

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/22 21:11:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630579.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_SRR630579 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR630579_1.fastq.gz SRR630579_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 22 21:11:23 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630579.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,519,228
Mapped reads	32,044,488 / 98.54%
Unmapped reads	474,740 / 1.46%
Mapped paired reads	32,044,488 / 98.54%
Mapped reads, first in pair	16,087,863 / 49.47%
Mapped reads, second in pair	15,956,625 / 49.07%
Mapped reads, both in pair	31,849,184 / 97.94%
Mapped reads, singletons	195,304 / 0.6%
Secondary alignments	0
Supplementary alignments	67,321 / 0.21%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	2,543,627 / 7.82%
Duplication rate	6.54%
Clipped reads	4,505,174 / 13.85%

2.2. ACGT Content

Number/percentage of A's	897,989,354 / 28.84%
Number/percentage of C's	633,966,482 / 20.36%
Number/percentage of T's	906,448,559 / 29.11%
Number/percentage of G's	674,659,789 / 21.67%
Number/percentage of N's	466,831 / 0.01%

GC Percentage	42.03%
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2.3. Coverage

Mean	1.0065
Standard Deviation	3.976

2.4. Mapping Quality

Mean Mapping Quality	54.03
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2.5. Insert size

Mean	31,550.4
Standard Deviation	1,787,071.99
P25/Median/P75	156 / 197 / 261

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	27,478,150
Insertions	556,878
Mapped reads with at least one insertion	1.71%
Deletions	1,756,562
Mapped reads with at least one deletion	5.33%
Homopolymer indels	54.17%

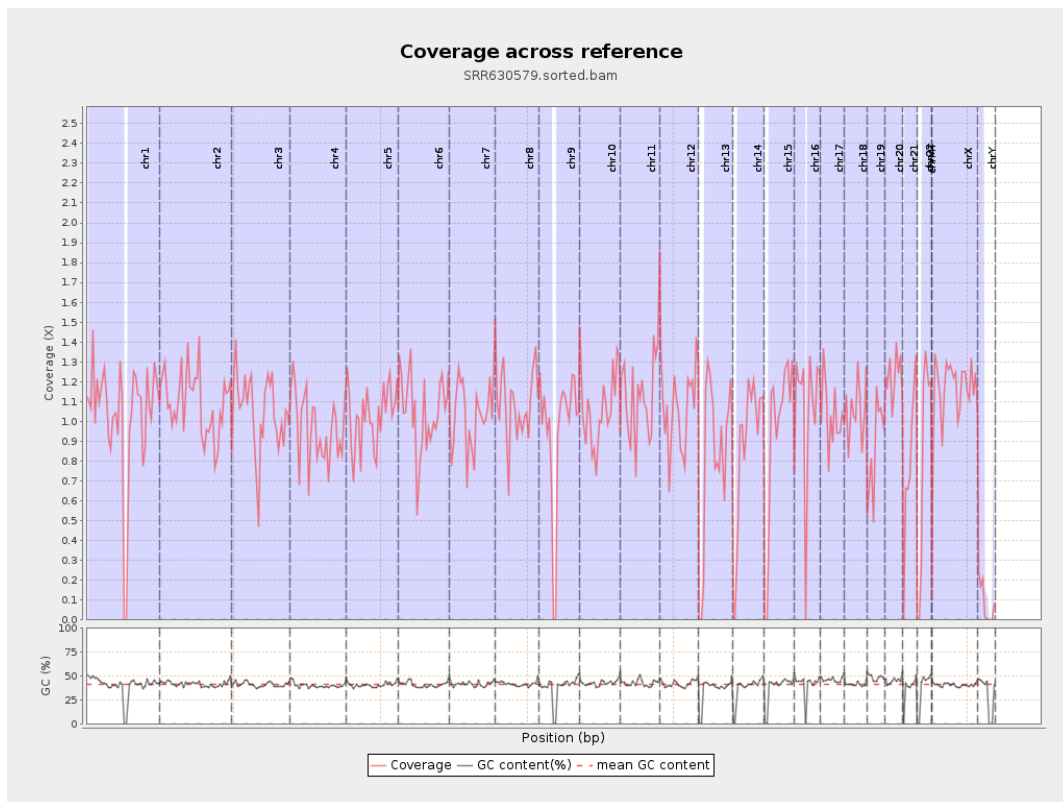
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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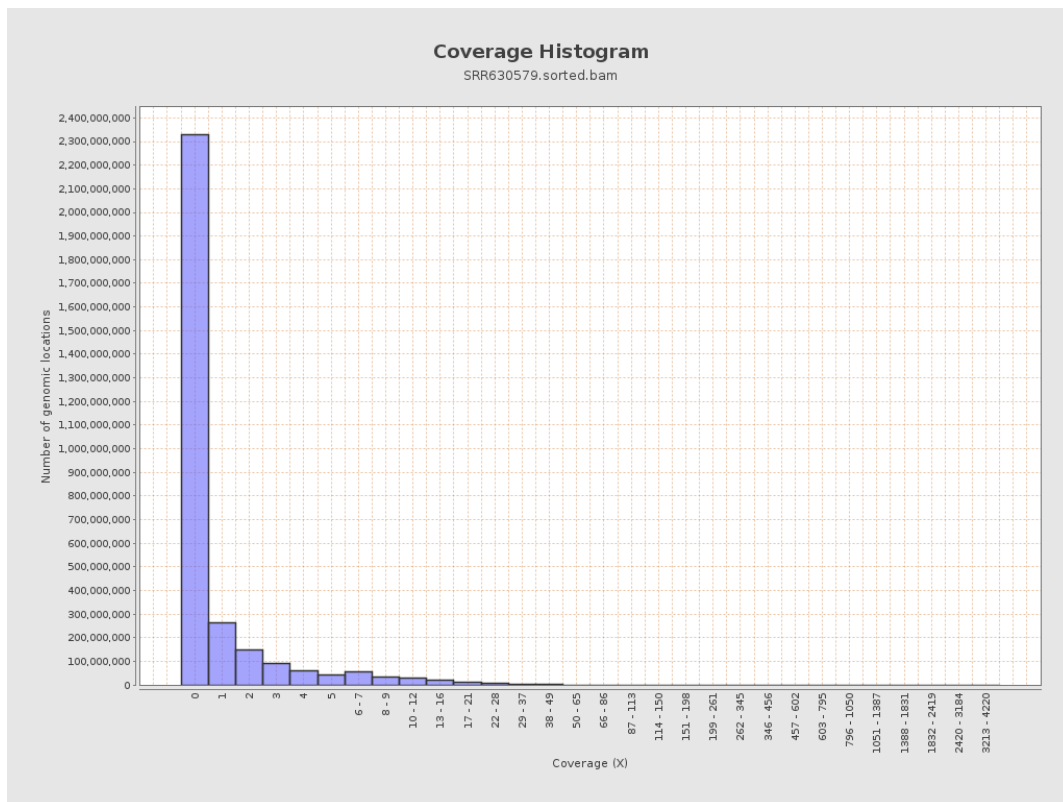
		bases	coverage	deviation
chr1	249250621	257552117	1.0333	5.7097
chr2	243199373	266272521	1.0949	5.4443
chr3	198022430	207667655	1.0487	3.0622
chr4	191154276	183954564	0.9623	3.4208
chr5	180915260	185961891	1.0279	3.0368
chr6	171115067	179556457	1.0493	3.1998
chr7	159138663	164065795	1.031	3.2077
chr8	146364022	157685285	1.0774	3.2578
chr9	141213431	133414719	0.9448	4.9446
chr10	135534747	144076469	1.063	3.4748
chr11	135006516	150661695	1.116	4.2679
chr12	133851895	141901050	1.0601	3.153
chr13	115169878	95635682	0.8304	2.6968
chr14	107349540	93451292	0.8705	2.8973
chr15	102531392	95864493	0.935	3.011
chr16	90354753	95115590	1.0527	5.8245
chr17	81195210	83093742	1.0234	3.5022
chr18	78077248	83092534	1.0642	5.1374
chr19	59128983	52043995	0.8802	3.872
chr20	63025520	77182676	1.2246	3.5514
chr21	48129895	39907176	0.8292	3.789
chr22	51304566	41488445	0.8087	2.9879
chrMT	16571	1746	0.1054	0.4122
chrX	155270560	181379287	1.1681	3.486

chrY	59373566	4858160	0.0818	2.7169
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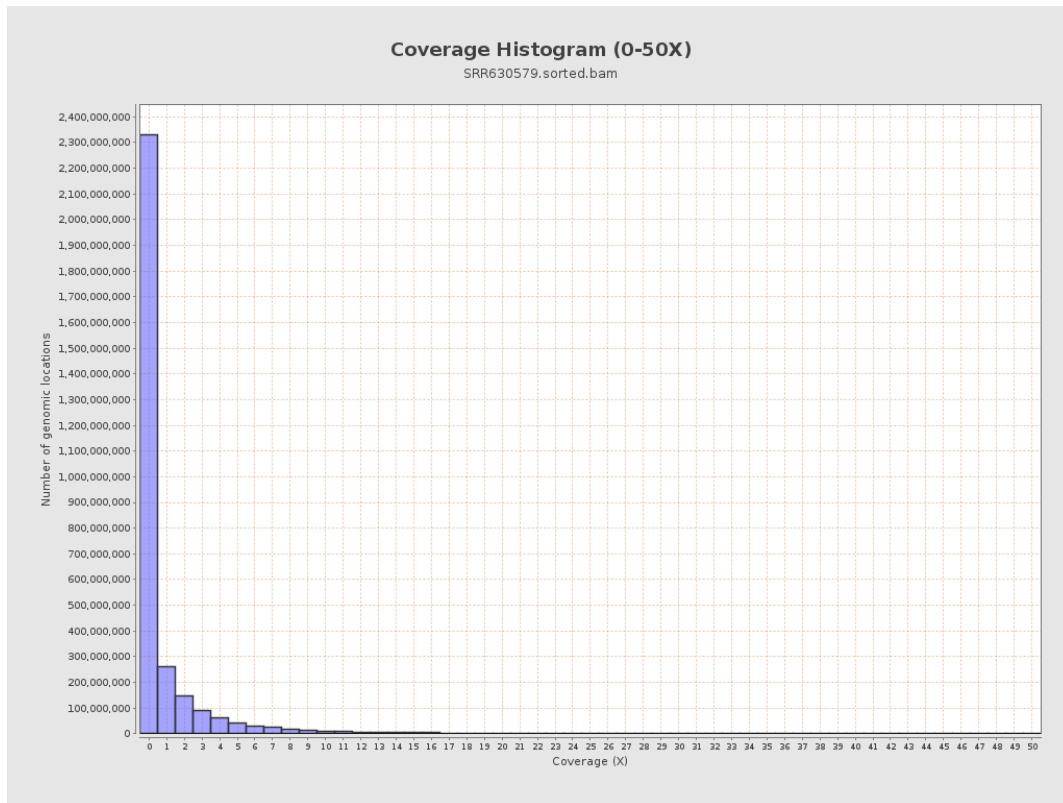
3. Results : Coverage across reference



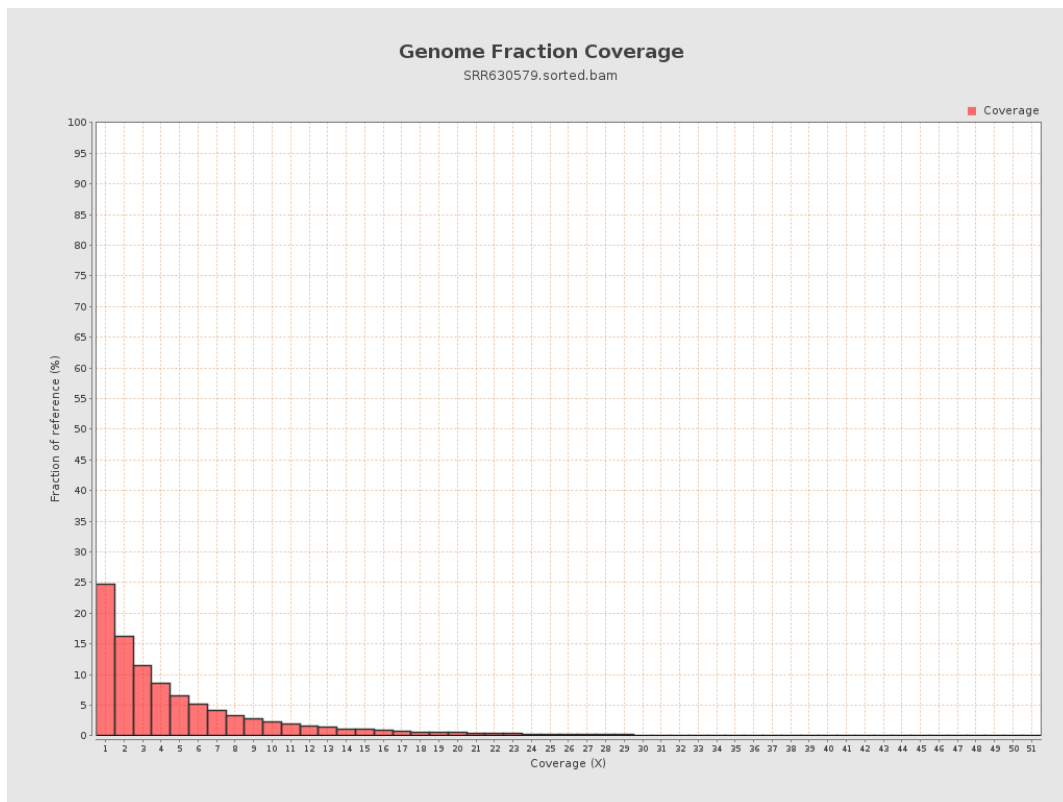
4. Results : Coverage Histogram



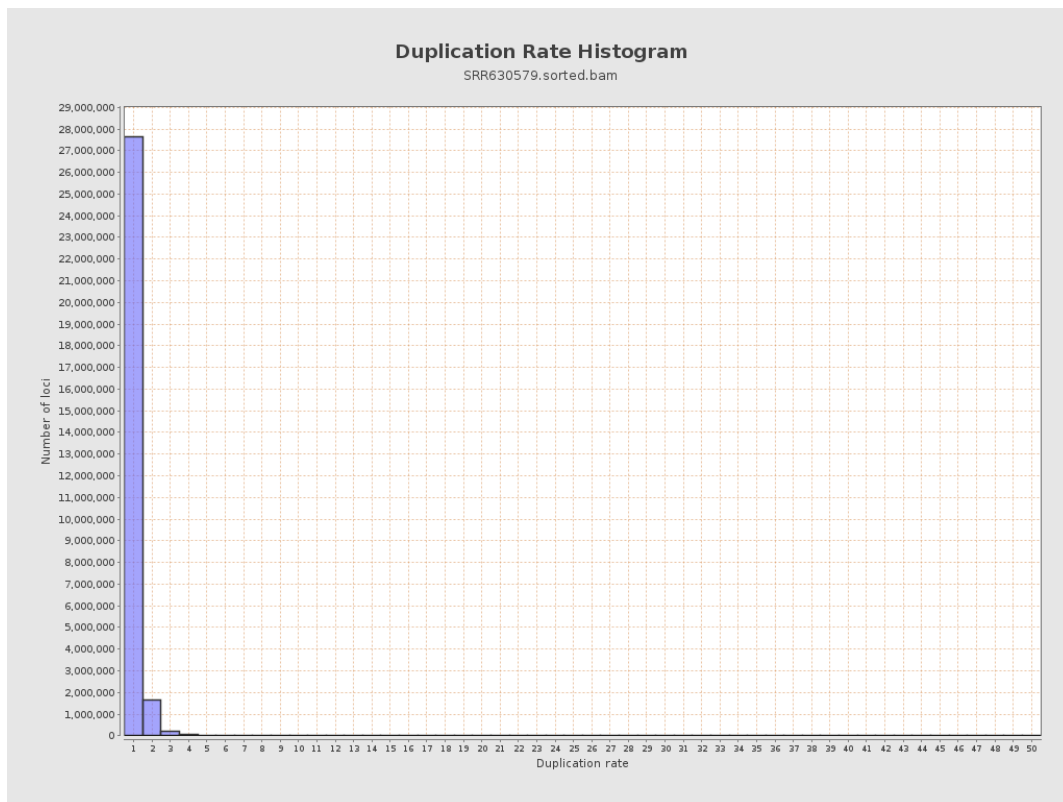
5. Results : Coverage Histogram (0-50X)



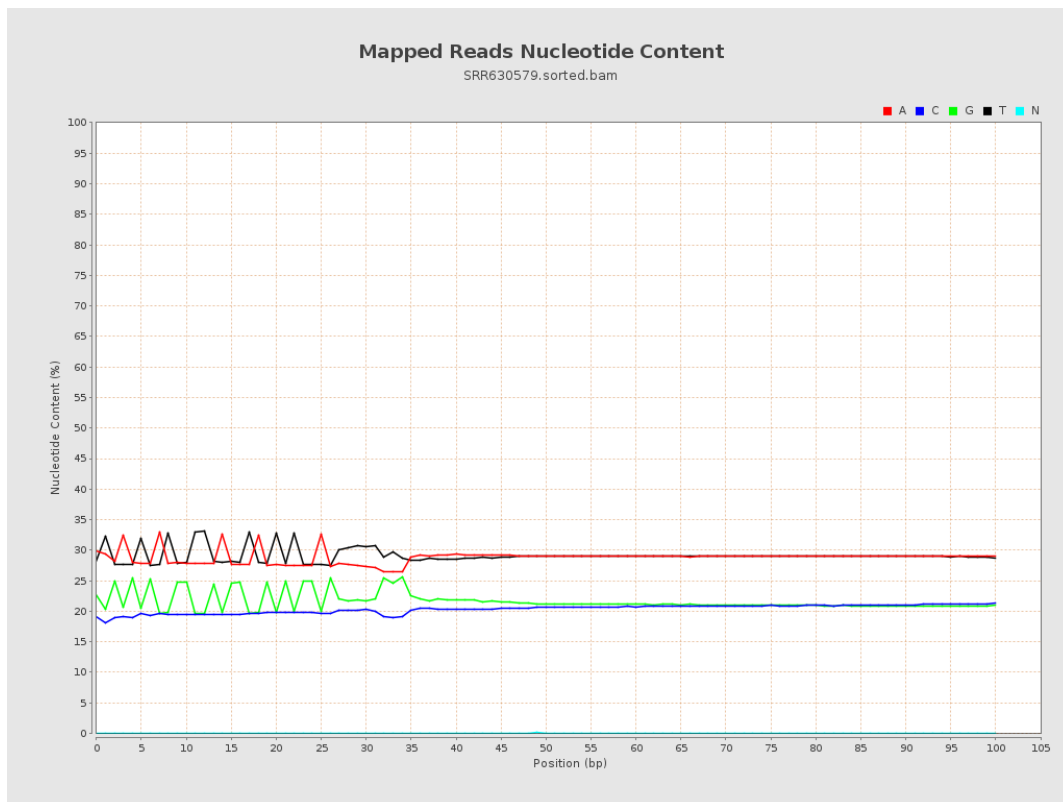
6. Results : Genome Fraction Coverage



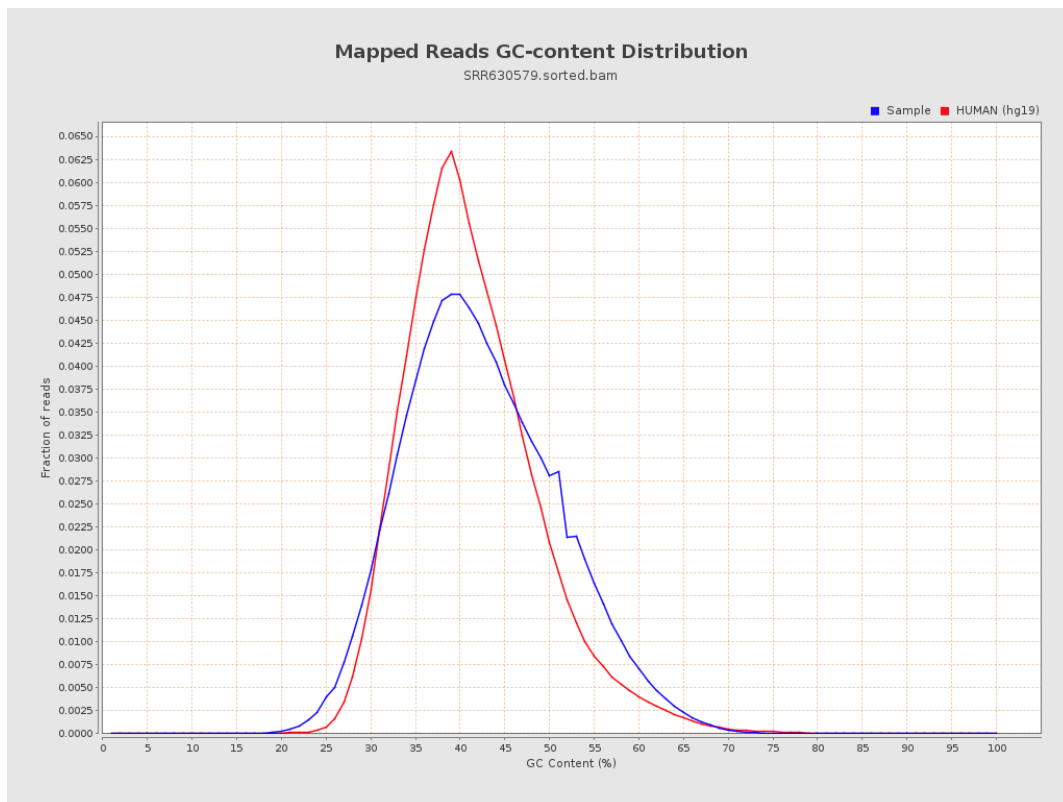
7. Results : Duplication Rate Histogram



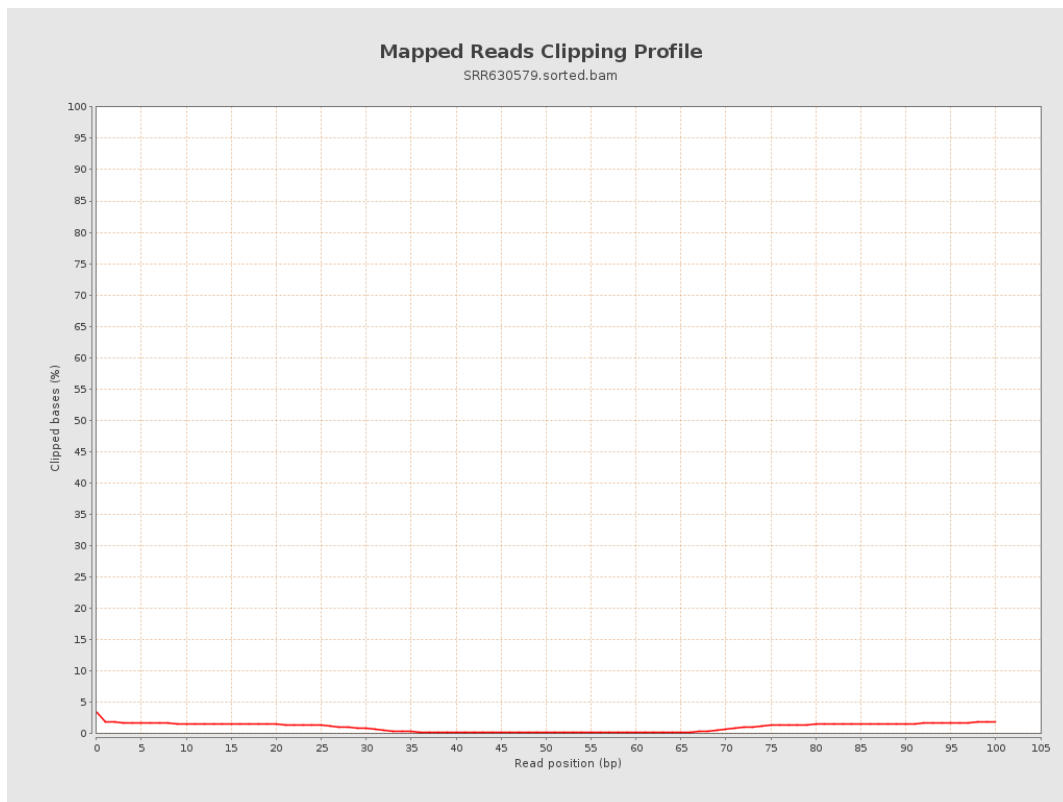
8. Results : Mapped Reads Nucleotide Content



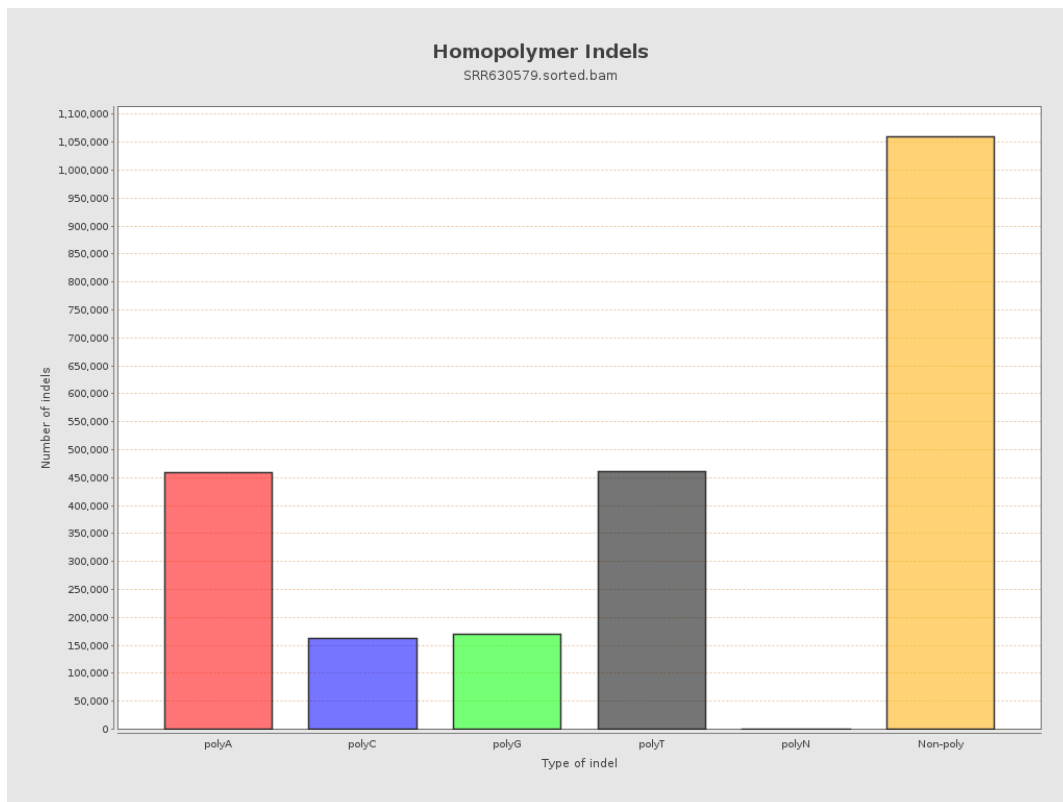
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



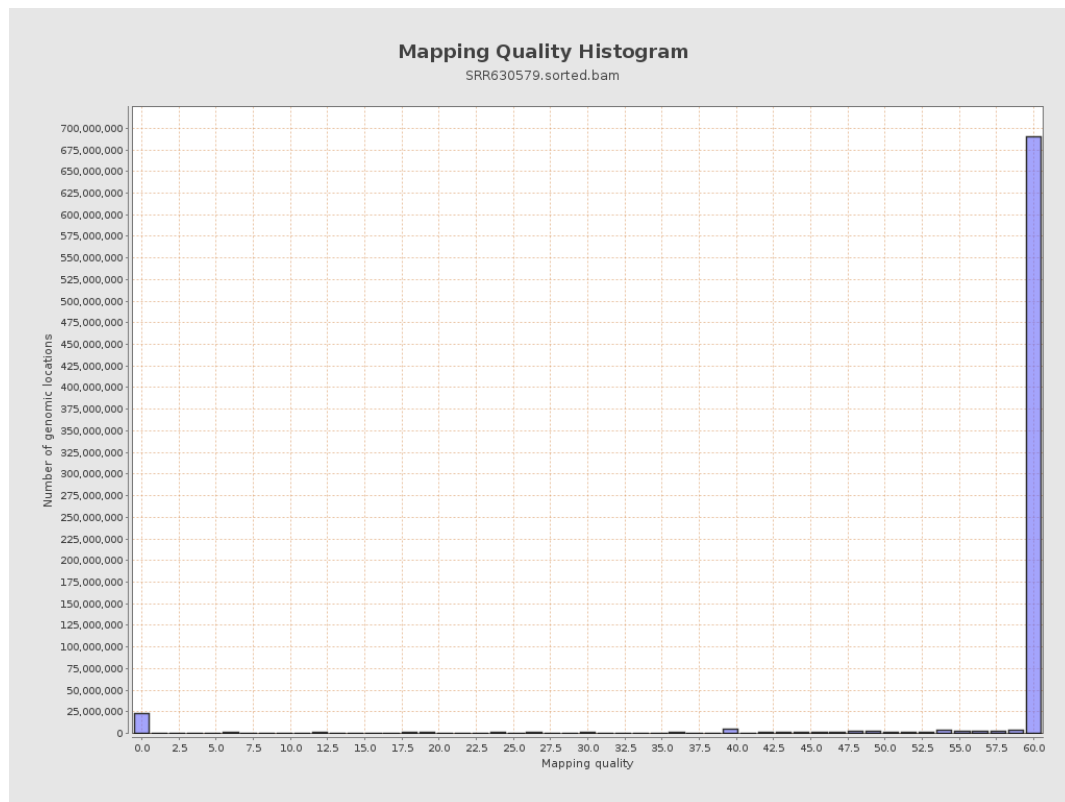
11. Results : Homopolymer Indels



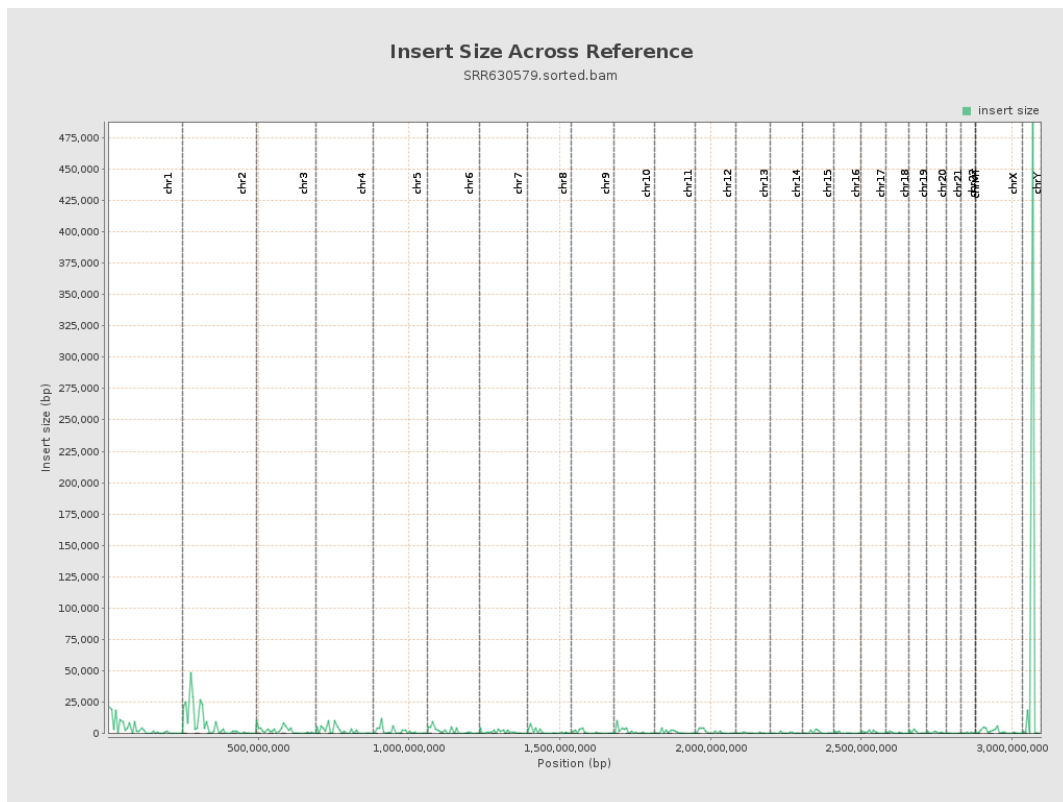
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

