

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 00:12:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818856.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_SRR1818856 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818856.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 00:11:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818856.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,867,052
Mapped reads	1,792,438 / 96%
Unmapped reads	74,614 / 4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,393 / 1.47%
Read min/max/mean length	30 / 101 / 101.57
Duplicated reads (estimated)	414,166 / 22.18%
Duplication rate	19.84%
Clipped reads	1,802,761 / 96.56%

2.2. ACGT Content

Number/percentage of A's	47,798,416 / 28.8%
Number/percentage of C's	35,204,484 / 21.21%
Number/percentage of T's	47,353,006 / 28.54%
Number/percentage of G's	35,587,897 / 21.45%
Number/percentage of N's	2,354 / 0%
GC Percentage	42.66%

2.3. Coverage

Mean	0.0536

Standard Deviation	0.6037
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2.4. Mapping Quality

Mean Mapping Quality	49.42
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2.5. Mismatches and indels

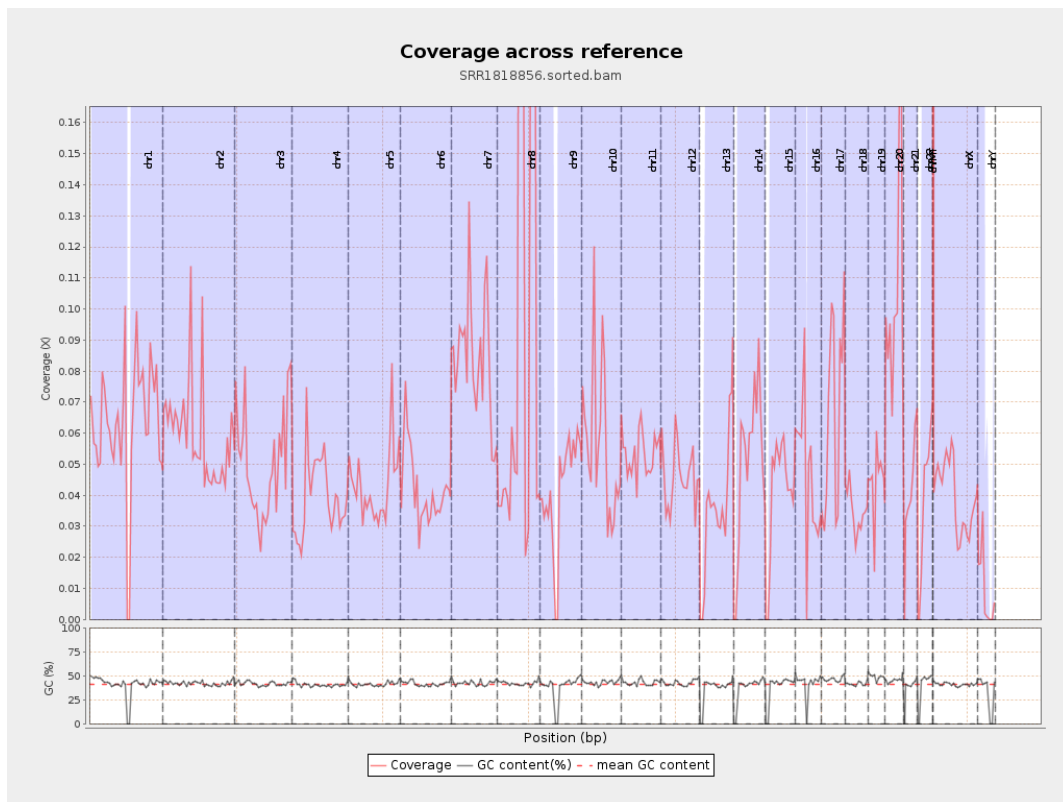
General error rate	0.64%
Mismatches	1,007,250
Insertions	24,880
Mapped reads with at least one insertion	1.35%
Deletions	53,737
Mapped reads with at least one deletion	2.92%
Homopolymer indels	39.6%

2.6. Chromosome stats

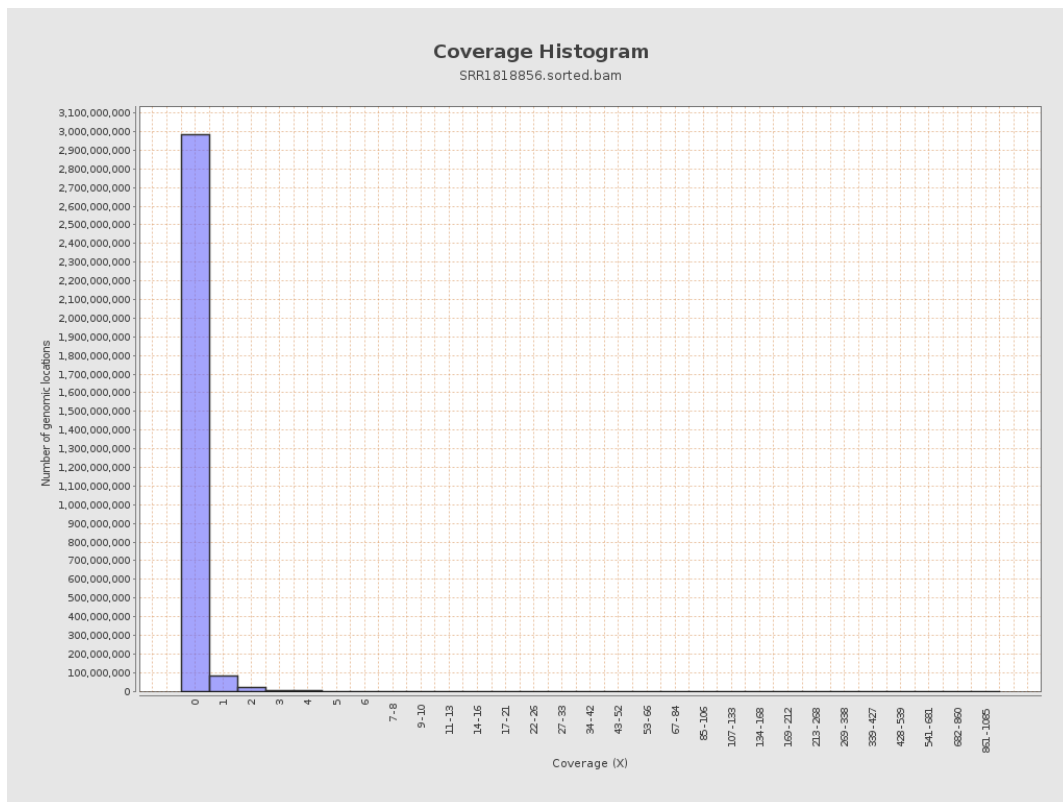
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15787477	0.0633	0.9199
chr2	243199373	14453378	0.0594	0.8967
chr3	198022430	9906475	0.05	0.3053
chr4	191154276	7609670	0.0398	0.3732
chr5	180915260	7824187	0.0432	0.3002
chr6	171115067	7172154	0.0419	0.3048
chr7	159138663	13327999	0.0838	1.1633

chr8	146364022	16841798	0.1151	0.583
chr9	141213431	5852410	0.0414	0.4708
chr10	135534747	7563602	0.0558	0.7992
chr11	135006516	7191474	0.0533	0.3794
chr12	133851895	6206566	0.0464	0.2932
chr13	115169878	4103923	0.0356	0.2556
chr14	107349540	5600642	0.0522	0.34
chr15	102531392	4105295	0.04	0.2727
chr16	90354753	4189457	0.0464	0.6826
chr17	81195210	5183569	0.0638	0.4355
chr18	78077248	2734119	0.035	0.5446
chr19	59128983	2617492	0.0443	0.8171
chr20	63025520	6856875	0.1088	0.4851
chr21	48129895	2003510	0.0416	0.3206
chr22	51304566	1909016	0.0372	0.2962
chrMT	16571	276882	16.7088	10.5363
chrX	155270560	6168711	0.0397	0.3142
chrY	59373566	564695	0.0095	0.7717

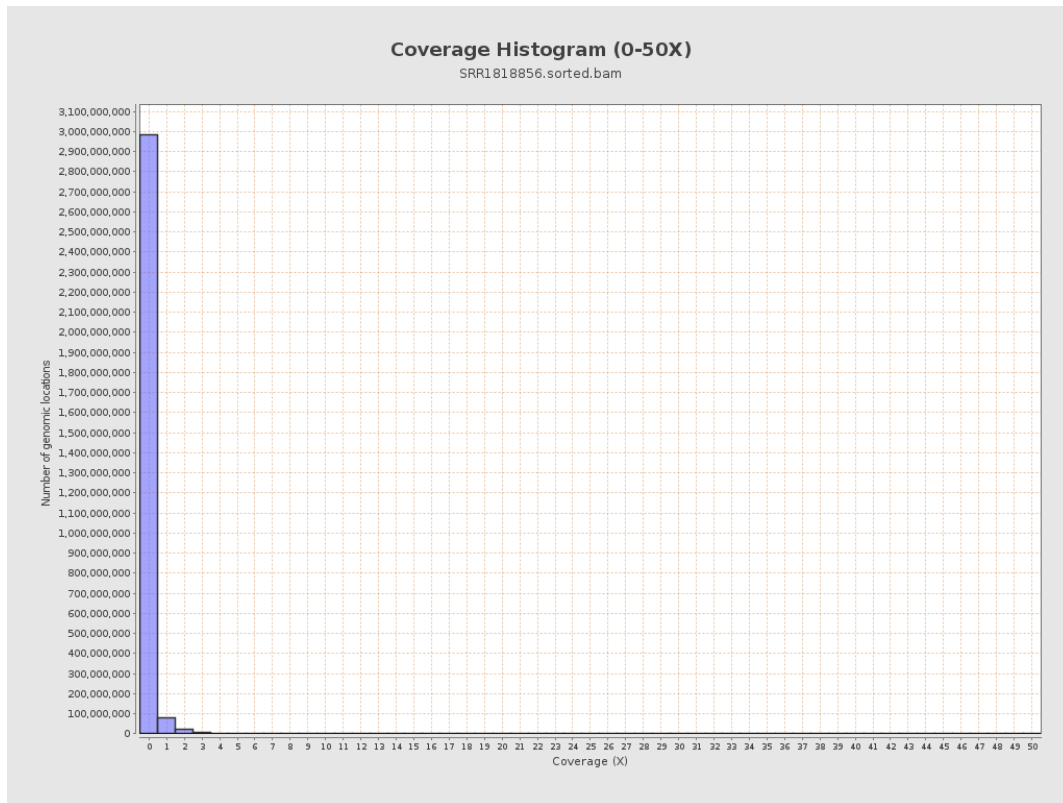
3. Results : Coverage across reference



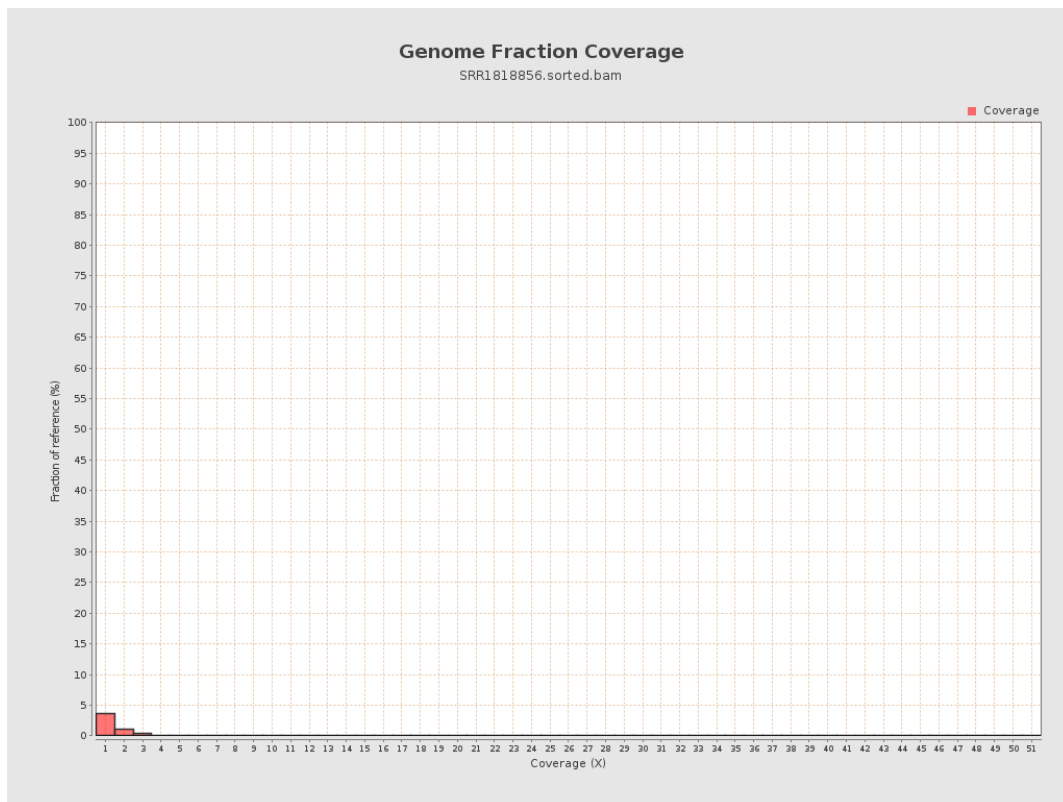
4. Results : Coverage Histogram



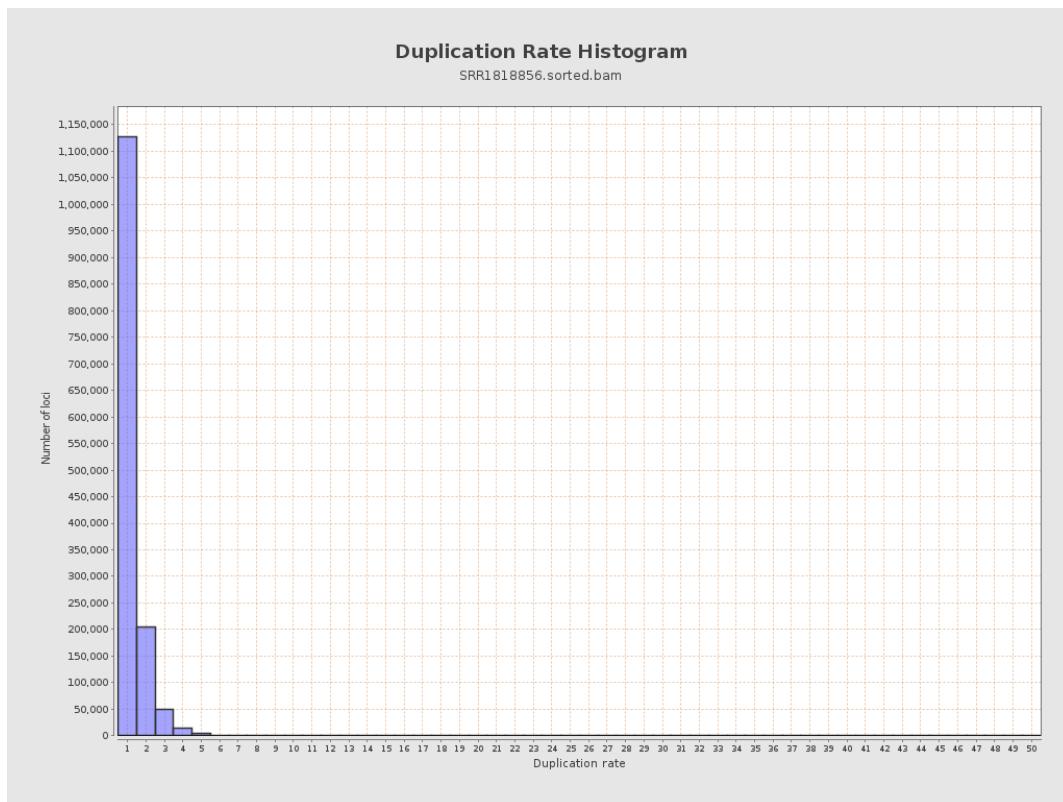
5. Results : Coverage Histogram (0-50X)



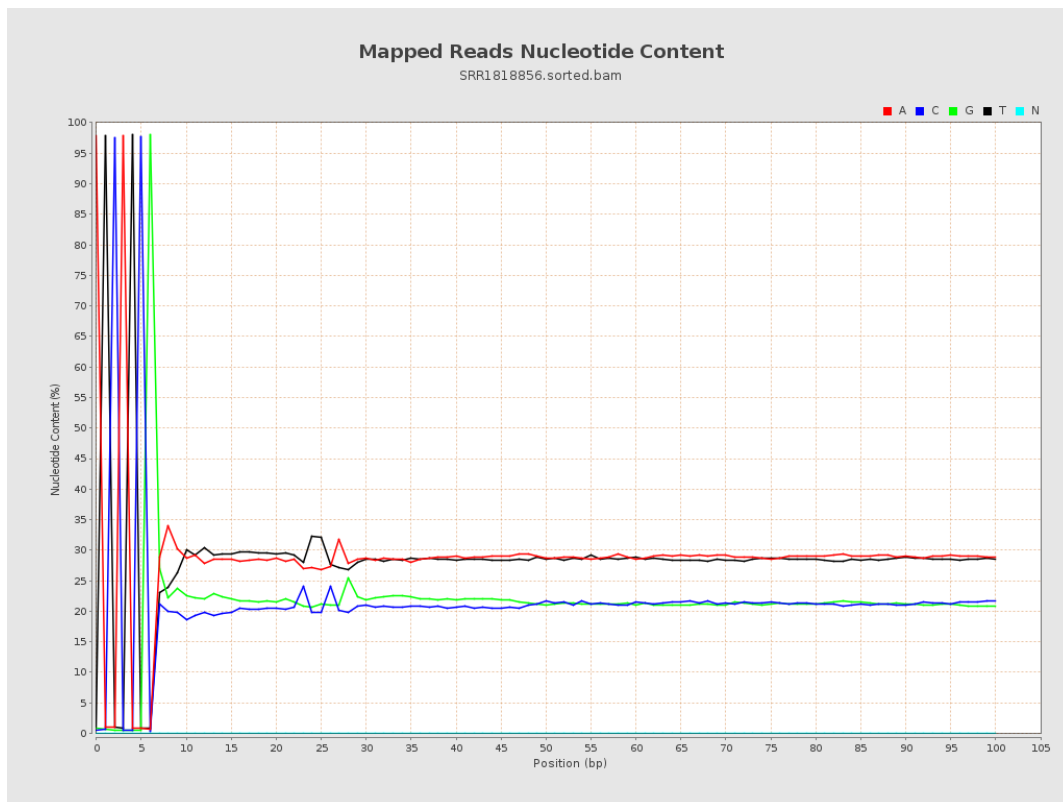
6. Results : Genome Fraction Coverage



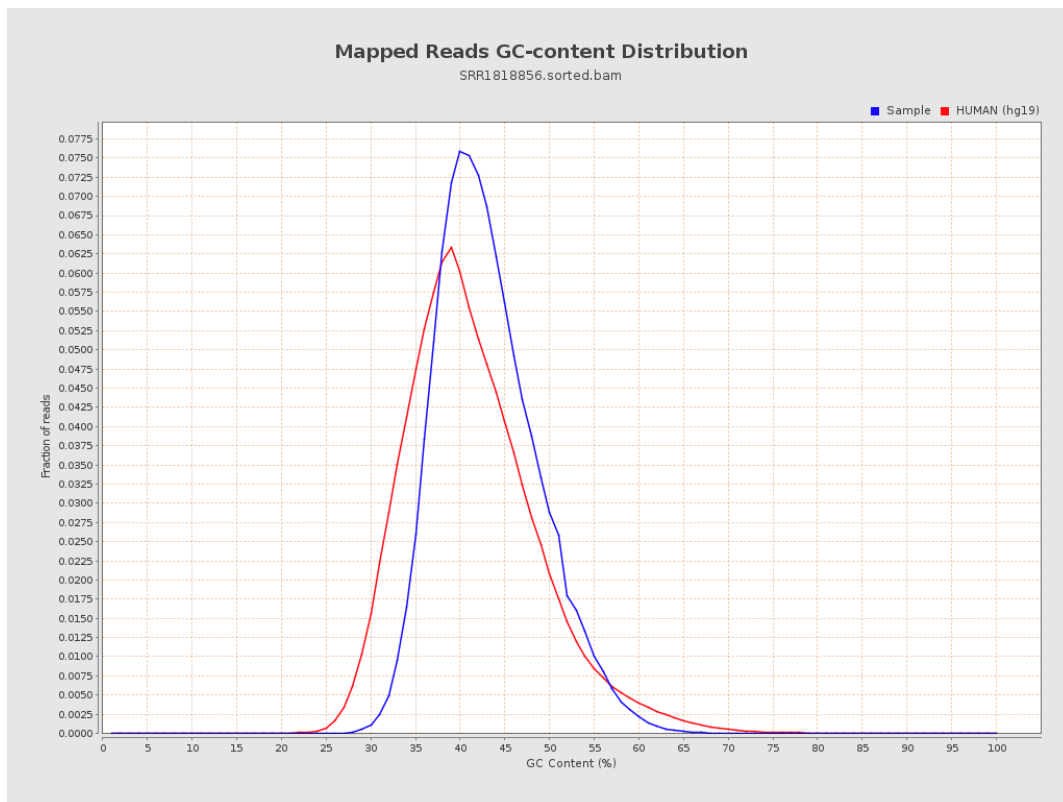
7. Results : Duplication Rate Histogram



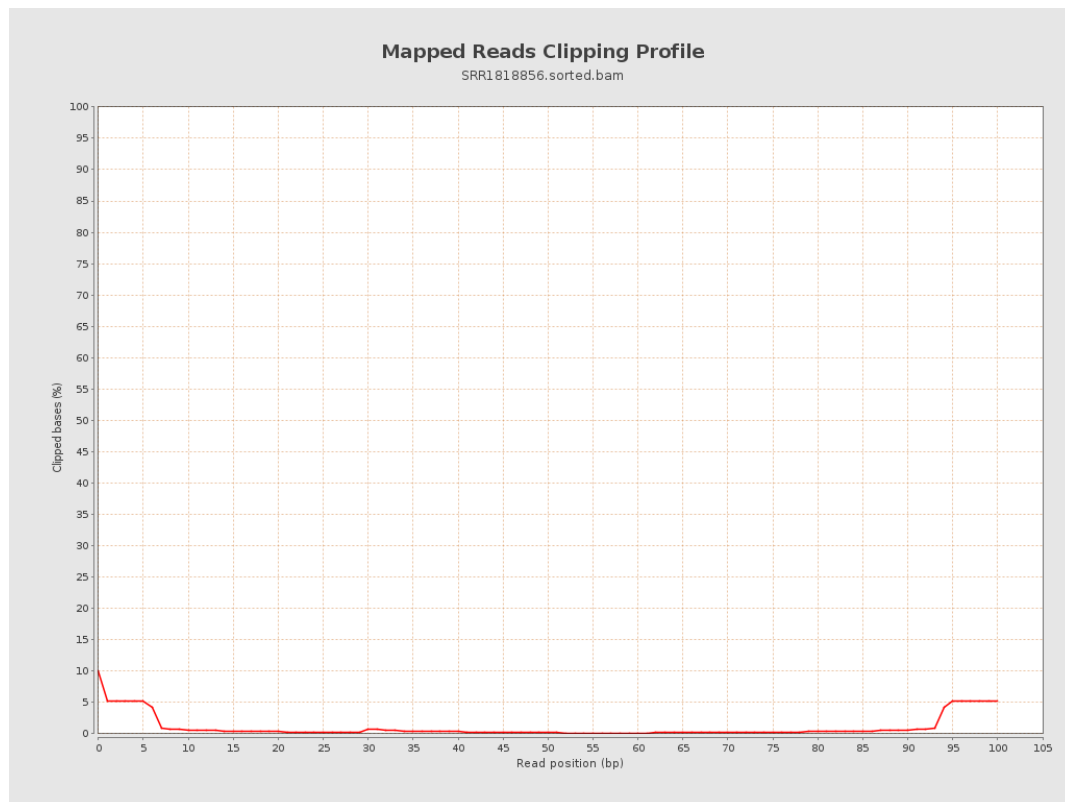
8. Results : Mapped Reads Nucleotide Content



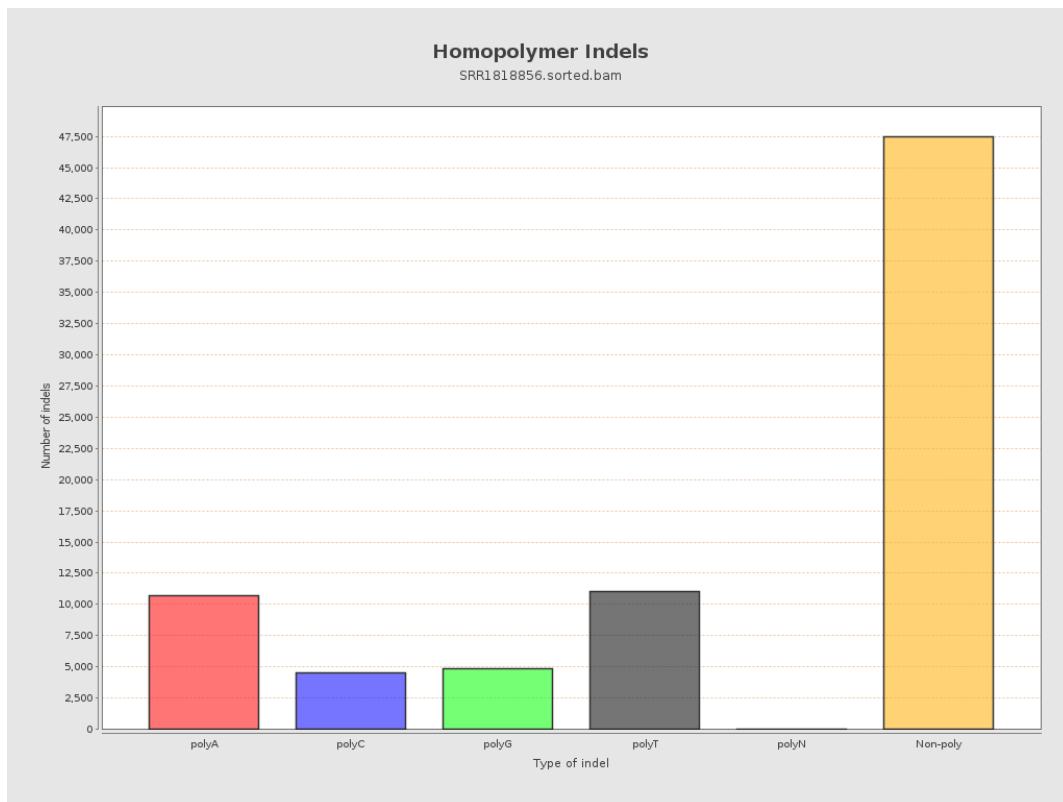
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

