

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 05:33:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618645.sorted.bam -c -nw 400 -hm 3
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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_SRR618645 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618645_1.fastq.gz SRR618645_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 05:33:00 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618645.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	43,856,208
Mapped reads	39,447,497 / 89.95%
Unmapped reads	4,408,711 / 10.05%
Mapped paired reads	39,447,497 / 89.95%
Mapped reads, first in pair	21,098,979 / 48.11%
Mapped reads, second in pair	18,348,518 / 41.84%
Mapped reads, both in pair	36,185,496 / 82.51%
Mapped reads, singletons	3,262,001 / 7.44%
Secondary alignments	0
Supplementary alignments	234,023 / 0.53%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	9,198,562 / 20.97%
Duplication rate	19.54%
Clipped reads	10,879,820 / 24.81%

2.2. ACGT Content

Number/percentage of A's	999,337,763 / 27.32%
Number/percentage of C's	788,769,825 / 21.56%
Number/percentage of T's	1,027,848,698 / 28.1%
Number/percentage of G's	841,920,989 / 23.02%
Number/percentage of N's	154,649 / 0%

GC Percentage	44.58%
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2.3. Coverage

Mean	1.1825
Standard Deviation	5.2766

2.4. Mapping Quality

Mean Mapping Quality	52.44
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2.5. Insert size

Mean	176,524.58
Standard Deviation	4,207,537.67
P25/Median/P75	212 / 237 / 264

2.6. Mismatches and indels

General error rate	1.39%
Mismatches	49,900,306
Insertions	694,497
Mapped reads with at least one insertion	1.73%
Deletions	1,884,090
Mapped reads with at least one deletion	4.65%
Homopolymer indels	52.36%

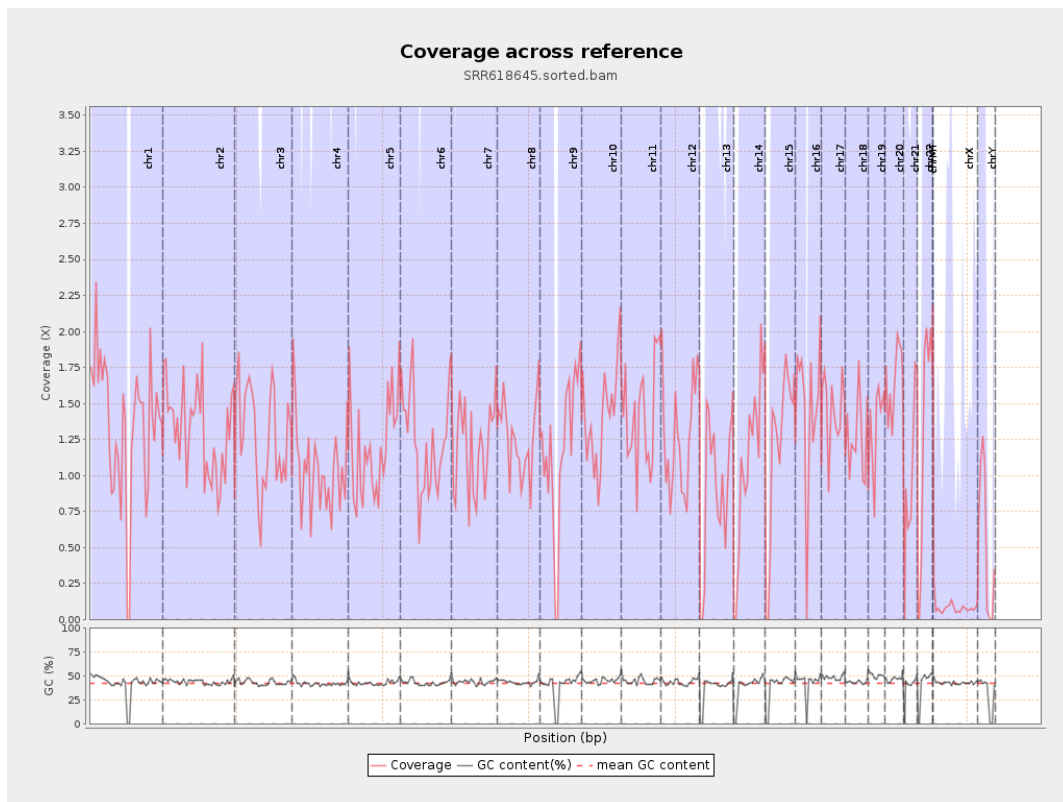
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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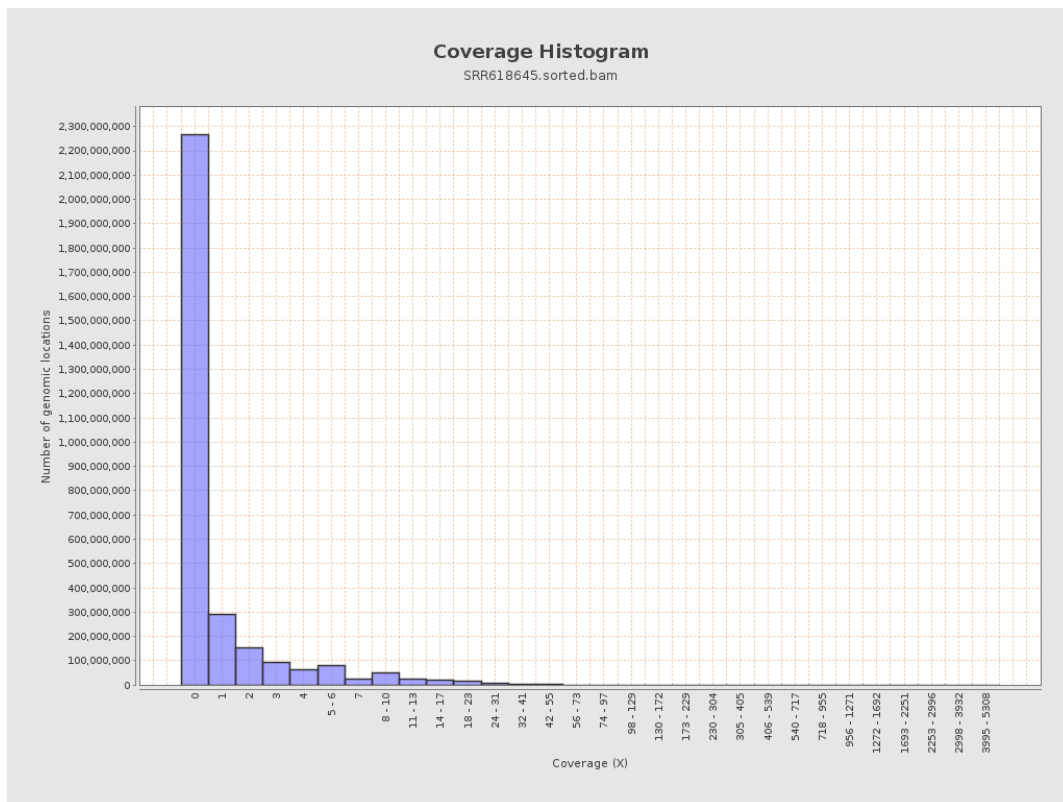
		bases	coverage	deviation
chr1	249250621	333385104	1.3375	6.6549
chr2	243199373	318923748	1.3114	6.7181
chr3	198022430	250421263	1.2646	4.5277
chr4	191154276	199287522	1.0425	4.2743
chr5	180915260	219173169	1.2115	4.5787
chr6	171115067	210098378	1.2278	4.3228
chr7	159138663	191767540	1.205	4.6048
chr8	146364022	183760288	1.2555	4.4799
chr9	141213431	166767077	1.181	5.716
chr10	135534747	190038032	1.4021	4.9538
chr11	135006516	190881867	1.4139	5.5785
chr12	133851895	170825345	1.2762	4.9279
chr13	115169878	103745054	0.9008	3.7241
chr14	107349540	117434229	1.0939	4.2031
chr15	102531392	122990035	1.1995	4.903
chr16	90354753	130197696	1.441	9.1678
chr17	81195210	118640929	1.4612	5.2325
chr18	78077248	97401113	1.2475	5.6589
chr19	59128983	78829291	1.3332	6.4377
chr20	63025520	104564221	1.6591	5.5157
chr21	48129895	49207395	1.0224	6.1159
chr22	51304566	66165197	1.2897	5.3362
chrMT	16571	36235	2.1867	6.6765
chrX	155270560	12655274	0.0815	2.0088

chrY	59373566	33466752	0.5637	4.3385
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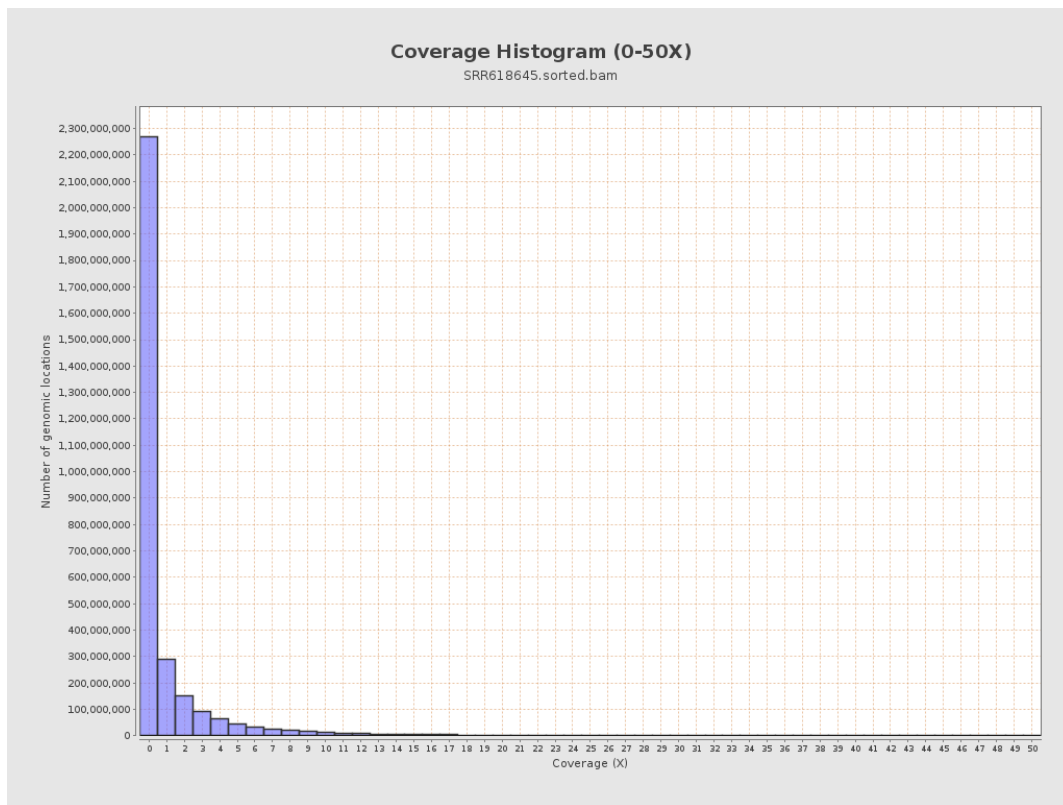
3. Results : Coverage across reference



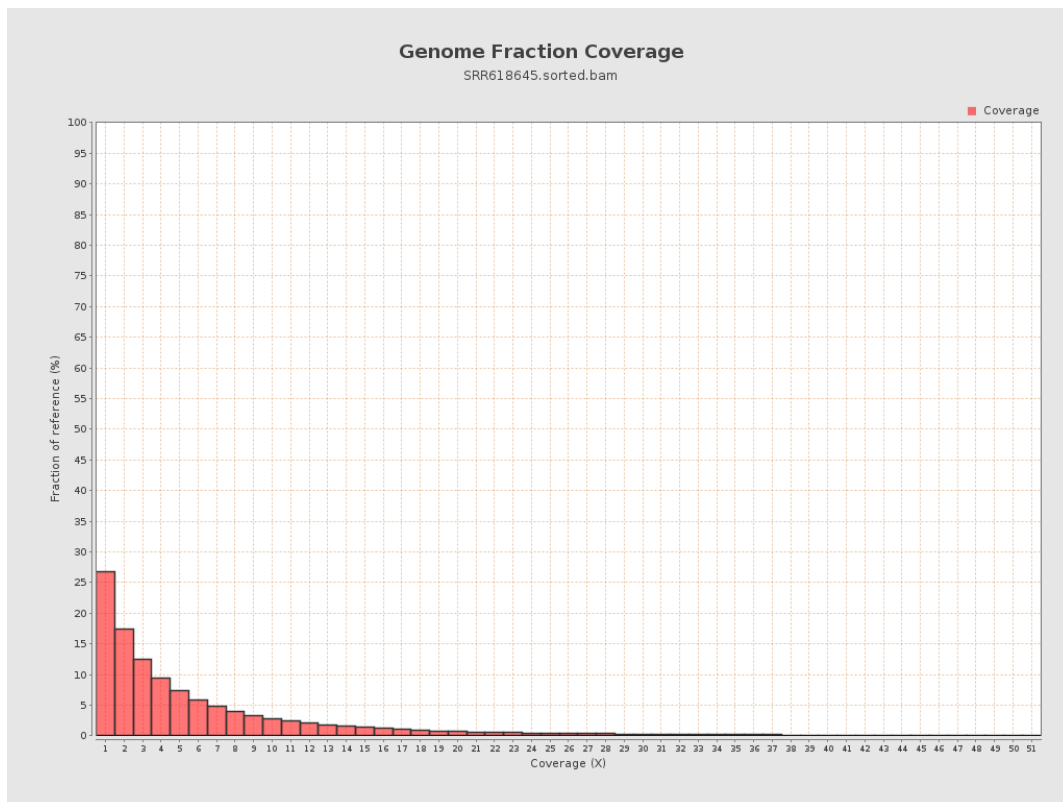
4. Results : Coverage Histogram



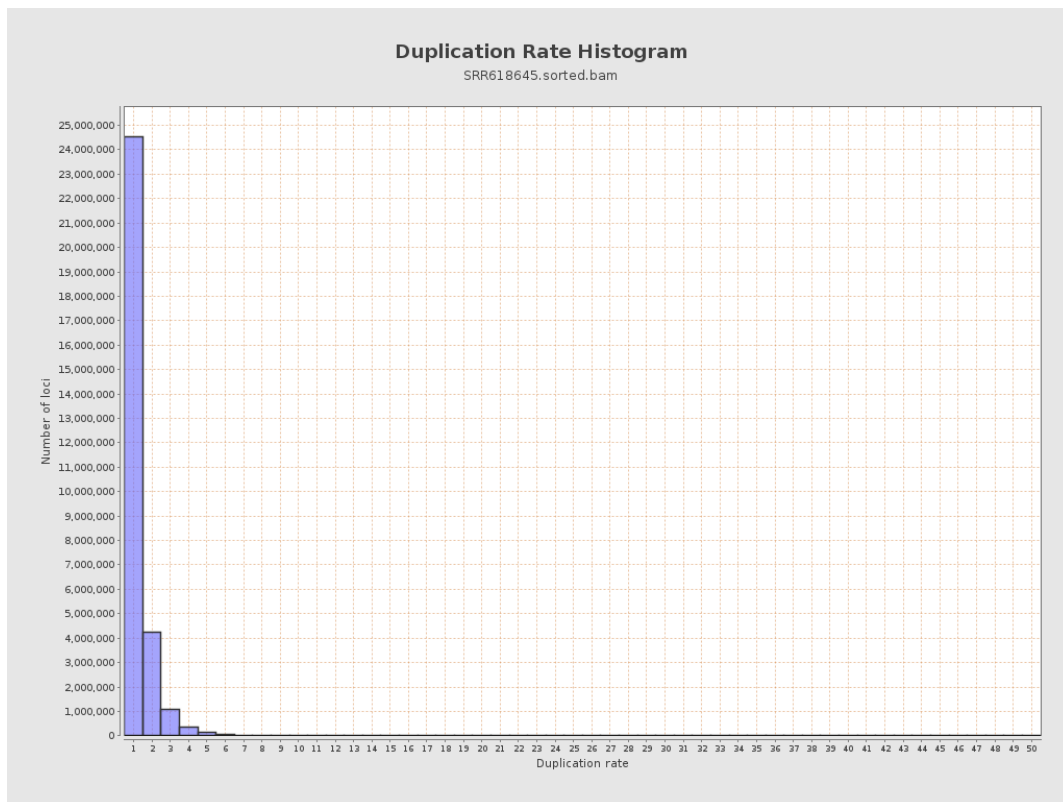
5. Results : Coverage Histogram (0-50X)



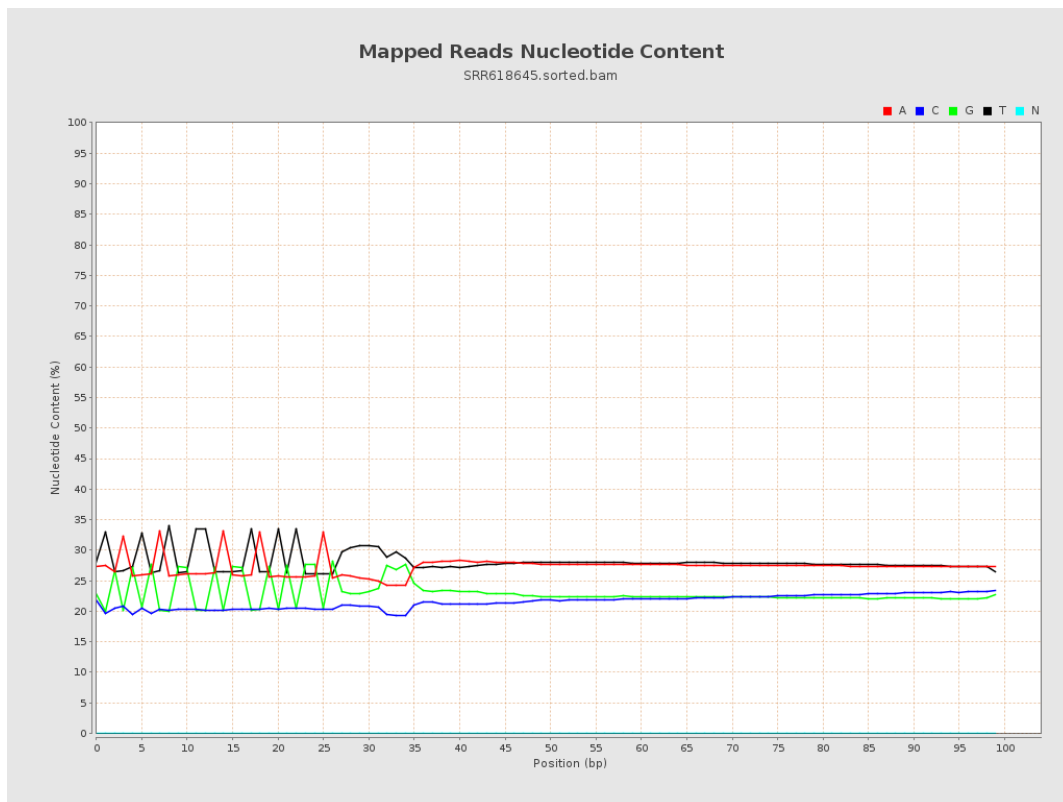
6. Results : Genome Fraction Coverage



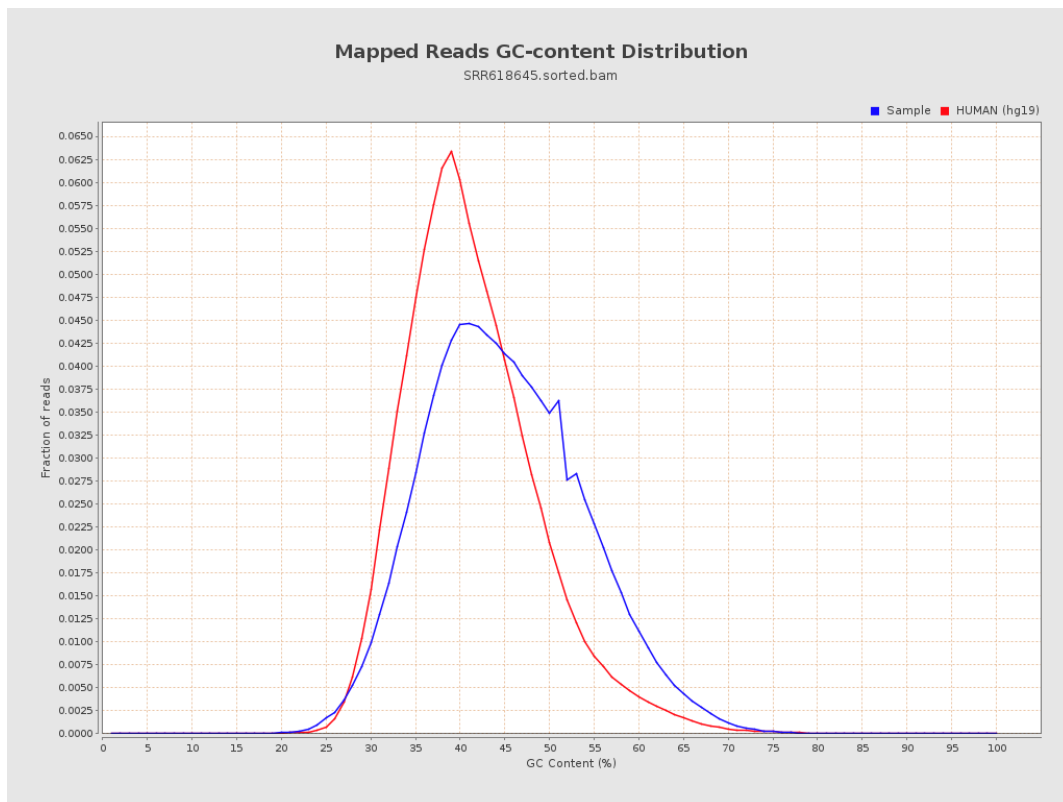
7. Results : Duplication Rate Histogram



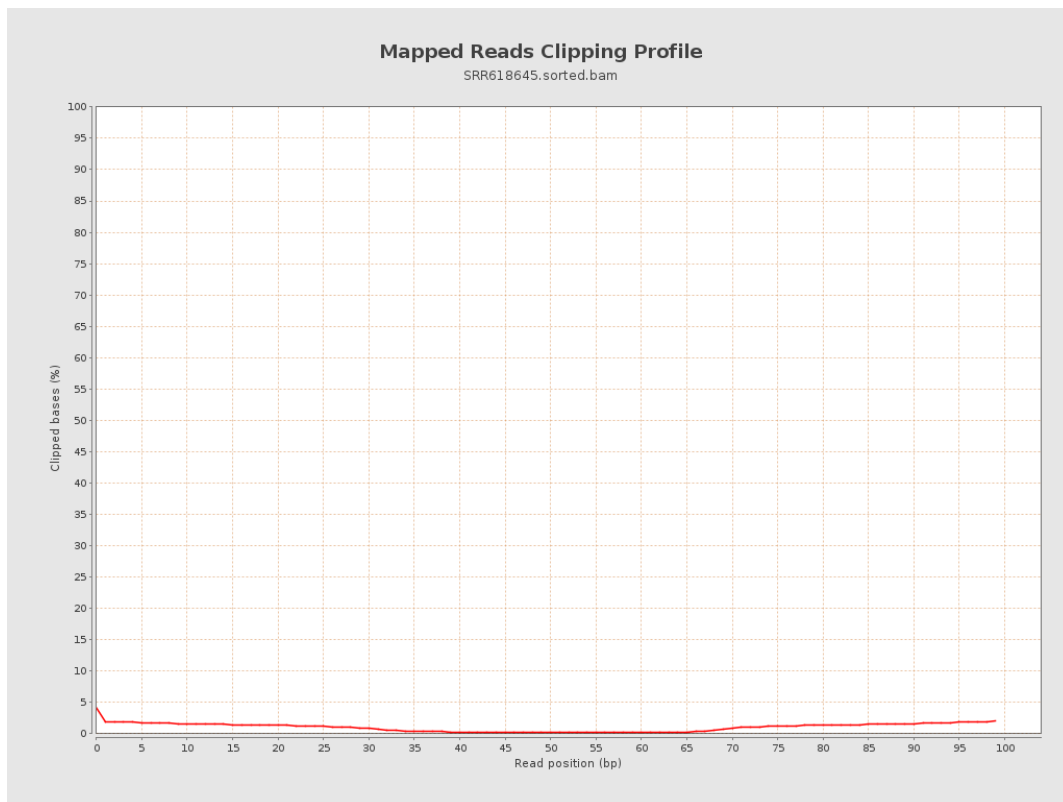
8. Results : Mapped Reads Nucleotide Content



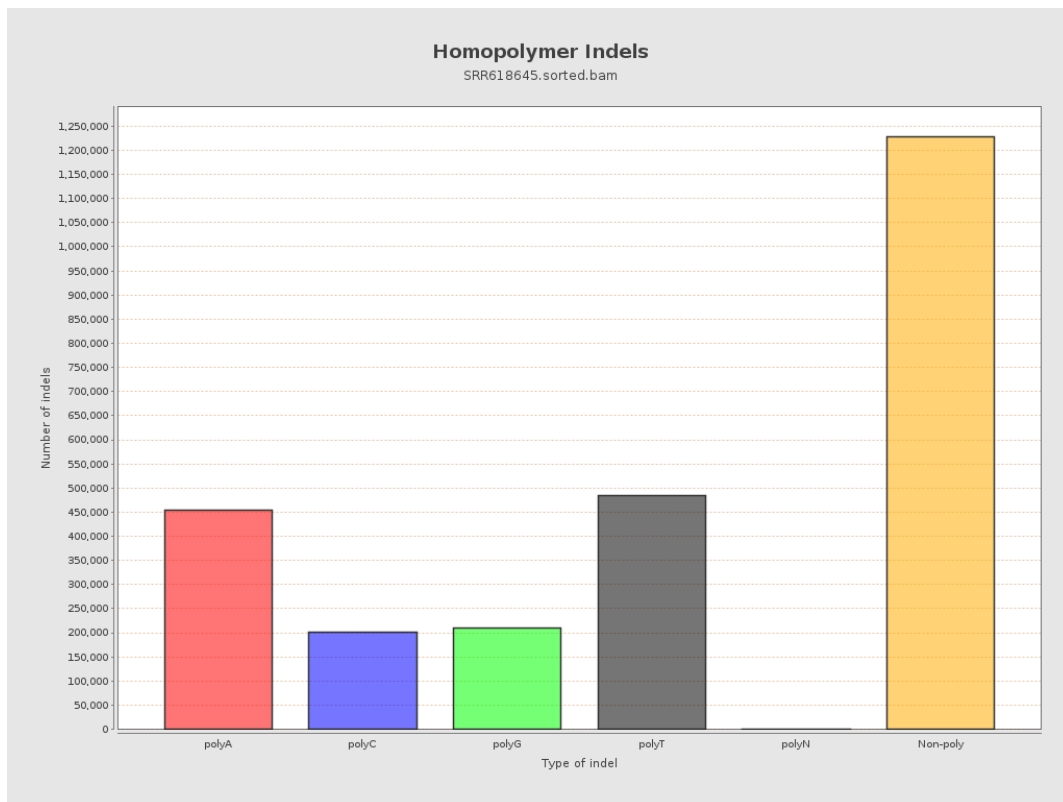
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



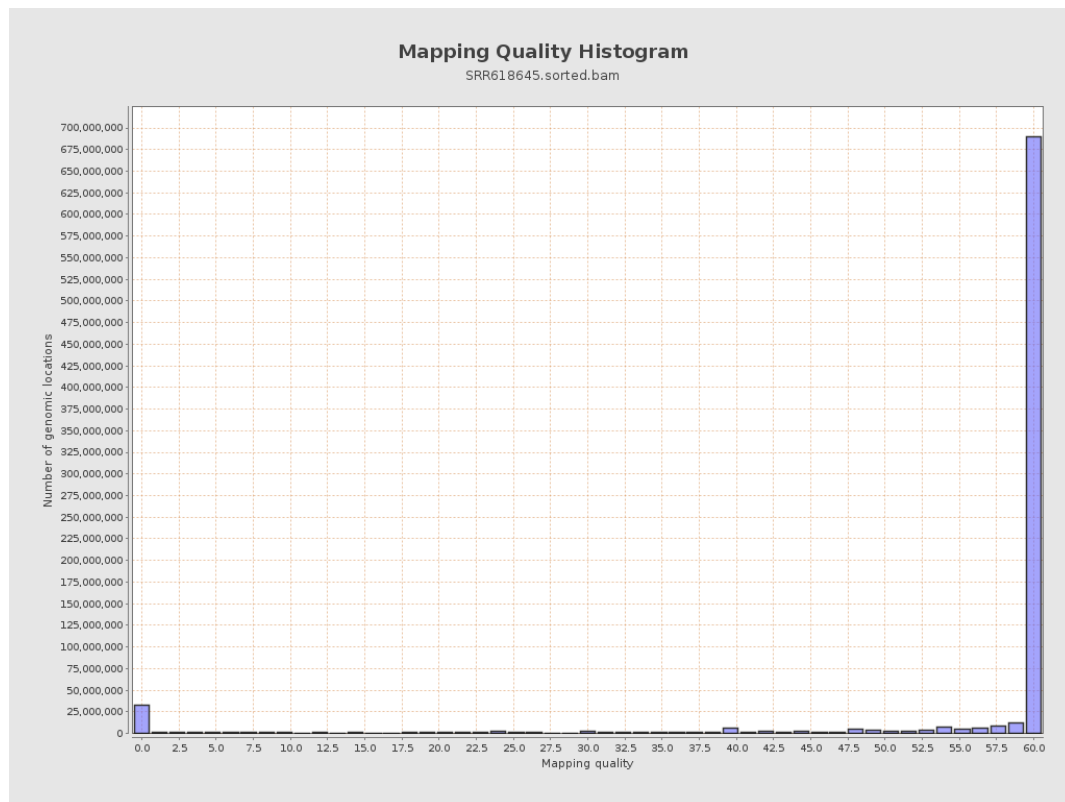
11. Results : Homopolymer Indels



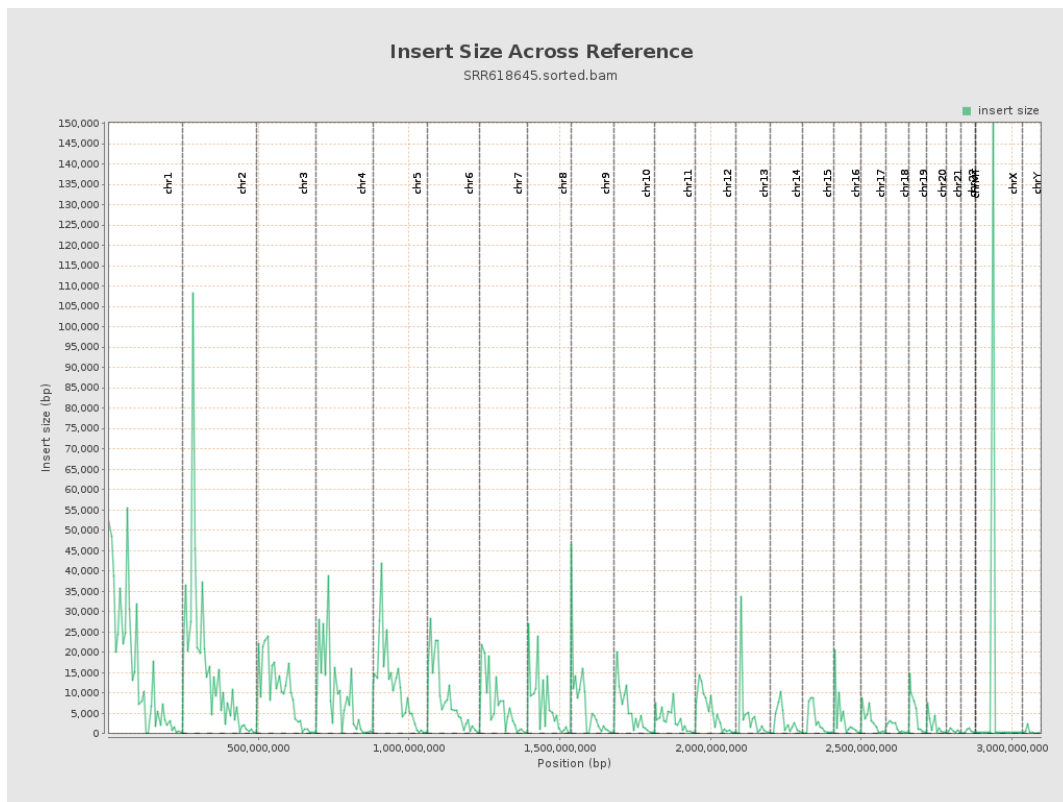
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

