

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 15:16:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618659.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_SRR618659 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618659.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 15:16:14 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618659.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	49,244,433
Mapped reads	33,816,899 / 68.67%
Unmapped reads	15,427,534 / 31.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	151,970 / 0.31%
Read min/max/mean length	30 / 100 / 100.12
Duplicated reads (estimated)	17,963,420 / 36.48%
Duplication rate	34.39%
Clipped reads	4,426,774 / 8.99%

2.2. ACGT Content

Number/percentage of A's	877,383,637 / 26.81%
Number/percentage of C's	759,080,891 / 23.19%
Number/percentage of T's	926,089,840 / 28.3%
Number/percentage of G's	709,376,126 / 21.67%
Number/percentage of N's	936,957 / 0.03%
GC Percentage	44.87%

2.3. Coverage

Mean	1.0579

Standard Deviation	18.6103
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2.4. Mapping Quality

Mean Mapping Quality	51.68
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2.5. Mismatches and indels

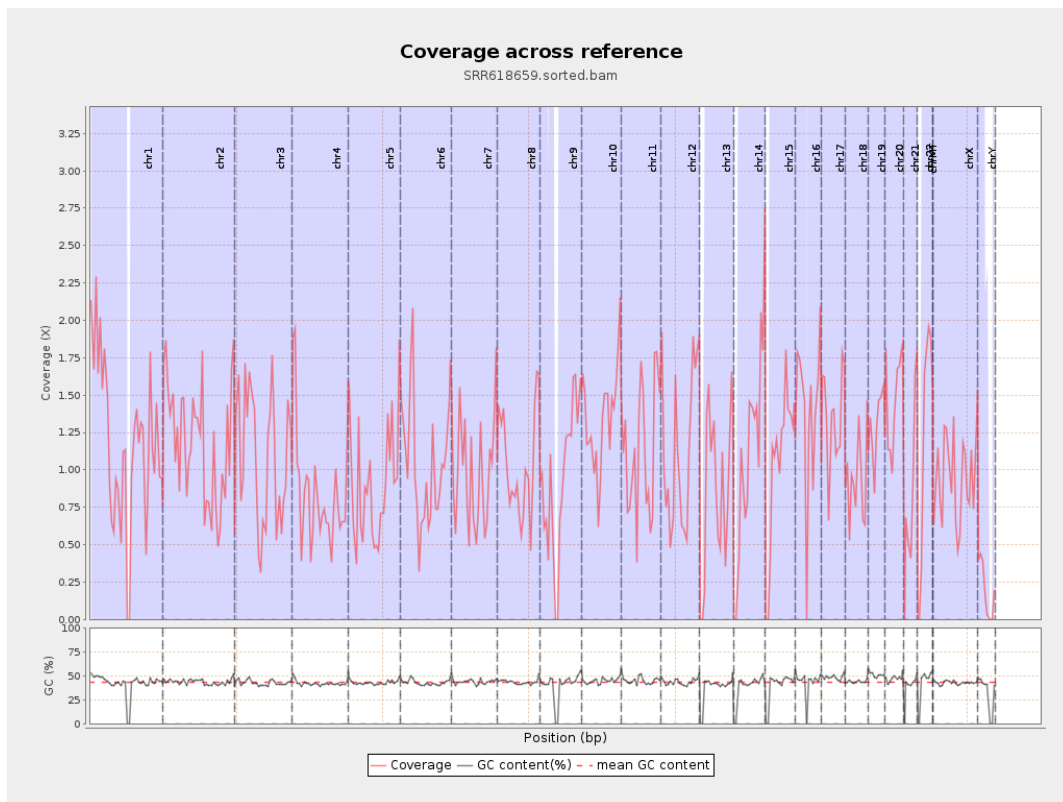
General error rate	0.83%
Mismatches	26,242,919
Insertions	578,067
Mapped reads with at least one insertion	1.67%
Deletions	1,468,712
Mapped reads with at least one deletion	4.23%
Homopolymer indels	52.02%

2.6. Chromosome stats

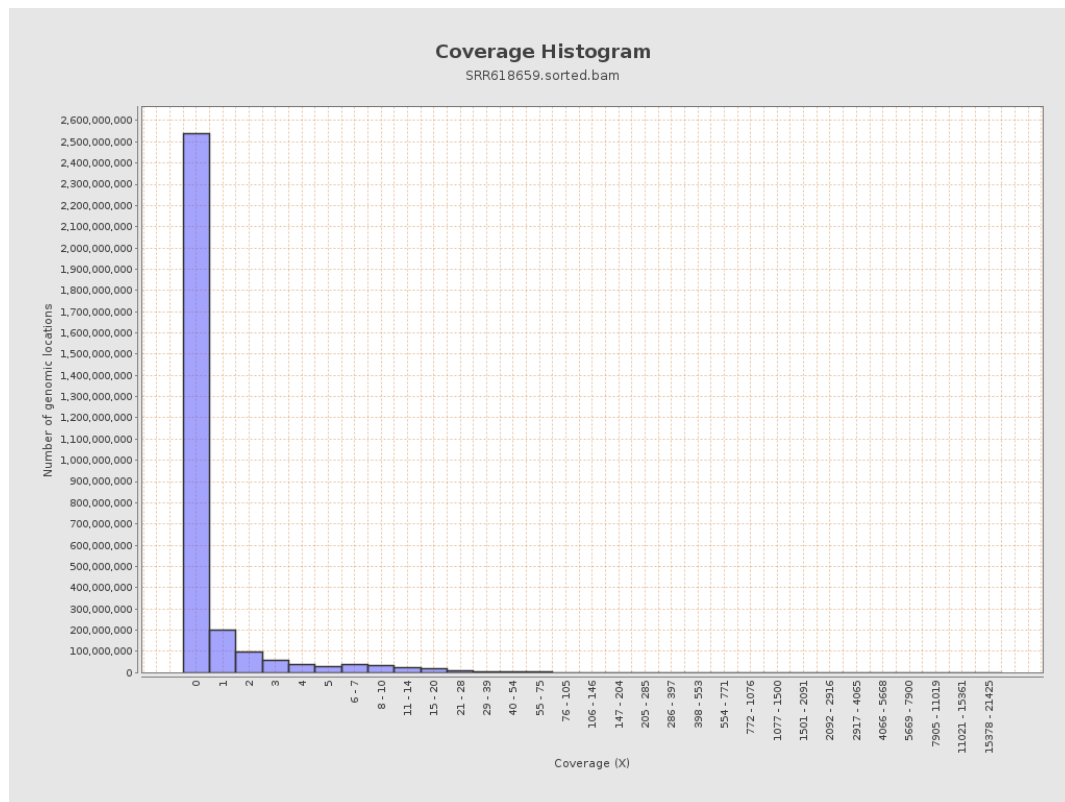
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	290670947	1.1662	22.3939
chr2	243199373	286475104	1.1779	19.225
chr3	198022430	213911064	1.0802	23.9976
chr4	191154276	159230514	0.833	16.2585
chr5	180915260	165966744	0.9174	14.1737
chr6	171115067	176747404	1.0329	12.9238
chr7	159138663	157612577	0.9904	22.2768

chr8	146364022	150380174	1.0274	16.3267
chr9	141213431	131866150	0.9338	23.9917
chr10	135534747	180583662	1.3324	19.7156
chr11	135006516	151775234	1.1242	11.265
chr12	133851895	152297840	1.1378	18.6101
chr13	115169878	99725711	0.8659	22.3695
chr14	107349540	114429925	1.066	19.1525
chr15	102531392	106924897	1.0429	18.0155
chr16	90354753	125336723	1.3872	22.4789
chr17	81195210	109115523	1.3439	18.3168
chr18	78077248	71524613	0.9161	14.3571
chr19	59128983	76469819	1.2933	10.7051
chr20	63025520	91735937	1.4555	10.9447
chr21	48129895	41425586	0.8607	11.9313
chr22	51304566	62291456	1.2142	18.5078
chrMT	16571	10598	0.6396	2.9115
chrX	155270560	146869810	0.9459	16.8177
chrY	59373566	11652342	0.1963	13.1636

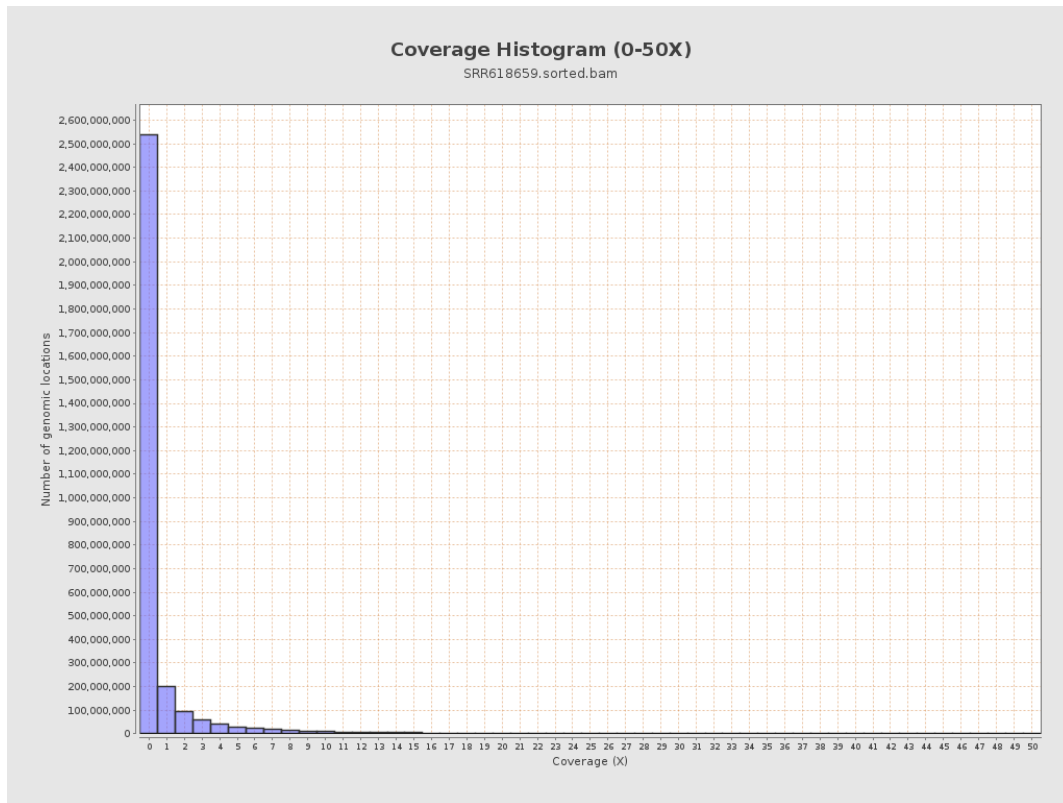
3. Results : Coverage across reference



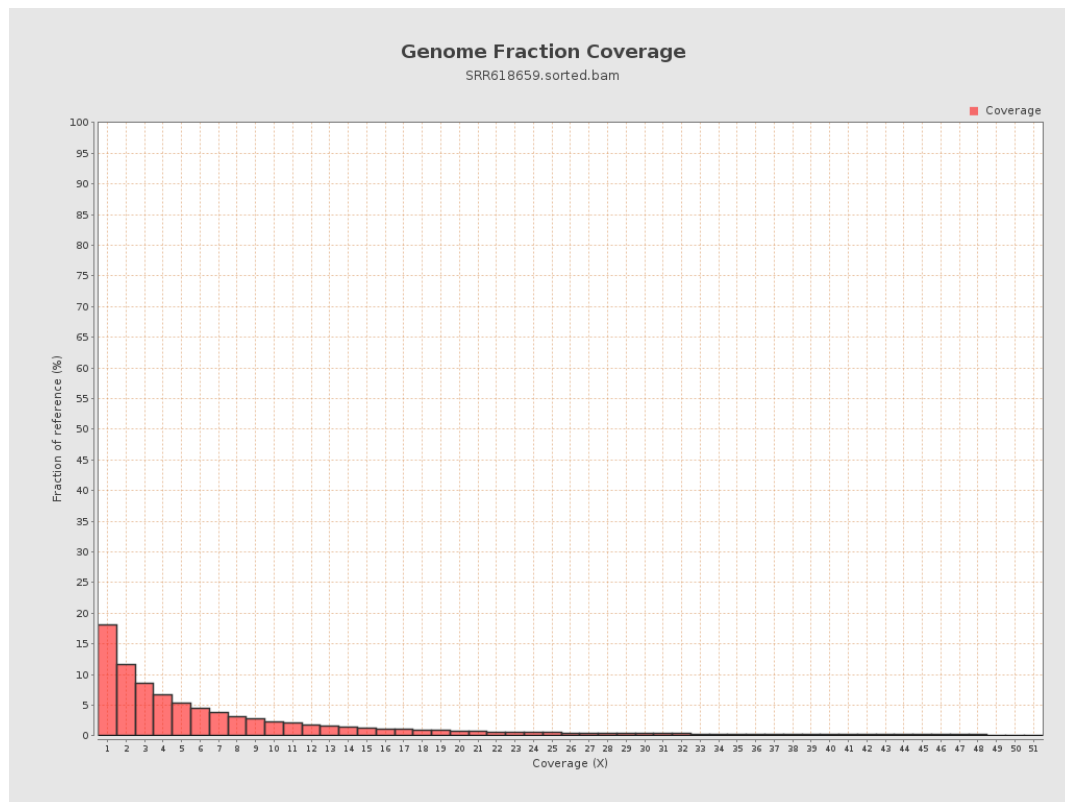
4. Results : Coverage Histogram



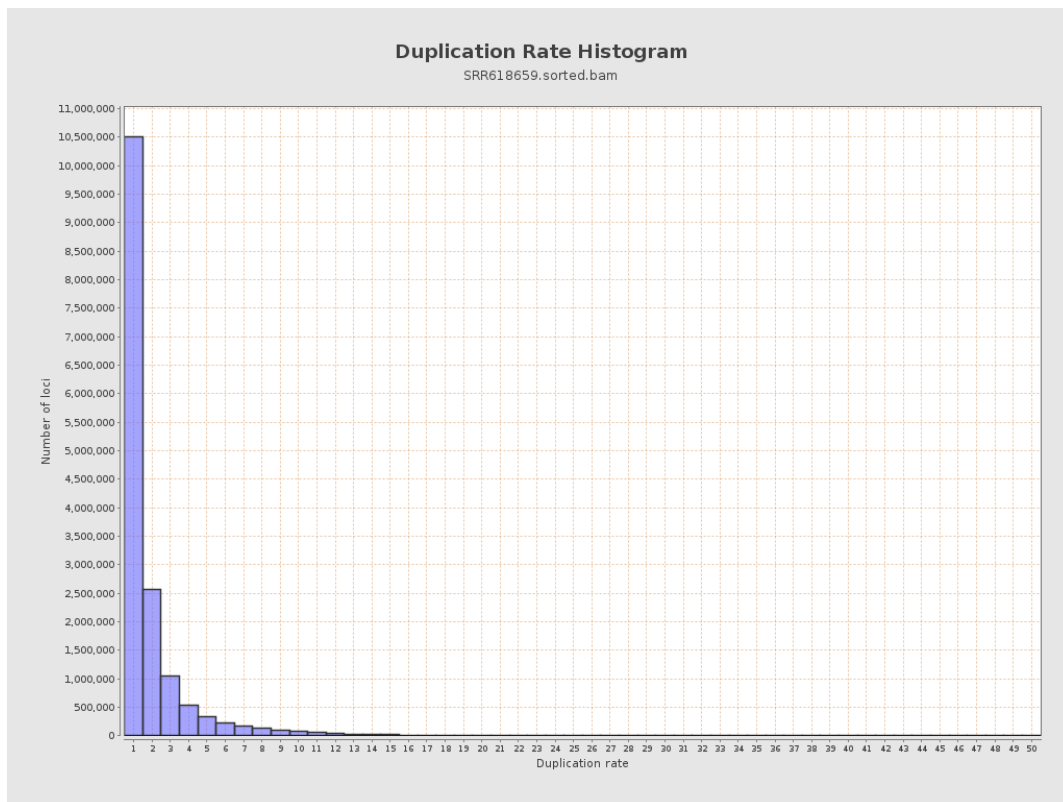
5. Results : Coverage Histogram (0-50X)



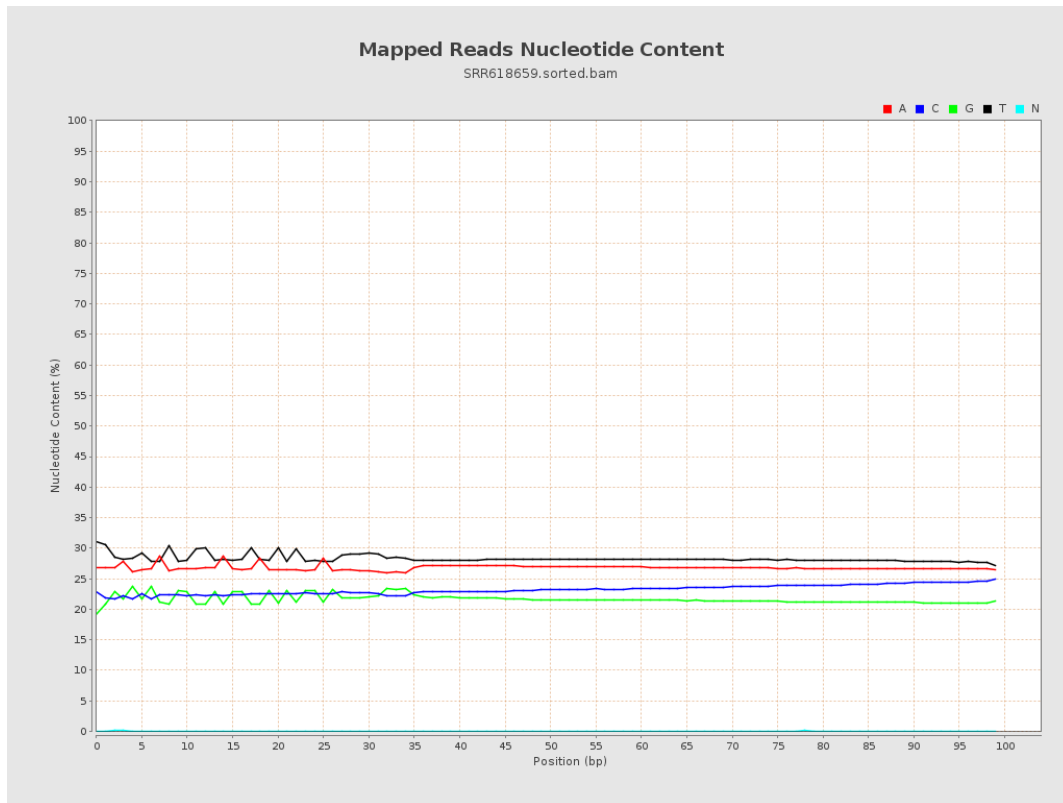
6. Results : Genome Fraction Coverage



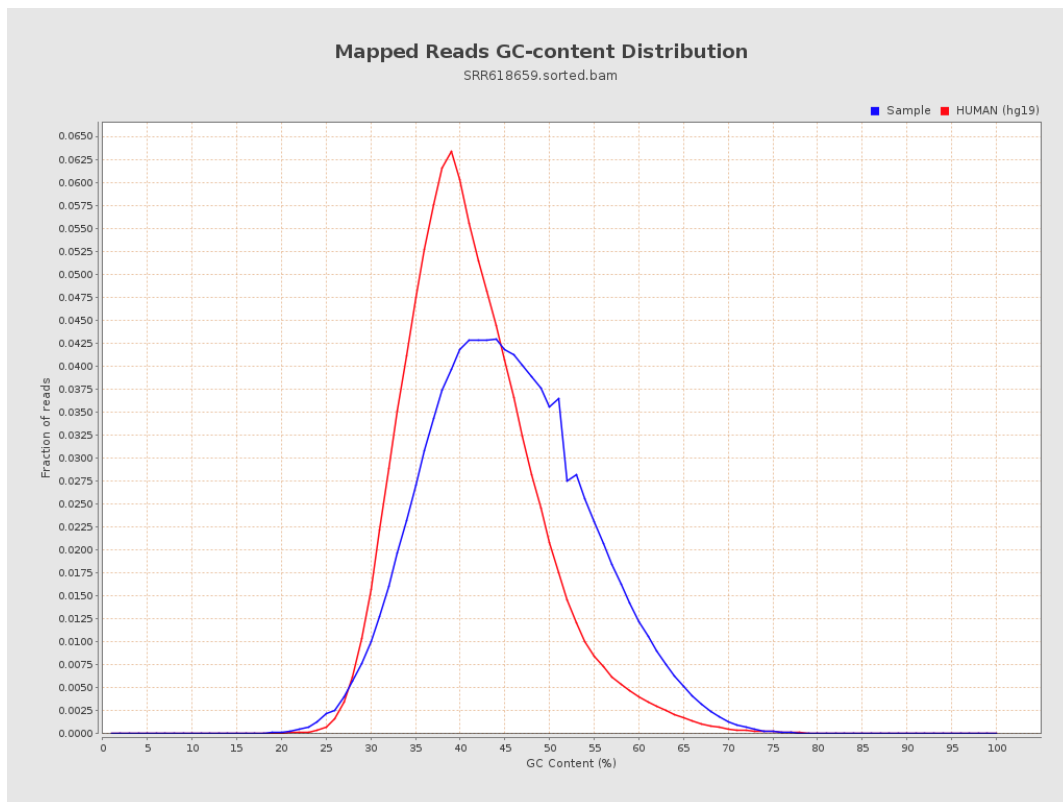
7. Results : Duplication Rate Histogram



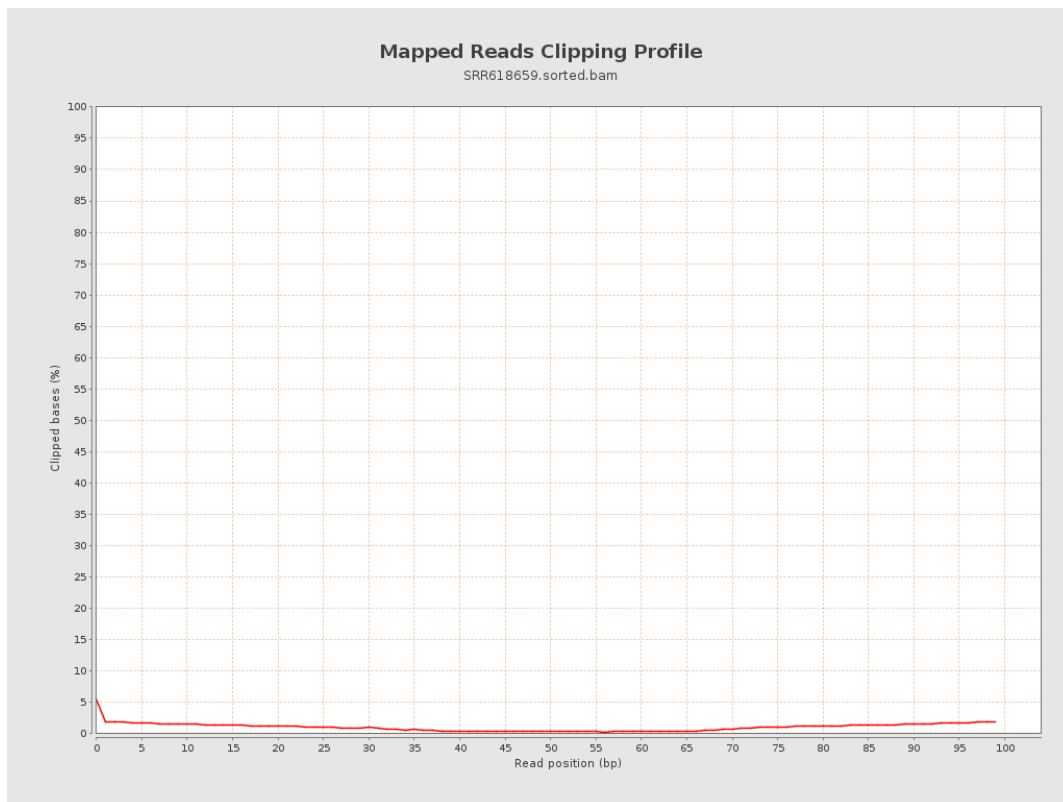
8. Results : Mapped Reads Nucleotide Content



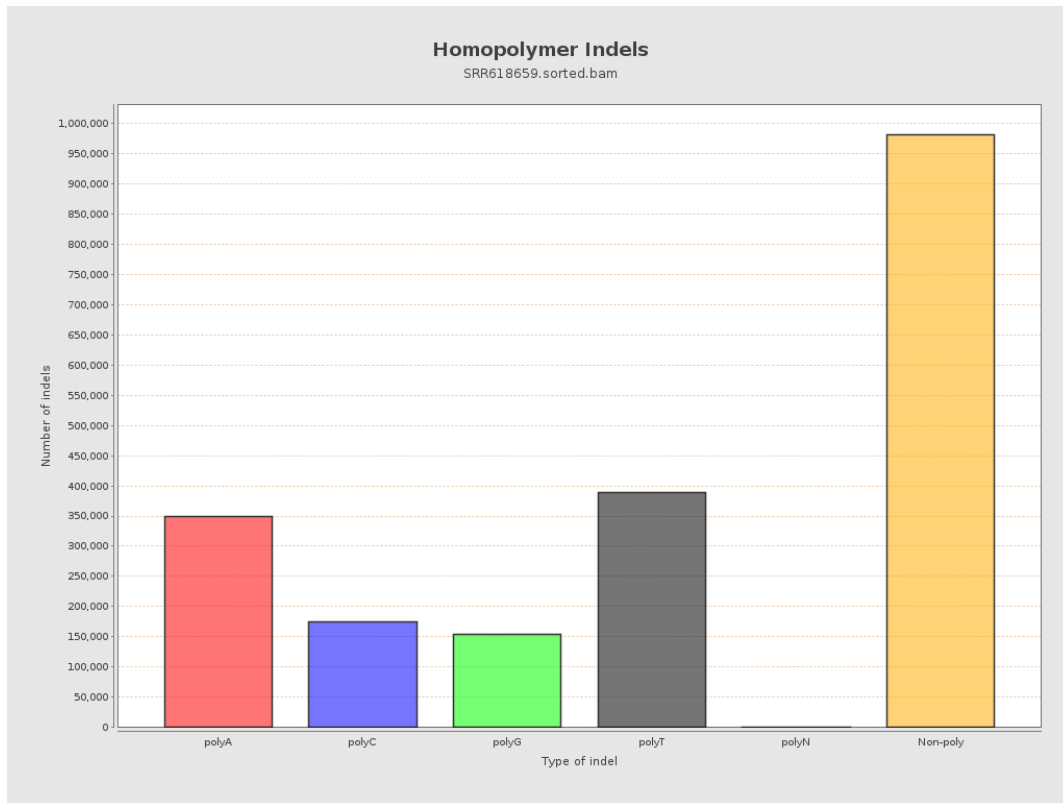
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

