

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 00:56:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618639.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_SRR618639 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618639_1.fastq.gz SRR618639_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 00:55:59 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618639.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	66,398,612
Mapped reads	59,034,321 / 88.91%
Unmapped reads	7,364,291 / 11.09%
Mapped paired reads	59,034,321 / 88.91%
Mapped reads, first in pair	31,971,569 / 48.15%
Mapped reads, second in pair	27,062,752 / 40.76%
Mapped reads, both in pair	53,442,358 / 80.49%
Mapped reads, singletons	5,591,963 / 8.42%
Secondary alignments	0
Supplementary alignments	320,796 / 0.48%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	13,045,487 / 19.65%
Duplication rate	18.23%
Clipped reads	17,722,053 / 26.69%

2.2. ACGT Content

Number/percentage of A's	1,462,211,173 / 26.98%
Number/percentage of C's	1,181,463,043 / 21.8%
Number/percentage of T's	1,504,407,840 / 27.76%
Number/percentage of G's	1,271,720,934 / 23.46%
Number/percentage of N's	322,608 / 0.01%

GC Percentage	45.26%
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2.3. Coverage

Mean	1.7521
Standard Deviation	7.3983

2.4. Mapping Quality

Mean Mapping Quality	53.25
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2.5. Insert size

Mean	156,500.2
Standard Deviation	3,940,226.59
P25/Median/P75	196 / 227 / 266

2.6. Mismatches and indels

General error rate	1.51%
Mismatches	80,444,148
Insertions	1,012,607
Mapped reads with at least one insertion	1.68%
Deletions	2,754,088
Mapped reads with at least one deletion	4.55%
Homopolymer indels	52.07%

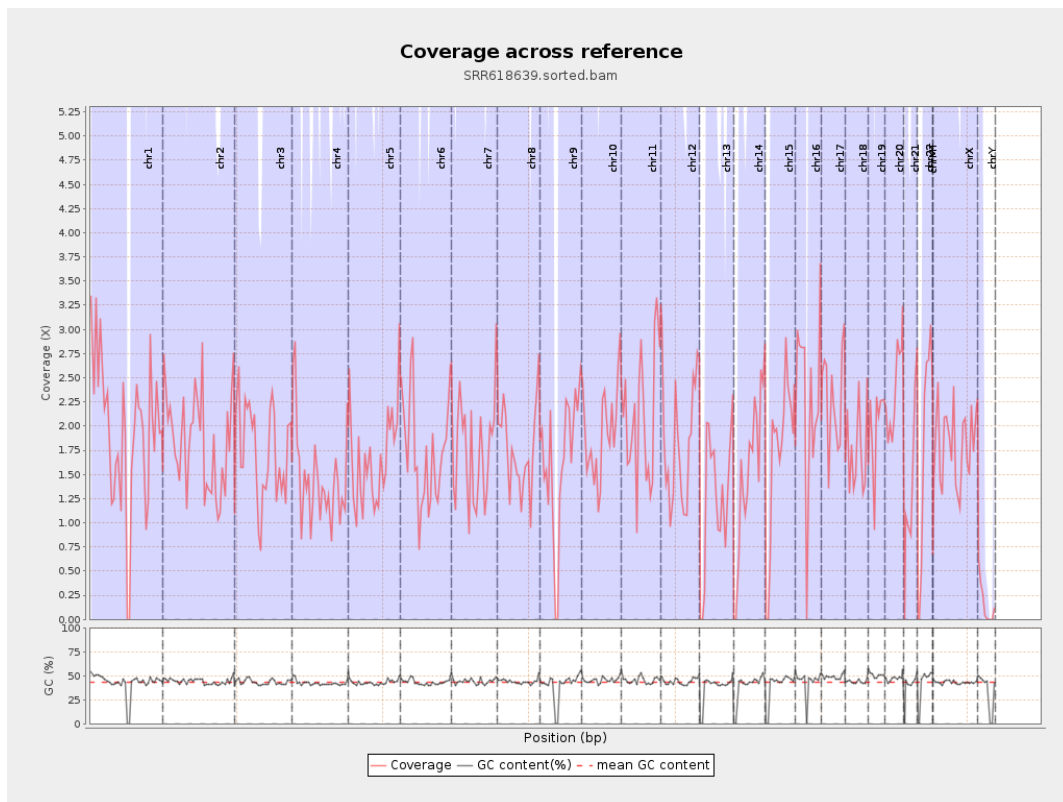
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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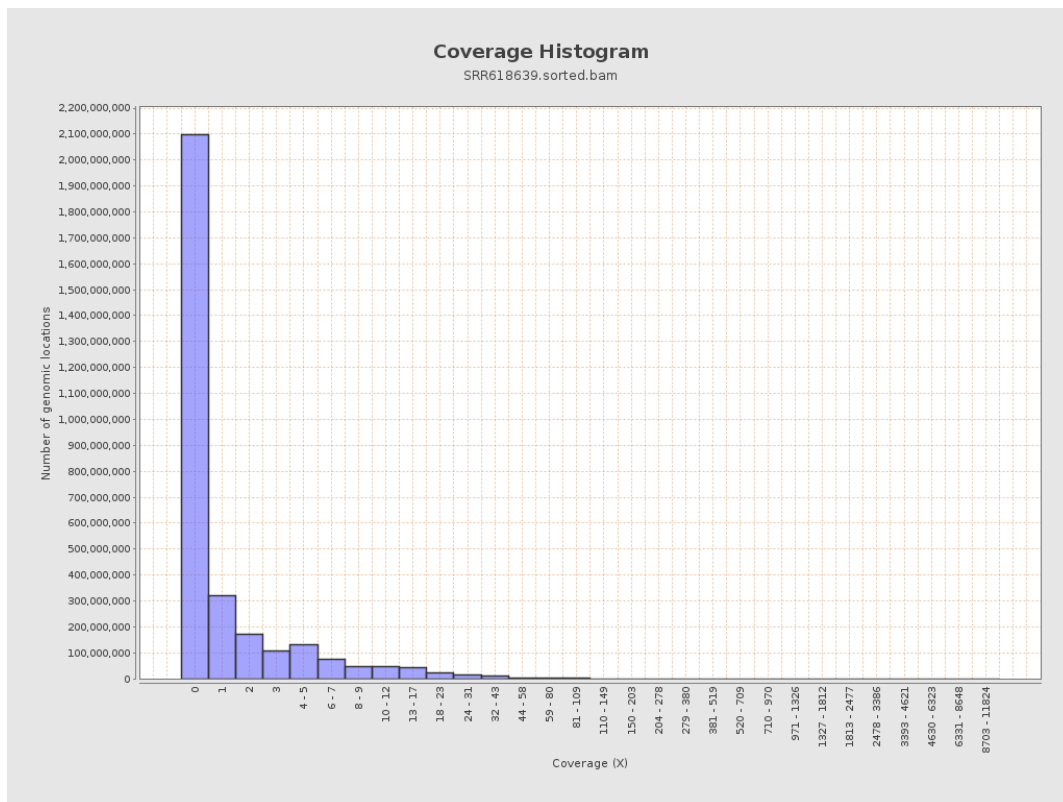
		bases	coverage	deviation
chr1	249250621	484351076	1.9432	7.9321
chr2	243199373	445590123	1.8322	10.2686
chr3	198022430	342896844	1.7316	5.829
chr4	191154276	276874297	1.4484	5.5213
chr5	180915260	306041658	1.6916	5.7955
chr6	171115067	294945976	1.7237	5.8104
chr7	159138663	279146436	1.7541	6.0684
chr8	146364022	255674757	1.7468	6.1965
chr9	141213431	230504609	1.6323	7.295
chr10	135534747	259528198	1.9148	6.8496
chr11	135006516	282711805	2.0941	7.1503
chr12	133851895	246859283	1.8443	6.7679
chr13	115169878	145004707	1.2591	4.9865
chr14	107349540	161084615	1.5006	5.639
chr15	102531392	174354493	1.7005	6.5101
chr16	90354753	203638660	2.2538	17.4351
chr17	81195210	184985221	2.2783	7.3676
chr18	78077248	134428683	1.7217	6.889
chr19	59128983	116770847	1.9748	7.114
chr20	63025520	148200155	2.3514	7.5024
chr21	48129895	68445548	1.4221	7.6451
chr22	51304566	91610022	1.7856	6.8577
chrMT	16571	10983	0.6628	1.6978
chrX	155270560	280809319	1.8085	5.6401

chrY	59373566	9496225	0.1599	5.9488
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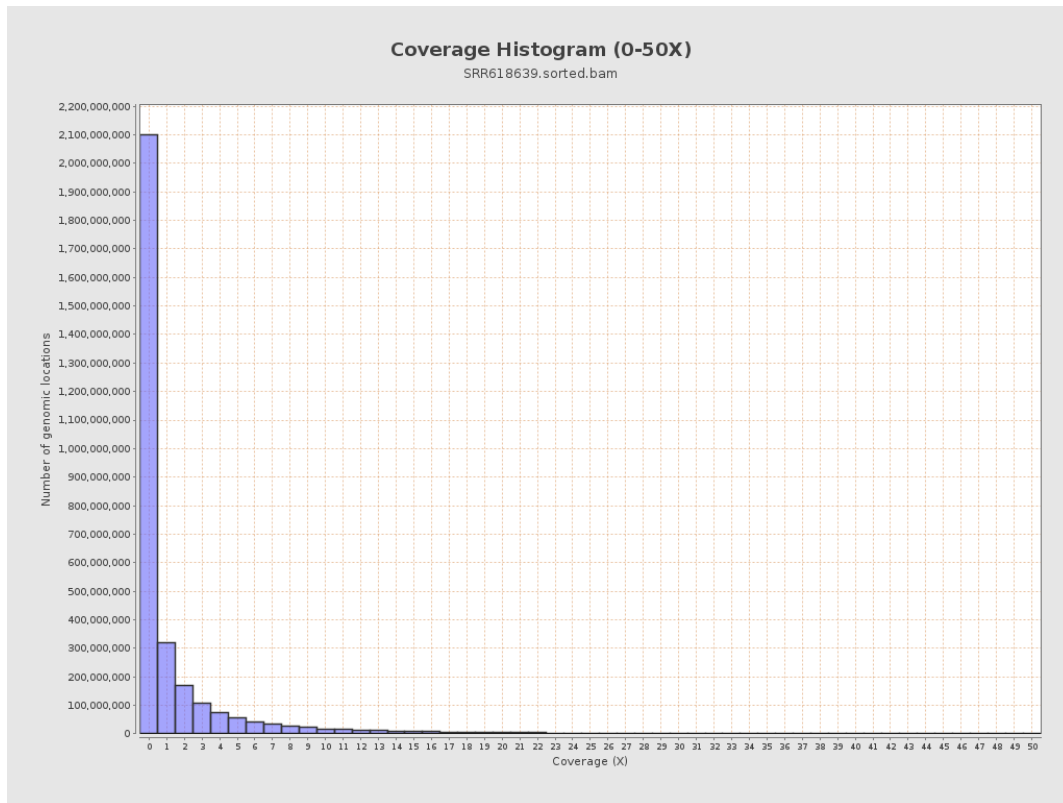
3. Results : Coverage across reference



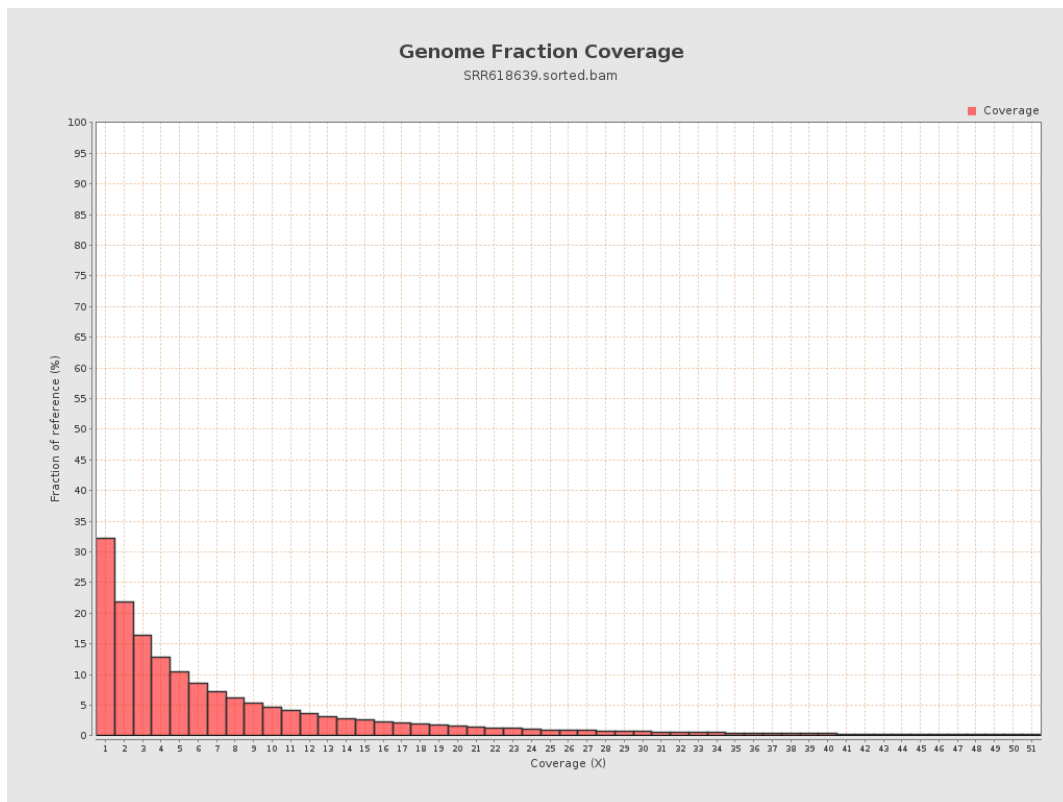
4. Results : Coverage Histogram



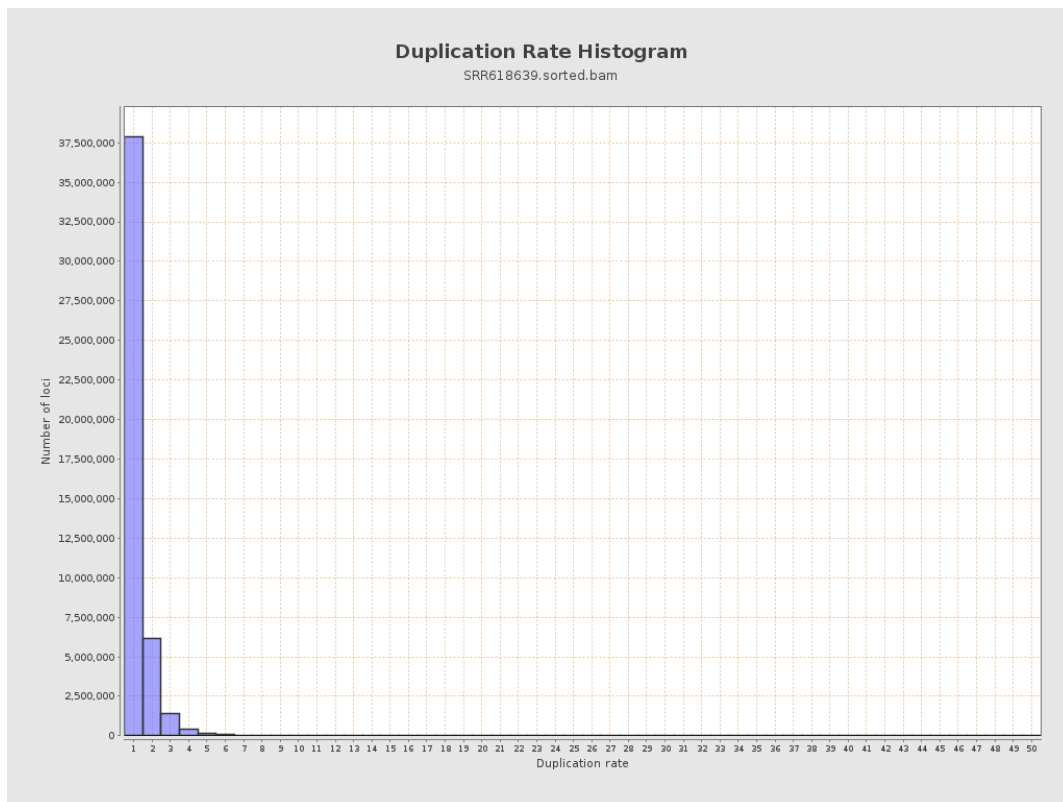
5. Results : Coverage Histogram (0-50X)



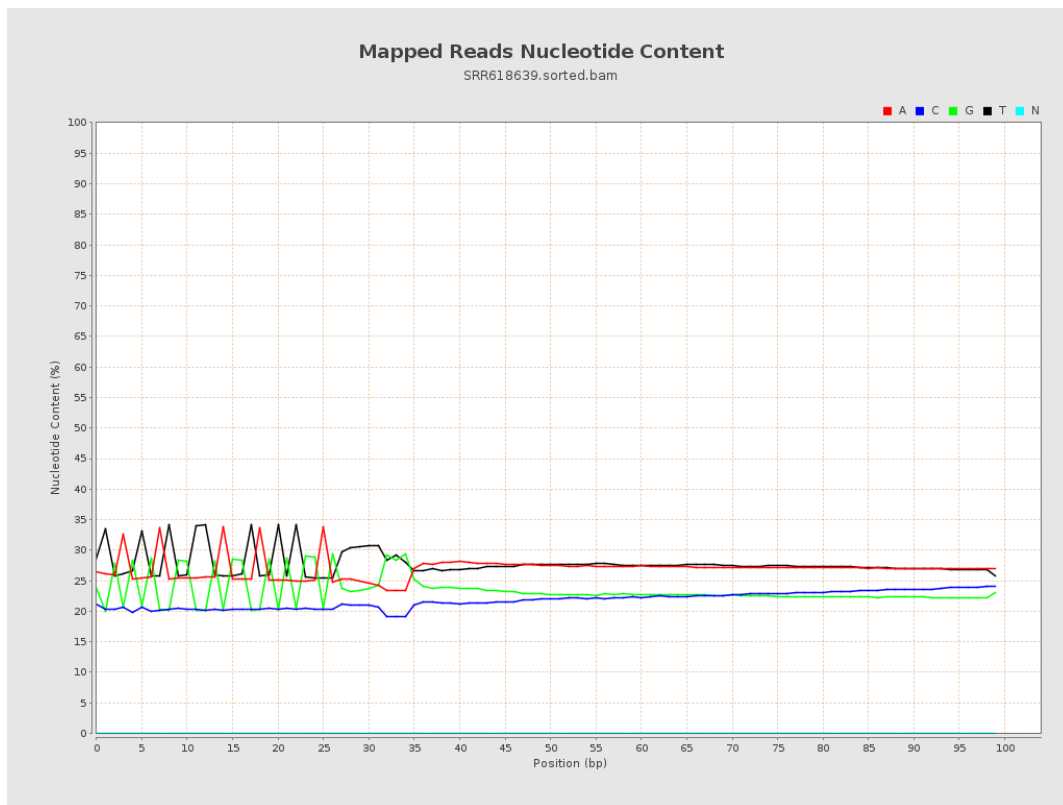
6. Results : Genome Fraction Coverage



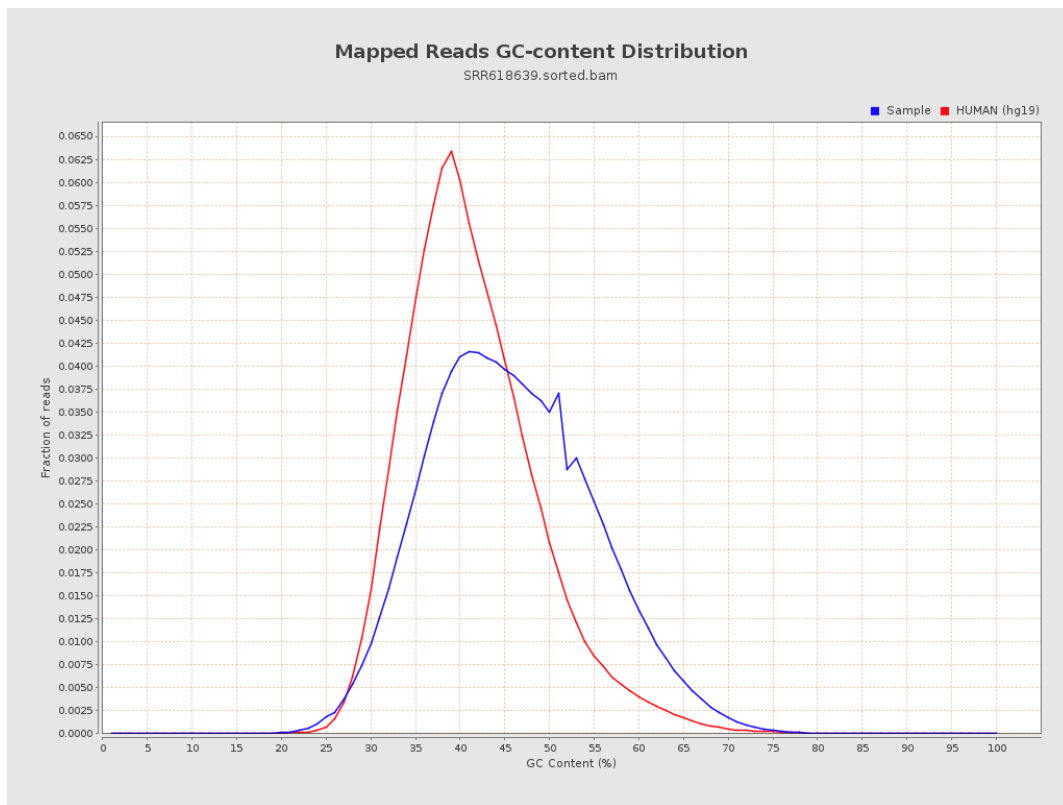
7. Results : Duplication Rate Histogram



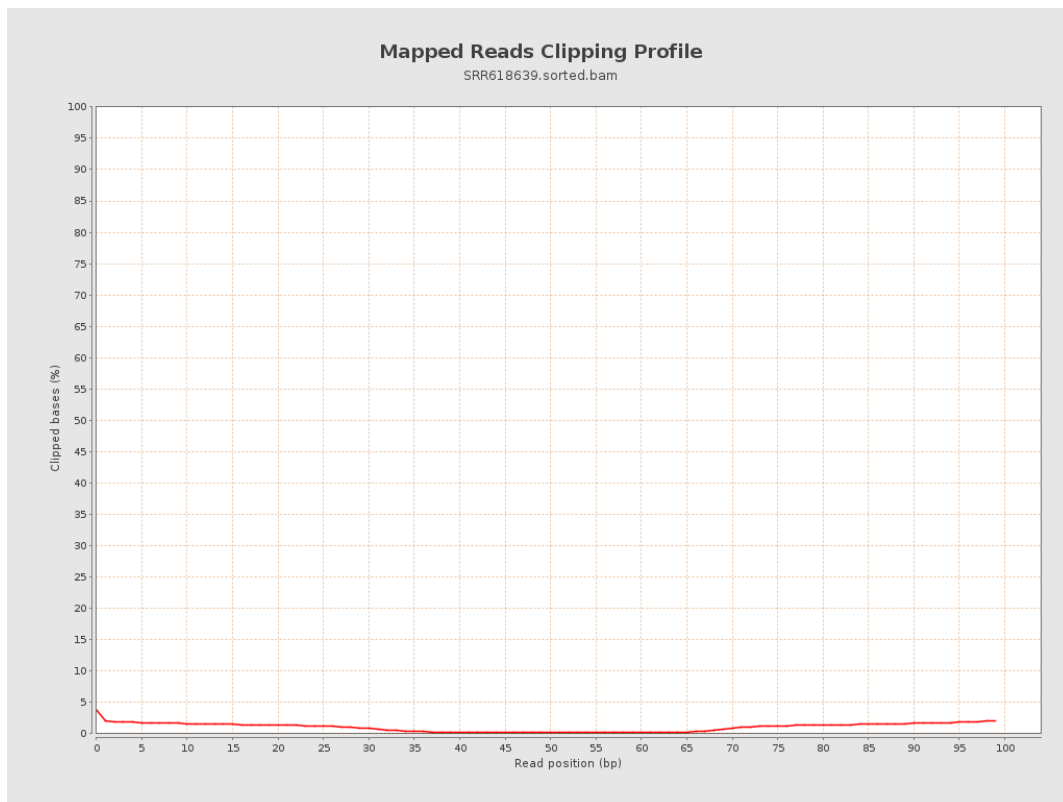
8. Results : Mapped Reads Nucleotide Content



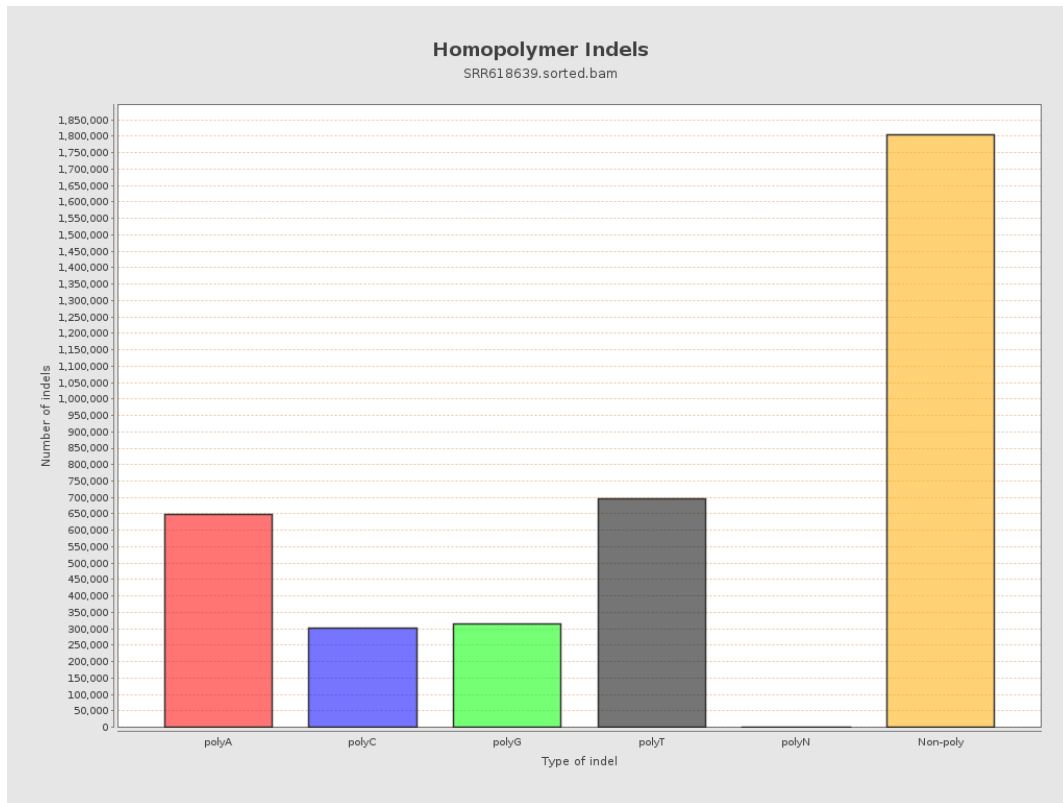
9. Results : Mapped Reads GC-content Distribution



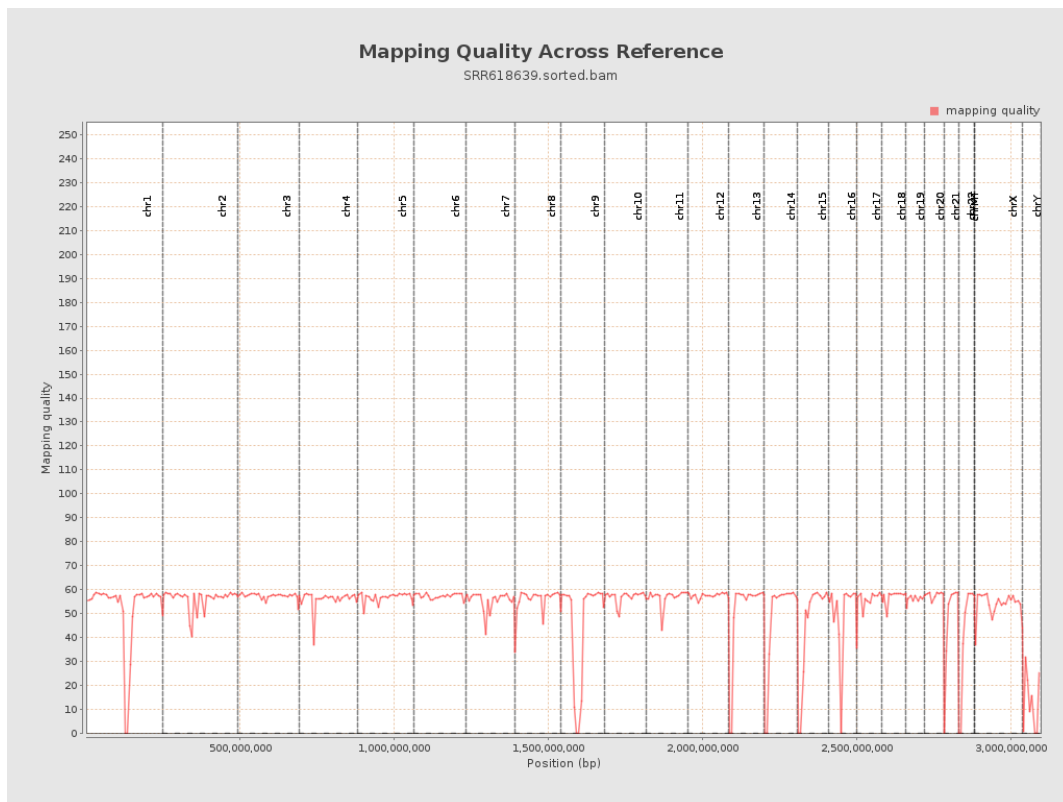
10. Results : Mapped Reads Clipping Profile



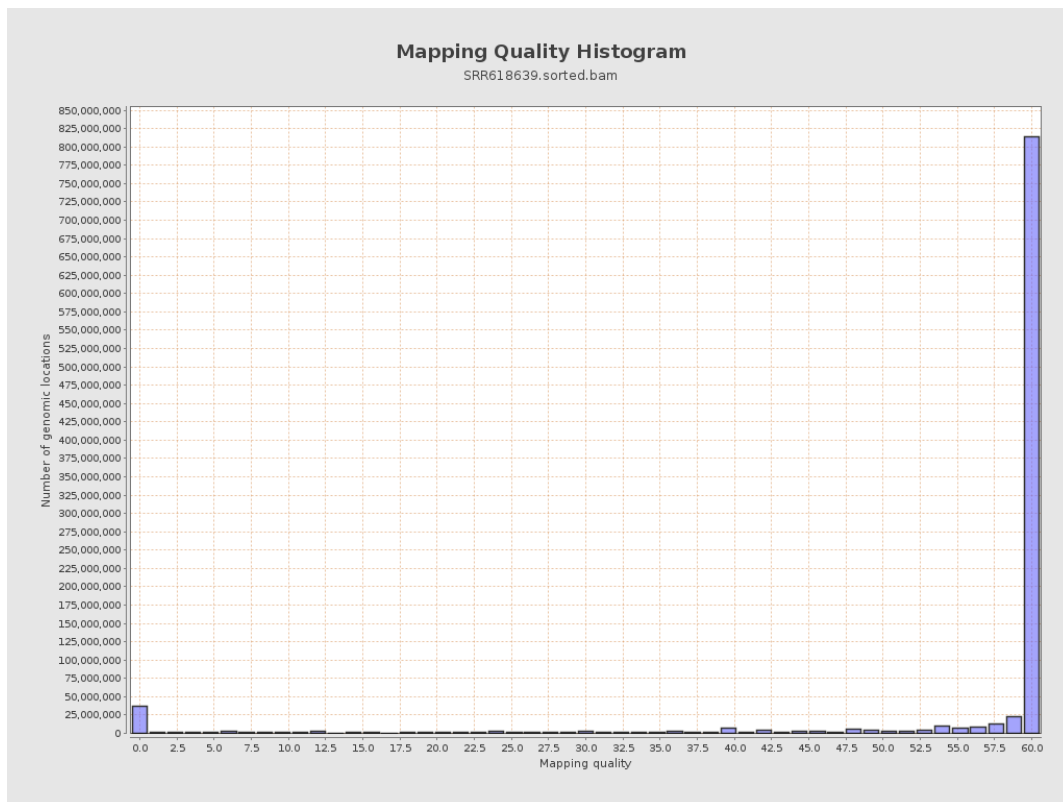
11. Results : Homopolymer Indels



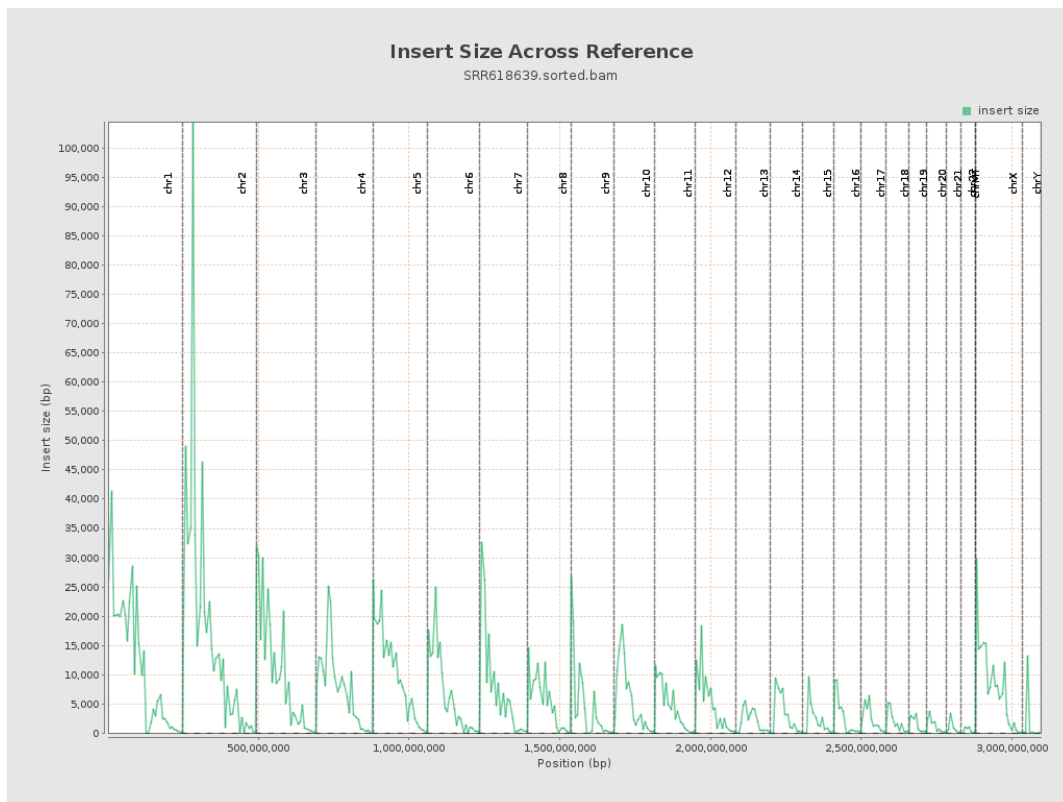
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

