

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 14:30:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818807.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_SRR1818807 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818807.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 14:30:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818807.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,167,502
Mapped reads	3,089,888 / 97.55%
Unmapped reads	77,614 / 2.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,290 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	1,685,257 / 53.2%
Duplication rate	44.73%
Clipped reads	3,102,522 / 97.95%

2.2. ACGT Content

Number/percentage of A's	59,000,886 / 28.1%
Number/percentage of C's	44,722,222 / 21.3%
Number/percentage of T's	60,130,904 / 28.64%
Number/percentage of G's	46,104,153 / 21.96%
Number/percentage of N's	12,423 / 0.01%
GC Percentage	43.26%

2.3. Coverage

Mean	0.0679

Standard Deviation	0.8582
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	47.64
----------------------	-------

2.5. Mismatches and indels

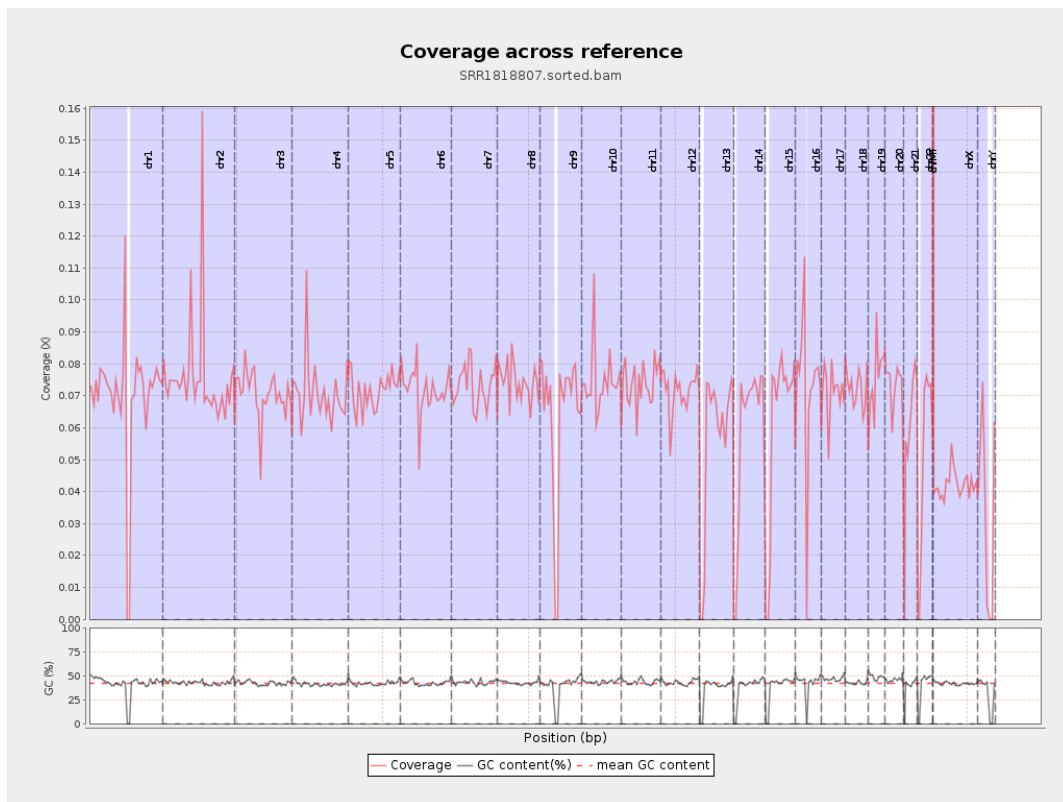
General error rate	0.52%
Mismatches	1,044,528
Insertions	20,129
Mapped reads with at least one insertion	0.64%
Deletions	52,692
Mapped reads with at least one deletion	1.69%
Homopolymer indels	40.83%

2.6. Chromosome stats

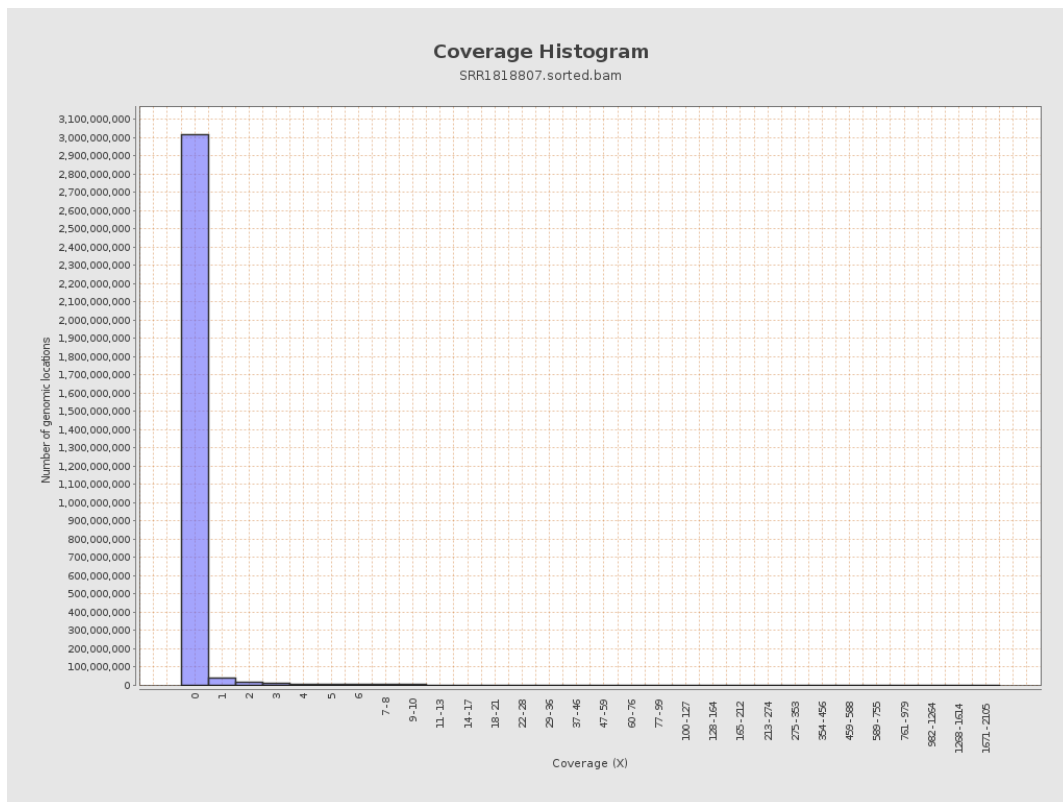
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17428718	0.0699	1.2791
chr2	243199373	18416653	0.0757	1.46
chr3	198022430	13961291	0.0705	0.5692
chr4	191154276	13564174	0.071	0.7038
chr5	180915260	12980681	0.0718	0.6059
chr6	171115067	12295881	0.0719	0.6565
chr7	159138663	11703381	0.0735	0.7155

chr8	146364022	10852325	0.0741	0.6777
chr9	141213431	8985789	0.0636	0.651
chr10	135534747	10049451	0.0741	0.9419
chr11	135006516	9945823	0.0737	0.6712
chr12	133851895	9602715	0.0717	0.6197
chr13	115169878	6446597	0.056	0.5054
chr14	107349540	6400063	0.0596	0.6224
chr15	102531392	6188396	0.0604	0.5394
chr16	90354753	6467972	0.0716	1.0288
chr17	81195210	5810183	0.0716	0.6354
chr18	78077248	5623236	0.072	0.8598
chr19	59128983	4466524	0.0755	1.0947
chr20	63025520	4615264	0.0732	0.6423
chr21	48129895	2896619	0.0602	0.5649
chr22	51304566	2572064	0.0501	0.5562
chrMT	16571	131160	7.915	7.9571
chrX	155270560	6572578	0.0423	0.5291
chrY	59373566	2080467	0.035	1.606

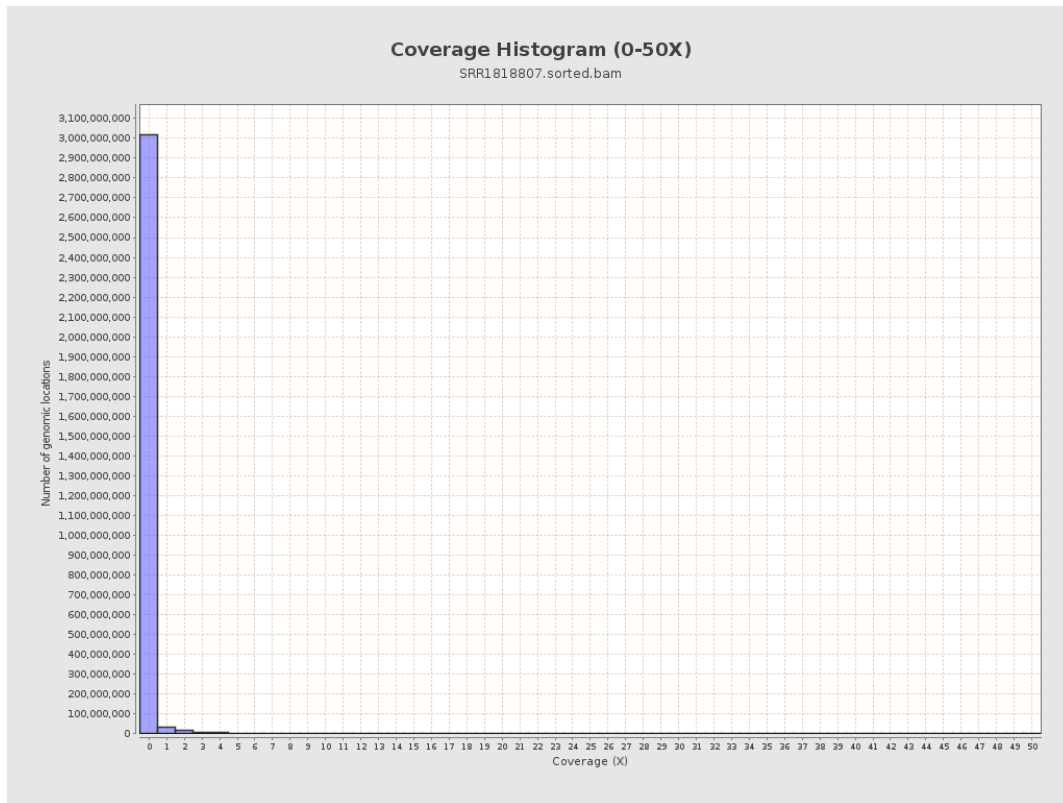
3. Results : Coverage across reference



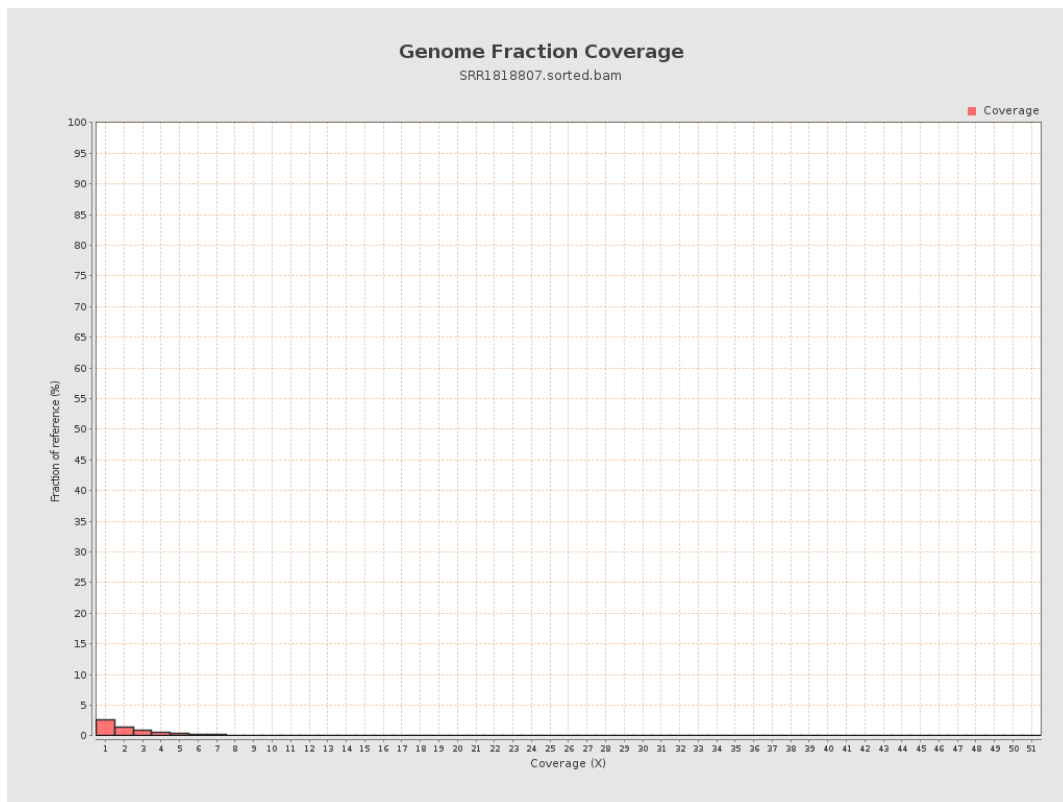
4. Results : Coverage Histogram



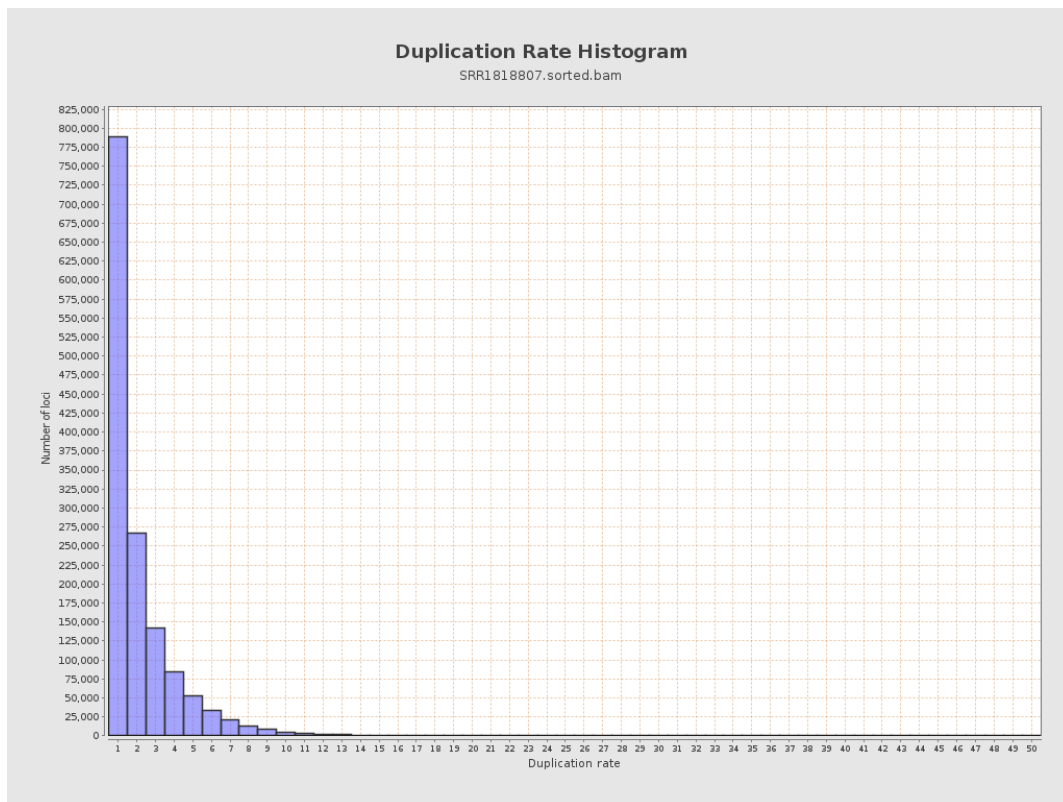
5. Results : Coverage Histogram (0-50X)



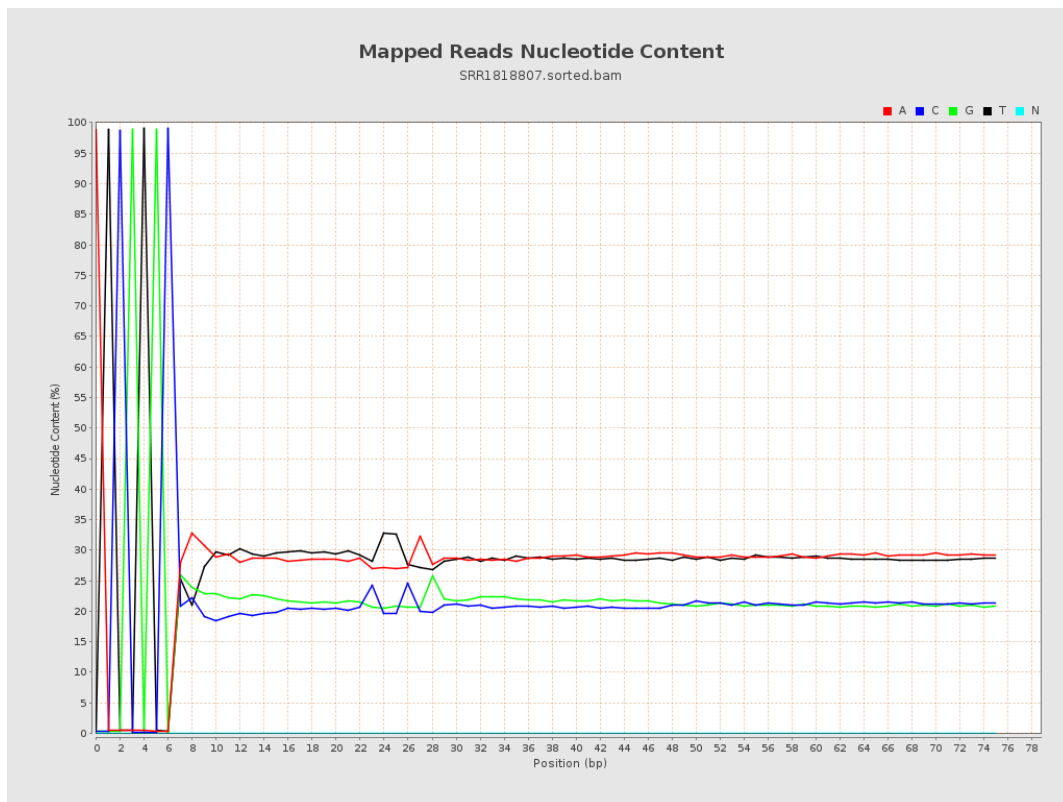
6. Results : Genome Fraction Coverage



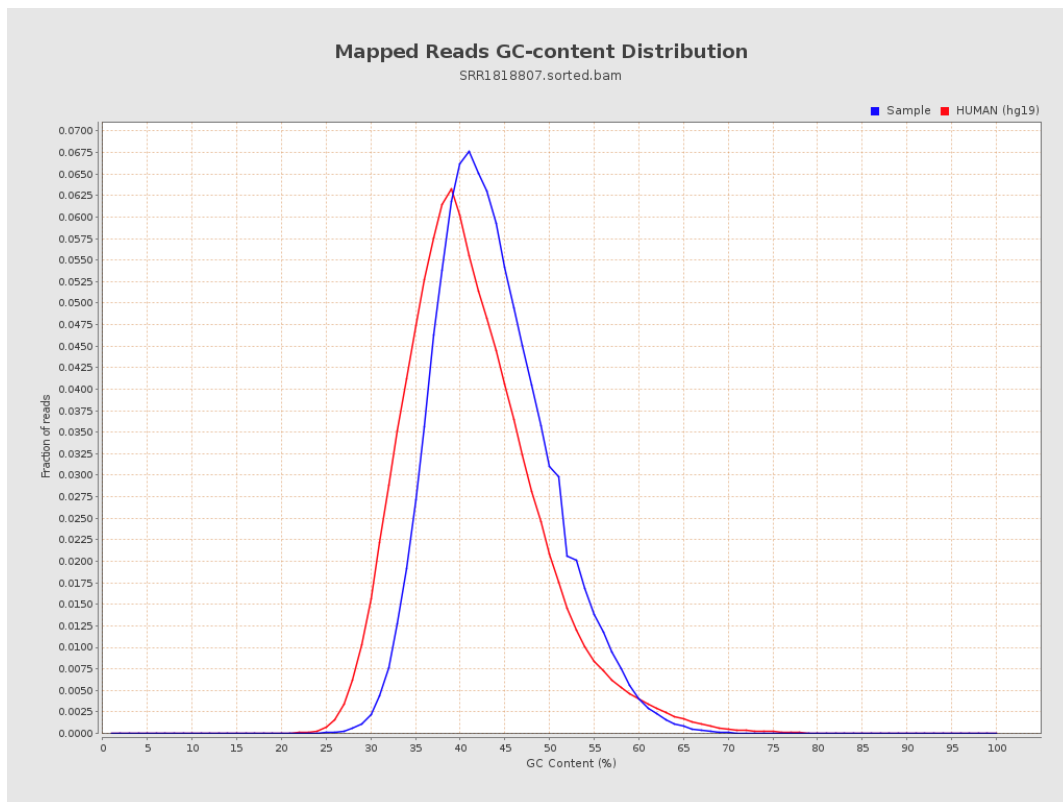
7. Results : Duplication Rate Histogram



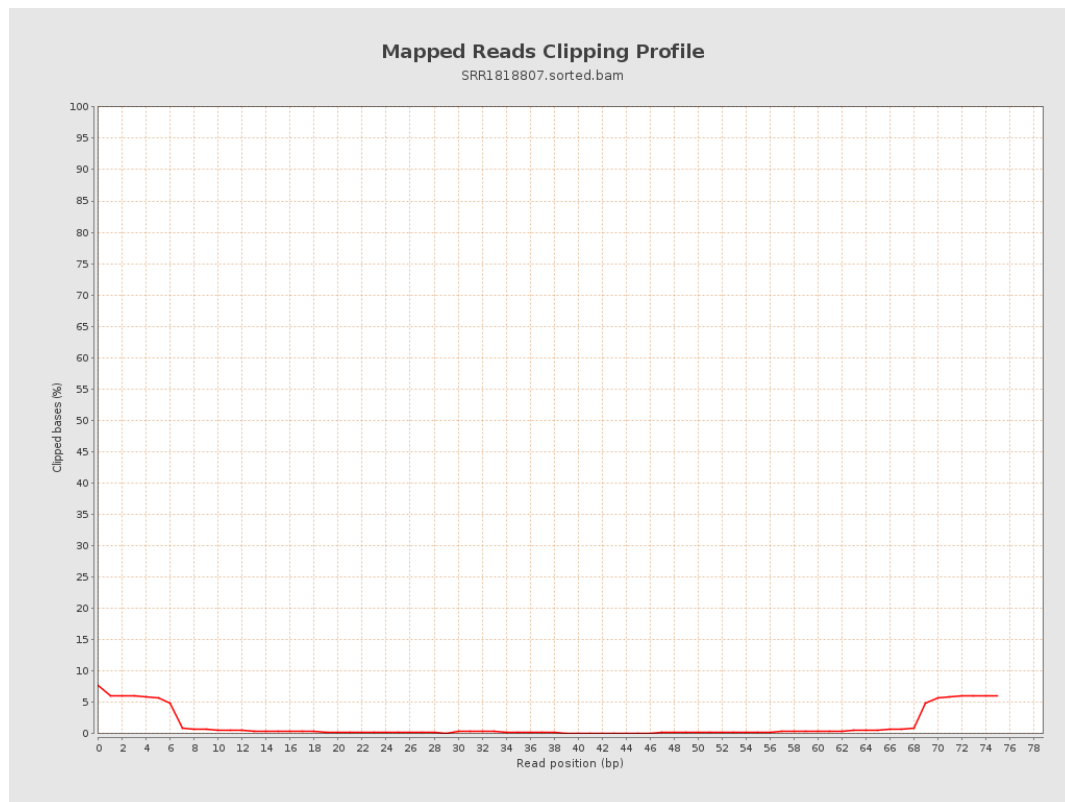
8. Results : Mapped Reads Nucleotide Content



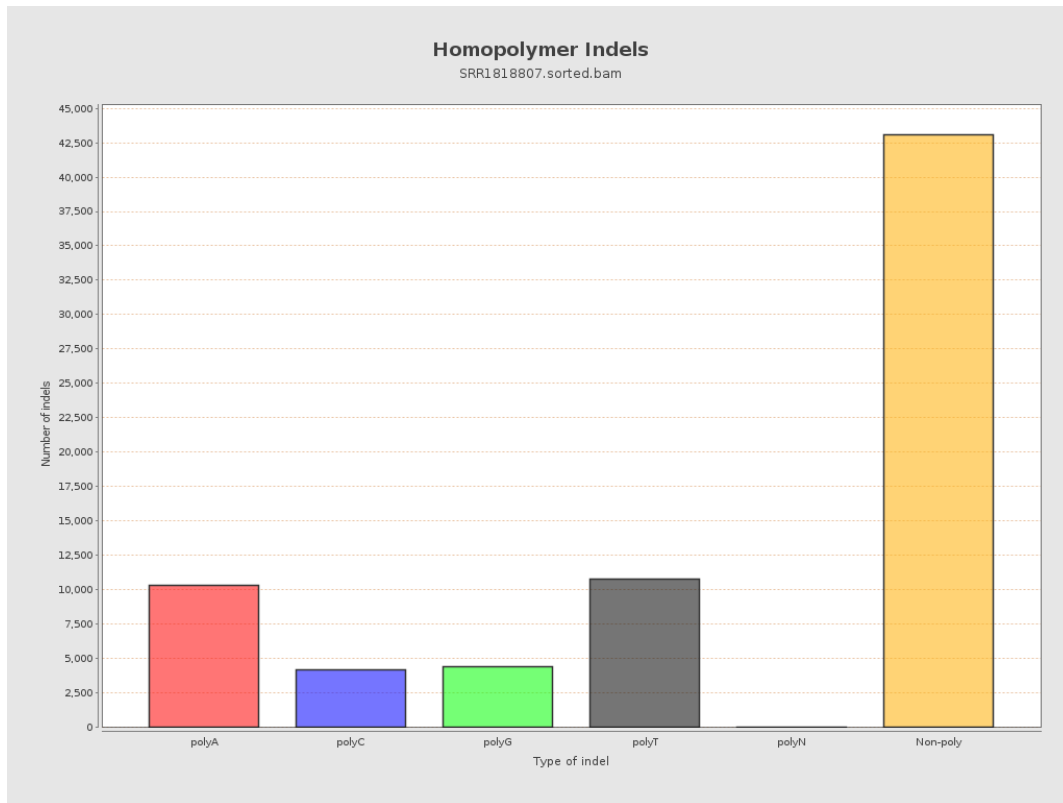
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

