

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 08:23:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354880.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_SRR22354880 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354880_1.fastq.gz SRR22354880_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 08:23:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354880.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,912,198
Mapped reads	19,771,418 / 99.29%
Unmapped reads	140,780 / 0.71%
Mapped paired reads	19,771,418 / 99.29%
Mapped reads, first in pair	9,895,855 / 49.7%
Mapped reads, second in pair	9,875,563 / 49.6%
Mapped reads, both in pair	19,728,188 / 99.08%
Mapped reads, singletons	43,230 / 0.22%
Secondary alignments	0
Supplementary alignments	446,248 / 2.24%
Read min/max/mean length	30 / 150 / 150.88
Duplicated reads (estimated)	7,126,359 / 35.79%
Duplication rate	33.68%
Clipped reads	7,512,750 / 37.73%

2.2. ACGT Content

Number/percentage of A's	756,558,841 / 28.7%
Number/percentage of C's	551,242,097 / 20.91%
Number/percentage of T's	765,991,443 / 29.06%
Number/percentage of G's	562,385,426 / 21.33%
Number/percentage of N's	12,419 / 0%

GC Percentage	42.24%
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2.3. Coverage

Mean	0.8521
Standard Deviation	19.9691

2.4. Mapping Quality

Mean Mapping Quality	54.03
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2.5. Insert size

Mean	201,368.41
Standard Deviation	5,132,622.02
P25/Median/P75	129 / 198 / 286

2.6. Mismatches and indels

General error rate	0.84%
Mismatches	20,576,657
Insertions	531,977
Mapped reads with at least one insertion	2.5%
Deletions	549,190
Mapped reads with at least one deletion	2.64%
Homopolymer indels	44.45%

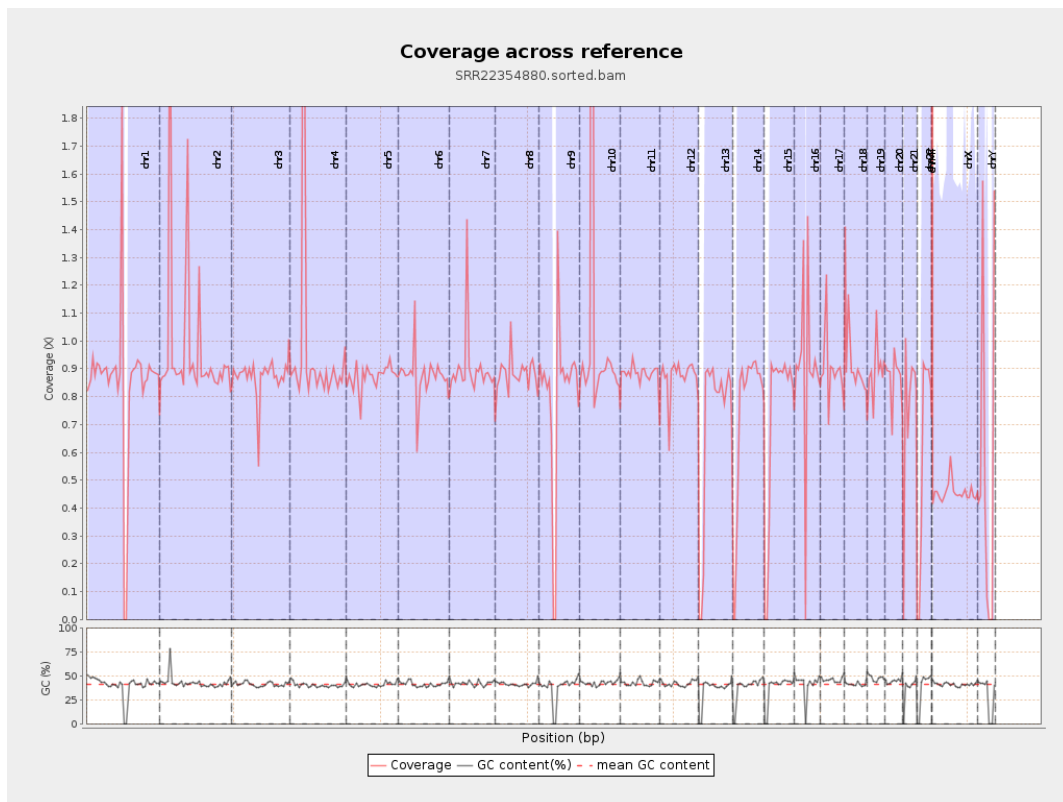
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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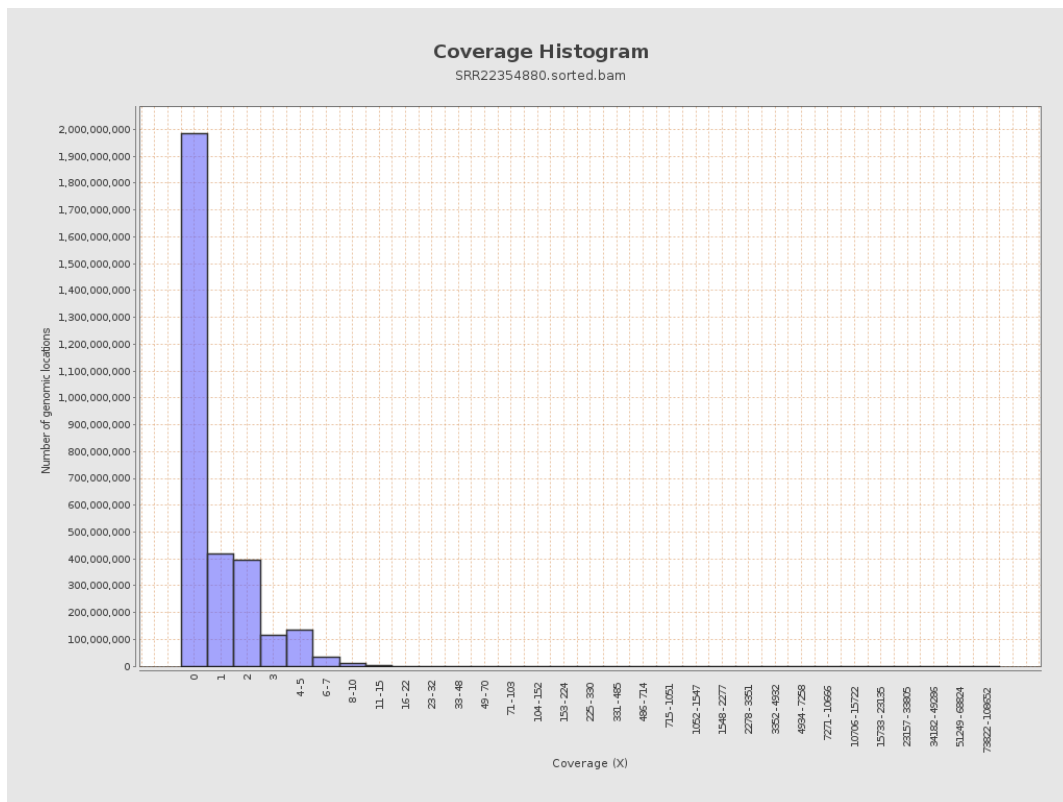
		bases	coverage	deviation
chr1	249250621	213867044	0.858	23.1127
chr2	243199373	238814541	0.982	58.0257
chr3	198022430	172306473	0.8701	1.8307
chr4	191154276	181744181	0.9508	14.6961
chr5	180915260	157651334	0.8714	1.5516
chr6	171115067	150093020	0.8771	3.4064
chr7	159138663	143287944	0.9004	12.4696
chr8	146364022	129585870	0.8854	3.6343
chr9	141213431	112216993	0.7947	12.8323
chr10	135534747	147581448	1.0889	30.824
chr11	135006516	119326444	0.8839	4.4328
chr12	133851895	116692555	0.8718	1.552
chr13	115169878	81764366	0.7099	1.3467
chr14	107349540	79477517	0.7404	3.2648
chr15	102531392	74081628	0.7225	1.3549
chr16	90354753	81601054	0.9031	5.7195
chr17	81195210	72600235	0.8941	4.9769
chr18	78077248	72032454	0.9226	10.5608
chr19	59128983	52542809	0.8886	11.7983
chr20	63025520	54763407	0.8689	4.7327
chr21	48129895	37116670	0.7712	7.2729
chr22	51304566	31515525	0.6143	2.4445
chrMT	16571	12497946	754.2059	178.1444
chrX	155270560	70786366	0.4559	1.7798

chrY	59373566	33807428	0.5694	17.5206
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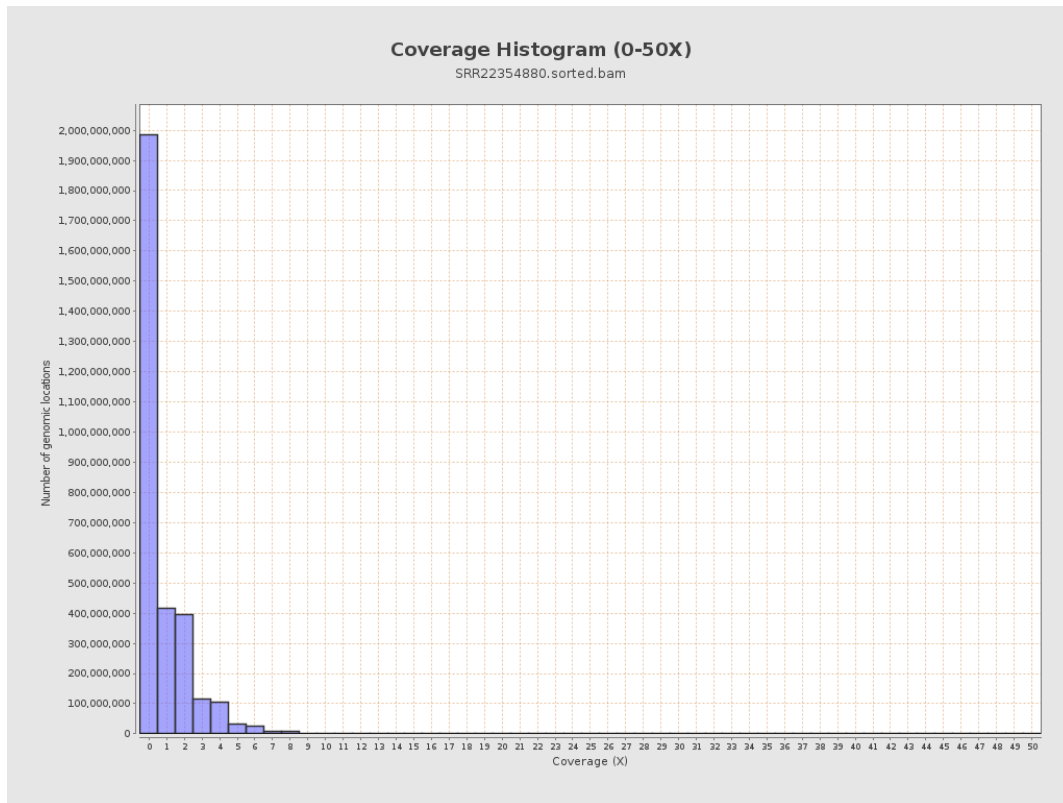
3. Results : Coverage across reference



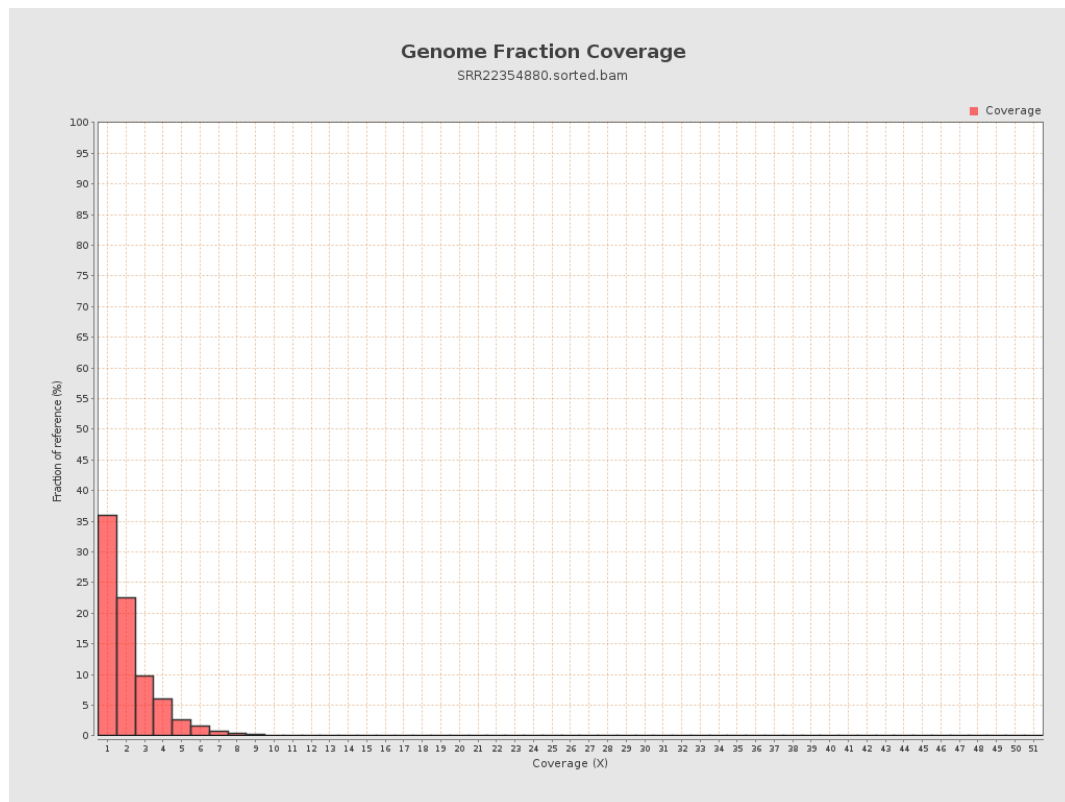
4. Results : Coverage Histogram



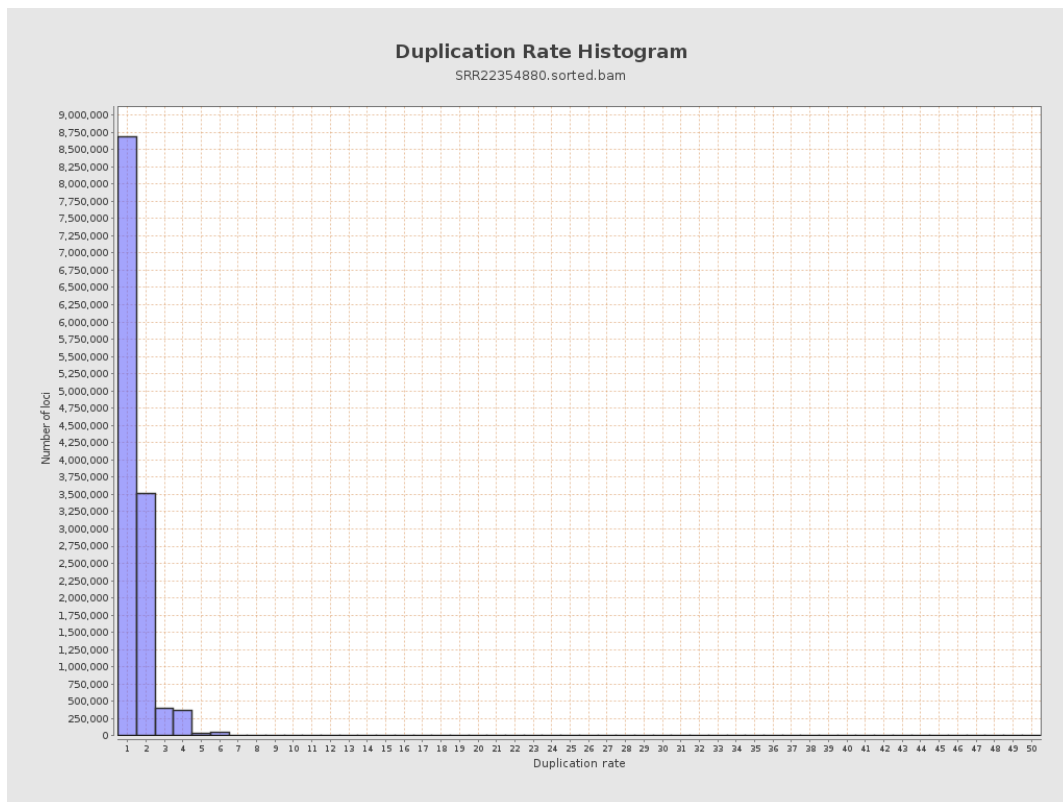
5. Results : Coverage Histogram (0-50X)



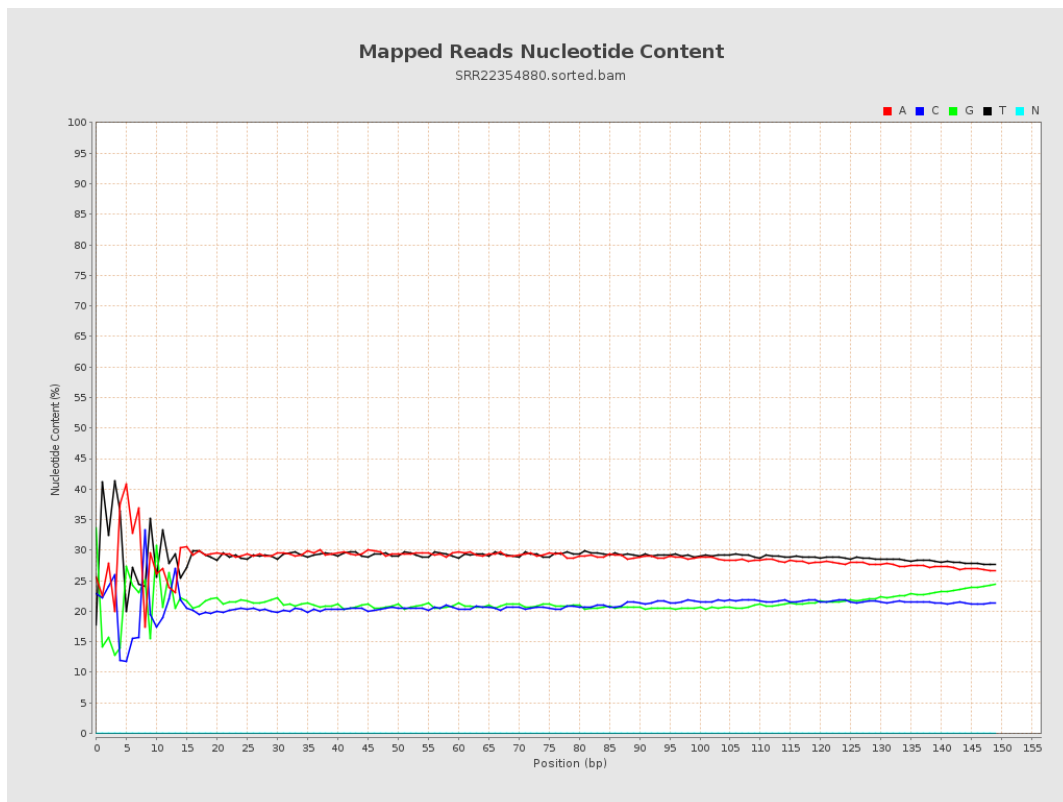
6. Results : Genome Fraction Coverage



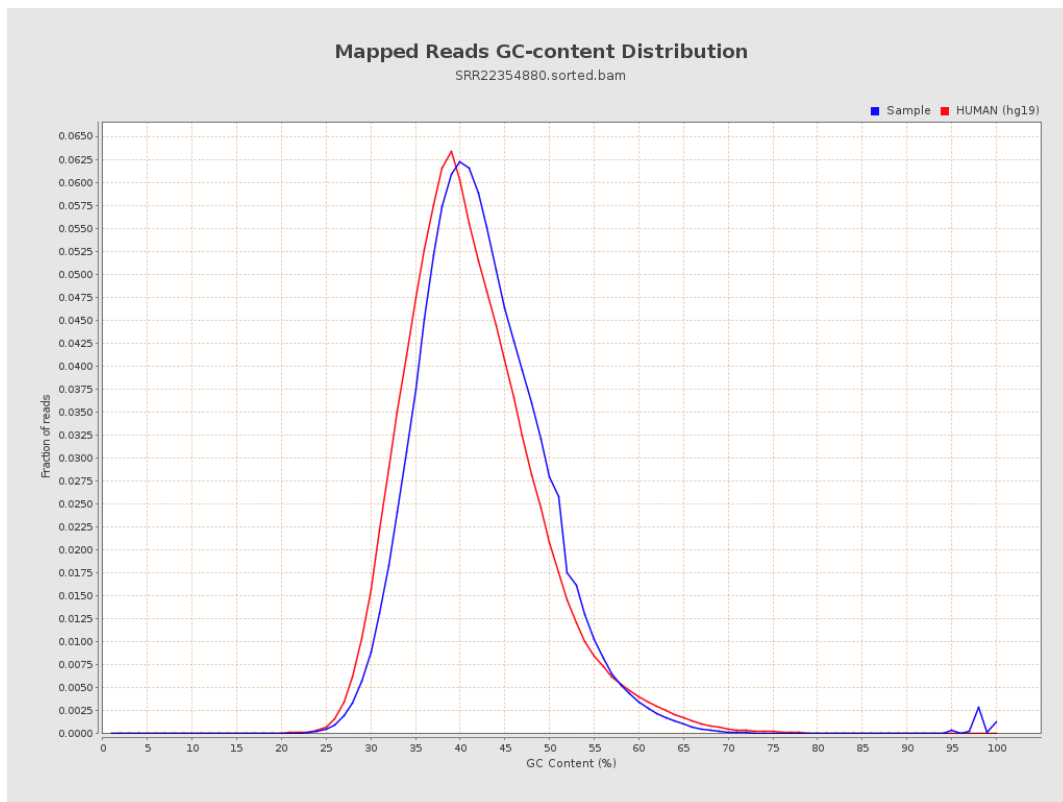
7. Results : Duplication Rate Histogram



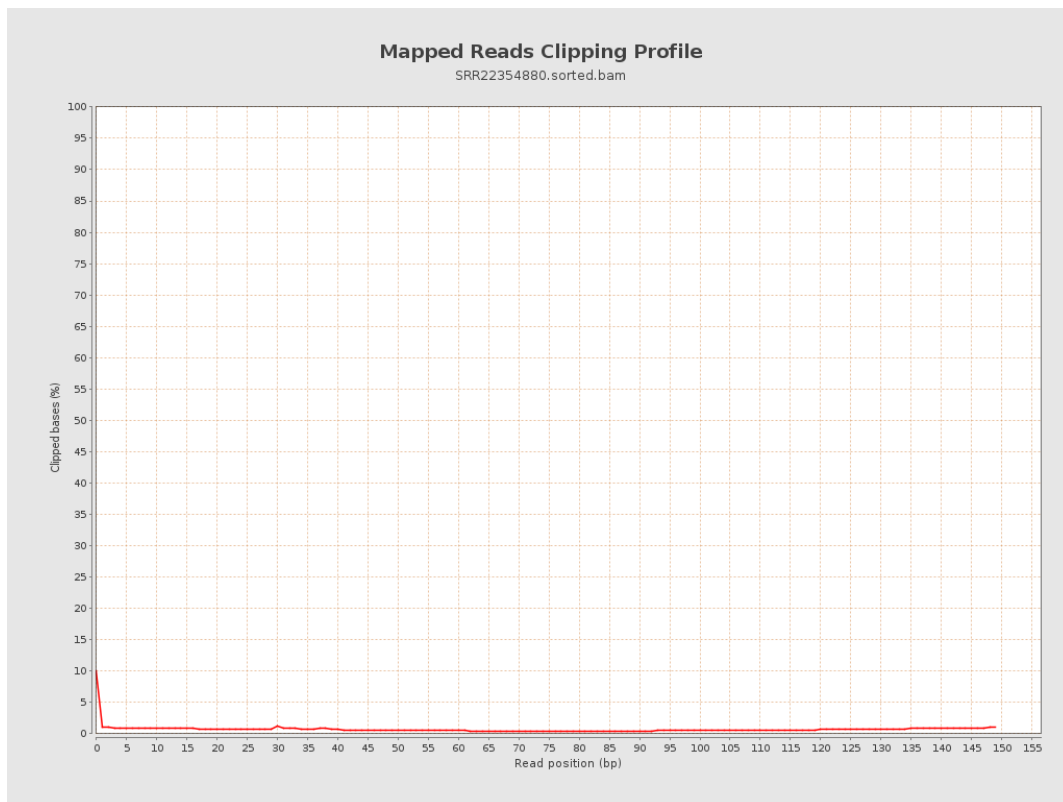
8. Results : Mapped Reads Nucleotide Content



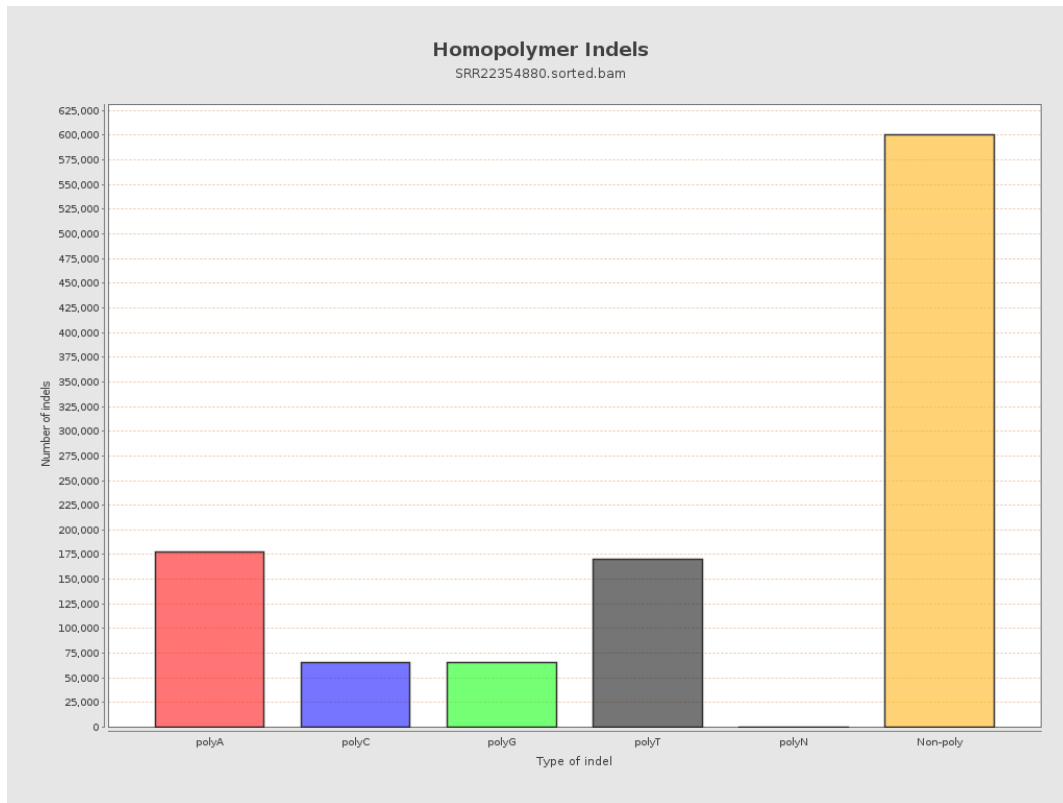
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



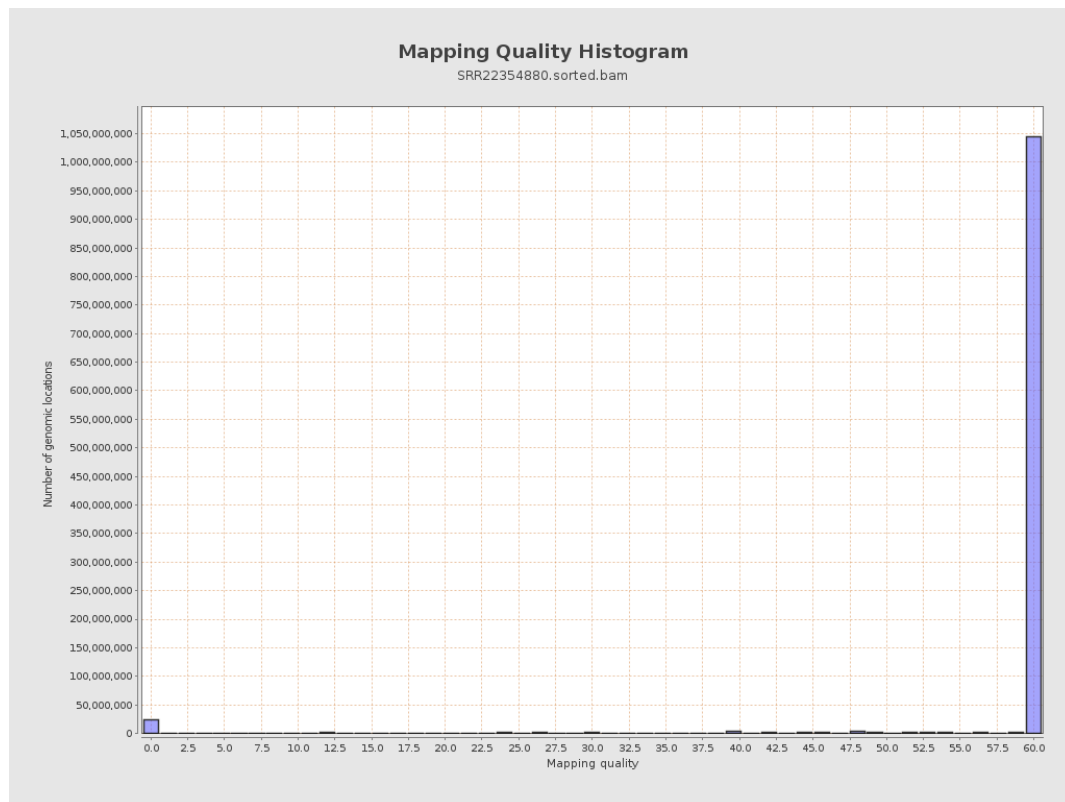
11. Results : Homopolymer Indels



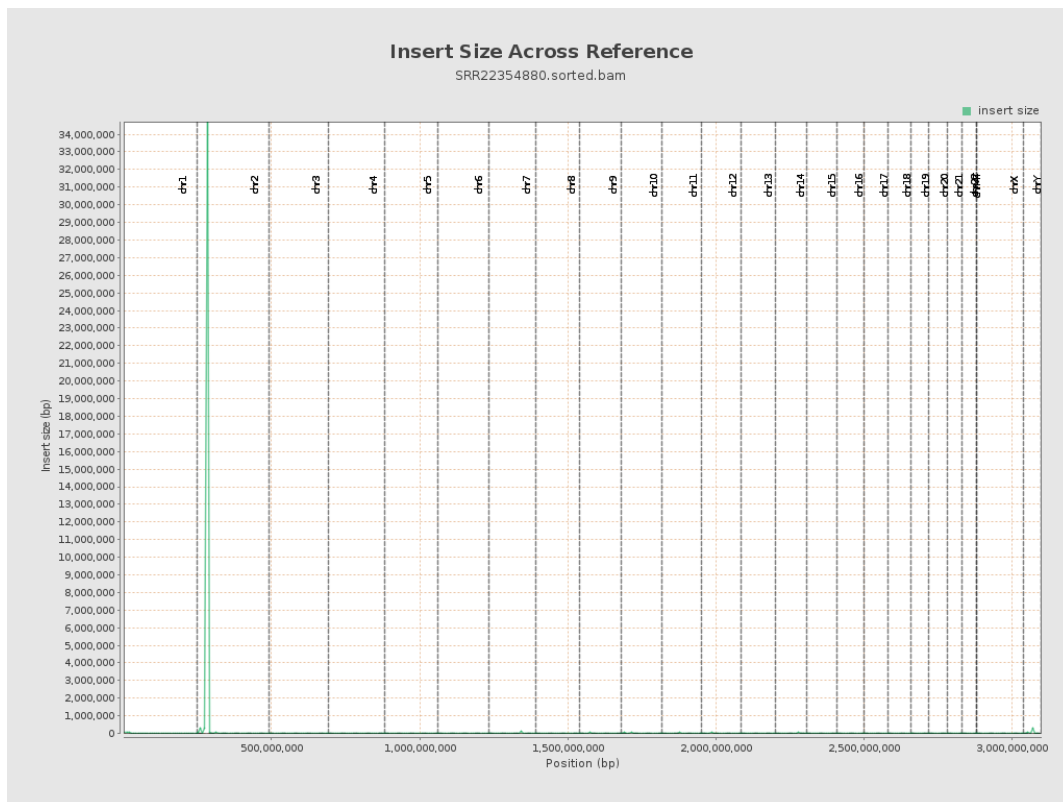
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

