

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/22 18:25:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630573.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_SRR630573 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR630573_1.fastq.gz SRR630573_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 22 18:25:01 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630573.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,928,508
Mapped reads	30,379,221 / 98.22%
Unmapped reads	549,287 / 1.78%
Mapped paired reads	30,379,221 / 98.22%
Mapped reads, first in pair	15,255,417 / 49.32%
Mapped reads, second in pair	15,123,804 / 48.9%
Mapped reads, both in pair	30,183,384 / 97.59%
Mapped reads, singletons	195,837 / 0.63%
Secondary alignments	0
Supplementary alignments	60,689 / 0.2%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	3,935,042 / 12.72%
Duplication rate	10.31%
Clipped reads	4,795,825 / 15.51%

2.2. ACGT Content

Number/percentage of A's	864,065,407 / 29.44%
Number/percentage of C's	574,467,559 / 19.57%
Number/percentage of T's	874,939,595 / 29.81%
Number/percentage of G's	620,863,326 / 21.16%
Number/percentage of N's	441,529 / 0.02%

GC Percentage	40.73%
---------------	--------

2.3. Coverage

Mean	0.9487
Standard Deviation	4.69

2.4. Mapping Quality

Mean Mapping Quality	53.02
----------------------	-------

2.5. Insert size

Mean	33,138.37
Standard Deviation	1,821,344.08
P25/Median/P75	167 / 210 / 274

2.6. Mismatches and indels

General error rate	0.93%
Mismatches	26,471,090
Insertions	543,356
Mapped reads with at least one insertion	1.76%
Deletions	1,645,150
Mapped reads with at least one deletion	5.27%
Homopolymer indels	54.51%

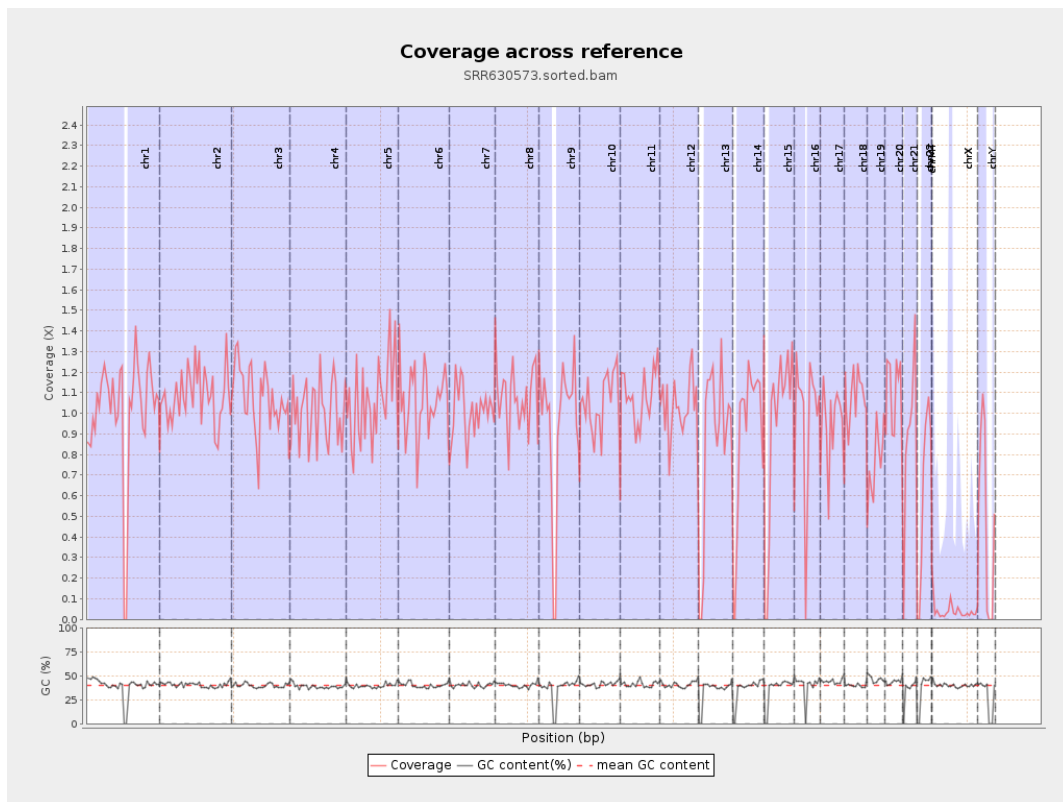
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

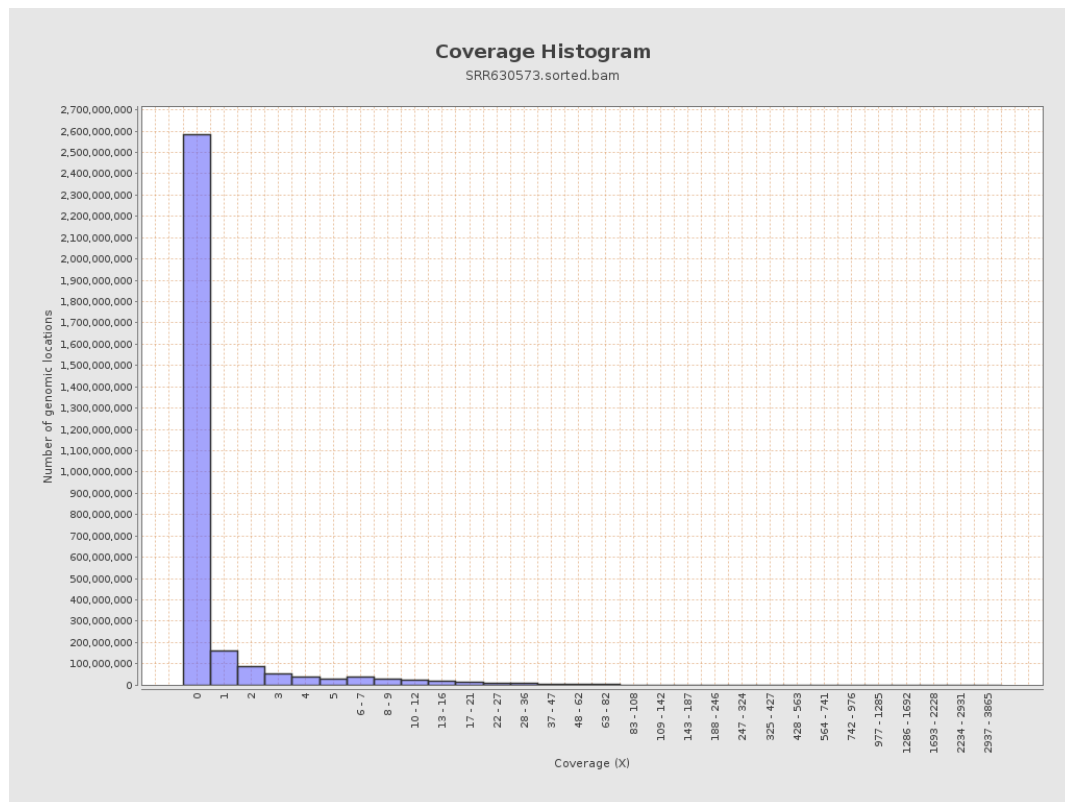
		bases	coverage	deviation
chr1	249250621	253774992	1.0182	5.9976
chr2	243199373	264950279	1.0894	5.5712
chr3	198022430	213015335	1.0757	4.3475
chr4	191154276	192422207	1.0066	4.3424
chr5	180915260	190985641	1.0557	4.2586
chr6	171115067	183135843	1.0702	4.508
chr7	159138663	159684817	1.0034	4.2728
chr8	146364022	155818062	1.0646	4.2755
chr9	141213431	132111793	0.9355	5.6721
chr10	135534747	143273621	1.0571	4.4714
chr11	135006516	145696727	1.0792	6.1084
chr12	133851895	137278263	1.0256	4.313
chr13	115169878	100010749	0.8684	3.8432
chr14	107349540	96931233	0.9029	3.9583
chr15	102531392	95305688	0.9295	4.0768
chr16	90354753	86441641	0.9567	5.1249
chr17	81195210	75998058	0.936	4.2521
chr18	78077248	84809075	1.0862	6.2181
chr19	59128983	44961062	0.7604	4.1727
chr20	63025520	68448629	1.086	4.5267
chr21	48129895	44057863	0.9154	4.6212
chr22	51304566	31737988	0.6186	3.2186
chrMT	16571	4316	0.2605	1.1263
chrX	155270560	5914444	0.0381	1.4046

chrY	59373566	30212095	0.5088	3.682
------	----------	----------	--------	-------

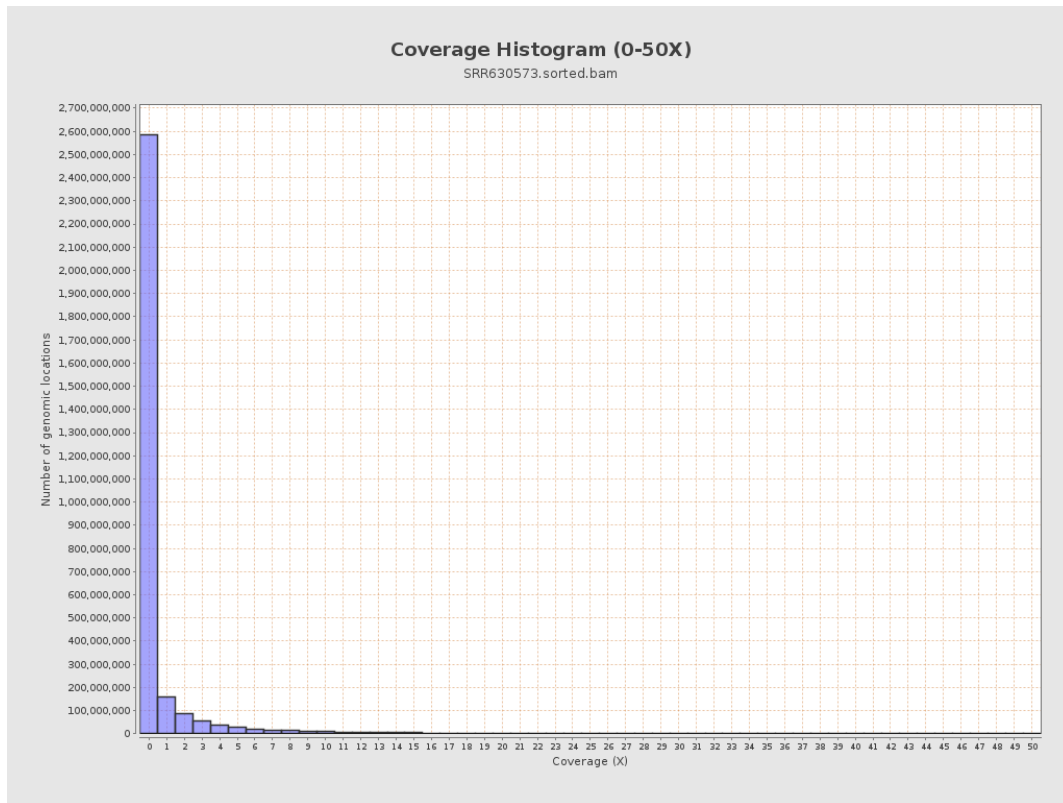
3. Results : Coverage across reference



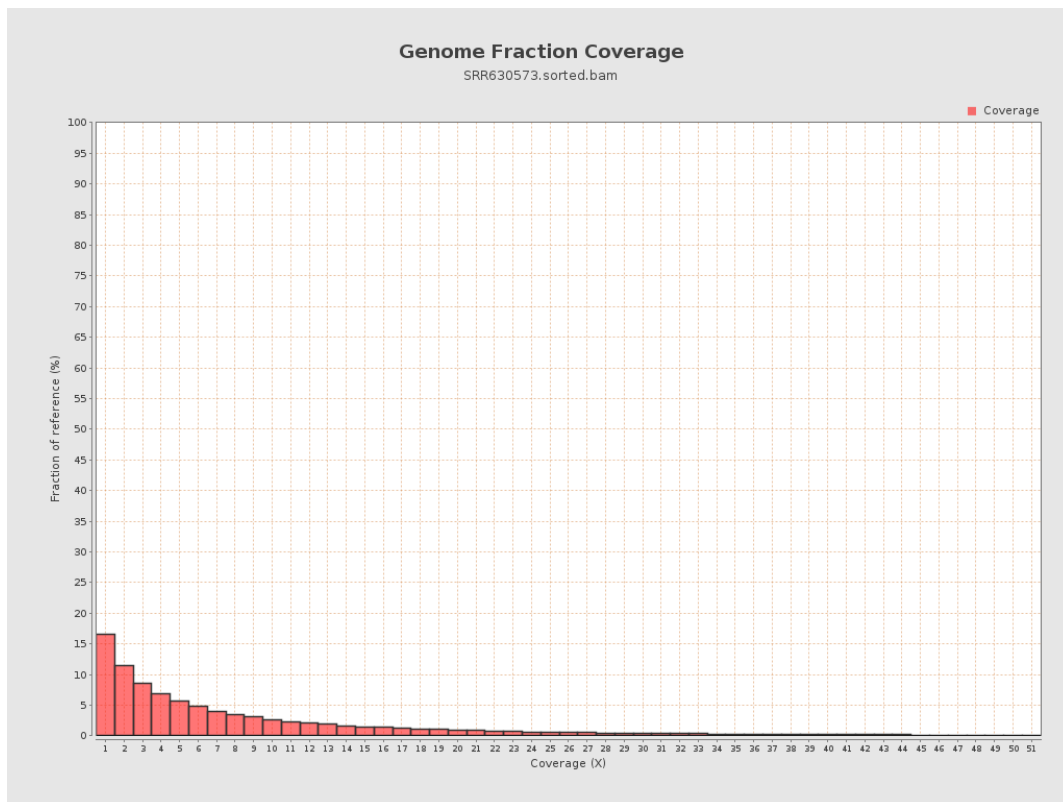
4. Results : Coverage Histogram



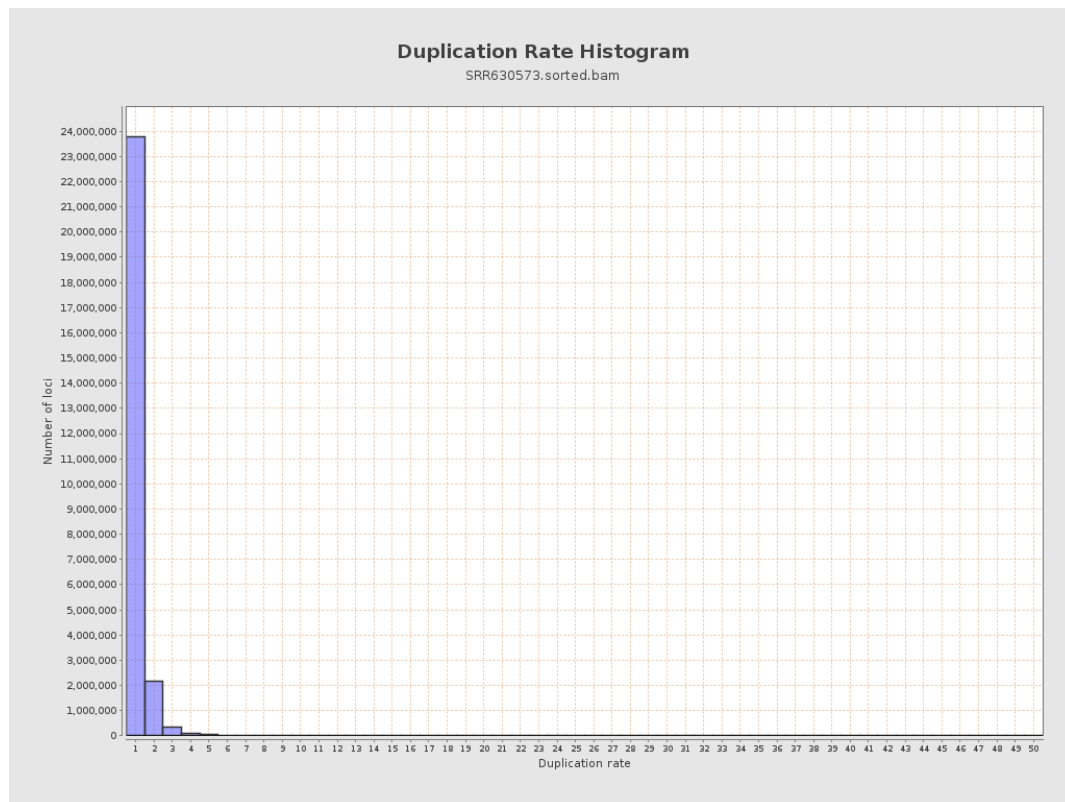
5. Results : Coverage Histogram (0-50X)



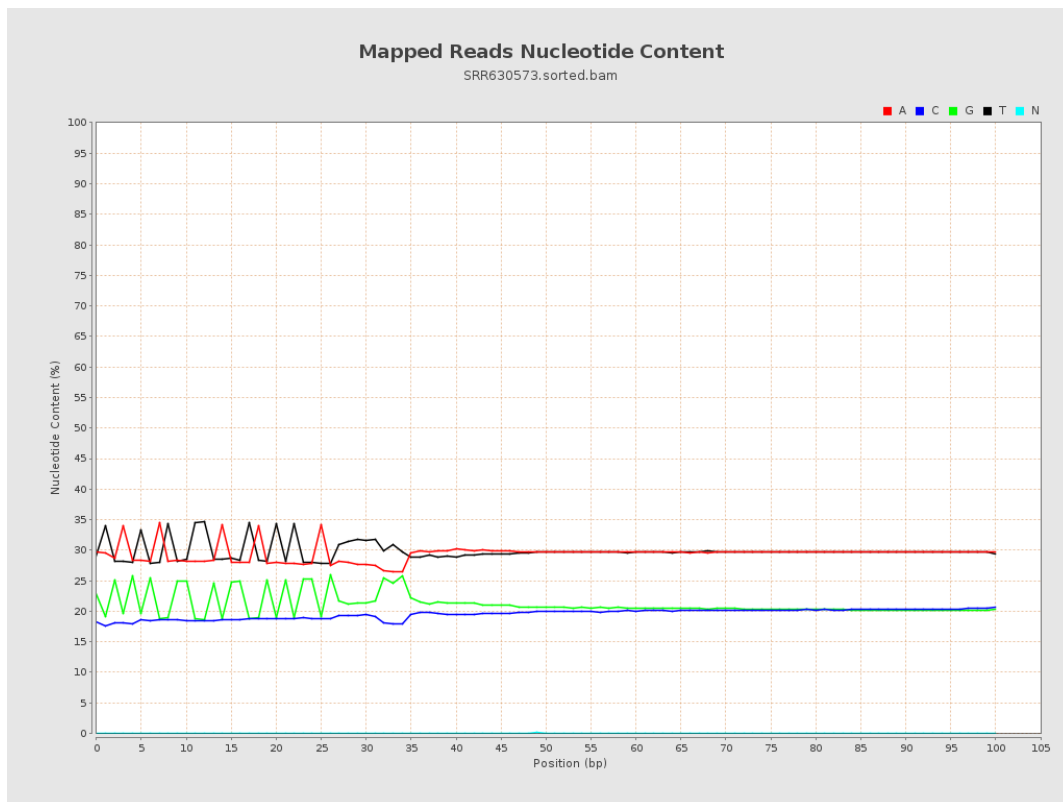
6. Results : Genome Fraction Coverage



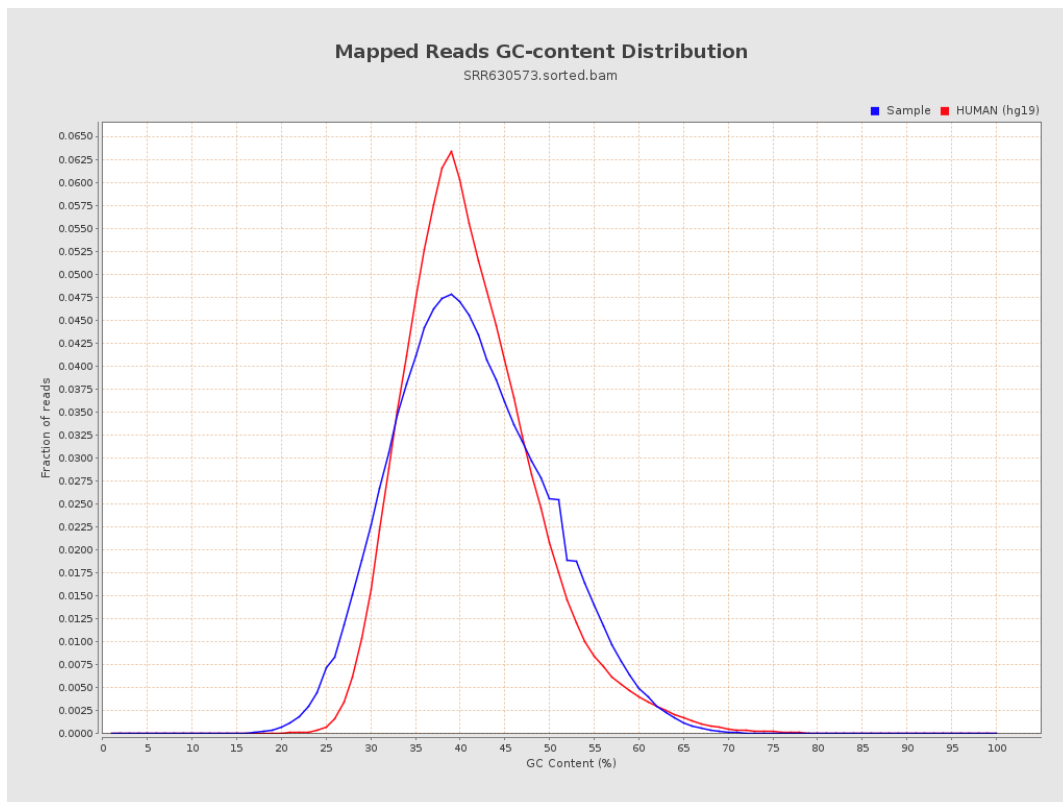
7. Results : Duplication Rate Histogram



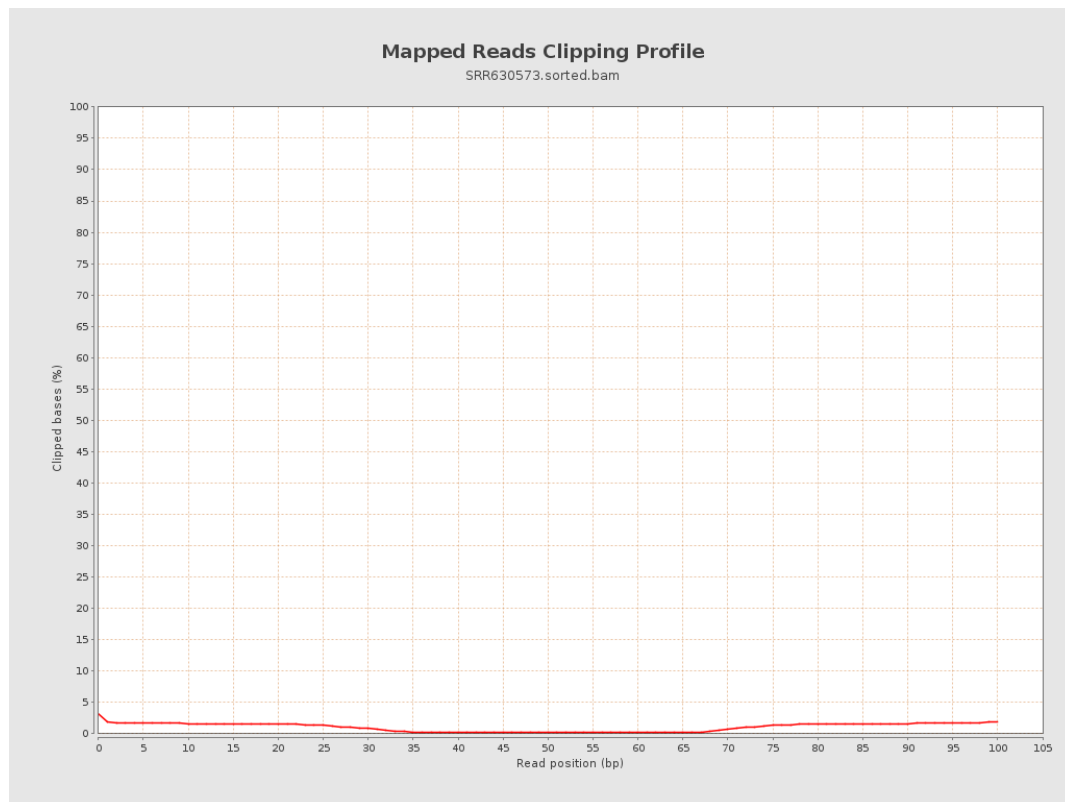
8. Results : Mapped Reads Nucleotide Content



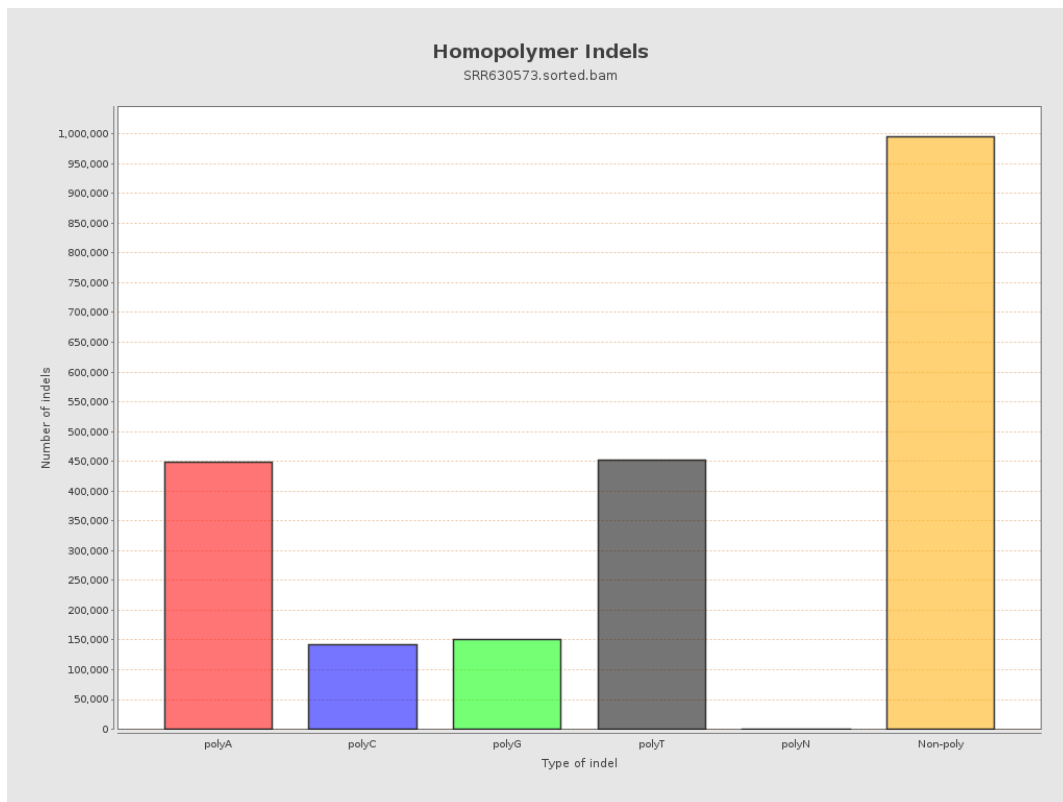
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



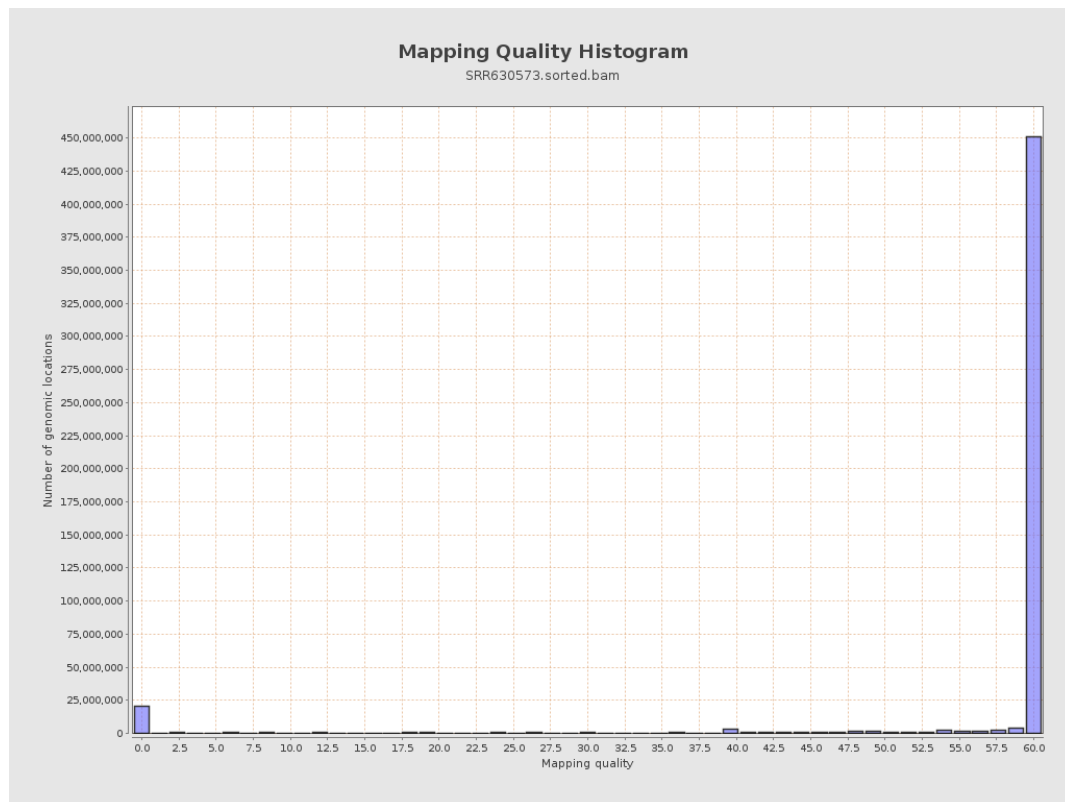
11. Results : Homopolymer Indels



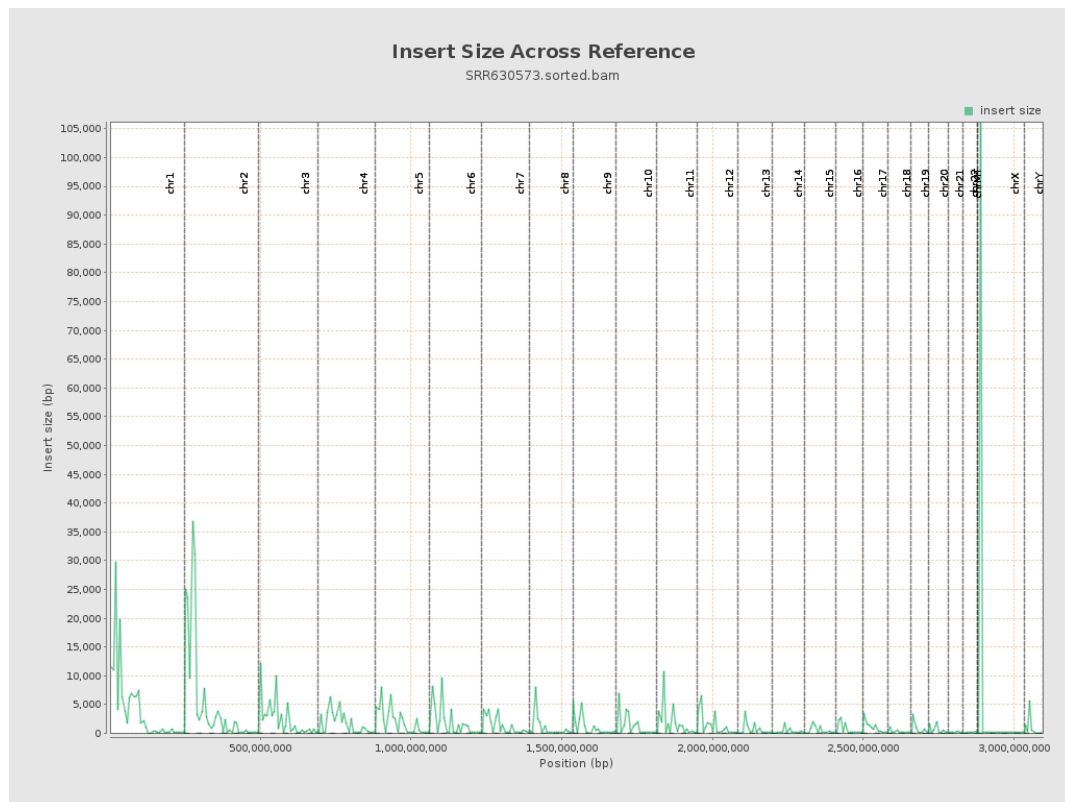
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

