

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 21:09:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618633.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_SRR618633 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618633_1.fastq.gz SRR618633_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 21:09:21 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618633.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,158,324
Mapped reads	20,839,378 / 94.05%
Unmapped reads	1,318,946 / 5.95%
Mapped paired reads	20,839,378 / 94.05%
Mapped reads, first in pair	10,647,208 / 48.05%
Mapped reads, second in pair	10,192,170 / 46%
Mapped reads, both in pair	20,197,046 / 91.15%
Mapped reads, singletons	642,332 / 2.9%
Secondary alignments	0
Supplementary alignments	99,985 / 0.45%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	4,445,163 / 20.06%
Duplication rate	18.57%
Clipped reads	4,840,574 / 21.85%

2.2. ACGT Content

Number/percentage of A's	539,007,926 / 27.57%
Number/percentage of C's	418,253,171 / 21.39%
Number/percentage of T's	548,842,160 / 28.07%
Number/percentage of G's	449,054,286 / 22.97%
Number/percentage of N's	72,967 / 0%

GC Percentage	44.36%
---------------	--------

2.3. Coverage

Mean	0.6321
Standard Deviation	2.6151

2.4. Mapping Quality

Mean Mapping Quality	53.35
----------------------	-------

2.5. Insert size

Mean	109,120.06
Standard Deviation	3,295,591.5
P25/Median/P75	172 / 198 / 232

2.6. Mismatches and indels

General error rate	1.25%
Mismatches	23,905,220
Insertions	372,353
Mapped reads with at least one insertion	1.76%
Deletions	1,059,232
Mapped reads with at least one deletion	4.95%
Homopolymer indels	52.97%

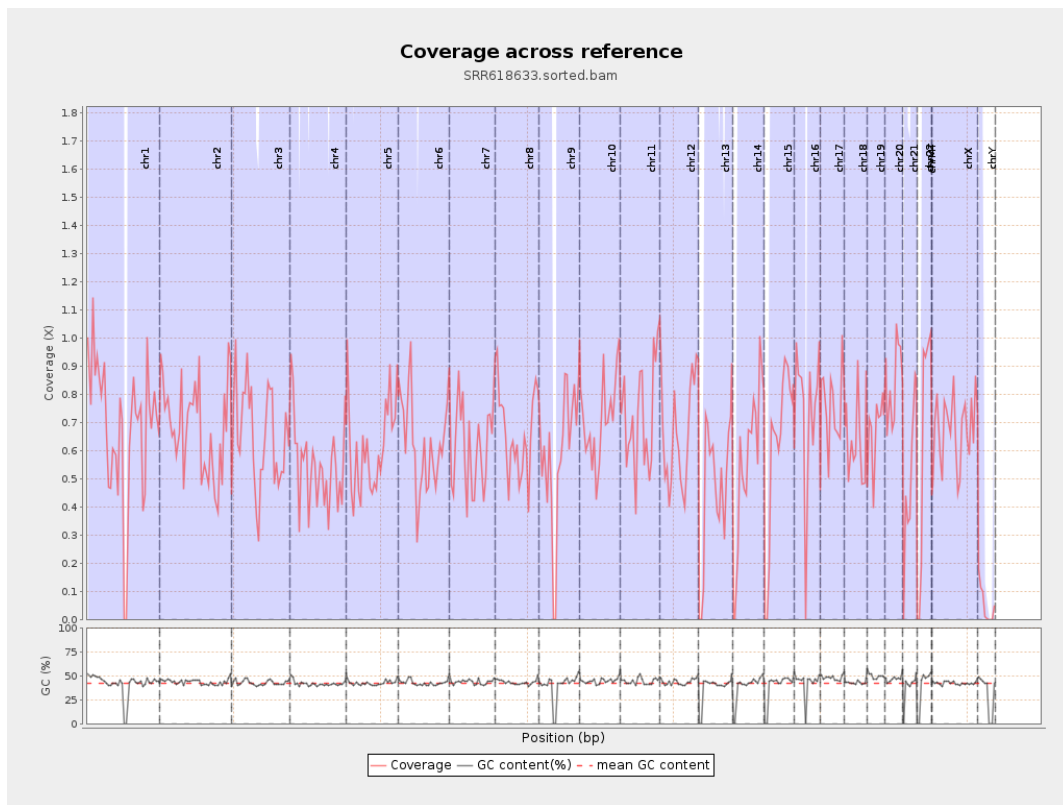
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

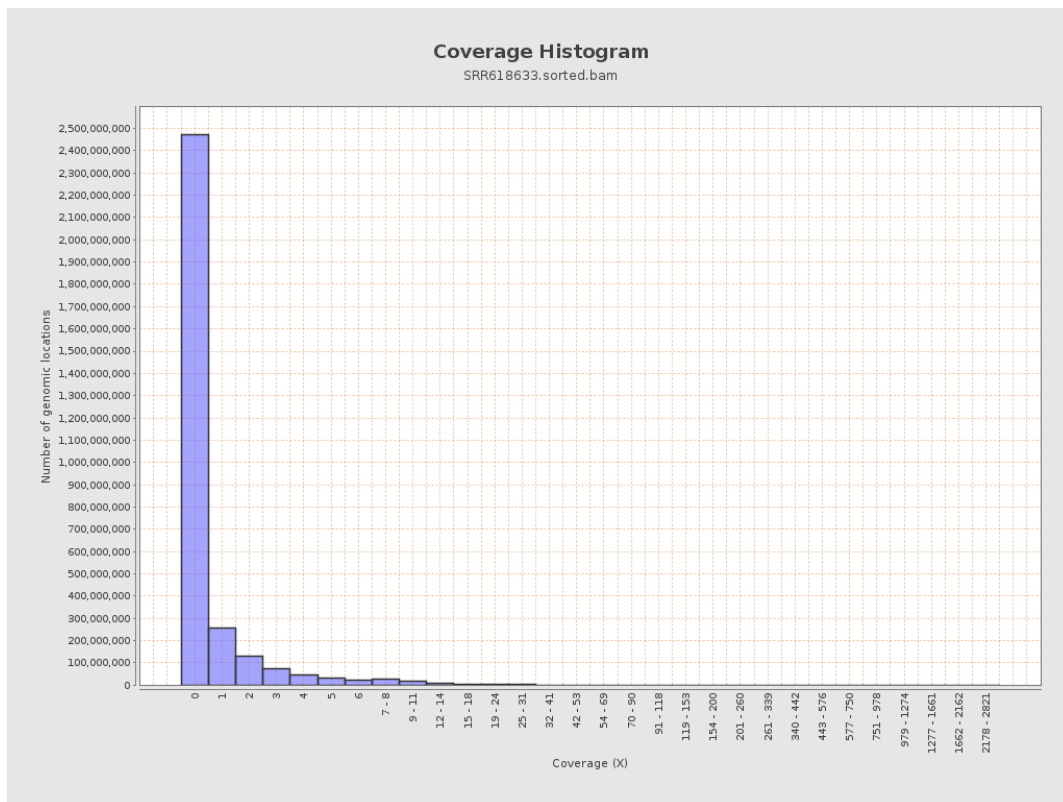
		bases	coverage	deviation
chr1	249250621	170562415	0.6843	3.2552
chr2	243199373	165153470	0.6791	3.1269
chr3	198022430	129617631	0.6546	2.2161
chr4	191154276	103693995	0.5425	2.1455
chr5	180915260	111729059	0.6176	2.1936
chr6	171115067	106691855	0.6235	2.1515
chr7	159138663	98136144	0.6167	2.2027
chr8	146364022	95815255	0.6546	2.4057
chr9	141213431	83166400	0.5889	2.8469
chr10	135534747	96099882	0.709	2.4208
chr11	135006516	97214963	0.7201	2.8071
chr12	133851895	88155927	0.6586	2.4612
chr13	115169878	53613697	0.4655	1.7462
chr14	107349540	59278148	0.5522	2.0785
chr15	102531392	62210455	0.6067	2.2672
chr16	90354753	65760915	0.7278	4.7849
chr17	81195210	61835401	0.7616	2.4906
chr18	78077248	49872966	0.6388	2.9326
chr19	59128983	40052096	0.6774	2.6504
chr20	63025520	53146230	0.8432	2.6663
chr21	48129895	24719533	0.5136	3.0648
chr22	51304566	32885997	0.641	2.4724
chrMT	16571	7309	0.4411	1.6714
chrX	155270560	104249017	0.6714	2.2352

chrY	59373566	3003992	0.0506	1.727
------	----------	---------	--------	-------

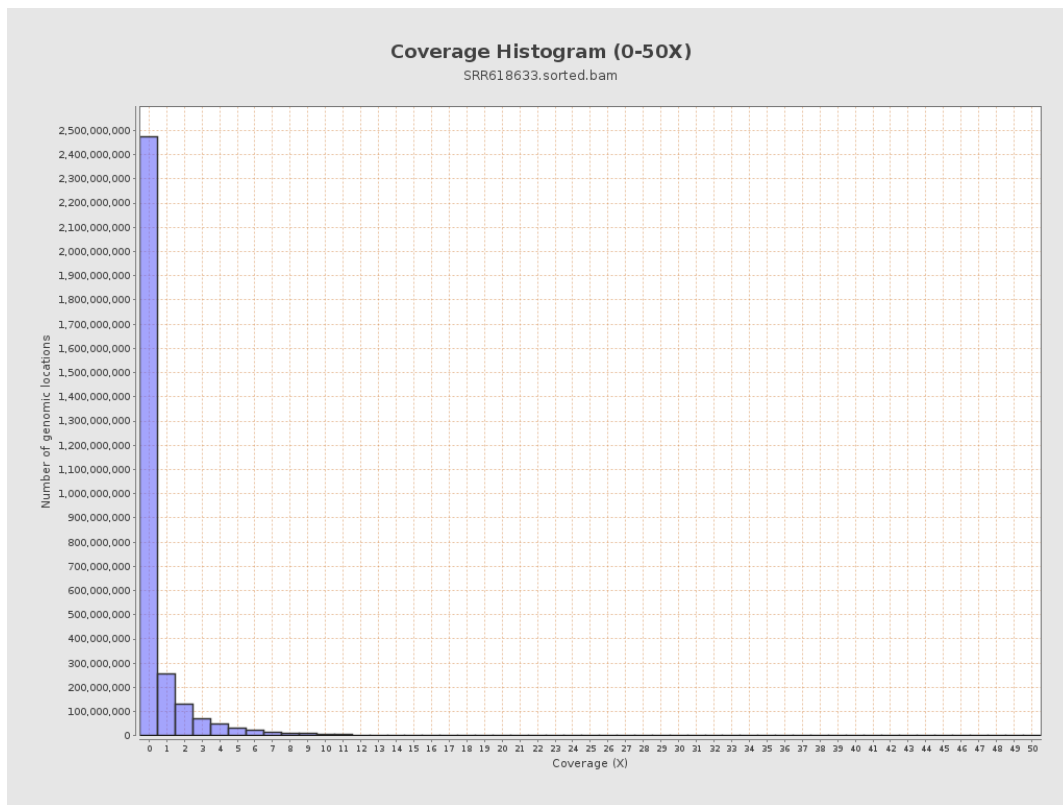
3. Results : Coverage across reference



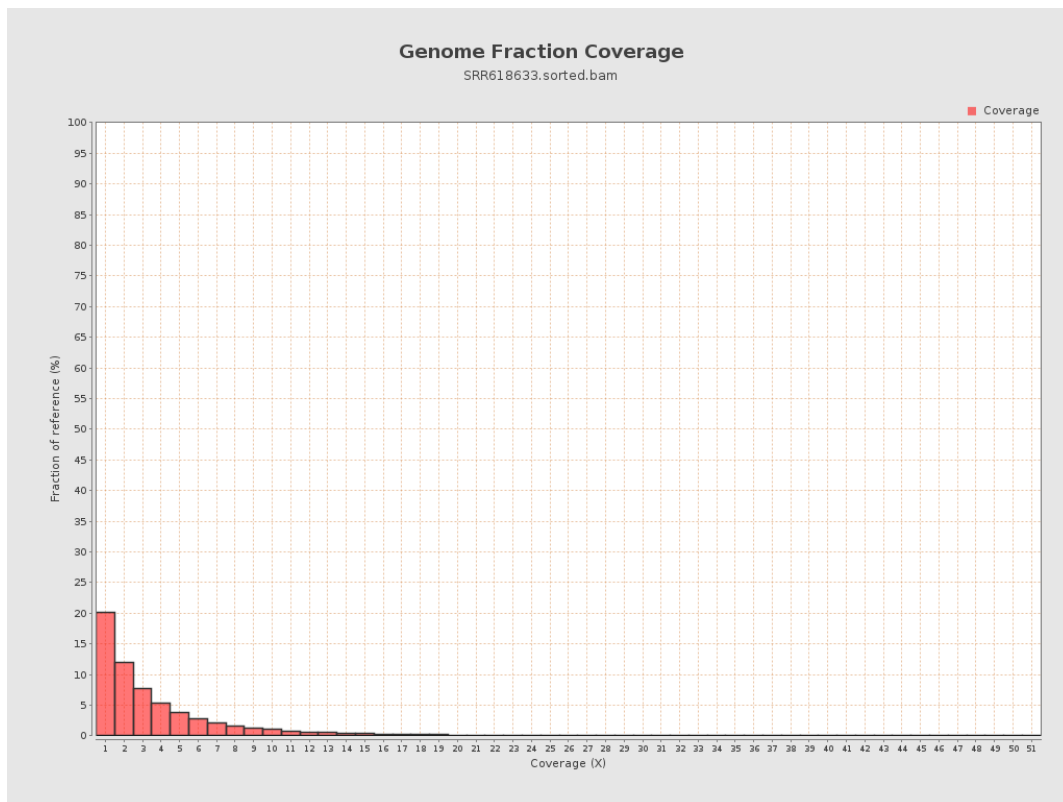
4. Results : Coverage Histogram



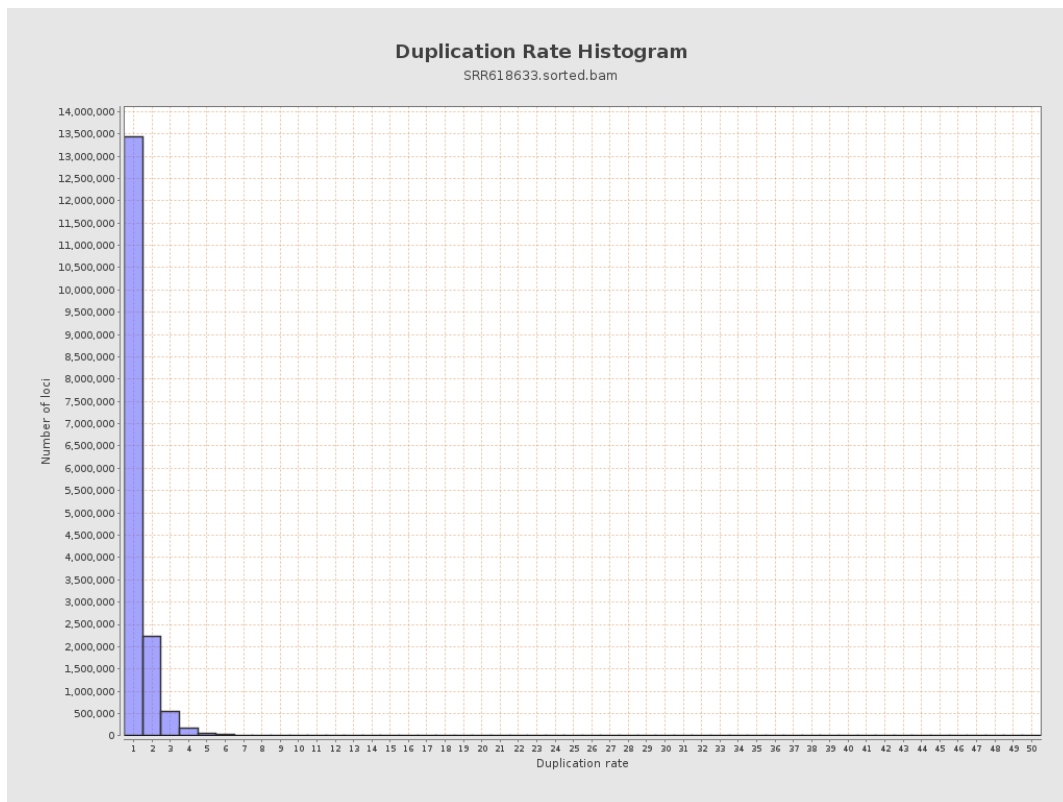
5. Results : Coverage Histogram (0-50X)



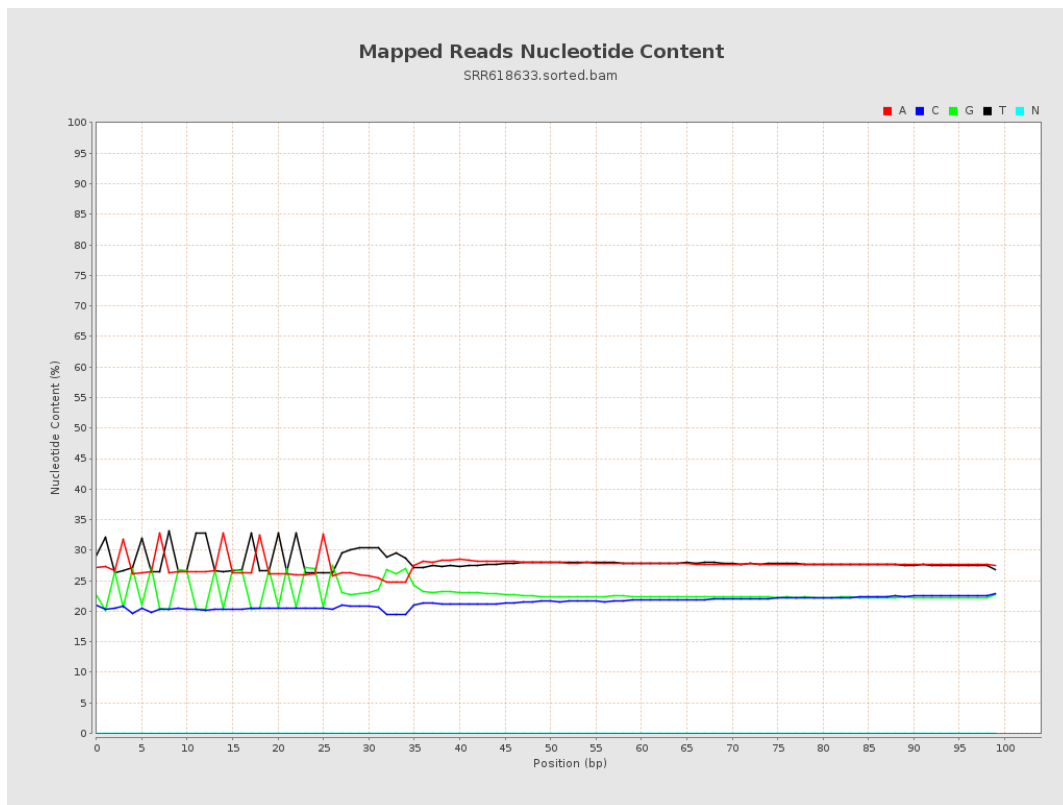
6. Results : Genome Fraction Coverage



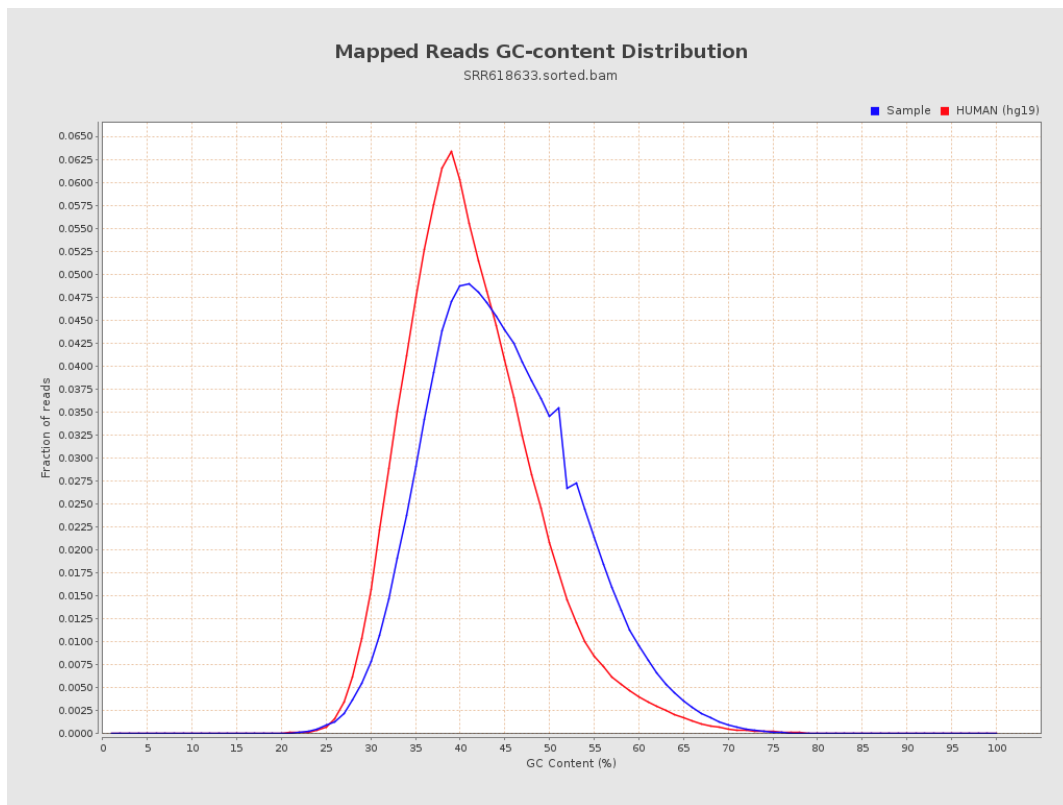
7. Results : Duplication Rate Histogram



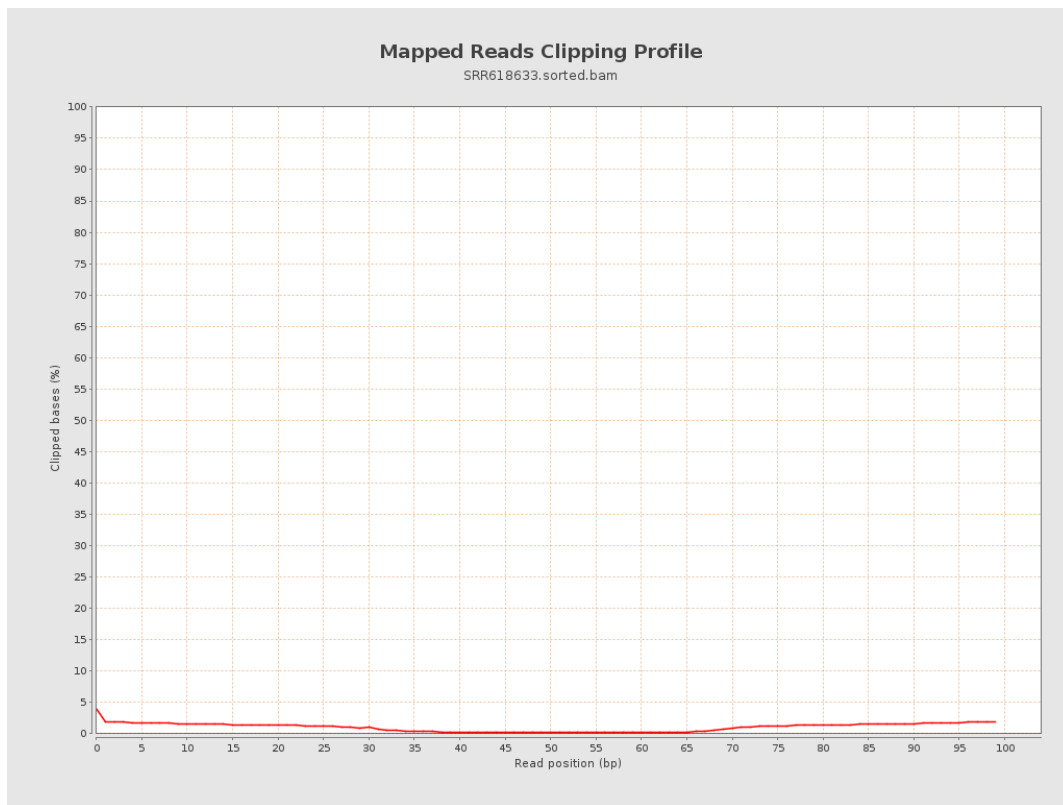
8. Results : Mapped Reads Nucleotide Content



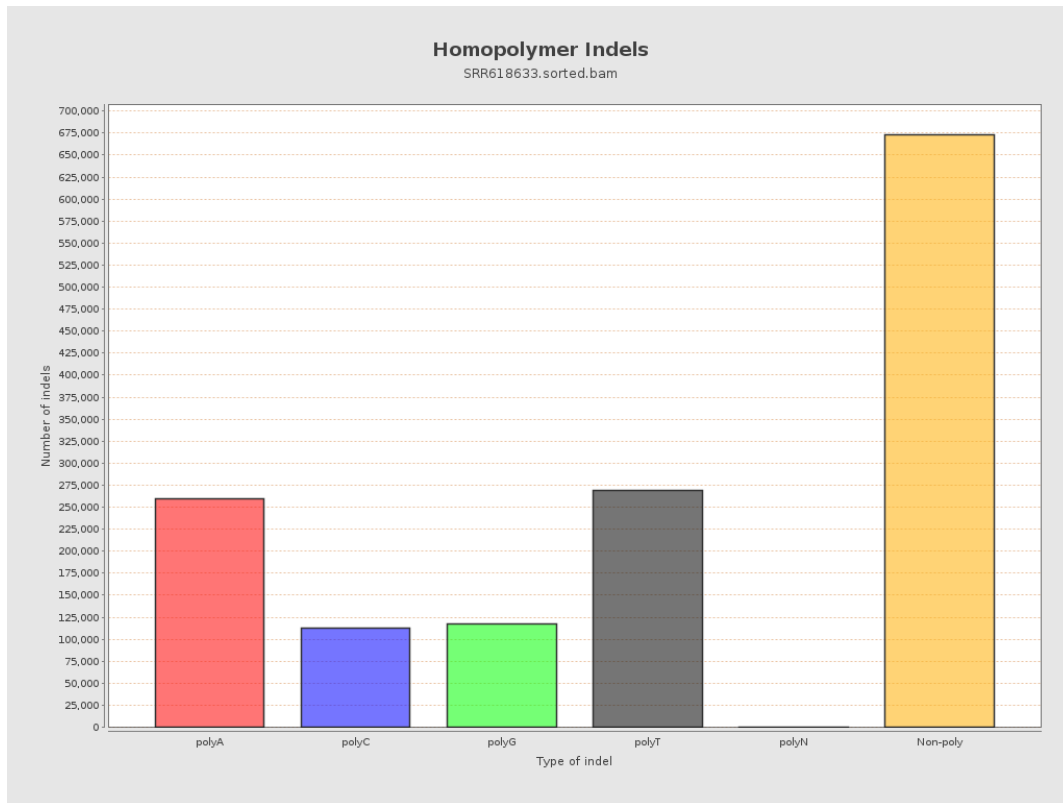
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



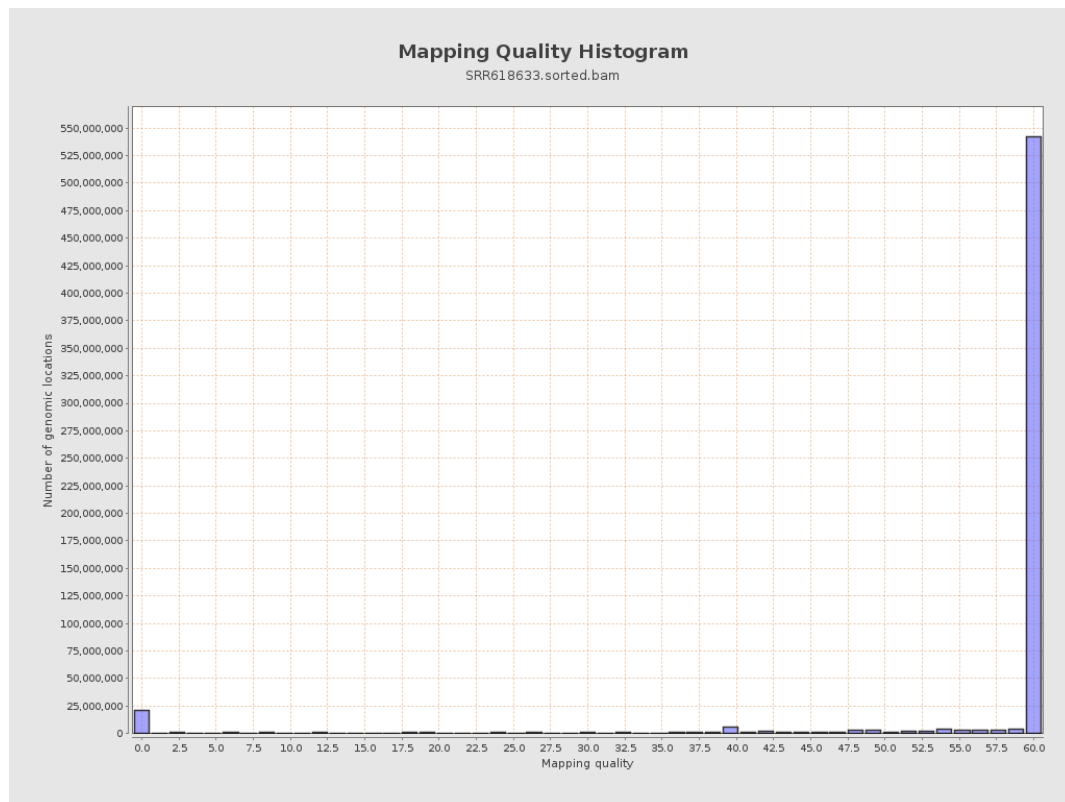
11. Results : Homopolymer Indels



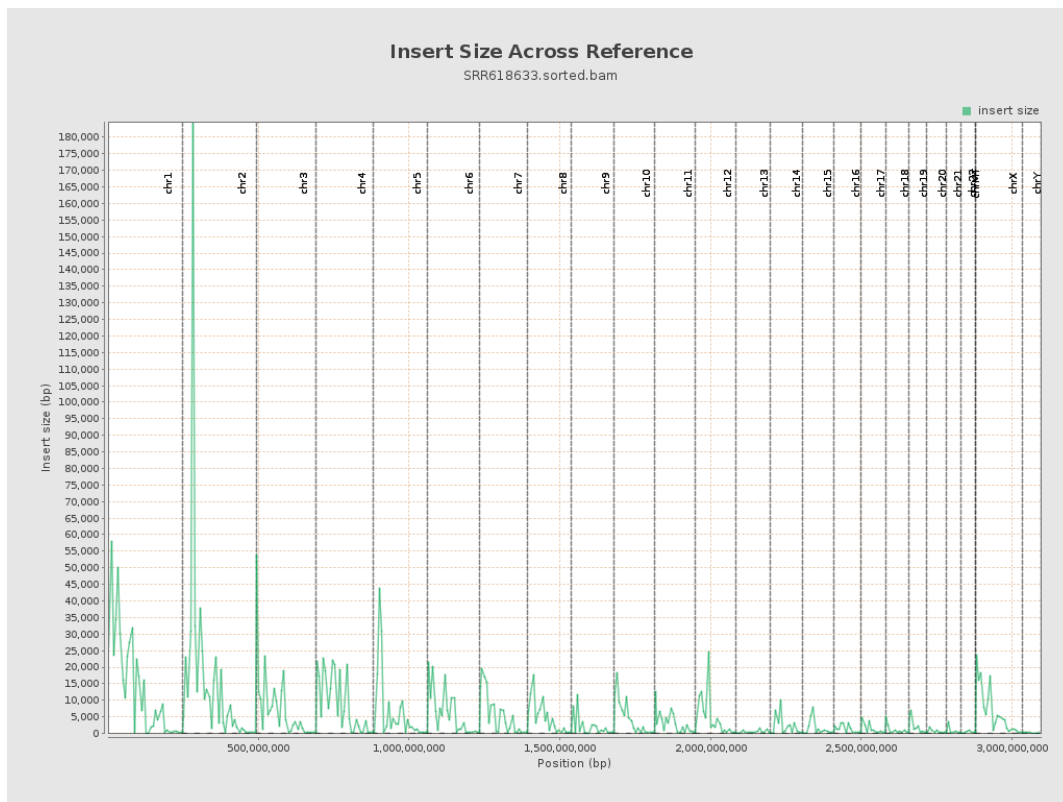
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

