

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:48:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081230.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_SRR3081230 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081230.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:48:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081230.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,155,947
Mapped reads	1,025,227 / 88.69%
Unmapped reads	130,720 / 11.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,056 / 1.13%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	33,251 / 2.88%
Duplication rate	2.87%
Clipped reads	545,000 / 47.15%

2.2. ACGT Content

Number/percentage of A's	19,203,522 / 28.77%
Number/percentage of C's	12,451,747 / 18.65%
Number/percentage of T's	20,949,140 / 31.38%
Number/percentage of G's	14,146,481 / 21.19%
Number/percentage of N's	4,551 / 0.01%
GC Percentage	39.84%

2.3. Coverage

Mean	0.0216

Standard Deviation	0.1841
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2.4. Mapping Quality

Mean Mapping Quality	45.72
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2.5. Mismatches and indels

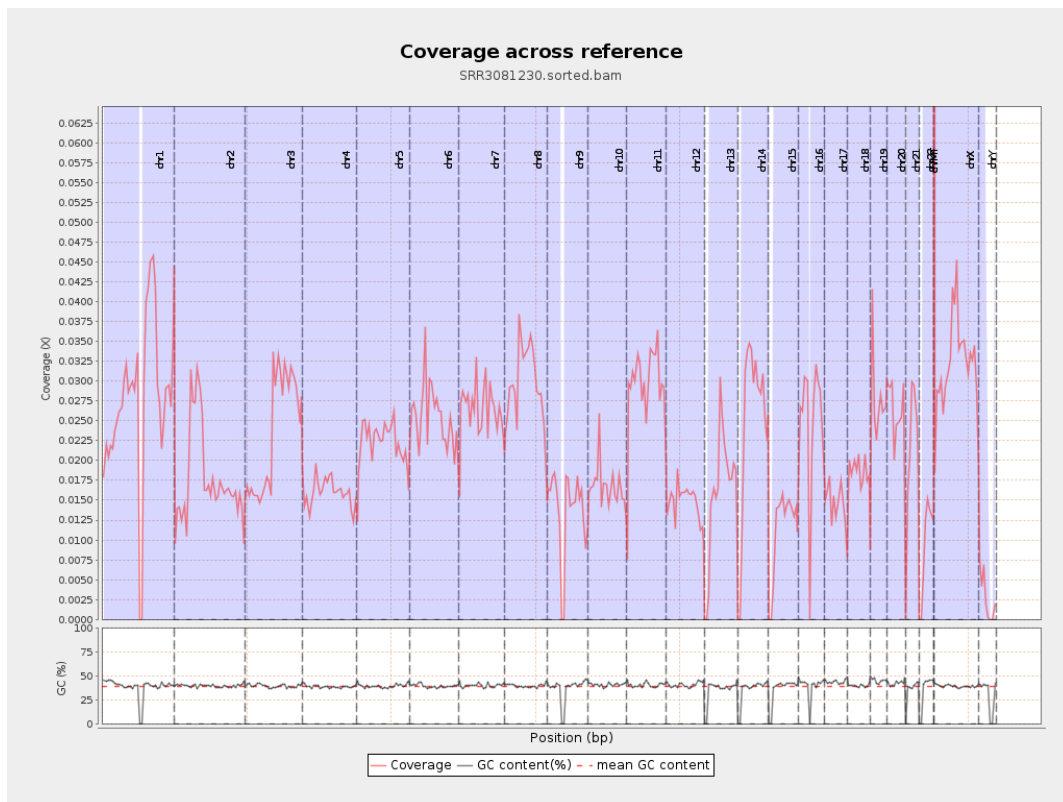
General error rate	0.86%
Mismatches	562,074
Insertions	5,111
Mapped reads with at least one insertion	0.49%
Deletions	15,370
Mapped reads with at least one deletion	1.49%
Homopolymer indels	48.76%

2.6. Chromosome stats

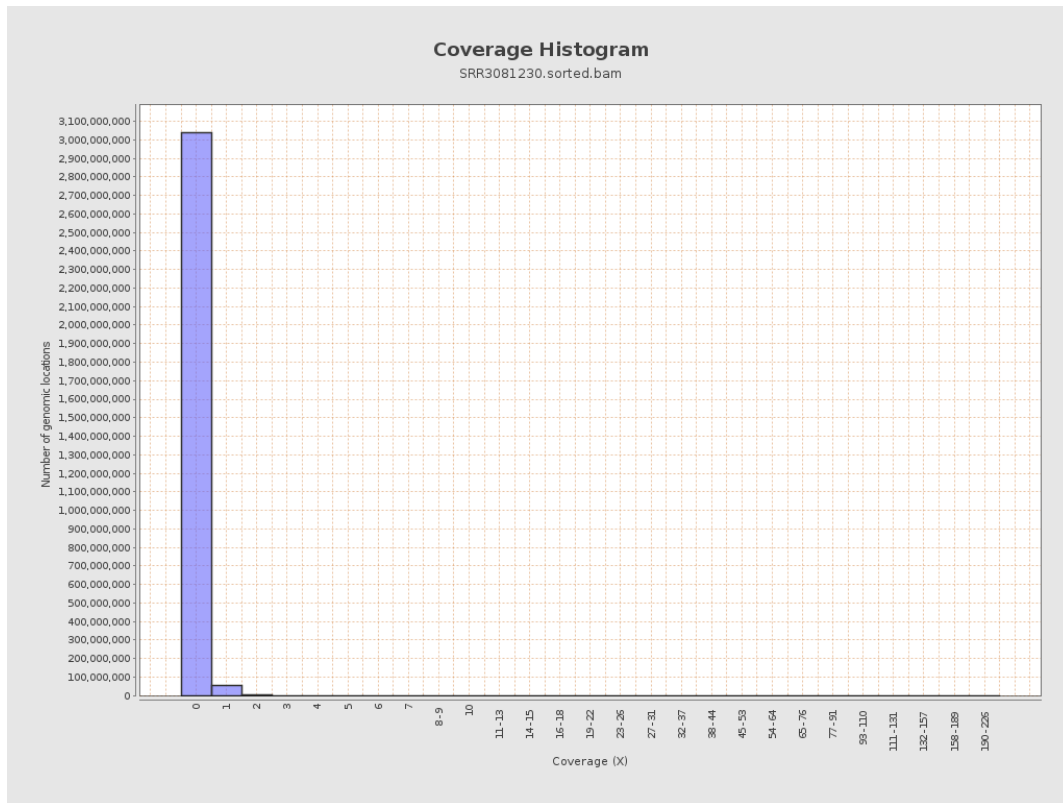
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6926617	0.0278	0.2571
chr2	243199373	4313551	0.0177	0.1881
chr3	198022430	4622997	0.0233	0.1696
chr4	191154276	3073330	0.0161	0.1416
chr5	180915260	4069597	0.0225	0.1658
chr6	171115067	4352352	0.0254	0.1893
chr7	159138663	4225842	0.0266	0.2172

chr8	146364022	4363778	0.0298	0.2262
chr9	141213431	1942353	0.0138	0.1433
chr10	135534747	2267515	0.0167	0.1701
chr11	135006516	4065547	0.0301	0.224
chr12	133851895	1975794	0.0148	0.1353
chr13	115169878	1866524	0.0162	0.1408
chr14	107349540	2691254	0.0251	0.177
chr15	102531392	1165153	0.0114	0.1199
chr16	90354753	2214202	0.0245	0.1751
chr17	81195210	1185439	0.0146	0.1419
chr18	78077248	1460511	0.0187	0.1894
chr19	59128983	1611543	0.0273	0.2222
chr20	63025520	1638410	0.026	0.1796
chr21	48129895	1024137	0.0213	0.1644
chr22	51304566	492246	0.0096	0.1076
chrMT	16571	34599	2.0879	2.1529
chrX	155270560	5039196	0.0325	0.2051
chrY	59373566	157915	0.0027	0.0599

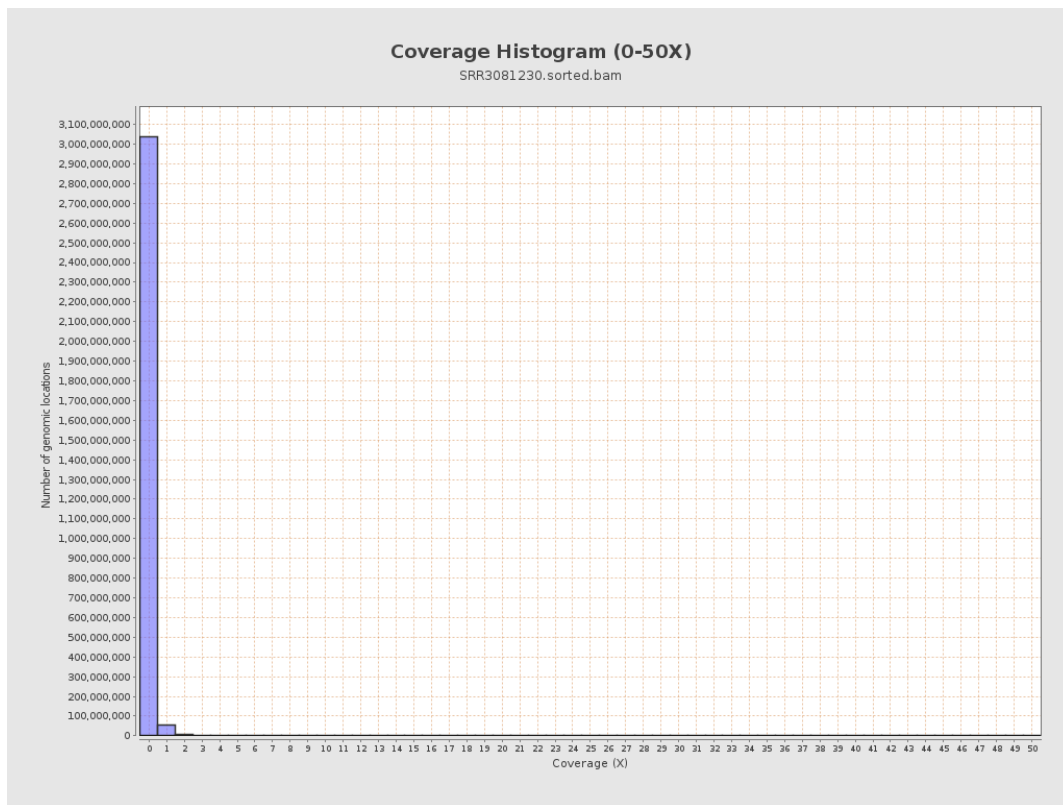
3. Results : Coverage across reference



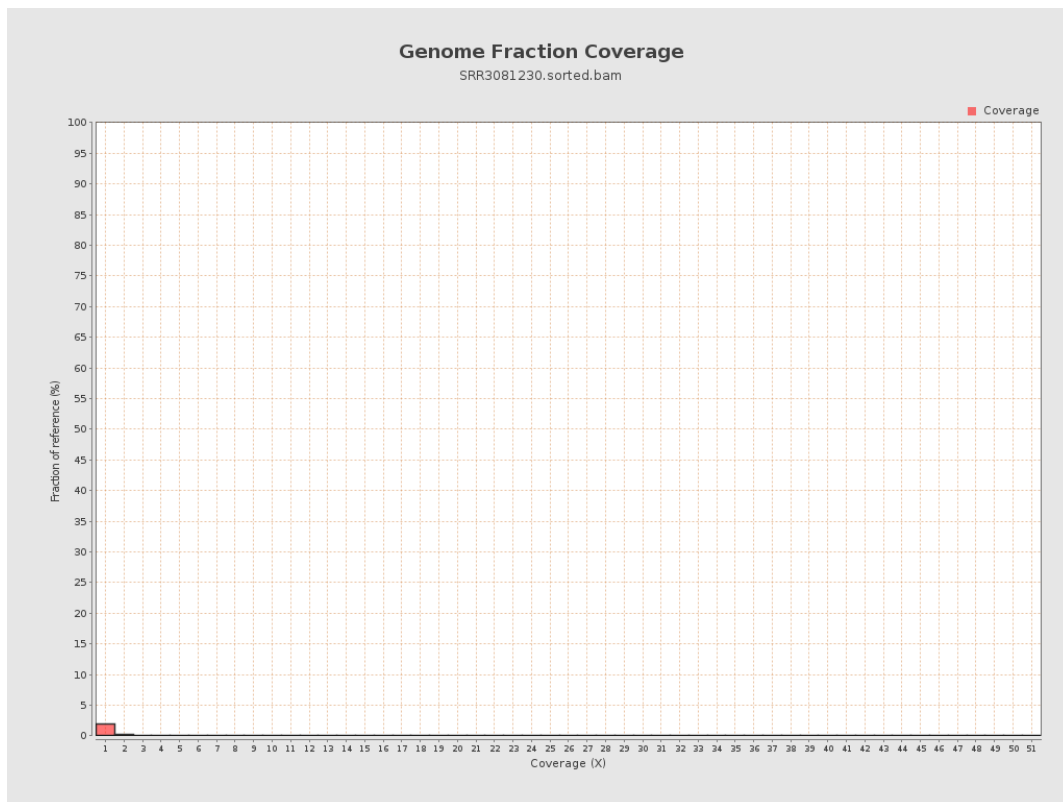
4. Results : Coverage Histogram



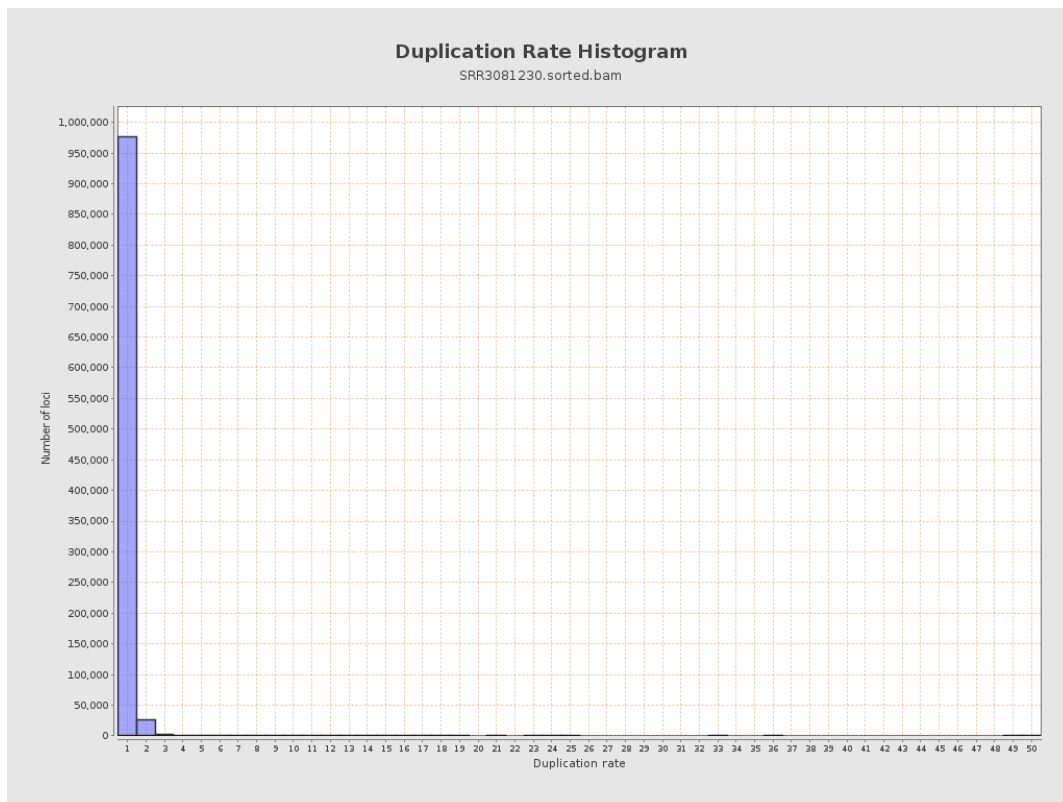
5. Results : Coverage Histogram (0-50X)



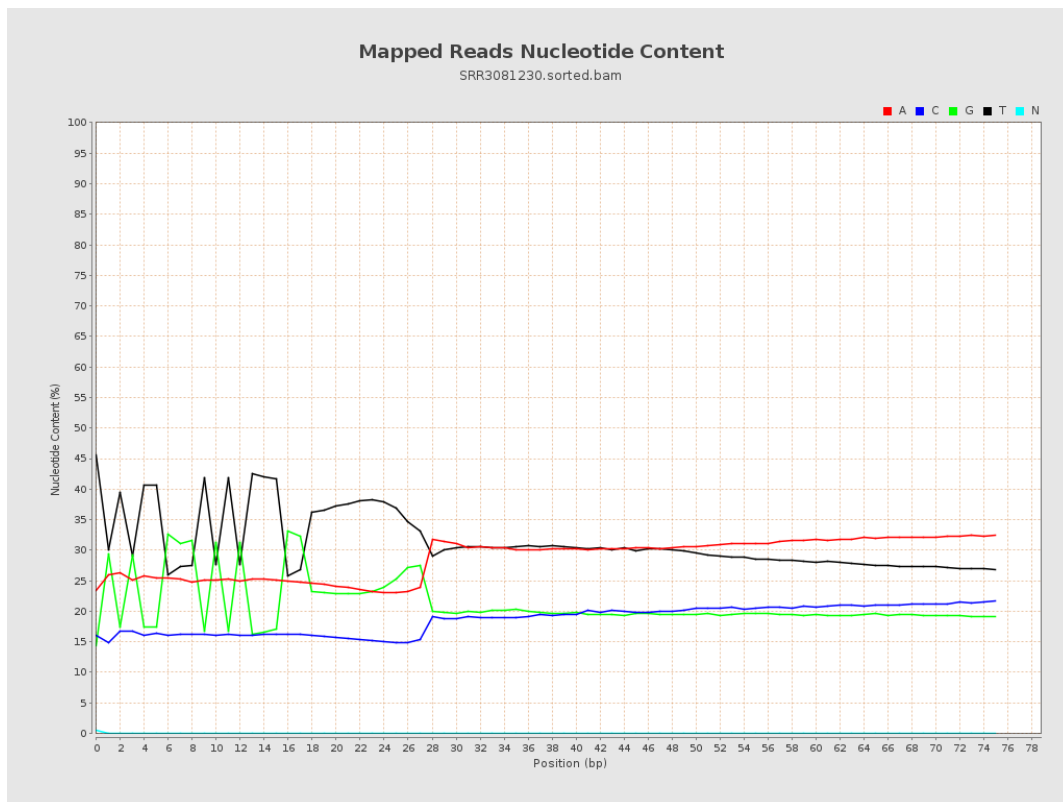
6. Results : Genome Fraction Coverage



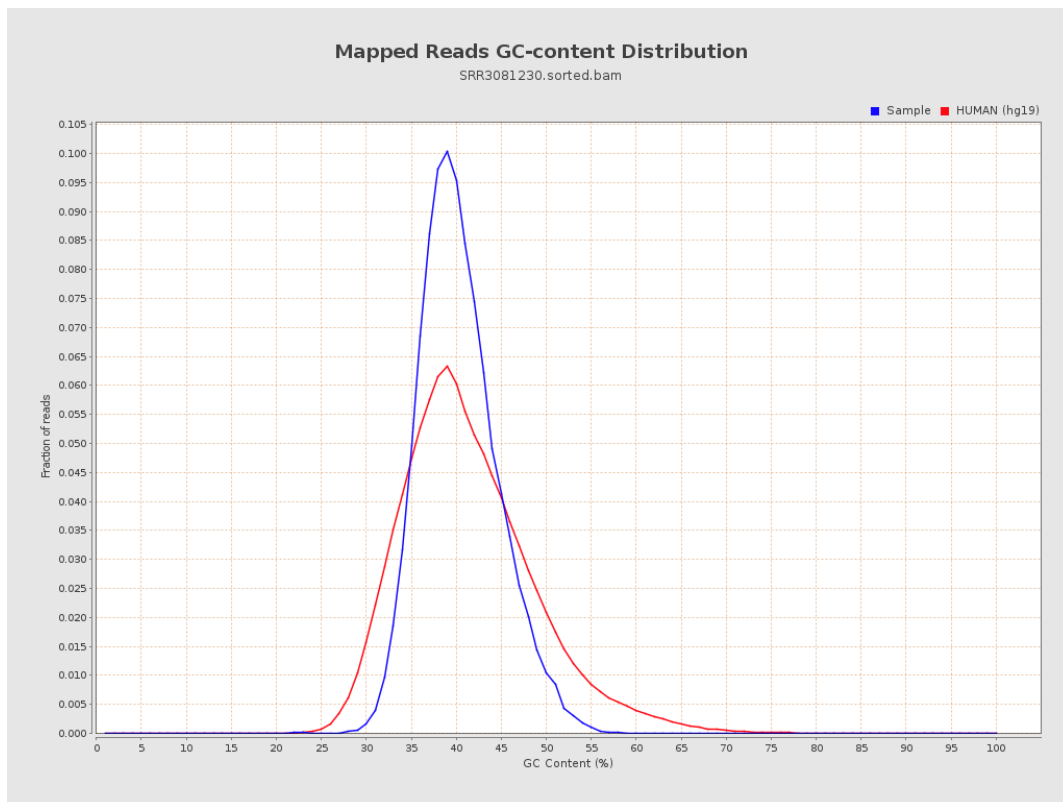
7. Results : Duplication Rate Histogram



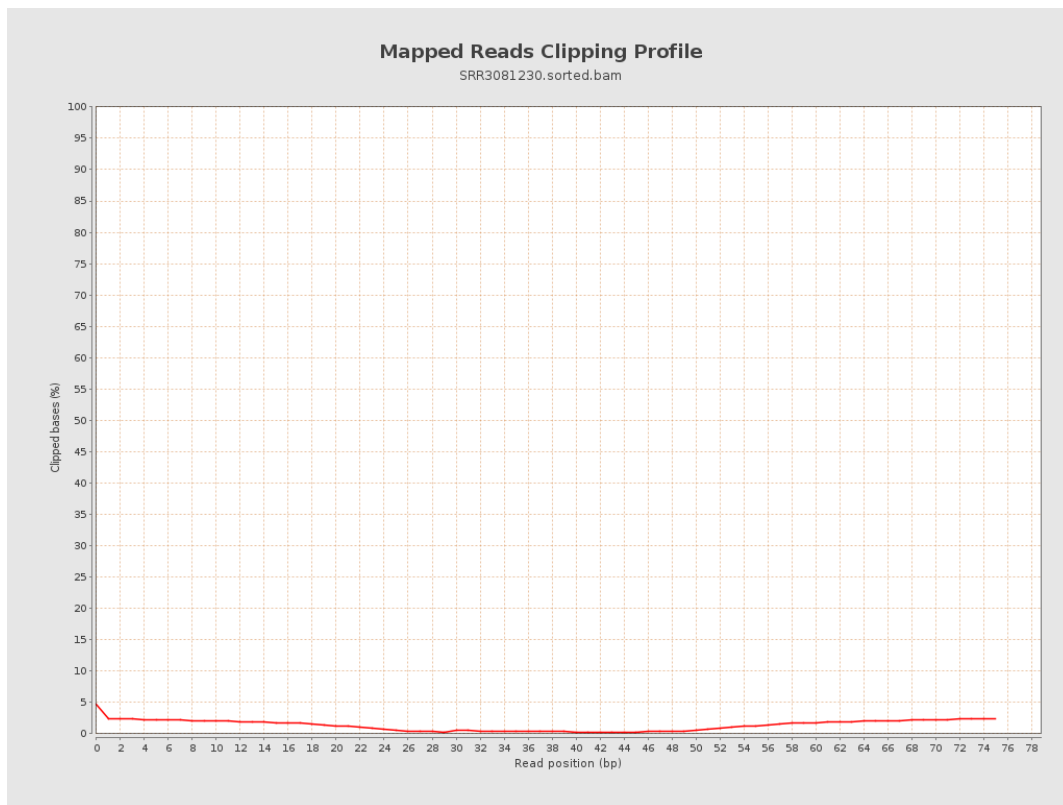
8. Results : Mapped Reads Nucleotide Content



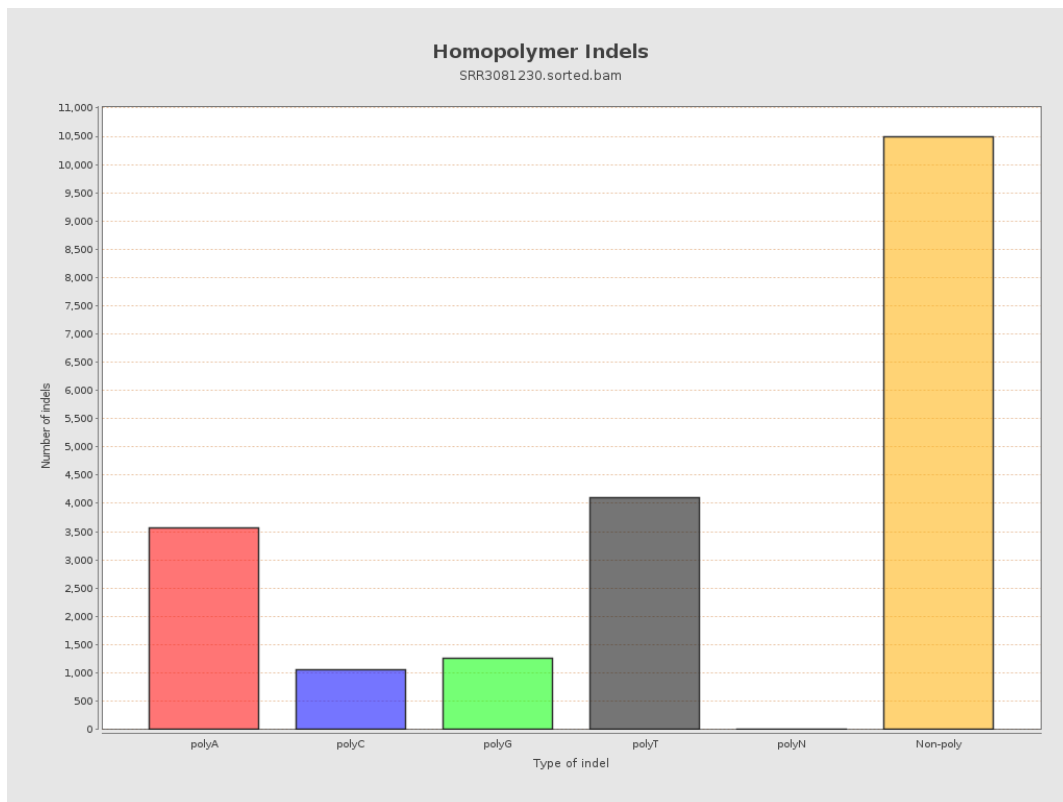
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

