

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/22 20:44:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630578.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_SRR630578 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR630578_1.fastq.gz SRR630578_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 22 20:44:42 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630578.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,916,924
Mapped reads	30,439,069 / 98.45%
Unmapped reads	477,855 / 1.55%
Mapped paired reads	30,439,069 / 98.45%
Mapped reads, first in pair	15,272,321 / 49.4%
Mapped reads, second in pair	15,166,748 / 49.06%
Mapped reads, both in pair	30,269,568 / 97.91%
Mapped reads, singletons	169,501 / 0.55%
Secondary alignments	0
Supplementary alignments	65,512 / 0.21%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	3,574,066 / 11.56%
Duplication rate	9.51%
Clipped reads	4,315,655 / 13.96%

2.2. ACGT Content

Number/percentage of A's	878,745,785 / 29.72%
Number/percentage of C's	576,124,349 / 19.49%
Number/percentage of T's	886,855,506 / 30%
Number/percentage of G's	614,467,113 / 20.78%
Number/percentage of N's	446,360 / 0.02%

GC Percentage	40.27%
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2.3. Coverage

Mean	0.9558
Standard Deviation	4.8058

2.4. Mapping Quality

Mean Mapping Quality	54.03
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2.5. Insert size

Mean	27,952.16
Standard Deviation	1,640,670.9
P25/Median/P75	158 / 198 / 260

2.6. Mismatches and indels

General error rate	0.93%
Mismatches	26,699,069
Insertions	556,911
Mapped reads with at least one insertion	1.8%
Deletions	1,672,965
Mapped reads with at least one deletion	5.34%
Homopolymer indels	54.58%

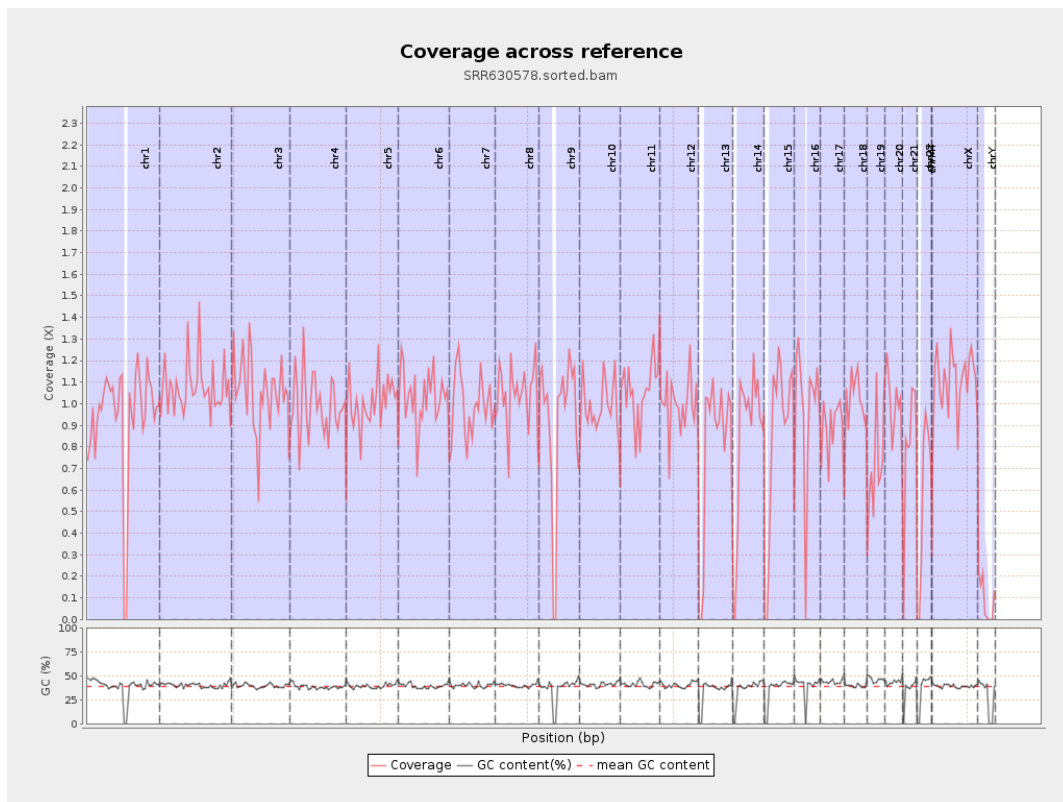
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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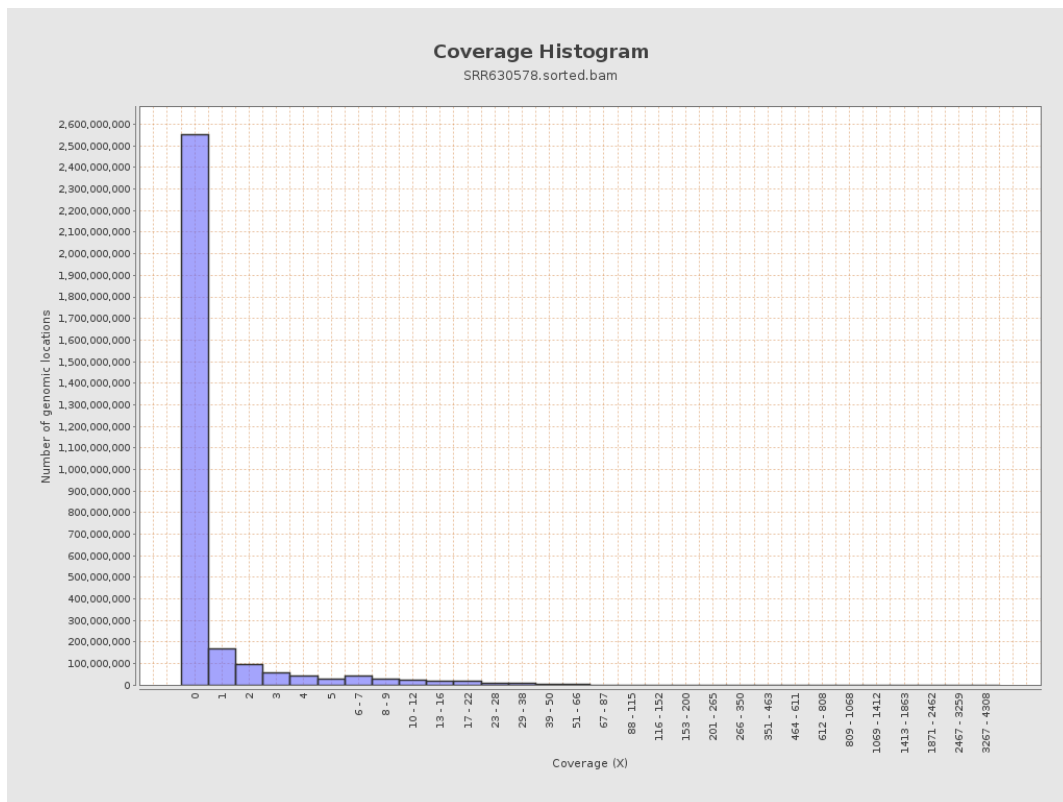
		bases	coverage	deviation
chr1	249250621	235096867	0.9432	6.1086
chr2	243199373	261369490	1.0747	5.7219
chr3	198022430	209008528	1.0555	4.1132
chr4	191154276	188769036	0.9875	4.8885
chr5	180915260	182562950	1.0091	4.0639
chr6	171115067	177110620	1.035	4.2982
chr7	159138663	157133397	0.9874	4.1048
chr8	146364022	152826749	1.0442	4.2164
chr9	141213431	126976664	0.8992	6.7711
chr10	135534747	135260836	0.998	4.509
chr11	135006516	141749723	1.0499	5.1429
chr12	133851895	133371825	0.9964	4.1374
chr13	115169878	92629097	0.8043	3.5142
chr14	107349540	91596283	0.8533	3.8497
chr15	102531392	86504375	0.8437	3.7271
chr16	90354753	85384061	0.945	5.1356
chr17	81195210	70799919	0.872	3.8957
chr18	78077248	80304689	1.0285	7.5711
chr19	59128983	41041115	0.6941	3.9807
chr20	63025520	62991798	0.9995	4.2296
chr21	48129895	39725475	0.8254	4.5507
chr22	51304566	29263907	0.5704	2.9948
chrMT	16571	4805	0.29	0.8358
chrX	155270560	172130578	1.1086	4.5627

chrY	59373566	5273502	0.0888	2.6932
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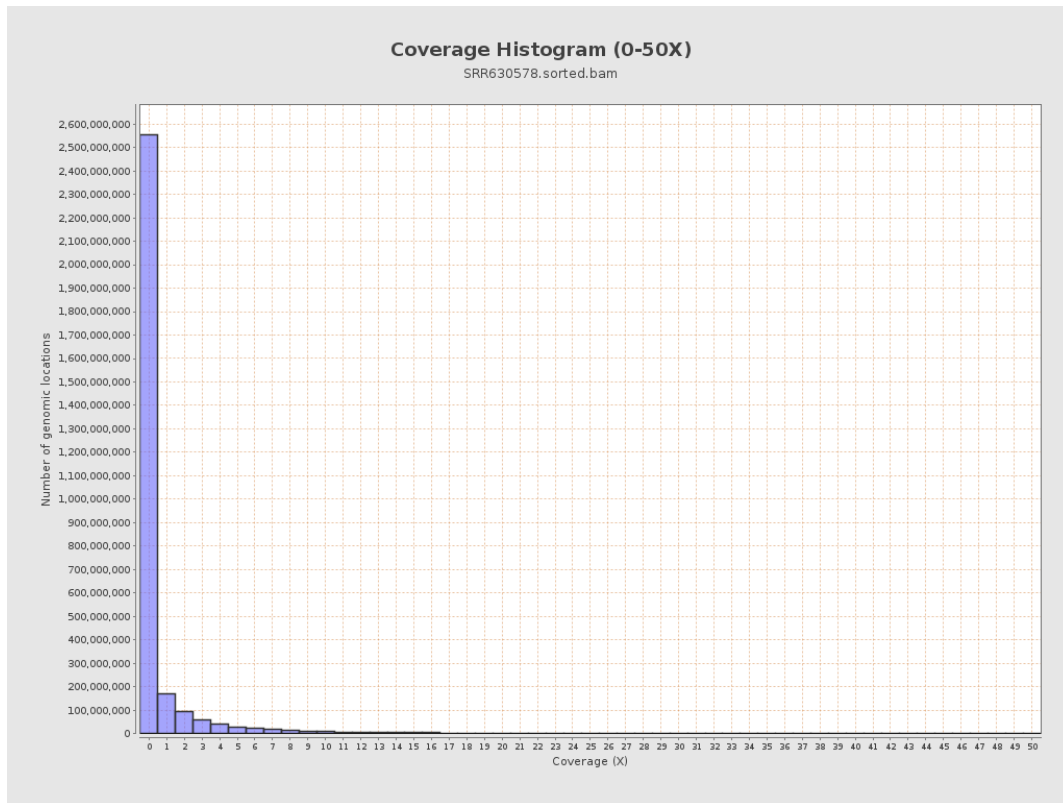
3. Results : Coverage across reference



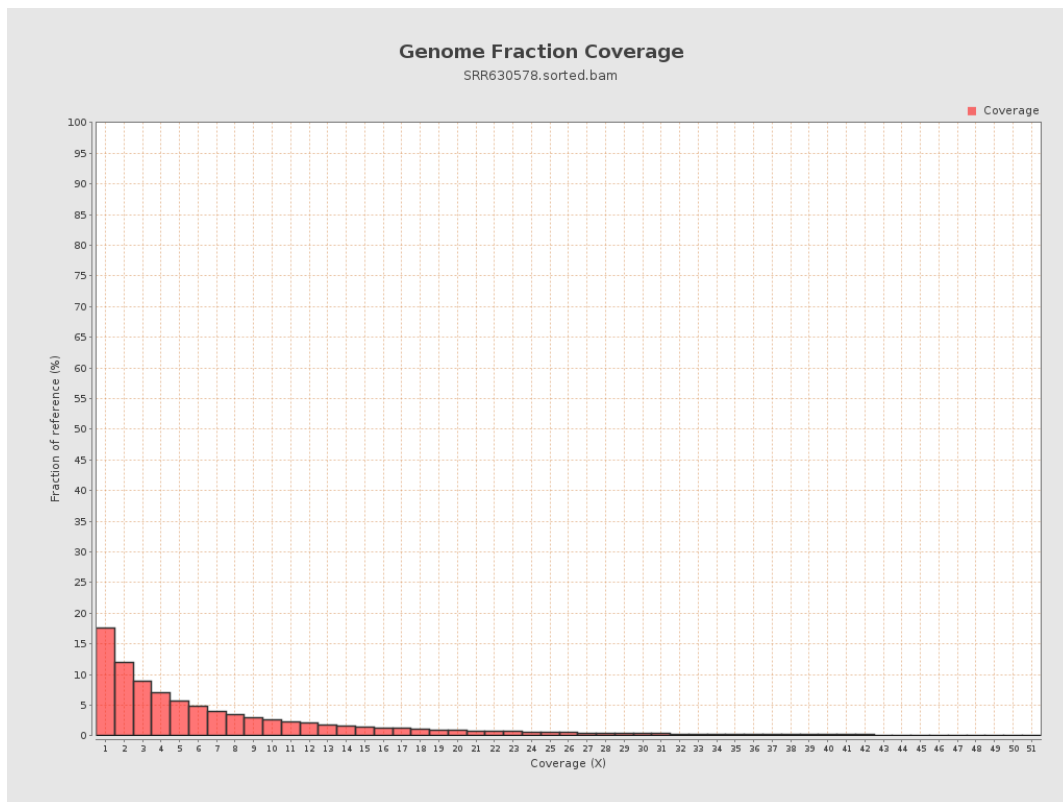
4. Results : Coverage Histogram



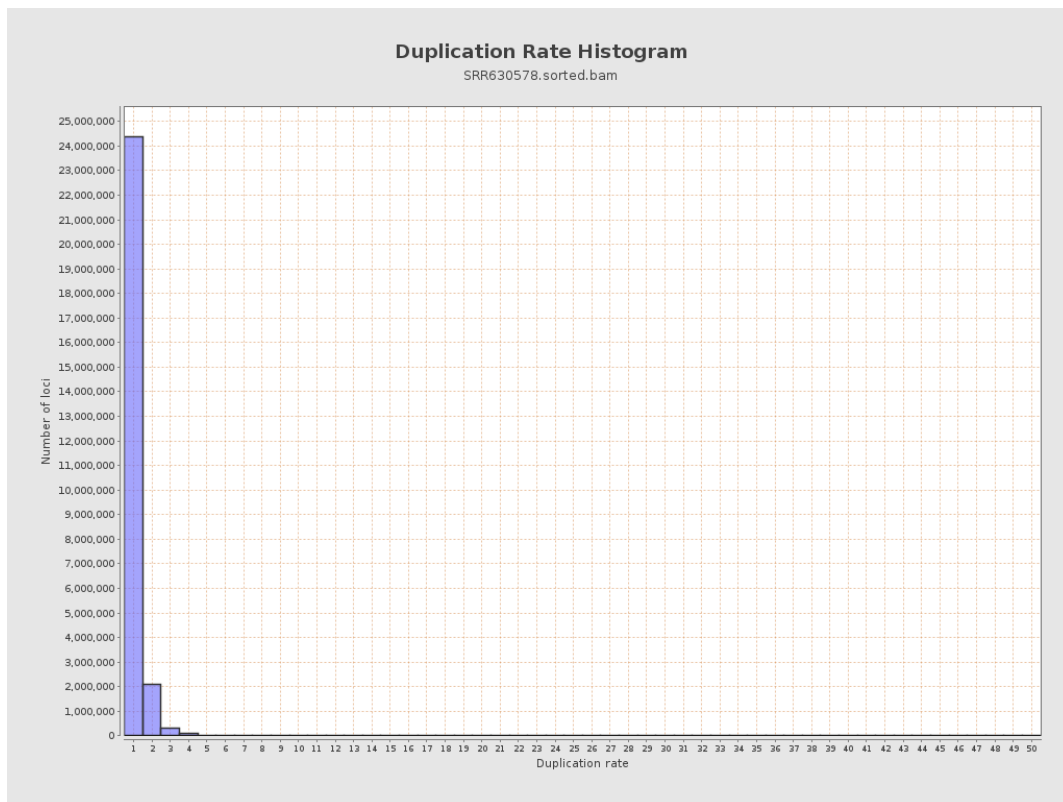
5. Results : Coverage Histogram (0-50X)



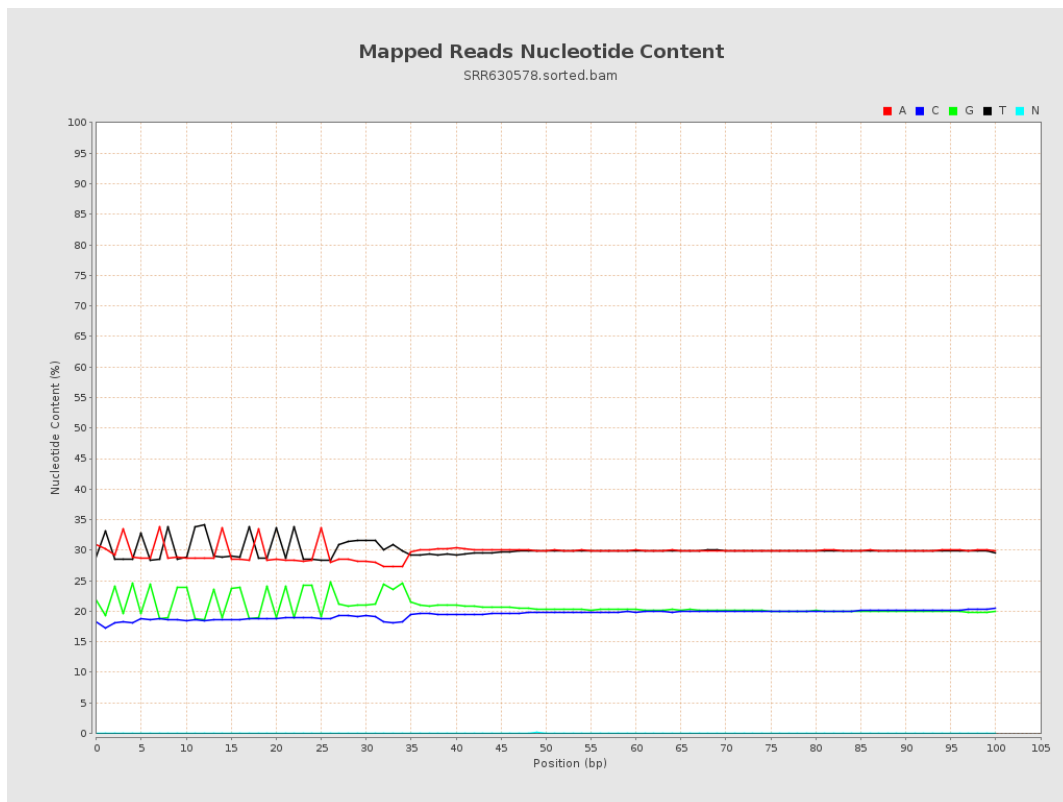
6. Results : Genome Fraction Coverage



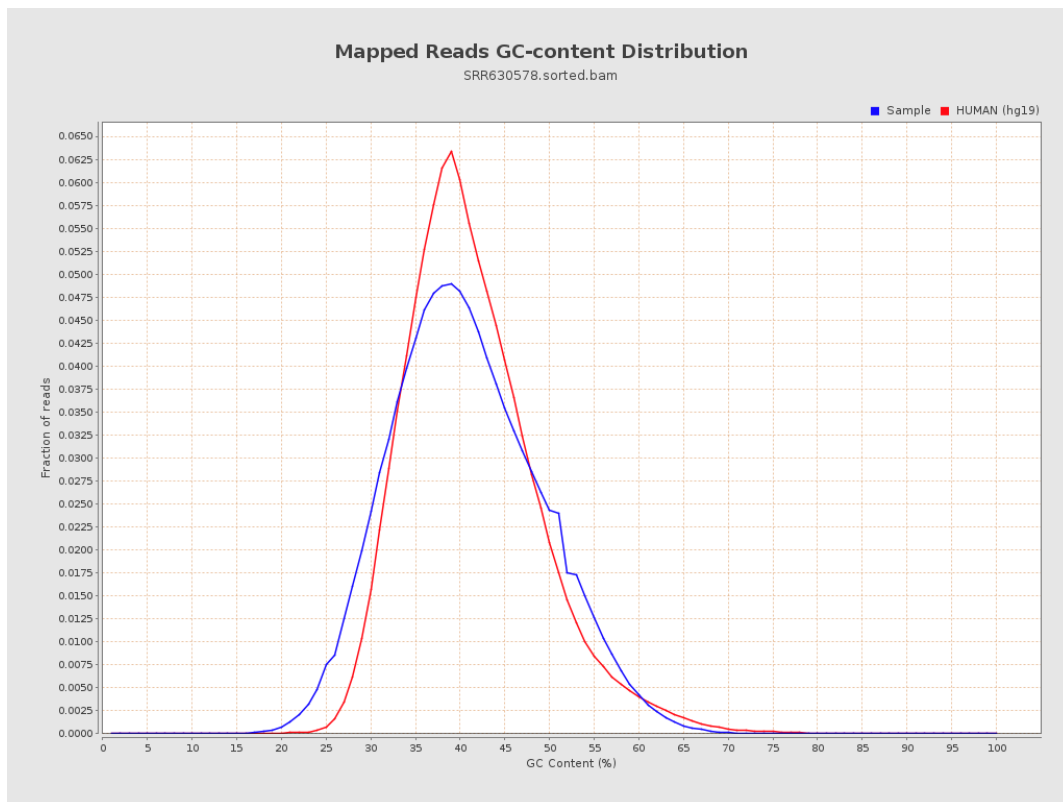
7. Results : Duplication Rate Histogram



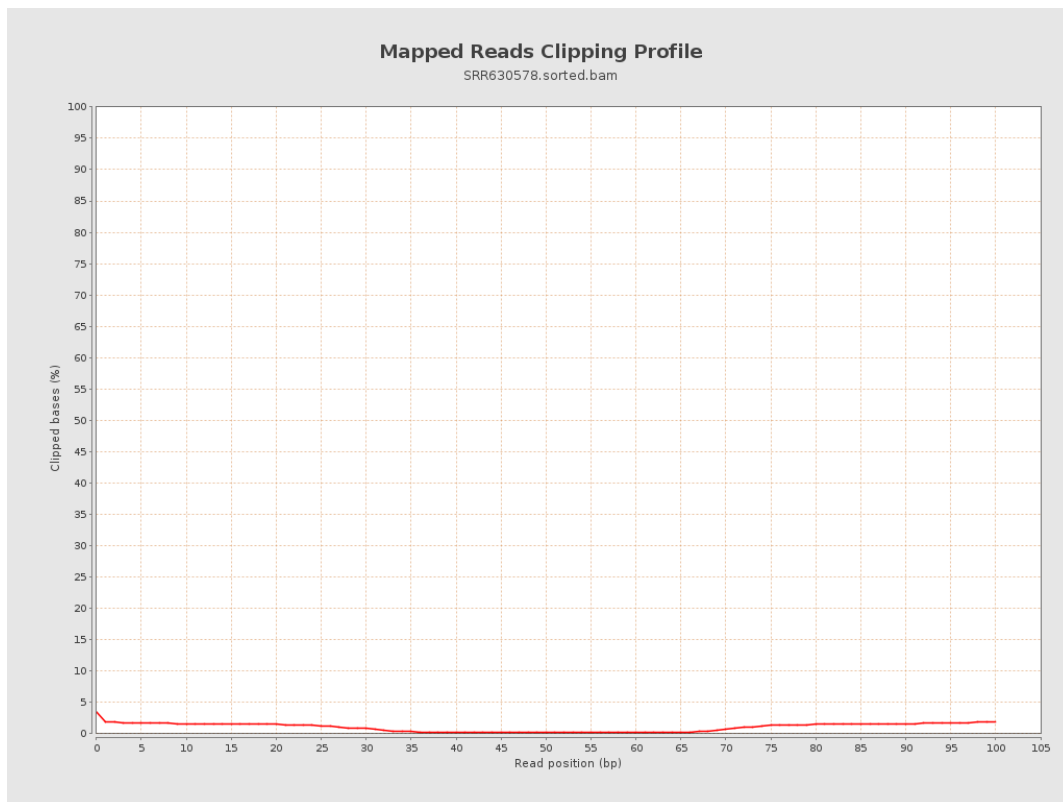
8. Results : Mapped Reads Nucleotide Content



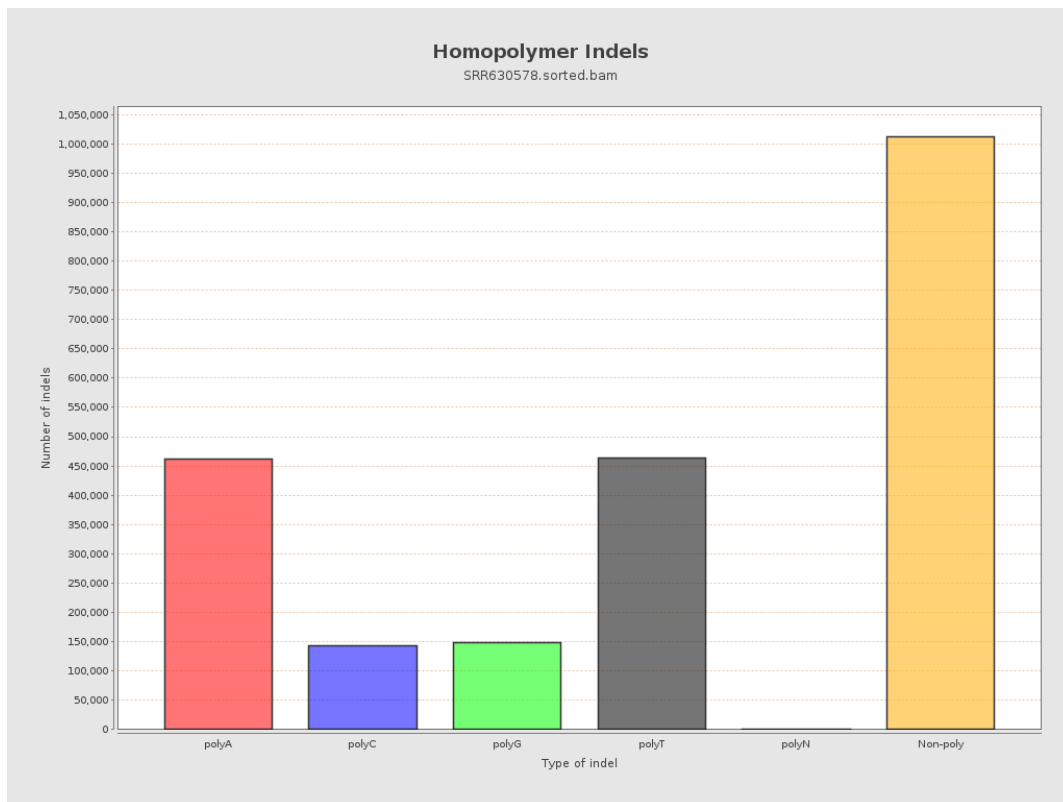
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



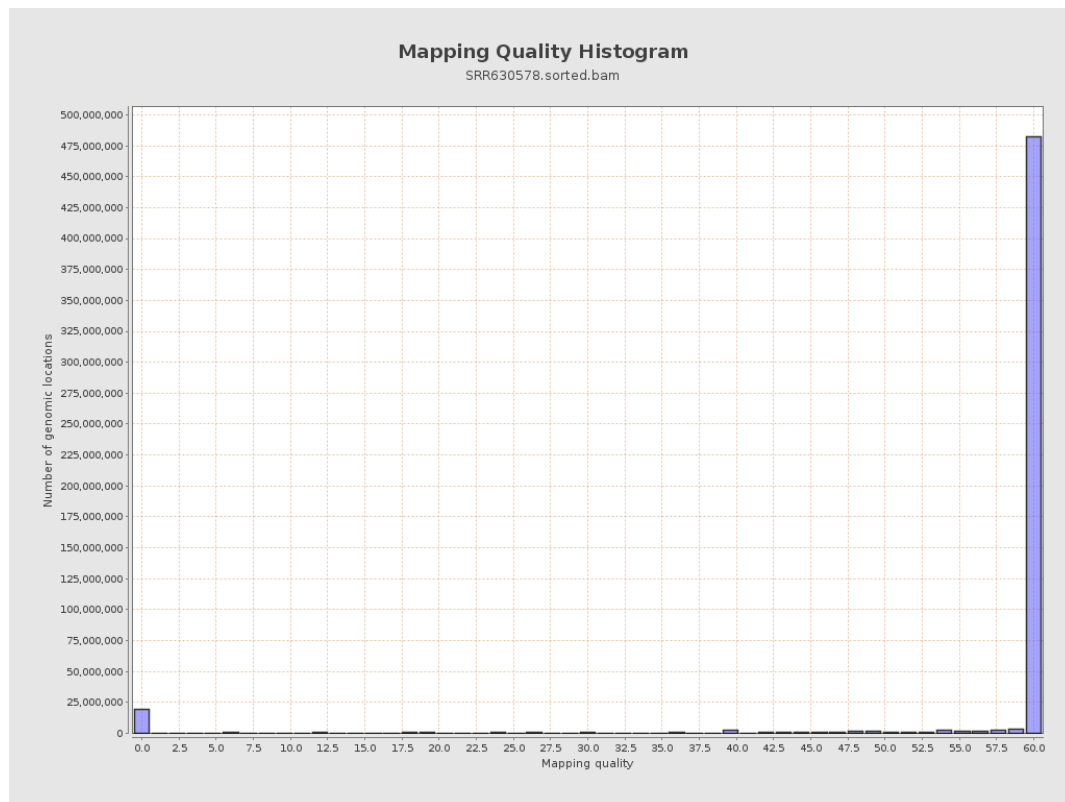
11. Results : Homopolymer Indels



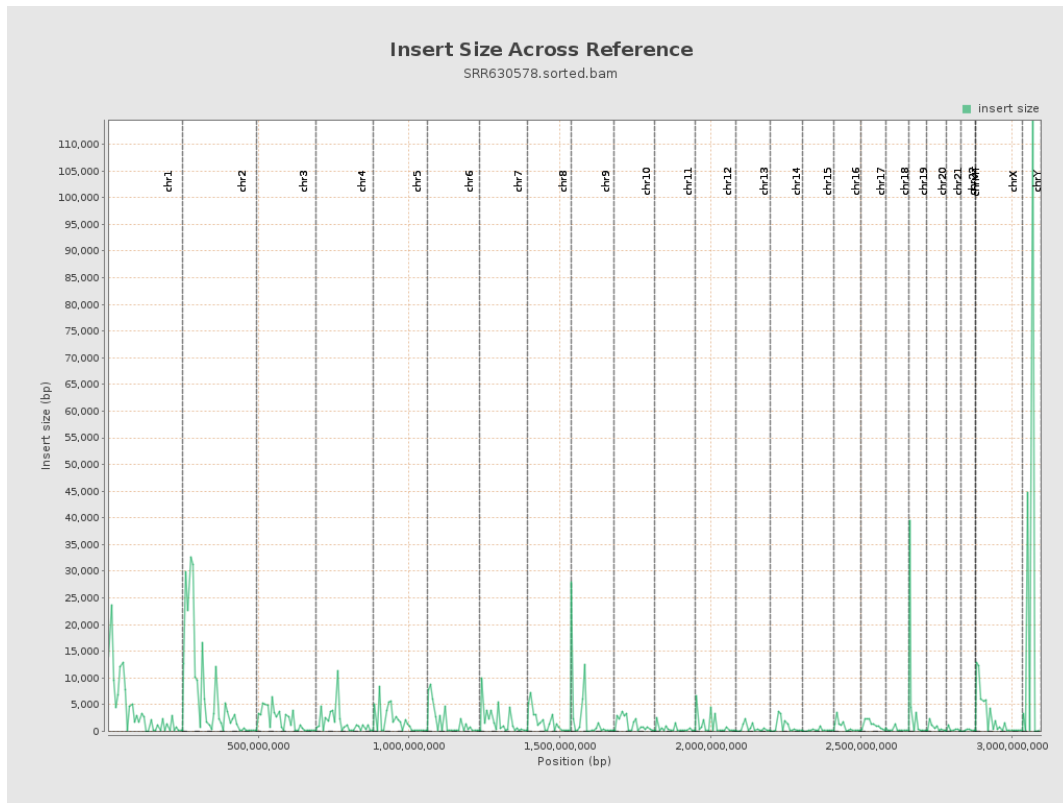
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

