

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 22:36:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231728.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_SRR6231728 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231728.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 22:36:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231728.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,285,229
Mapped reads	4,931,253 / 93.3%
Unmapped reads	353,976 / 6.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	41,229 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	554,072 / 10.48%
Duplication rate	4.77%
Clipped reads	1,835,248 / 34.72%

2.2. ACGT Content

Number/percentage of A's	88,959,730 / 26.38%
Number/percentage of C's	61,354,158 / 18.2%
Number/percentage of T's	96,877,975 / 28.73%
Number/percentage of G's	89,935,325 / 26.67%
Number/percentage of N's	73,668 / 0.02%
GC Percentage	44.87%

2.3. Coverage

Mean	0.109

Standard Deviation	39.0257
--------------------	---------

2.4. Mapping Quality

Mean Mapping Quality	44.87
----------------------	-------

2.5. Mismatches and indels

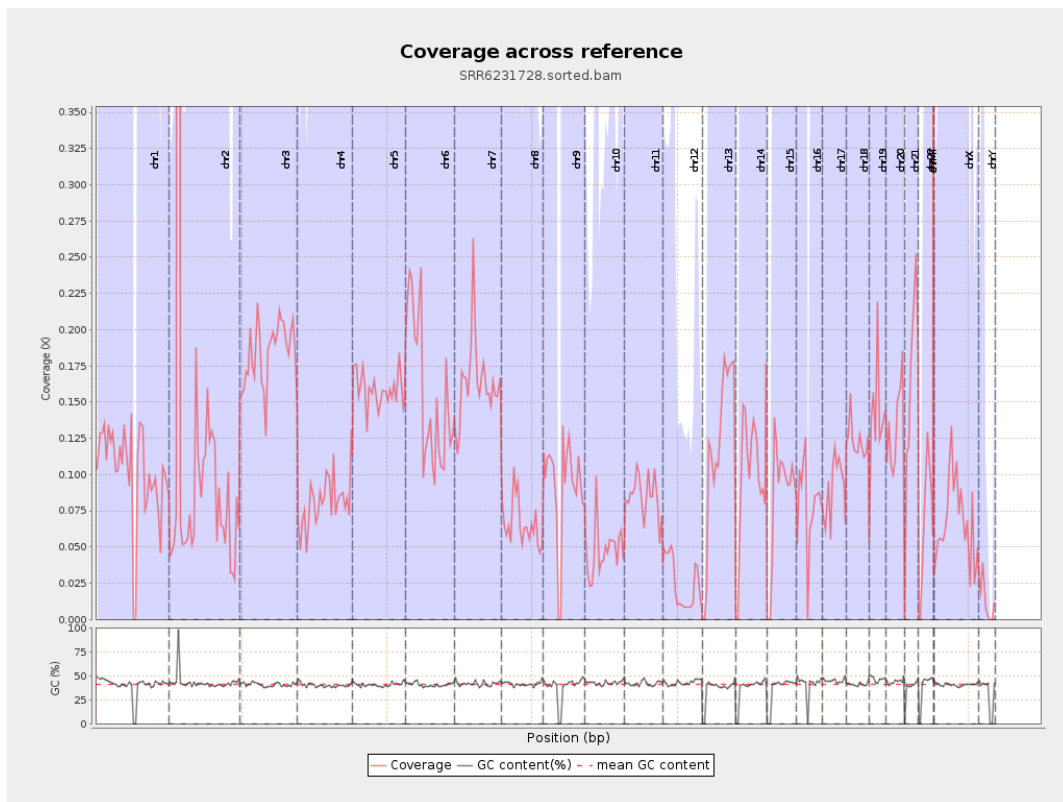
General error rate	0.66%
Mismatches	2,172,340
Insertions	23,392
Mapped reads with at least one insertion	0.47%
Deletions	77,727
Mapped reads with at least one deletion	1.56%
Homopolymer indels	46.43%

2.6. Chromosome stats

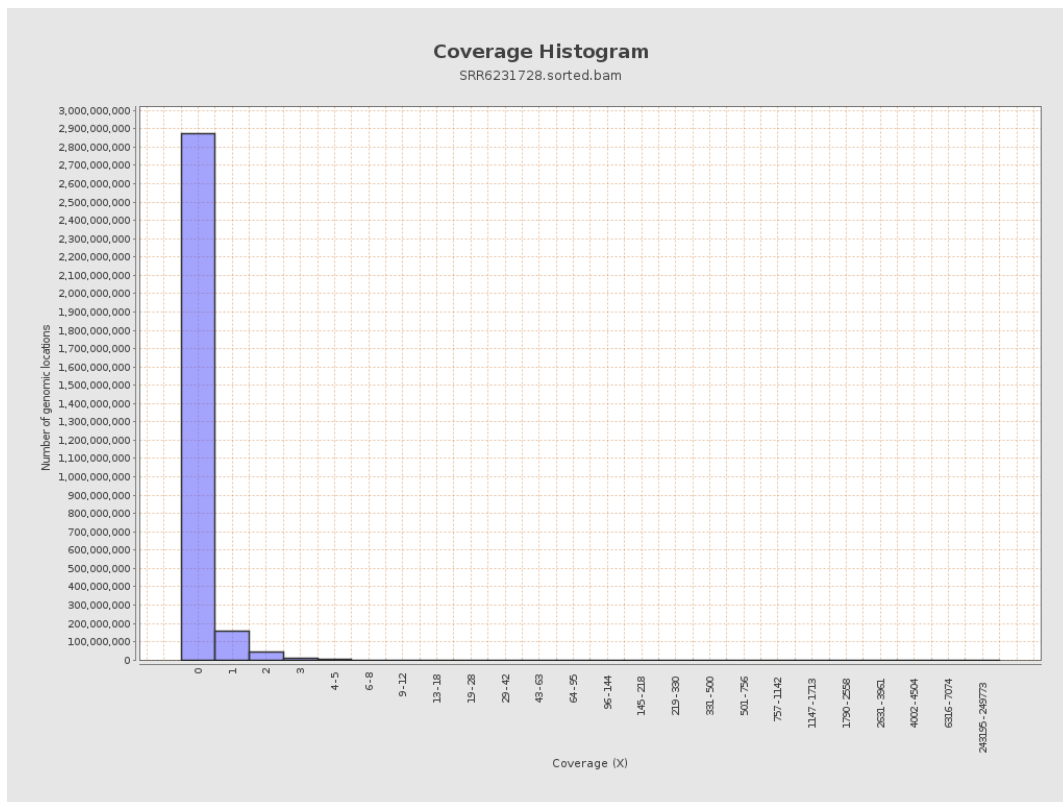
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	25272826	0.1014	1.3821
chr2	243199373	38754673	0.1594	139.205
chr3	198022430	36430987	0.184	0.5834
chr4	191154276	15399339	0.0806	0.4085
chr5	180915260	28613843	0.1582	0.5453
chr6	171115067	26837062	0.1568	0.7674
chr7	159138663	26227569	0.1648	1.7436

chr8	146364022	9667613	0.0661	0.8776
chr9	141213431	12949126	0.0917	0.786
chr10	135534747	6353669	0.0469	0.5552
chr11	135006516	11330507	0.0839	0.8039
chr12	133851895	3246033	0.0243	0.2524
chr13	115169878	13662682	0.1186	0.4656
chr14	107349540	10343922	0.0964	0.5725
chr15	102531392	8764577	0.0855	0.3918
chr16	90354753	7301706	0.0808	0.4682
chr17	81195210	7351952	0.0905	0.5145
chr18	78077248	9641871	0.1235	1.6367
chr19	59128983	8467040	0.1432	1.0203
chr20	63025520	8289808	0.1315	0.5267
chr21	48129895	7752832	0.1611	0.6072
chr22	51304566	3460095	0.0674	0.3474
chrMT	16571	12114	0.731	1.0893
chrX	155270560	10470578	0.0674	0.493
chrY	59373566	725752	0.0122	0.237

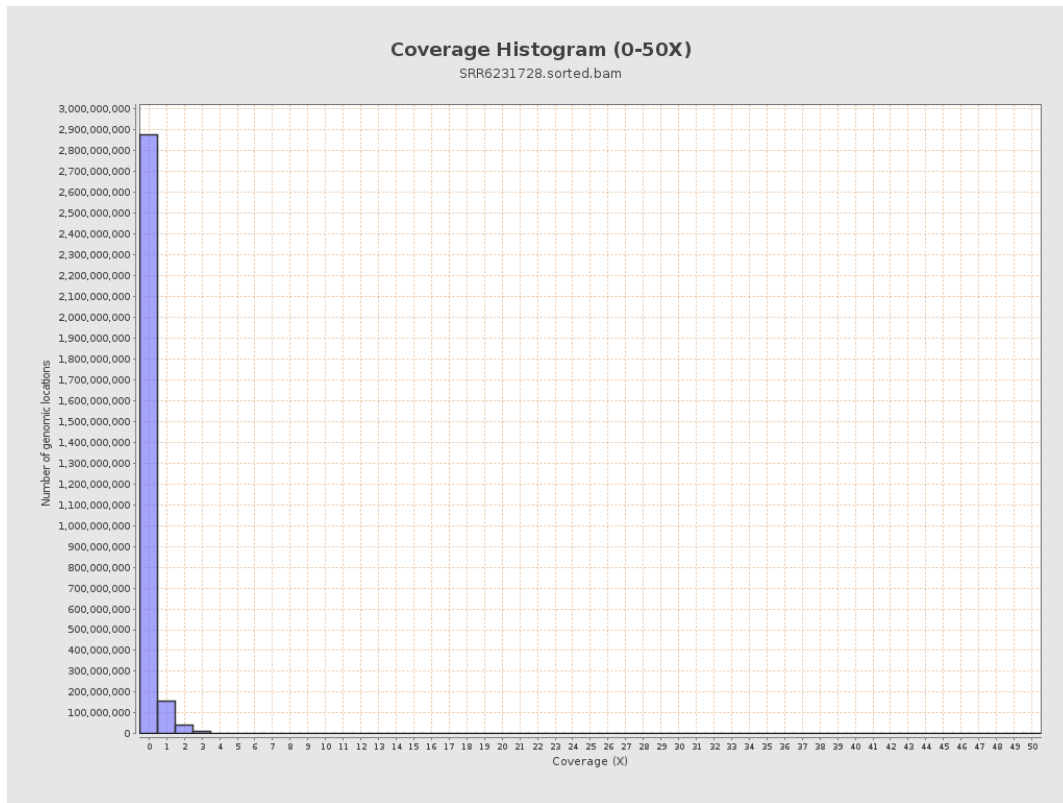
3. Results : Coverage across reference



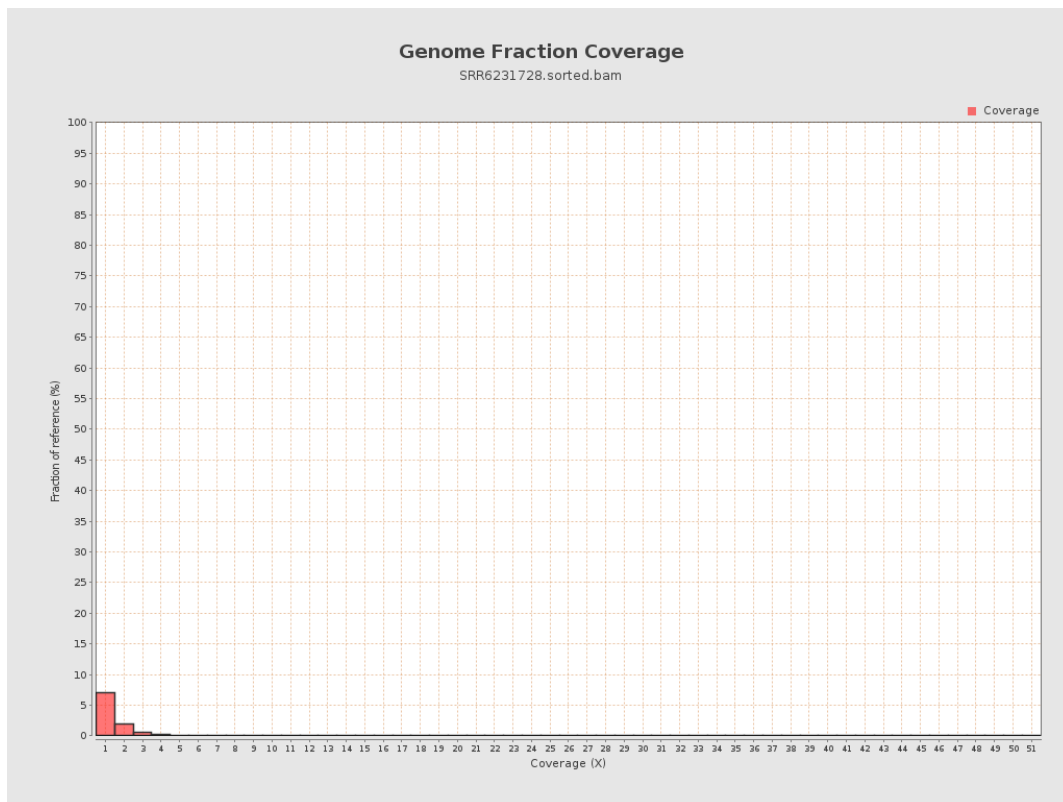
4. Results : Coverage Histogram



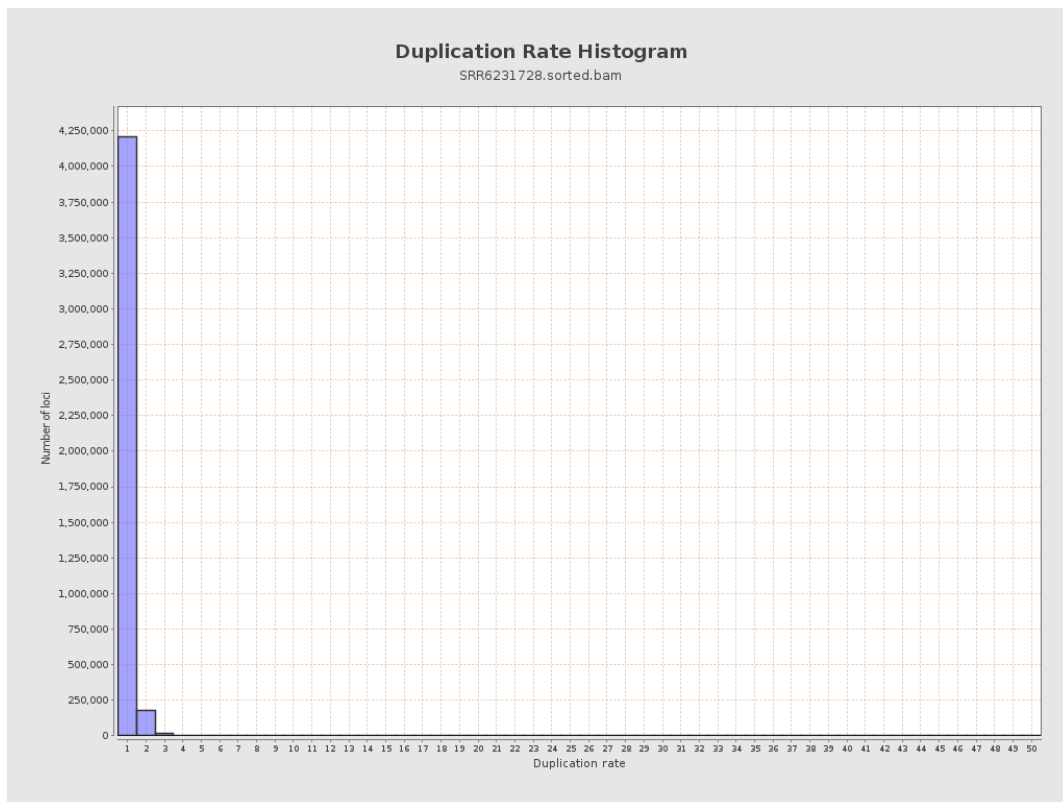
5. Results : Coverage Histogram (0-50X)



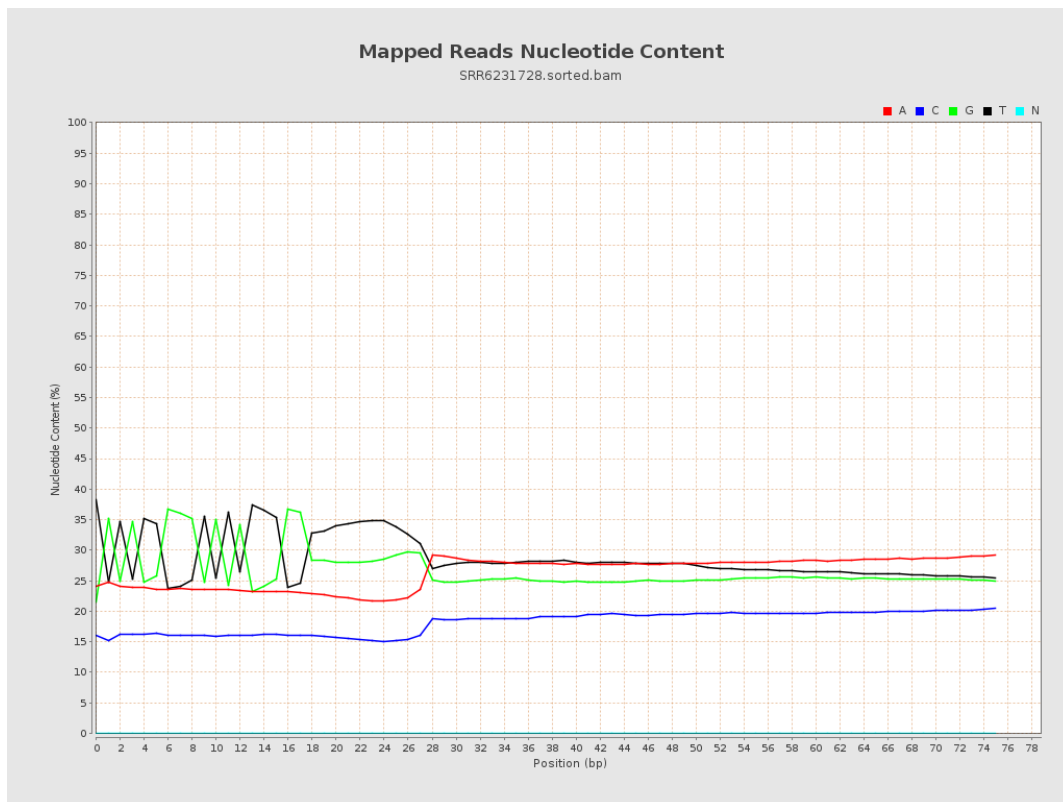
6. Results : Genome Fraction Coverage



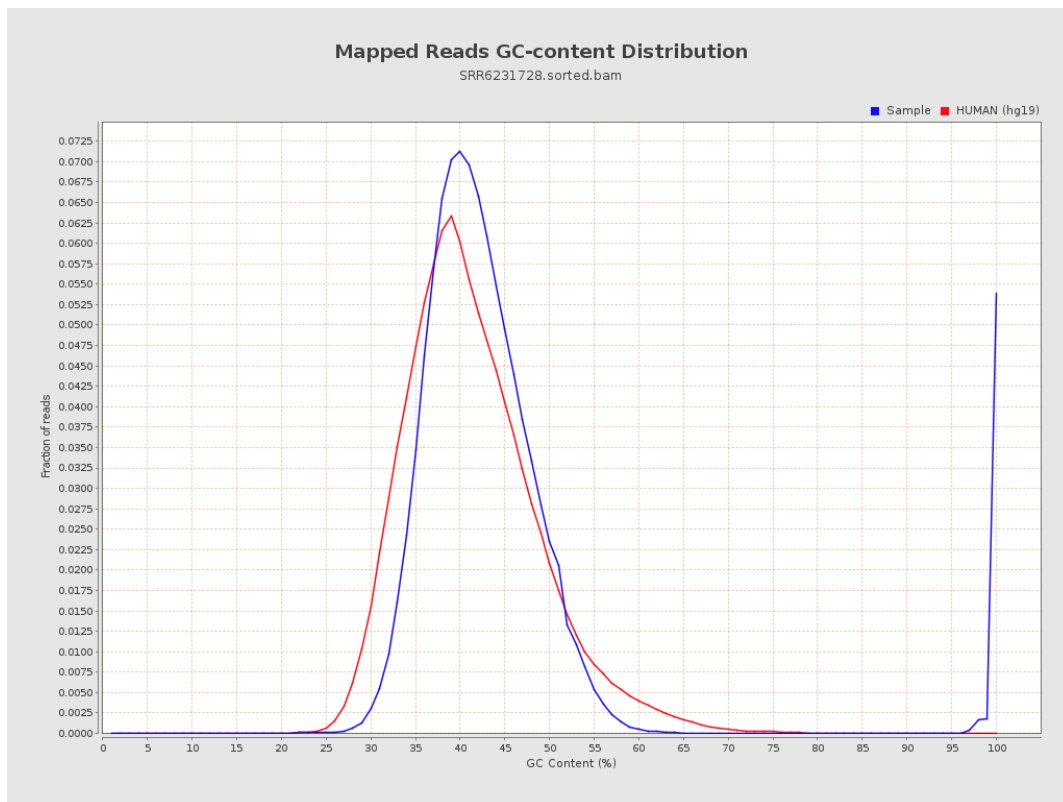
7. Results : Duplication Rate Histogram



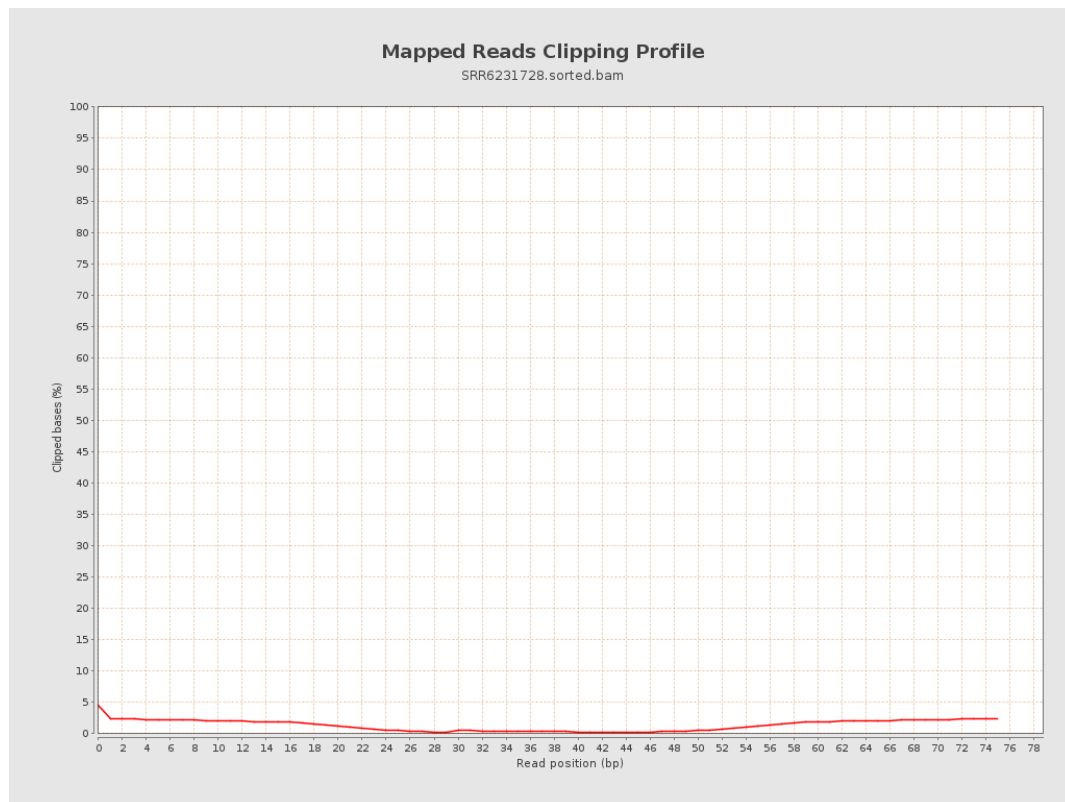
8. Results : Mapped Reads Nucleotide Content



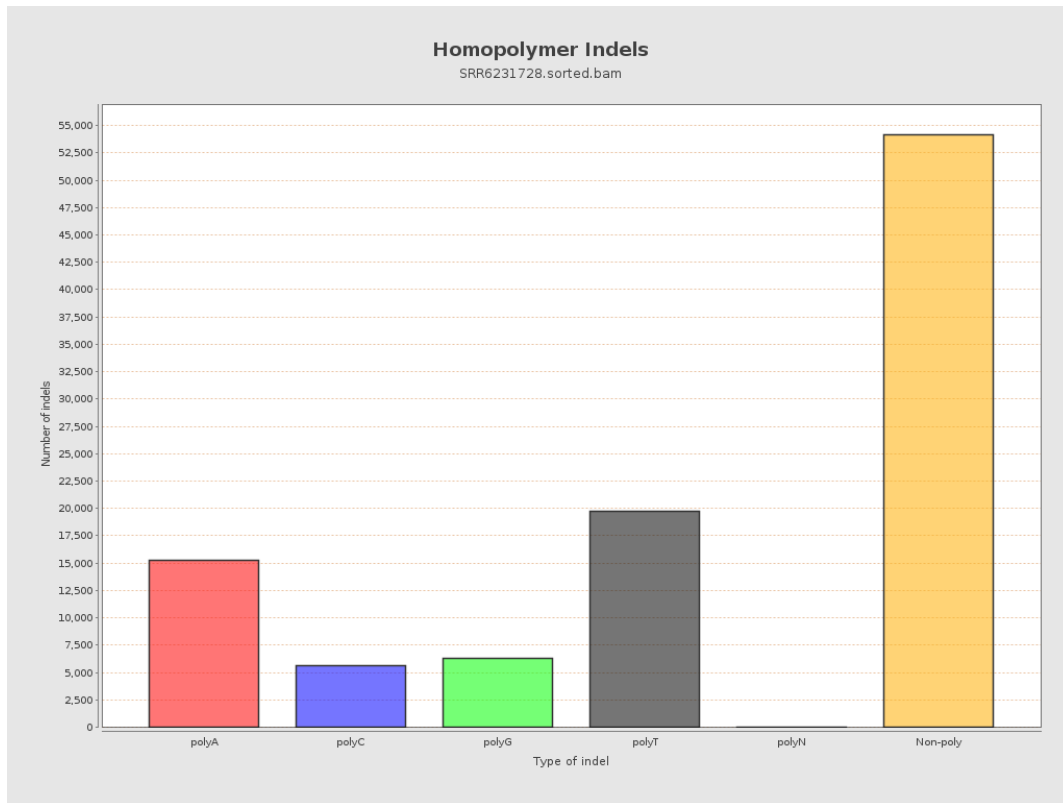
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

