

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 23:42:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174036.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_SRR10174036 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174036_1.fastq.gz SRR10174036_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 23:42:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174036.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,002,952
Mapped reads	3,889,667 / 97.17%
Unmapped reads	113,285 / 2.83%
Mapped paired reads	3,889,667 / 97.17%
Mapped reads, first in pair	1,950,526 / 48.73%
Mapped reads, second in pair	1,939,141 / 48.44%
Mapped reads, both in pair	3,814,116 / 95.28%
Mapped reads, singletons	75,551 / 1.89%
Secondary alignments	0
Supplementary alignments	387,603 / 9.68%
Read min/max/mean length	30 / 133 / 128.12
Duplicated reads (estimated)	3,030,398 / 75.7%
Duplication rate	64.87%
Clipped reads	1,598,820 / 39.94%

2.2. ACGT Content

Number/percentage of A's	137,598,548 / 30.03%
Number/percentage of C's	90,014,834 / 19.64%
Number/percentage of T's	137,403,706 / 29.99%
Number/percentage of G's	93,190,239 / 20.34%
Number/percentage of N's	4,969 / 0%

GC Percentage	39.98%
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2.3. Coverage

Mean	0.1481
Standard Deviation	2.2621

2.4. Mapping Quality

Mean Mapping Quality	52.75
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2.5. Insert size

Mean	885,505.9
Standard Deviation	8,848,622.9
P25/Median/P75	144 / 201 / 287

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	4,770,394
Insertions	49,146
Mapped reads with at least one insertion	1.22%
Deletions	106,807
Mapped reads with at least one deletion	2.67%
Homopolymer indels	42.29%

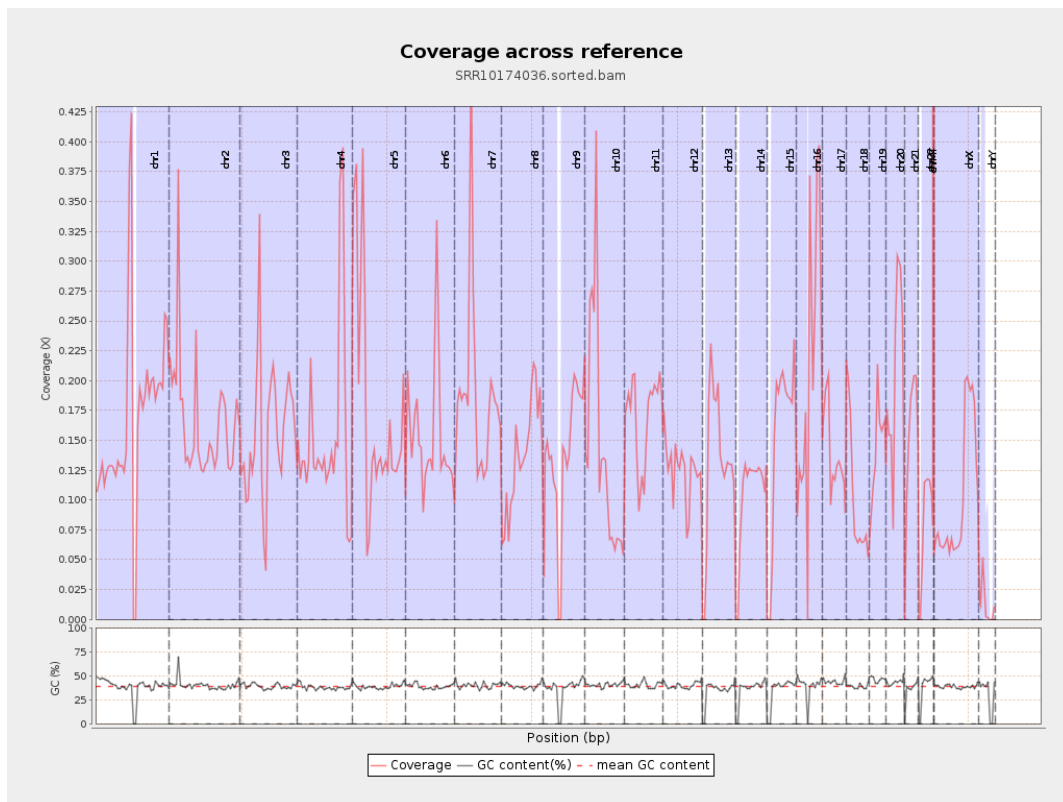
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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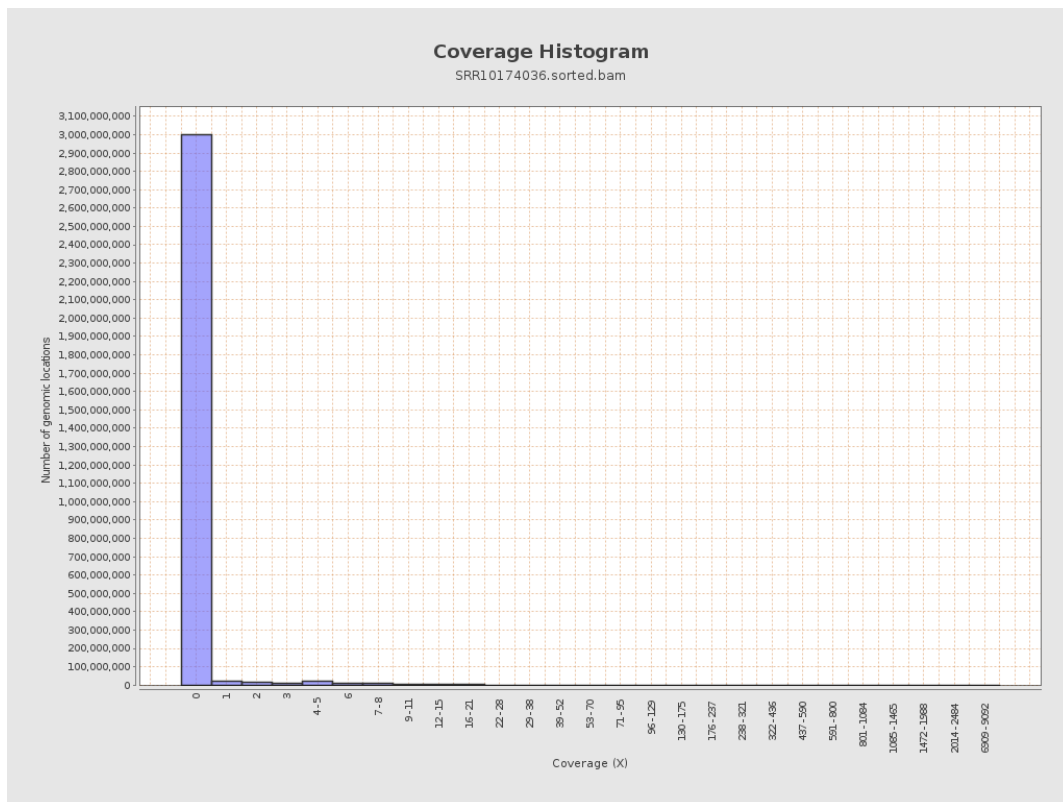
		bases	coverage	deviation
chr1	249250621	41768208	0.1676	1.8714
chr2	243199373	40357330	0.1659	6.3981
chr3	198022430	31056601	0.1568	1.1569
chr4	191154276	28608723	0.1497	1.4009
chr5	180915260	32022711	0.177	1.2272
chr6	171115067	26654555	0.1558	1.1969
chr7	159138663	29804758	0.1873	2.0694
chr8	146364022	20281383	0.1386	1.2392
chr9	141213431	19485685	0.138	1.2858
chr10	135534747	19298280	0.1424	2.4099
chr11	135006516	22794924	0.1688	1.2114
chr12	133851895	16663813	0.1245	1.0306
chr13	115169878	15054185	0.1307	1.0588
chr14	107349540	11016565	0.1026	0.9309
chr15	102531392	15715121	0.1533	1.1213
chr16	90354753	18968301	0.2099	1.8054
chr17	81195210	11109249	0.1368	1.1557
chr18	78077248	7915359	0.1014	1.7007
chr19	59128983	8464076	0.1431	1.7692
chr20	63025520	12906173	0.2048	1.3103
chr21	48129895	7275565	0.1512	1.1916
chr22	51304566	4049004	0.0789	0.769
chrMT	16571	768052	46.3492	37.7352
chrX	155270560	15762512	0.1015	0.9318

chrY	59373566	678793	0.0114	0.557
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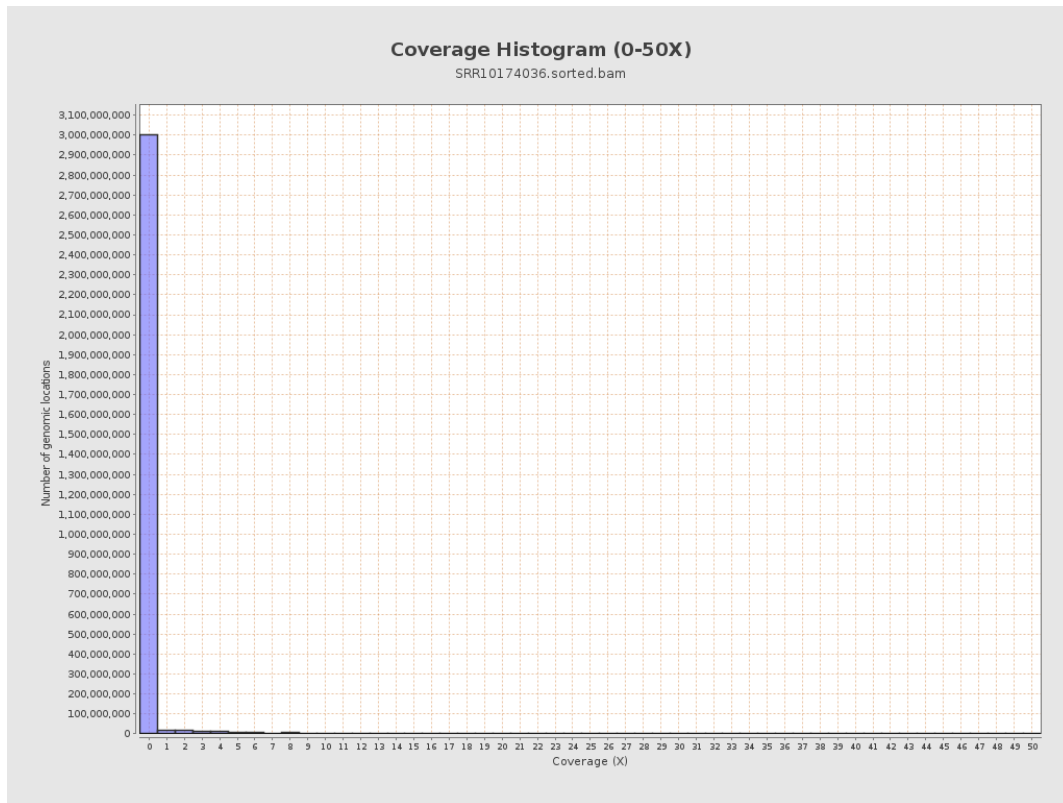
3. Results : Coverage across reference



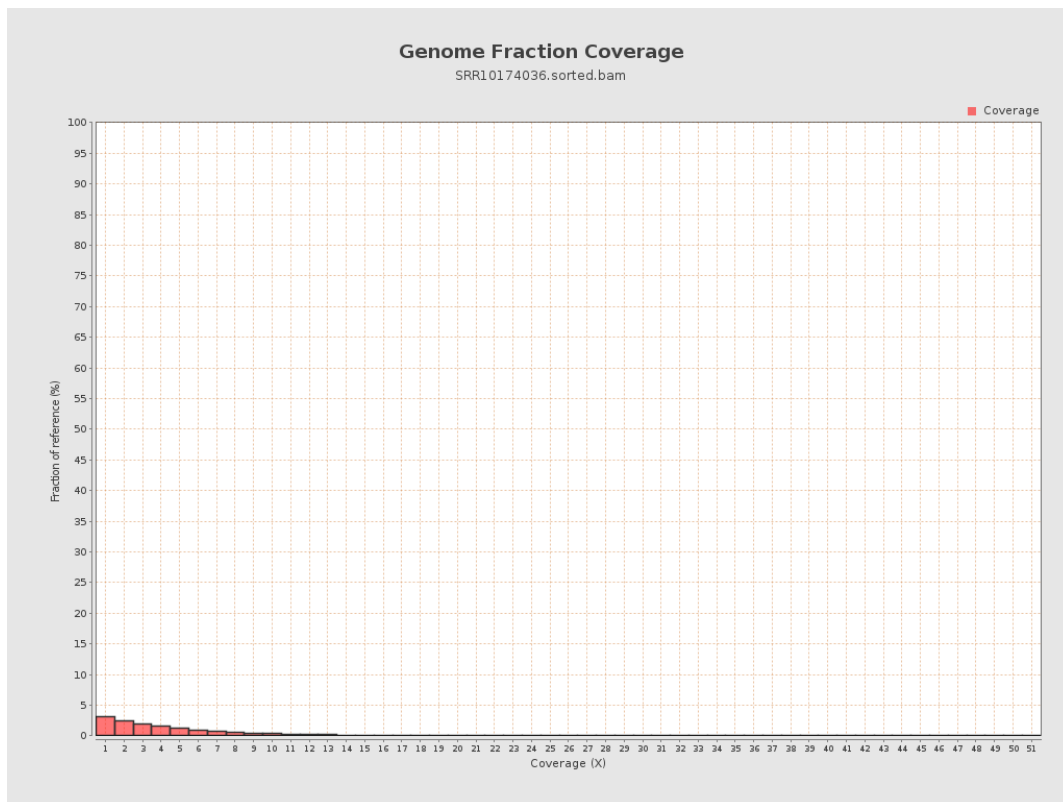
4. Results : Coverage Histogram



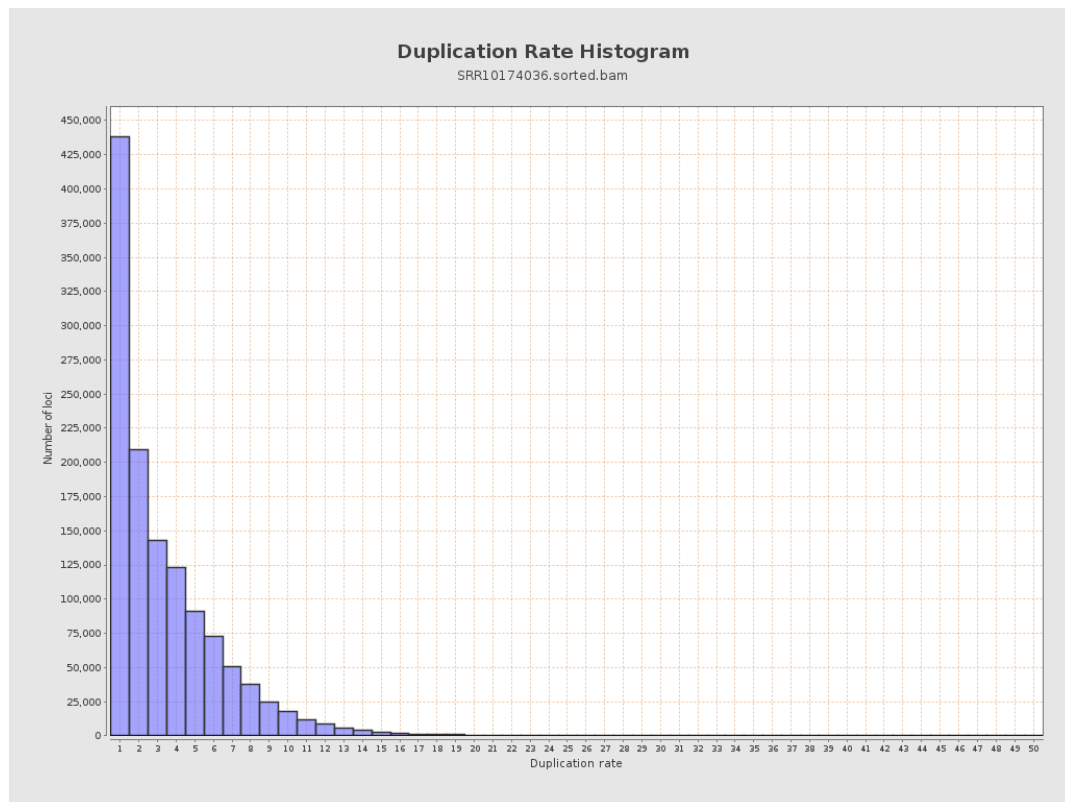
5. Results : Coverage Histogram (0-50X)



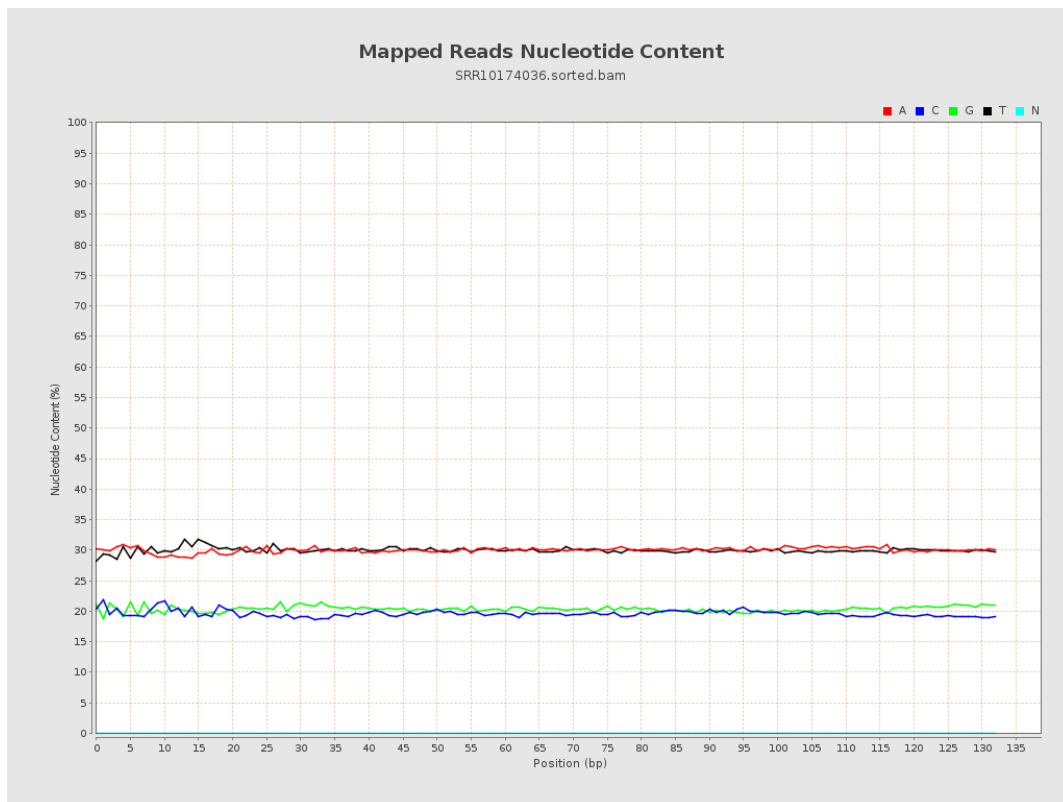
6. Results : Genome Fraction Coverage



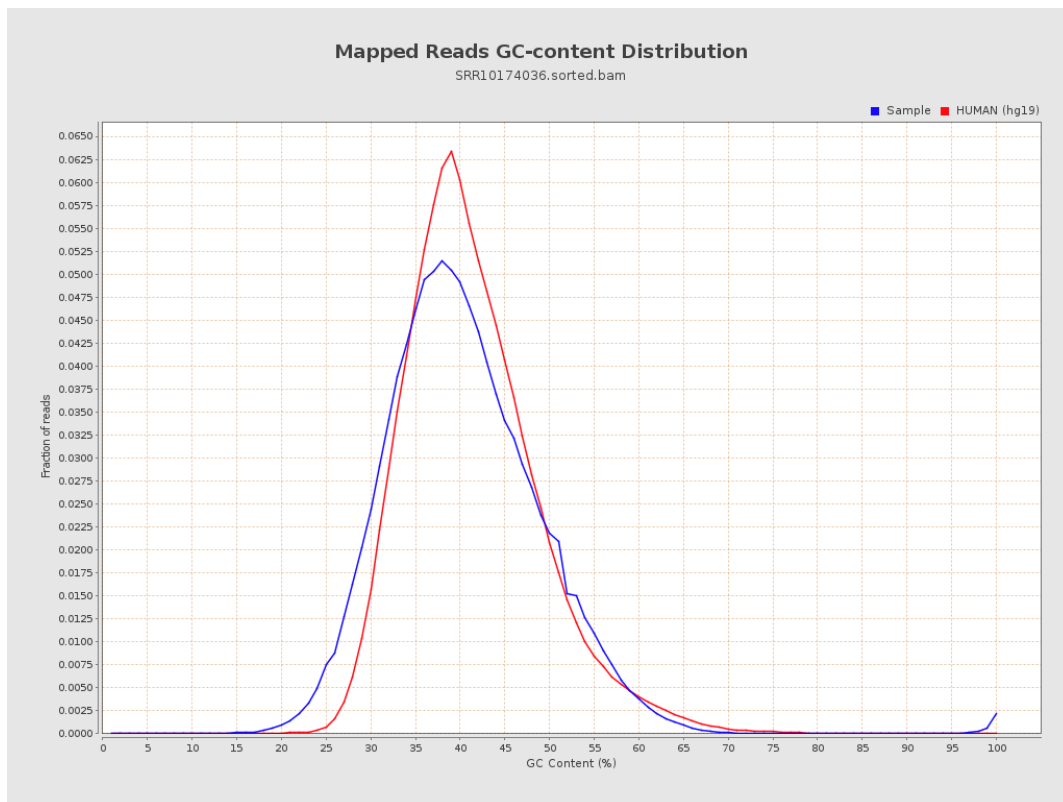
7. Results : Duplication Rate Histogram



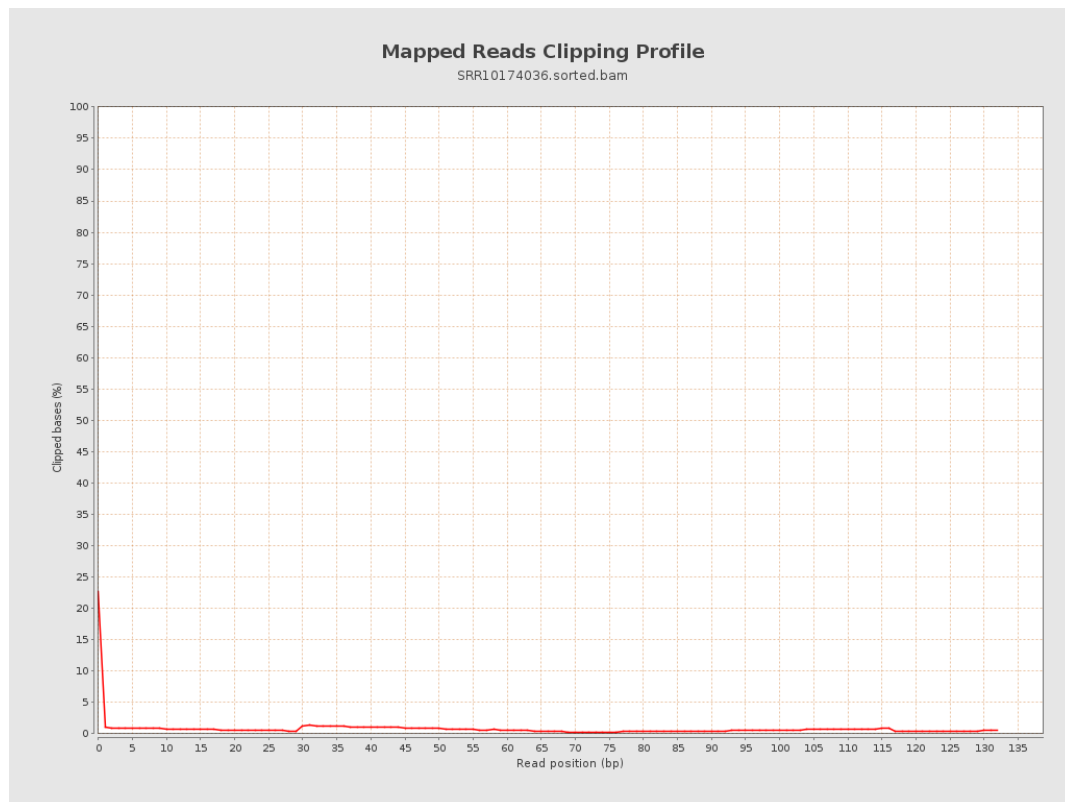
8. Results : Mapped Reads Nucleotide Content



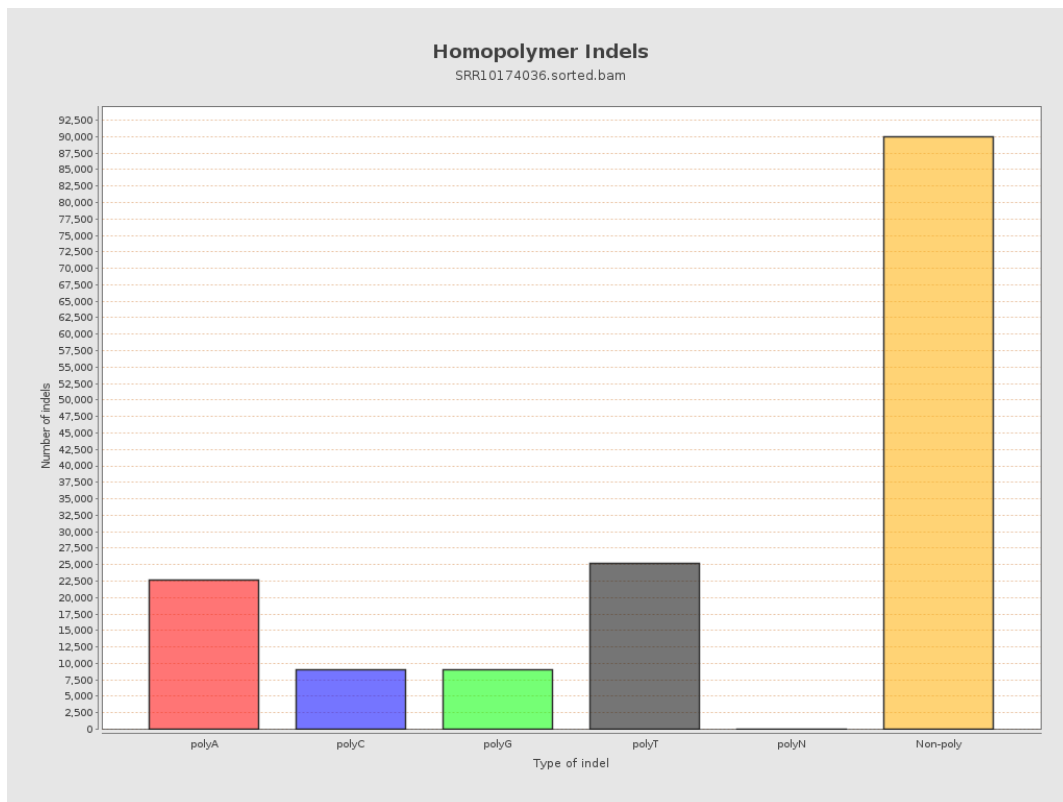
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



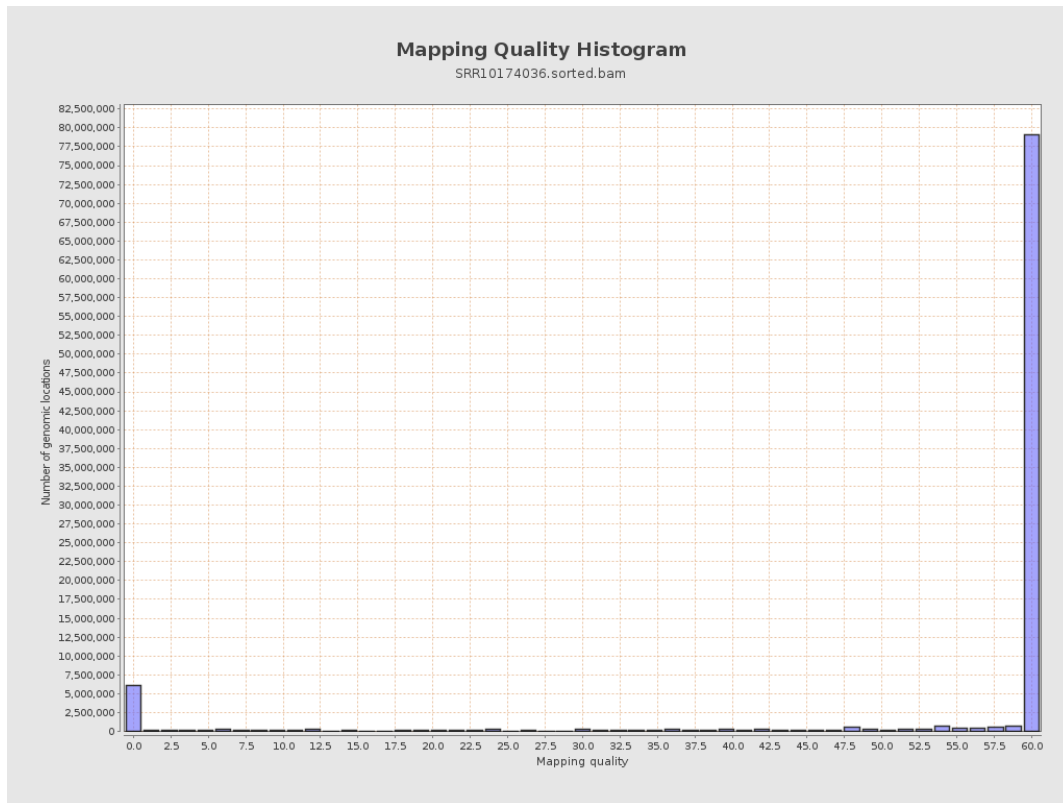
11. Results : Homopolymer Indels



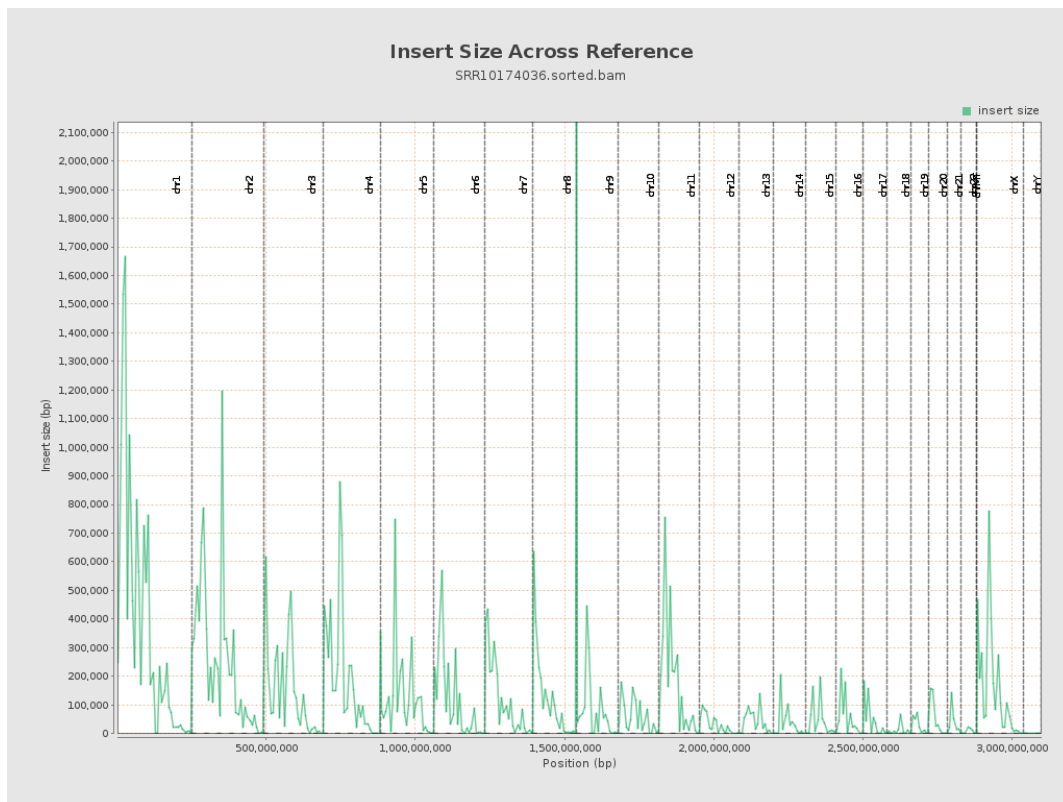
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

