

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 05:43:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174078.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_SRR10174078 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174078_1.fastq.gz SRR10174078_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 05:43:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174078.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,996,868
Mapped reads	4,881,230 / 97.69%
Unmapped reads	115,638 / 2.31%
Mapped paired reads	4,881,230 / 97.69%
Mapped reads, first in pair	2,441,847 / 48.87%
Mapped reads, second in pair	2,439,383 / 48.82%
Mapped reads, both in pair	4,804,102 / 96.14%
Mapped reads, singletons	77,128 / 1.54%
Secondary alignments	0
Supplementary alignments	660,740 / 13.22%
Read min/max/mean length	30 / 133 / 126.57
Duplicated reads (estimated)	4,038,972 / 80.83%
Duplication rate	67.6%
Clipped reads	2,519,964 / 50.43%

2.2. ACGT Content

Number/percentage of A's	163,969,363 / 29.42%
Number/percentage of C's	112,544,595 / 20.2%
Number/percentage of T's	162,736,135 / 29.2%
Number/percentage of G's	118,014,743 / 21.18%
Number/percentage of N's	4,452 / 0%

GC Percentage	41.37%
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2.3. Coverage

Mean	0.1802
Standard Deviation	3.5839

2.4. Mapping Quality

Mean Mapping Quality	52.32
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2.5. Insert size

Mean	1,085,806.47
Standard Deviation	9,724,046.47
P25/Median/P75	111 / 164 / 253

2.6. Mismatches and indels

General error rate	0.96%
Mismatches	5,148,235
Insertions	67,118
Mapped reads with at least one insertion	1.32%
Deletions	201,293
Mapped reads with at least one deletion	4.01%
Homopolymer indels	39.97%

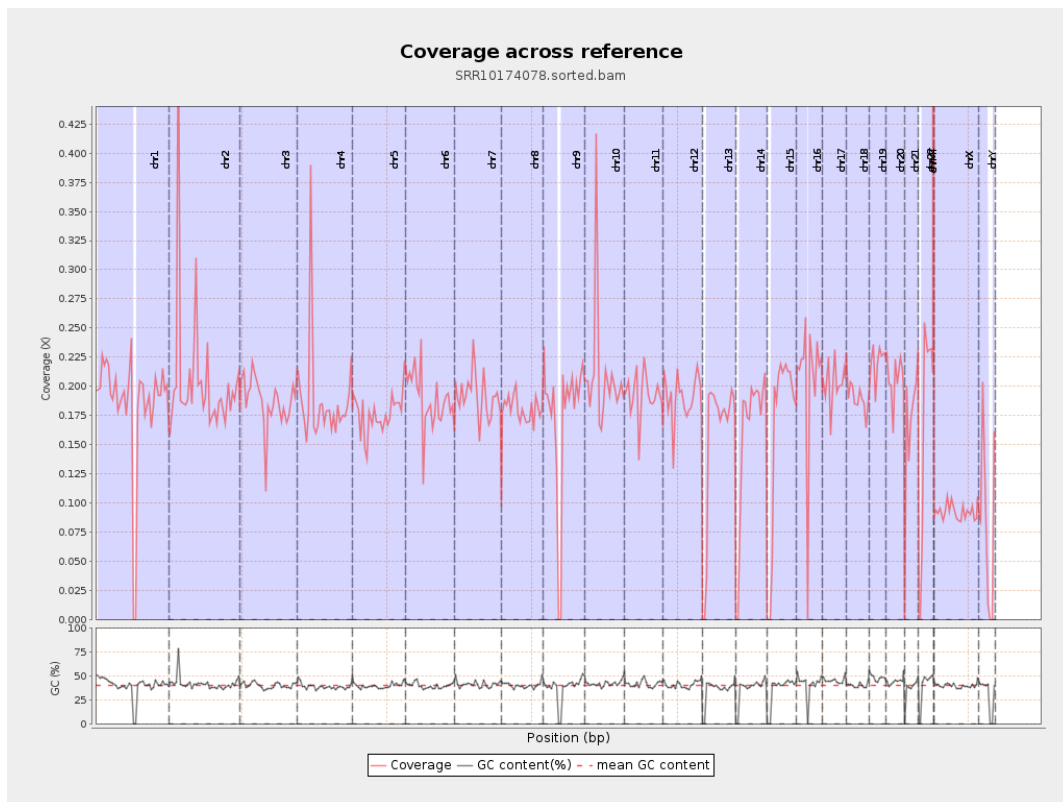
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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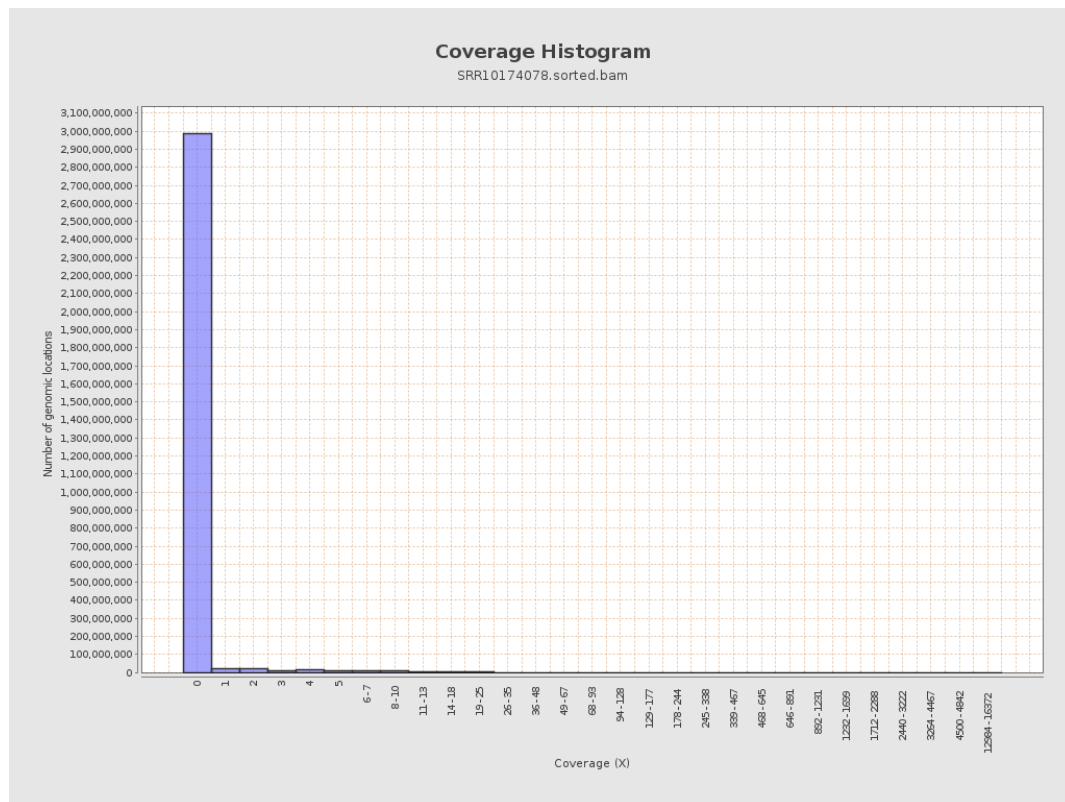
		bases	coverage	deviation
chr1	249250621	46246300	0.1855	1.9943
chr2	243199373	49921922	0.2053	11.4812
chr3	198022430	37123935	0.1875	1.3214
chr4	191154276	35658093	0.1865	1.909
chr5	180915260	31818858	0.1759	1.2733
chr6	171115067	32279495	0.1886	1.5198
chr7	159138663	30456189	0.1914	1.7715
chr8	146364022	26441356	0.1807	2.0367
chr9	141213431	24175017	0.1712	1.8167
chr10	135534747	28123326	0.2075	2.2385
chr11	135006516	26097453	0.1933	1.4102
chr12	133851895	25457393	0.1902	1.366
chr13	115169878	17796538	0.1545	1.1965
chr14	107349540	16939619	0.1578	1.2183
chr15	102531392	16865180	0.1645	1.2525
chr16	90354753	18550402	0.2053	1.6128
chr17	81195210	16419288	0.2022	1.5049
chr18	78077248	14880191	0.1906	2.3012
chr19	59128983	13050496	0.2207	1.7053
chr20	63025520	12953830	0.2055	1.4737
chr21	48129895	8118834	0.1687	1.6485
chr22	51304566	8344754	0.1627	1.3629
chrMT	16571	1015705	61.2941	52.6797
chrX	155270560	14305771	0.0921	0.9275

chrY	59373566	4691099	0.079	1.3944
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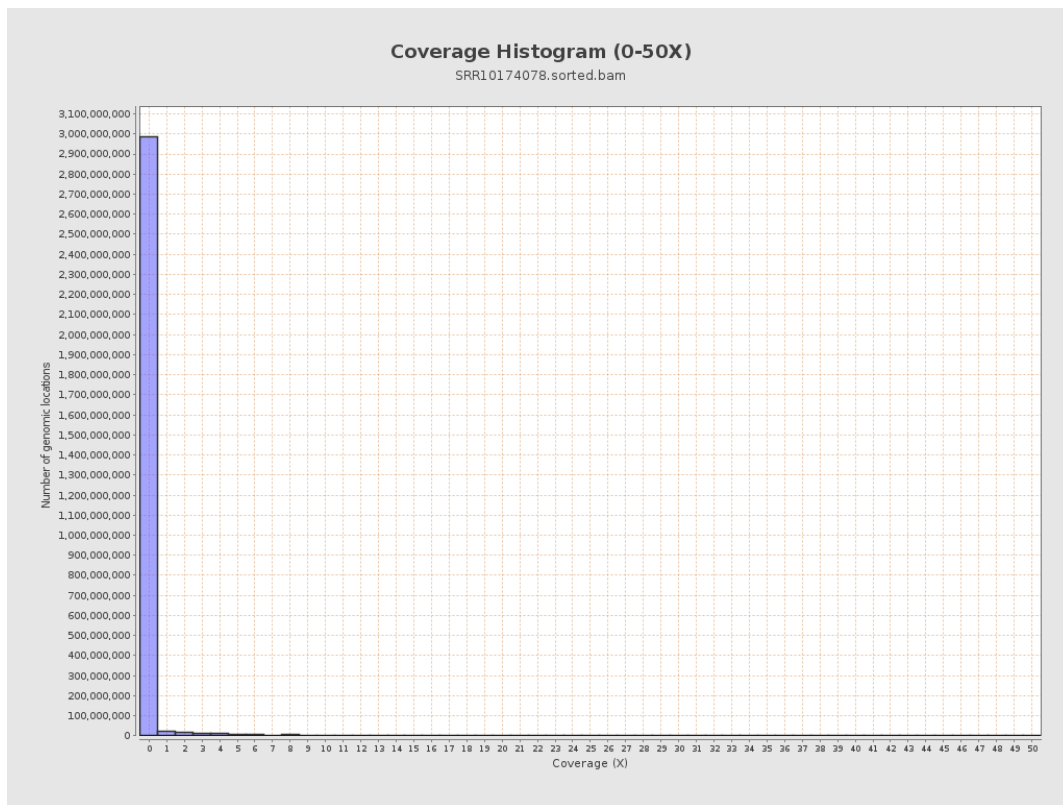
3. Results : Coverage across reference



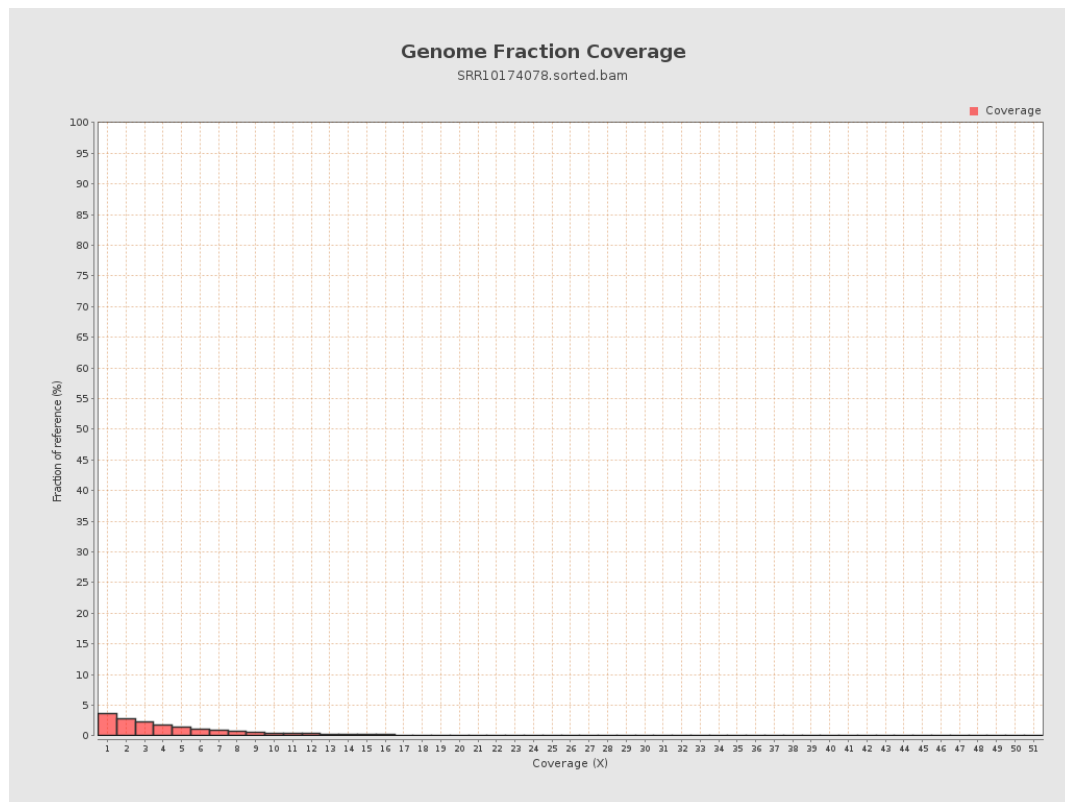
4. Results : Coverage Histogram



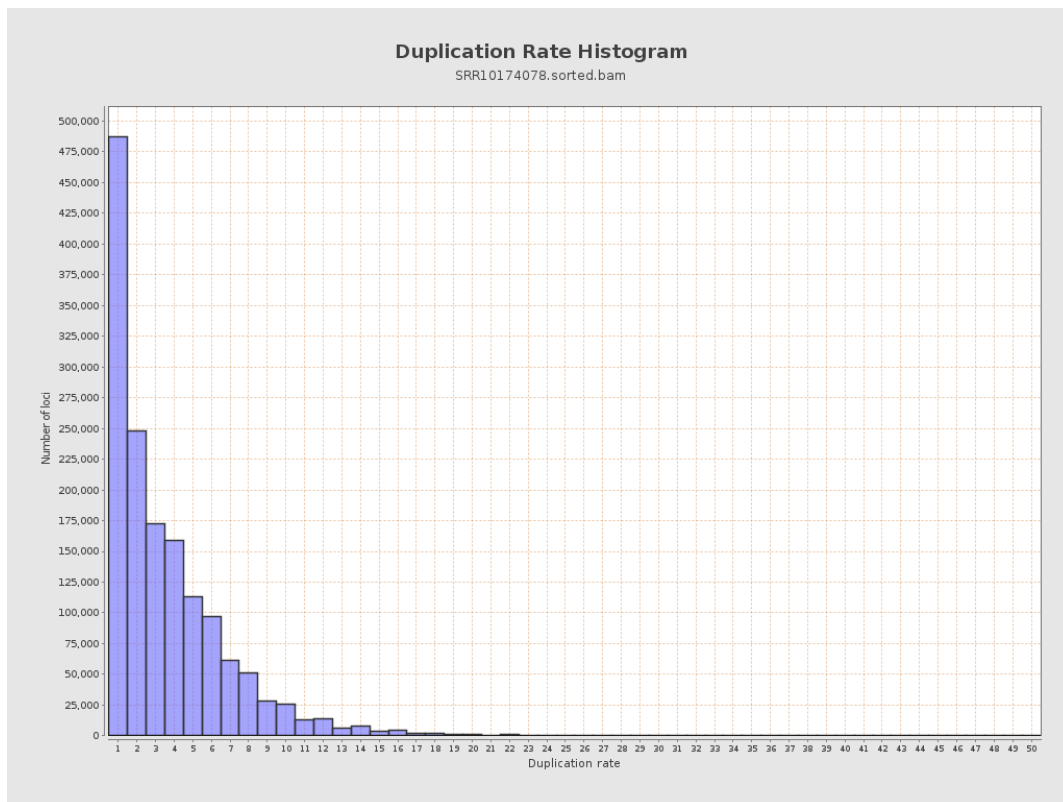
5. Results : Coverage Histogram (0-50X)



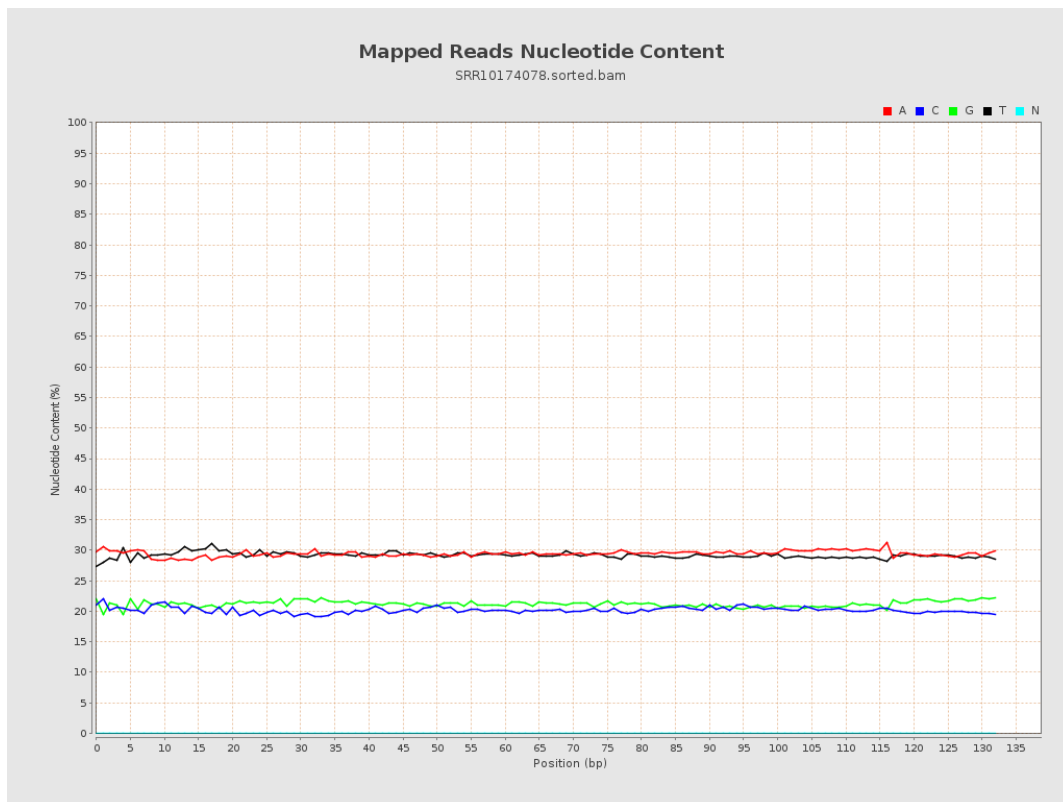
6. Results : Genome Fraction Coverage



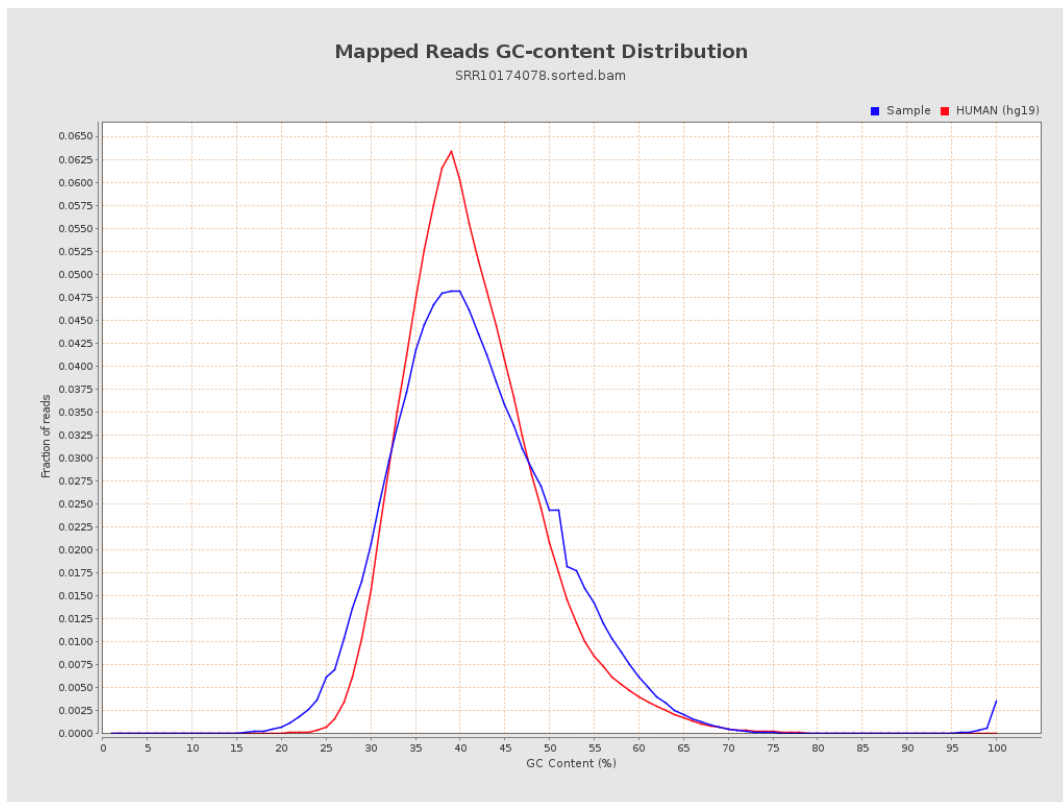
7. Results : Duplication Rate Histogram



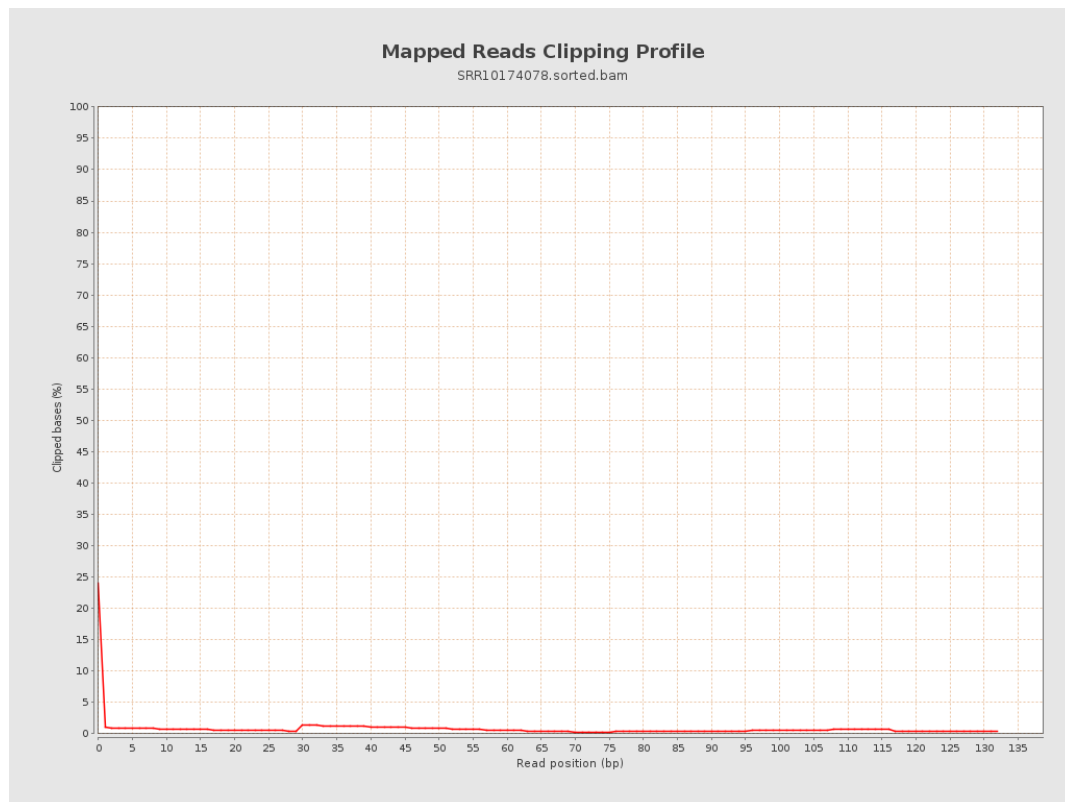
8. Results : Mapped Reads Nucleotide Content



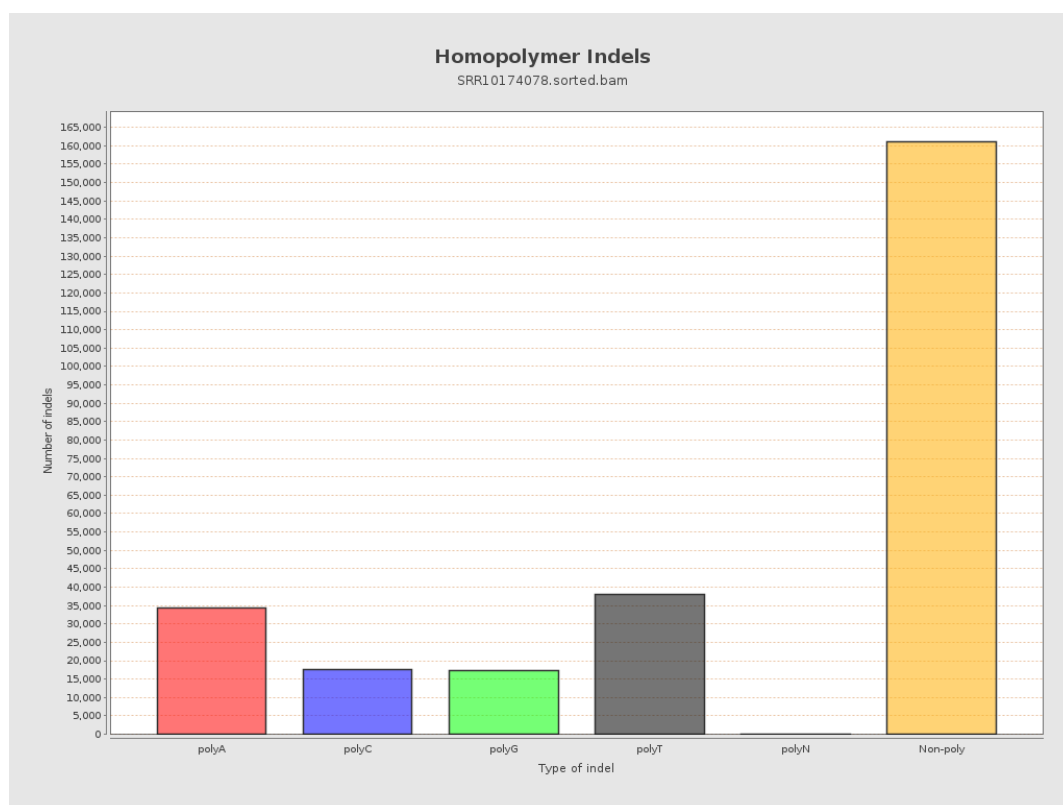
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



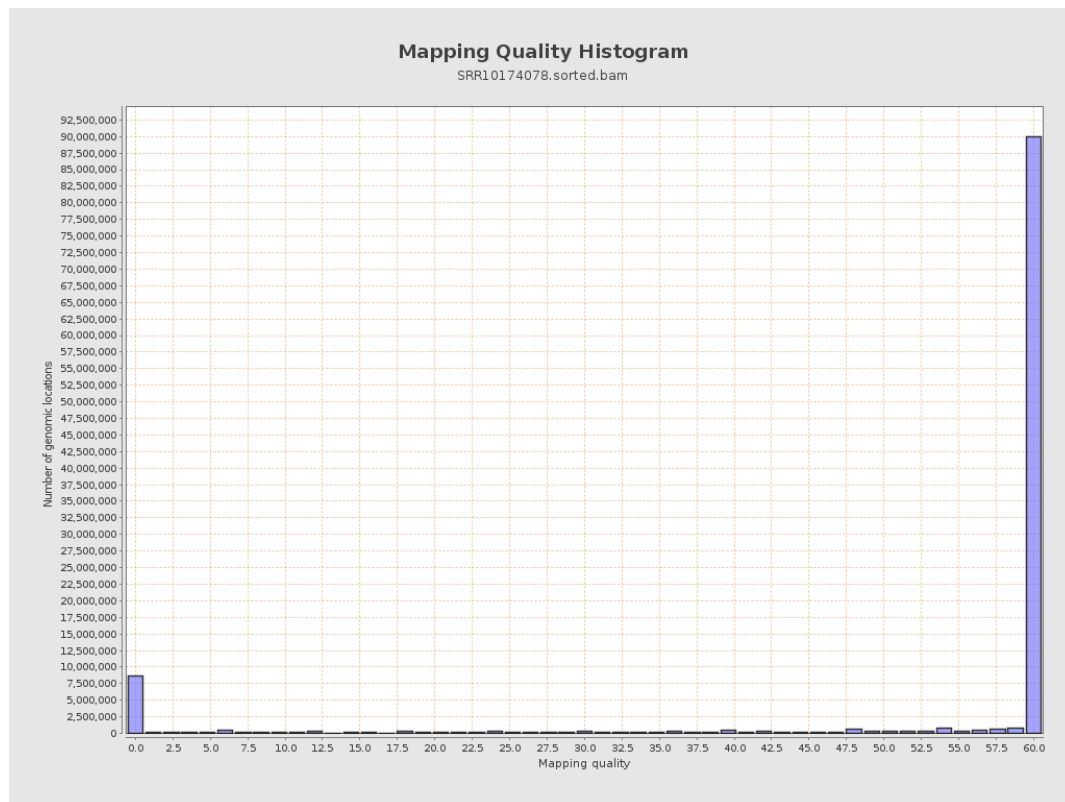
11. Results : Homopolymer Indels



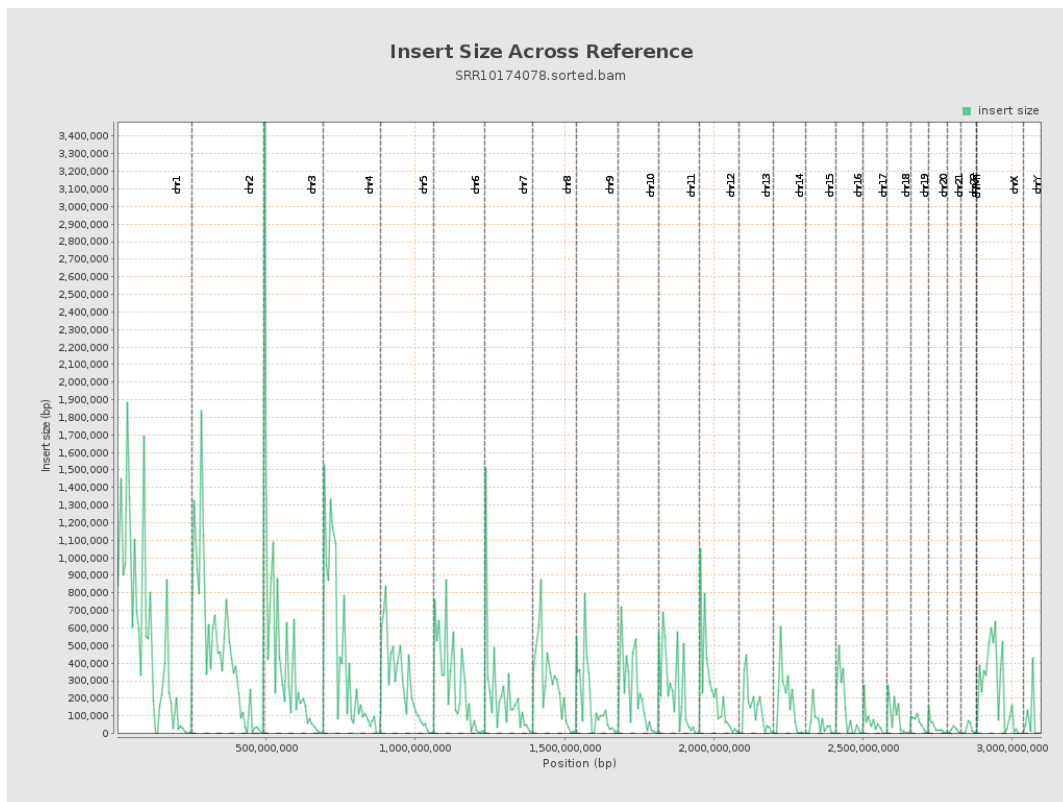
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

