

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 14:34:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084802.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_SRR3084802 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084802.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 14:34:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084802.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,023,940
Mapped reads	1,800,470 / 88.96%
Unmapped reads	223,470 / 11.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,231 / 0.95%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	83,011 / 4.1%
Duplication rate	4.1%
Clipped reads	798,867 / 39.47%

2.2. ACGT Content

Number/percentage of A's	32,668,873 / 27.18%
Number/percentage of C's	22,332,912 / 18.58%
Number/percentage of T's	37,996,549 / 31.61%
Number/percentage of G's	27,170,613 / 22.61%
Number/percentage of N's	17,037 / 0.01%
GC Percentage	41.19%

2.3. Coverage

Mean	0.0388

Standard Deviation	0.2645
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2.4. Mapping Quality

Mean Mapping Quality	45.32
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2.5. Mismatches and indels

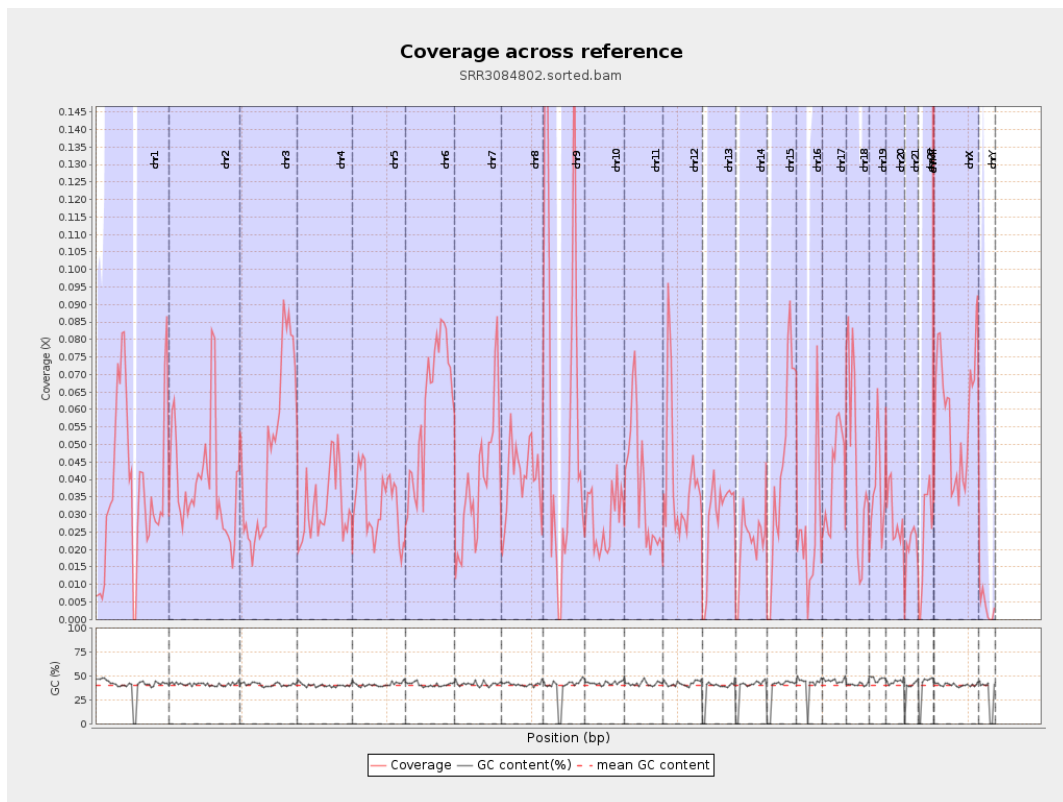
General error rate	0.78%
Mismatches	919,564
Insertions	9,093
Mapped reads with at least one insertion	0.5%
Deletions	27,160
Mapped reads with at least one deletion	1.49%
Homopolymer indels	48.29%

2.6. Chromosome stats

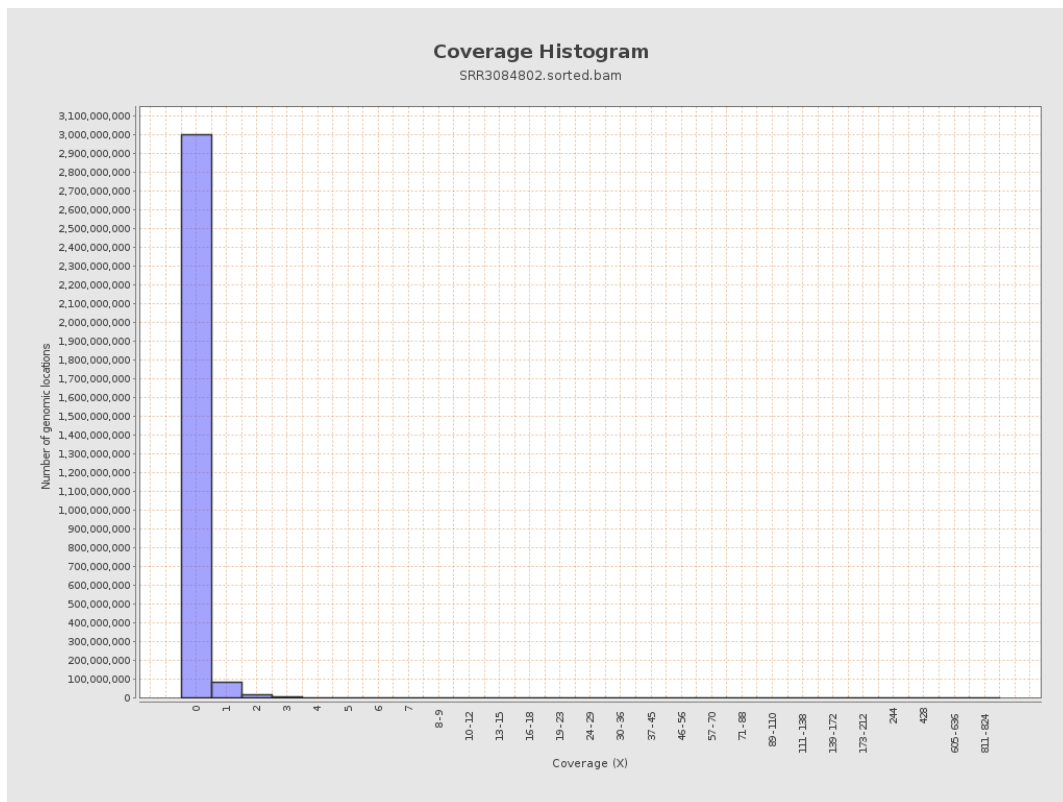
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9323143	0.0374	0.2905
chr2	243199373	9407473	0.0387	0.4126
chr3	198022430	9601820	0.0485	0.2592
chr4	191154276	6190521	0.0324	0.2151
chr5	180915260	5926946	0.0328	0.2116
chr6	171115067	10298871	0.0602	0.306
chr7	159138663	6201268	0.039	0.2456

chr8	146364022	5922639	0.0405	0.2595
chr9	141213431	8511796	0.0603	0.3171
chr10	135534747	3879318	0.0286	0.2032
chr11	135006516	5082094	0.0376	0.2436
chr12	133851895	5230288	0.0391	0.2328
chr13	115169878	3296596	0.0286	0.1982
chr14	107349540	2291909	0.0213	0.1708
chr15	102531392	4514000	0.044	0.2549
chr16	90354753	2227449	0.0247	0.187
chr17	81195210	3334874	0.0411	0.2395
chr18	78077248	3517048	0.045	0.3232
chr19	59128983	2272253	0.0384	0.2553
chr20	63025520	1832636	0.0291	0.1994
chr21	48129895	966131	0.0201	0.1668
chr22	51304566	1212313	0.0236	0.1794
chrMT	16571	21432	1.2933	1.4813
chrX	155270560	8946914	0.0576	0.2881
chrY	59373566	220377	0.0037	0.078

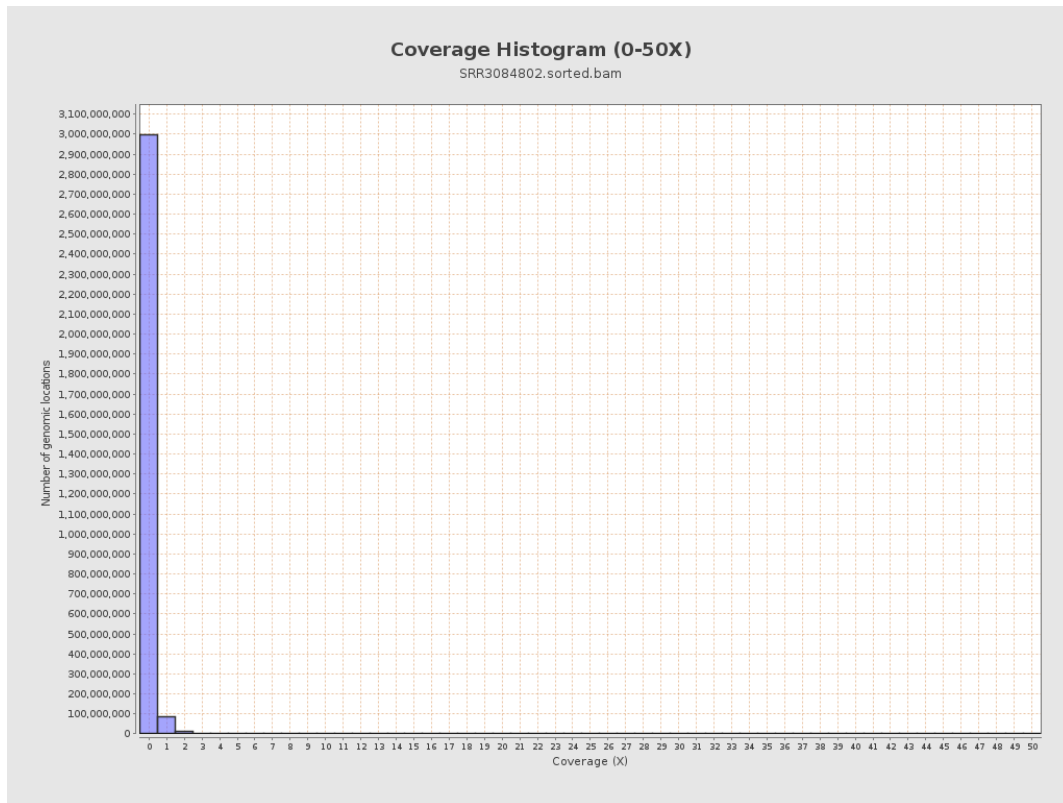
3. Results : Coverage across reference



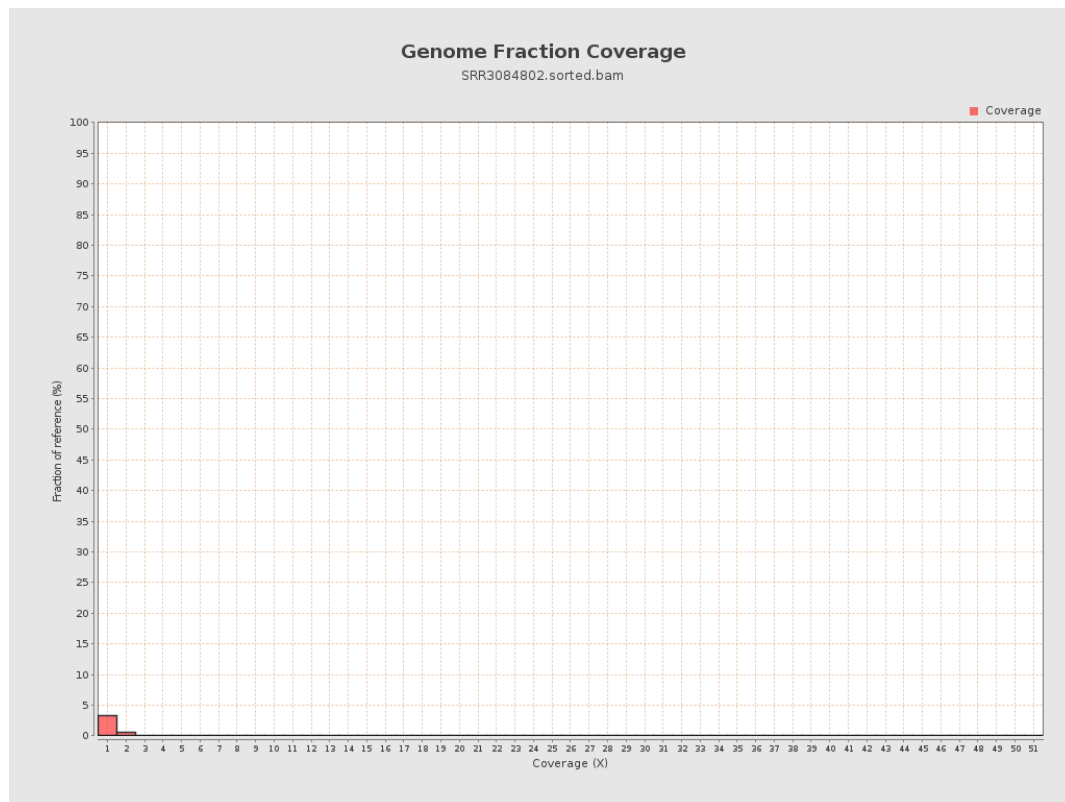
4. Results : Coverage Histogram



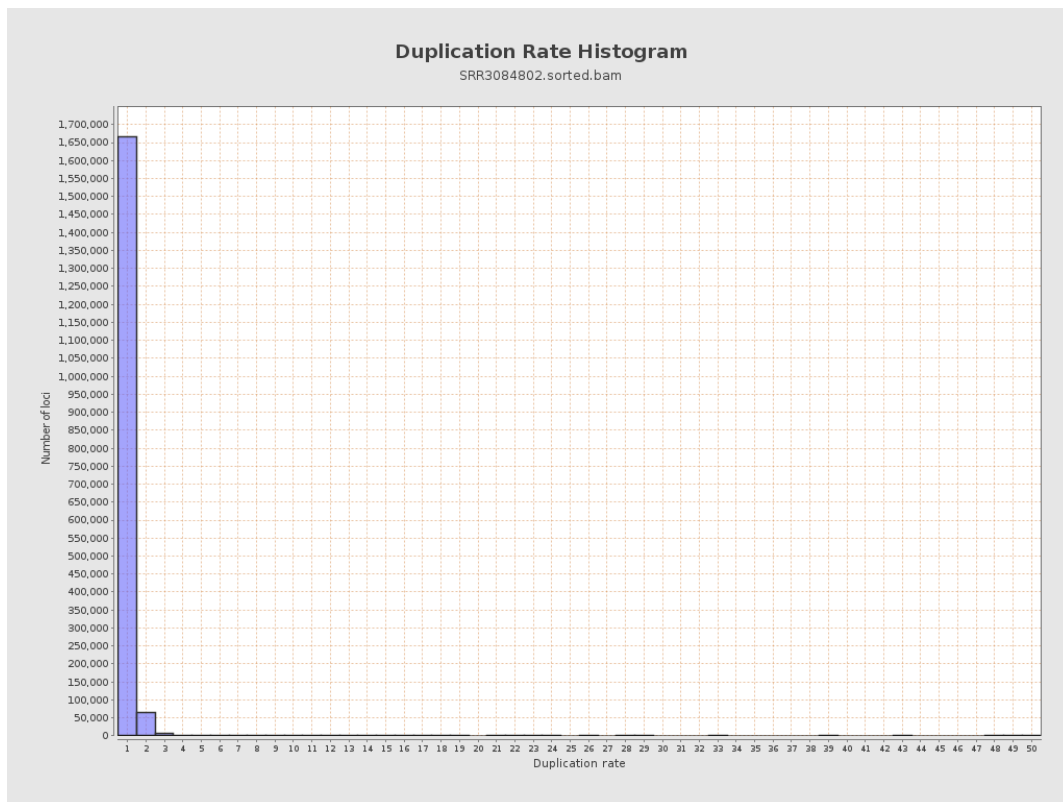
5. Results : Coverage Histogram (0-50X)



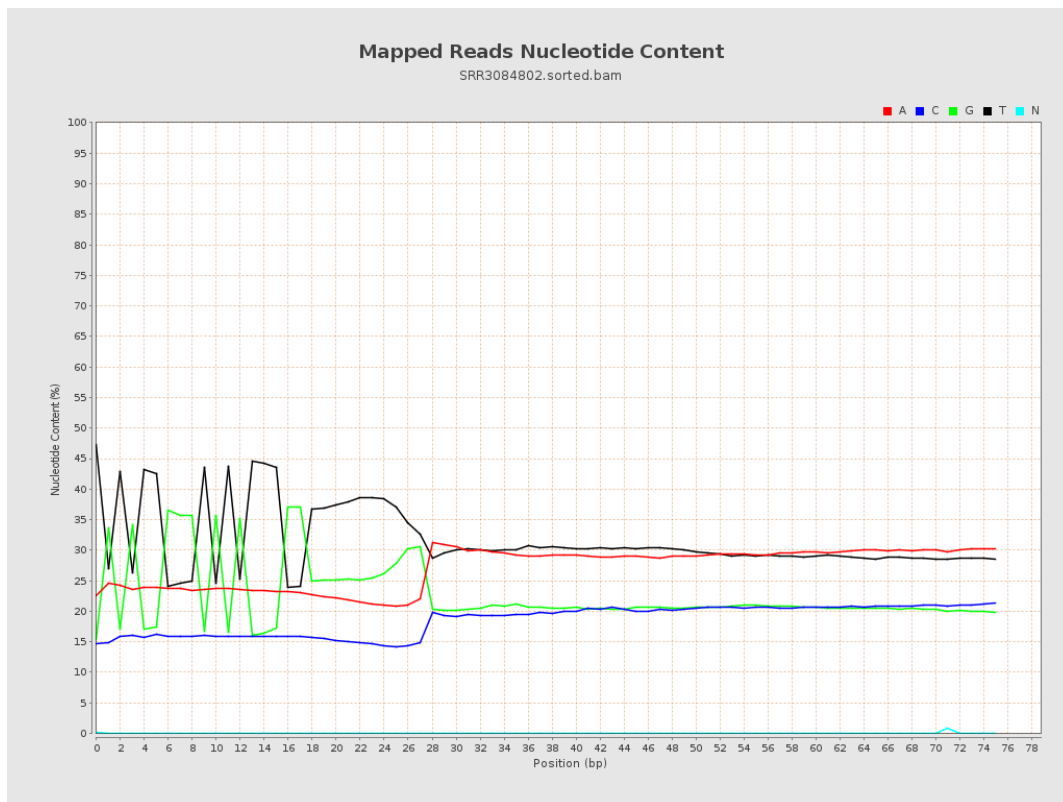
6. Results : Genome Fraction Coverage



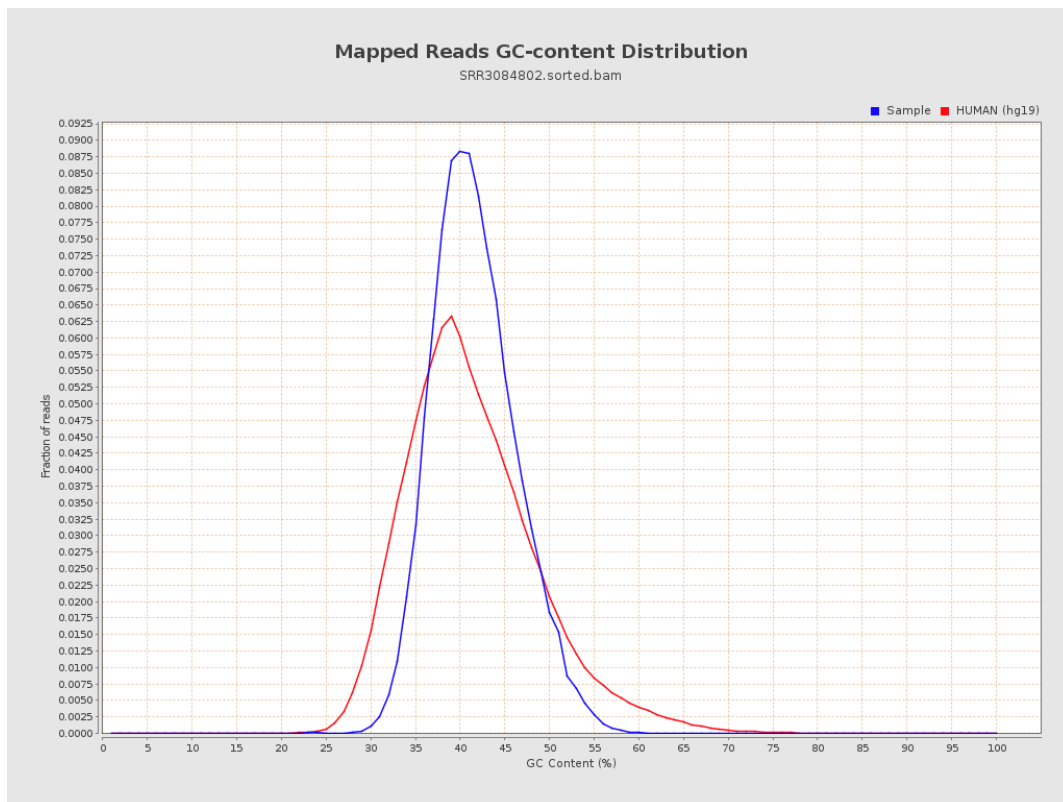
7. Results : Duplication Rate Histogram



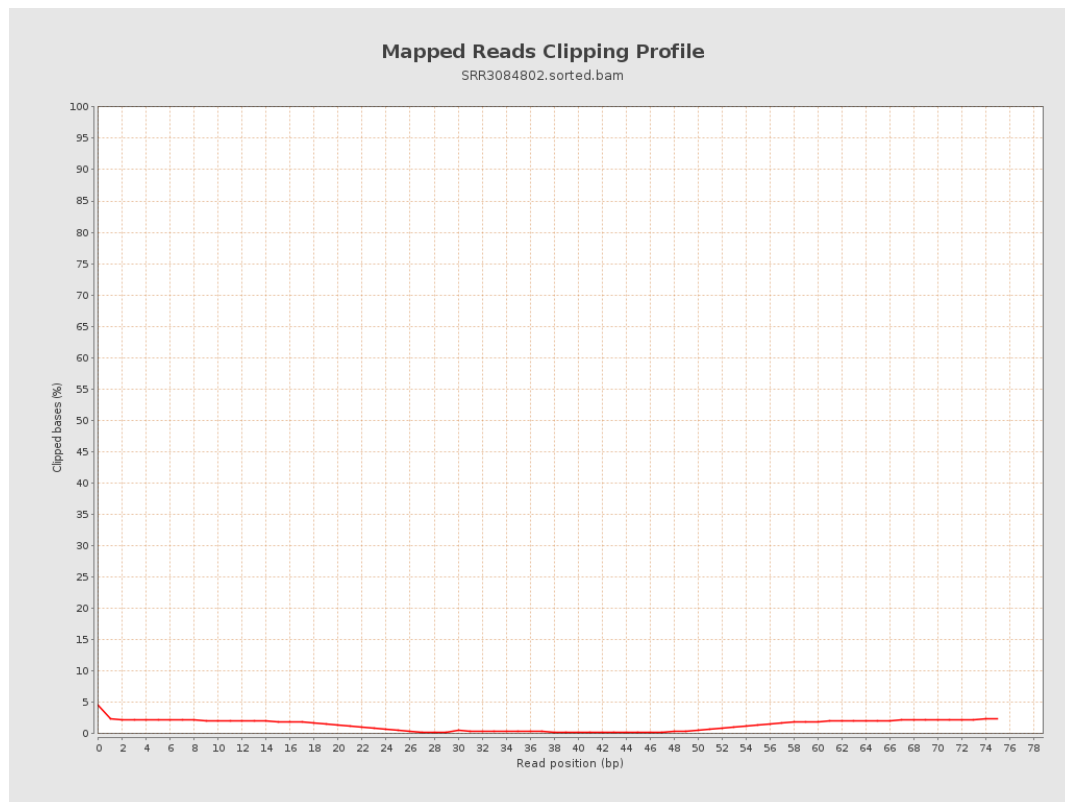
8. Results : Mapped Reads Nucleotide Content



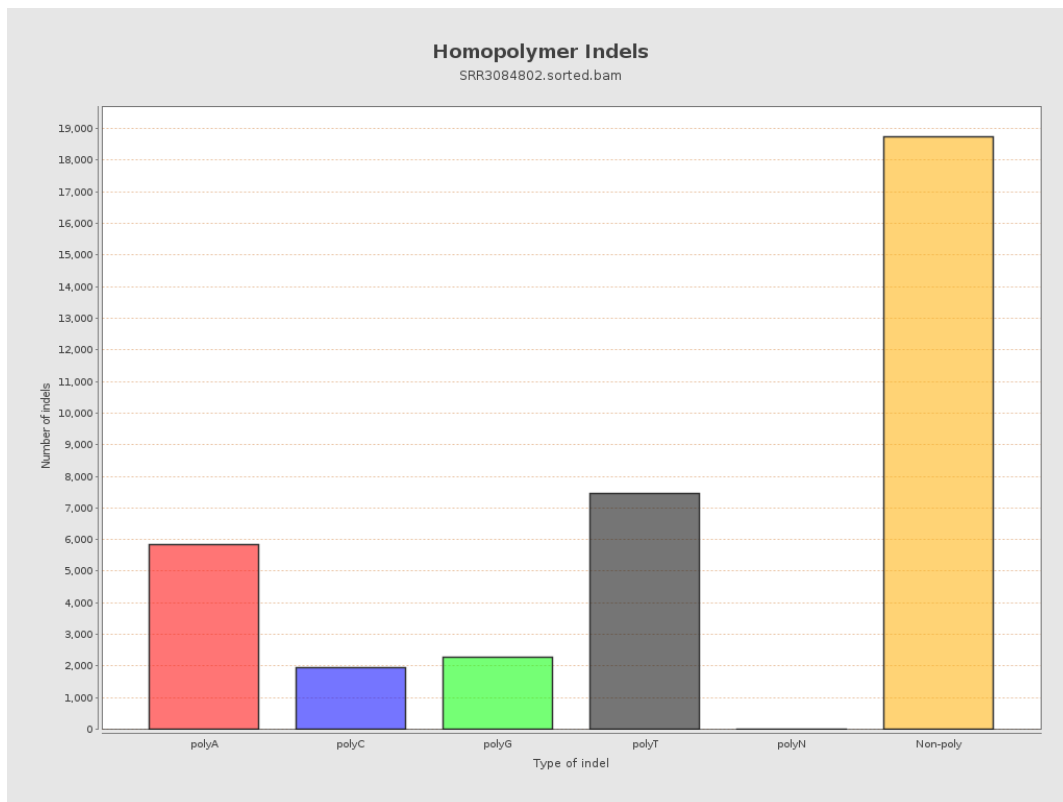
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

