

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 20:56:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174011.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_SRR10174011 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174011_1.fastq.gz SRR10174011_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 20:56:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174011.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,710,968
Mapped reads	5,563,979 / 97.43%
Unmapped reads	146,989 / 2.57%
Mapped paired reads	5,563,979 / 97.43%
Mapped reads, first in pair	2,785,450 / 48.77%
Mapped reads, second in pair	2,778,529 / 48.65%
Mapped reads, both in pair	5,465,112 / 95.7%
Mapped reads, singletons	98,867 / 1.73%
Secondary alignments	0
Supplementary alignments	545,055 / 9.54%
Read min/max/mean length	30 / 133 / 127.77
Duplicated reads (estimated)	4,373,976 / 76.59%
Duplication rate	65.38%
Clipped reads	2,265,766 / 39.67%

2.2. ACGT Content

Number/percentage of A's	197,409,640 / 30.18%
Number/percentage of C's	127,966,482 / 19.56%
Number/percentage of T's	196,796,755 / 30.08%
Number/percentage of G's	131,957,048 / 20.17%
Number/percentage of N's	7,579 / 0%

GC Percentage	39.74%
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2.3. Coverage

Mean	0.2114
Standard Deviation	3.1936

2.4. Mapping Quality

Mean Mapping Quality	52.66
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2.5. Insert size

Mean	805,728.19
Standard Deviation	8,151,201.83
P25/Median/P75	142 / 200 / 286

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	6,570,616
Insertions	70,243
Mapped reads with at least one insertion	1.21%
Deletions	144,517
Mapped reads with at least one deletion	2.53%
Homopolymer indels	42.77%

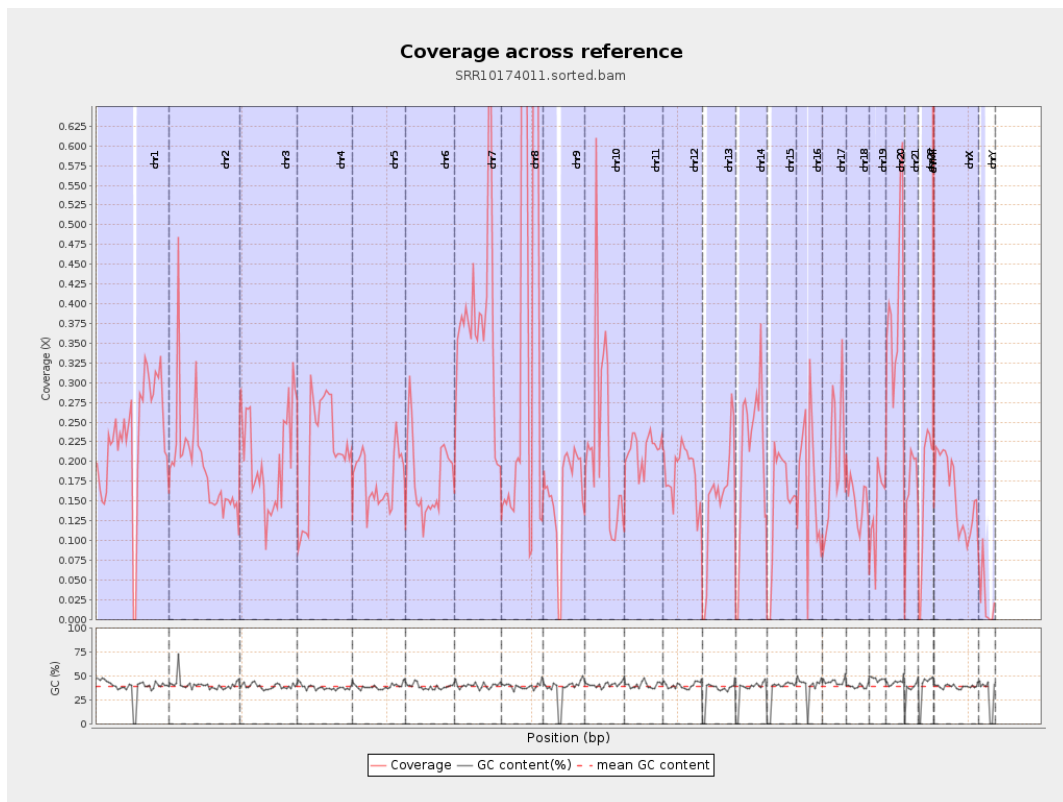
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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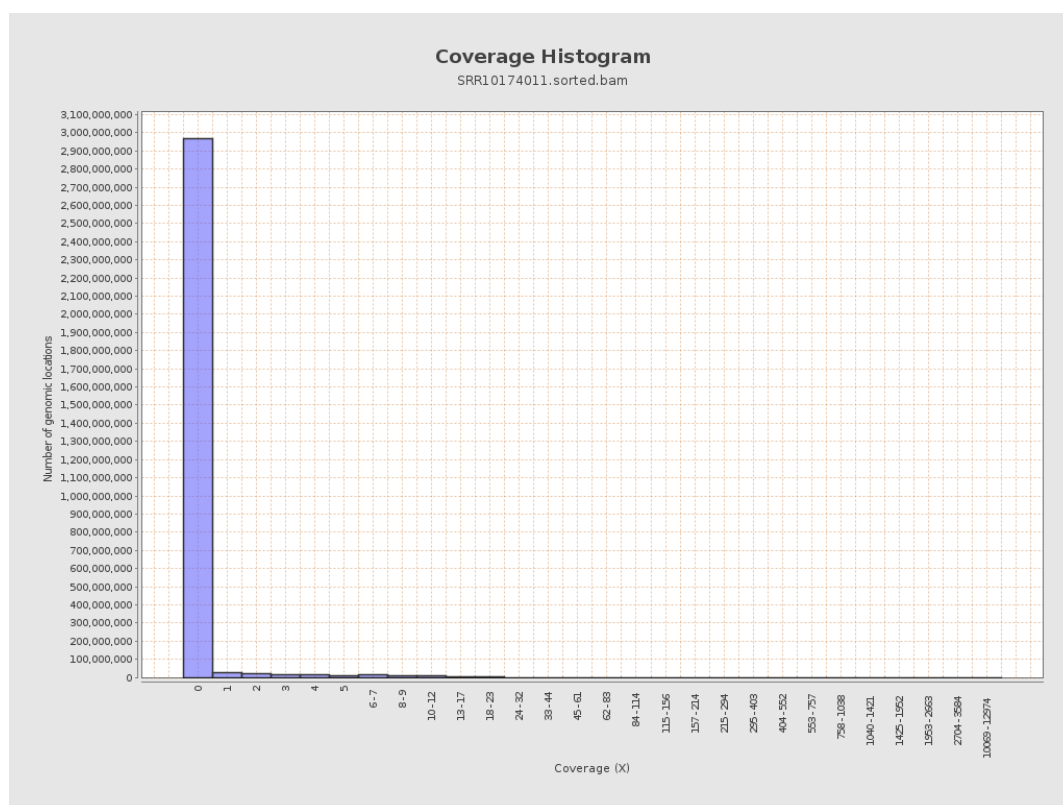
		bases	coverage	deviation
chr1	249250621	57234141	0.2296	1.8782
chr2	243199373	47217738	0.1942	9.1418
chr3	198022430	40658810	0.2053	1.3436
chr4	191154276	40690231	0.2129	1.993
chr5	180915260	32160146	0.1778	1.2354
chr6	171115067	30315316	0.1772	1.294
chr7	159138663	59918321	0.3765	3.7957
chr8	146364022	63040655	0.4307	2.5912
chr9	141213431	22618506	0.1602	1.5184
chr10	135534747	30608379	0.2258	4.0885
chr11	135006516	28946332	0.2144	1.4114
chr12	133851895	24803255	0.1853	1.2745
chr13	115169878	17597696	0.1528	1.168
chr14	107349540	22702368	0.2115	1.3648
chr15	102531392	15351944	0.1497	1.123
chr16	90354753	15554984	0.1722	1.7114
chr17	81195210	16073429	0.198	1.4866
chr18	78077248	11840760	0.1517	2.0956
chr19	59128983	8392128	0.1419	1.4305
chr20	63025520	25053644	0.3975	1.9108
chr21	48129895	7877782	0.1637	1.3144
chr22	51304566	8169596	0.1592	1.1108
chrMT	16571	1667942	100.6543	72.393
chrX	155270560	24584952	0.1583	1.1829

chrY	59373566	1426795	0.024	1.1246
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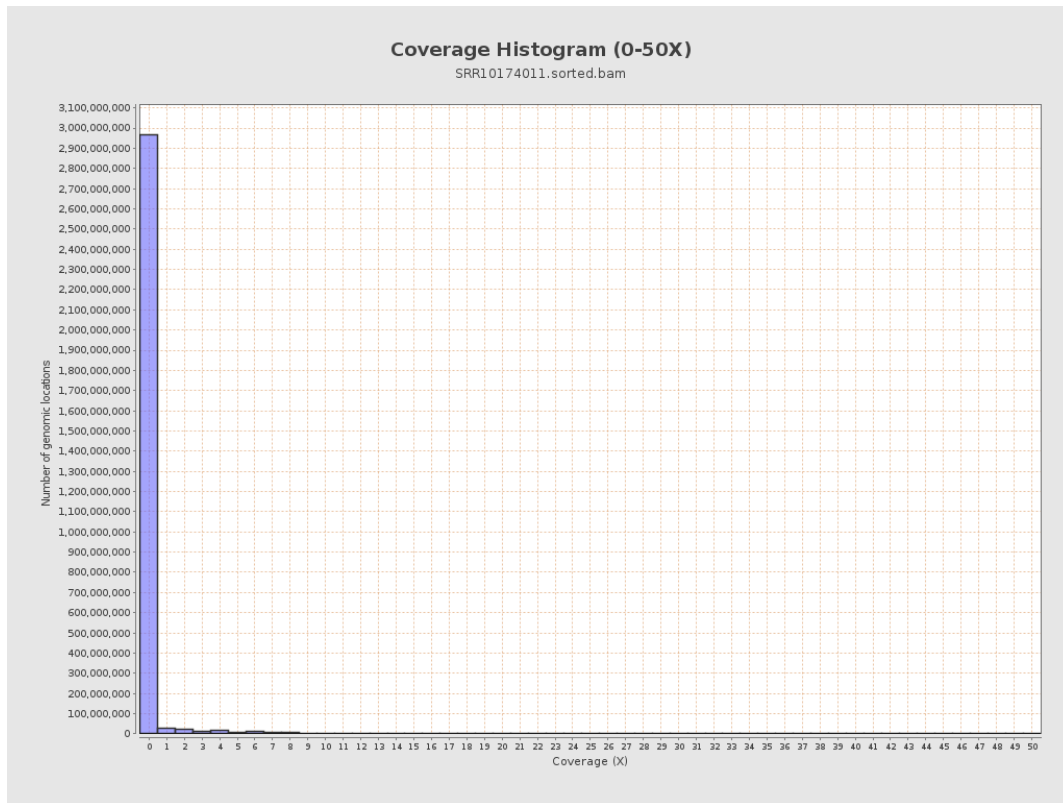
3. Results : Coverage across reference



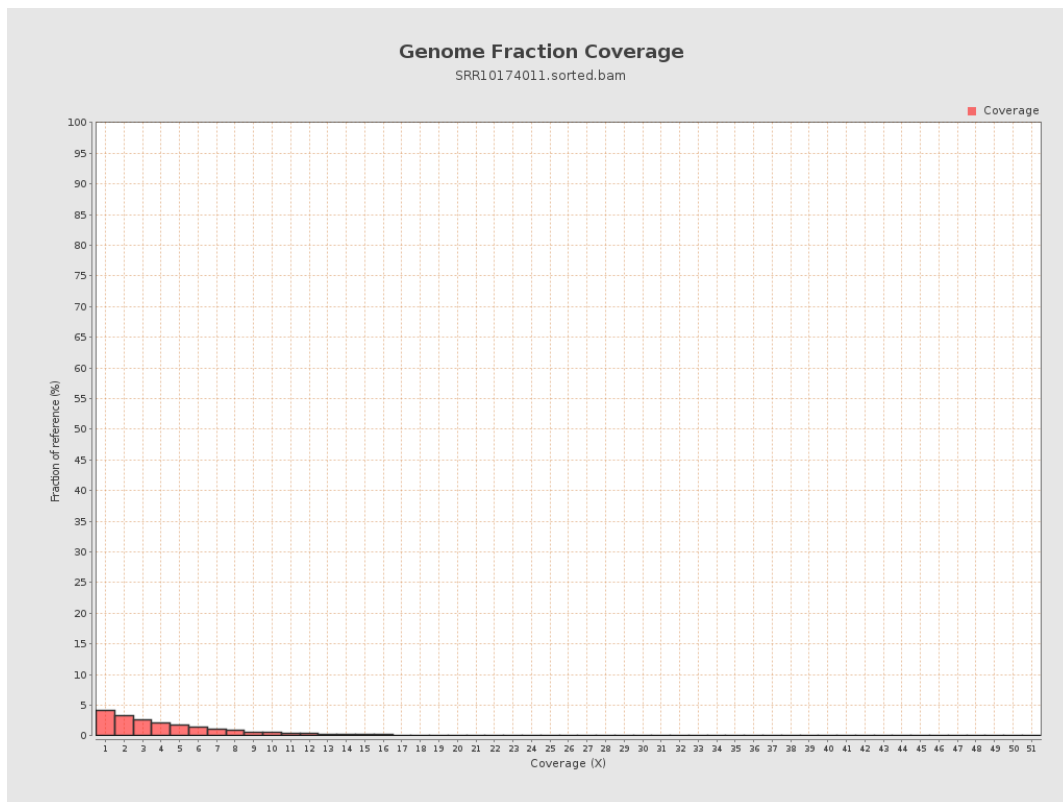
4. Results : Coverage Histogram



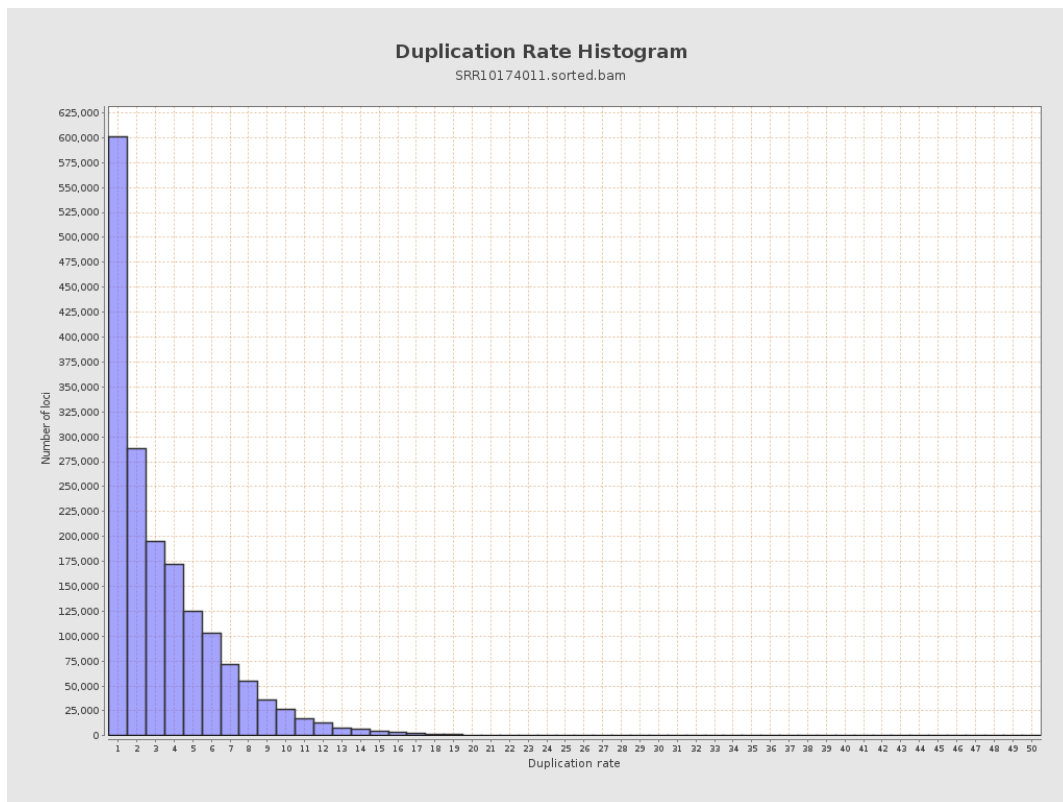
5. Results : Coverage Histogram (0-50X)



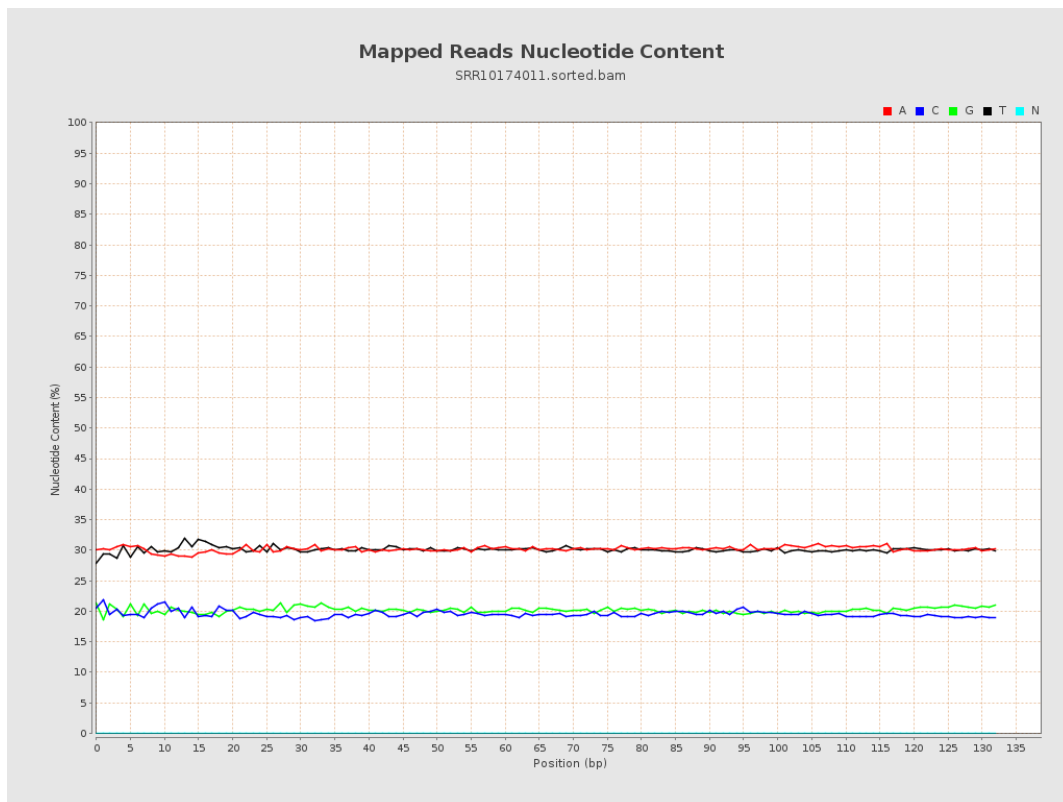
6. Results : Genome Fraction Coverage



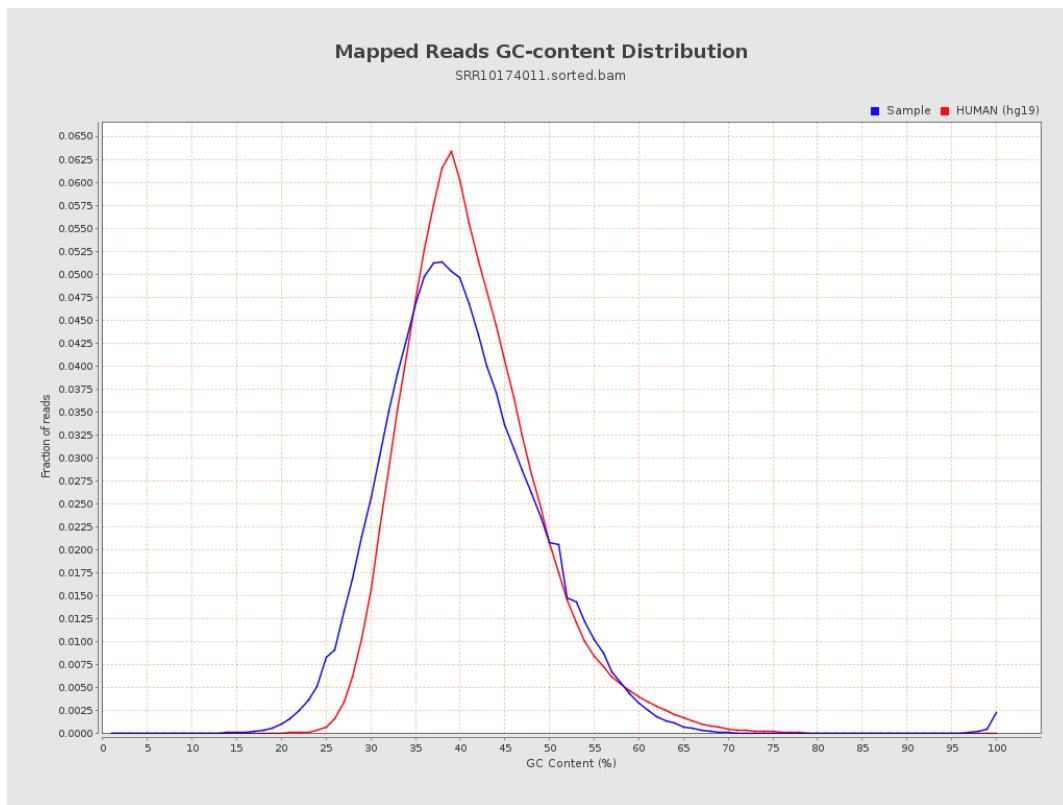
7. Results : Duplication Rate Histogram



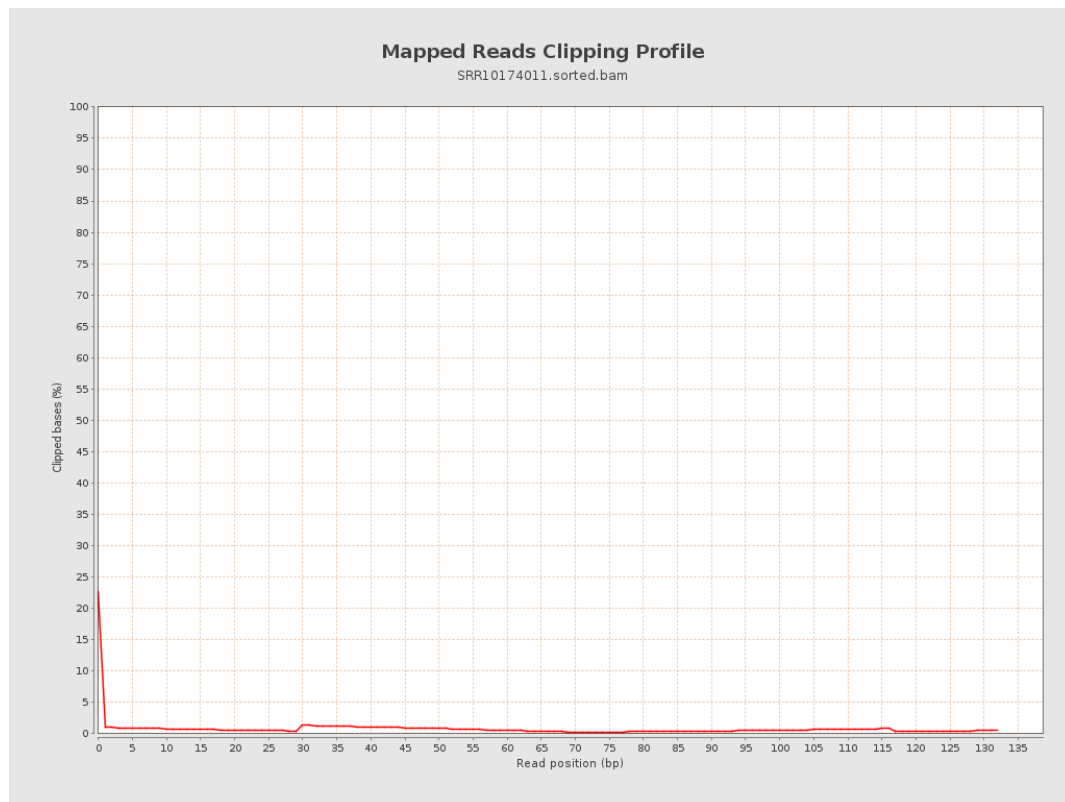
8. Results : Mapped Reads Nucleotide Content



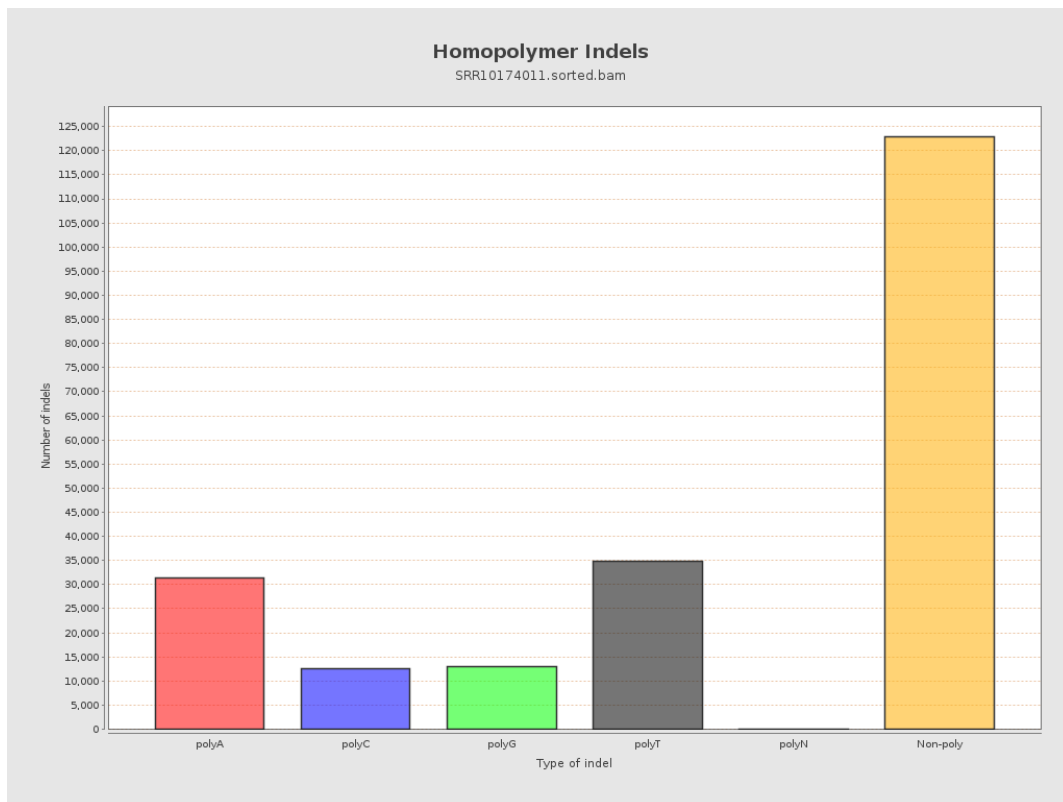
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



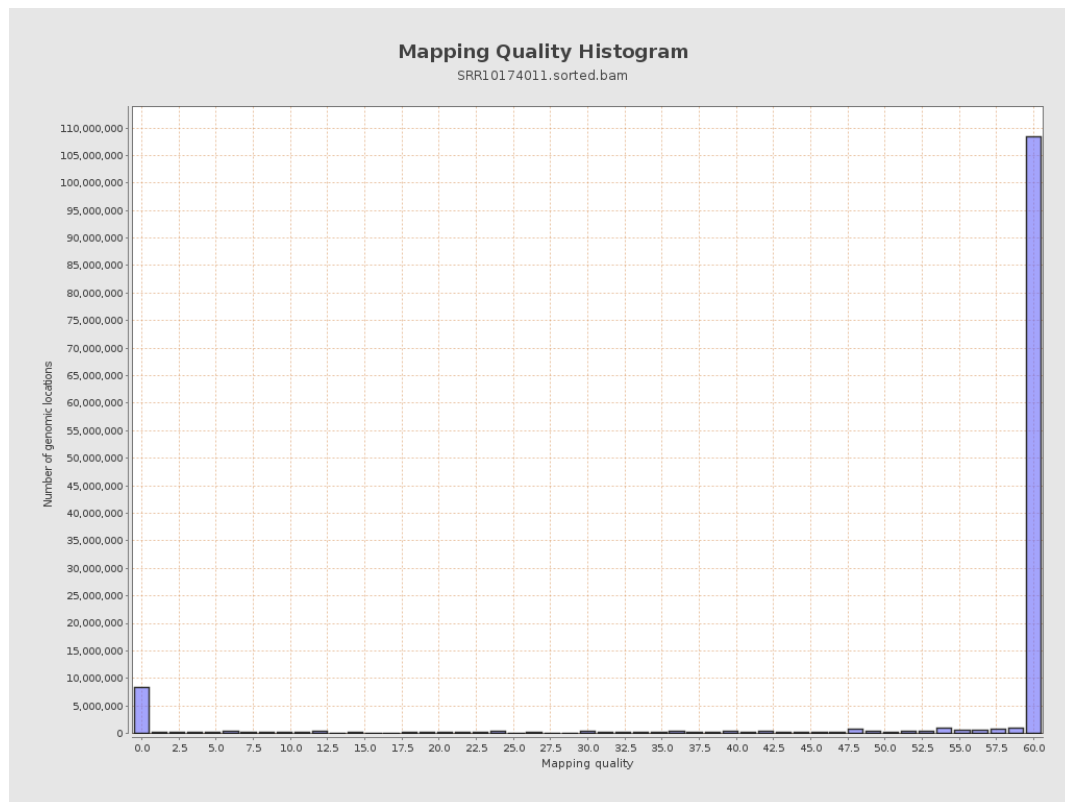
11. Results : Homopolymer Indels



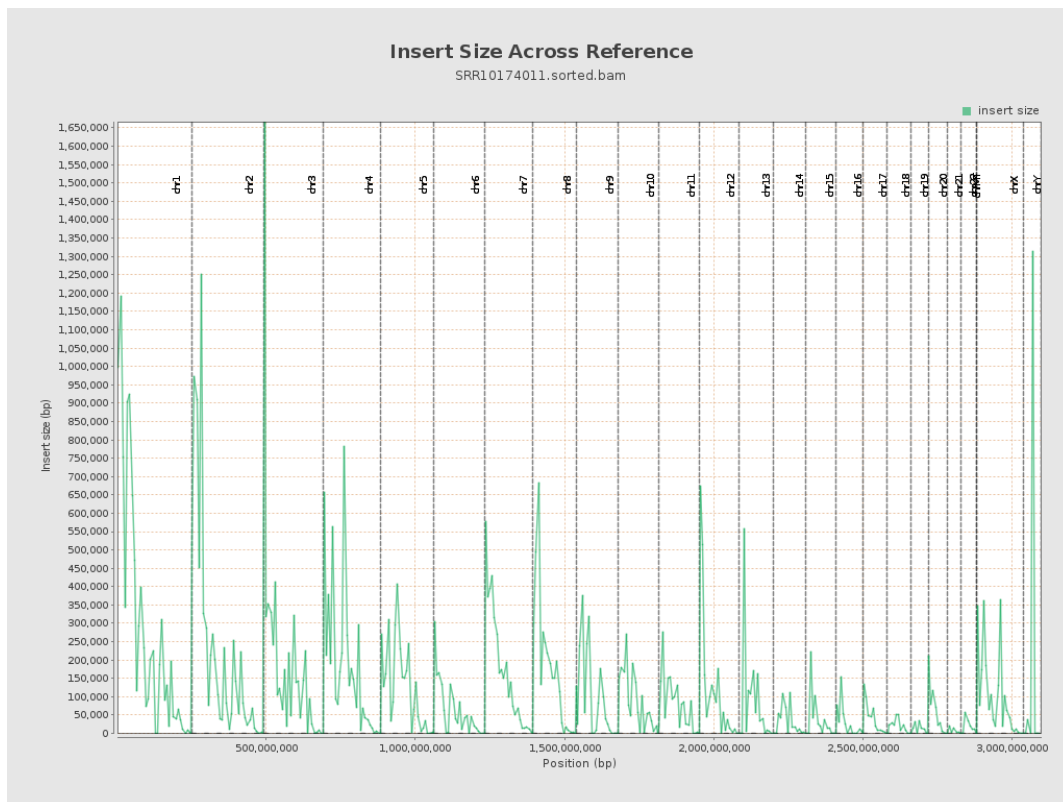
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

