

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/17 20:14:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618572.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_SRR618572 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618572.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 17 20:14:01 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618572.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	70,723,199
Mapped reads	68,588,141 / 96.98%
Unmapped reads	2,135,058 / 3.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	84,375 / 0.12%
Read min/max/mean length	30 / 100 / 100.05
Duplicated reads (estimated)	28,524,472 / 40.33%
Duplication rate	32.87%
Clipped reads	5,829,169 / 8.24%

2.2. ACGT Content

Number/percentage of A's	1,768,653,428 / 26.33%
Number/percentage of C's	1,586,298,470 / 23.62%
Number/percentage of T's	1,788,295,223 / 26.62%
Number/percentage of G's	1,571,699,768 / 23.4%
Number/percentage of N's	2,009,272 / 0.03%
GC Percentage	47.02%

2.3. Coverage

Mean	2.1711

Standard Deviation	20.082
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2.4. Mapping Quality

Mean Mapping Quality	49.89
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2.5. Mismatches and indels

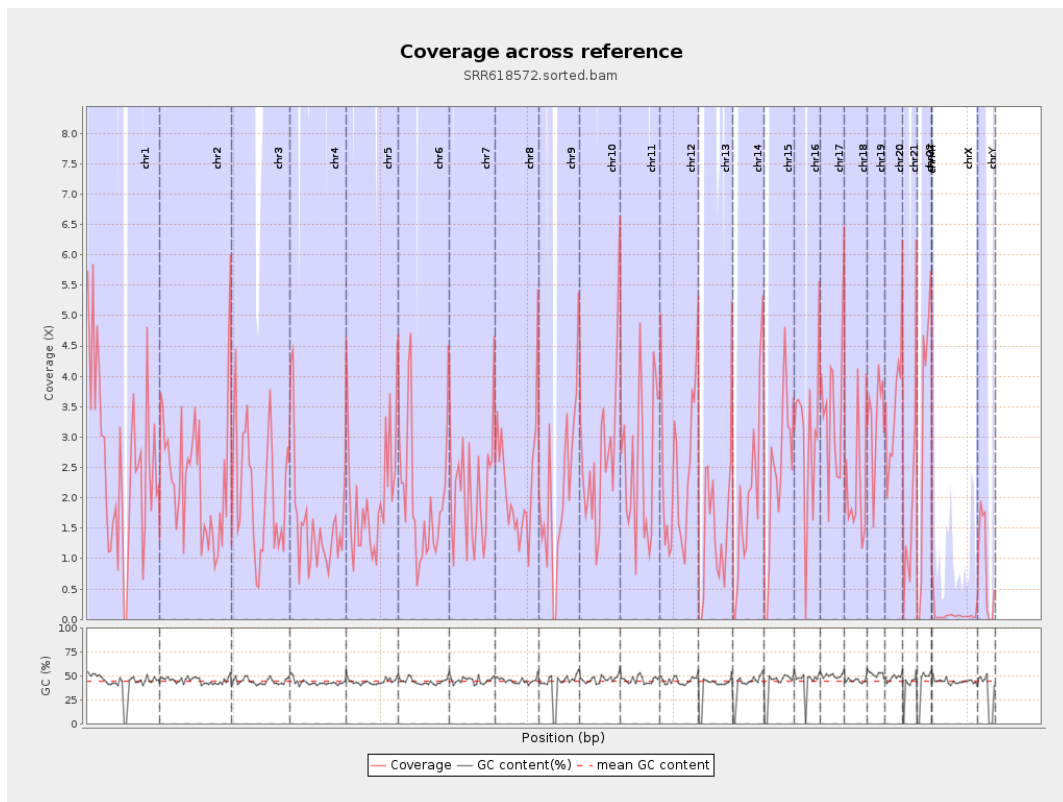
General error rate	0.87%
Mismatches	57,029,902
Insertions	1,034,003
Mapped reads with at least one insertion	1.48%
Deletions	2,781,270
Mapped reads with at least one deletion	3.97%
Homopolymer indels	52.98%

2.6. Chromosome stats

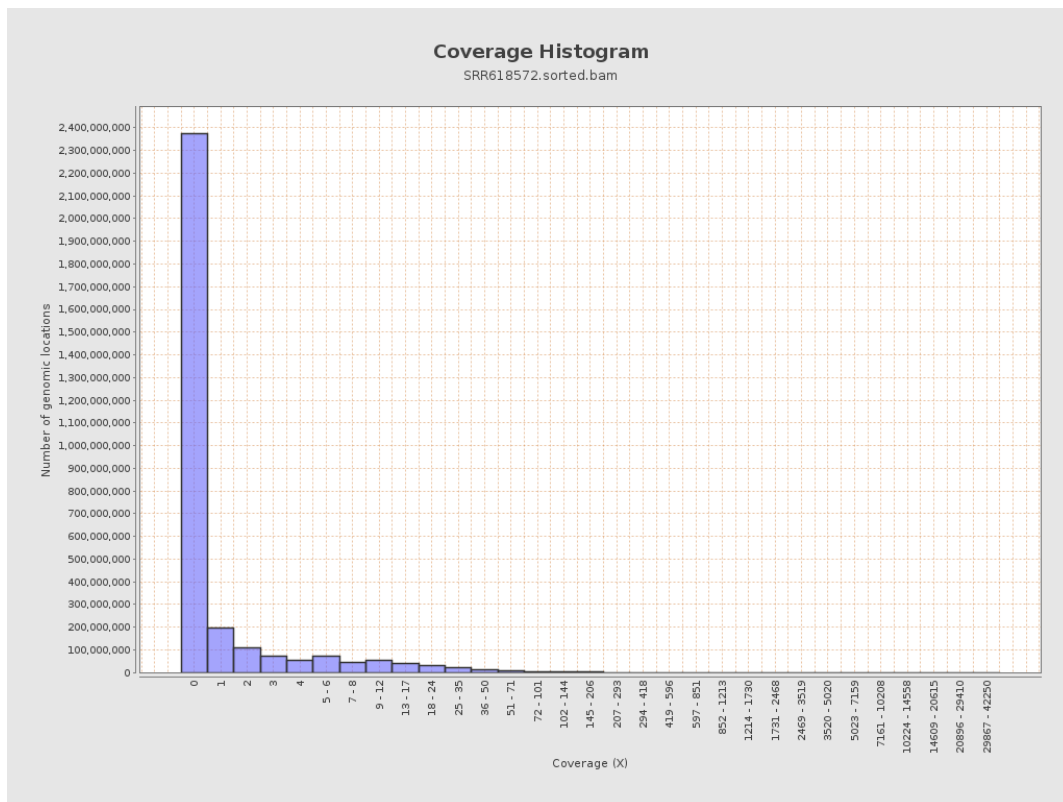
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	636778068	2.5548	19.7329
chr2	243199373	563720981	2.3179	19.4553
chr3	198022430	420779158	2.1249	21.6133
chr4	191154276	296503668	1.5511	21.4329
chr5	180915260	370281517	2.0467	33.3278
chr6	171115067	336203320	1.9648	16.3022
chr7	159138663	340004737	2.1365	18.8788

chr8	146364022	324133350	2.2146	22.7603
chr9	141213431	305546473	2.1637	16.4542
chr10	135534747	361005943	2.6636	19.4783
chr11	135006516	358709204	2.657	18.9286
chr12	133851895	321274554	2.4002	20.0595
chr13	115169878	164446908	1.4279	14.3568
chr14	107349540	216998939	2.0214	14.3606
chr15	102531392	241762469	2.3579	20.8082
chr16	90354753	272737181	3.0185	24.0095
chr17	81195210	281224026	3.4636	21.0877
chr18	78077248	170341181	2.1817	17.536
chr19	59128983	198967557	3.365	16.7457
chr20	63025520	216631679	3.4372	15.6288
chr21	48129895	91564558	1.9024	16.2792
chr22	51304566	166554944	3.2464	31.5118
chrMT	16571	13803	0.833	3.1958
chrX	155270560	11541340	0.0743	3.5872
chrY	59373566	53253519	0.8969	10.4906

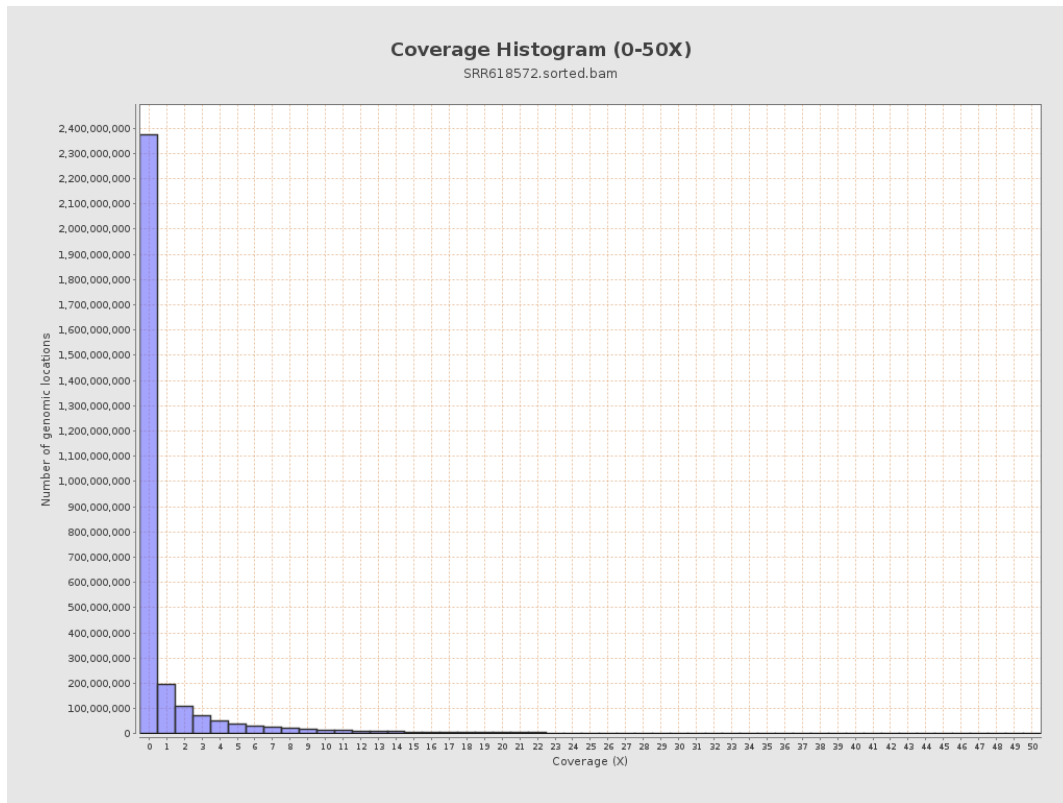
3. Results : Coverage across reference



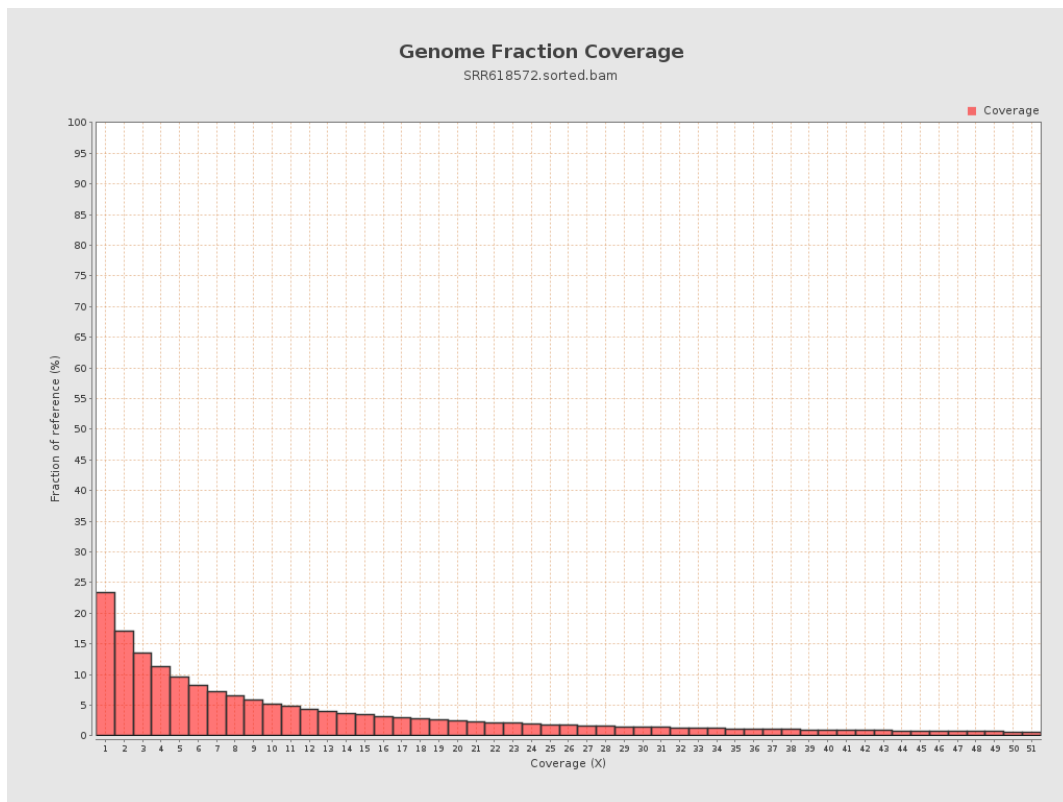
4. Results : Coverage Histogram



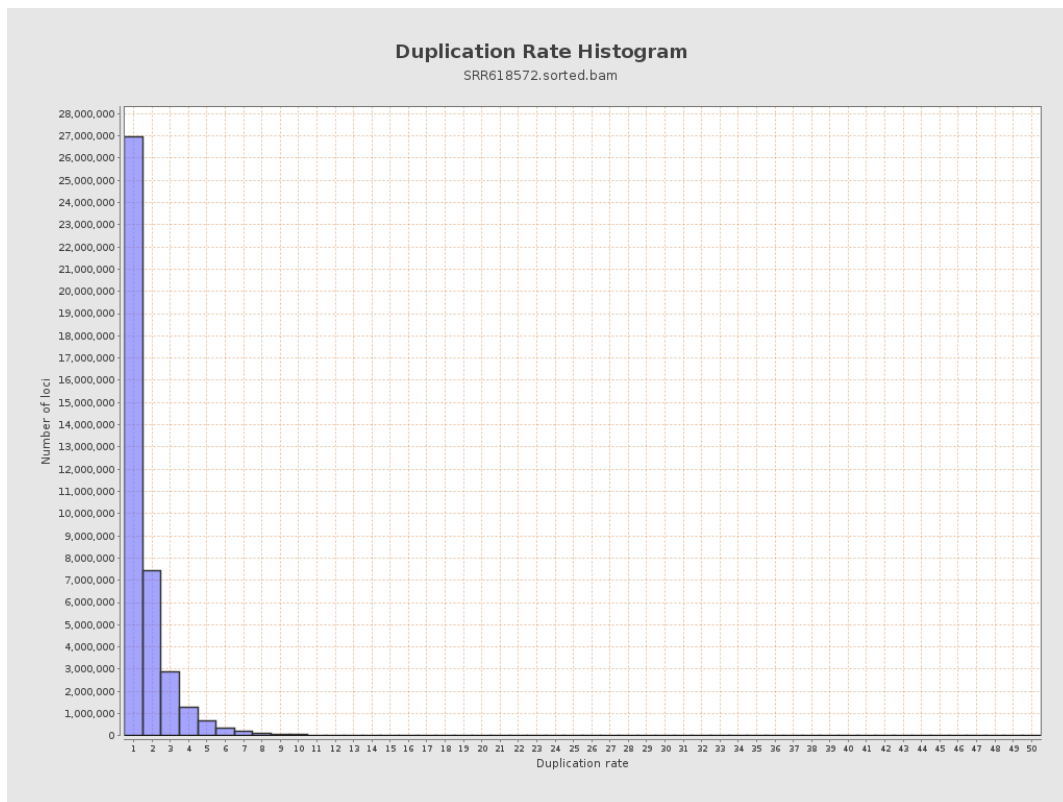
5. Results : Coverage Histogram (0-50X)



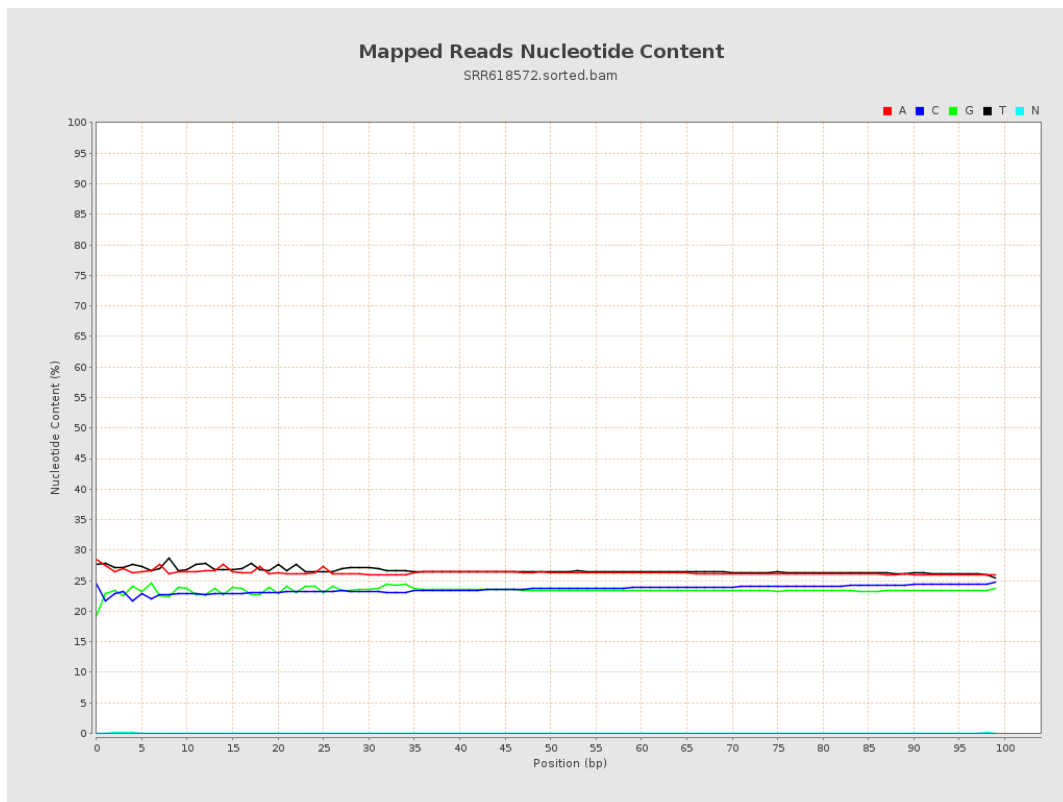
6. Results : Genome Fraction Coverage



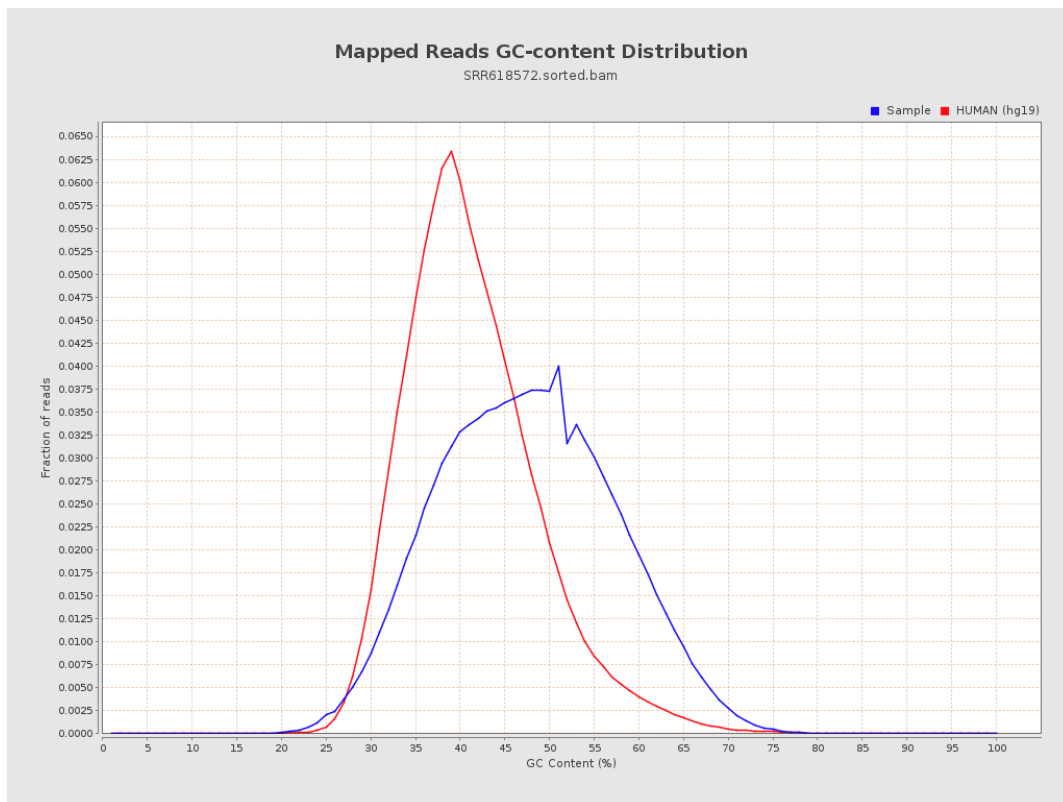
7. Results : Duplication Rate Histogram



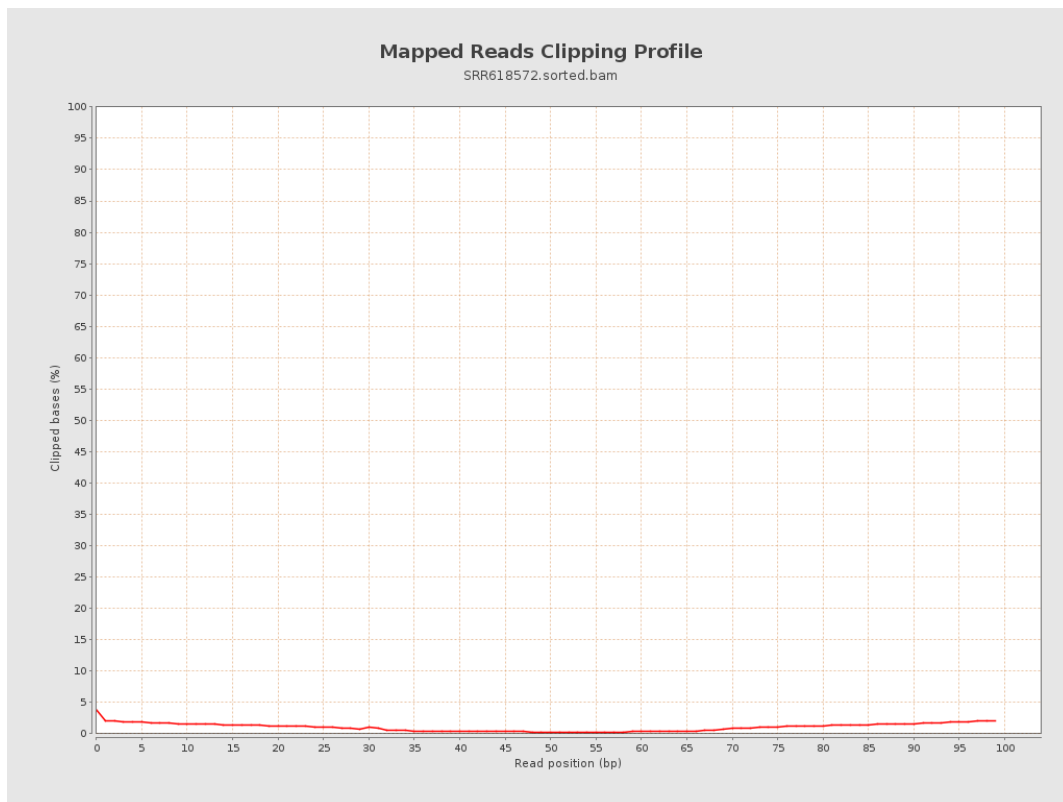
8. Results : Mapped Reads Nucleotide Content



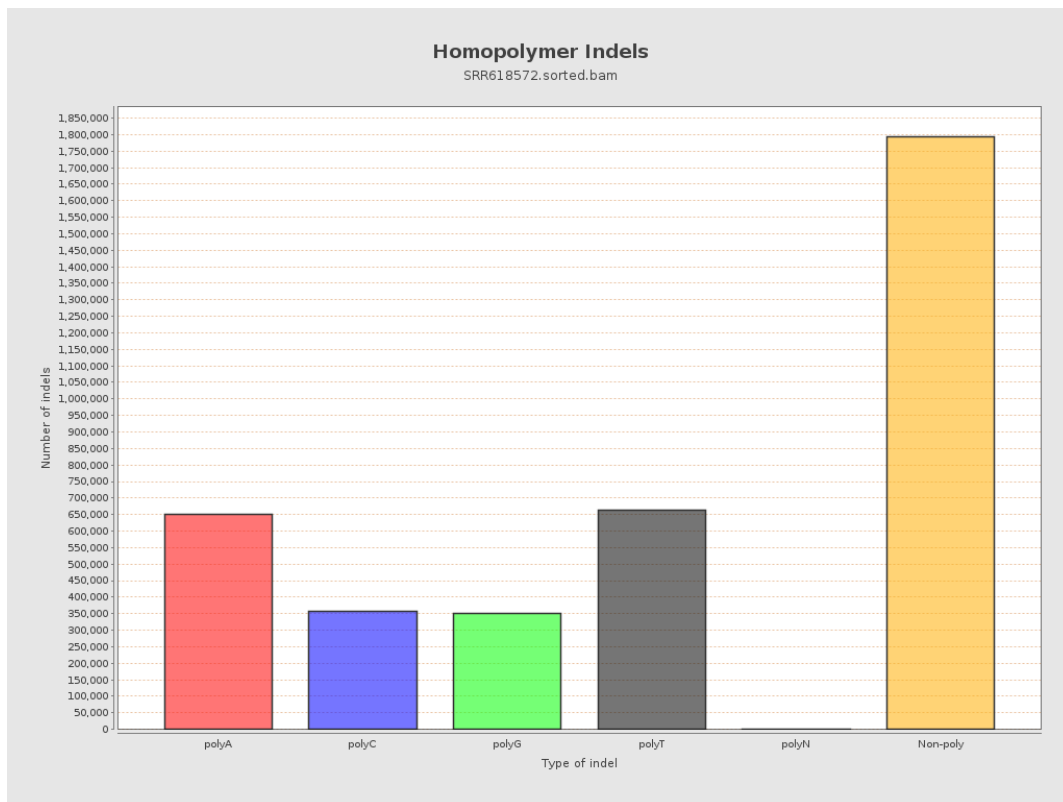
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

