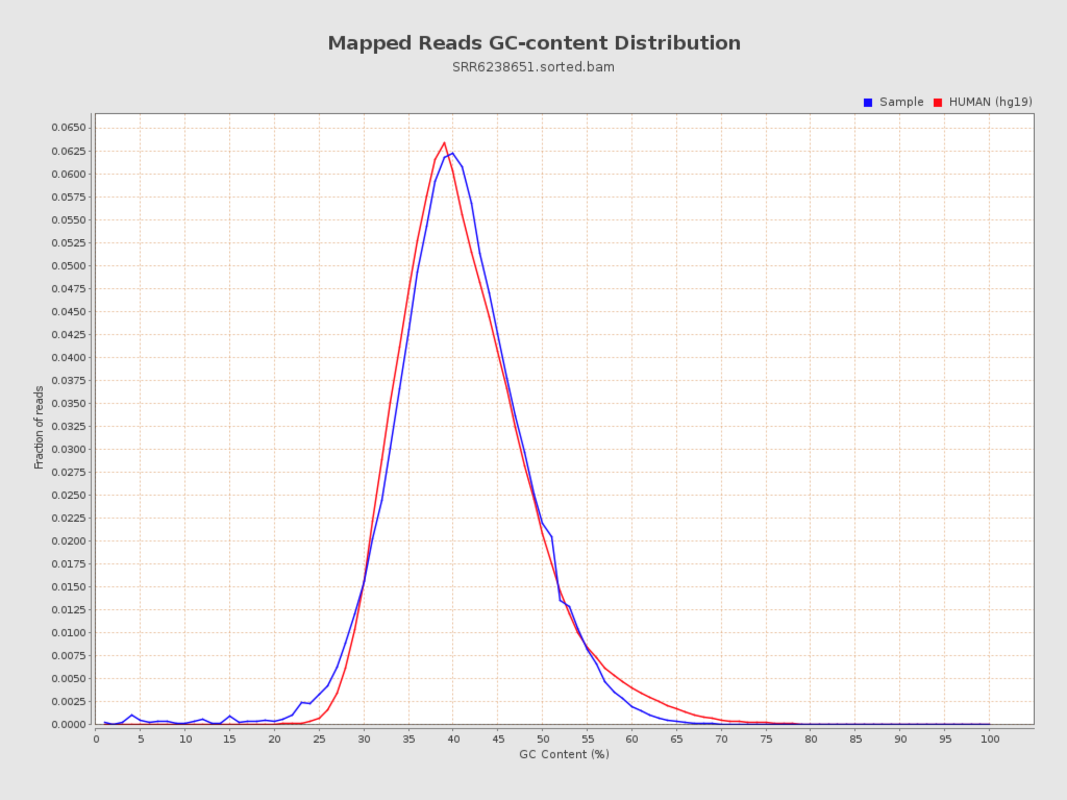
7. Results : Duplication Rate Histogram



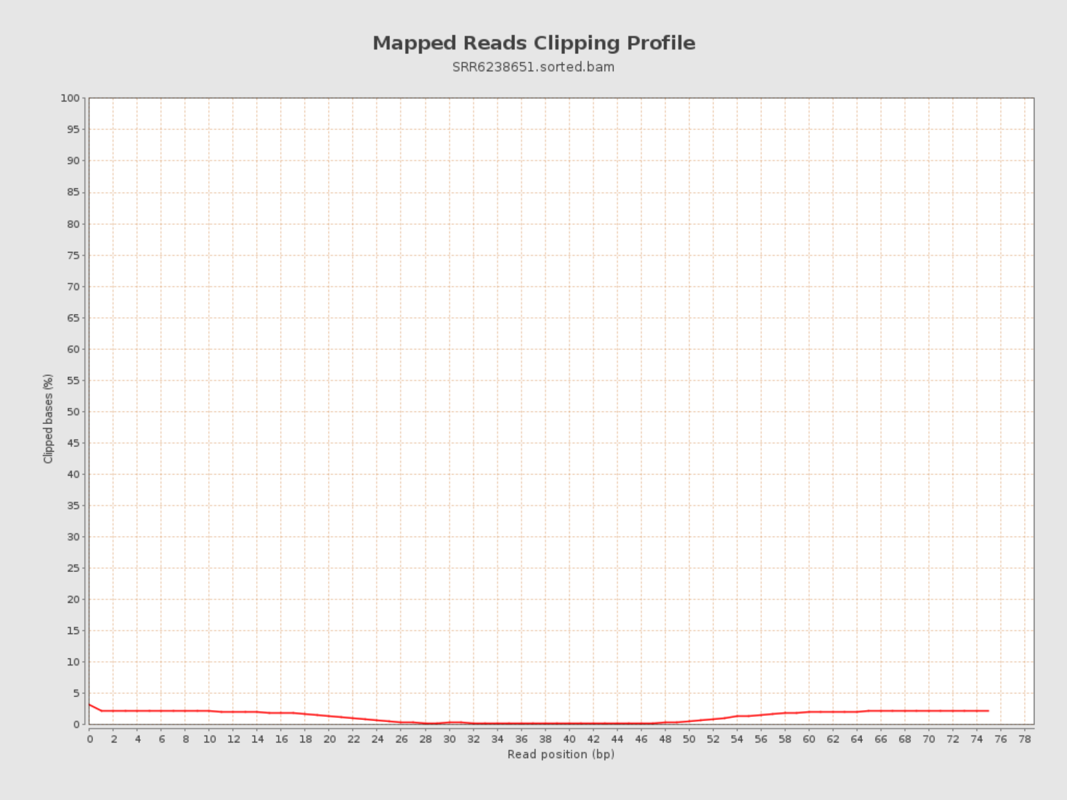
8. Results : Mapped Reads Nucleotide Content



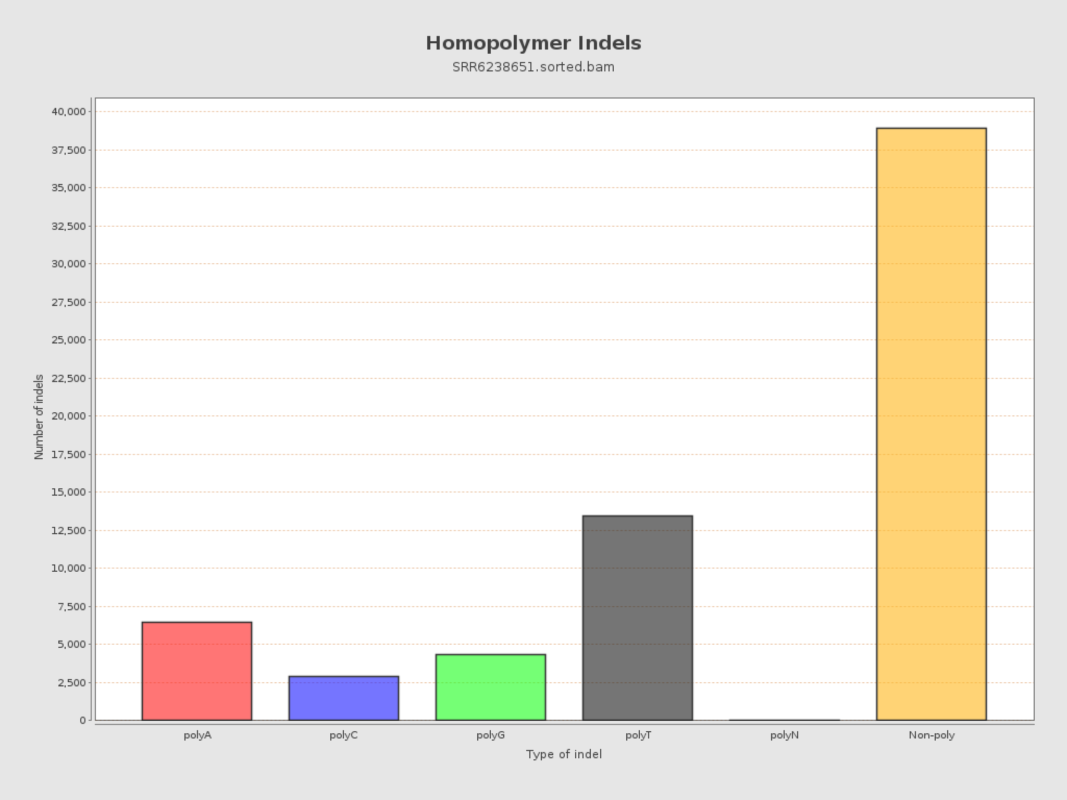
9. Results : Mapped Reads GC-content Distribution



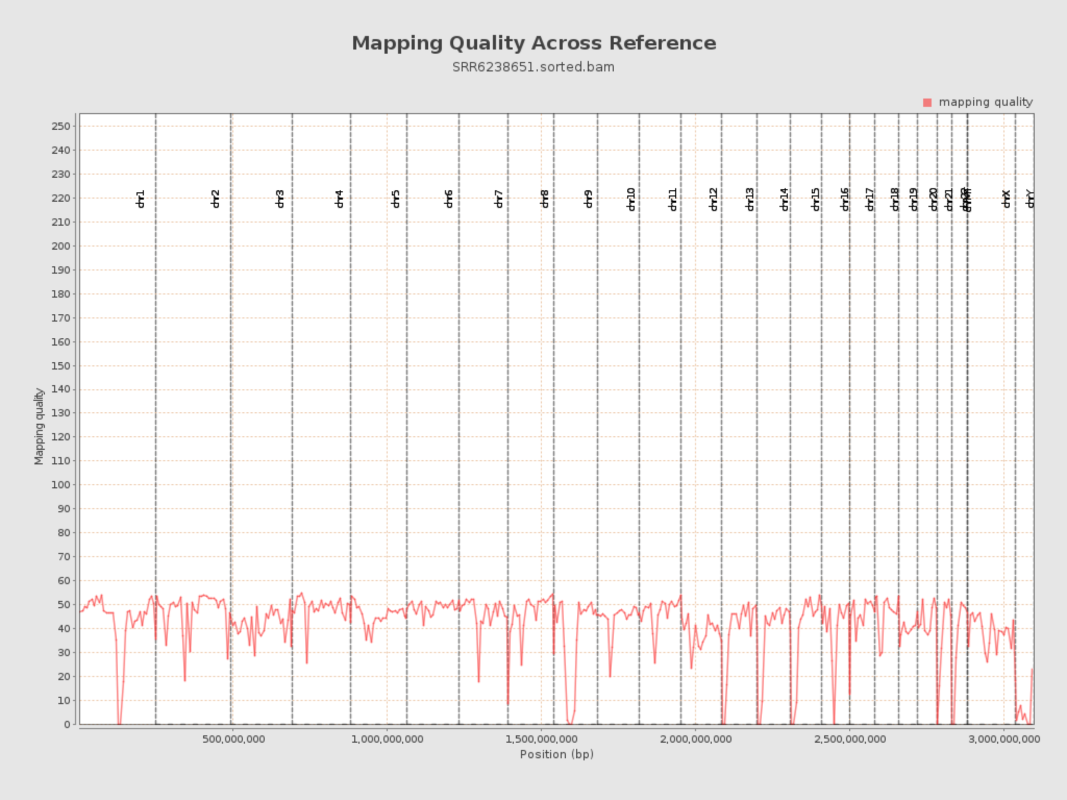
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram