

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 22:17:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818847.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_SRR1818847 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818847.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 22:17:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818847.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,761,509
Mapped reads	1,700,056 / 96.51%
Unmapped reads	61,453 / 3.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,138 / 1.6%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	395,436 / 22.45%
Duplication rate	20.23%
Clipped reads	1,715,544 / 97.39%

2.2. ACGT Content

Number/percentage of A's	45,701,164 / 29.06%
Number/percentage of C's	33,072,451 / 21.03%
Number/percentage of T's	45,524,638 / 28.95%
Number/percentage of G's	32,964,583 / 20.96%
Number/percentage of N's	2,364 / 0%
GC Percentage	41.99%

2.3. Coverage

Mean	0.0508

Standard Deviation	0.5756
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	49.37
----------------------	-------

2.5. Mismatches and indels

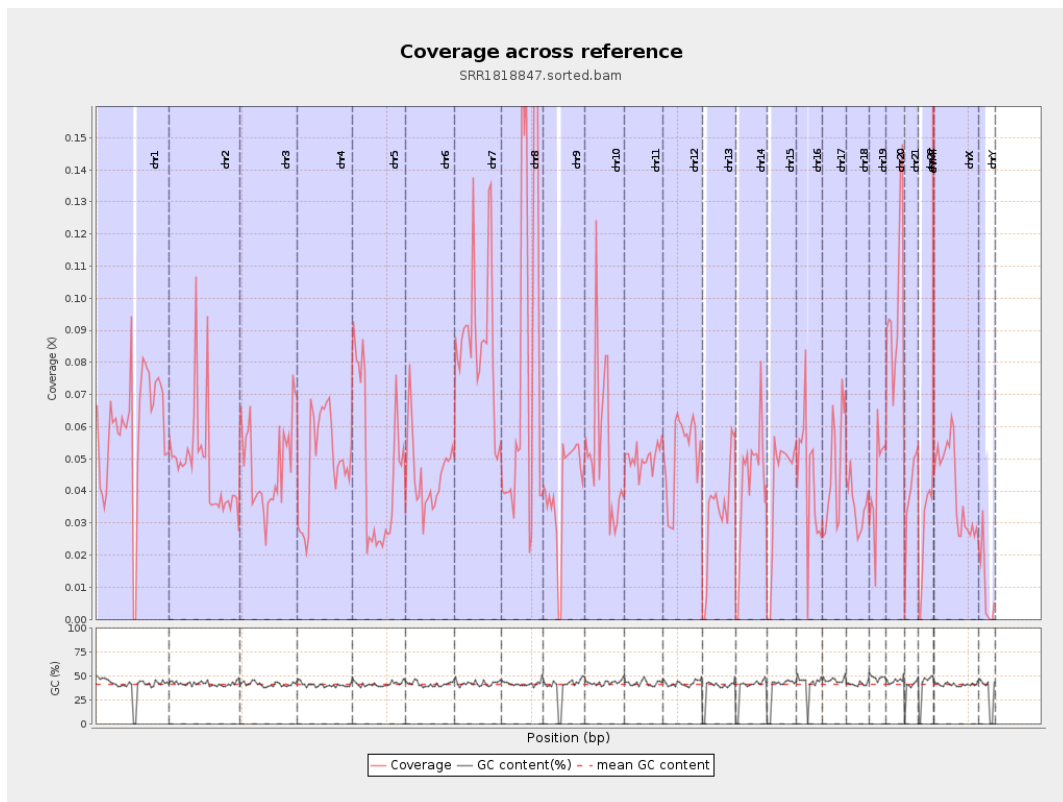
General error rate	0.64%
Mismatches	957,329
Insertions	21,455
Mapped reads with at least one insertion	1.22%
Deletions	51,303
Mapped reads with at least one deletion	2.95%
Homopolymer indels	40.64%

2.6. Chromosome stats

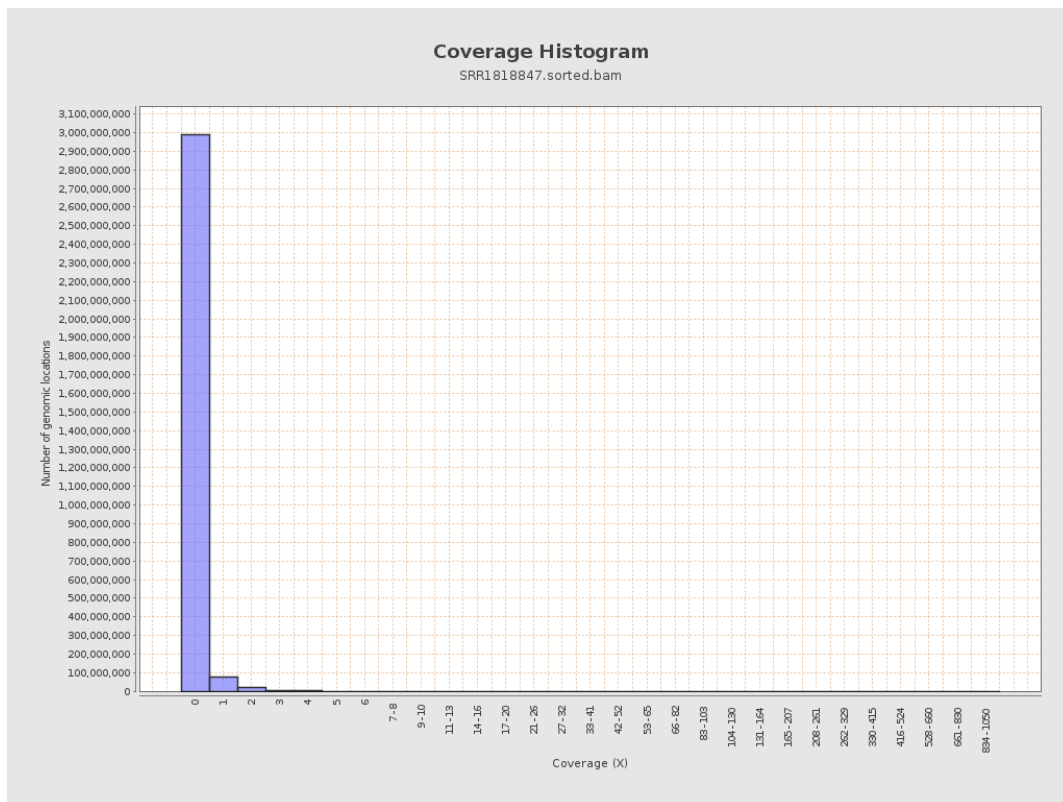
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14674658	0.0589	0.8507
chr2	243199373	11634768	0.0478	0.8388
chr3	198022430	9532651	0.0481	0.299
chr4	191154276	9314413	0.0487	0.3805
chr5	180915260	8496636	0.047	0.3108
chr6	171115067	7723124	0.0451	0.3142
chr7	159138663	13882170	0.0872	1.1674

chr8	146364022	13278079	0.0907	0.5072
chr9	141213431	5700133	0.0404	0.4655
chr10	135534747	7167271	0.0529	0.7817
chr11	135006516	6774060	0.0502	0.3604
chr12	133851895	6937474	0.0518	0.3099
chr13	115169878	3873772	0.0336	0.2454
chr14	107349540	4544954	0.0423	0.3107
chr15	102531392	4290943	0.0419	0.2761
chr16	90354753	3857117	0.0427	0.6314
chr17	81195210	3801663	0.0468	0.3728
chr18	78077248	2767057	0.0354	0.5484
chr19	59128983	2557530	0.0433	0.7233
chr20	63025520	6195296	0.0983	0.4562
chr21	48129895	1907213	0.0396	0.3173
chr22	51304566	1370192	0.0267	0.2459
chrMT	16571	211987	12.7926	8.3288
chrX	155270560	6312280	0.0407	0.3248
chrY	59373566	559393	0.0094	0.6761

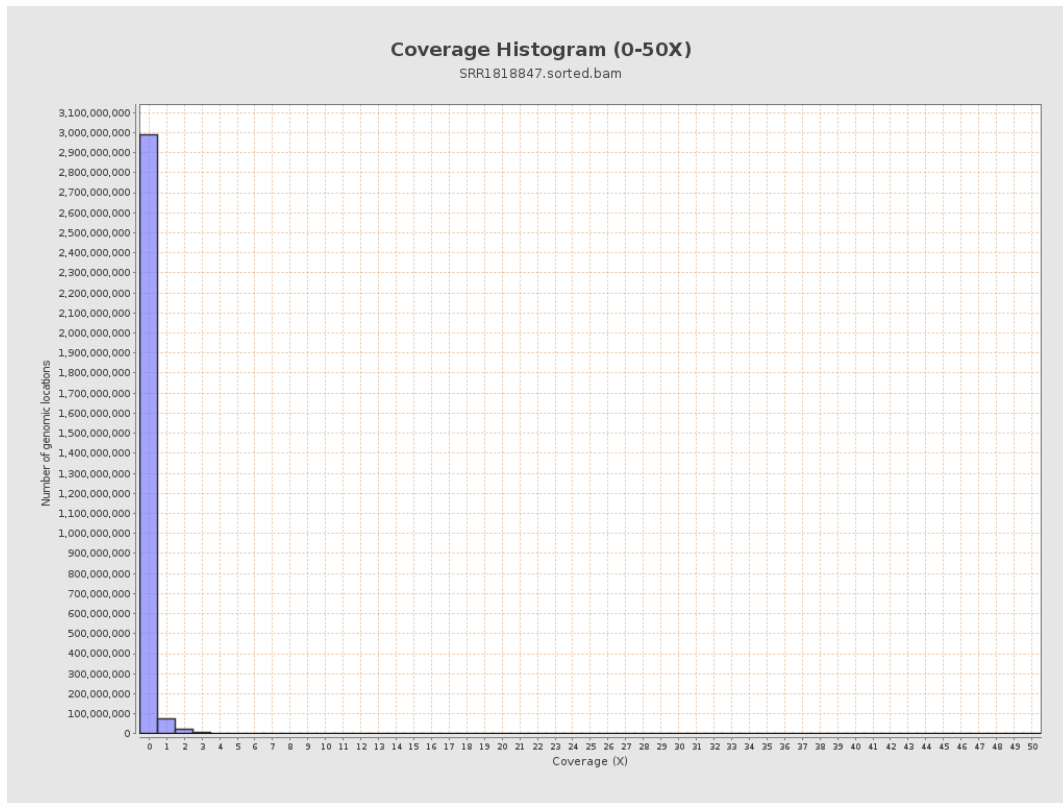
3. Results : Coverage across reference



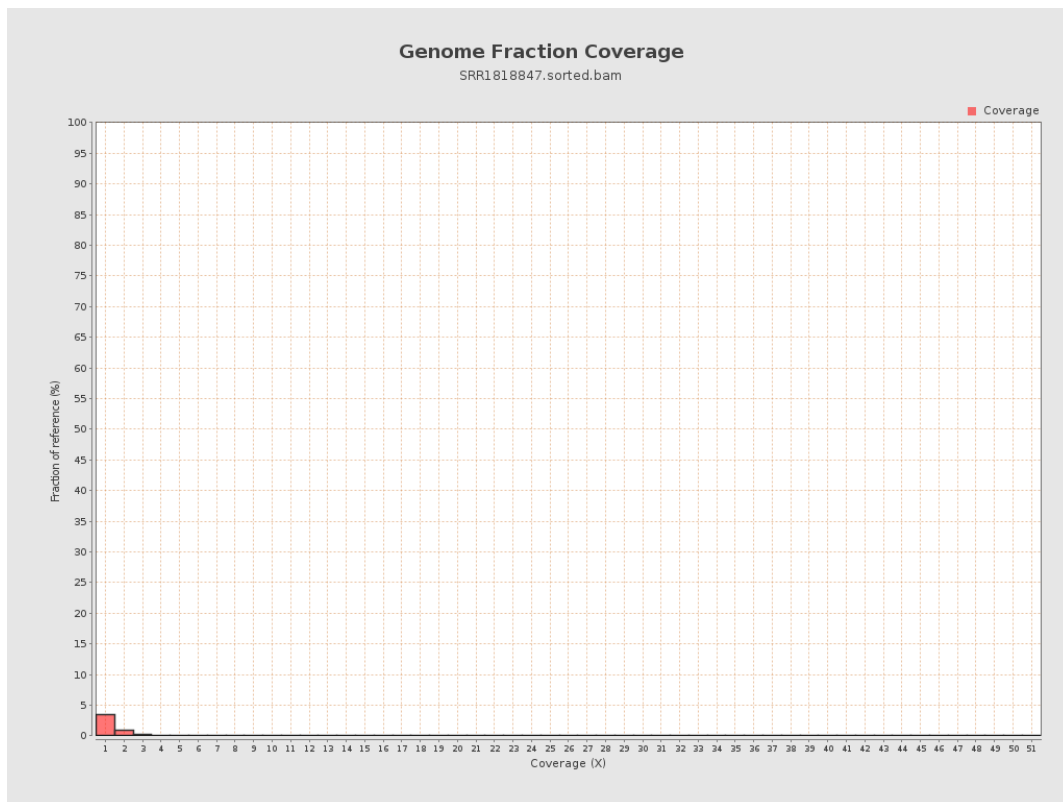
4. Results : Coverage Histogram



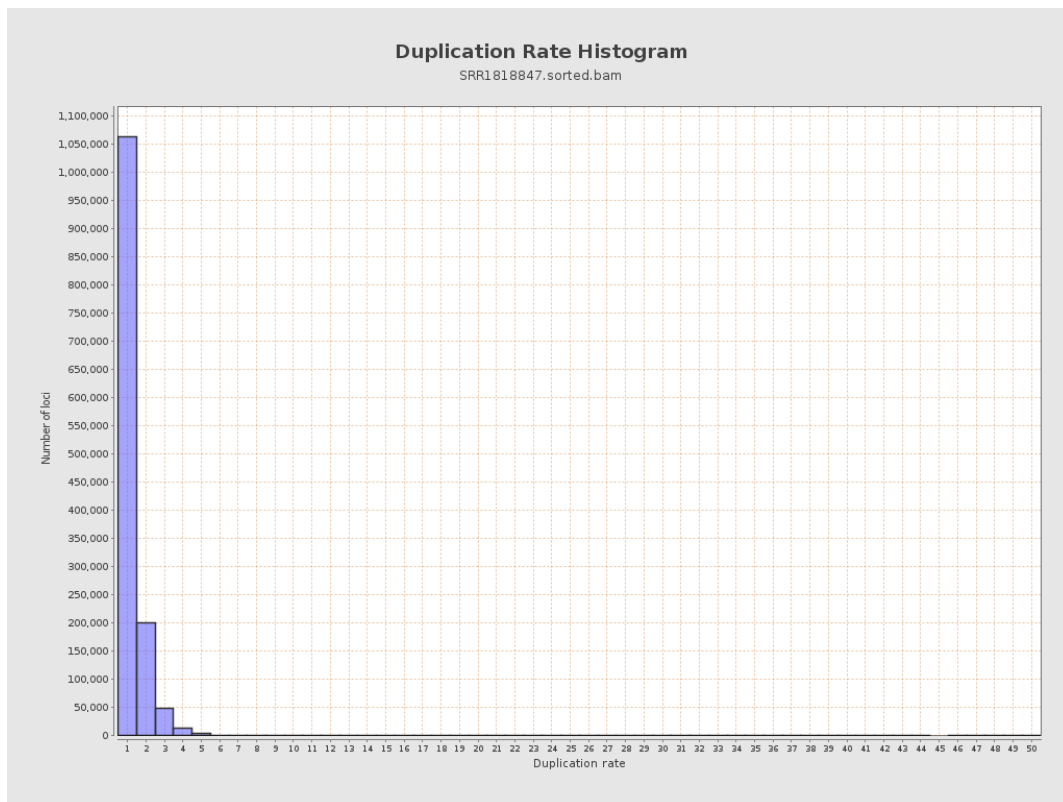
5. Results : Coverage Histogram (0-50X)



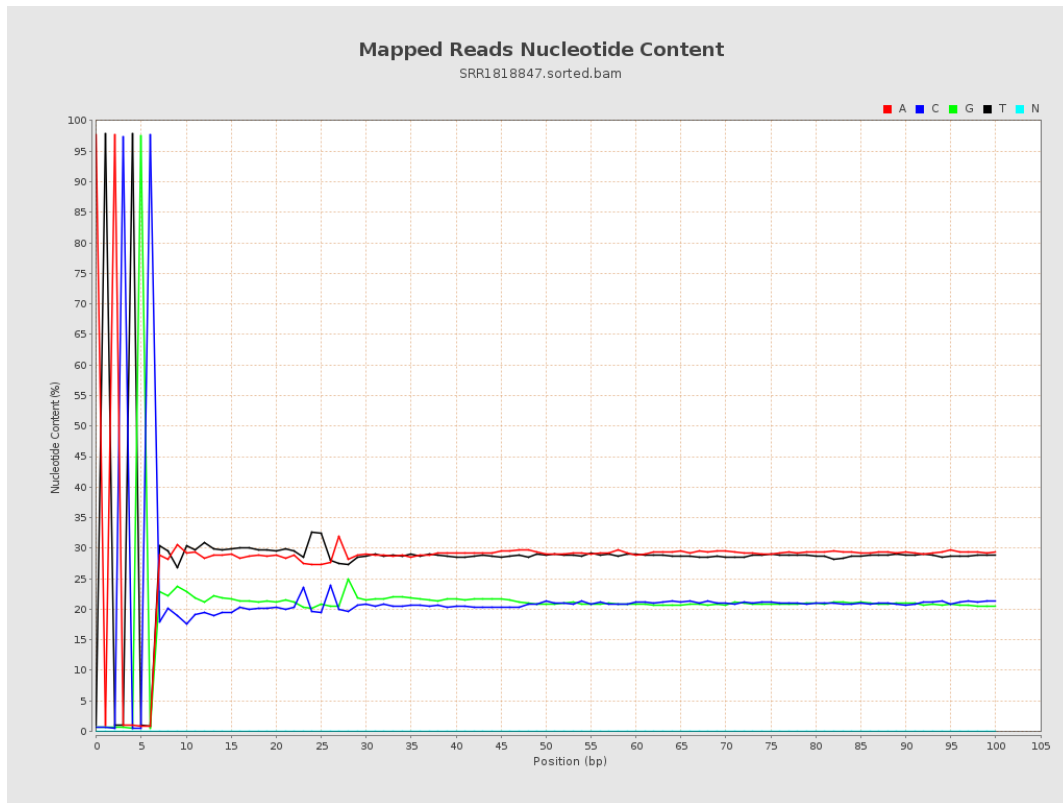
6. Results : Genome Fraction Coverage



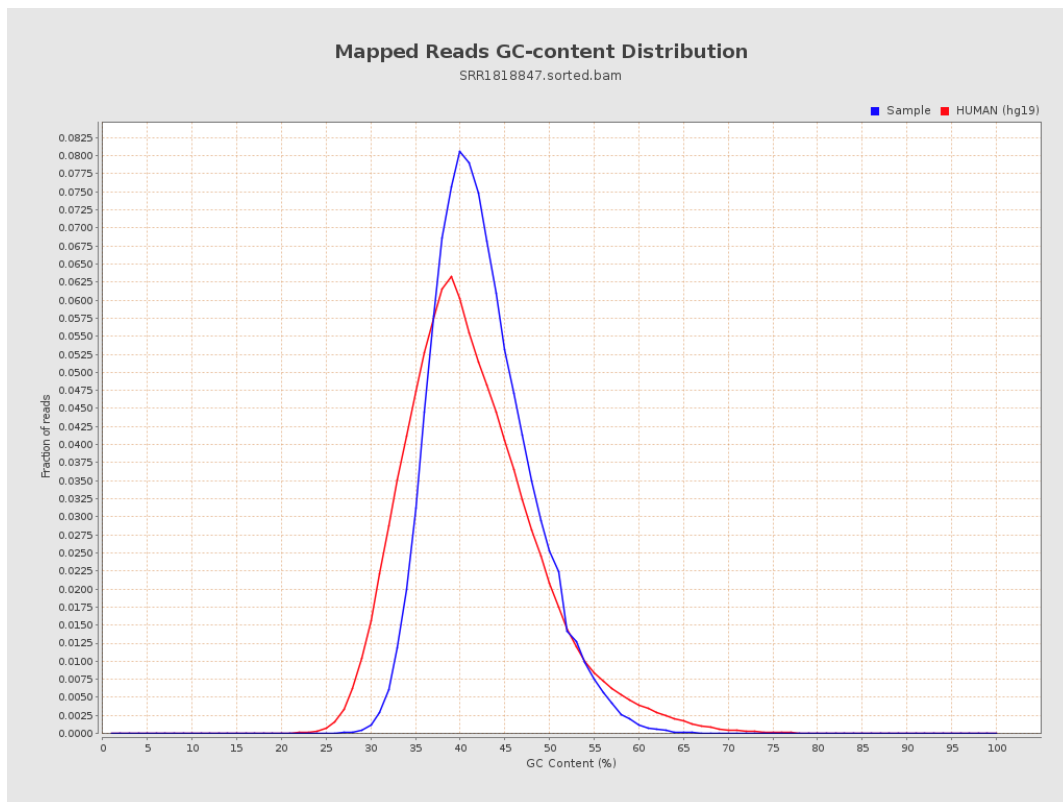
7. Results : Duplication Rate Histogram



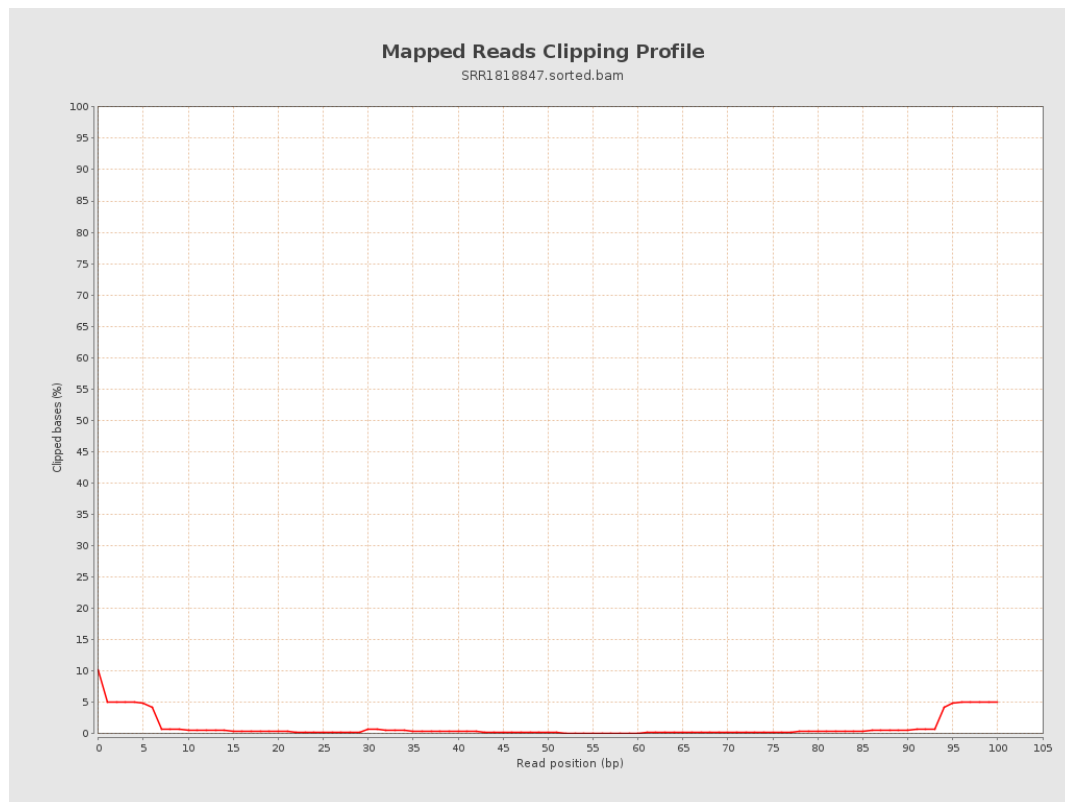
8. Results : Mapped Reads Nucleotide Content



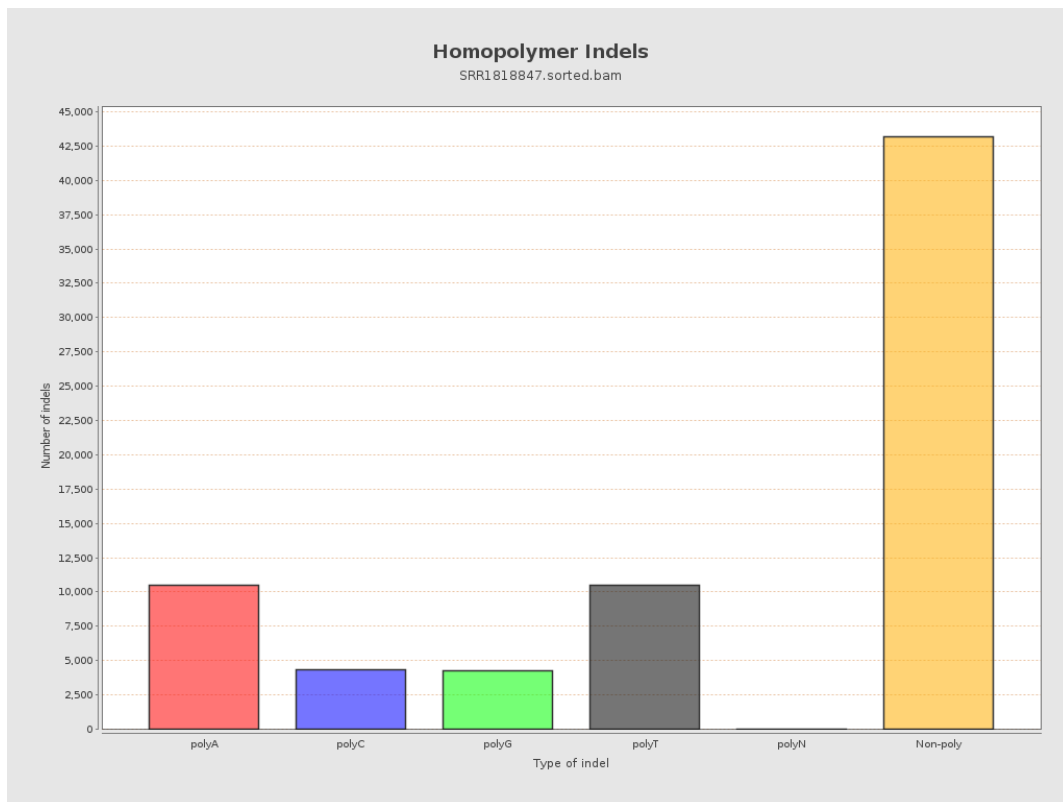
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

