Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 11:07:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238056.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_SRR6238056 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238056.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 11:07:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238056.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,575,900
Mapped reads	2,350,543 / 91.25%
Unmapped reads	225,357 / 8.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,555 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	98,250 / 3.81%
Duplication rate	3.15%
Clipped reads	945,818 / 36.72%

2.2. ACGT Content

Number/percentage of A's	43,551,453 / 27.52%
Number/percentage of C's	30,065,495 / 18.99%
Number/percentage of T's	49,306,664 / 31.15%
Number/percentage of G's	35,336,179 / 22.32%
Number/percentage of N's	21,737 / 0.01%
GC Percentage	41.32%

2.3. Coverage

Mean	0.0512

Standard Deviation	0.4588

2.4. Mapping Quality

Mean Mapping Quality	46.45

2.5. Mismatches and indels

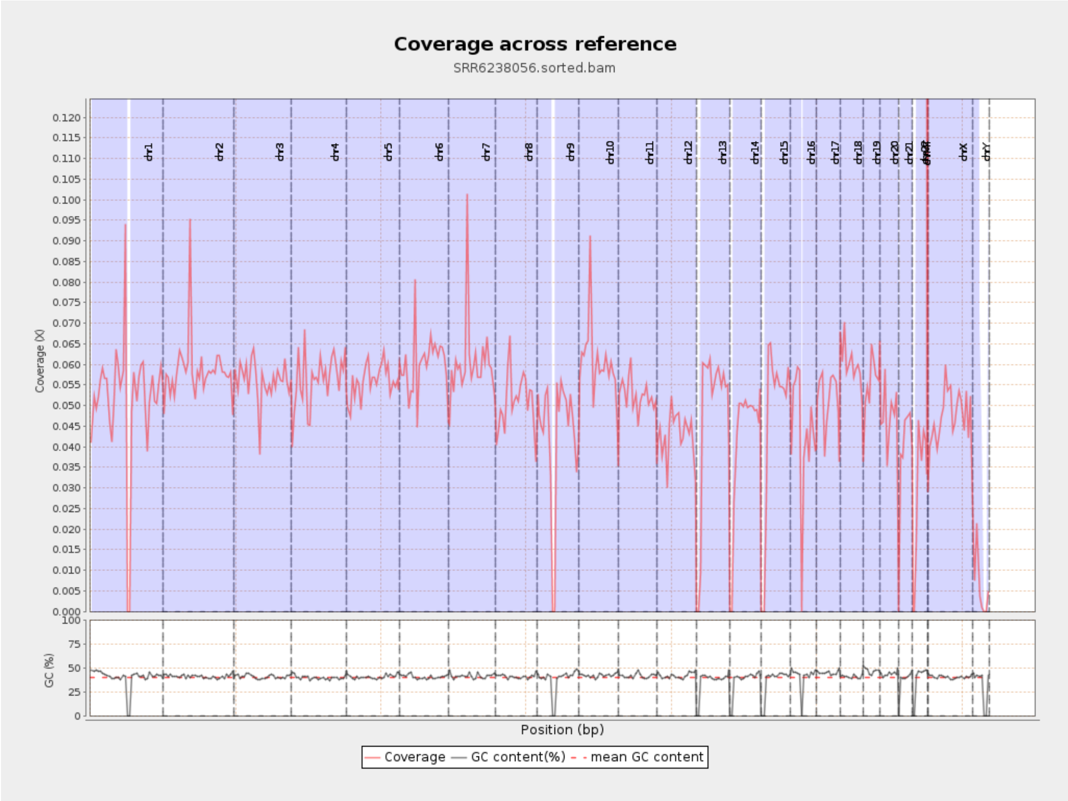
General error rate	0.75%
Mismatches	1,161,393
Insertions	10,864
Mapped reads with at least one insertion	0.46%
Deletions	41,482
Mapped reads with at least one deletion	1.74%
Homopolymer indels	46.41%

2.6. Chromosome stats

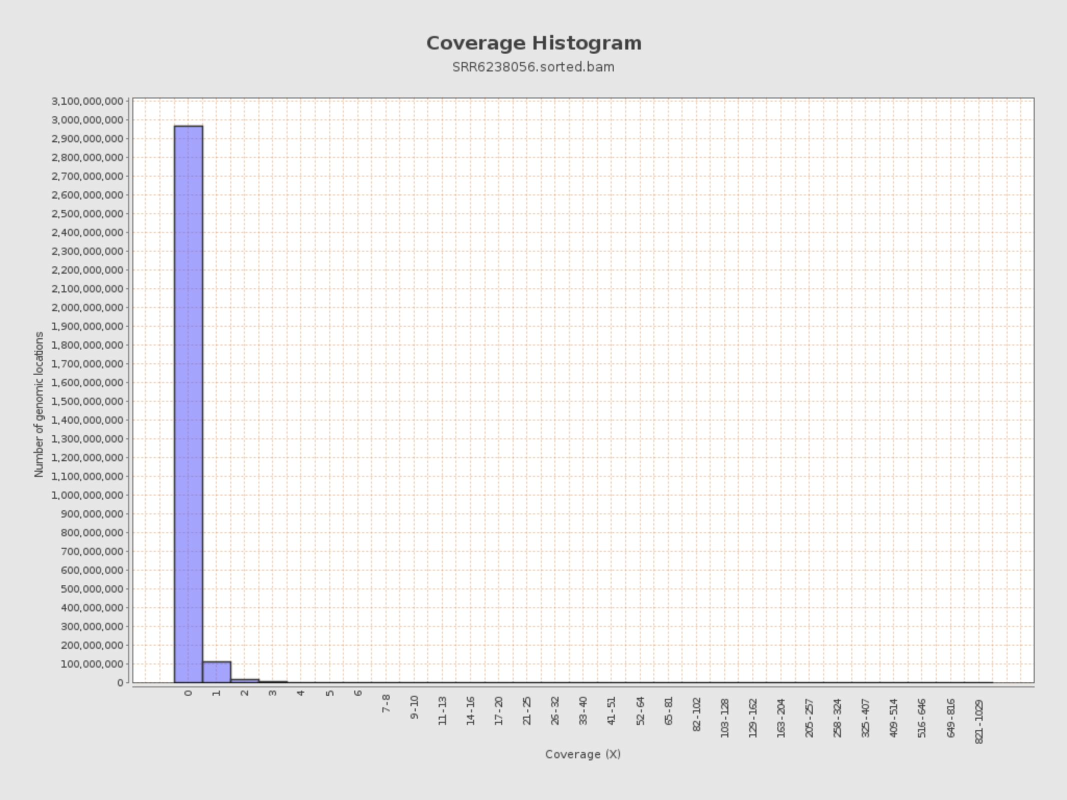
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12785076	0.0513	0.9243
chr2	243199373	14257813	0.0586	0.4807
chr3	198022430	11096649	0.056	0.2764
chr4	191154276	10778339	0.0564	0.2933
chr5	180915260	10123466	0.056	0.2764
chr6	171115067	10298498	0.0602	0.3684
chr7	159138663	9682340	0.0608	0.6949

chr8	146364022	7424940	0.0507	0.5442
chr9	141213431	5993966	0.0424	0.3824
chr10	135534747	8244227	0.0608	0.4443
chr11	135006516	7034923	0.0521	0.3516
chr12	133851895	5763526	0.0431	0.2466
chr13	115169878	5474989	0.0475	0.2533
chr14	107349540	4432330	0.0413	0.2573
chr15	102531392	4823096	0.047	0.2529
chr16	90354753	3916679	0.0433	0.2784
chr17	81195210	4150693	0.0511	0.3068
chr18	78077248	4704826	0.0603	0.7395
chr19	59128983	3304872	0.0559	0.5674
chr20	63025520	2958468	0.0469	0.2631
chr21	48129895	1879662	0.0391	0.2514
chr22	51304566	1502235	0.0293	0.1973
chrMT	16571	25383	1.5318	1.5549
chrX	155270560	7323667	0.0472	0.2827
chrY	59373566	374715	0.0063	0.1711

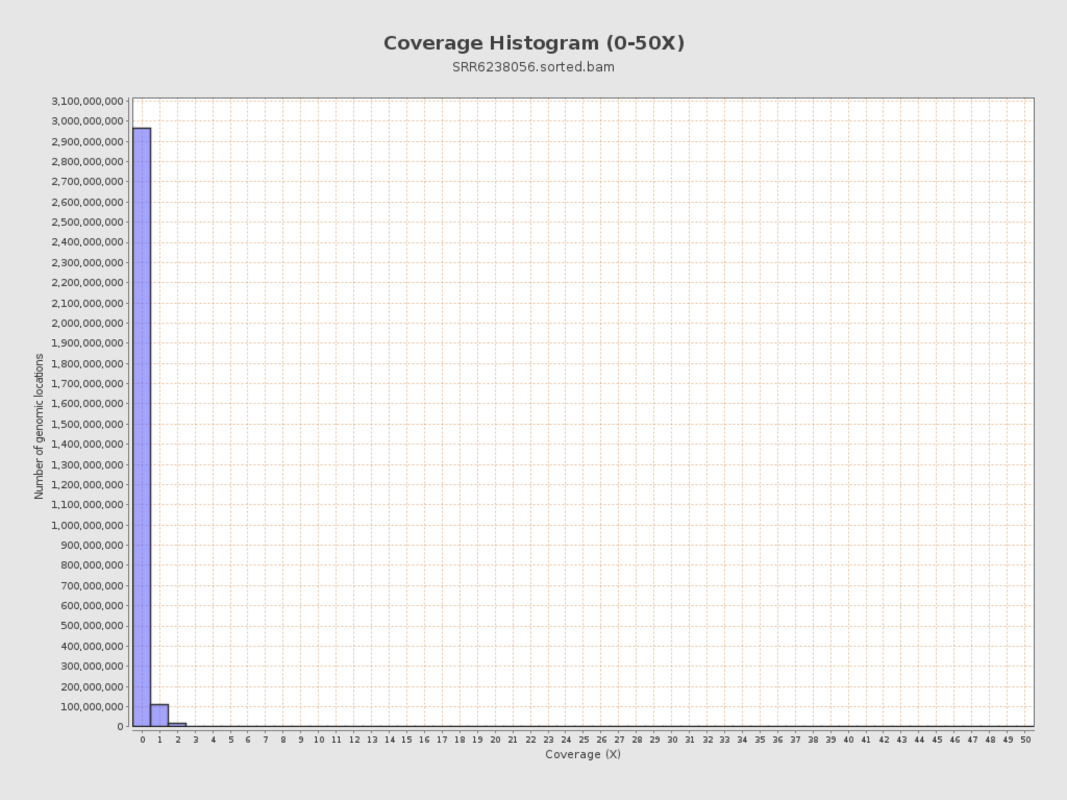
3. Results : Coverage across reference



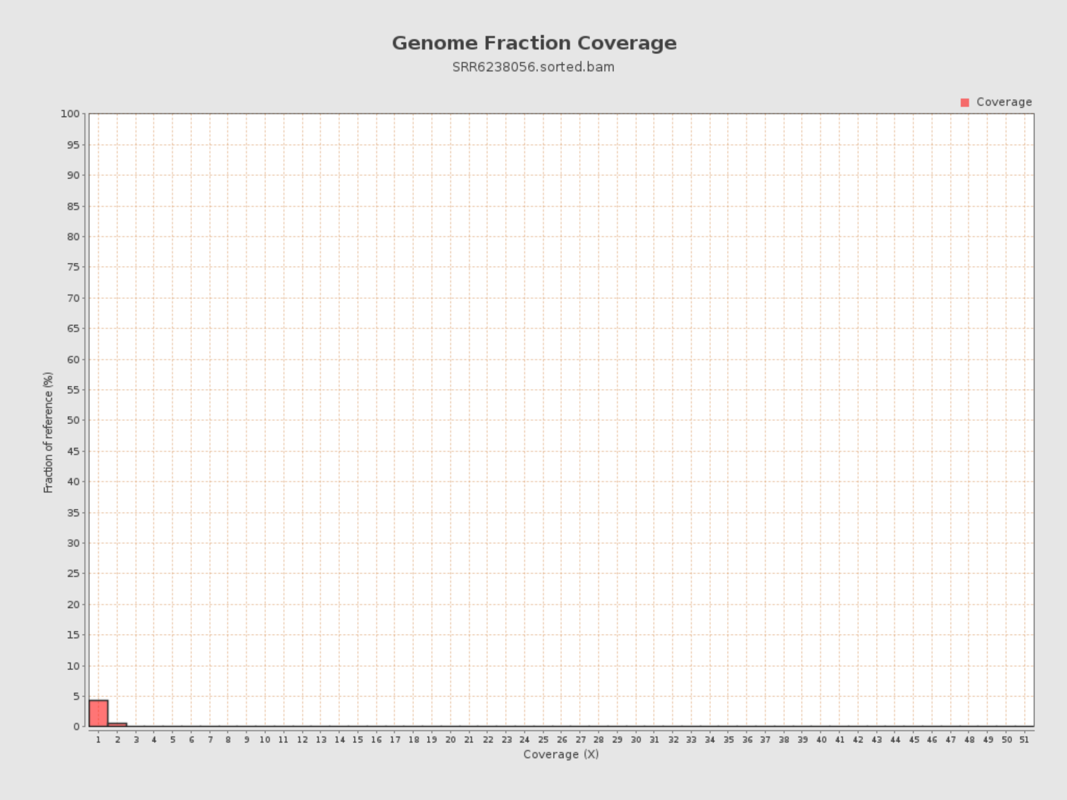
4. Results : Coverage Histogram



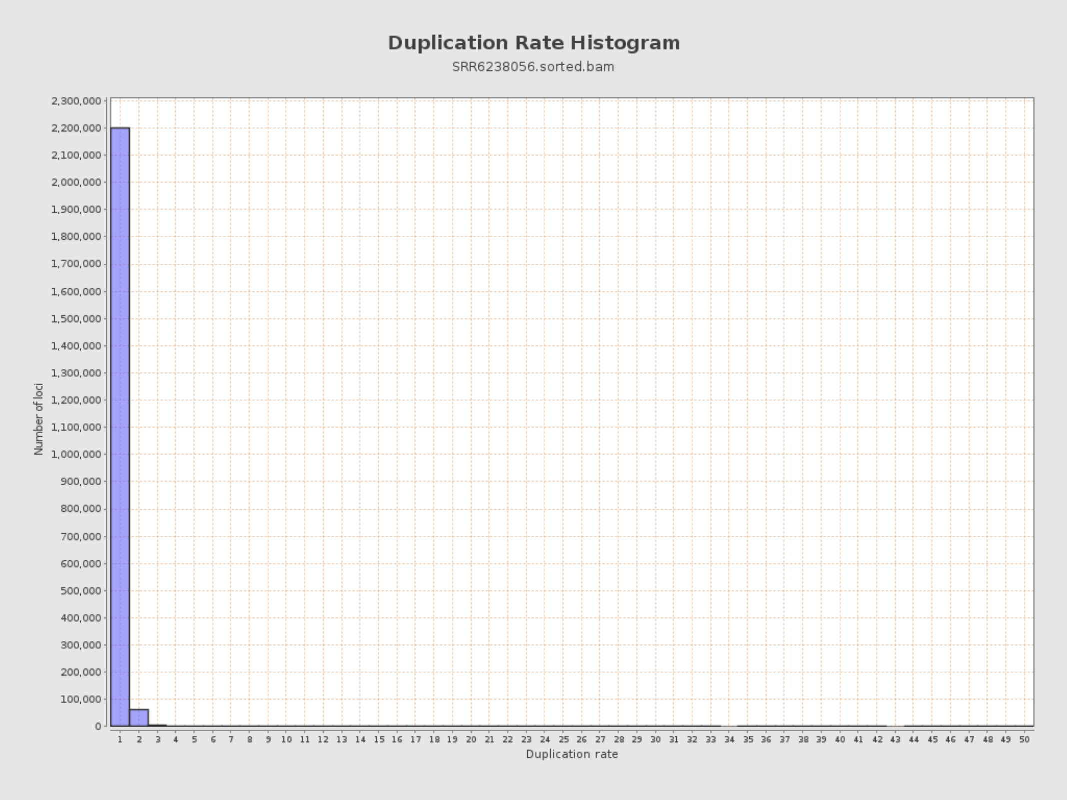
5. Results : Coverage Histogram (0-50X)



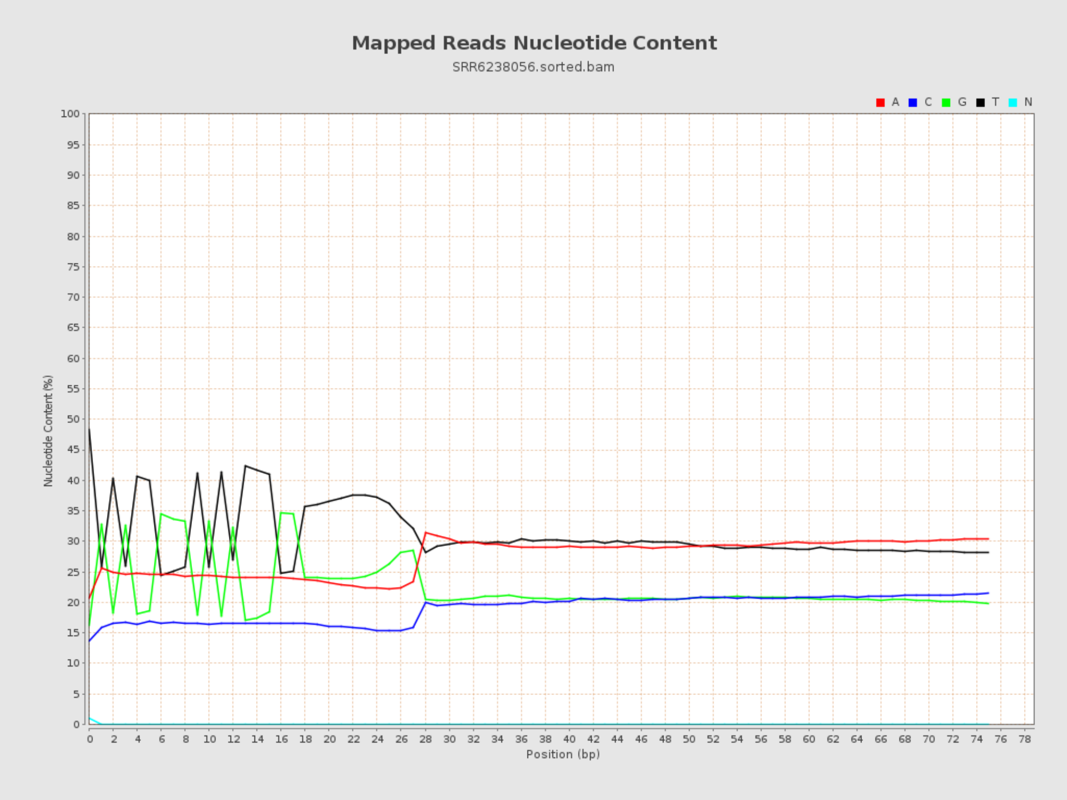
6. Results : Genome Fraction Coverage



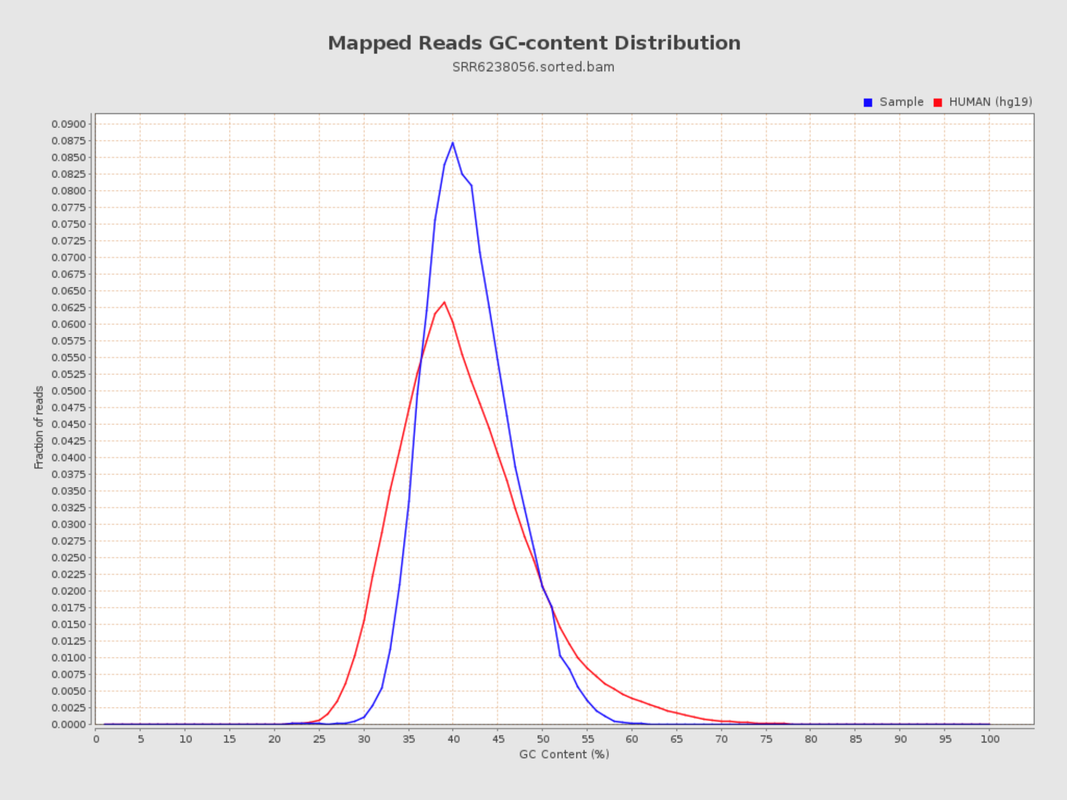
7. Results : Duplication Rate Histogram



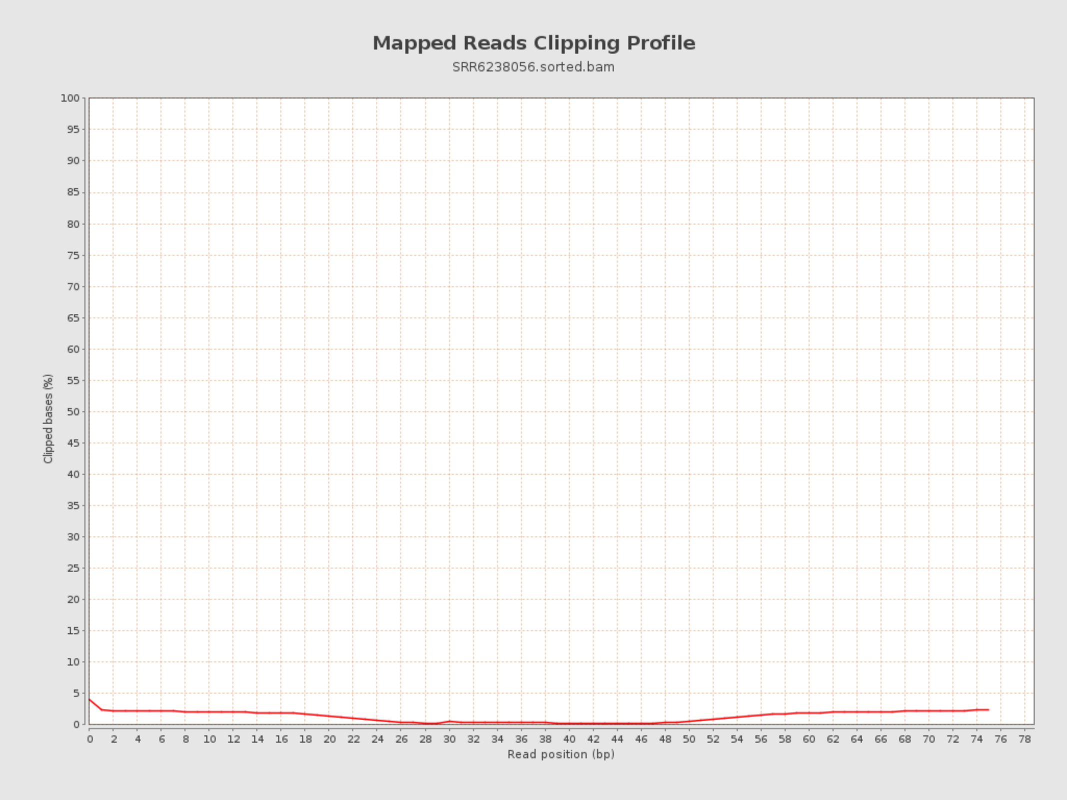
8. Results : Mapped Reads Nucleotide Content



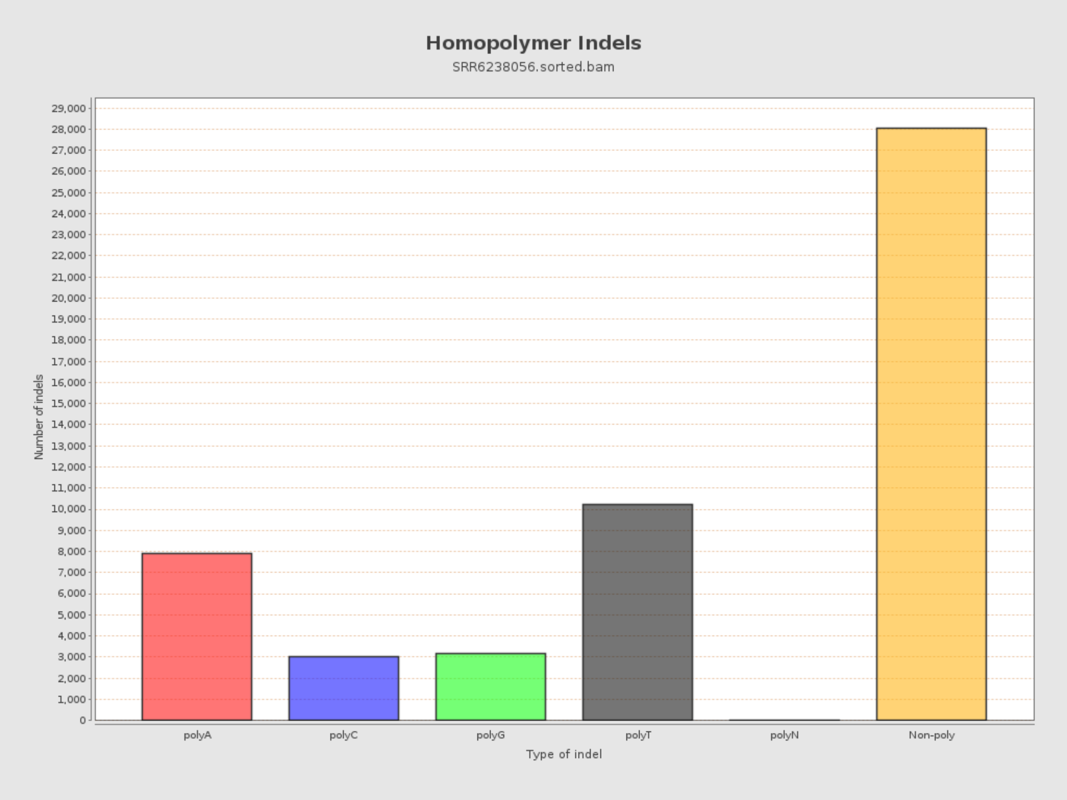
9. Results : Mapped Reads GC-content Distribution



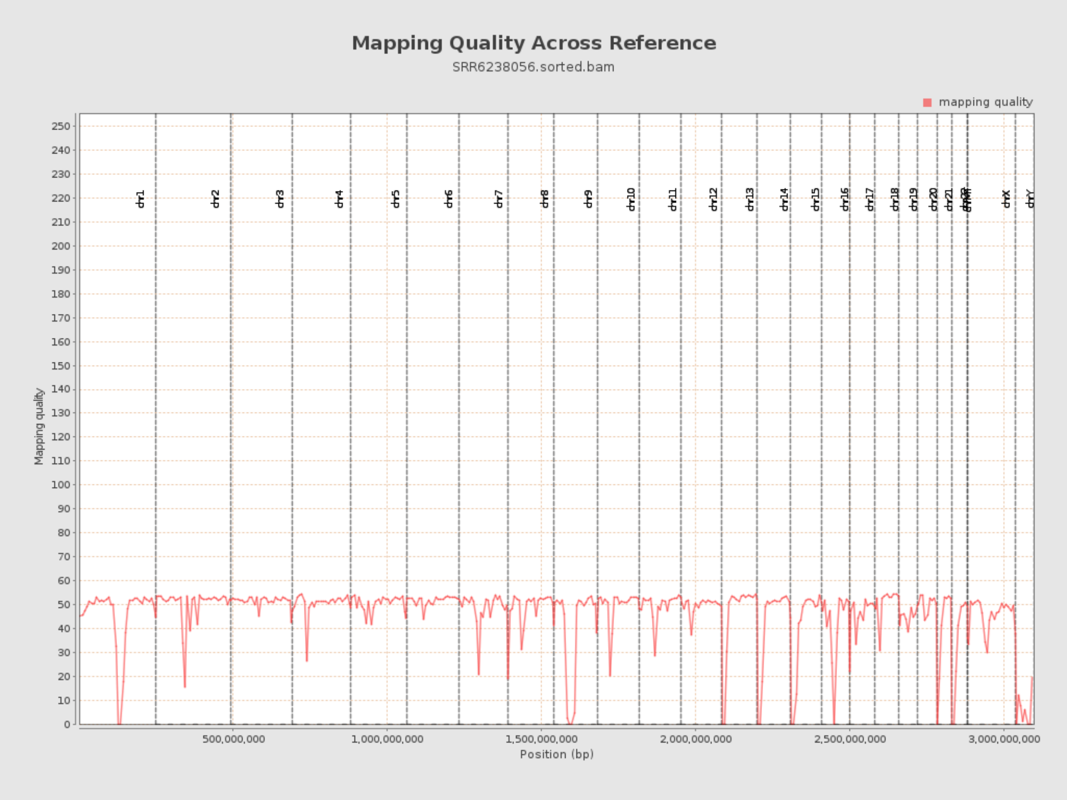
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram