

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/22 20:19:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630577.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_SRR630577 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR630577_1.fastq.gz SRR630577_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 22 20:19:51 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630577.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	31,132,806
Mapped reads	30,746,217 / 98.76%
Unmapped reads	386,589 / 1.24%
Mapped paired reads	30,746,217 / 98.76%
Mapped reads, first in pair	15,438,984 / 49.59%
Mapped reads, second in pair	15,307,233 / 49.17%
Mapped reads, both in pair	30,551,926 / 98.13%
Mapped reads, singletons	194,291 / 0.62%
Secondary alignments	0
Supplementary alignments	69,387 / 0.22%
Read min/max/mean length	30 / 101 / 101.09
Duplicated reads (estimated)	4,065,608 / 13.06%
Duplication rate	10.97%
Clipped reads	3,849,816 / 12.37%

2.2. ACGT Content

Number/percentage of A's	883,974,579 / 29.44%
Number/percentage of C's	597,254,487 / 19.89%
Number/percentage of T's	891,006,810 / 29.68%
Number/percentage of G's	629,613,885 / 20.97%
Number/percentage of N's	454,962 / 0.02%

GC Percentage	40.86%
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2.3. Coverage

Mean	0.9705
Standard Deviation	5.1239

2.4. Mapping Quality

Mean Mapping Quality	53.95
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2.5. Insert size

Mean	33,118.4
Standard Deviation	1,813,719.81
P25/Median/P75	156 / 199 / 264

2.6. Mismatches and indels

General error rate	0.92%
Mismatches	26,825,536
Insertions	549,027
Mapped reads with at least one insertion	1.75%
Deletions	1,552,937
Mapped reads with at least one deletion	4.91%
Homopolymer indels	54%

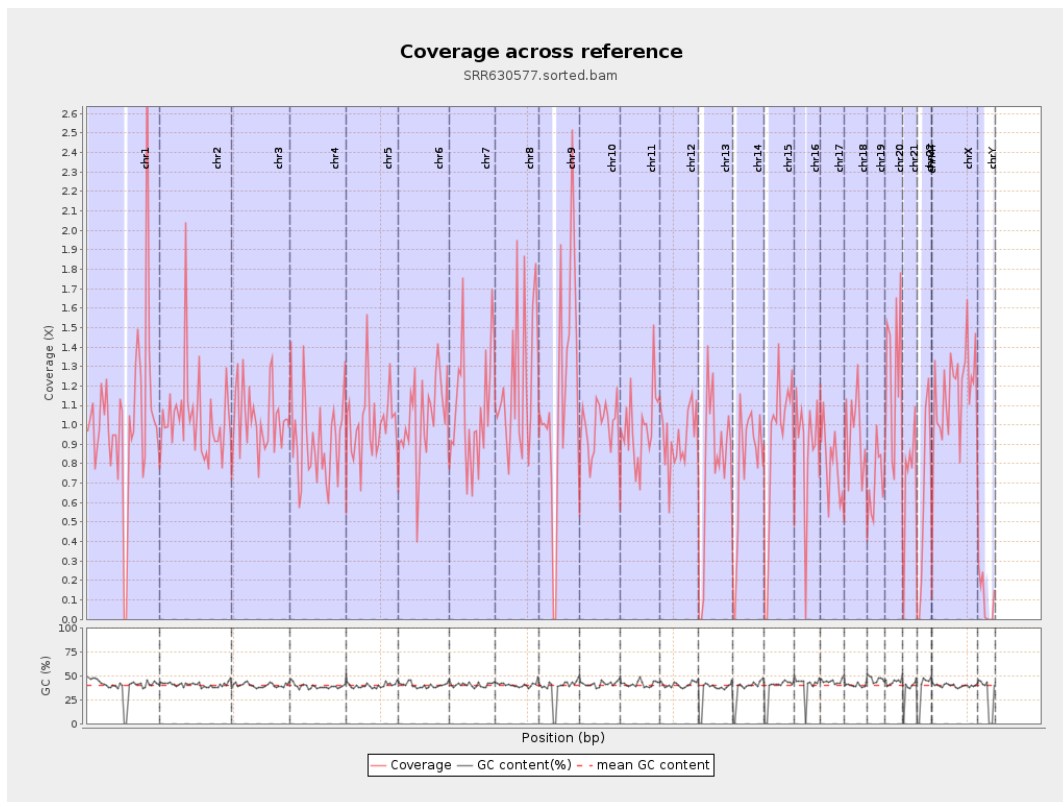
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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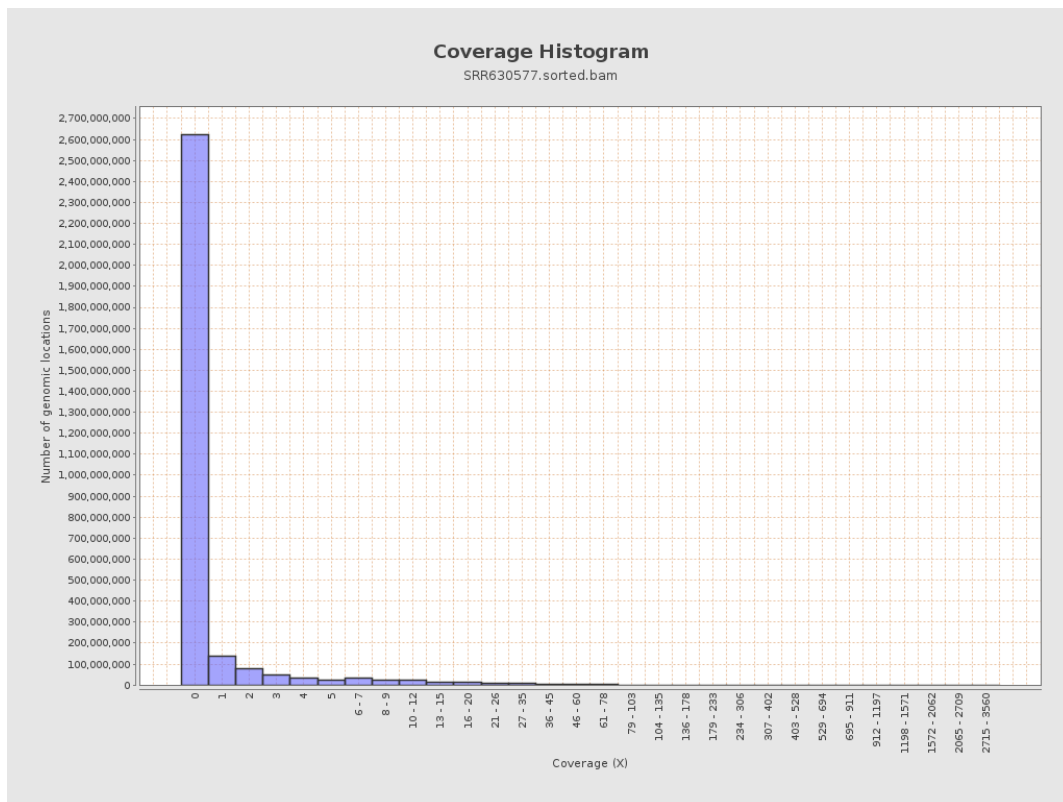
		bases	coverage	deviation
chr1	249250621	255114147	1.0235	6.156
chr2	243199373	252039224	1.0363	6.165
chr3	198022430	204645878	1.0334	4.6213
chr4	191154276	173830068	0.9094	5.141
chr5	180915260	181461284	1.003	4.484
chr6	171115067	179873274	1.0512	4.8634
chr7	159138663	171691593	1.0789	4.9101
chr8	146364022	178160318	1.2172	5.2676
chr9	141213431	157226194	1.1134	6.2457
chr10	135534747	133702050	0.9865	5.1791
chr11	135006516	132876657	0.9842	5.1663
chr12	133851895	124494169	0.9301	4.2094
chr13	115169878	91203818	0.7919	3.9417
chr14	107349540	84677289	0.7888	4.0582
chr15	102531392	92341310	0.9006	4.4373
chr16	90354753	77802210	0.8611	5.8742
chr17	81195210	64053831	0.7889	4.0411
chr18	78077248	75923721	0.9724	6.06
chr19	59128983	41391073	0.7	4.3158
chr20	63025520	77318295	1.2268	5.3167
chr21	48129895	36318327	0.7546	5.282
chr22	51304566	30717343	0.5987	3.5437
chrMT	16571	1713	0.1034	0.4264
chrX	155270560	181683337	1.1701	5.1514

chrY	59373566	5899355	0.0994	3.2469
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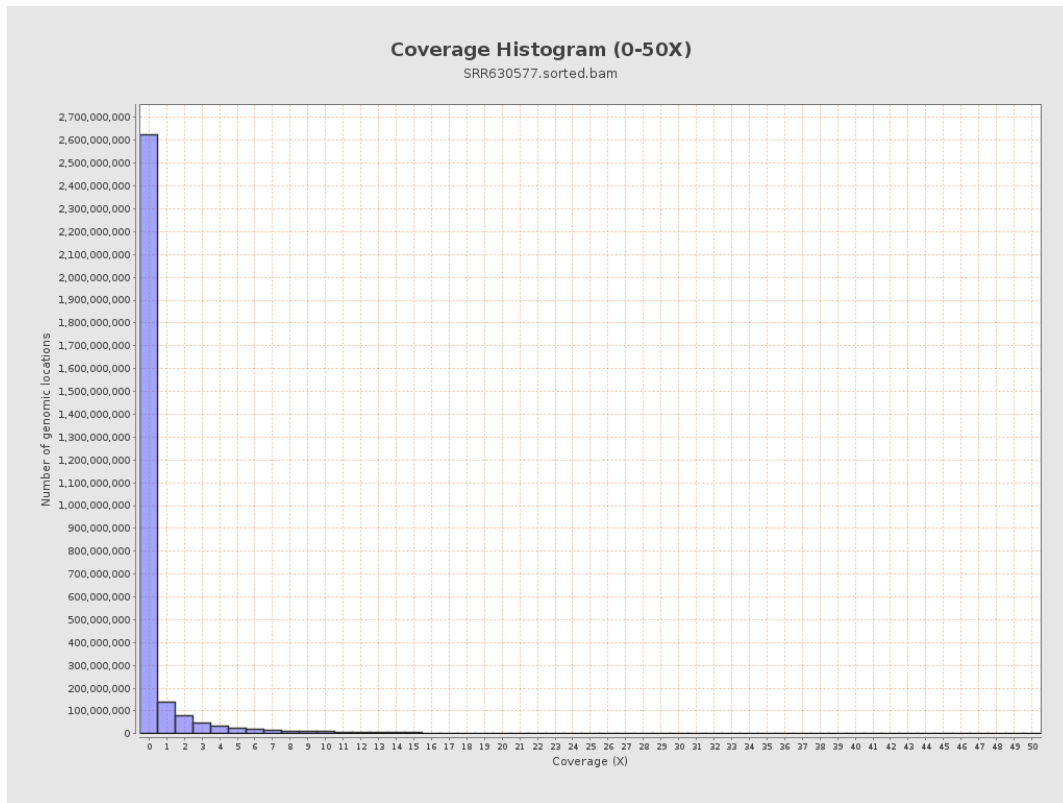
3. Results : Coverage across reference



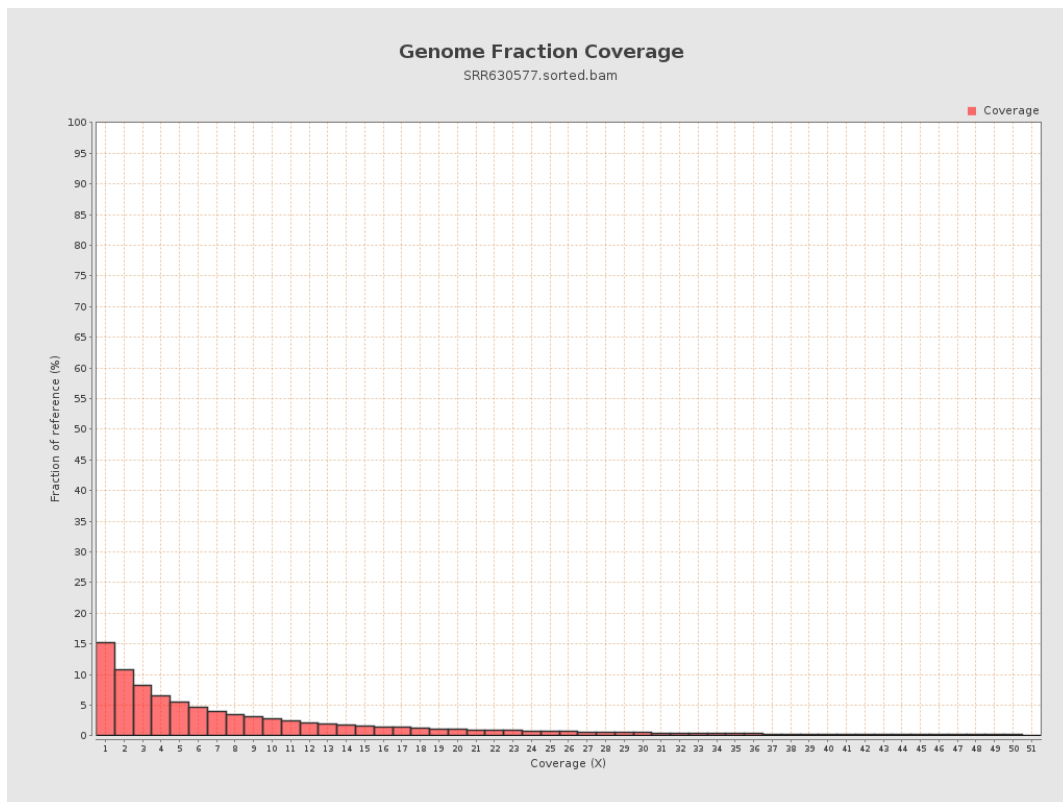
4. Results : Coverage Histogram



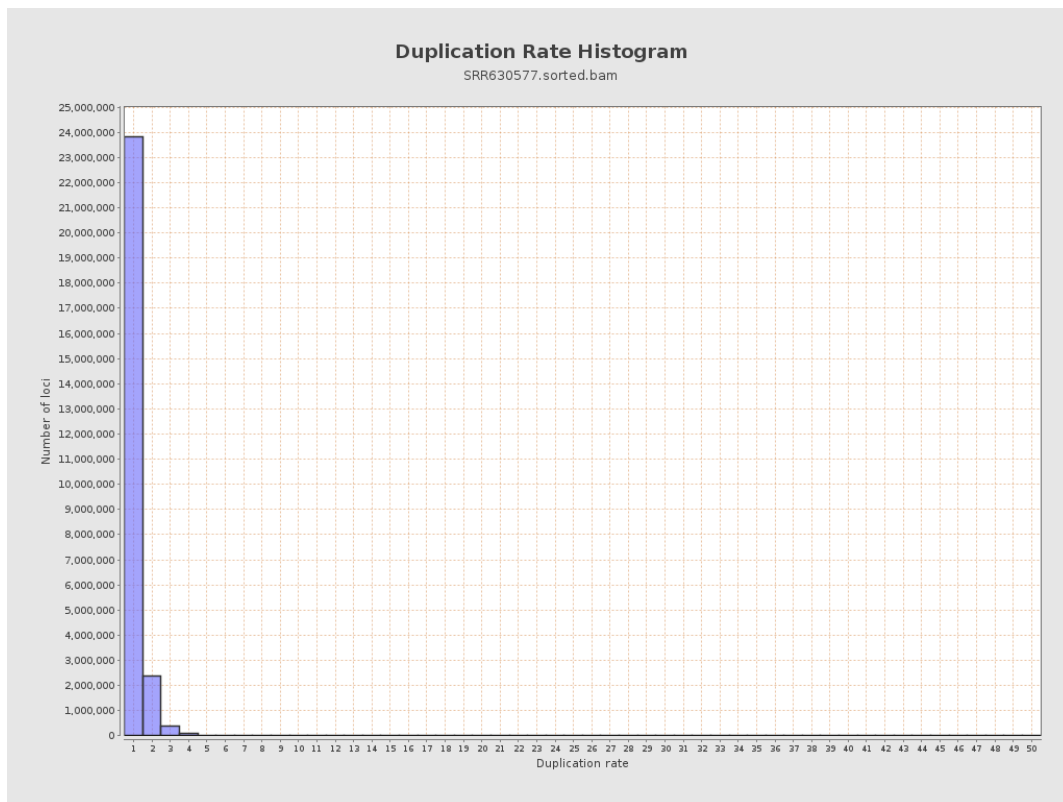
5. Results : Coverage Histogram (0-50X)



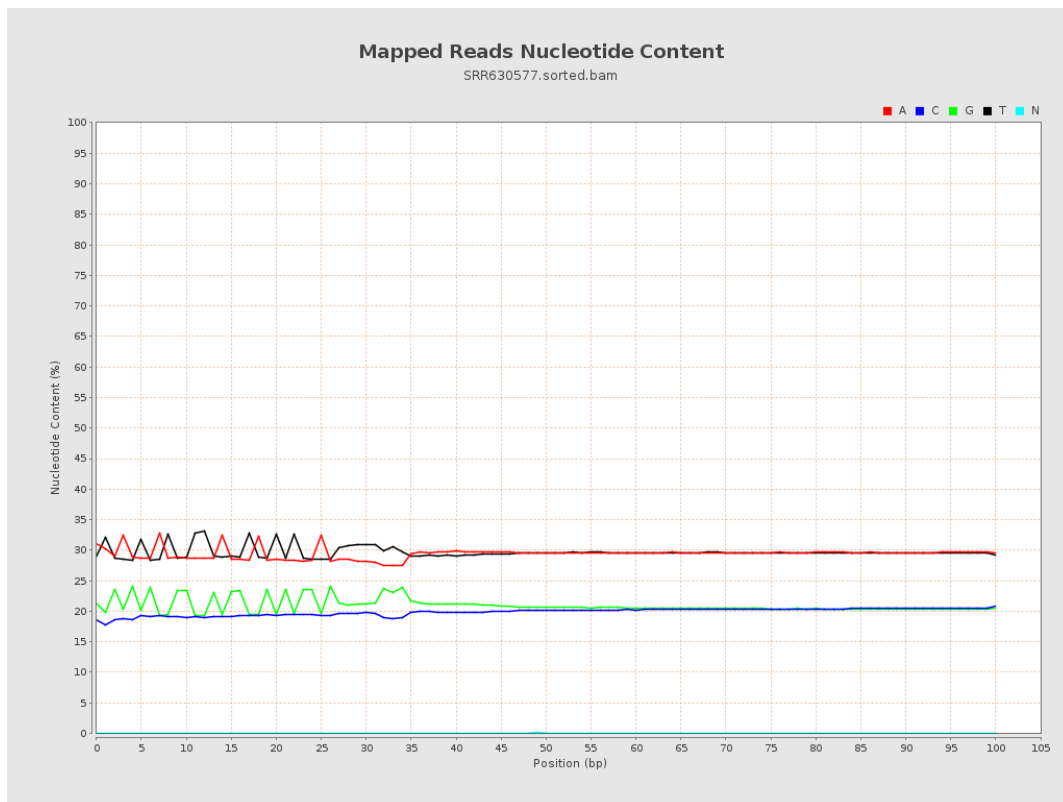
6. Results : Genome Fraction Coverage



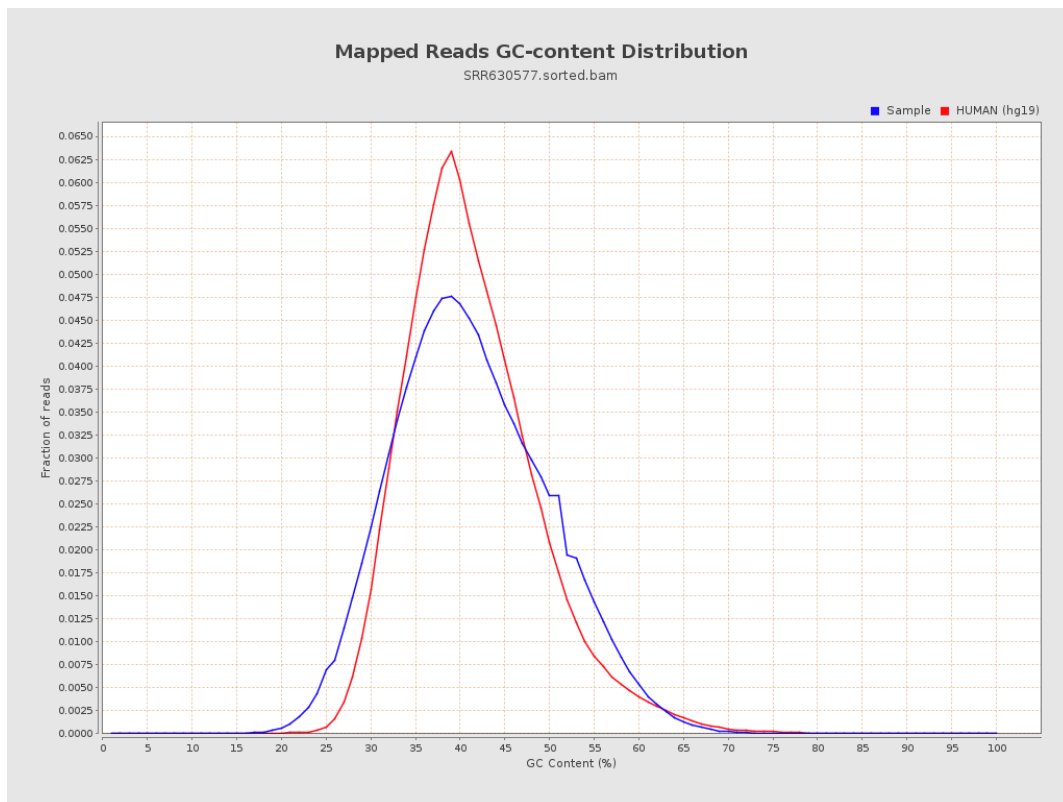
7. Results : Duplication Rate Histogram



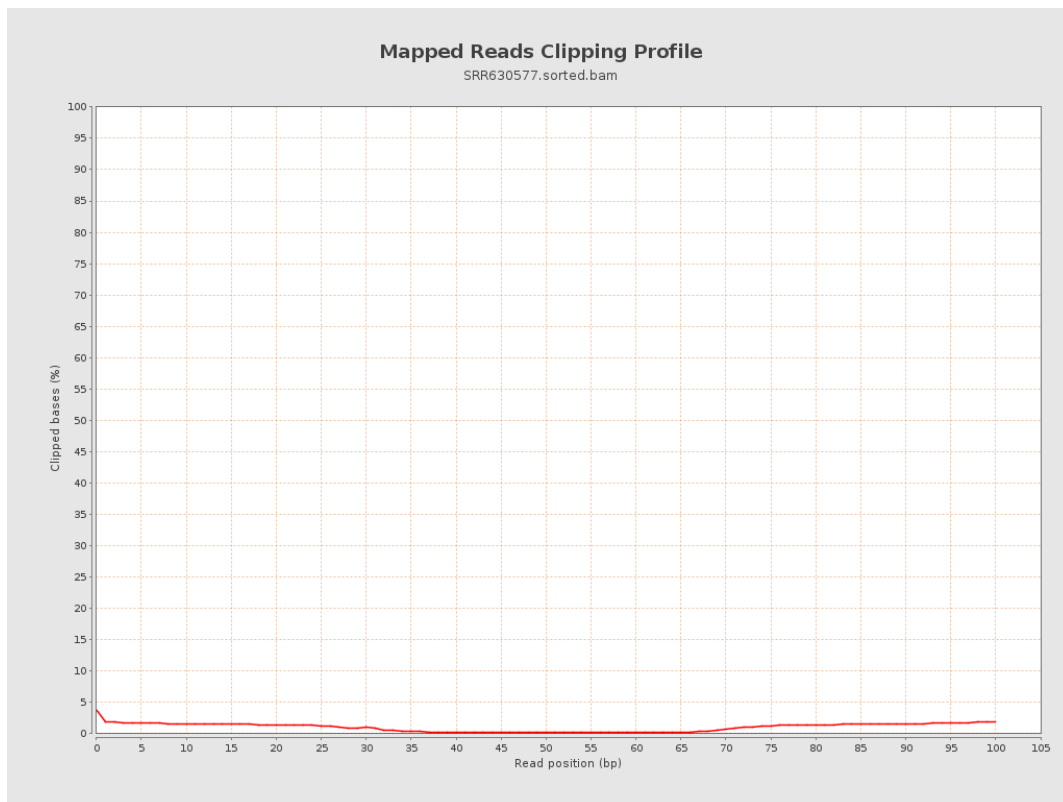
8. Results : Mapped Reads Nucleotide Content



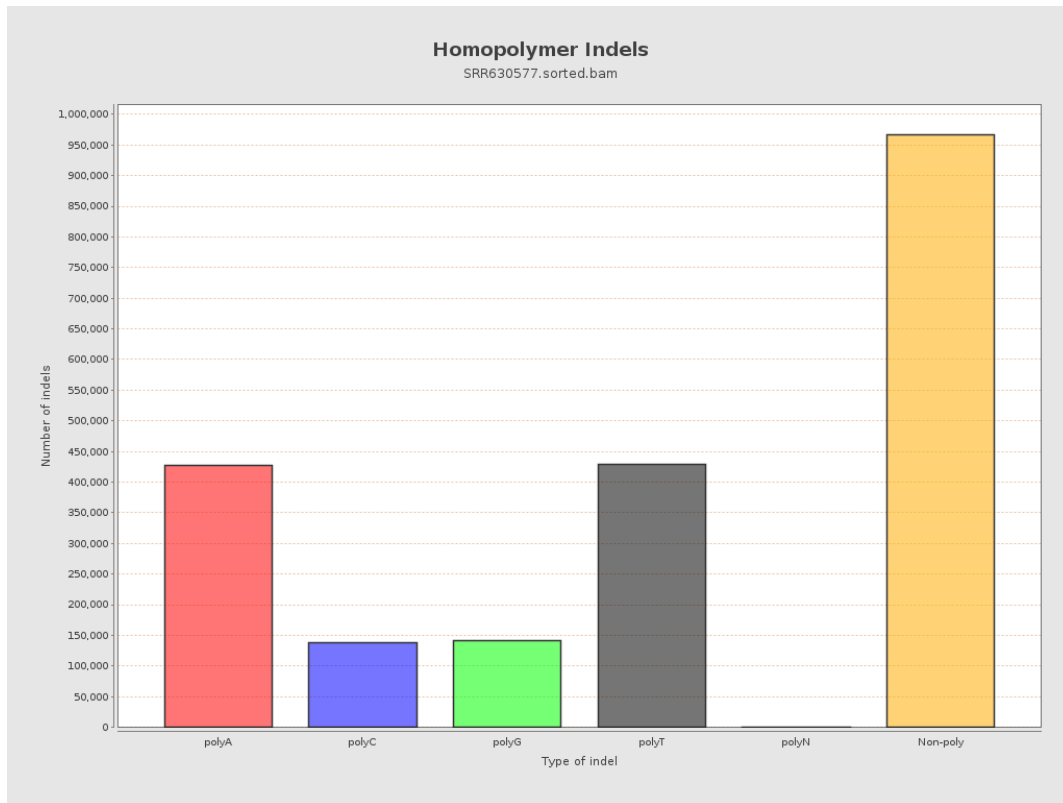
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



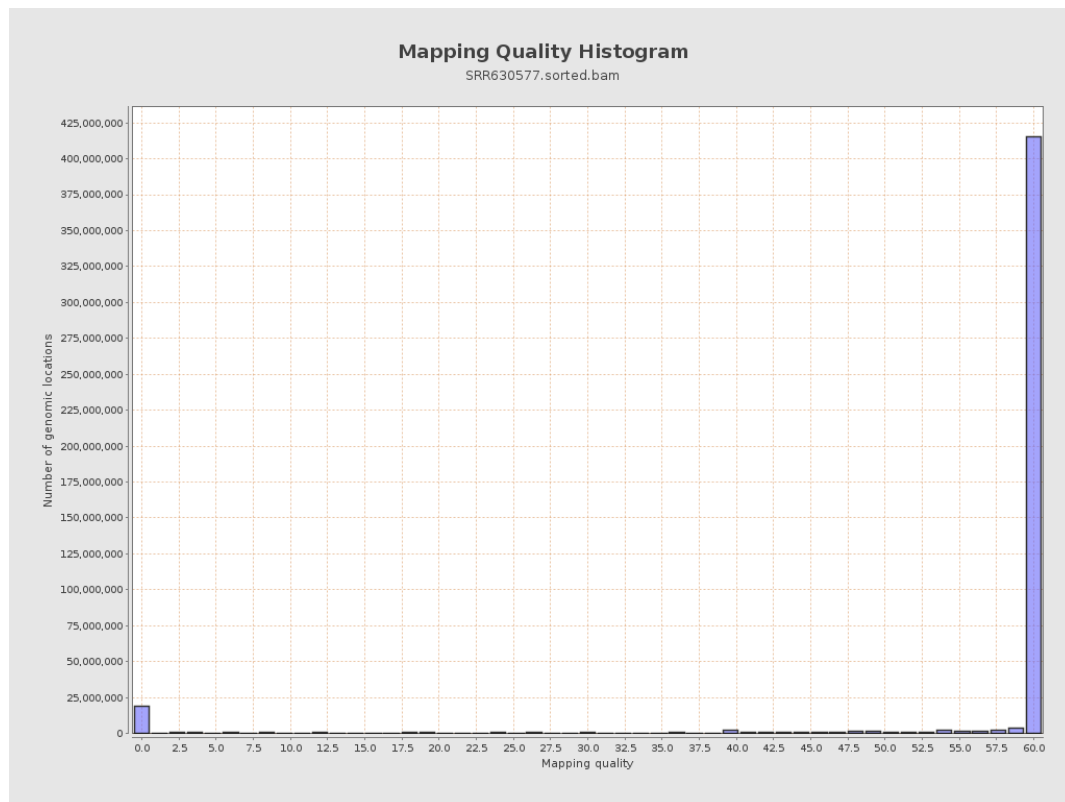
11. Results : Homopolymer Indels



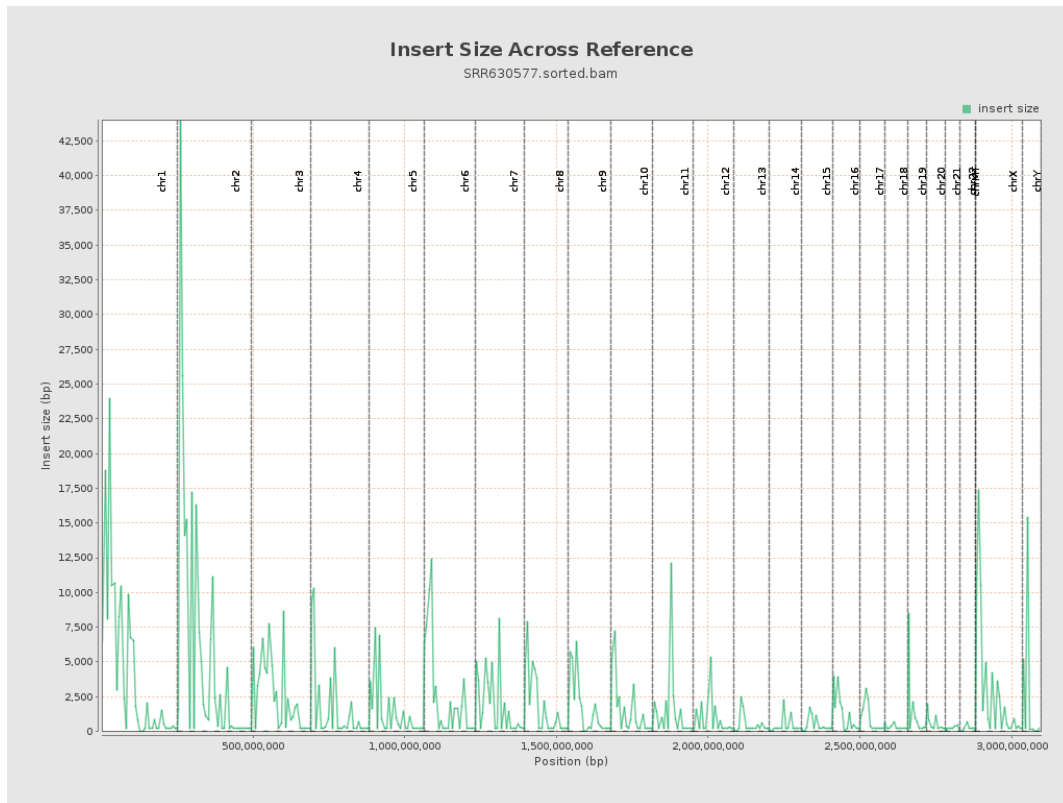
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

