Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 00:50:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238652.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_SRR6238652 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238652.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 00:50:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238652.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,618,867
Mapped reads	3,231,946 / 89.31%
Unmapped reads	386,921 / 10.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,398 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	953,970 / 26.36%
Duplication rate	20.4%
Clipped reads	2,057,988 / 56.87%

2.2. ACGT Content

Number/percentage of A's	50,108,117 / 25.2%
Number/percentage of C's	34,506,150 / 17.35%
Number/percentage of T's	67,330,548 / 33.85%
Number/percentage of G's	46,931,088 / 23.6%
Number/percentage of N's	4,435 / 0%
GC Percentage	40.95%

2.3. Coverage

Mean	0.0643

Standard Deviation	1.0692

2.4. Mapping Quality

Mean Mapping Quality	37.67

2.5. Mismatches and indels

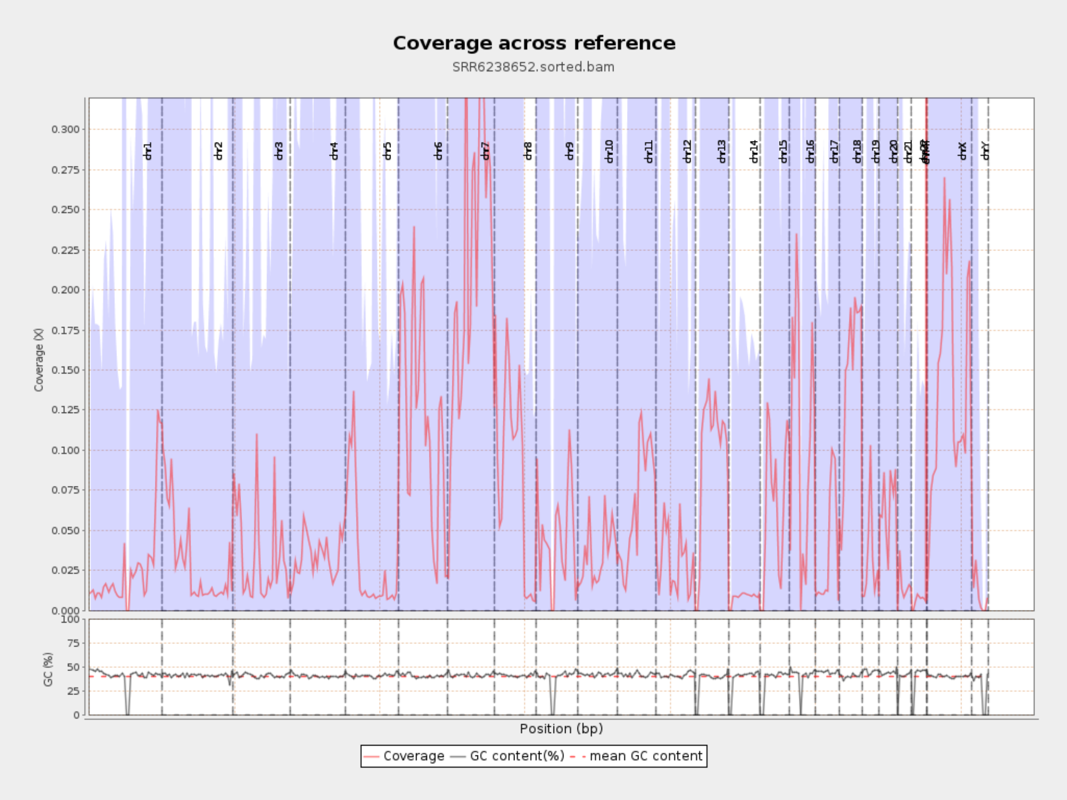
General error rate	0.58%
Mismatches	1,122,945
Insertions	12,998
Mapped reads with at least one insertion	0.4%
Deletions	52,414
Mapped reads with at least one deletion	1.61%
Homopolymer indels	41.57%

2.6. Chromosome stats

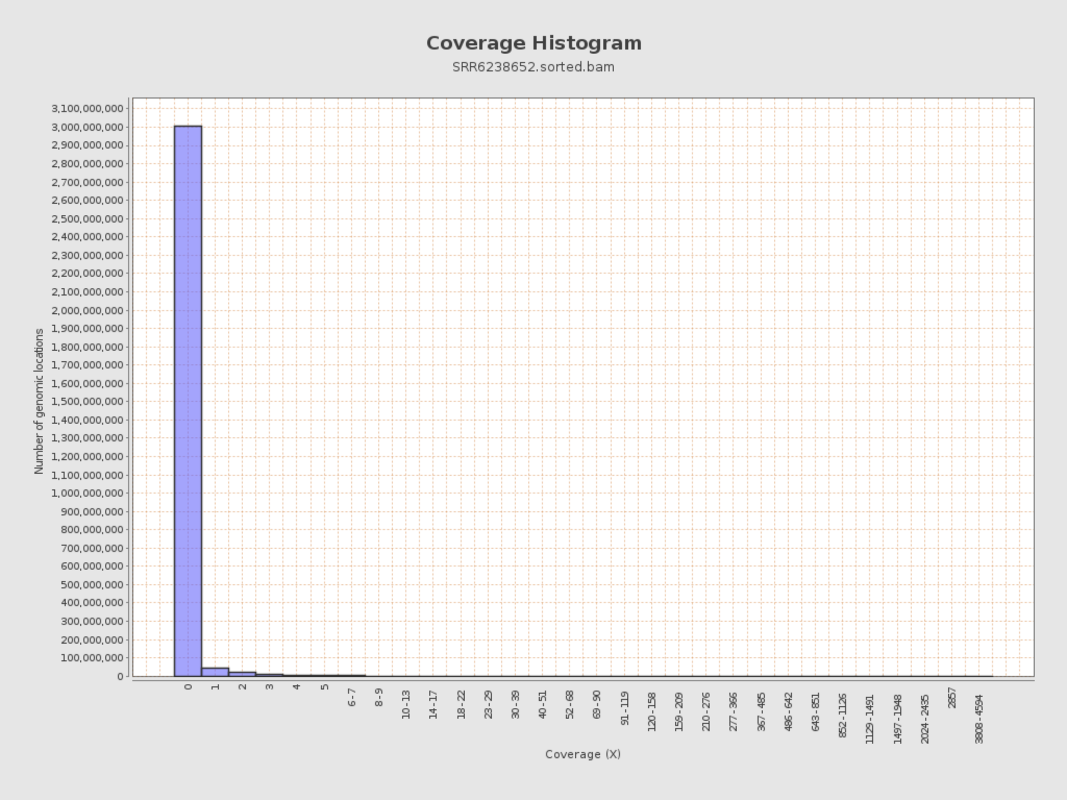
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6395285	0.0257	0.8
chr2	243199373	7573876	0.0311	2.0396
chr3	198022430	7044351	0.0356	0.3711
chr4	191154276	6490454	0.034	0.367
chr5	180915260	5689607	0.0314	0.3463
chr6	171115067	20908447	0.1222	1.0204
chr7	159138663	34960240	0.2197	2.8905

chr8	146364022	12372173	0.0845	0.7773
chr9	141213431	6428320	0.0455	0.5405
chr10	135534747	4704578	0.0347	0.5943
chr11	135006516	9063689	0.0671	0.5316
chr12	133851895	4128758	0.0308	0.3598
chr13	115169878	11476842	0.0997	0.7089
chr14	107349540	886295	0.0083	0.2465
chr15	102531392	6817356	0.0665	0.6001
chr16	90354753	10224769	0.1132	0.7048
chr17	81195210	2945222	0.0363	0.3642
chr18	78077248	11332831	0.1451	1.7546
chr19	59128983	1948198	0.0329	0.6505
chr20	63025520	4085610	0.0648	0.5016
chr21	48129895	753373	0.0157	0.2873
chr22	51304566	310678	0.0061	0.1197
chrMT	16571	34293	2.0695	3.2556
chrX	155270560	21773976	0.1402	0.7721
chrY	59373566	621135	0.0105	0.3587

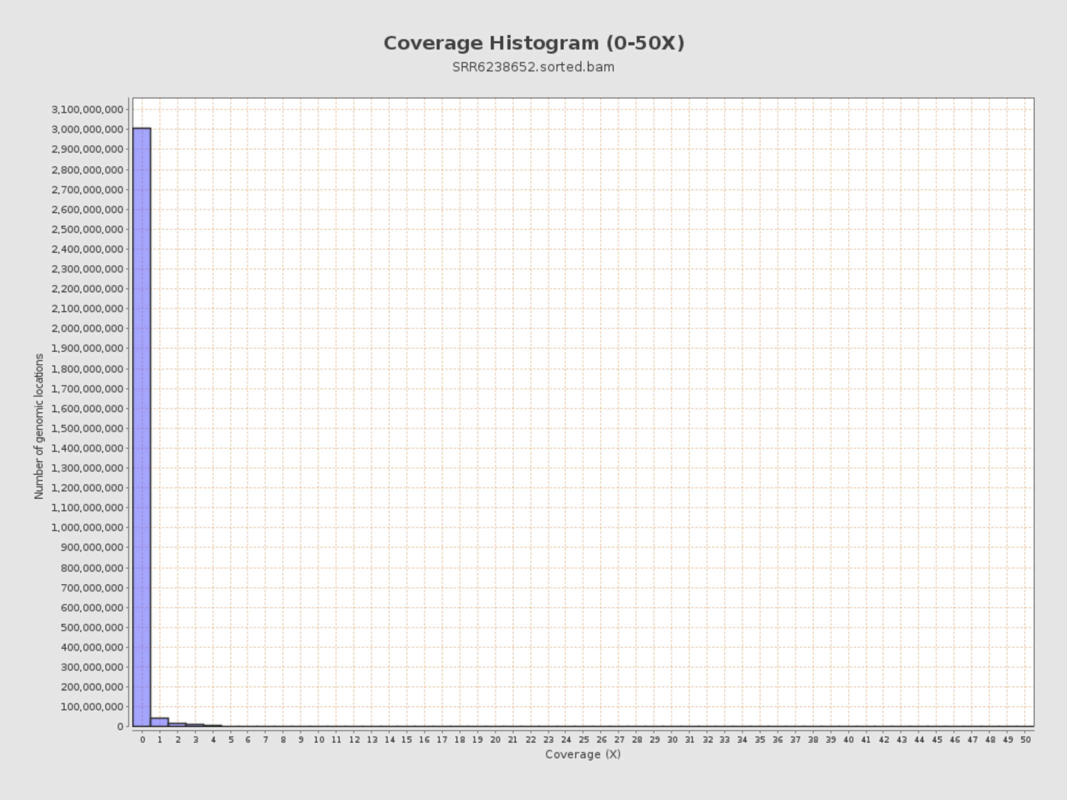
3. Results : Coverage across reference



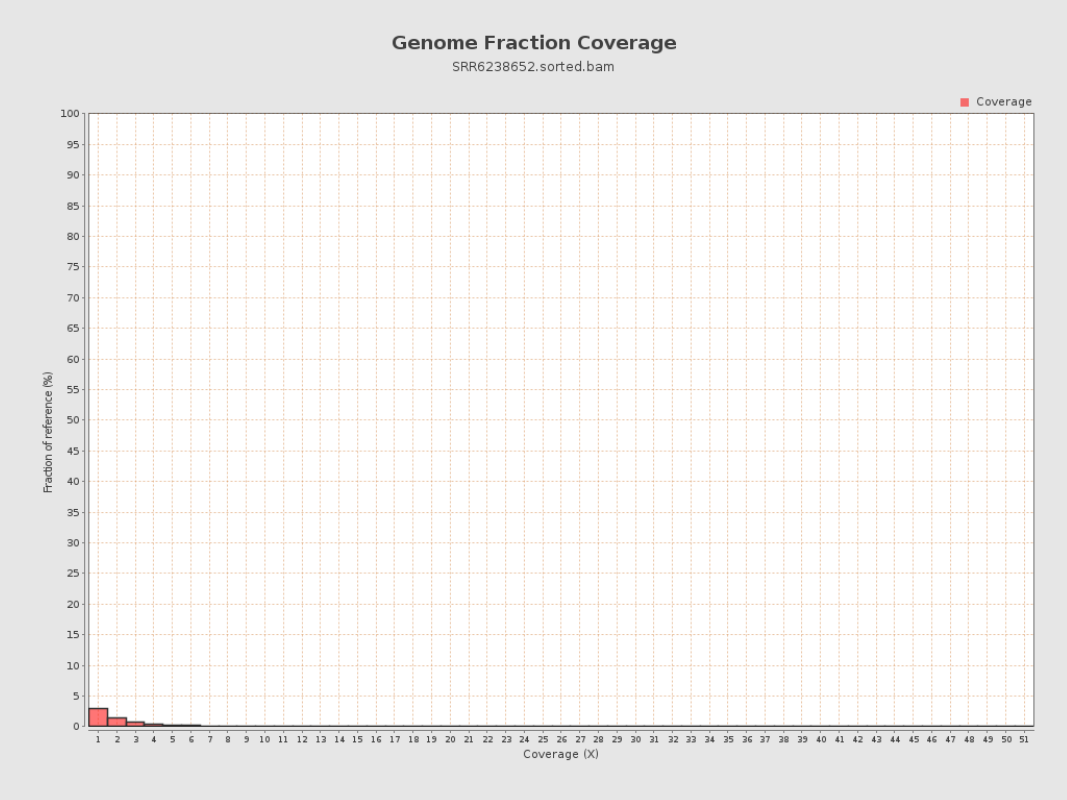
4. Results : Coverage Histogram



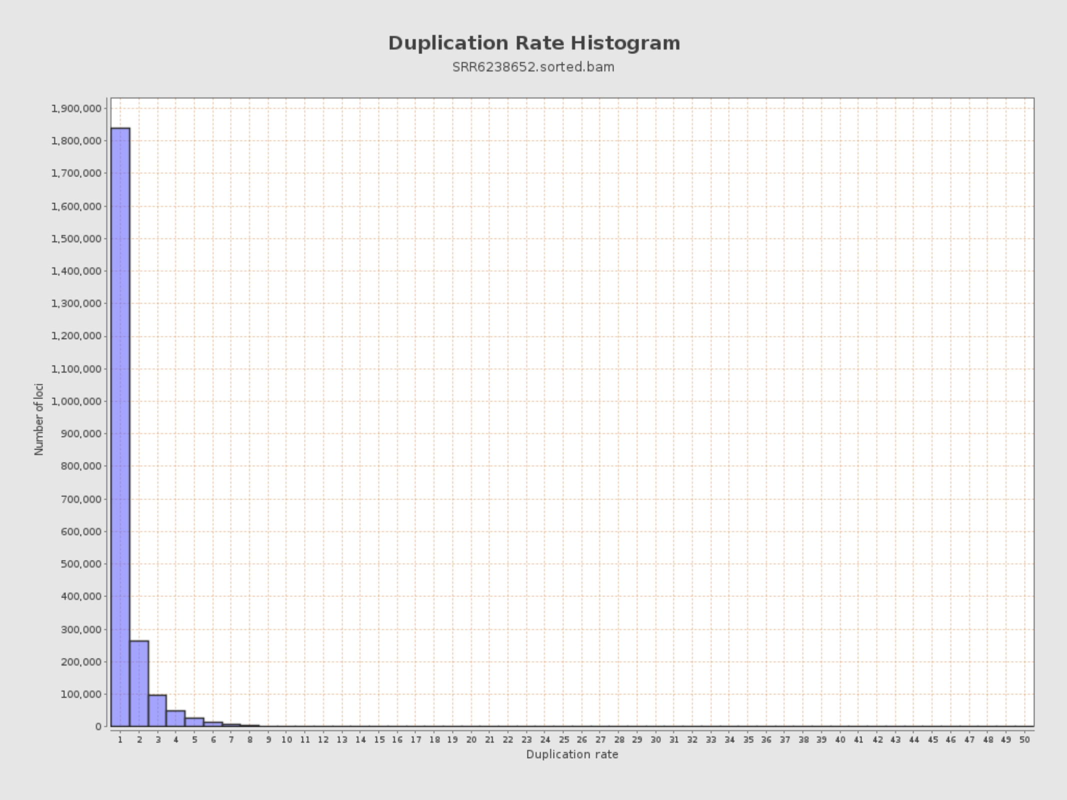
5. Results : Coverage Histogram (0-50X)



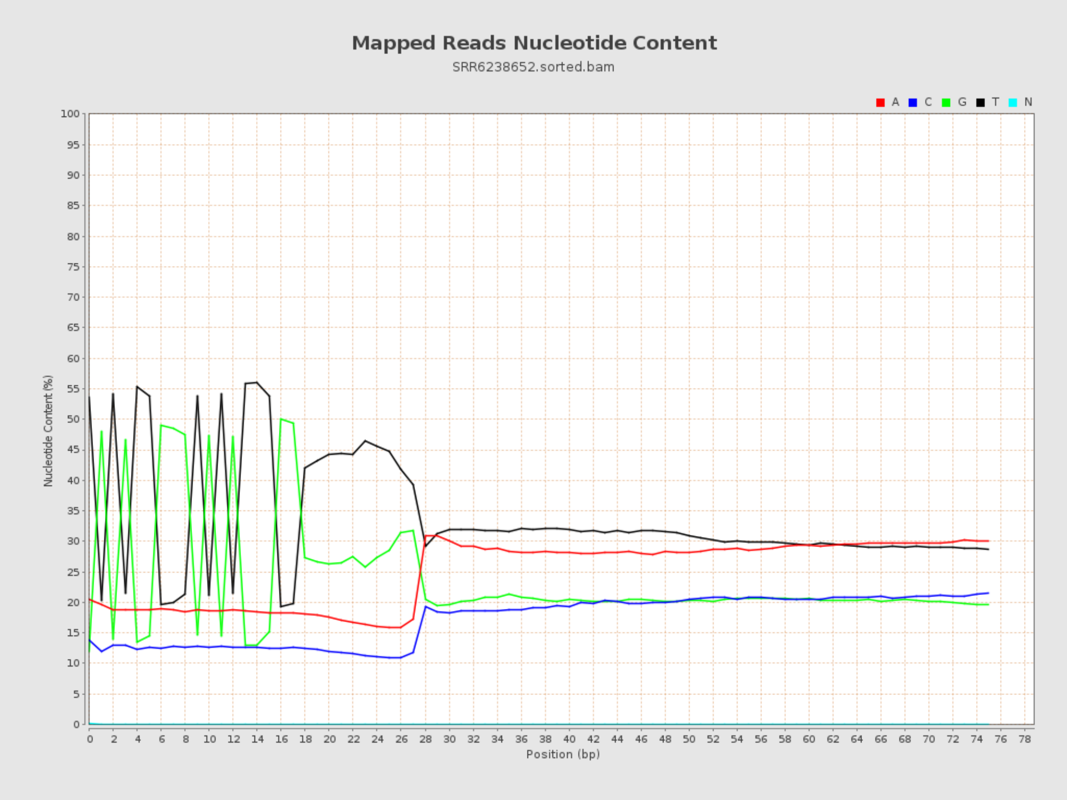
6. Results : Genome Fraction Coverage



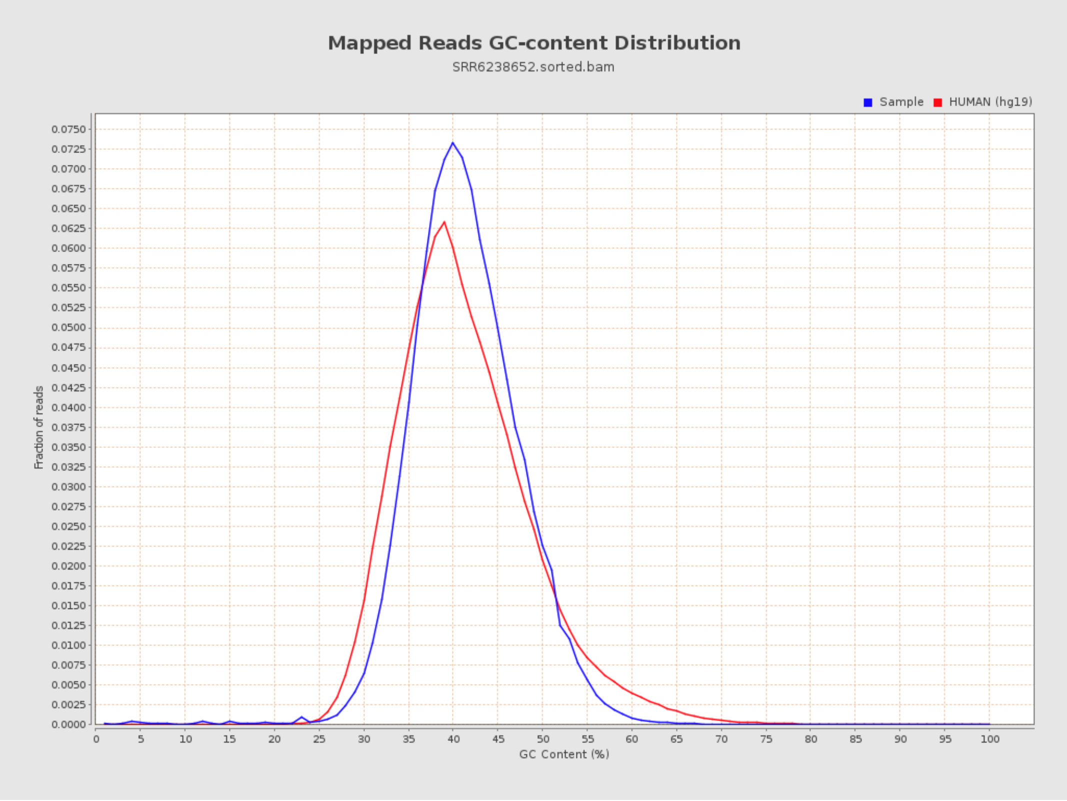
7. Results : Duplication Rate Histogram



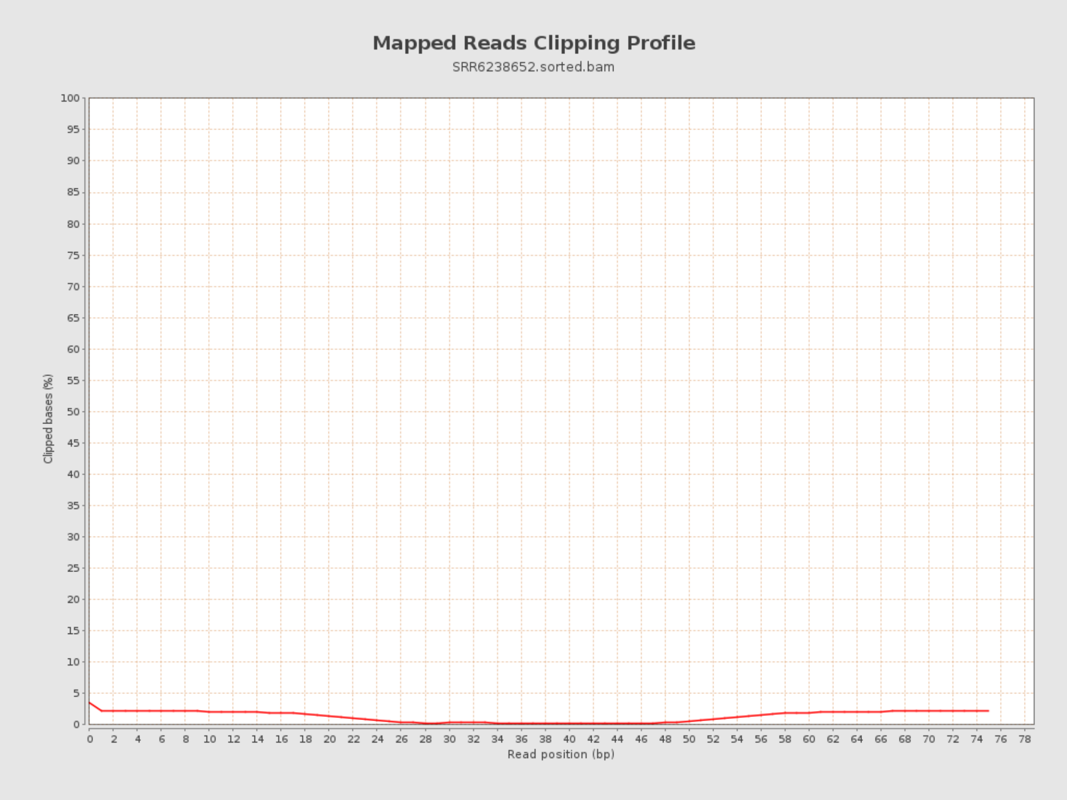
8. Results : Mapped Reads Nucleotide Content



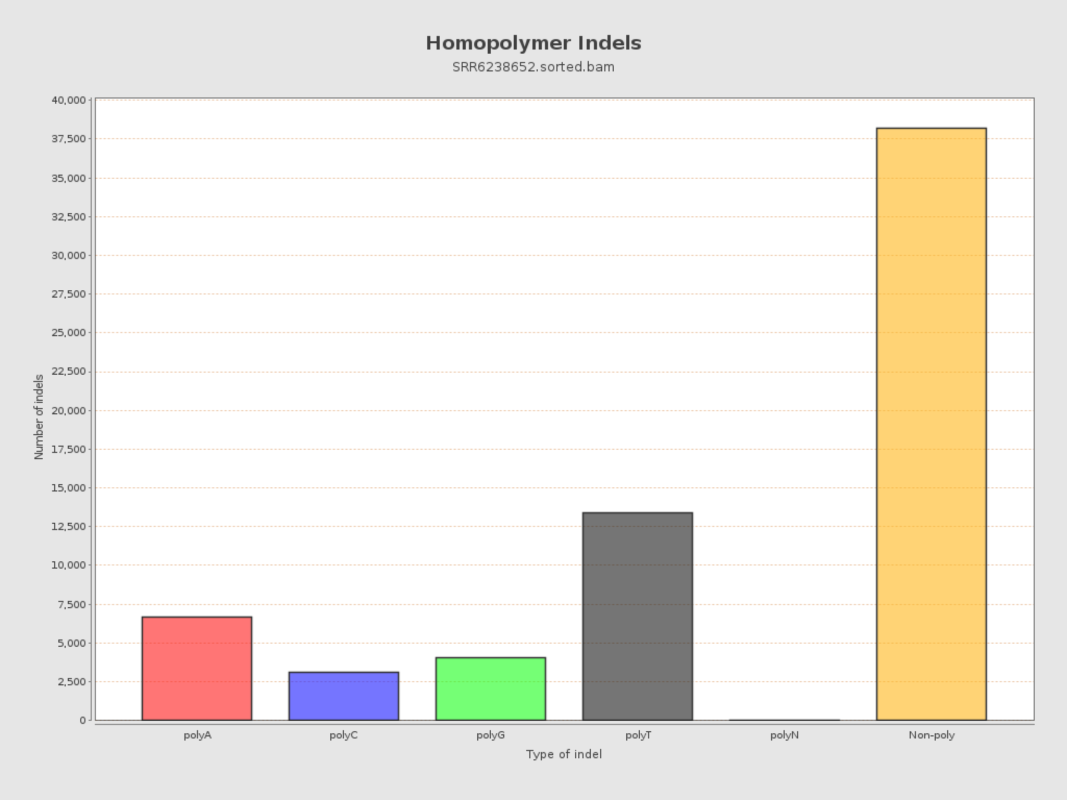
9. Results : Mapped Reads GC-content Distribution



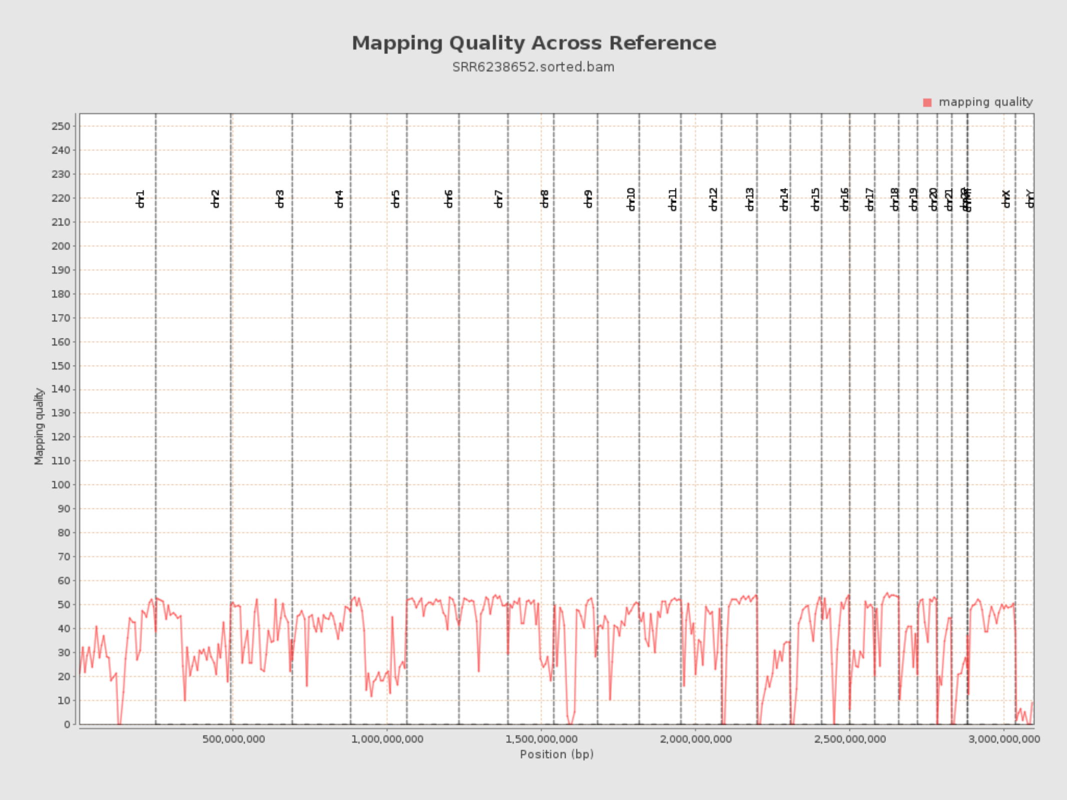
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram