

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 22:05:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618635.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_SRR618635 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618635_1.fastq.gz SRR618635_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 22:05:38 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618635.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,568,612
Mapped reads	23,920,811 / 80.9%
Unmapped reads	5,647,801 / 19.1%
Mapped paired reads	23,920,811 / 80.9%
Mapped reads, first in pair	12,286,712 / 41.55%
Mapped reads, second in pair	11,634,099 / 39.35%
Mapped reads, both in pair	22,483,144 / 76.04%
Mapped reads, singletons	1,437,667 / 4.86%
Secondary alignments	0
Supplementary alignments	115,762 / 0.39%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	11,915,952 / 40.3%
Duplication rate	35.47%
Clipped reads	6,700,731 / 22.66%

2.2. ACGT Content

Number/percentage of A's	595,636,659 / 27.03%
Number/percentage of C's	483,147,356 / 21.92%
Number/percentage of T's	606,632,419 / 27.52%
Number/percentage of G's	517,059,041 / 23.46%
Number/percentage of N's	1,500,051 / 0.07%

GC Percentage	45.38%
---------------	--------

2.3. Coverage

Mean	0.7124
Standard Deviation	5.0901

2.4. Mapping Quality

Mean Mapping Quality	52.16
----------------------	-------

2.5. Insert size

Mean	106,674.27
Standard Deviation	3,323,629.18
P25/Median/P75	176 / 209 / 249

2.6. Mismatches and indels

General error rate	1.41%
Mismatches	30,512,677
Insertions	417,091
Mapped reads with at least one insertion	1.71%
Deletions	1,061,118
Mapped reads with at least one deletion	4.33%
Homopolymer indels	51.64%

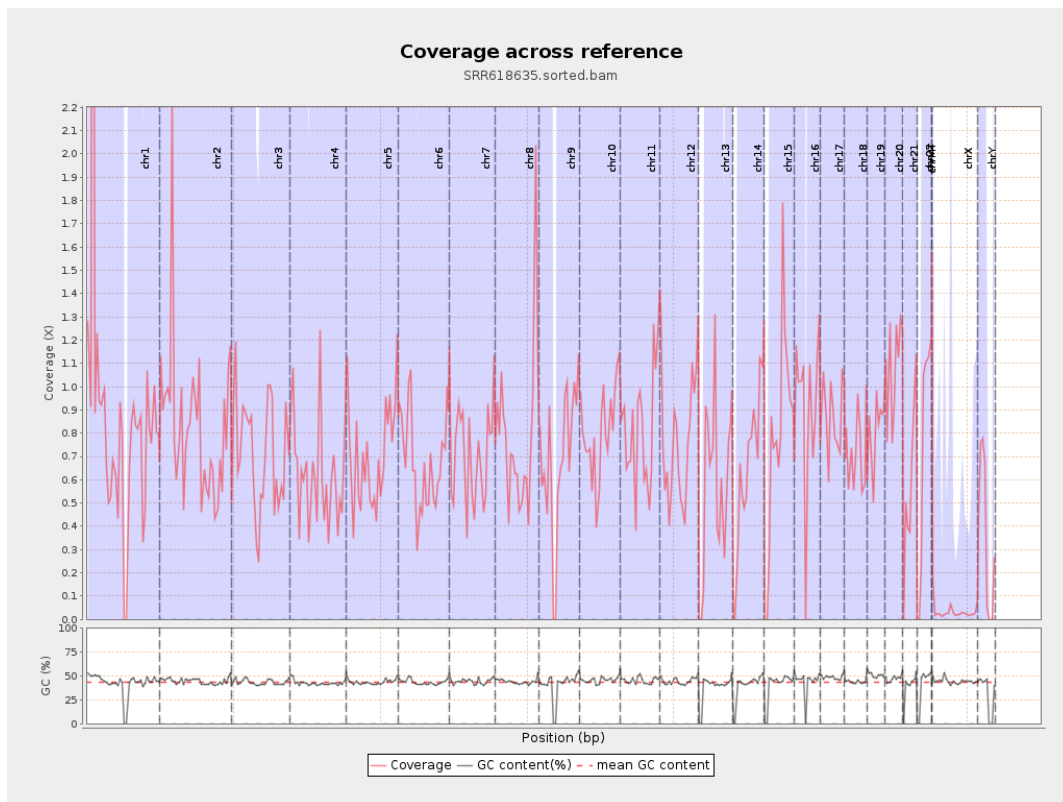
2.7. Chromosome stats

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

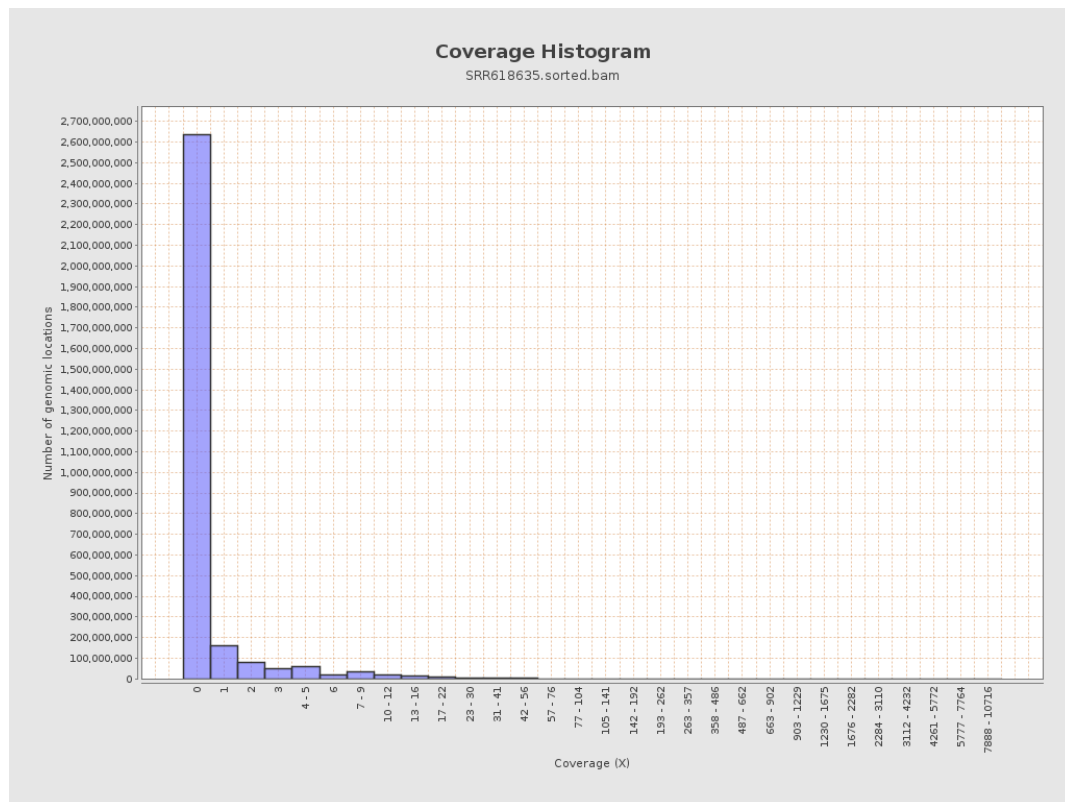
		bases	coverage	deviation
chr1	249250621	217859063	0.8741	10.6314
chr2	243199373	201790449	0.8297	5.8572
chr3	198022430	142302034	0.7186	3.0203
chr4	191154276	117437476	0.6144	5.4571
chr5	180915260	128551543	0.7106	3.082
chr6	171115067	115945663	0.6776	3.1721
chr7	159138663	113278770	0.7118	3.424
chr8	146364022	114674003	0.7835	4.7406
chr9	141213431	98040773	0.6943	3.9221
chr10	135534747	109092811	0.8049	3.3759
chr11	135006516	110391227	0.8177	3.6797
chr12	133851895	101693257	0.7597	3.5622
chr13	115169878	66519292	0.5776	3.7611
chr14	107349540	68402407	0.6372	3.114
chr15	102531392	80188530	0.7821	5.349
chr16	90354753	81897085	0.9064	9.4169
chr17	81195210	71050487	0.8751	3.5979
chr18	78077248	56195740	0.7197	3.6172
chr19	59128983	47652742	0.8059	3.8823
chr20	63025520	67672204	1.0737	4.6648
chr21	48129895	28988404	0.6023	4.2669
chr22	51304566	38953110	0.7593	3.5692
chrMT	16571	26286	1.5863	7.6922
chrX	155270560	4857666	0.0313	0.9203

chrY	59373566	22018329	0.3708	3.247
------	----------	----------	--------	-------

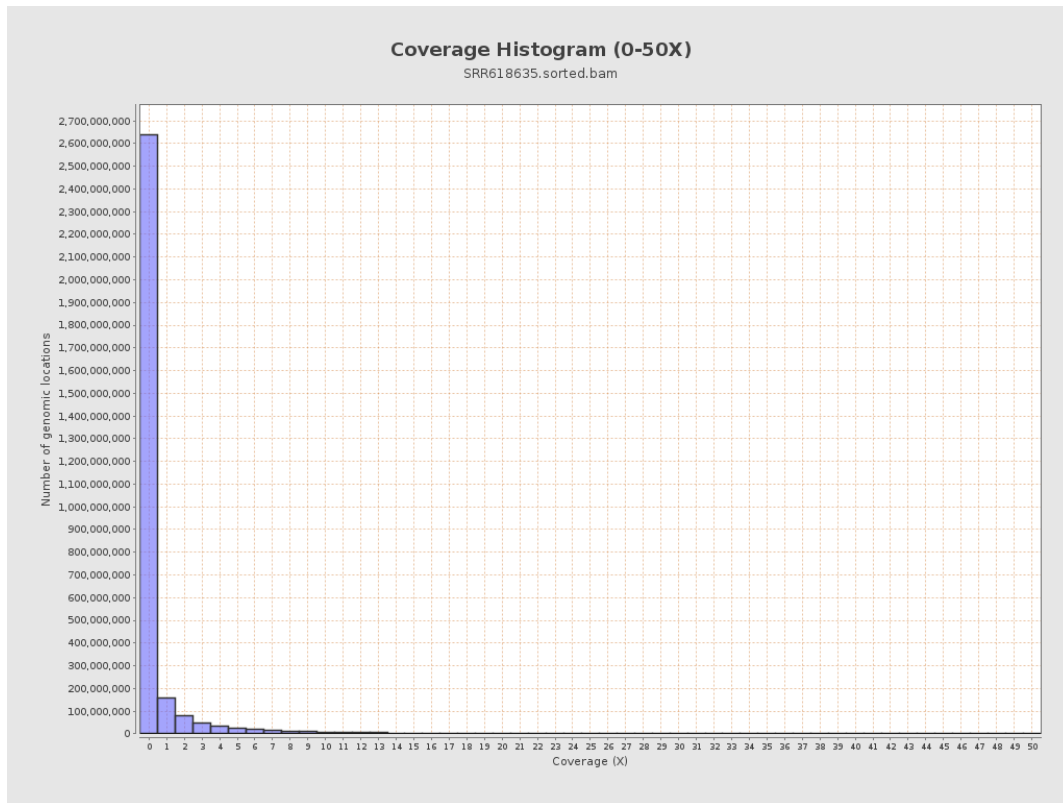
3. Results : Coverage across reference



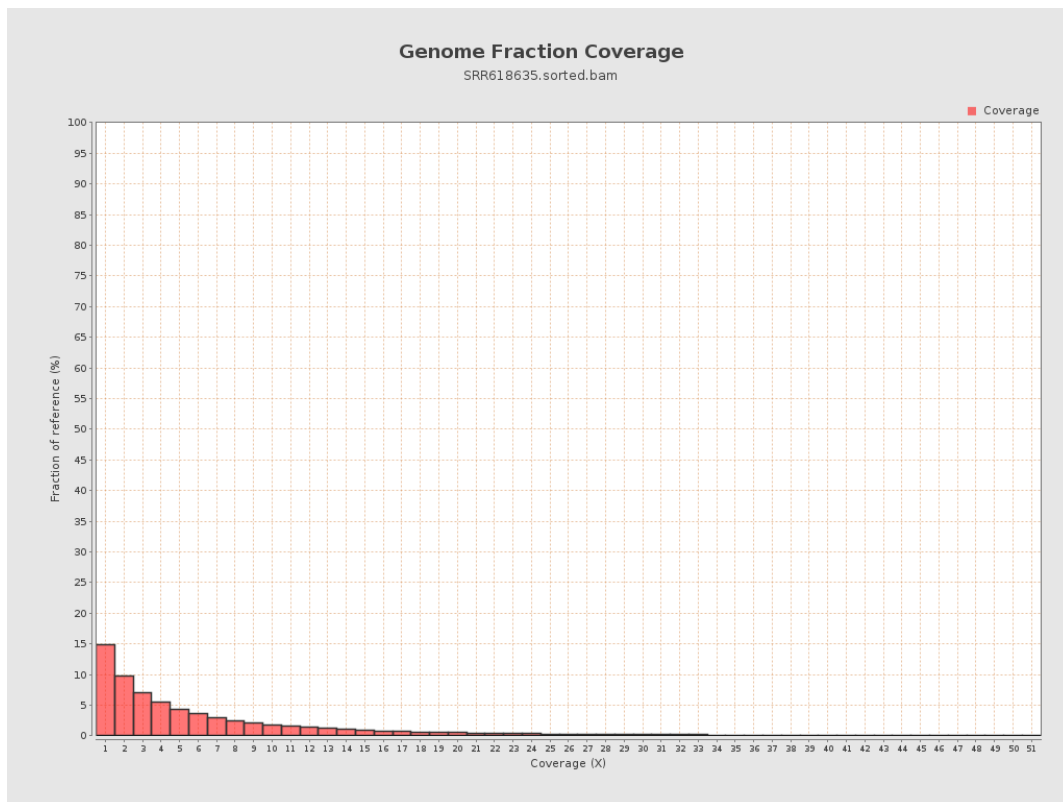
4. Results : Coverage Histogram



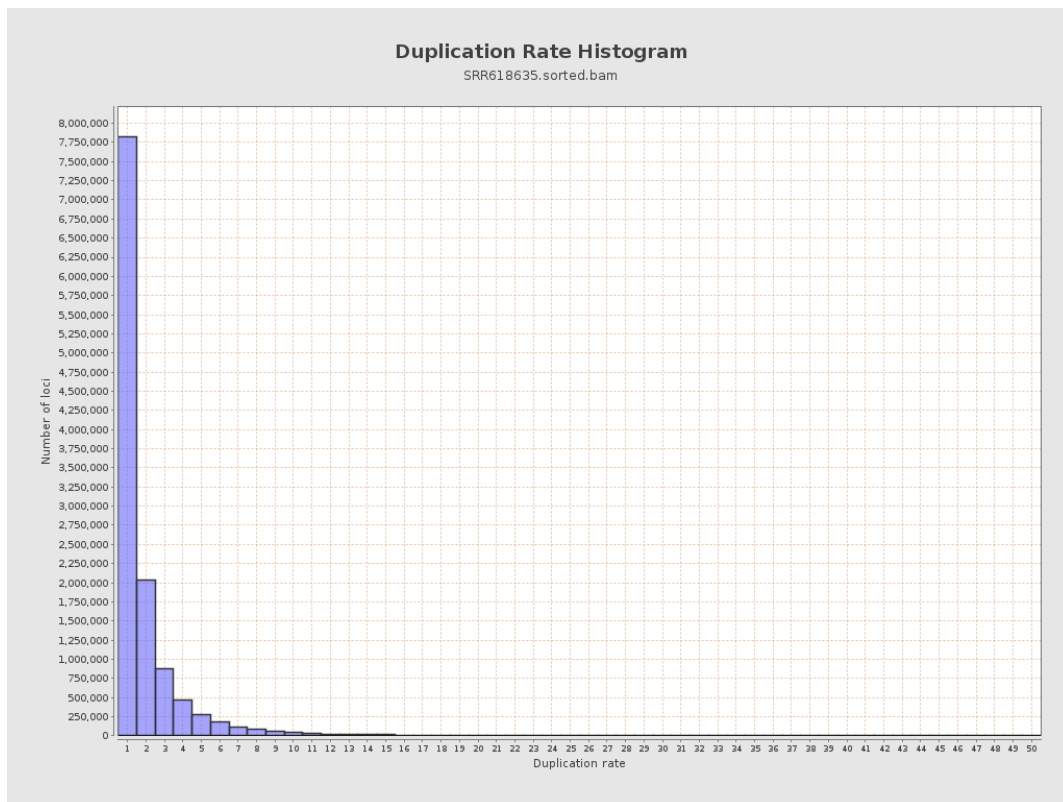
5. Results : Coverage Histogram (0-50X)



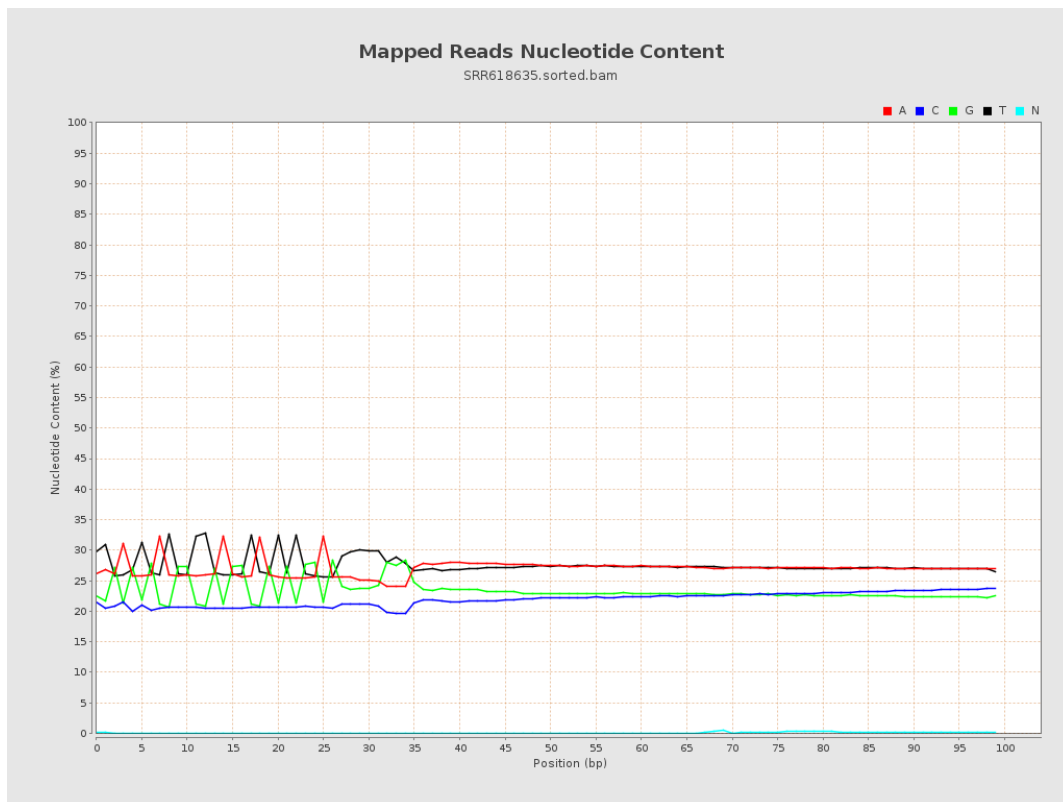
6. Results : Genome Fraction Coverage



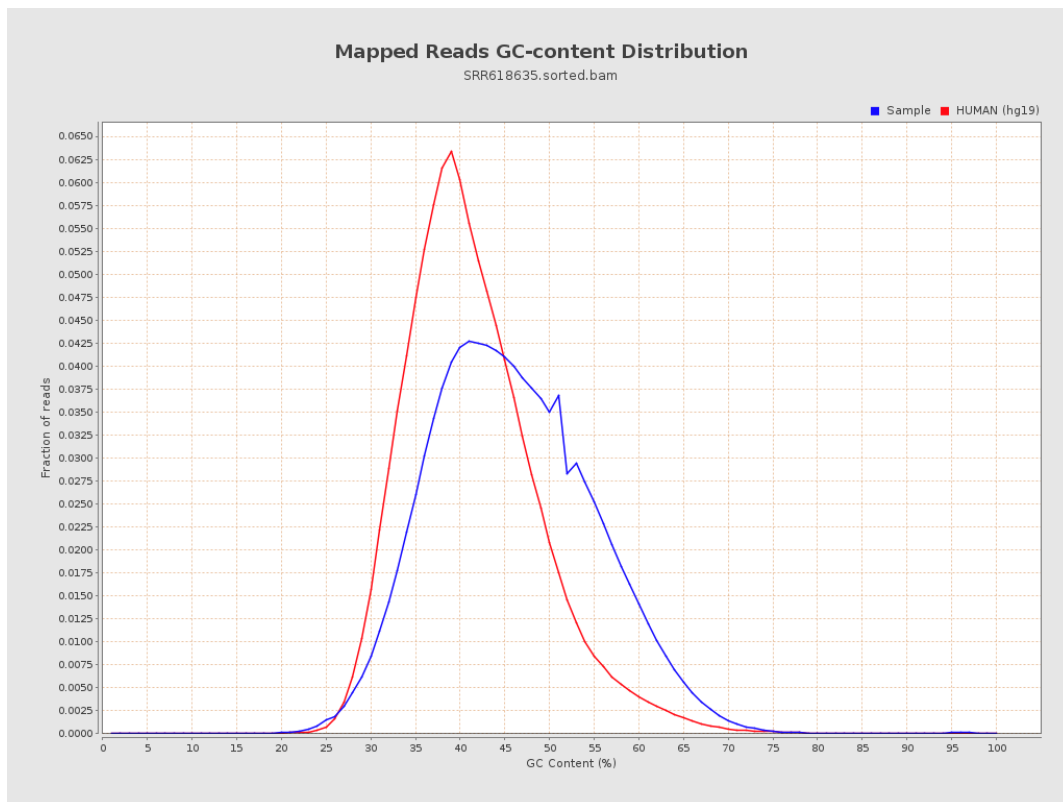
7. Results : Duplication Rate Histogram



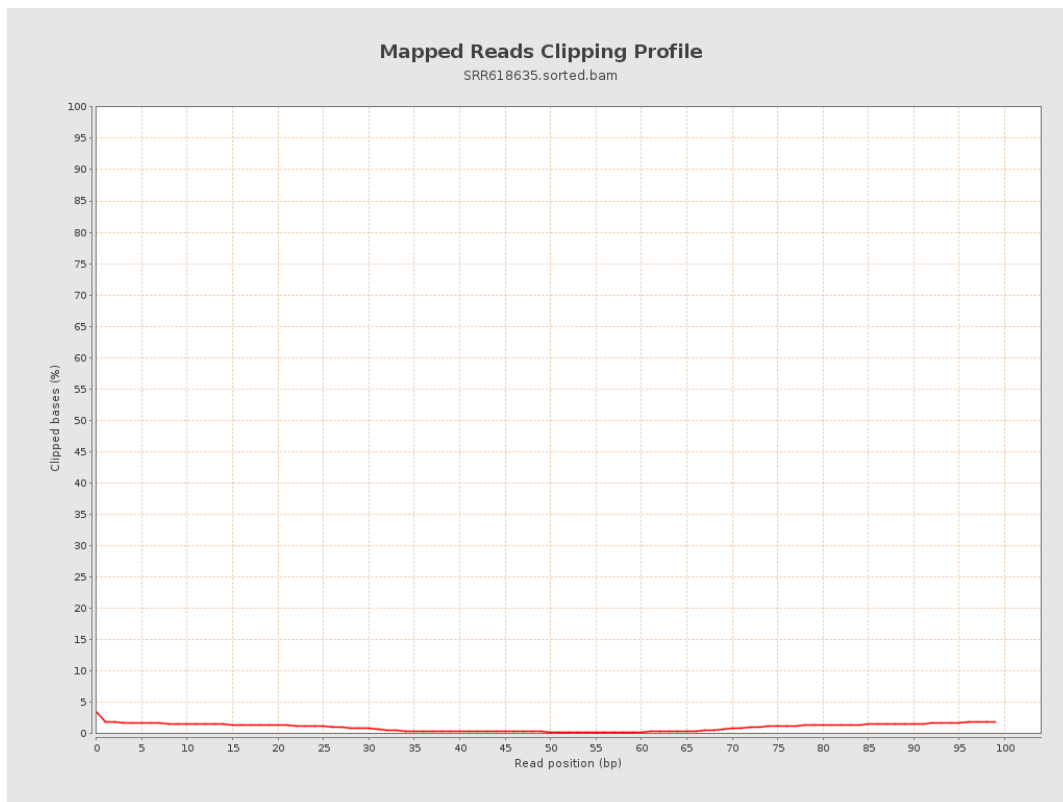
8. Results : Mapped Reads Nucleotide Content



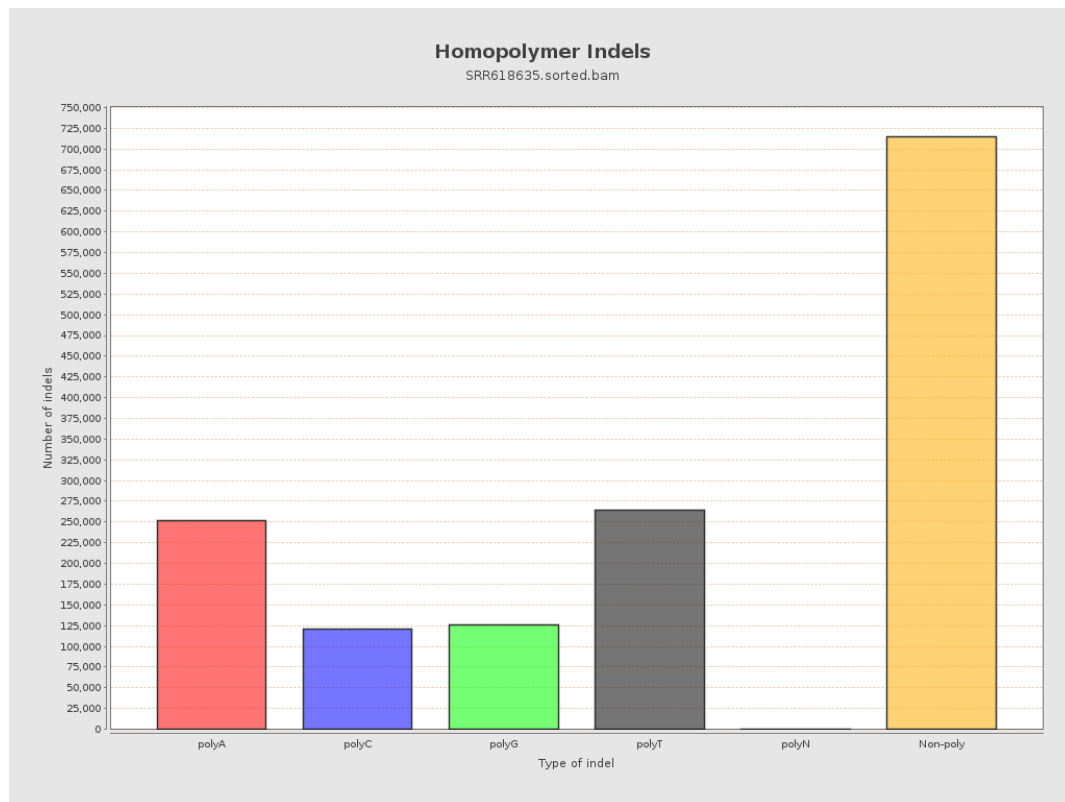
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



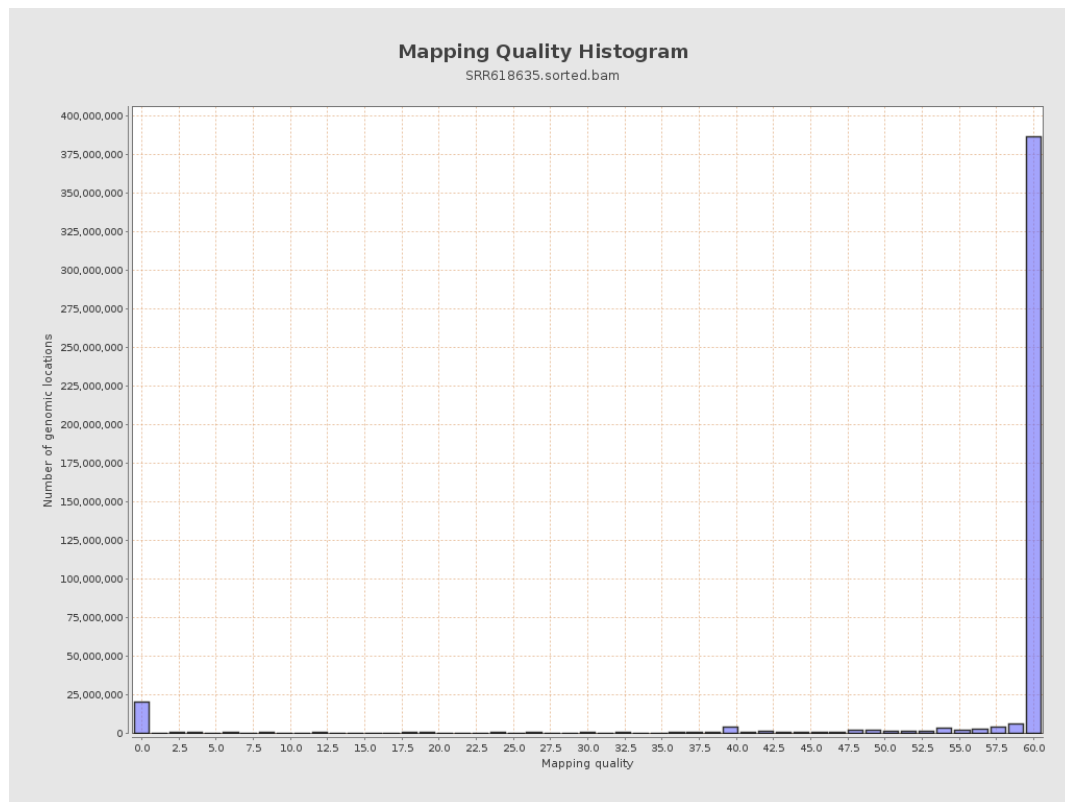
11. Results : Homopolymer Indels



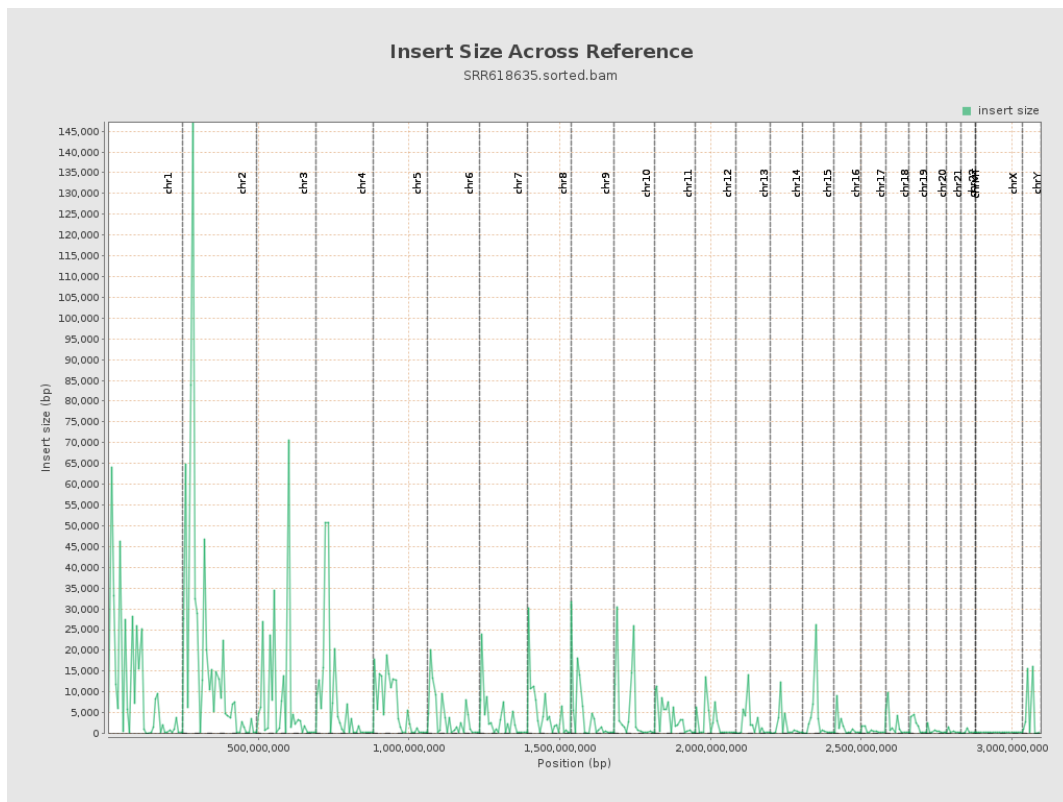
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

