

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 20:38:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230381.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_SRR6230381 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230381.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 20:38:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230381.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,492,068
Mapped reads	1,889,955 / 75.84%
Unmapped reads	602,113 / 24.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,378 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	126,181 / 5.06%
Duplication rate	5.63%
Clipped reads	908,317 / 36.45%

2.2. ACGT Content

Number/percentage of A's	33,821,543 / 27.27%
Number/percentage of C's	21,453,701 / 17.3%
Number/percentage of T's	41,826,920 / 33.73%
Number/percentage of G's	26,680,541 / 21.51%
Number/percentage of N's	236,803 / 0.19%
GC Percentage	38.81%

2.3. Coverage

Mean	0.0401

Standard Deviation	0.3404
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2.4. Mapping Quality

Mean Mapping Quality	44.25
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2.5. Mismatches and indels

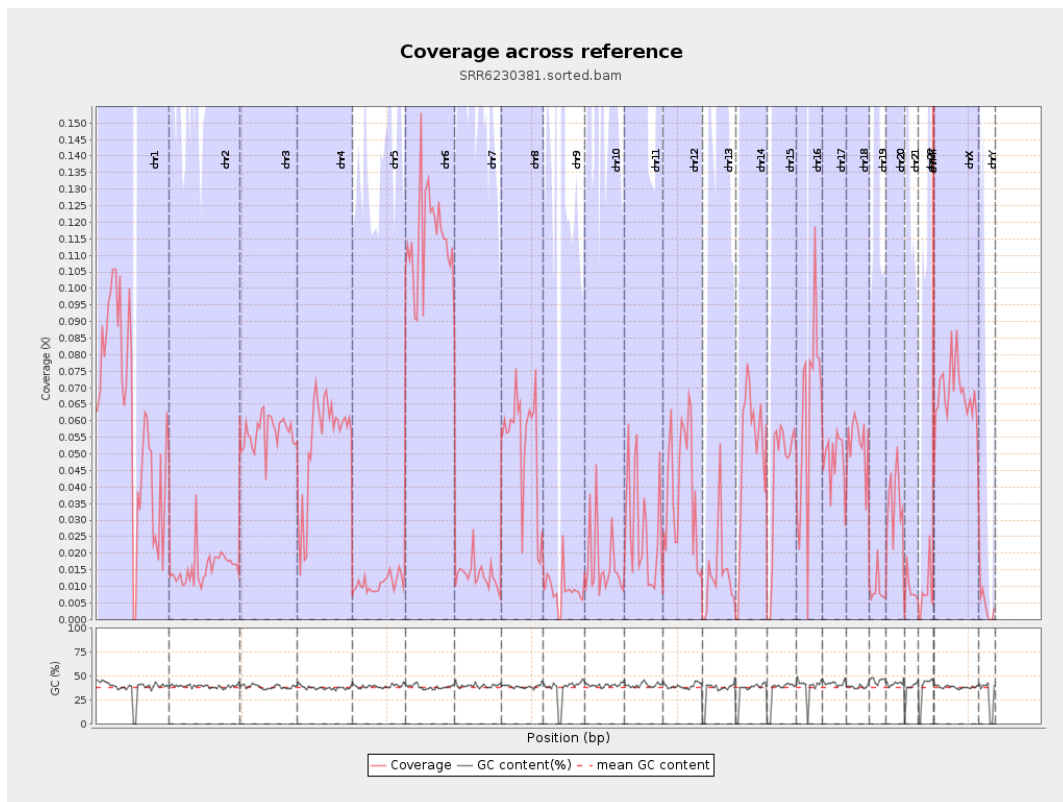
General error rate	1.06%
Mismatches	1,298,744
Insertions	10,305
Mapped reads with at least one insertion	0.54%
Deletions	32,043
Mapped reads with at least one deletion	1.68%
Homopolymer indels	48.52%

2.6. Chromosome stats

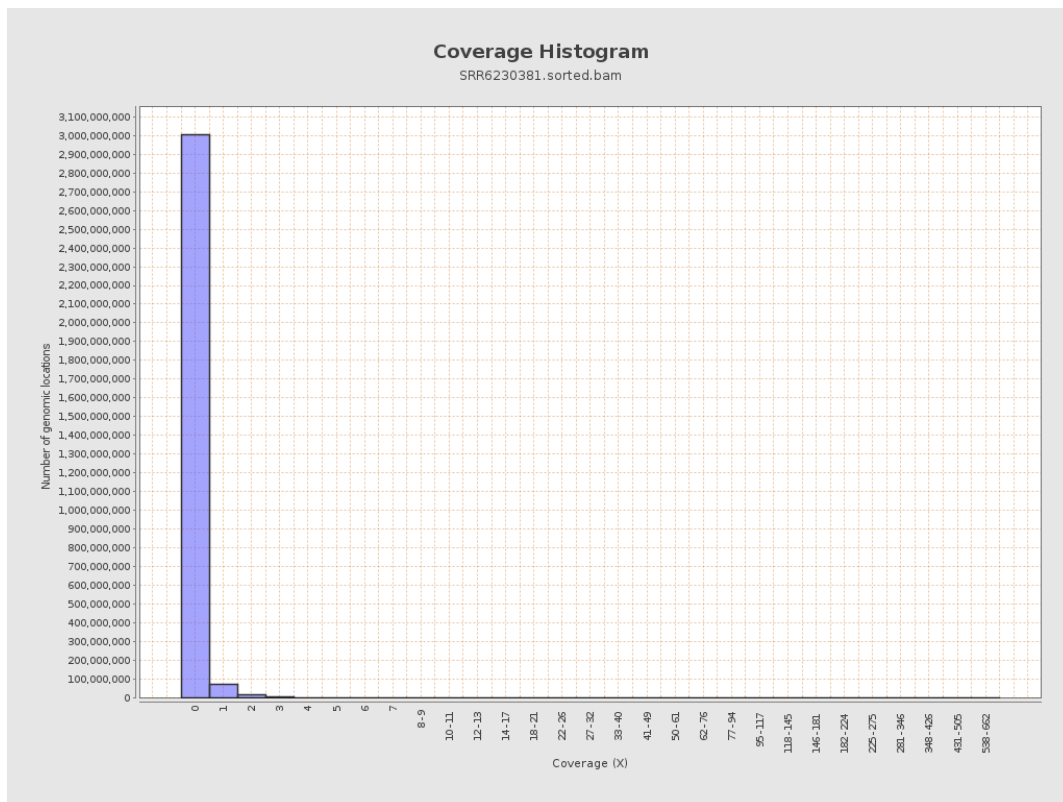
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15187911	0.0609	0.547
chr2	243199373	3813245	0.0157	0.2913
chr3	198022430	11204595	0.0566	0.3028
chr4	191154276	10237070	0.0536	0.2937
chr5	180915260	1966608	0.0109	0.1265
chr6	171115067	19689192	0.1151	0.5908
chr7	159138663	2146446	0.0135	0.2093

chr8	146364022	7770880	0.0531	0.4918
chr9	141213431	1255487	0.0089	0.212
chr10	135534747	2228047	0.0164	0.34
chr11	135006516	3584233	0.0265	0.2396
chr12	133851895	5252143	0.0392	0.2539
chr13	115169878	1629057	0.0141	0.1478
chr14	107349540	5370615	0.05	0.2882
chr15	102531392	4446742	0.0434	0.2624
chr16	90354753	5733828	0.0635	0.3346
chr17	81195210	3891102	0.0479	0.2828
chr18	78077248	4157452	0.0532	0.4384
chr19	59128983	544453	0.0092	0.3473
chr20	63025520	2213863	0.0351	0.2377
chr21	48129895	433750	0.009	0.1198
chr22	51304566	427827	0.0083	0.1085
chrMT	16571	56542	3.4121	2.7739
chrX	155270560	10546772	0.0679	0.361
chrY	59373566	283085	0.0048	0.0899

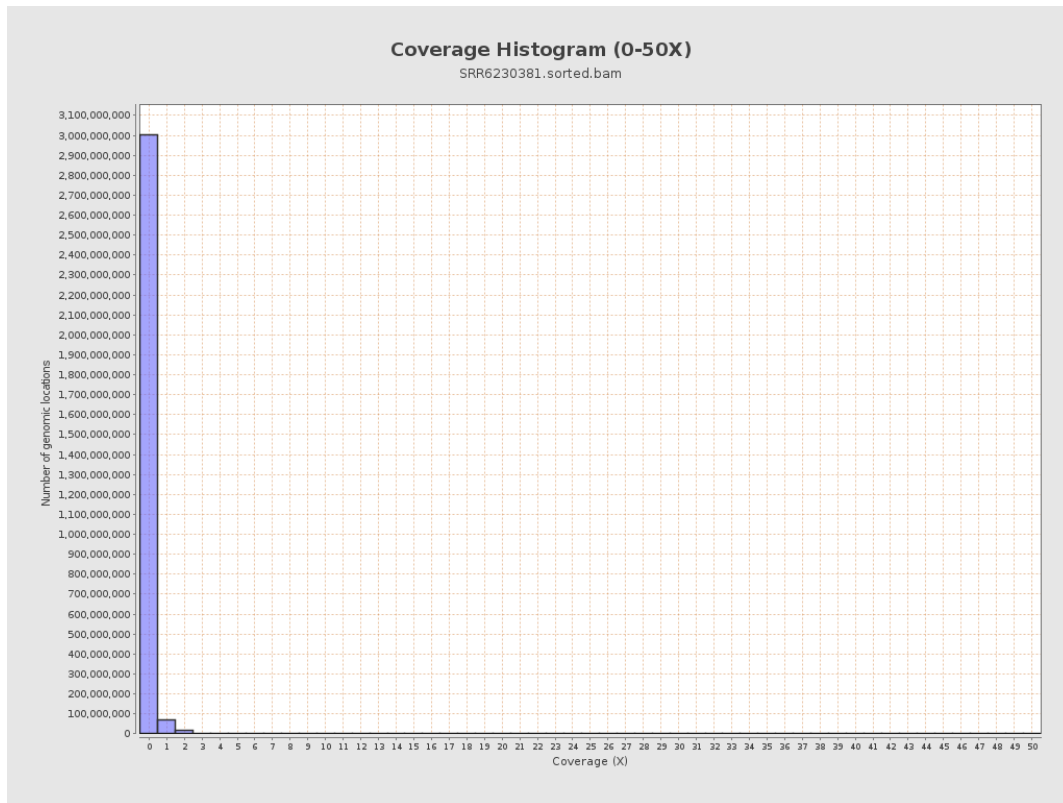
3. Results : Coverage across reference



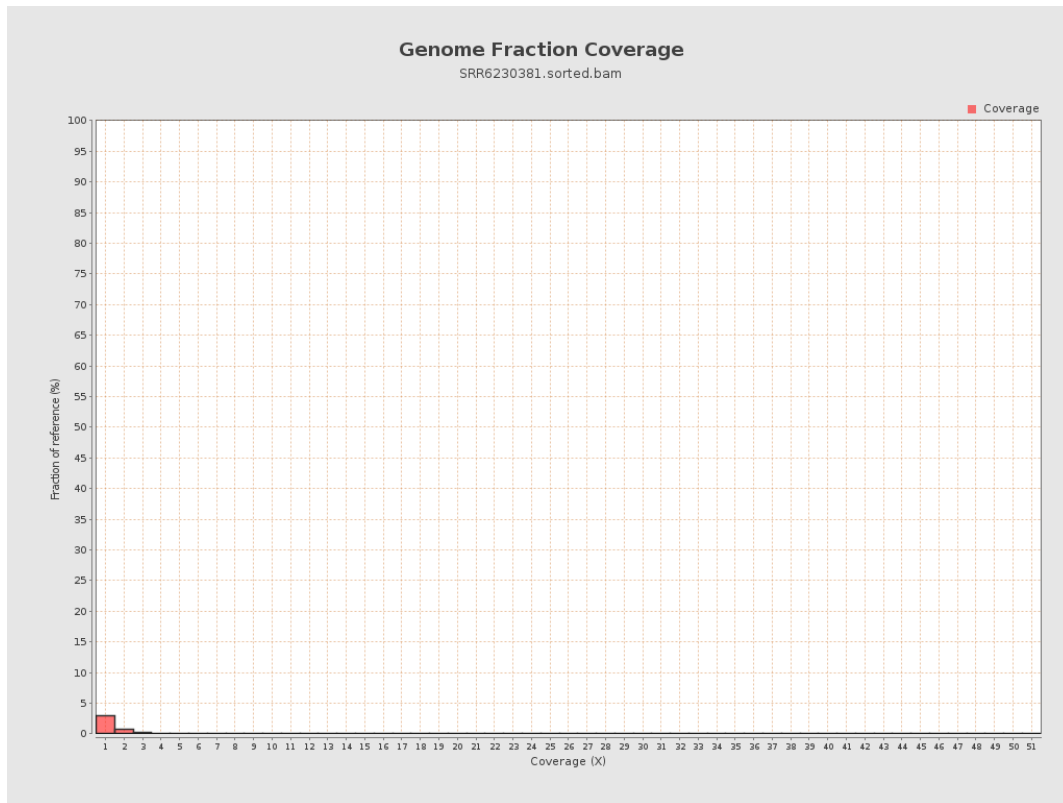
4. Results : Coverage Histogram



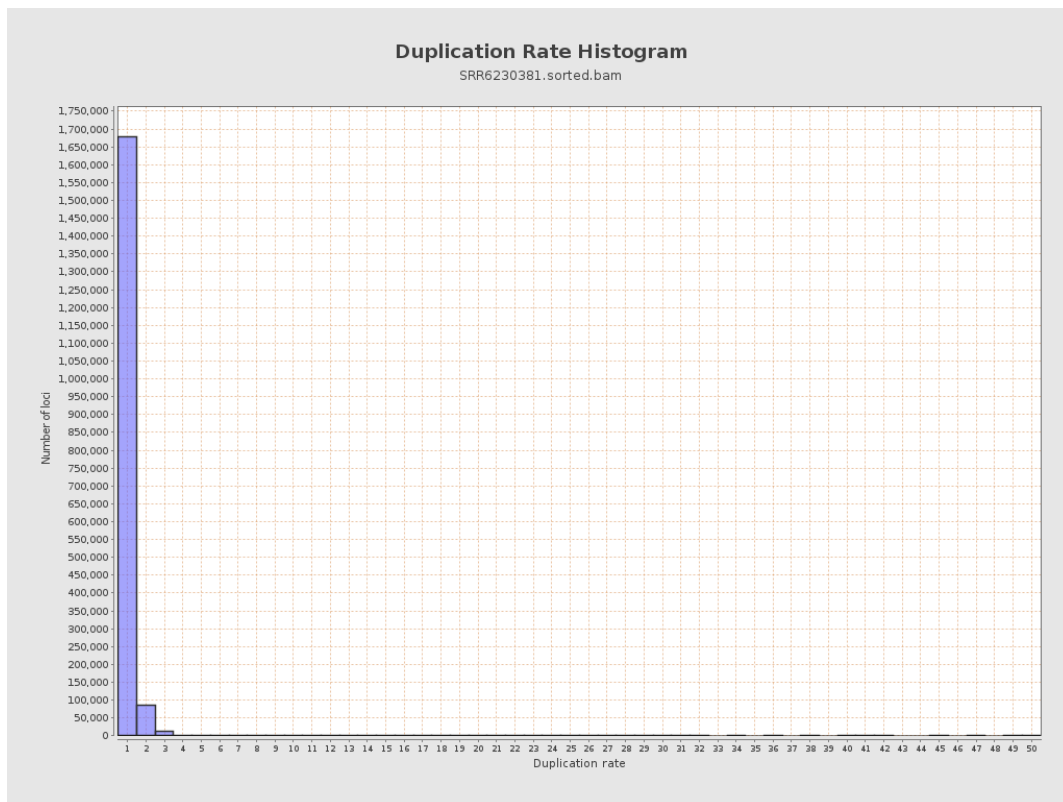
5. Results : Coverage Histogram (0-50X)



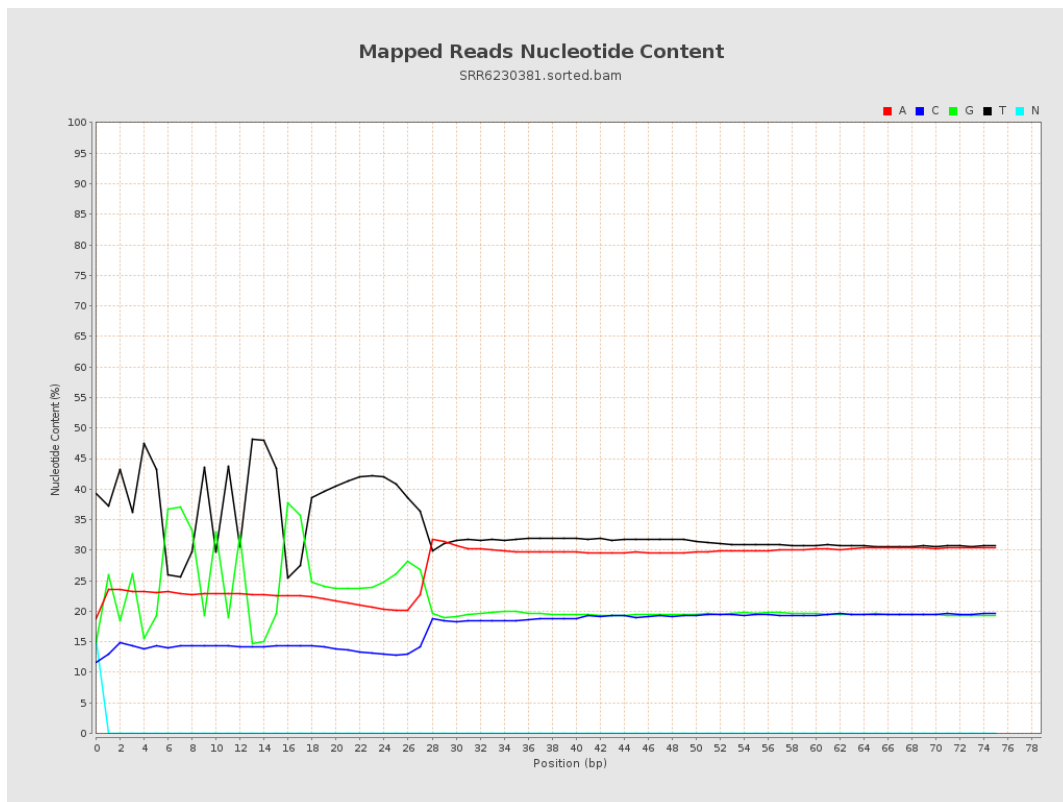
6. Results : Genome Fraction Coverage



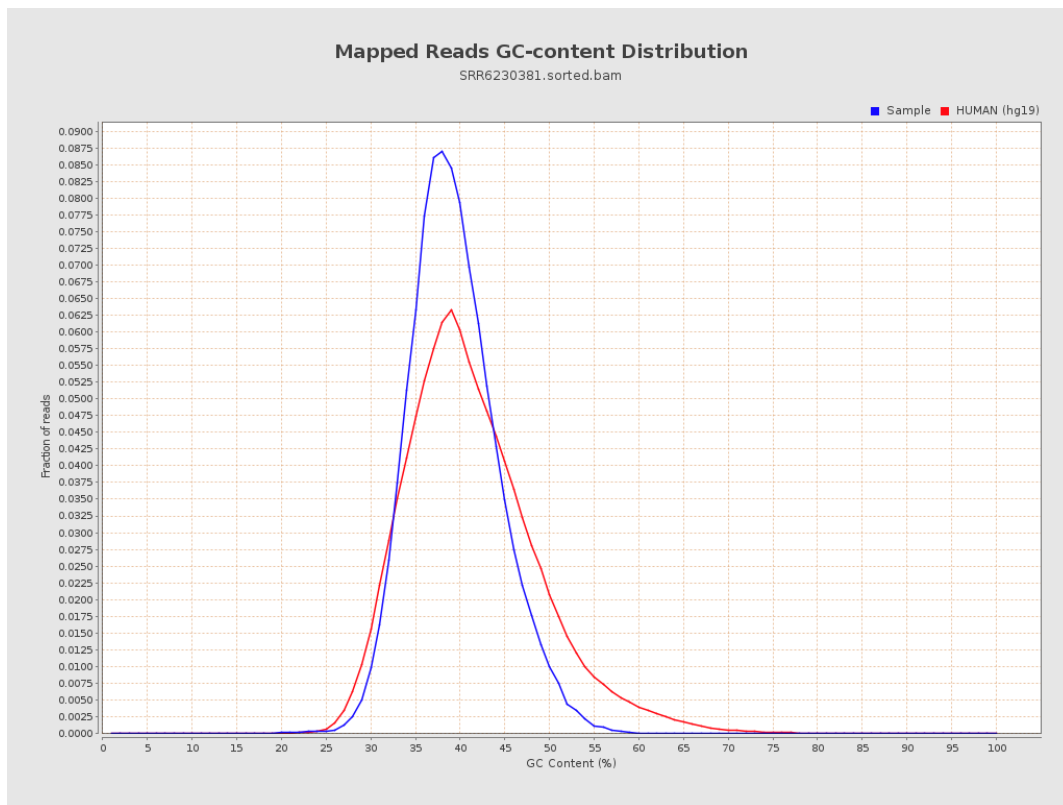
7. Results : Duplication Rate Histogram



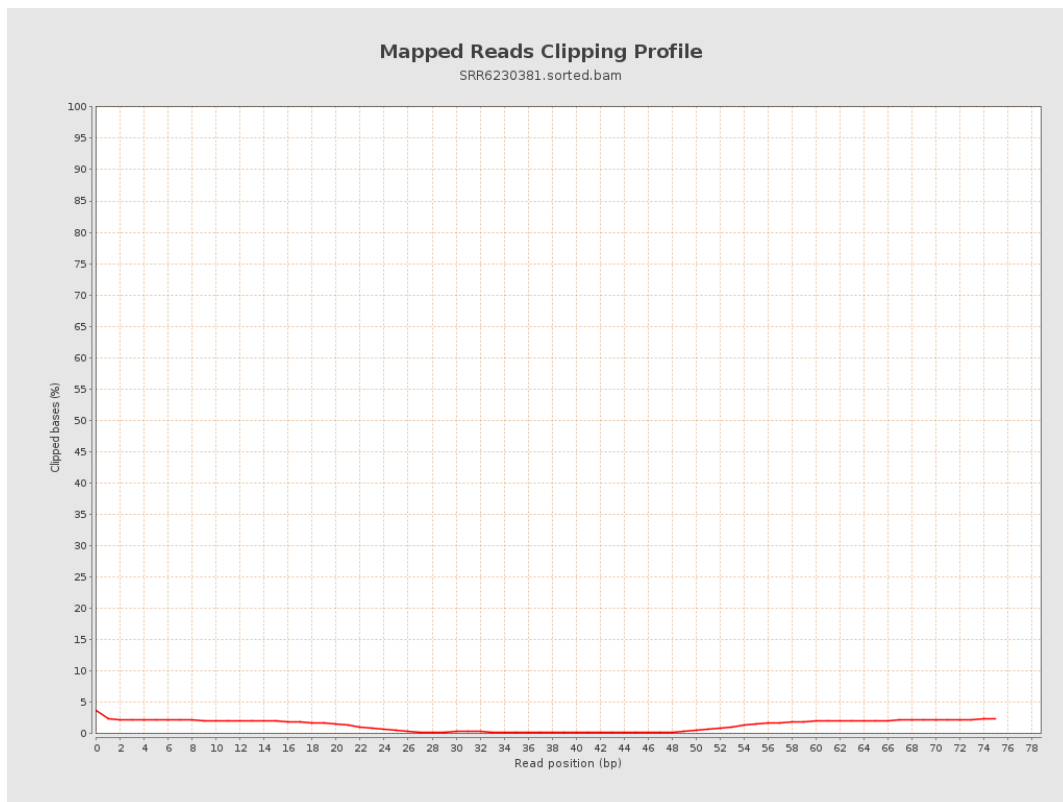
8. Results : Mapped Reads Nucleotide Content



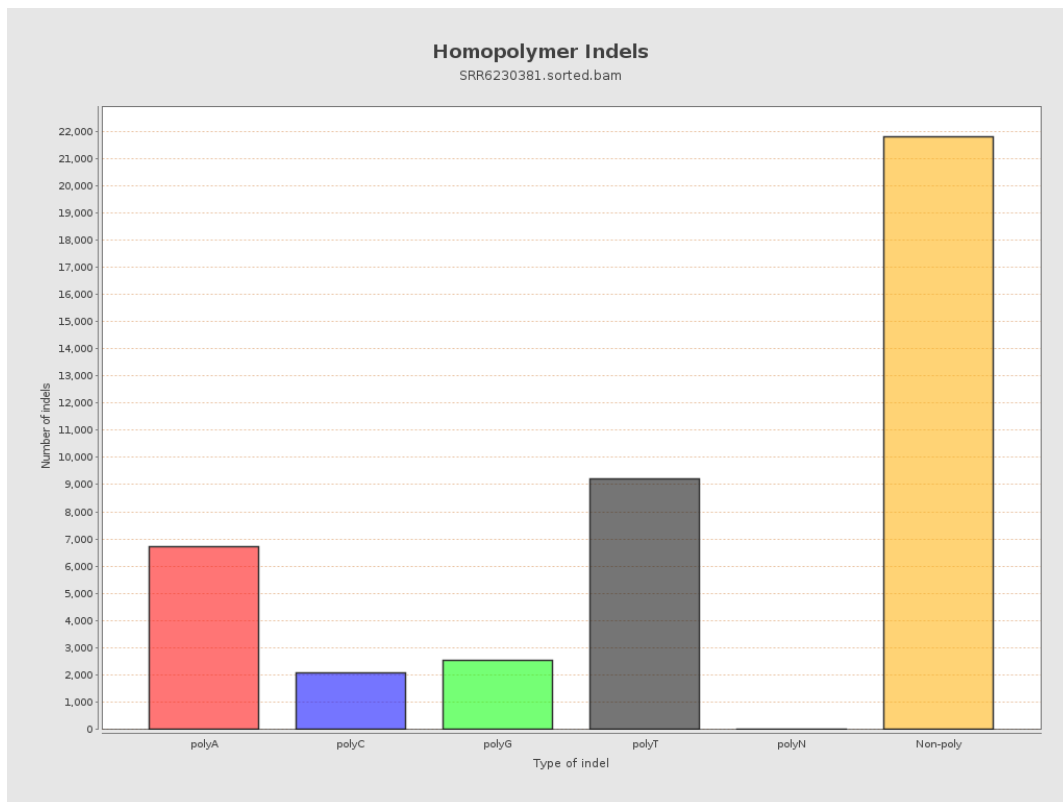
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

