

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/06 10:38:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR26104295.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_SRR26104295 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR26104295_1.fastq.gz SRR26104295_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 06 10:38:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR26104295.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	640,573,026
Mapped reads	598,815,986 / 93.48%
Unmapped reads	41,757,040 / 6.52%
Mapped paired reads	598,815,986 / 93.48%
Mapped reads, first in pair	309,780,312 / 48.36%
Mapped reads, second in pair	289,035,674 / 45.12%
Mapped reads, both in pair	577,253,112 / 90.12%
Mapped reads, singletons	21,562,874 / 3.37%
Secondary alignments	0
Supplementary alignments	304,734 / 0.05%
Read min/max/mean length	30 / 97 / 91.02
Duplicated reads (estimated)	392,759,896 / 61.31%
Duplication rate	51.6%
Clipped reads	552,925,797 / 86.32%

2.2. ACGT Content

Number/percentage of A's	9,219,411,007 / 26.83%
Number/percentage of C's	8,114,553,064 / 23.62%
Number/percentage of T's	9,850,024,547 / 28.67%
Number/percentage of G's	7,169,036,365 / 20.86%
Number/percentage of N's	7,918,736 / 0.02%

GC Percentage	44.48%
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2.3. Coverage

Mean	11.1009
Standard Deviation	119.632

2.4. Mapping Quality

Mean Mapping Quality	50.41
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2.5. Insert size

Mean	14,660.25
Standard Deviation	1,103,662.94
P25/Median/P75	44 / 54 / 65

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	139,495,456
Insertions	1,811,001
Mapped reads with at least one insertion	0.3%
Deletions	2,036,046
Mapped reads with at least one deletion	0.34%
Homopolymer indels	36%

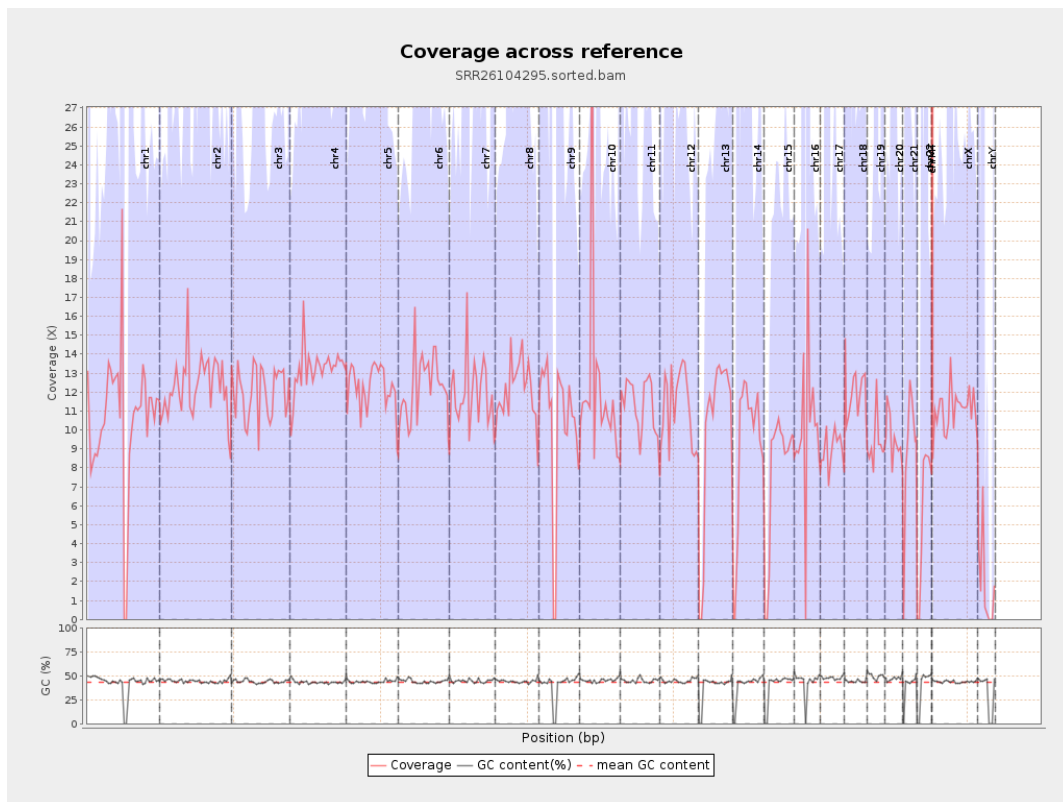
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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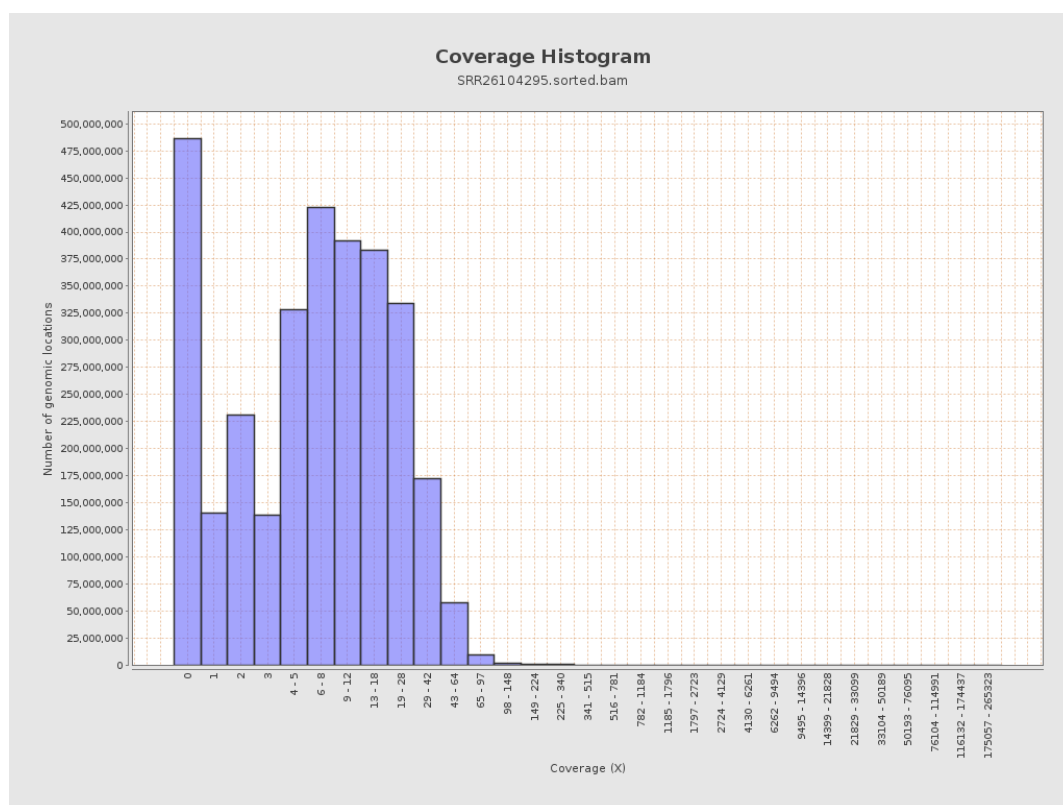
		bases	coverage	deviation
chr1	249250621	2659056363	10.6682	246.963
chr2	243199373	2991017091	12.2986	60.2509
chr3	198022430	2364082891	11.9385	31.1843
chr4	191154276	2521864353	13.1928	36.8771
chr5	180915260	2204734361	12.1866	30.3139
chr6	171115067	2118366983	12.3798	40.6329
chr7	159138663	1891499091	11.8859	96.8399
chr8	146364022	1778880222	12.1538	72.7817
chr9	141213431	1438100249	10.1839	51.2138
chr10	135534747	1652287030	12.1909	175.0236
chr11	135006516	1526369024	11.3059	48.6573
chr12	133851895	1498397033	11.1944	22.0222
chr13	115169878	1170218879	10.1608	21.9285
chr14	107349540	983902191	9.1654	23.8535
chr15	102531392	789080653	7.696	12.4988
chr16	90354753	923678565	10.2228	76.5399
chr17	81195210	727343868	8.958	29.2127
chr18	78077248	929966196	11.9108	99.3371
chr19	59128983	549682680	9.2963	166.8803
chr20	63025520	599456228	9.5113	19.3695
chr21	48129895	442781853	9.1997	37.0012
chr22	51304566	303207468	5.91	87.7928
chrMT	16571	476966194	28,783.1871	12,198.6066
chrX	155270560	1717131469	11.059	28.7547

chrY	59373566	107018142	1.8025	56.2835
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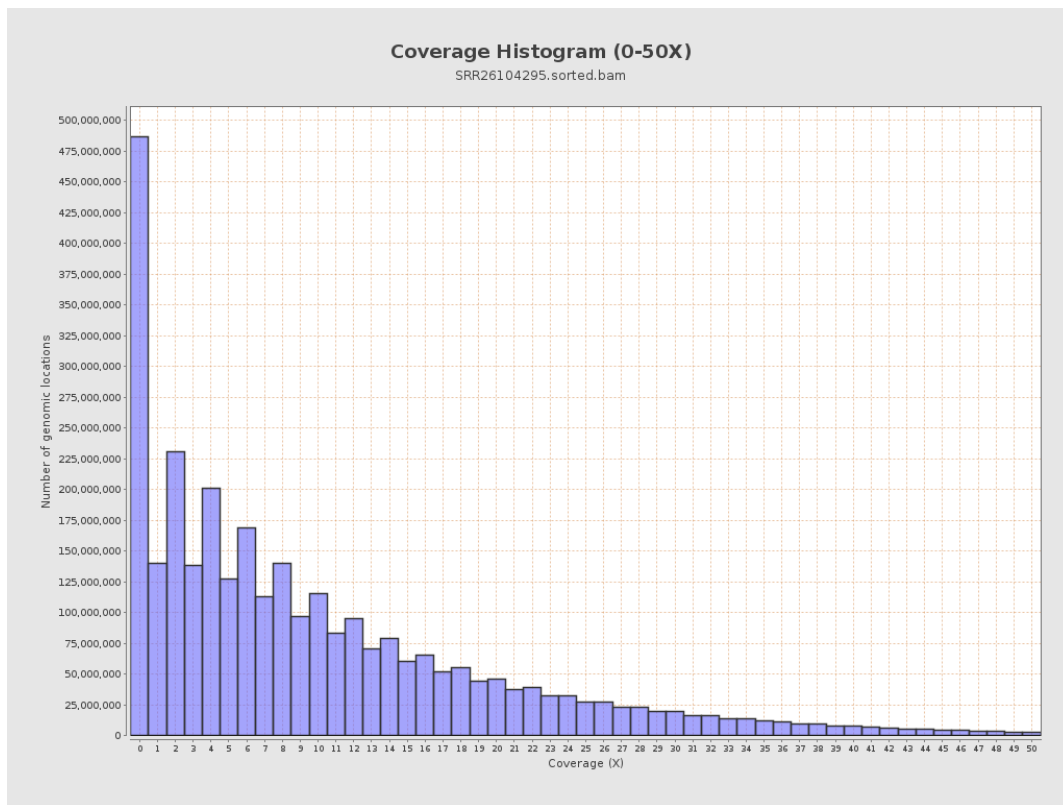
3. Results : Coverage across reference



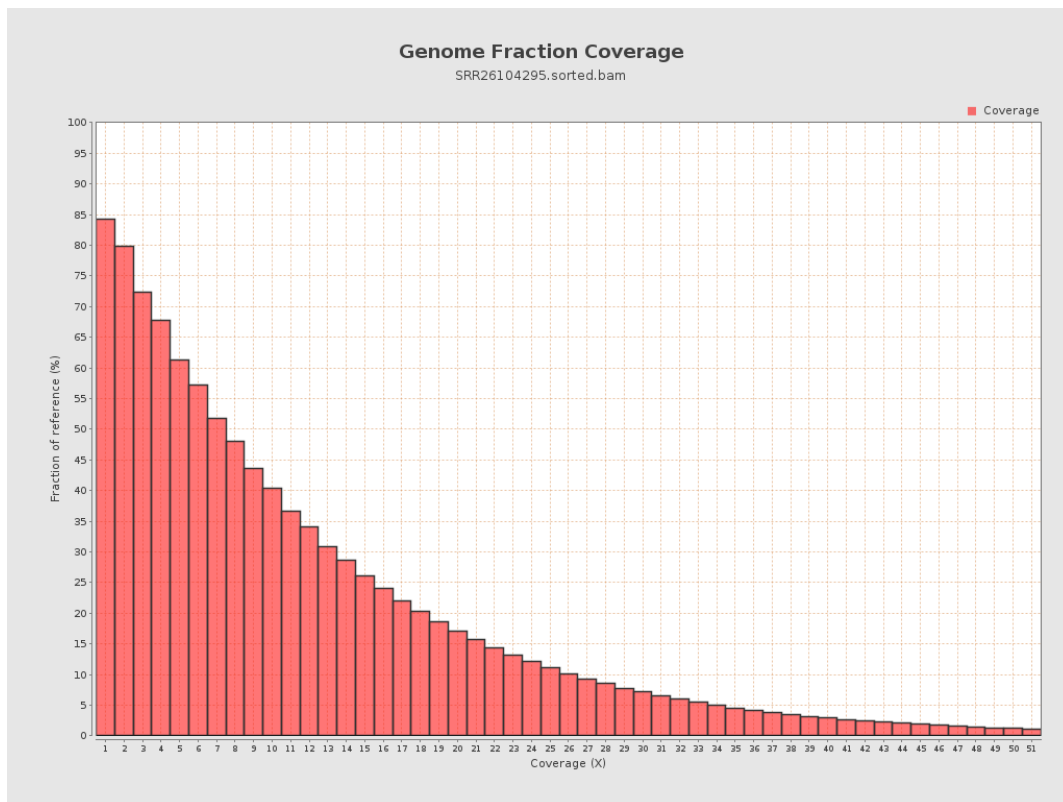
4. Results : Coverage Histogram



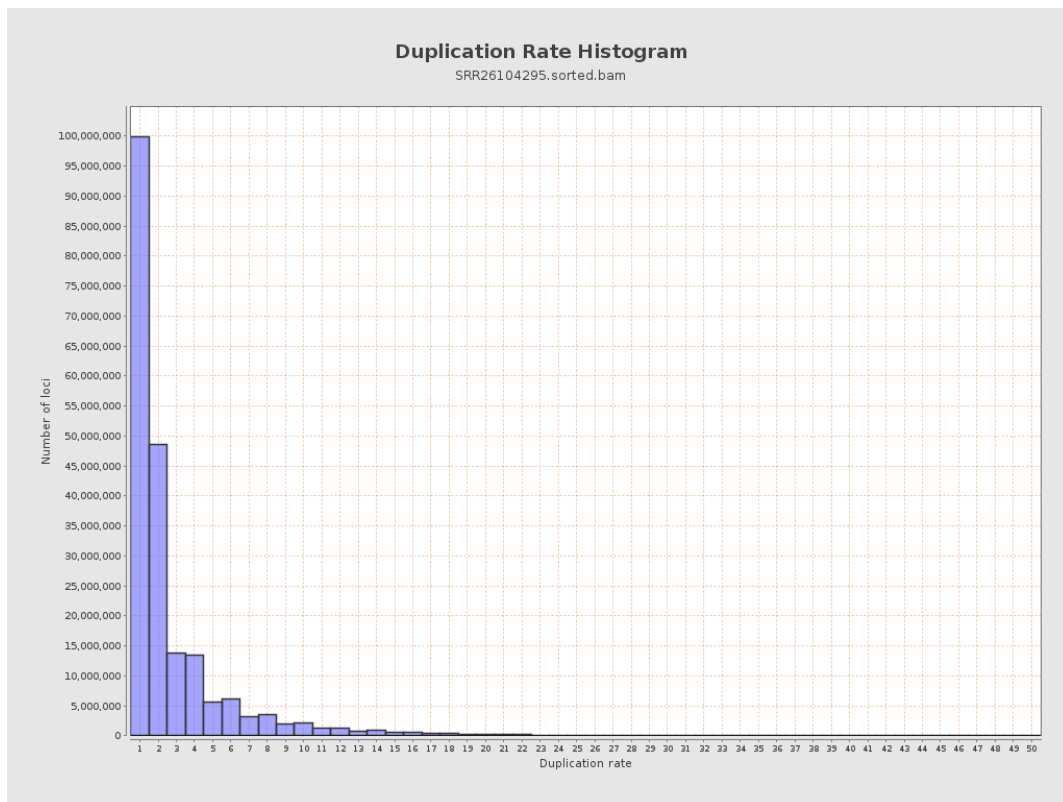
5. Results : Coverage Histogram (0-50X)



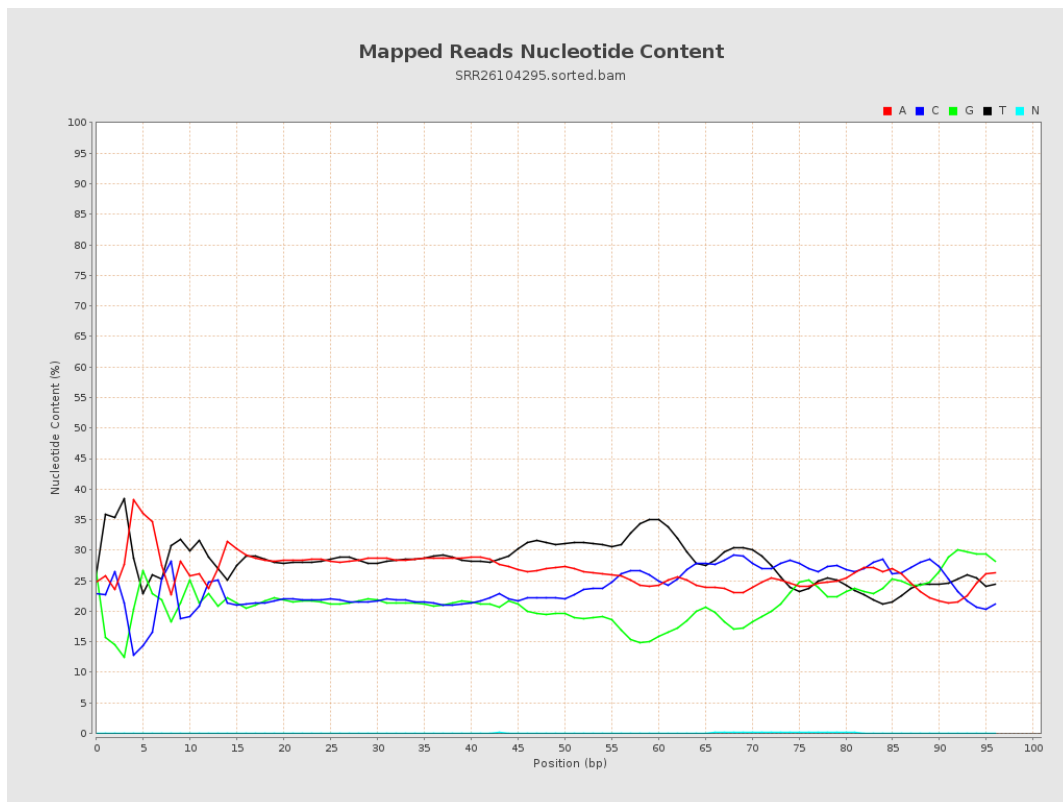
6. Results : Genome Fraction Coverage



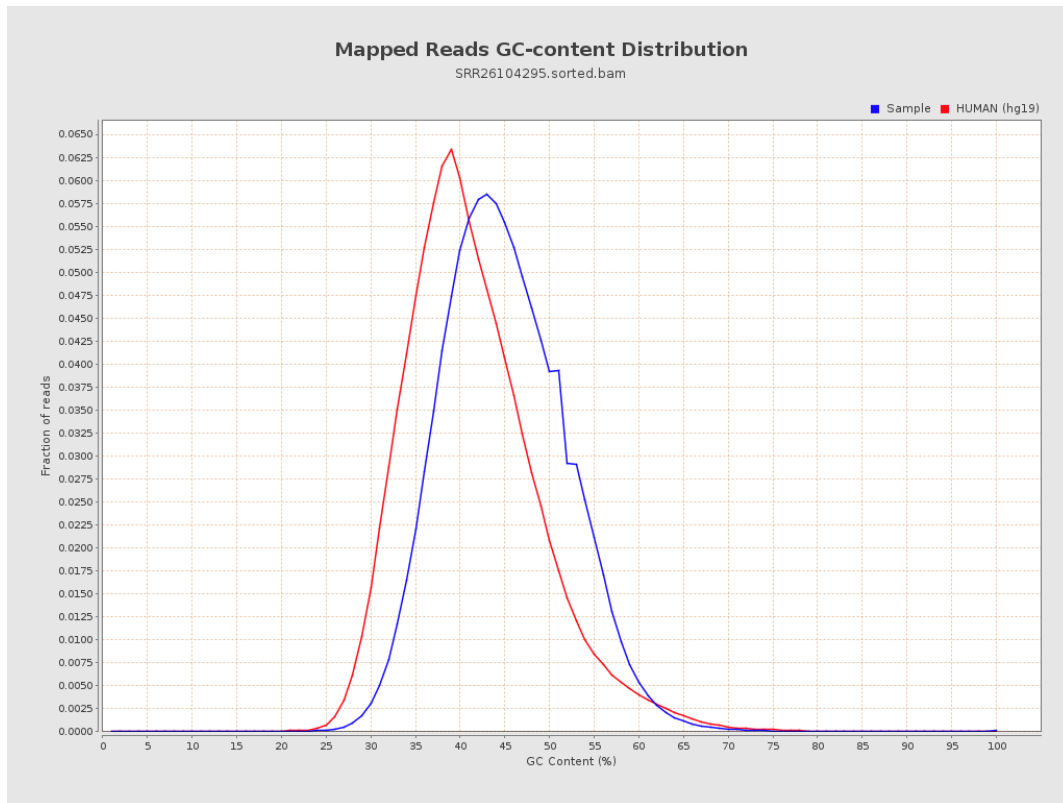
7. Results : Duplication Rate Histogram



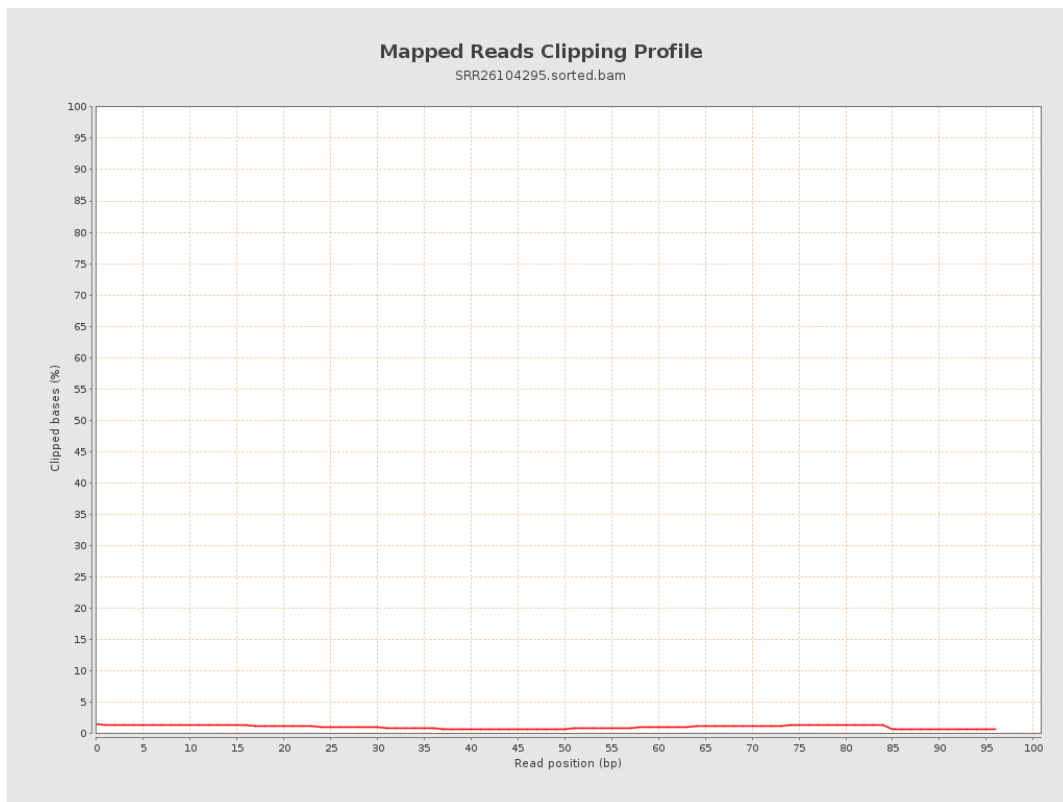
8. Results : Mapped Reads Nucleotide Content



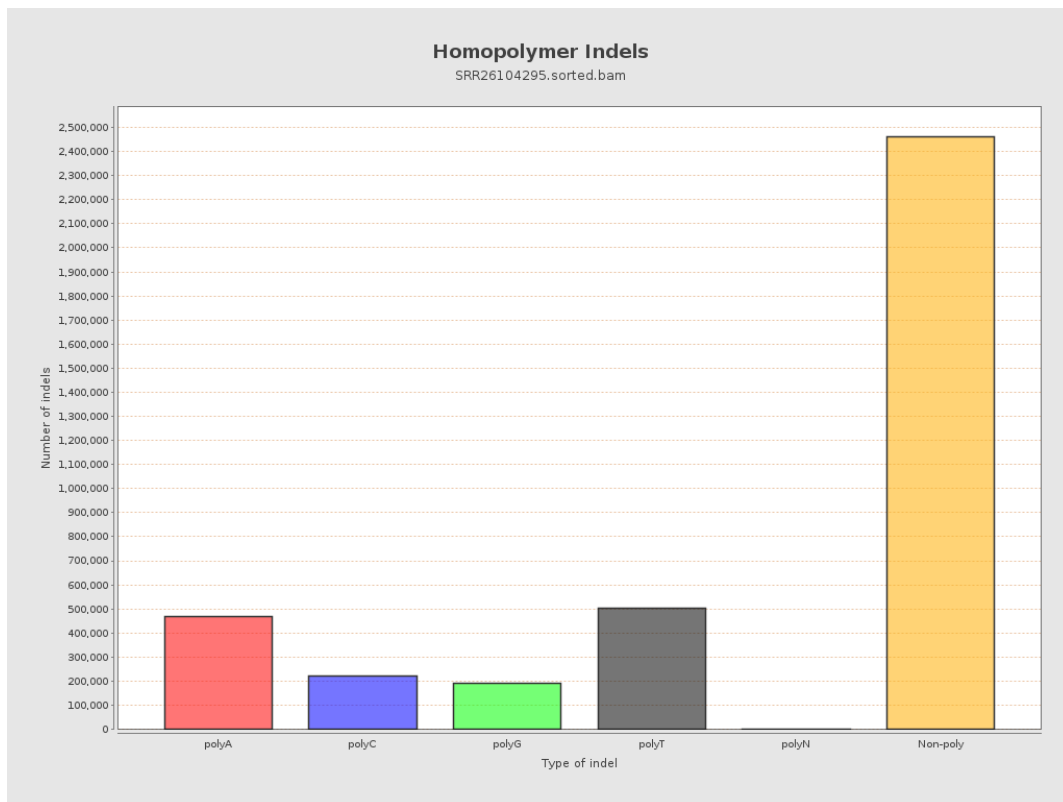
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



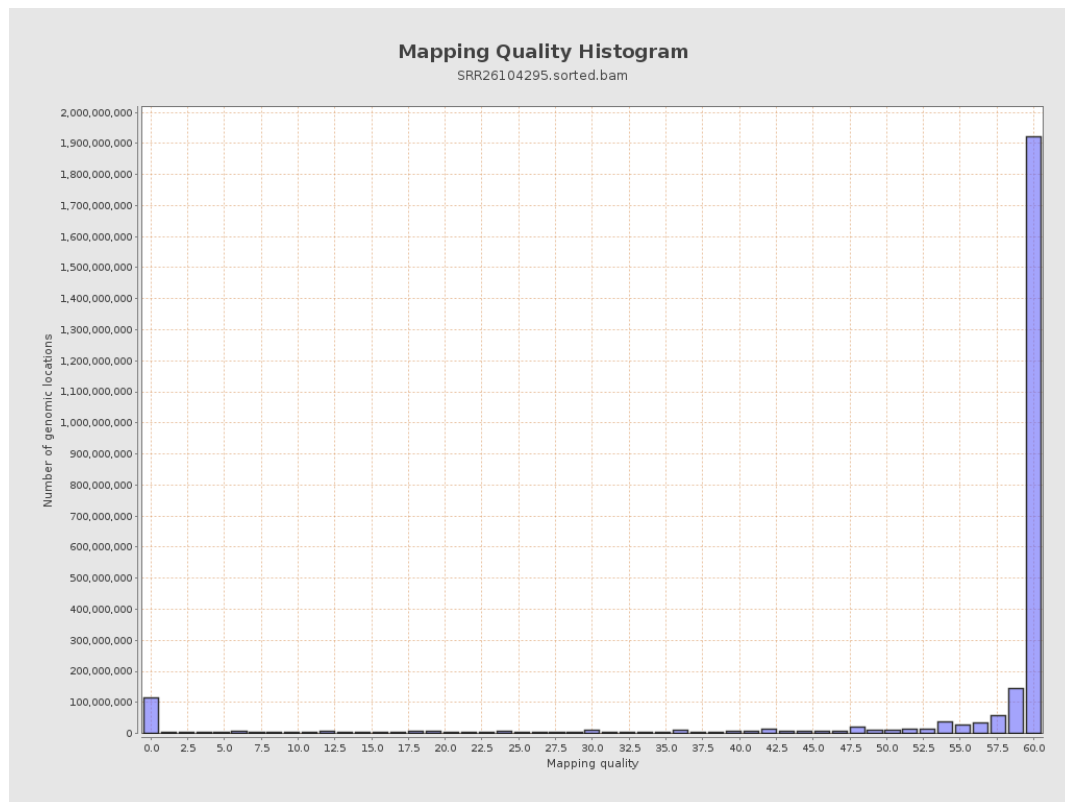
11. Results : Homopolymer Indels



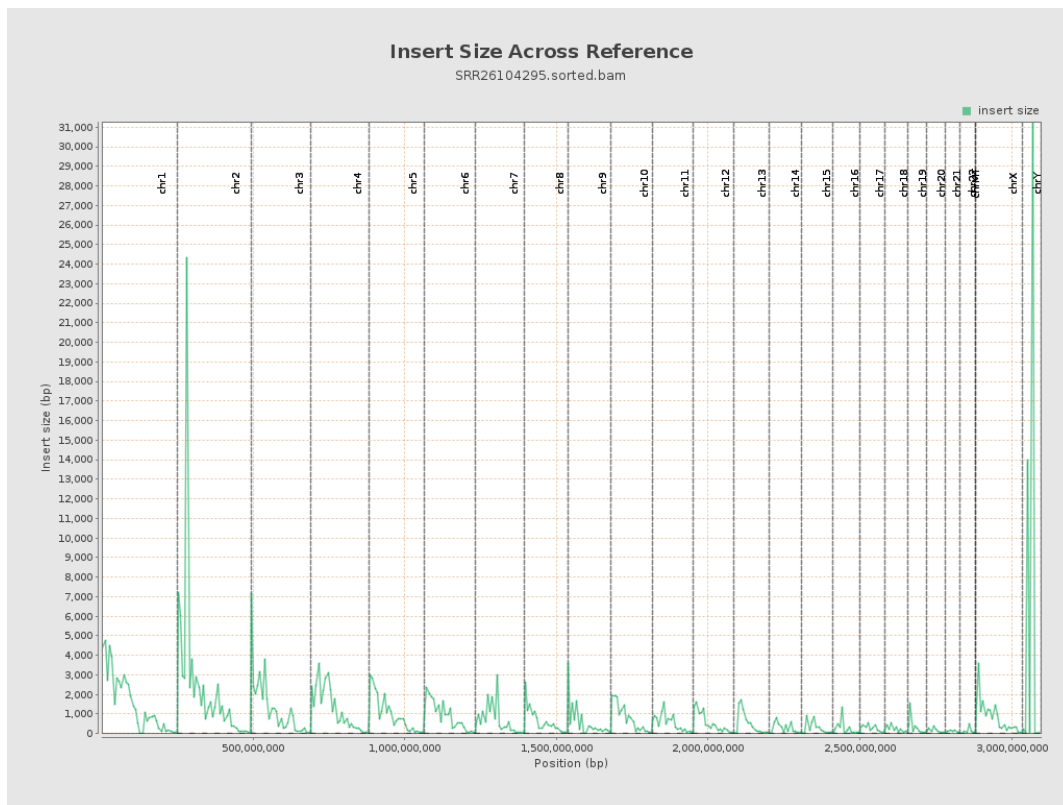
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

