

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 04:55:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618644.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_SRR618644 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618644_1.fastq.gz SRR618644_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 04:55:25 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618644.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	47,802,900
Mapped reads	42,433,358 / 88.77%
Unmapped reads	5,369,542 / 11.23%
Mapped paired reads	42,433,358 / 88.77%
Mapped reads, first in pair	23,042,847 / 48.2%
Mapped reads, second in pair	19,390,511 / 40.56%
Mapped reads, both in pair	38,378,496 / 80.28%
Mapped reads, singletons	4,054,862 / 8.48%
Secondary alignments	0
Supplementary alignments	118,910 / 0.25%
Read min/max/mean length	30 / 100 / 100.1
Duplicated reads (estimated)	8,304,021 / 17.37%
Duplication rate	17%
Clipped reads	10,787,499 / 22.57%

2.2. ACGT Content

Number/percentage of A's	1,076,361,479 / 27.2%
Number/percentage of C's	877,273,976 / 22.17%
Number/percentage of T's	1,092,827,174 / 27.61%
Number/percentage of G's	909,951,770 / 22.99%
Number/percentage of N's	1,212,208 / 0.03%

GC Percentage	45.16%
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2.3. Coverage

Mean	1.2793
Standard Deviation	5.1971

2.4. Mapping Quality

Mean Mapping Quality	52.87
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2.5. Insert size

Mean	92,565.89
Standard Deviation	3,058,211.74
P25/Median/P75	178 / 201 / 227

2.6. Mismatches and indels

General error rate	1.6%
Mismatches	62,400,595
Insertions	722,703
Mapped reads with at least one insertion	1.67%
Deletions	2,027,496
Mapped reads with at least one deletion	4.66%
Homopolymer indels	52.5%

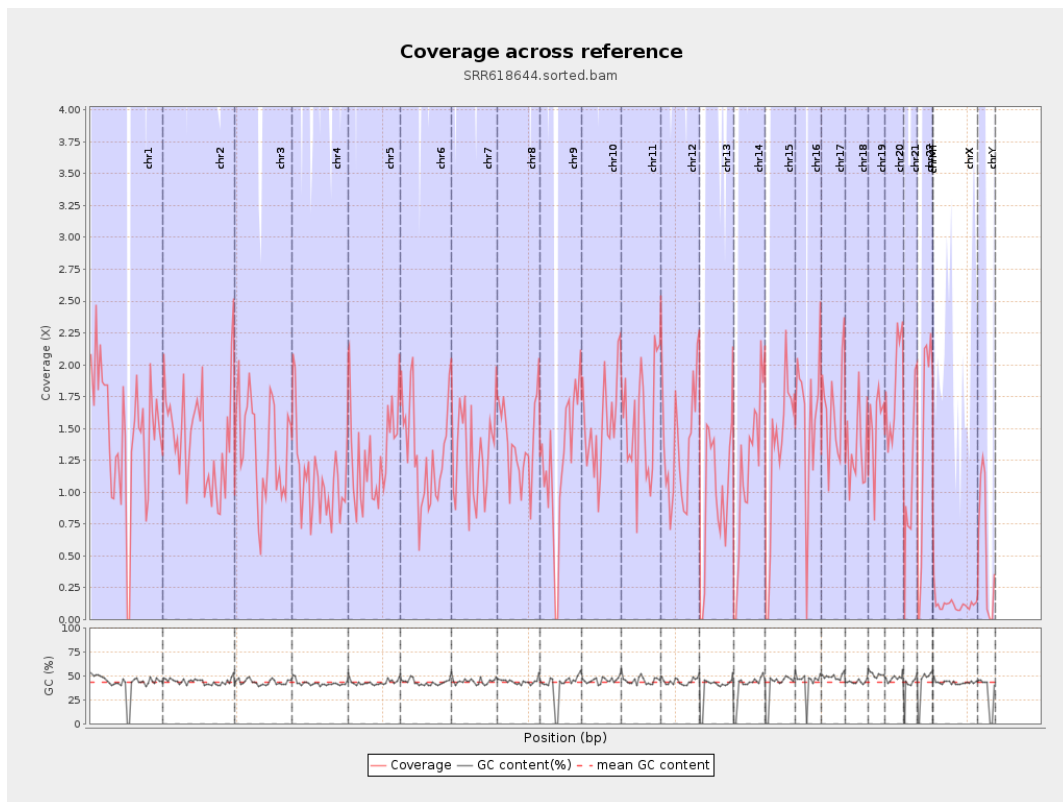
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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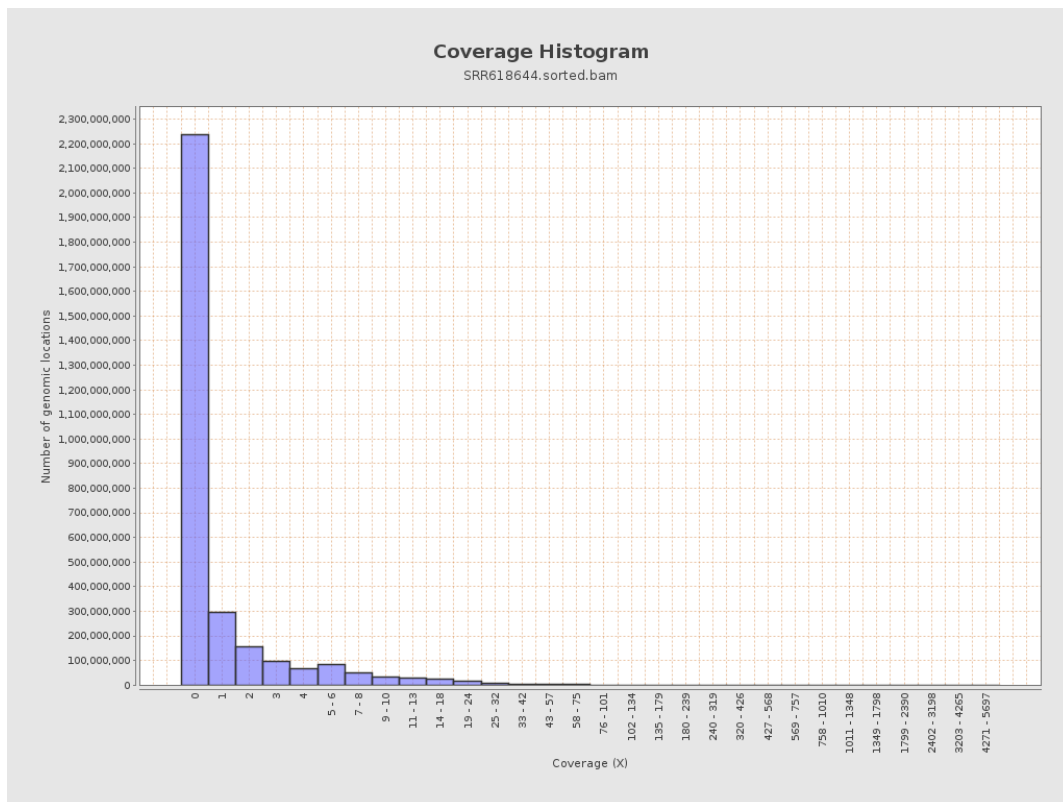
		bases	coverage	deviation
chr1	249250621	361345028	1.4497	5.9548
chr2	243199373	344147106	1.4151	6.7062
chr3	198022430	265406938	1.3403	4.5423
chr4	191154276	210636424	1.1019	4.3047
chr5	180915260	233613196	1.2913	4.6825
chr6	171115067	222509652	1.3004	4.399
chr7	159138663	208154589	1.308	4.4994
chr8	146364022	202794968	1.3856	4.9911
chr9	141213431	175483239	1.2427	5.2838
chr10	135534747	206510655	1.5237	5.1858
chr11	135006516	210150407	1.5566	5.4962
chr12	133851895	184209845	1.3762	4.9137
chr13	115169878	111962954	0.9722	3.6581
chr14	107349540	126556375	1.1789	4.3433
chr15	102531392	133370868	1.3008	4.89
chr16	90354753	143861961	1.5922	8.9382
chr17	81195210	132597628	1.6331	5.3157
chr18	78077248	102711590	1.3155	5.0754
chr19	59128983	89832728	1.5193	5.5103
chr20	63025520	114935961	1.8236	5.7551
chr21	48129895	53917988	1.1203	6.7003
chr22	51304566	72830879	1.4196	5.3859
chrMT	16571	15035	0.9073	2.1285
chrX	155270560	18320121	0.118	2.0818

chrY	59373566	34545328	0.5818	4.2787
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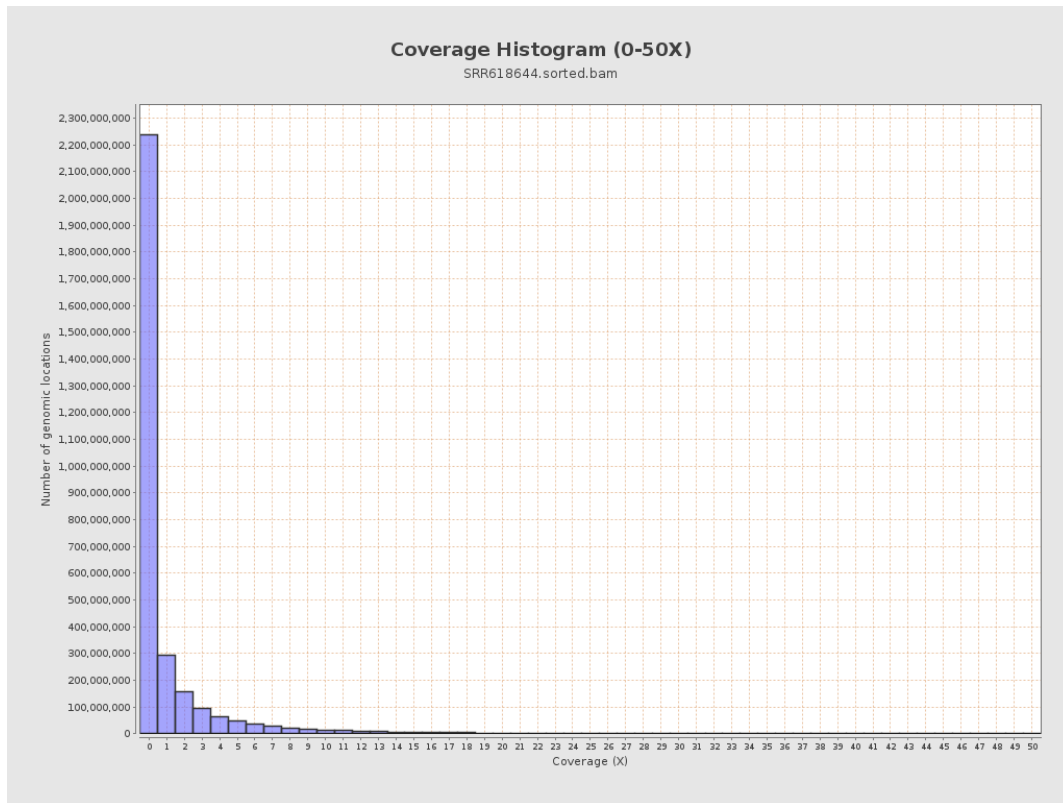
3. Results : Coverage across reference



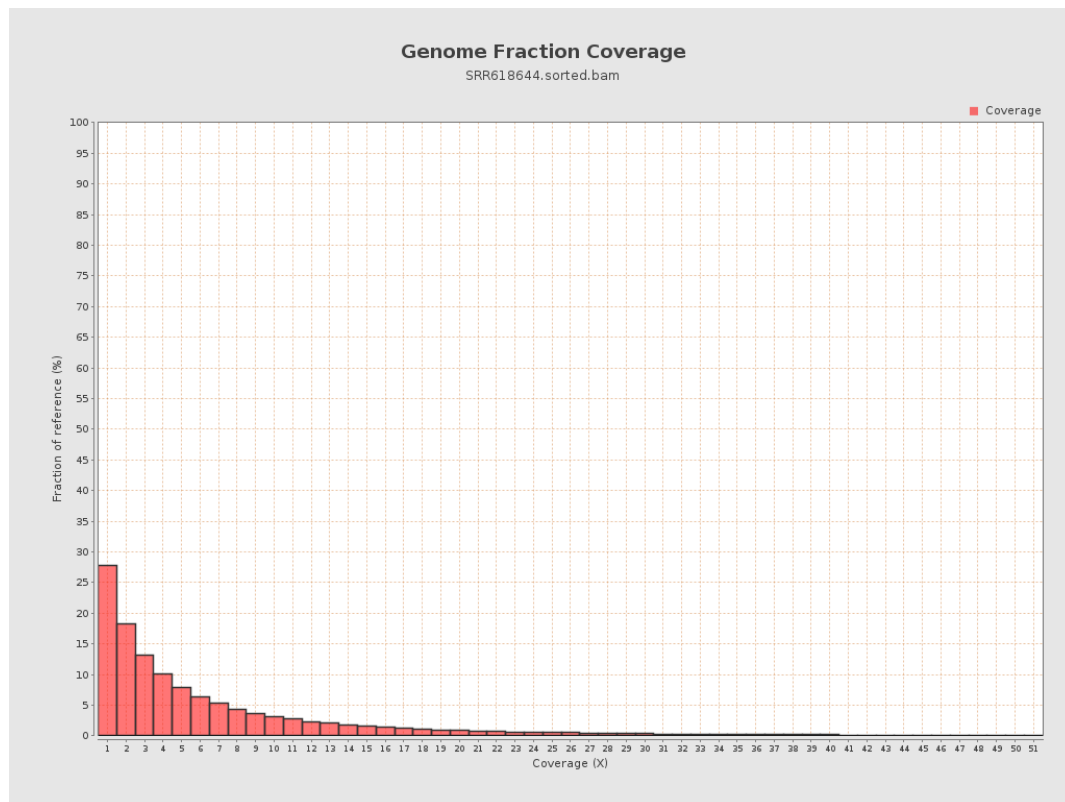
4. Results : Coverage Histogram



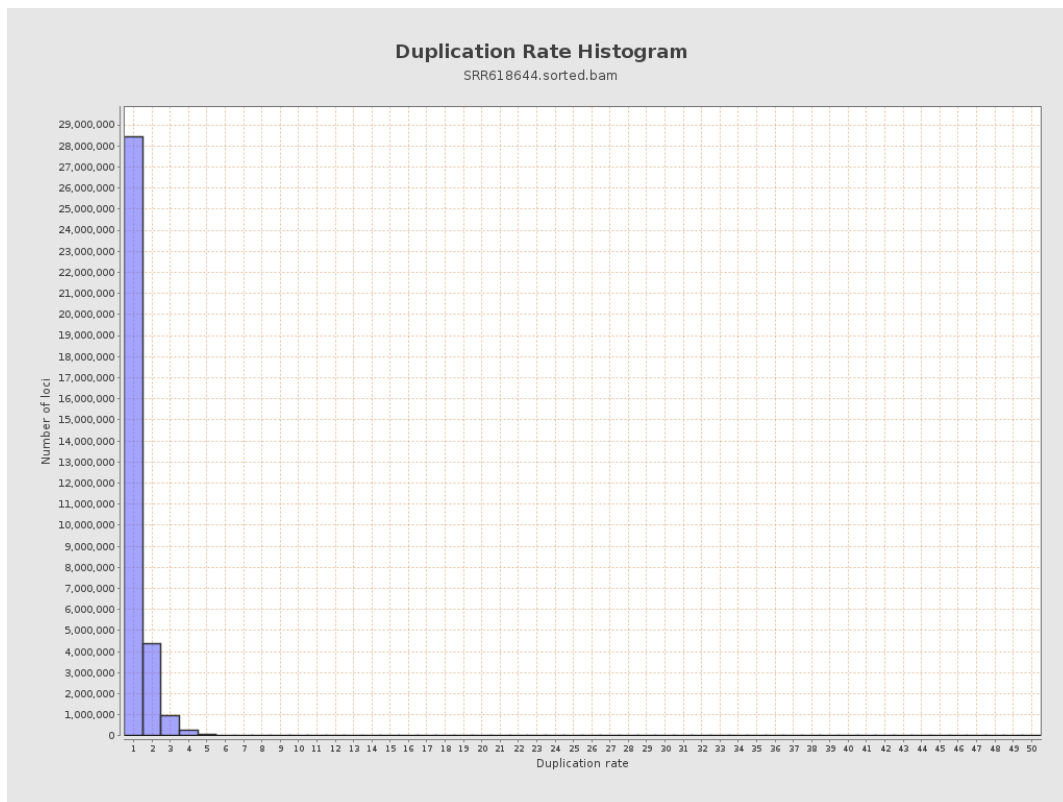
5. Results : Coverage Histogram (0-50X)



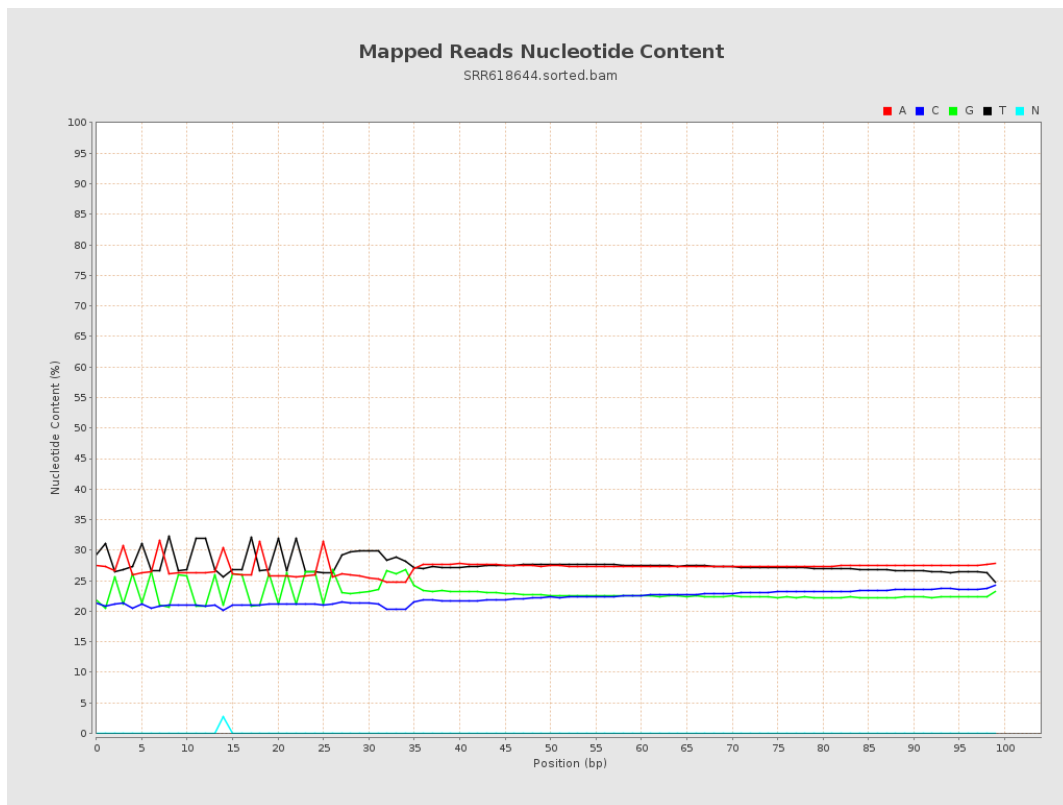
6. Results : Genome Fraction Coverage



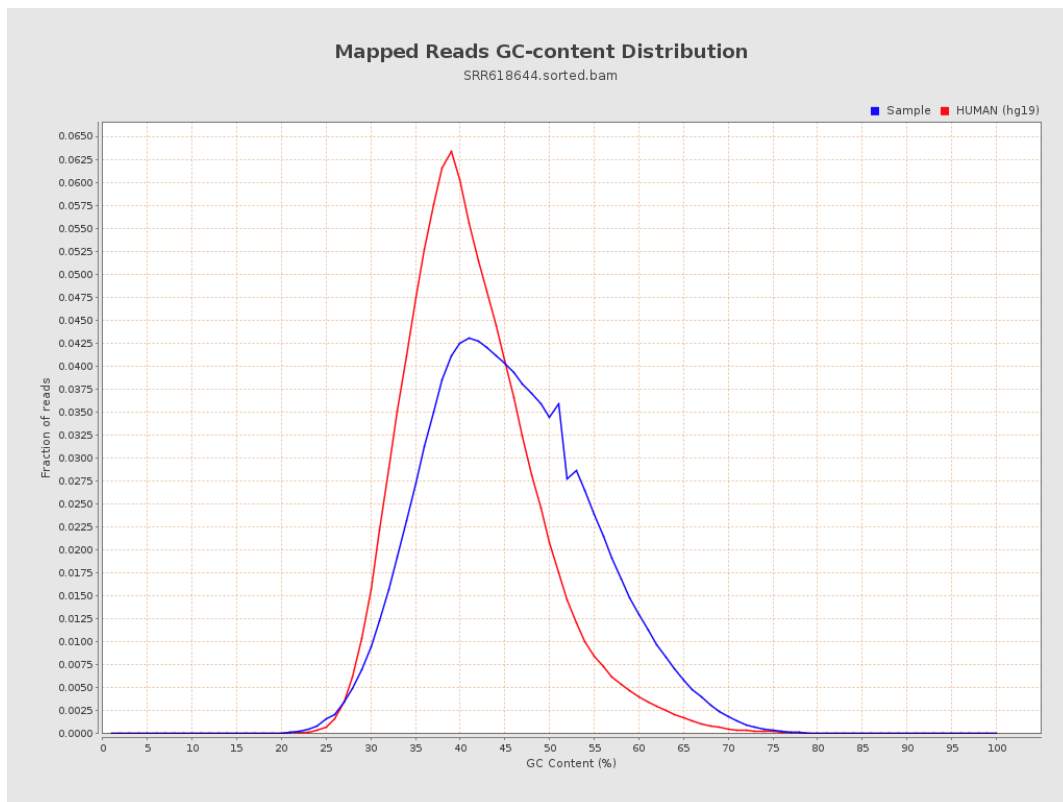
7. Results : Duplication Rate Histogram



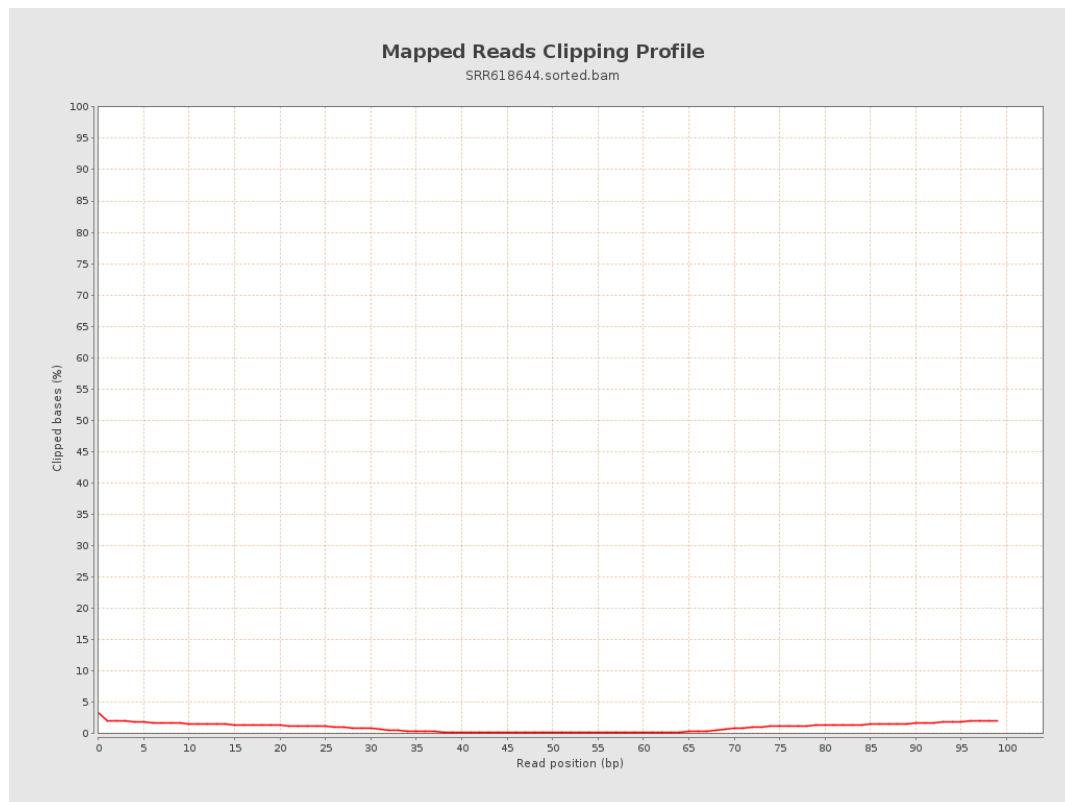
8. Results : Mapped Reads Nucleotide Content



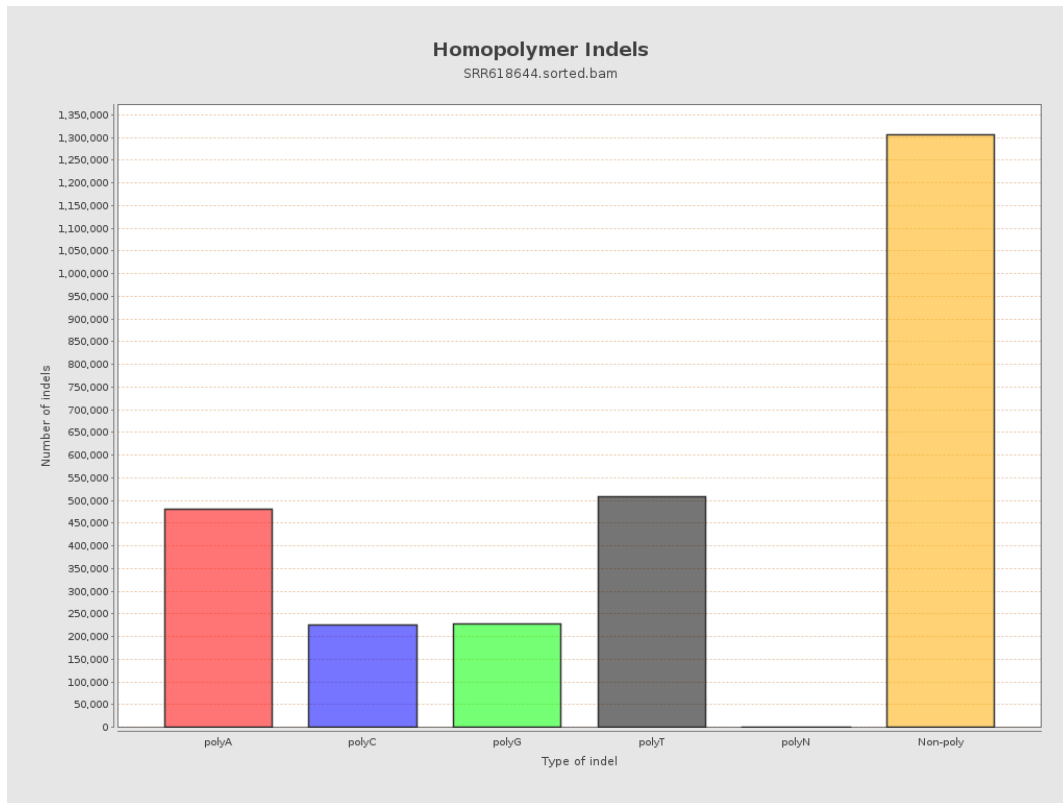
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



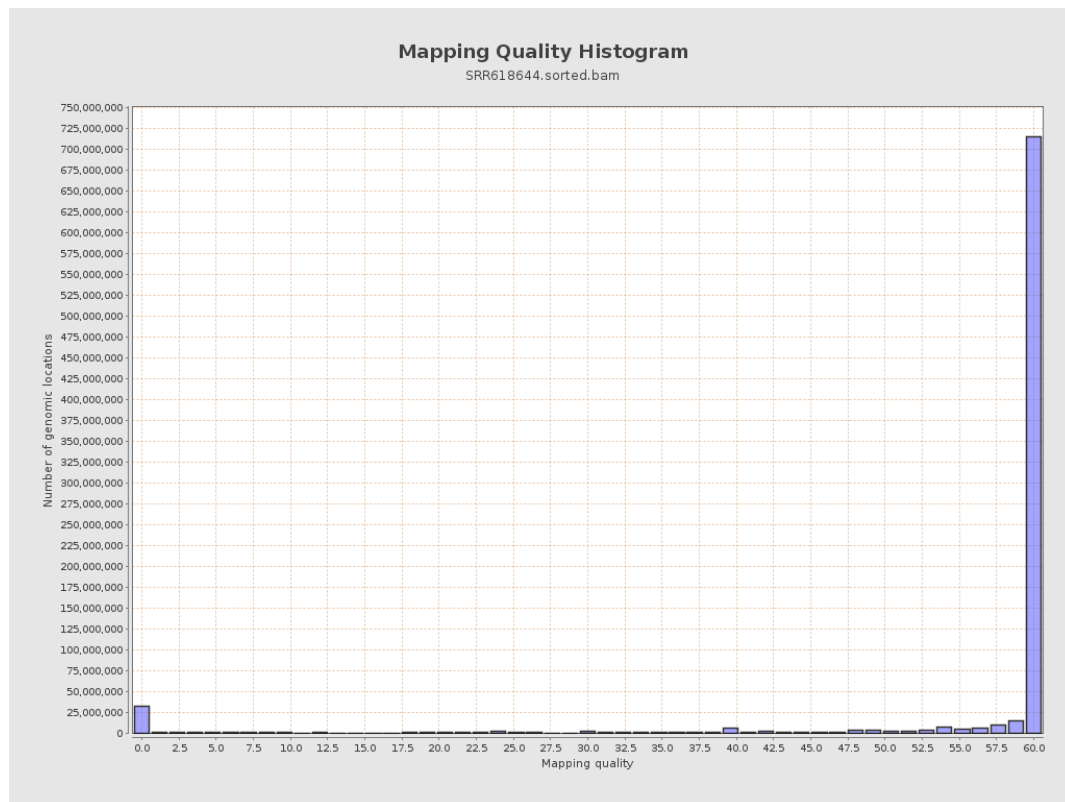
11. Results : Homopolymer Indels



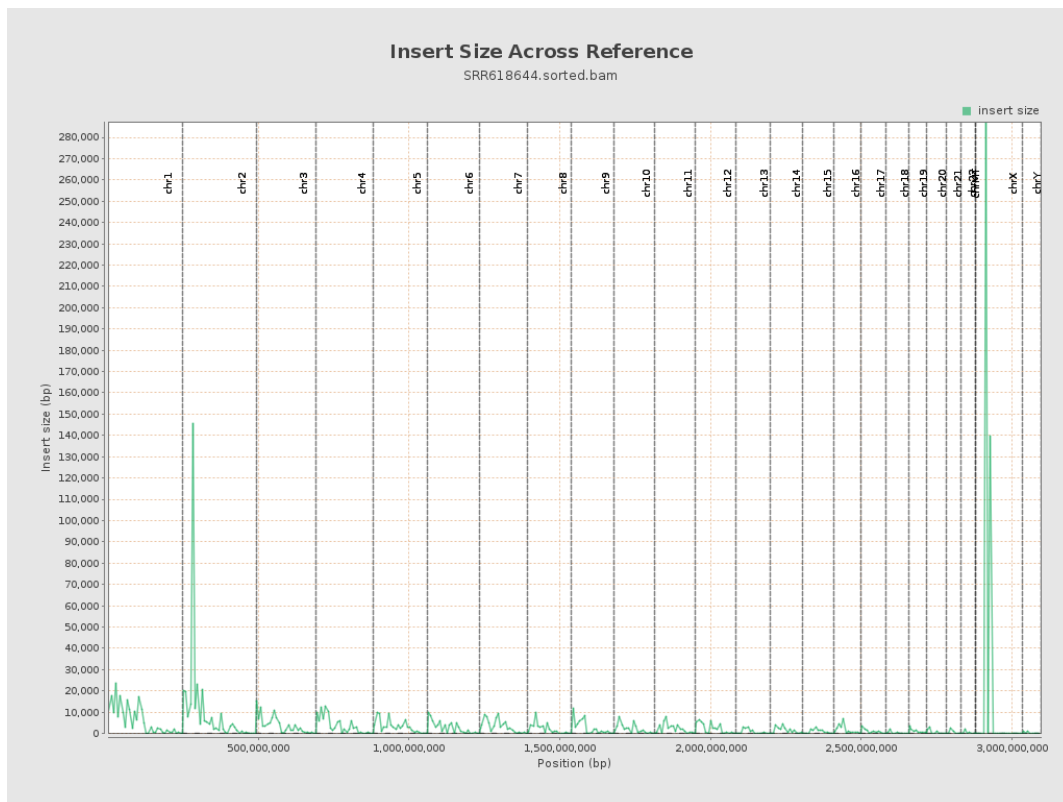
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

