

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/30 23:43:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16352026.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_SRR16352026 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16352026_1.fastq.gz SRR16352026_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Jan 30 23:43:36 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16352026.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	706,023,892
Mapped reads	684,502,335 / 96.95%
Unmapped reads	21,521,557 / 3.05%
Mapped paired reads	684,502,335 / 96.95%
Mapped reads, first in pair	343,700,333 / 48.68%
Mapped reads, second in pair	340,802,002 / 48.27%
Mapped reads, both in pair	679,959,958 / 96.31%
Mapped reads, singletons	4,542,377 / 0.64%
Secondary alignments	0
Supplementary alignments	30,251,242 / 4.28%
Read min/max/mean length	30 / 150 / 152.11
Duplicated reads (estimated)	232,389,336 / 32.92%
Duplication rate	28.5%
Clipped reads	446,783,673 / 63.28%

2.2. ACGT Content

Number/percentage of A's	27,499,606,608 / 28.95%
Number/percentage of C's	19,856,006,598 / 20.91%
Number/percentage of T's	27,433,733,409 / 28.88%
Number/percentage of G's	20,180,026,396 / 21.25%
Number/percentage of N's	8,182,231 / 0.01%

GC Percentage	42.15%
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2.3. Coverage

Mean	30.7106
Standard Deviation	333.7994

2.4. Mapping Quality

Mean Mapping Quality	53.83
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2.5. Insert size

Mean	84,361.93
Standard Deviation	2,815,289.33
P25/Median/P75	201 / 270 / 387

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	851,622,364
Insertions	17,515,758
Mapped reads with at least one insertion	2.42%
Deletions	56,031,578
Mapped reads with at least one deletion	7.81%
Homopolymer indels	45.37%

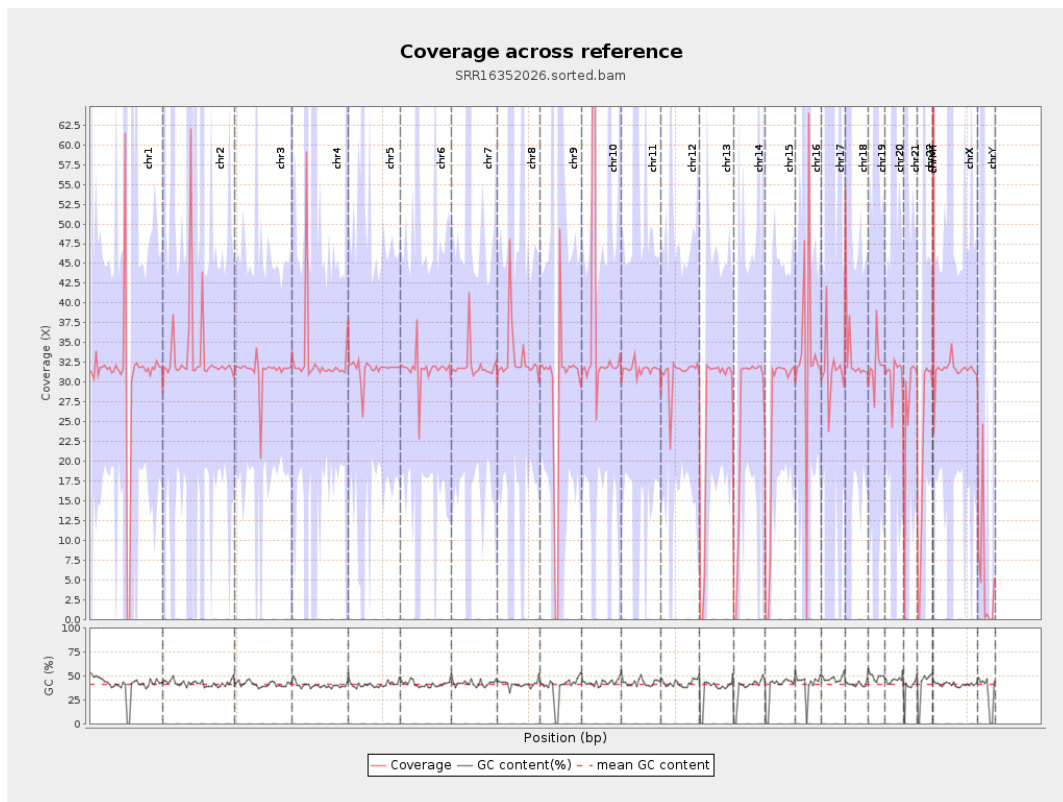
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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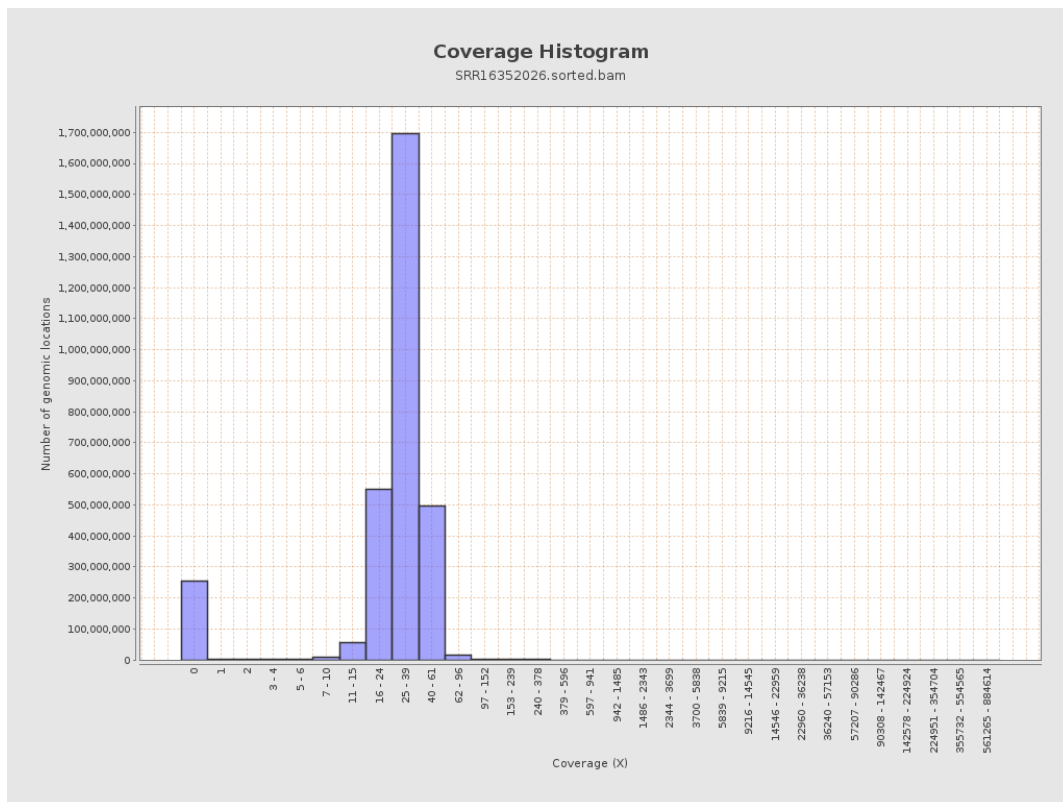
		bases	coverage	deviation
chr1	249250621	7636506490	30.6379	690.5723
chr2	243199373	8134429490	33.4476	284.8032
chr3	198022430	6213664871	31.3786	29.9423
chr4	191154276	6289957362	32.9051	251.3513
chr5	180915260	5717339955	31.6023	26.3444
chr6	171115067	5405397723	31.5893	81.6763
chr7	159138663	5108165967	32.0988	220.9141
chr8	146364022	4837773957	33.053	703.1415
chr9	141213431	4110435638	29.108	358.2115
chr10	135534747	4894787738	36.1146	661.2784
chr11	135006516	4266512641	31.6023	128.3327
chr12	133851895	4165154478	31.1176	20.0838
chr13	115169878	3034283838	26.3462	18.6516
chr14	107349540	2822605327	26.2936	26.605
chr15	102531392	2589770919	25.2583	18.0371
chr16	90354753	3024980061	33.4789	243.5197
chr17	81195210	2575591046	31.721	147.4441
chr18	78077248	2596524178	33.2558	345.0677
chr19	59128983	1901938392	32.1659	380.534
chr20	63025520	1940226516	30.7848	69.8405
chr21	48129895	1315251854	27.3271	108.7344
chr22	51304566	1118967072	21.8103	30.1259
chrMT	16571	168425294	10,163.8582	1,252.3697
chrX	155270560	4885829742	31.4666	71.1997

chrY	59373566	316230100	5.3261	271.988
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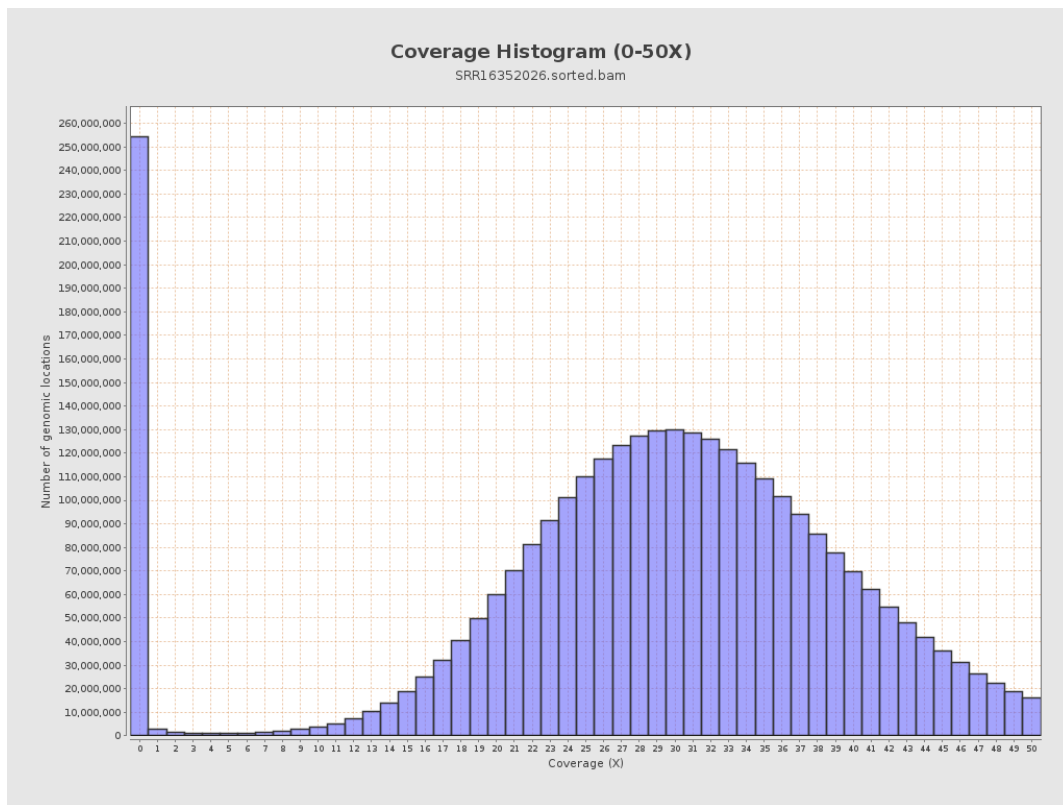
3. Results : Coverage across reference



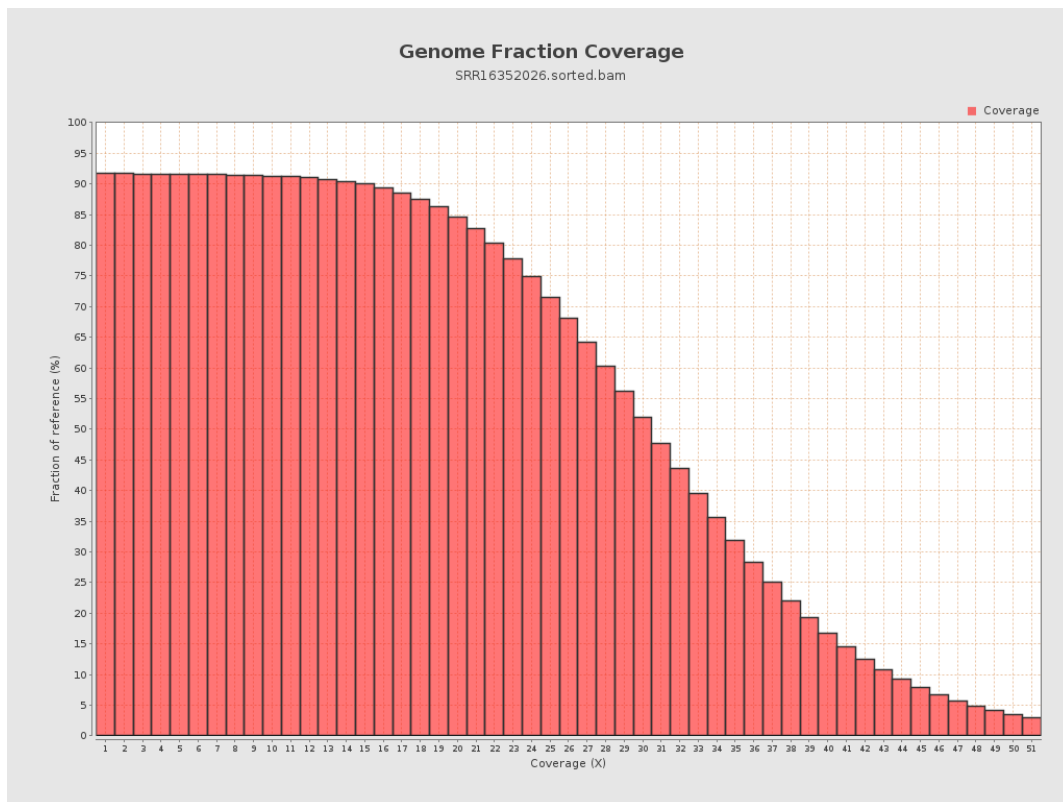
4. Results : Coverage Histogram



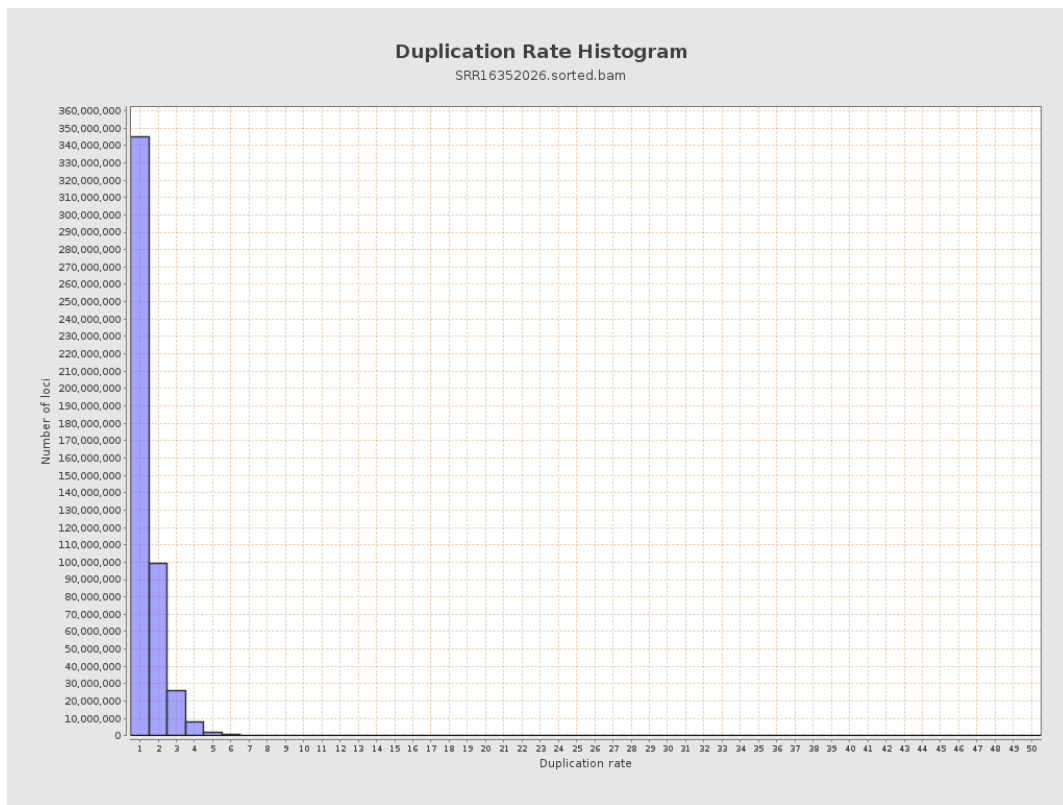
5. Results : Coverage Histogram (0-50X)



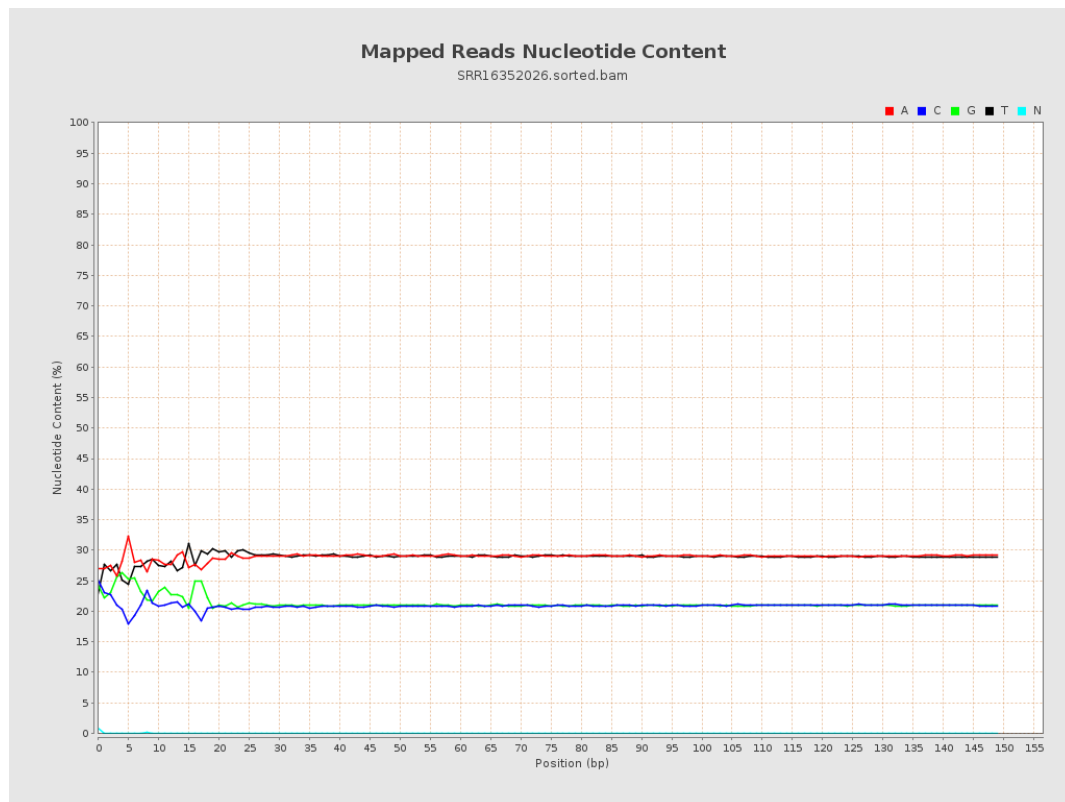
6. Results : Genome Fraction Coverage



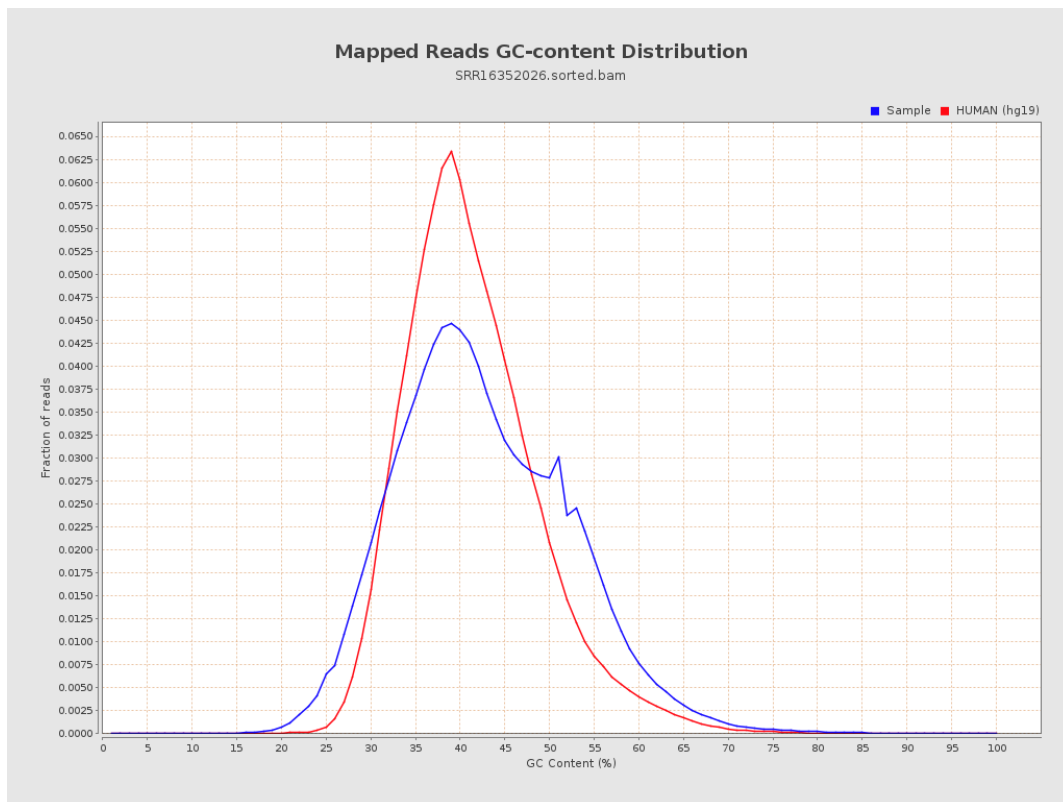
7. Results : Duplication Rate Histogram



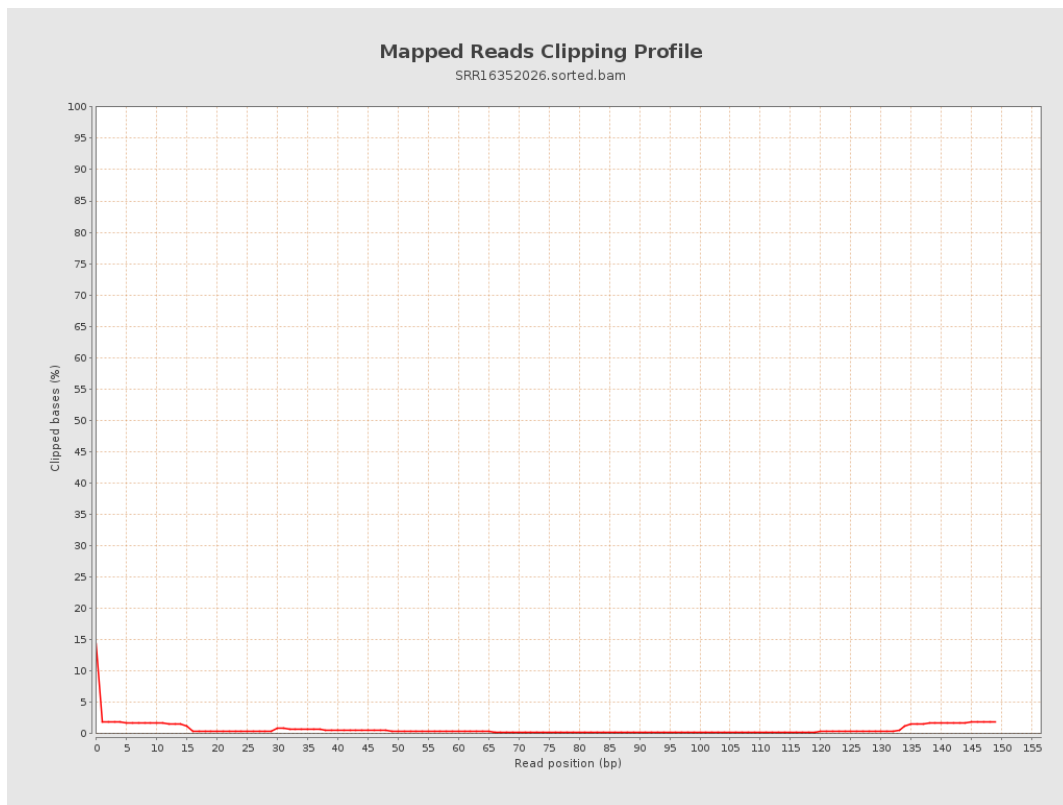
8. Results : Mapped Reads Nucleotide Content



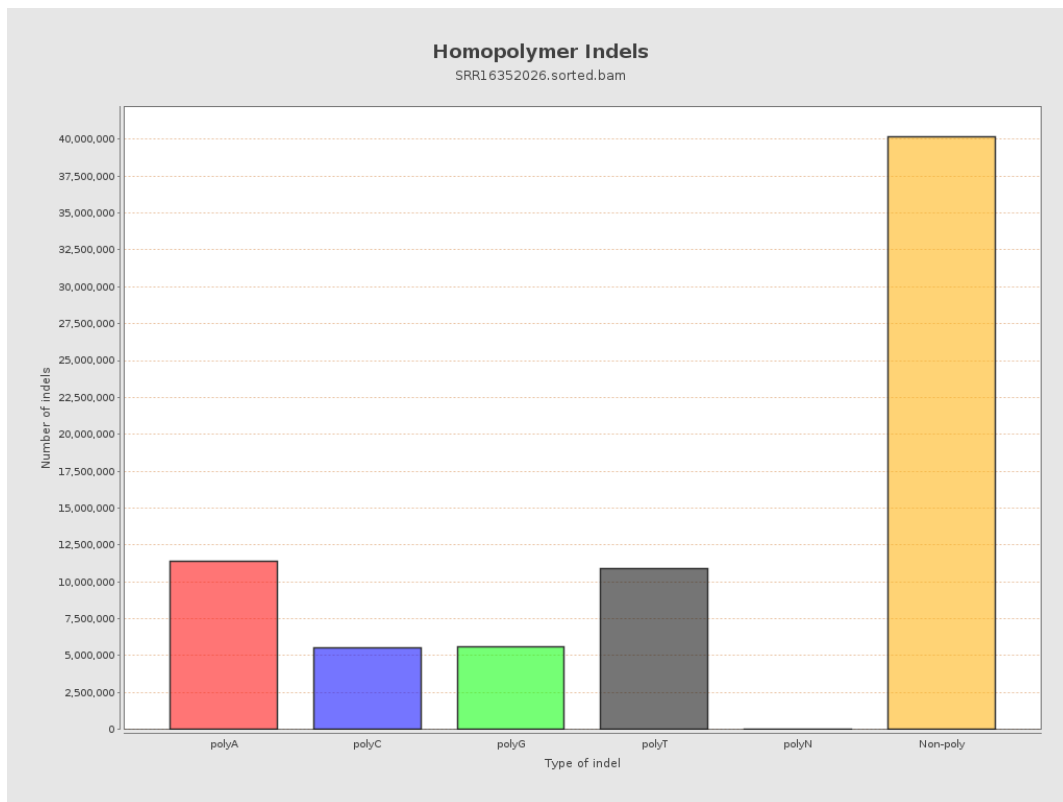
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



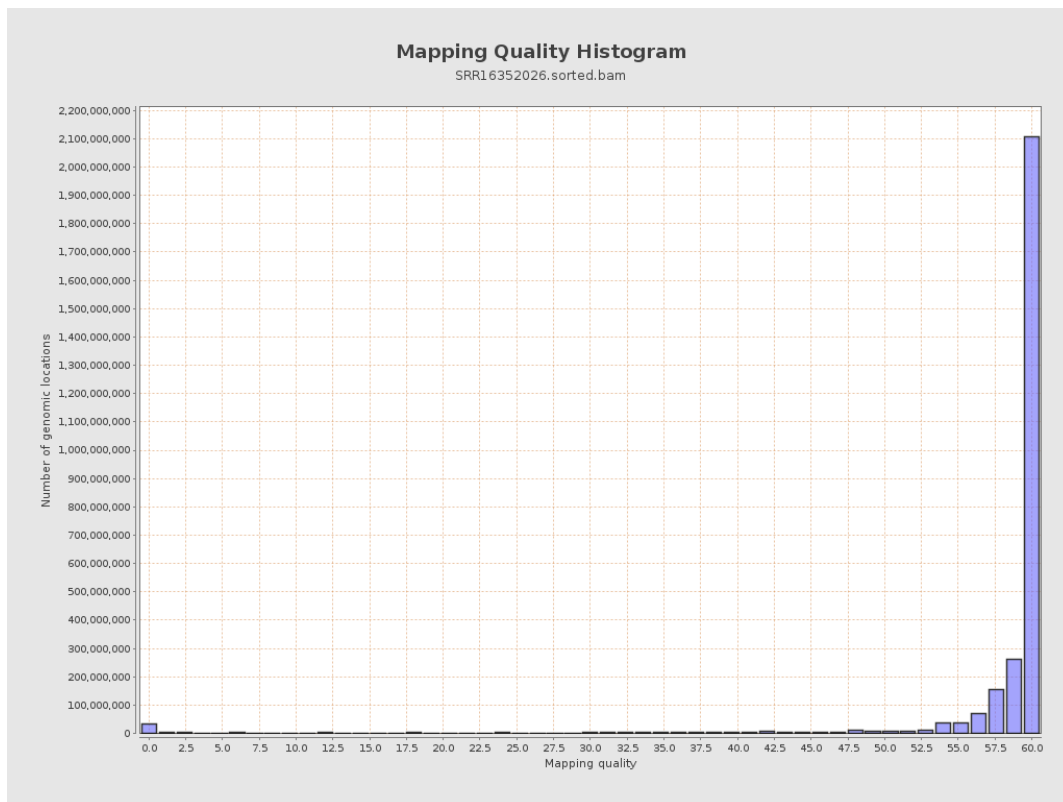
11. Results : Homopolymer Indels



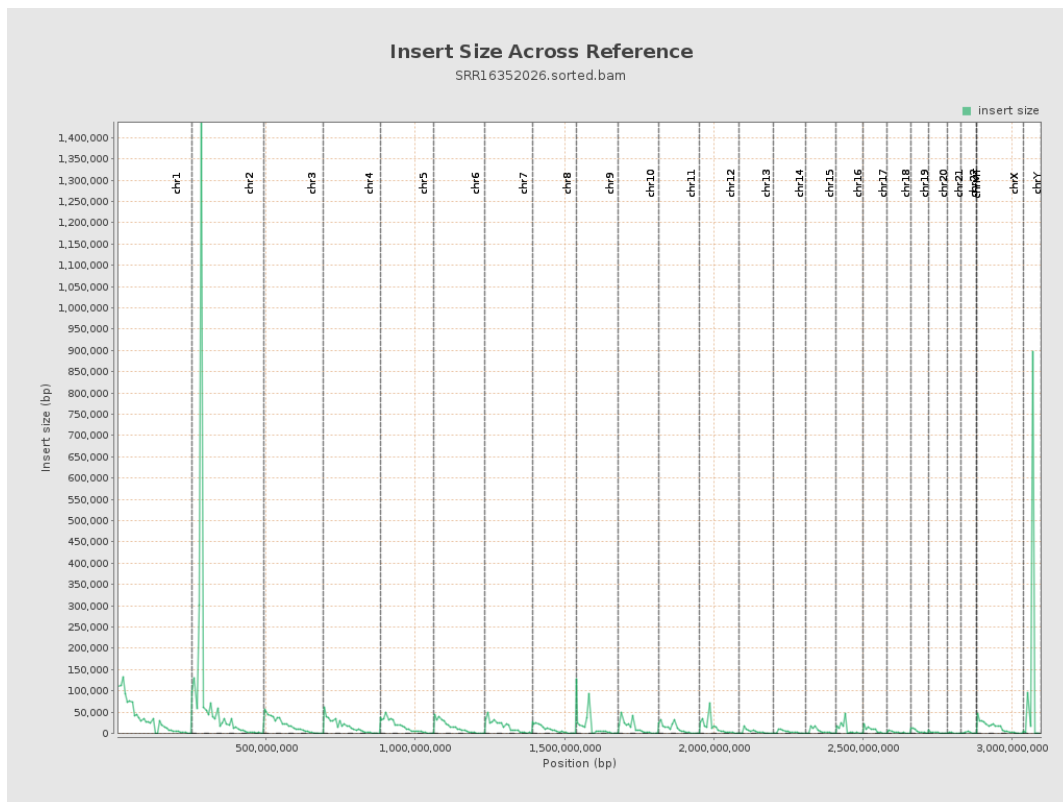
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

