

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 01:53:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618640.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_SRR618640 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618640_1.fastq.gz SRR618640_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 01:53:17 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618640.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	65,677,912
Mapped reads	51,125,044 / 77.84%
Unmapped reads	14,552,868 / 22.16%
Mapped paired reads	51,125,044 / 77.84%
Mapped reads, first in pair	27,458,198 / 41.81%
Mapped reads, second in pair	23,666,846 / 36.03%
Mapped reads, both in pair	46,595,168 / 70.94%
Mapped reads, singletons	4,529,876 / 6.9%
Secondary alignments	0
Supplementary alignments	127,437 / 0.19%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	10,785,543 / 16.42%
Duplication rate	17.79%
Clipped reads	11,547,371 / 17.58%

2.2. ACGT Content

Number/percentage of A's	1,304,636,675 / 27.11%
Number/percentage of C's	1,071,409,747 / 22.26%
Number/percentage of T's	1,335,834,884 / 27.76%
Number/percentage of G's	1,100,746,525 / 22.87%
Number/percentage of N's	219,320 / 0%

GC Percentage	45.13%
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2.3. Coverage

Mean	1.5558
Standard Deviation	7.5303

2.4. Mapping Quality

Mean Mapping Quality	53.7
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2.5. Insert size

Mean	99,430.34
Standard Deviation	3,177,155.45
P25/Median/P75	176 / 206 / 248

2.6. Mismatches and indels

General error rate	1.49%
Mismatches	70,452,865
Insertions	880,468
Mapped reads with at least one insertion	1.69%
Deletions	2,402,440
Mapped reads with at least one deletion	4.58%
Homopolymer indels	52.37%

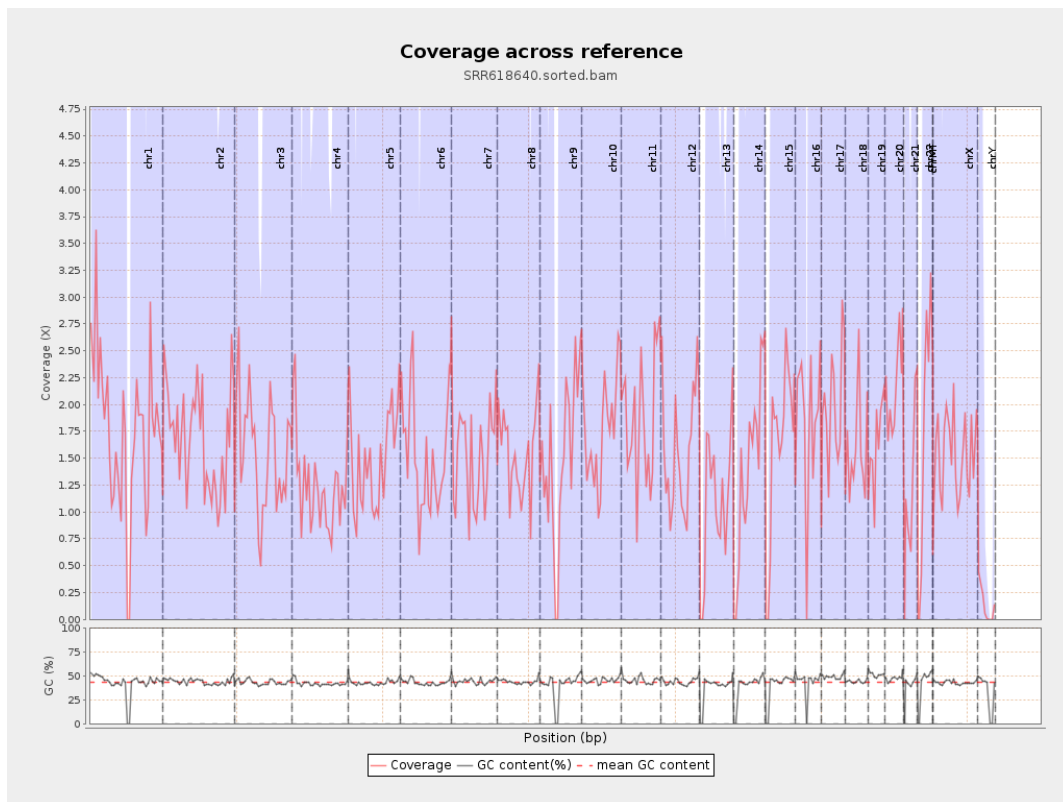
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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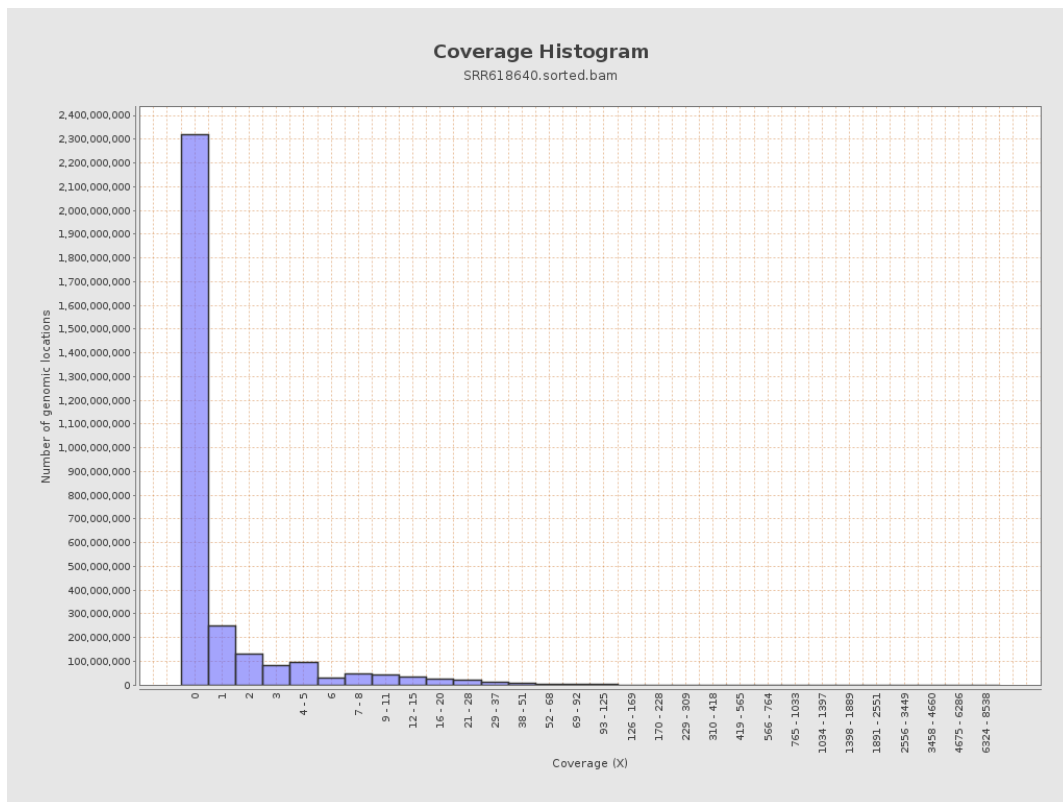
		bases	coverage	deviation
chr1	249250621	432318315	1.7345	8.0702
chr2	243199373	409605038	1.6842	8.989
chr3	198022430	304923971	1.5398	7.7656
chr4	191154276	236160293	1.2354	6.0418
chr5	180915260	271703502	1.5018	6.9347
chr6	171115067	259032725	1.5138	6.2423
chr7	159138663	243623206	1.5309	6.6545
chr8	146364022	226659715	1.5486	6.8135
chr9	141213431	211248264	1.496	7.4821
chr10	135534747	238583802	1.7603	7.1615
chr11	135006516	251197549	1.8606	8.5643
chr12	133851895	212032180	1.5841	7.6173
chr13	115169878	125364892	1.0885	5.2485
chr14	107349540	149489551	1.3925	6.4227
chr15	102531392	164086505	1.6004	7.2817
chr16	90354753	165531525	1.832	12.6085
chr17	81195210	161398849	1.9878	8.3813
chr18	78077248	121763593	1.5595	6.9326
chr19	59128983	96253283	1.6279	7.164
chr20	63025520	136120251	2.1598	8.2828
chr21	48129895	60491811	1.2568	8.7988
chr22	51304566	91017464	1.7741	8.5202
chrMT	16571	9849	0.5944	2.0707
chrX	155270560	239300695	1.5412	6.185

chrY	59373566	8245118	0.1389	4.3977
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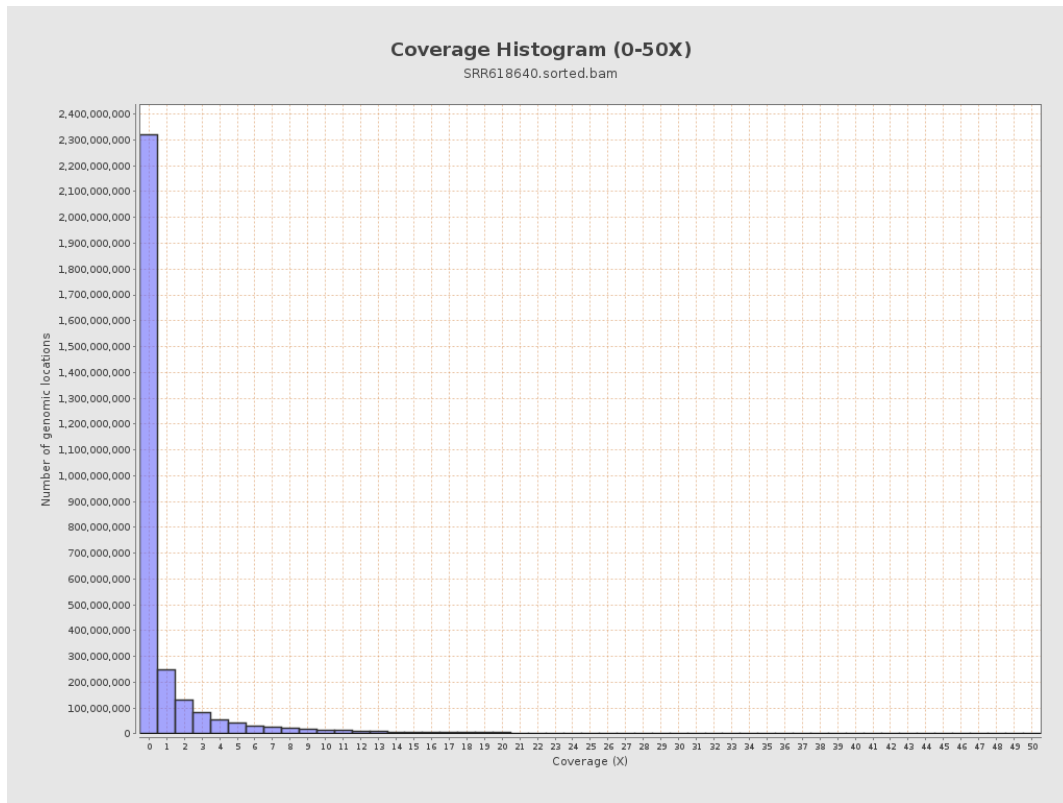
3. Results : Coverage across reference



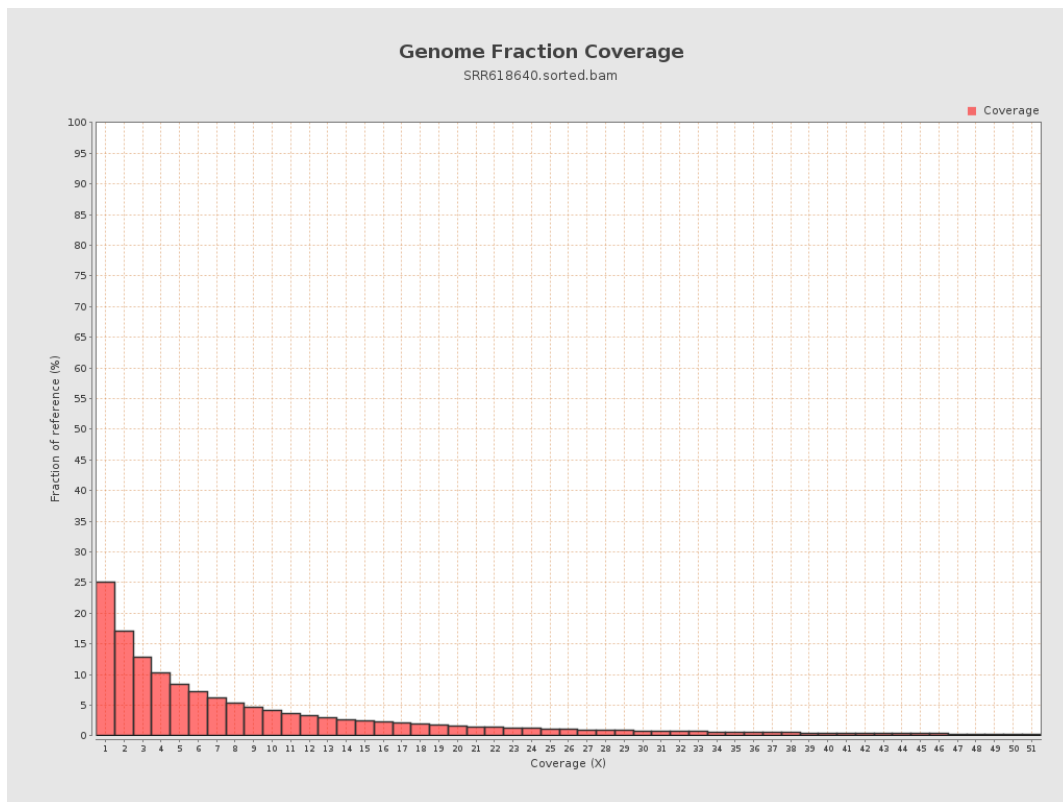
4. Results : Coverage Histogram



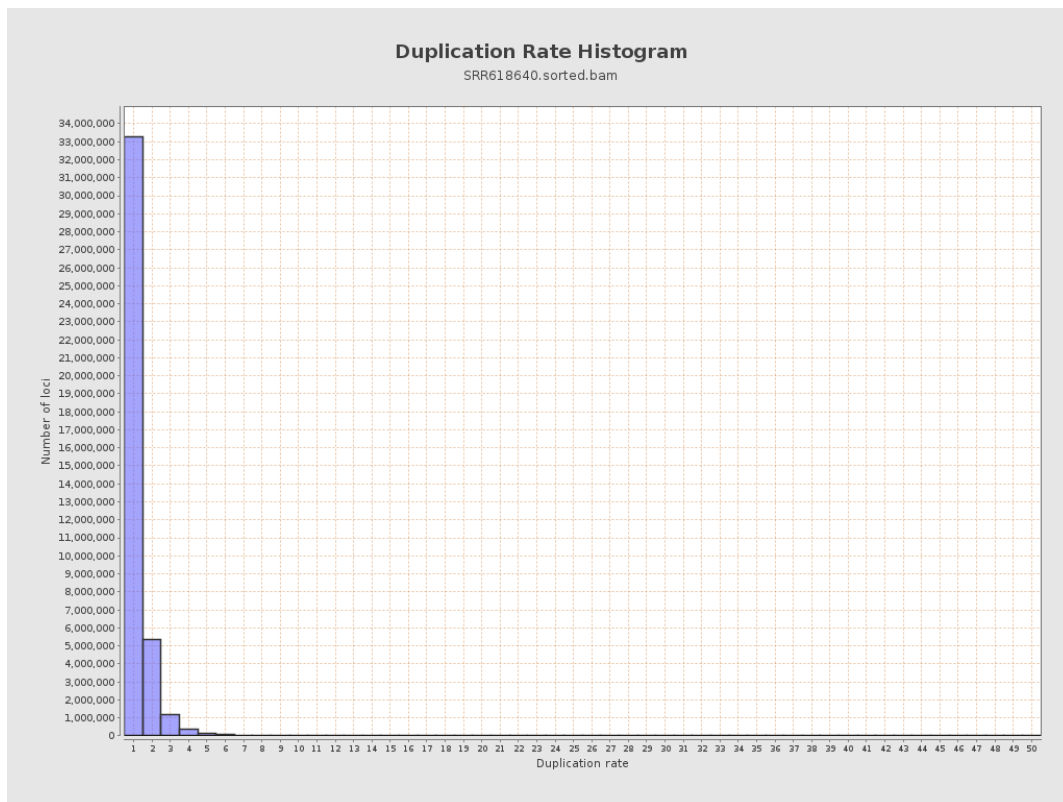
5. Results : Coverage Histogram (0-50X)



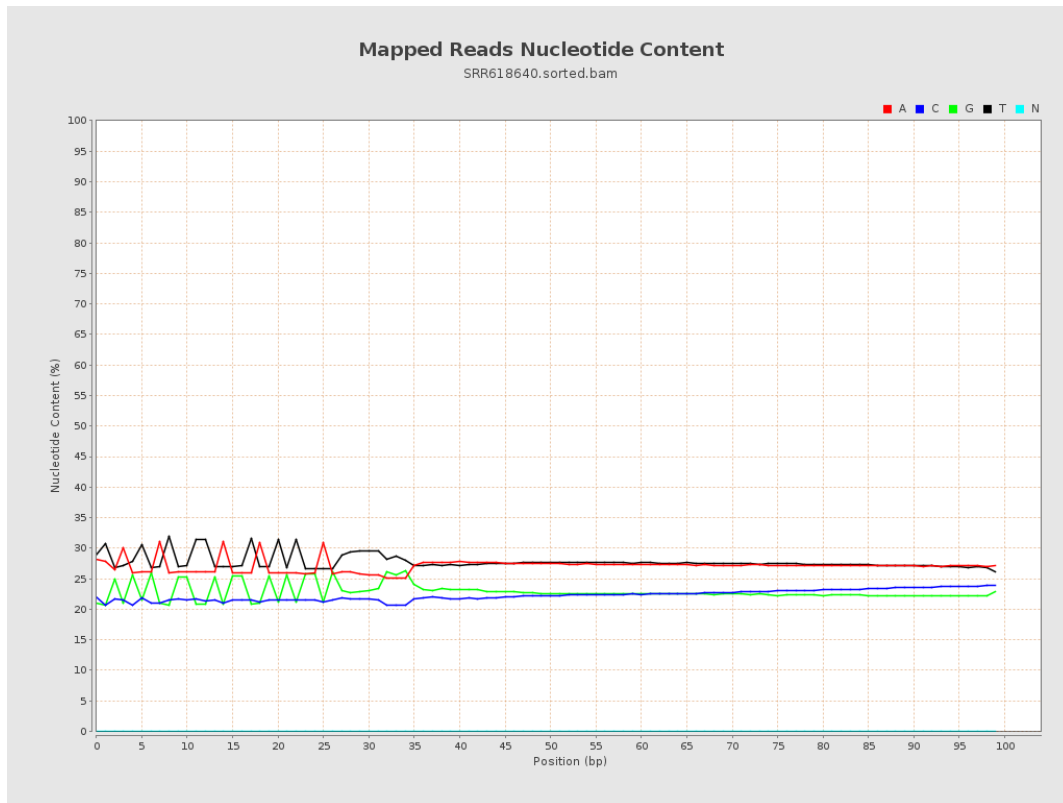
6. Results : Genome Fraction Coverage



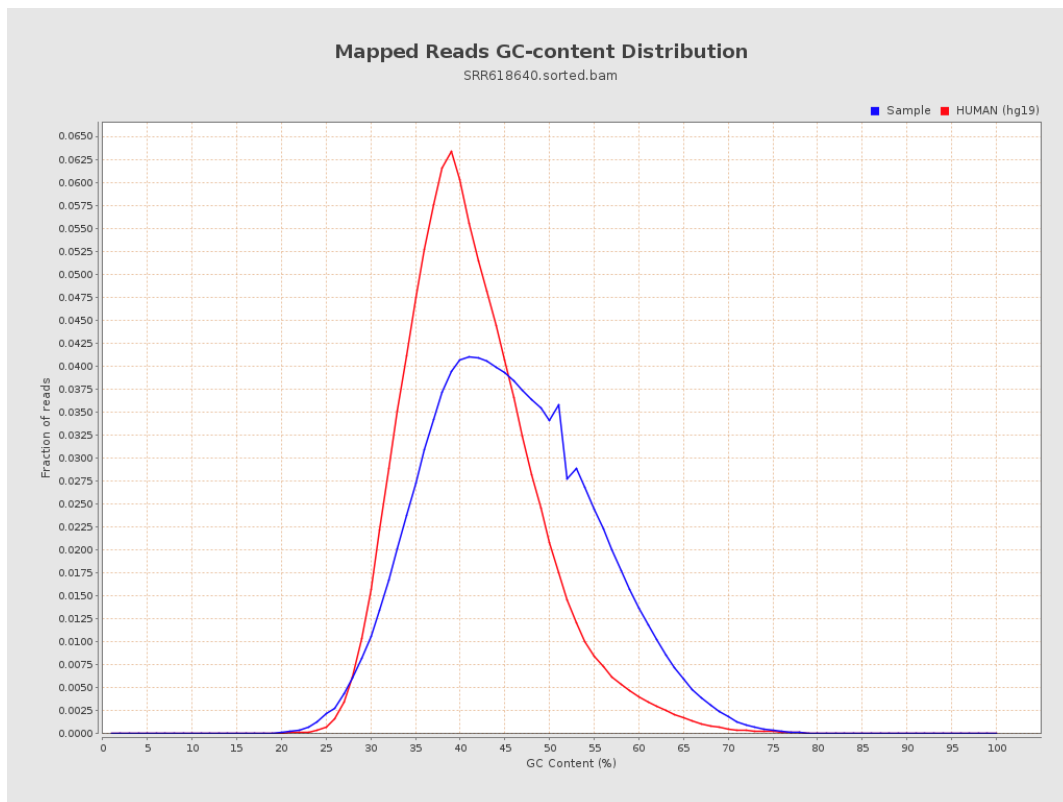
7. Results : Duplication Rate Histogram



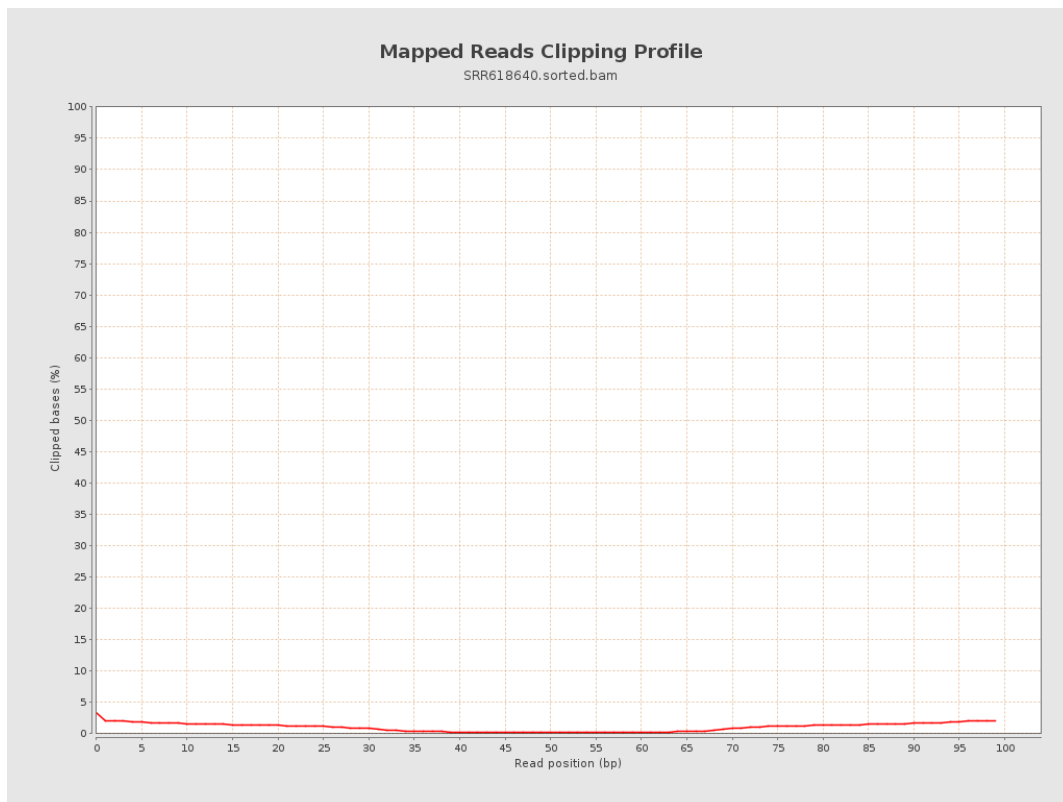
8. Results : Mapped Reads Nucleotide Content



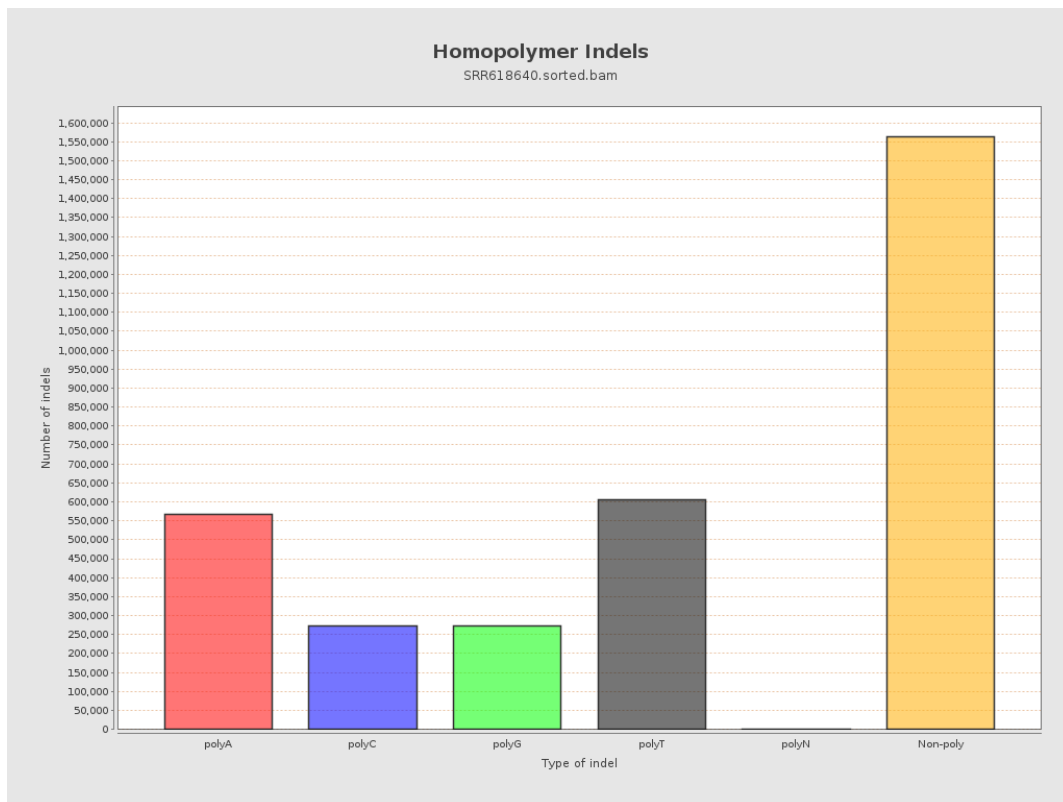
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



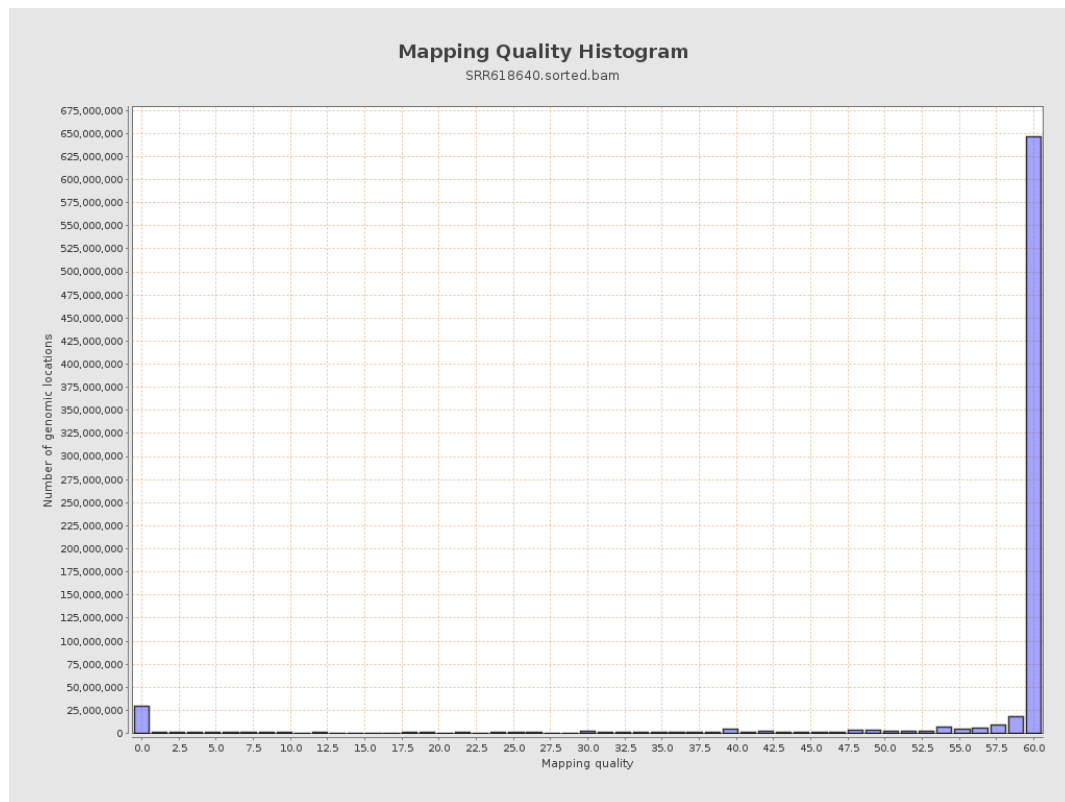
11. Results : Homopolymer Indels



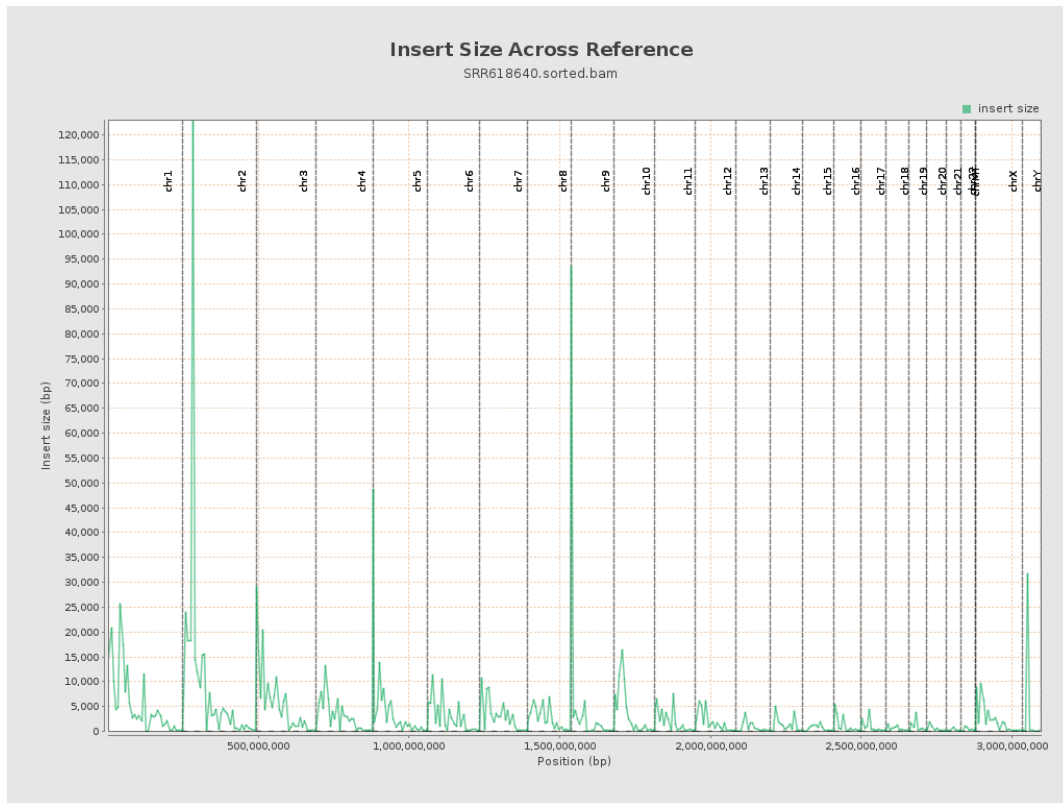
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

