

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 18:00:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818826.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_SRR1818826 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818826.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 18:00:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818826.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,378,267
Mapped reads	1,336,965 / 97%
Unmapped reads	41,302 / 3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,338 / 0.82%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	608,468 / 44.15%
Duplication rate	37.81%
Clipped reads	1,333,273 / 96.74%

2.2. ACGT Content

Number/percentage of A's	24,935,466 / 27.44%
Number/percentage of C's	18,819,403 / 20.71%
Number/percentage of T's	26,808,403 / 29.5%
Number/percentage of G's	20,294,454 / 22.34%
Number/percentage of N's	5,306 / 0.01%
GC Percentage	43.05%

2.3. Coverage

Mean	0.0294

Standard Deviation	0.4173
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2.4. Mapping Quality

Mean Mapping Quality	47.81
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2.5. Mismatches and indels

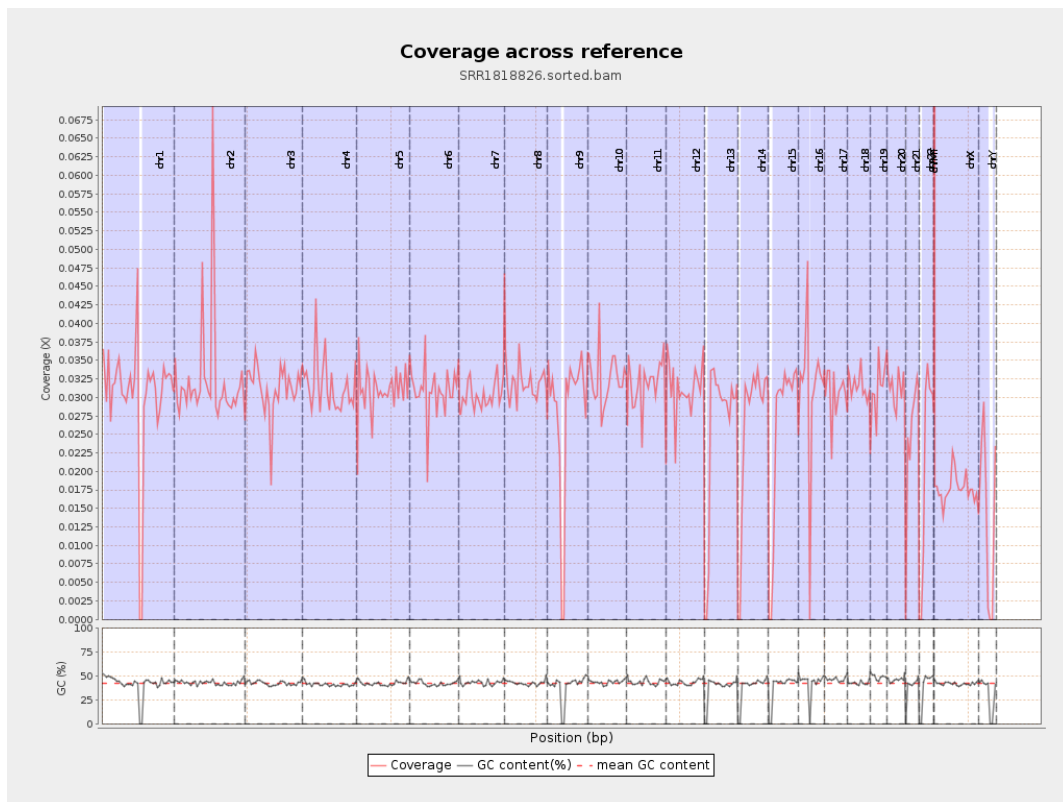
General error rate	0.53%
Mismatches	458,259
Insertions	12,984
Mapped reads with at least one insertion	0.96%
Deletions	23,611
Mapped reads with at least one deletion	1.75%
Homopolymer indels	41.21%

2.6. Chromosome stats

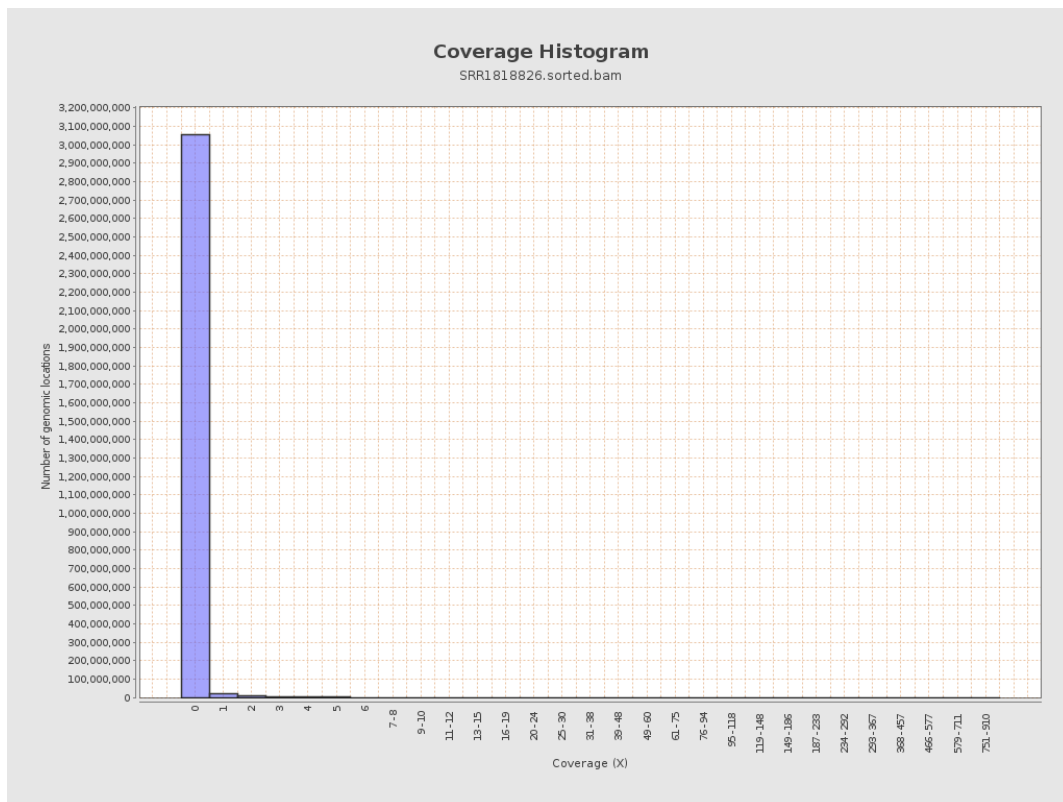
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7516180	0.0302	0.5392
chr2	243199373	7831750	0.0322	0.6891
chr3	198022430	6179315	0.0312	0.3285
chr4	191154276	6030499	0.0315	0.3643
chr5	180915260	5664812	0.0313	0.3354
chr6	171115067	5288678	0.0309	0.3547
chr7	159138663	4803883	0.0302	0.3455

chr8	146364022	4678178	0.032	0.3557
chr9	141213431	3942428	0.0279	0.3446
chr10	135534747	4414153	0.0326	0.457
chr11	135006516	4317693	0.032	0.3623
chr12	133851895	4198606	0.0314	0.3415
chr13	115169878	2958518	0.0257	0.2986
chr14	107349540	2820918	0.0263	0.3213
chr15	102531392	2622044	0.0256	0.2994
chr16	90354753	2775166	0.0307	0.4928
chr17	81195210	2467296	0.0304	0.3437
chr18	78077248	2471167	0.0317	0.4191
chr19	59128983	1850048	0.0313	0.4633
chr20	63025520	1964778	0.0312	0.3495
chr21	48129895	1207752	0.0251	0.3124
chr22	51304566	1108386	0.0216	0.2968
chrMT	16571	192905	11.6411	11.1223
chrX	155270560	2753078	0.0177	0.2643
chrY	59373566	843718	0.0142	0.663

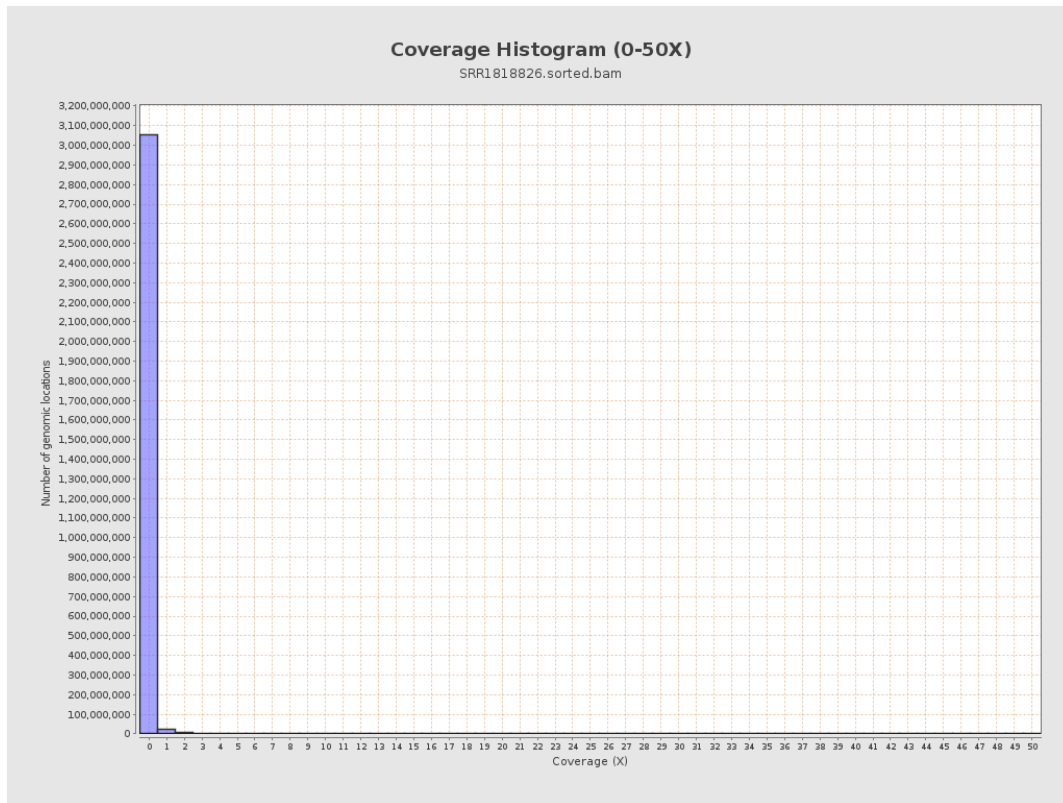
3. Results : Coverage across reference



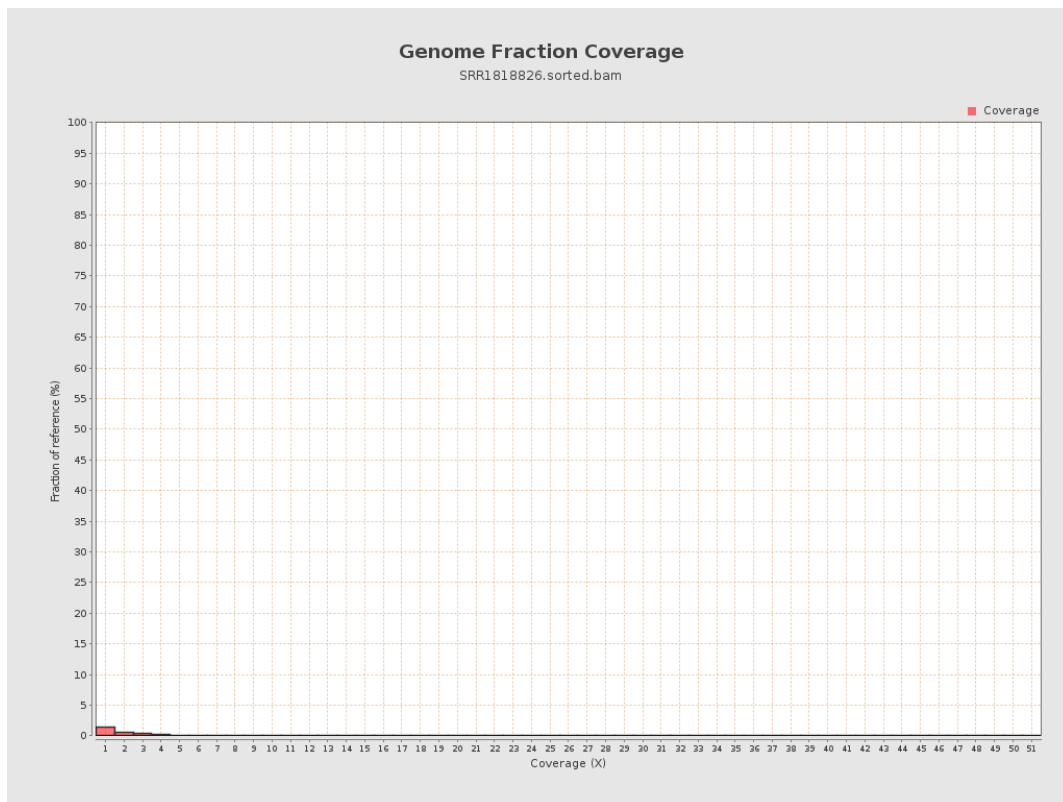
4. Results : Coverage Histogram



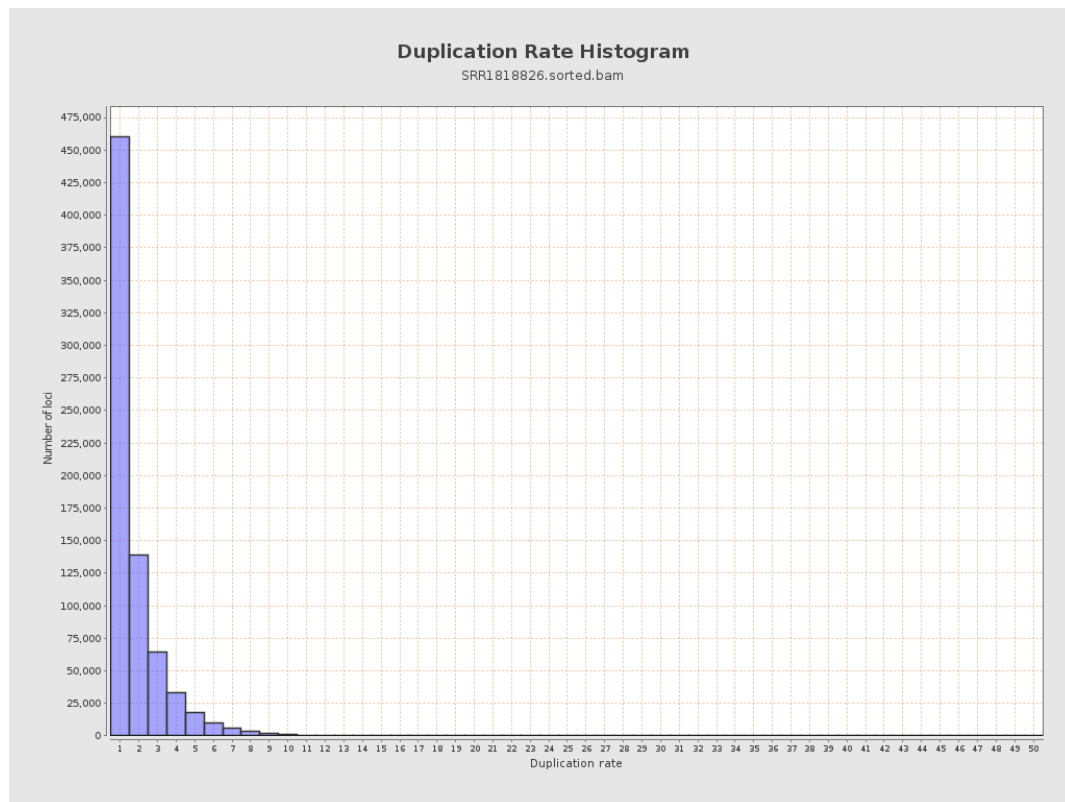
5. Results : Coverage Histogram (0-50X)



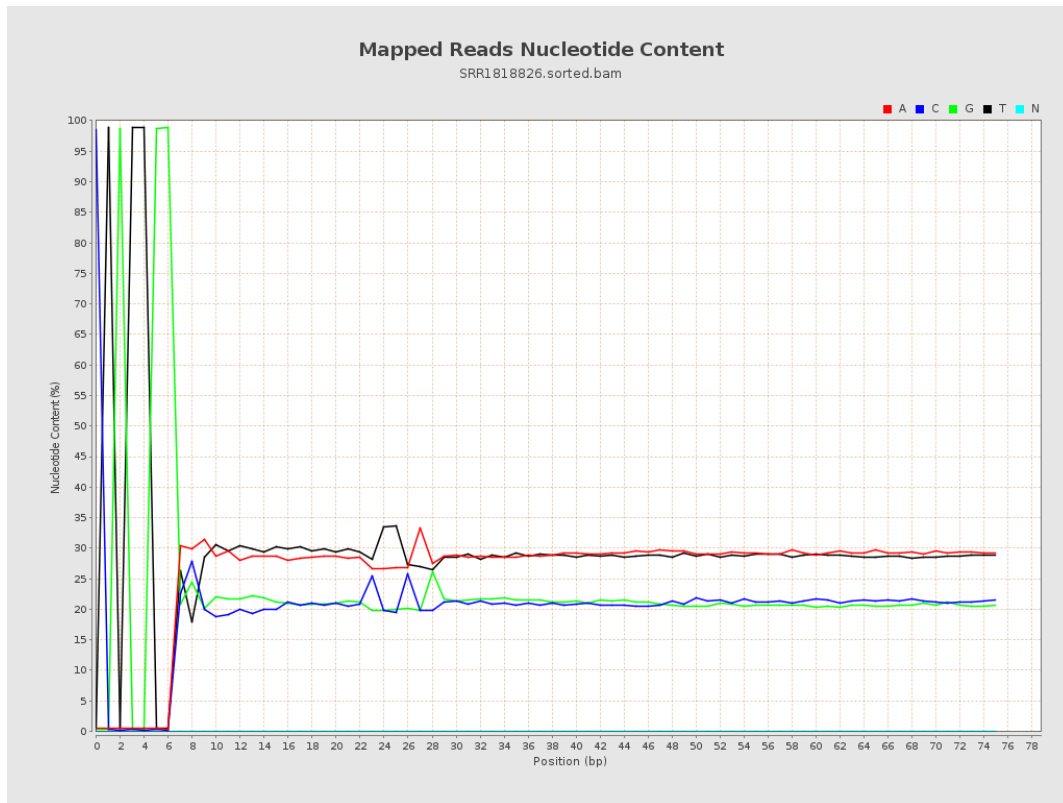
6. Results : Genome Fraction Coverage



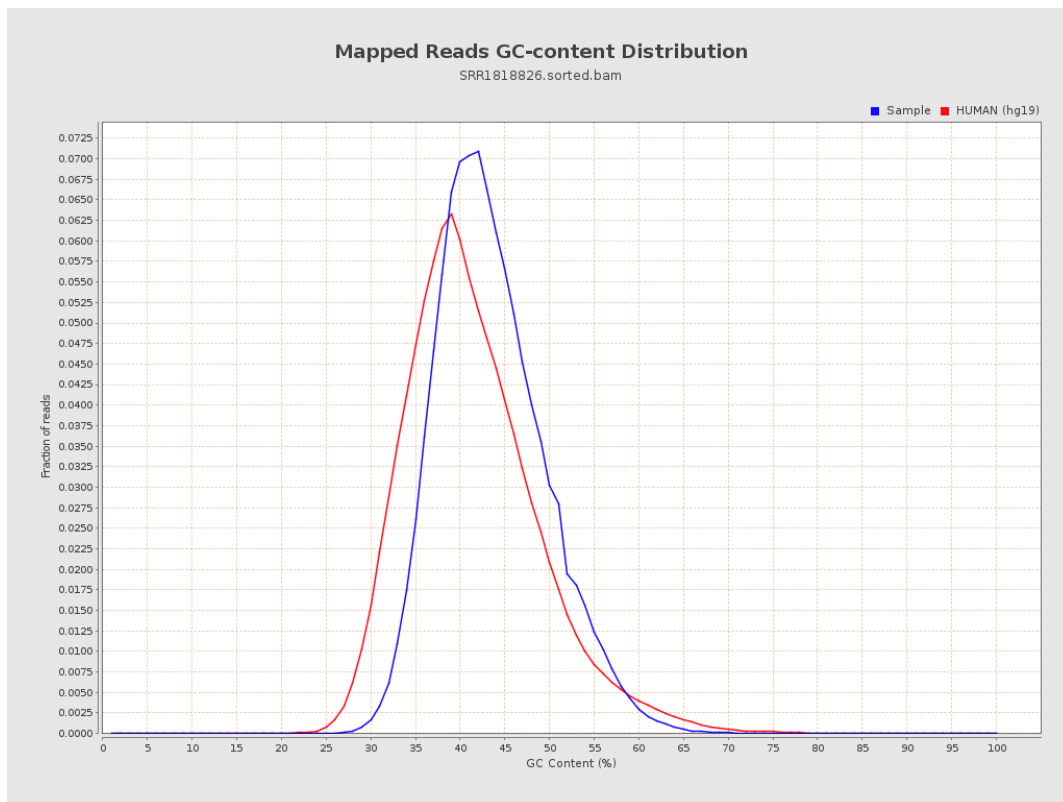
7. Results : Duplication Rate Histogram



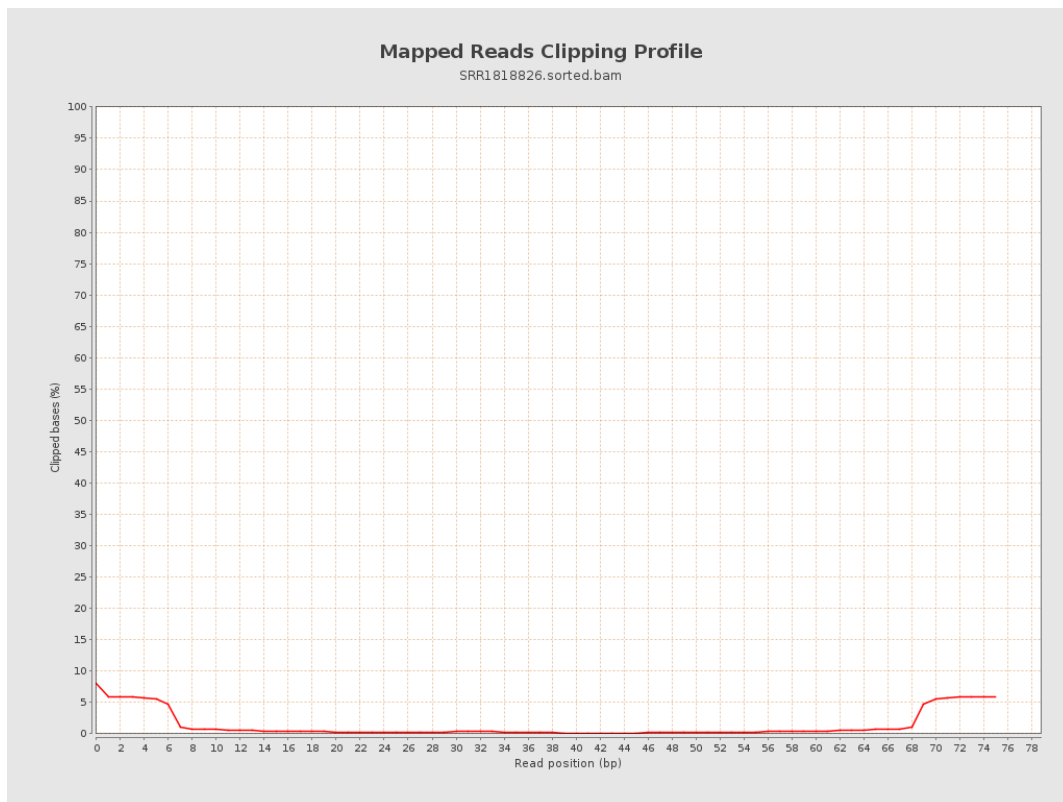
8. Results : Mapped Reads Nucleotide Content



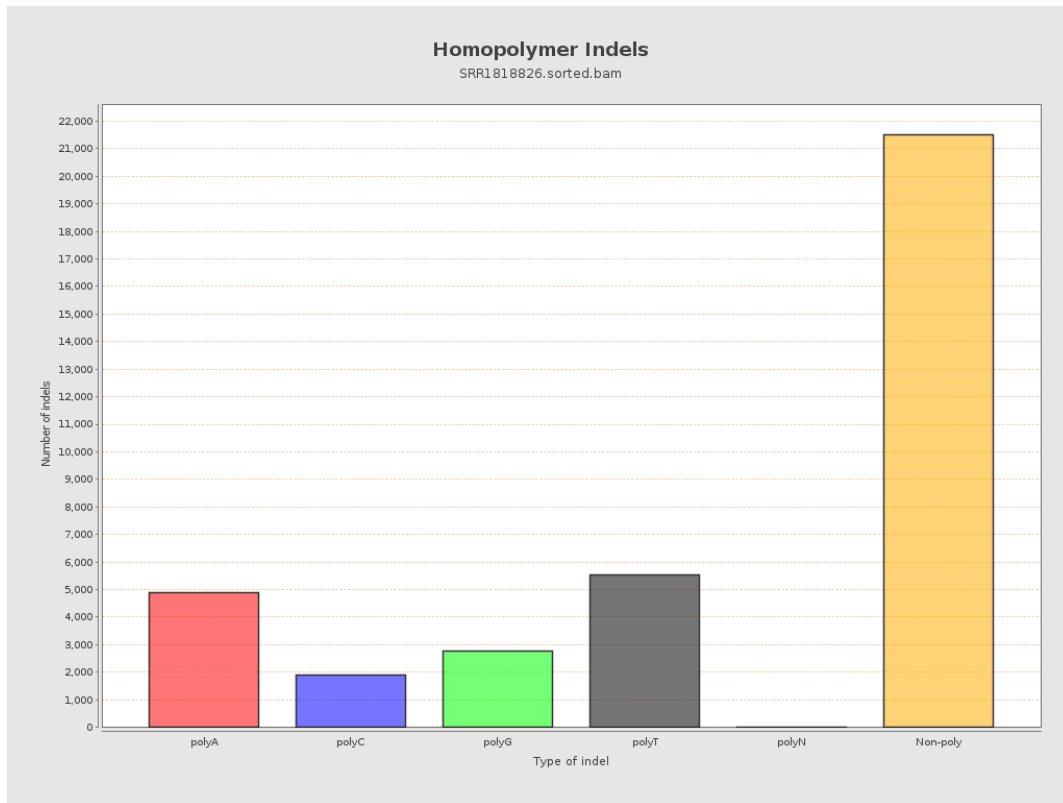
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

