

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 21:38:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618634.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_SRR618634 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618634_1.fastq.gz SRR618634_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 21:38:00 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618634.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	36,528,284
Mapped reads	24,117,144 / 66.02%
Unmapped reads	12,411,140 / 33.98%
Mapped paired reads	24,117,144 / 66.02%
Mapped reads, first in pair	12,972,414 / 35.51%
Mapped reads, second in pair	11,144,730 / 30.51%
Mapped reads, both in pair	21,023,500 / 57.55%
Mapped reads, singletons	3,093,644 / 8.47%
Secondary alignments	0
Supplementary alignments	160,382 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	9,468,564 / 25.92%
Duplication rate	29.74%
Clipped reads	7,066,491 / 19.35%

2.2. ACGT Content

Number/percentage of A's	606,433,732 / 27.39%
Number/percentage of C's	481,072,070 / 21.73%
Number/percentage of T's	626,437,111 / 28.29%
Number/percentage of G's	499,123,188 / 22.54%
Number/percentage of N's	1,192,904 / 0.05%

GC Percentage	44.27%
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2.3. Coverage

Mean	0.7158
Standard Deviation	4.6656

2.4. Mapping Quality

Mean Mapping Quality	53.1
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2.5. Insert size

Mean	197,354.28
Standard Deviation	4,445,832.06
P25/Median/P75	172 / 207 / 251

2.6. Mismatches and indels

General error rate	1.51%
Mismatches	32,758,393
Insertions	434,109
Mapped reads with at least one insertion	1.77%
Deletions	1,126,106
Mapped reads with at least one deletion	4.55%
Homopolymer indels	51.62%

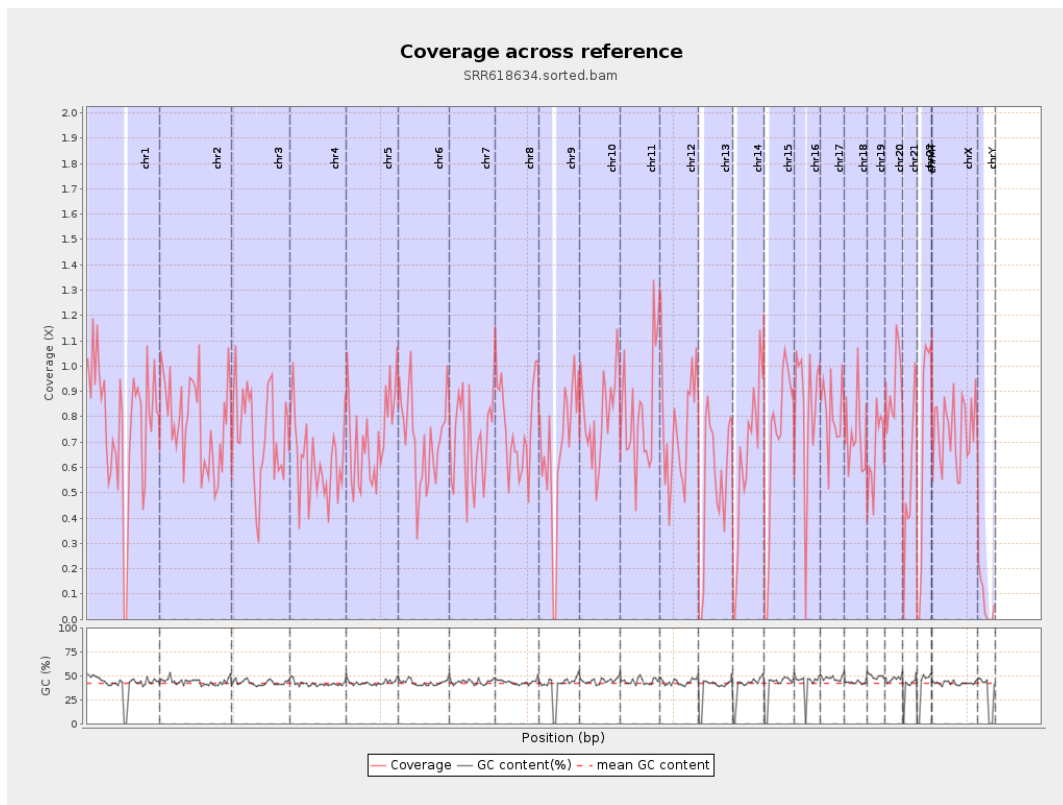
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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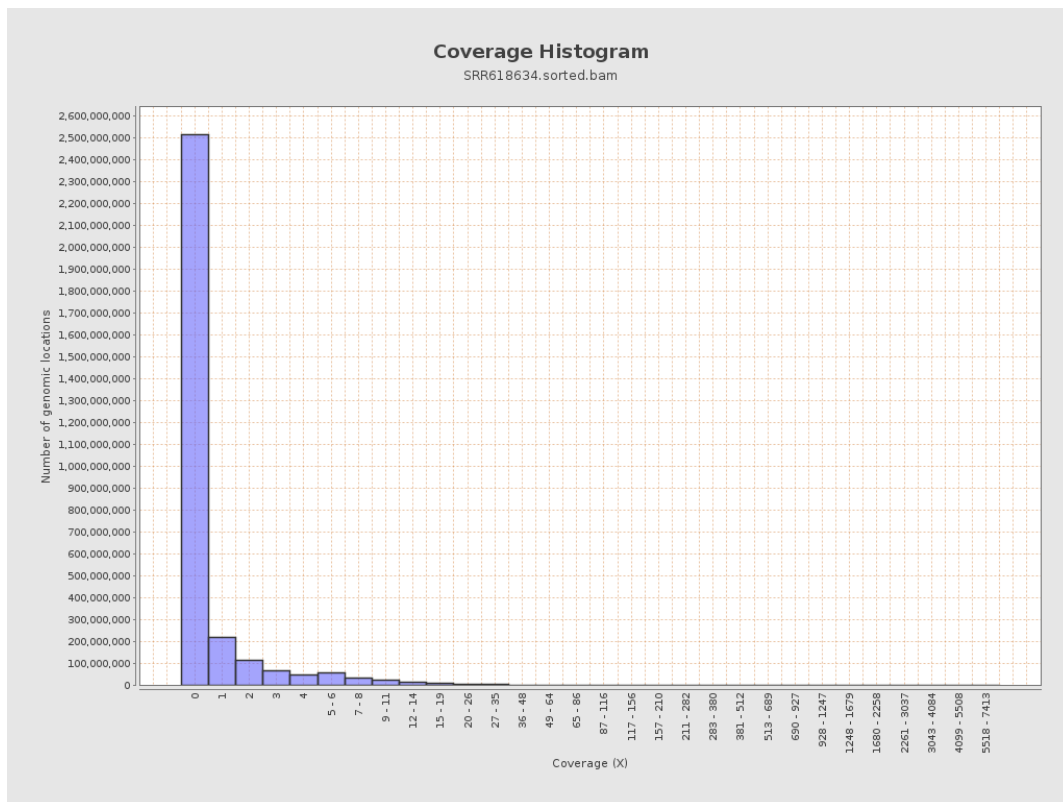
		bases	coverage	deviation
chr1	249250621	192437671	0.7721	4.5532
chr2	243199373	189716982	0.7801	7.0292
chr3	198022430	145992537	0.7373	3.9256
chr4	191154276	118462014	0.6197	4.0941
chr5	180915260	130753914	0.7227	4.1966
chr6	171115067	122384953	0.7152	3.5247
chr7	159138663	111663810	0.7017	4.4464
chr8	146364022	110190710	0.7529	5.0167
chr9	141213431	94295276	0.6678	4.6505
chr10	135534747	110038960	0.8119	5.7281
chr11	135006516	109757961	0.813	4.5591
chr12	133851895	101011720	0.7547	6.5219
chr13	115169878	62054814	0.5388	3.2077
chr14	107349540	68065709	0.6341	4.2408
chr15	102531392	71564027	0.698	3.6152
chr16	90354753	73936901	0.8183	6.3219
chr17	81195210	65977746	0.8126	3.9551
chr18	78077248	57483527	0.7362	3.9802
chr19	59128983	39666485	0.6708	3.3724
chr20	63025520	58316241	0.9253	3.4784
chr21	48129895	27791918	0.5774	3.4943
chr22	51304566	35382693	0.6897	4.5309
chrMT	16571	18902	1.1407	4.7211
chrX	155270560	114804469	0.7394	3.3657

chrY	59373566	4040757	0.0681	2.4392
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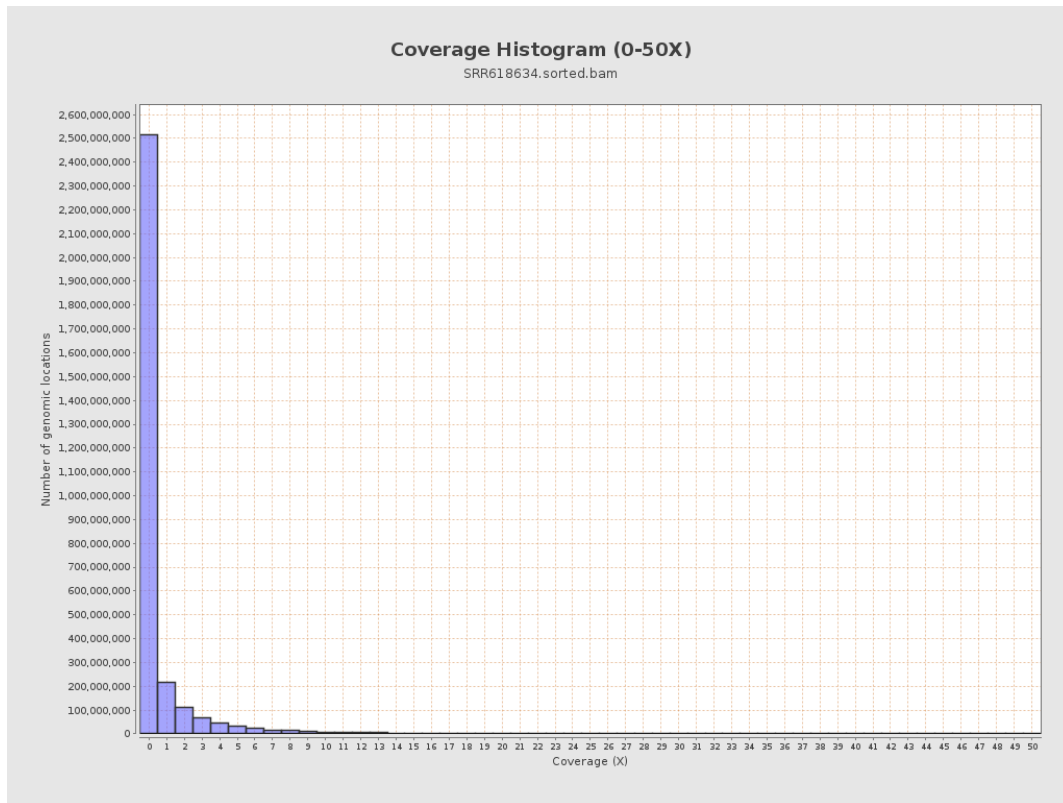
3. Results : Coverage across reference



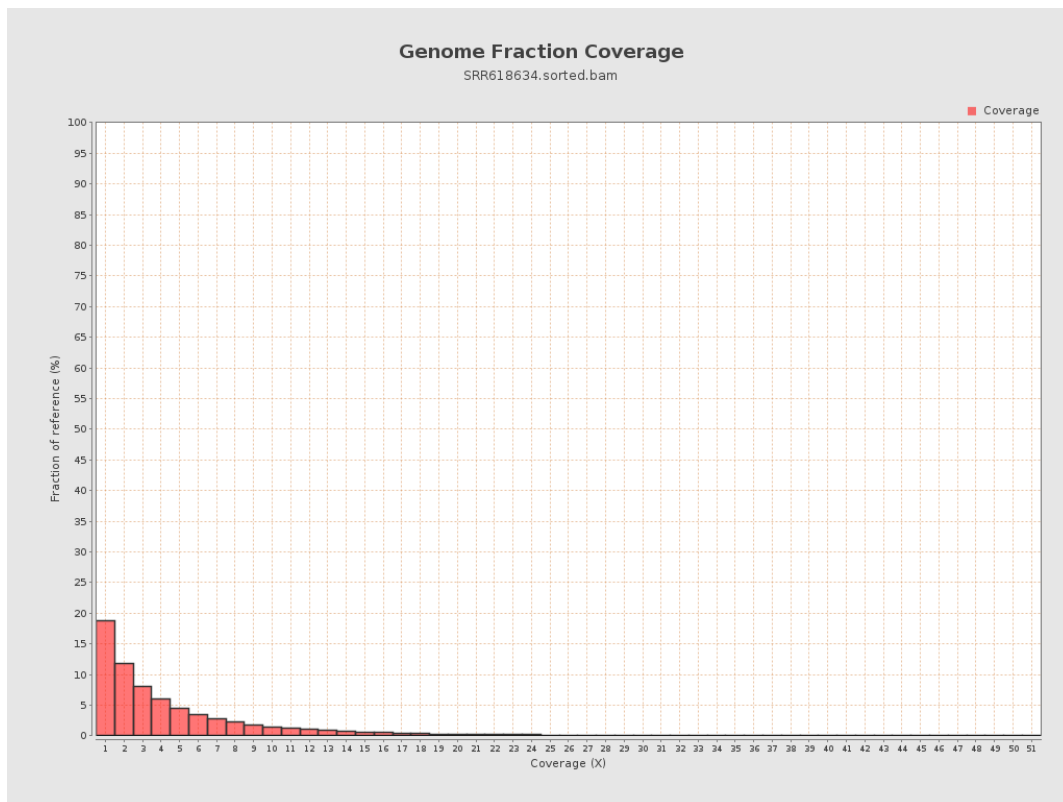
4. Results : Coverage Histogram



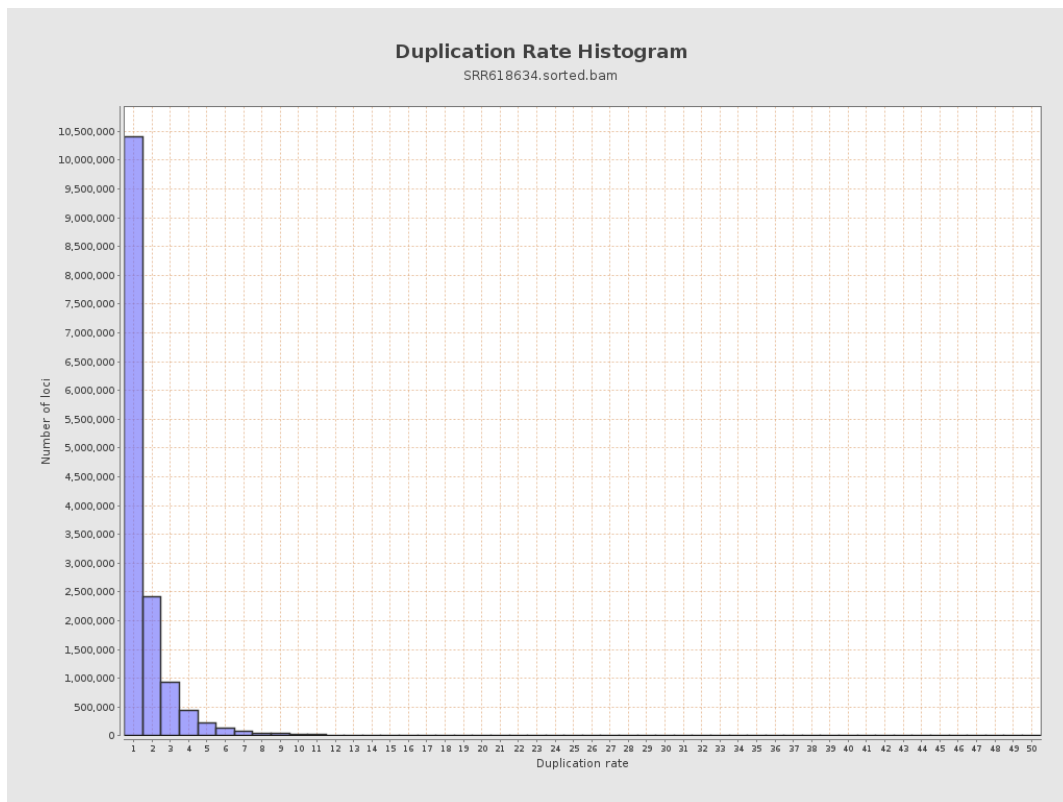
5. Results : Coverage Histogram (0-50X)



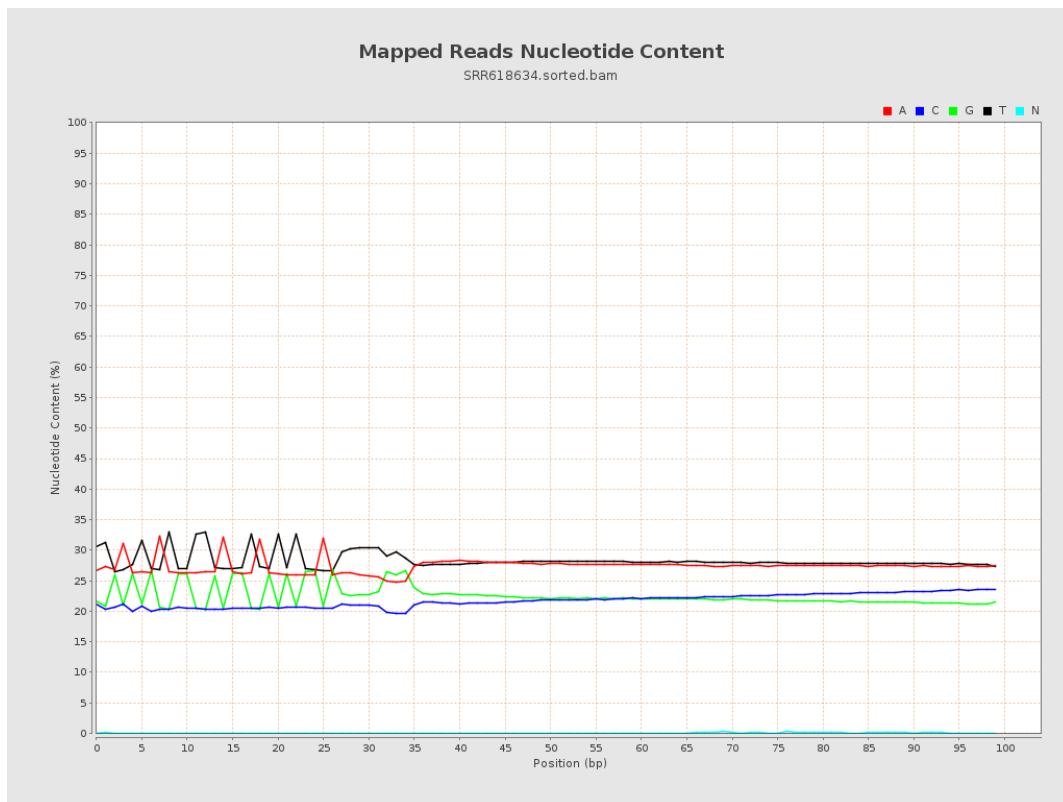
6. Results : Genome Fraction Coverage



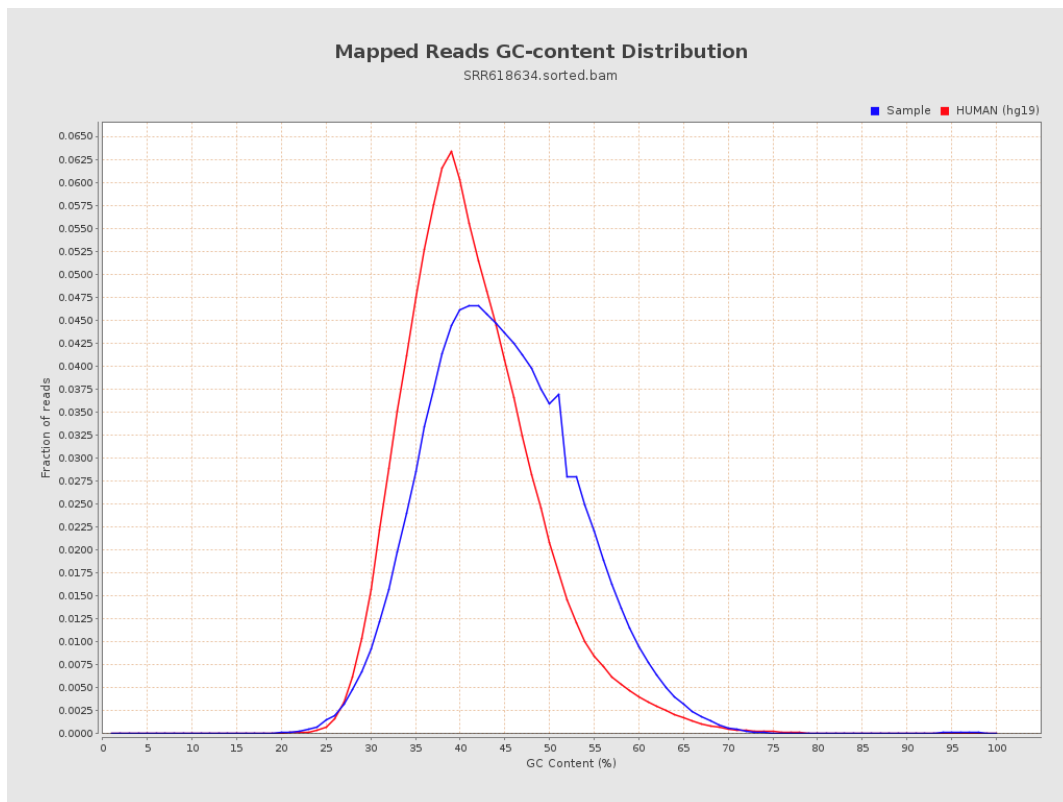
7. Results : Duplication Rate Histogram



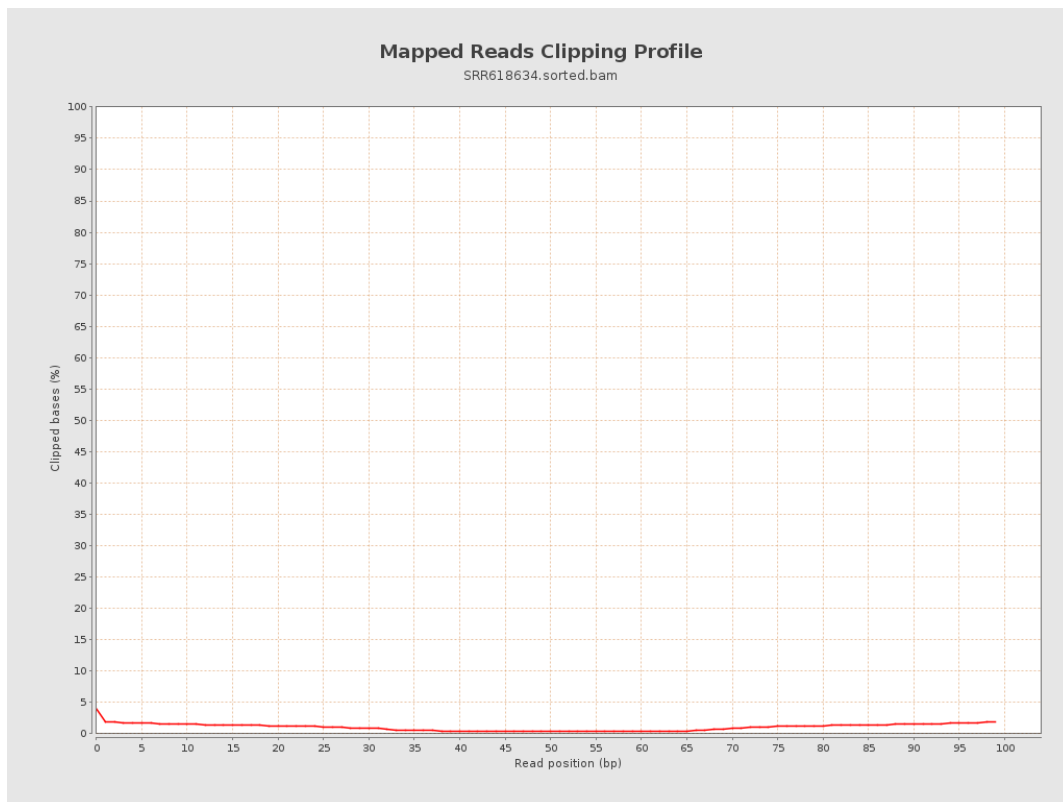
8. Results : Mapped Reads Nucleotide Content



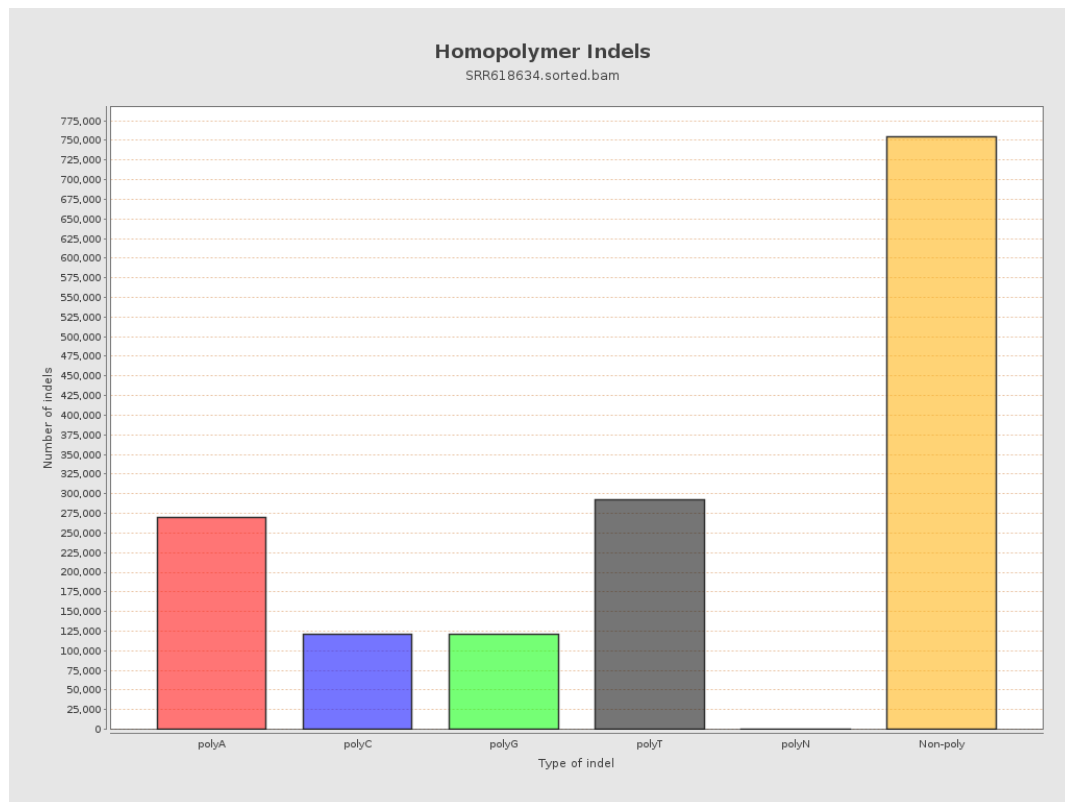
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



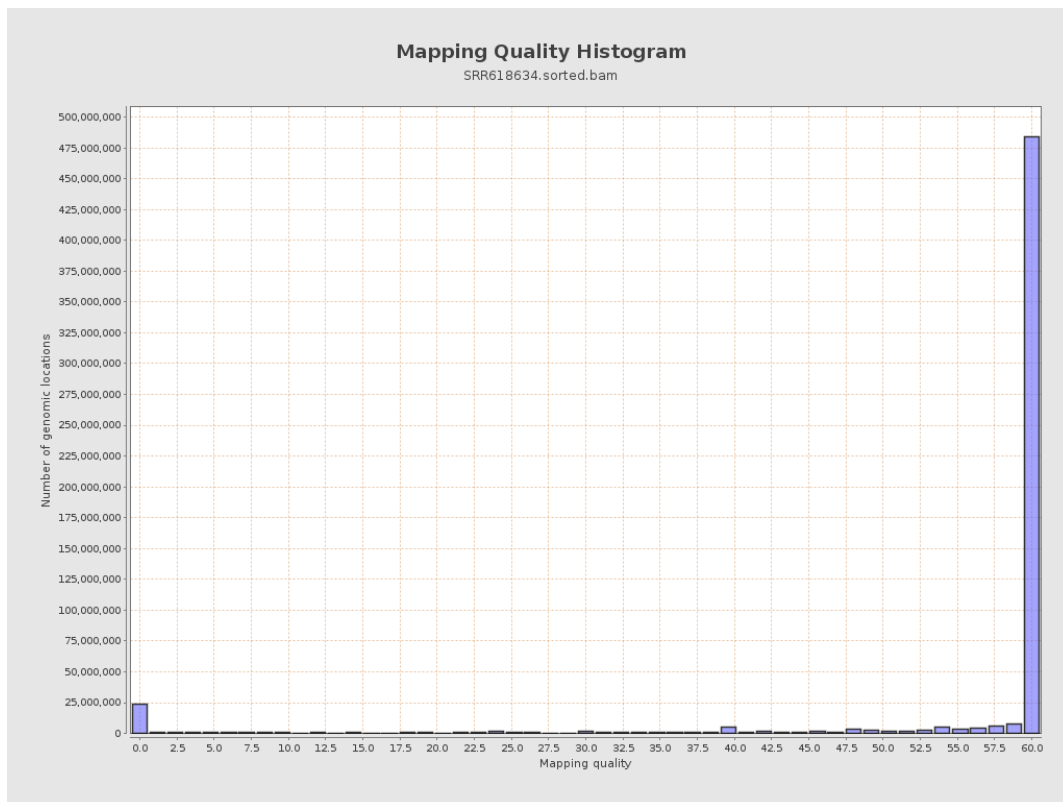
11. Results : Homopolymer Indels



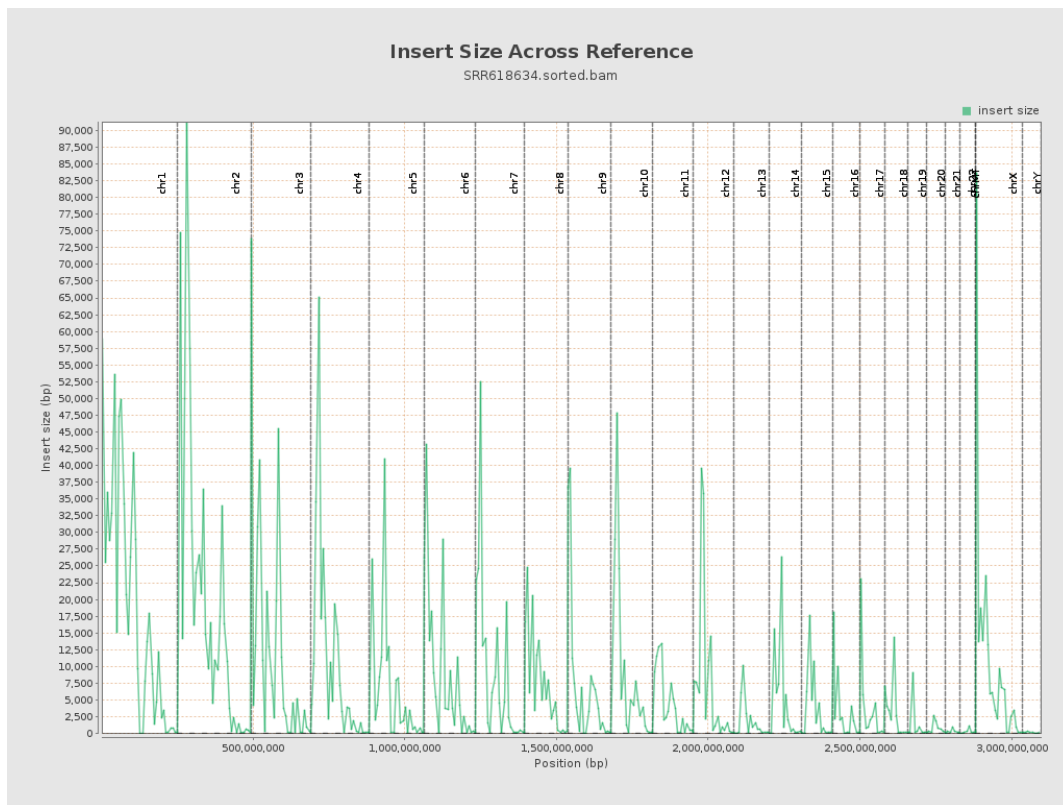
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

