

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 06:00:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR26104291.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_SRR26104291 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR26104291_1.fastq.gz SRR26104291_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 06:00:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR26104291.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	162,355,664
Mapped reads	158,723,288 / 97.76%
Unmapped reads	3,632,376 / 2.24%
Mapped paired reads	158,723,288 / 97.76%
Mapped reads, first in pair	80,012,295 / 49.28%
Mapped reads, second in pair	78,710,993 / 48.48%
Mapped reads, both in pair	157,124,850 / 96.78%
Mapped reads, singletons	1,598,438 / 0.98%
Secondary alignments	0
Supplementary alignments	154,596 / 0.1%
Read min/max/mean length	30 / 97 / 91.04
Duplicated reads (estimated)	80,557,116 / 49.62%
Duplication rate	36.87%
Clipped reads	34,971,530 / 21.54%

2.2. ACGT Content

Number/percentage of A's	4,236,664,261 / 31.23%
Number/percentage of C's	2,549,015,498 / 18.79%
Number/percentage of T's	4,285,344,401 / 31.59%
Number/percentage of G's	2,488,402,566 / 18.34%
Number/percentage of N's	7,136,867 / 0.05%

GC Percentage	37.13%
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2.3. Coverage

Mean	4.3835
Standard Deviation	91.528

2.4. Mapping Quality

Mean Mapping Quality	53.16
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2.5. Insert size

Mean	10,594.95
Standard Deviation	997,469.49
P25/Median/P75	100 / 164 / 256

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	84,623,068
Insertions	1,276,856
Mapped reads with at least one insertion	0.79%
Deletions	1,537,644
Mapped reads with at least one deletion	0.95%
Homopolymer indels	44.3%

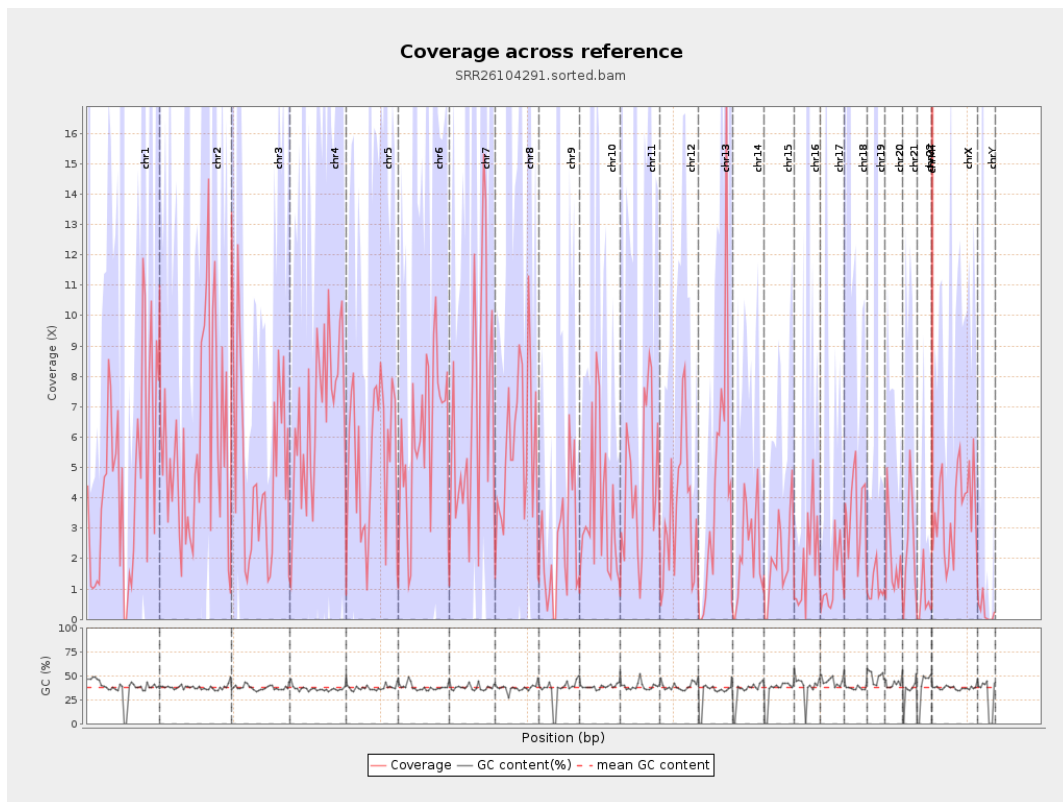
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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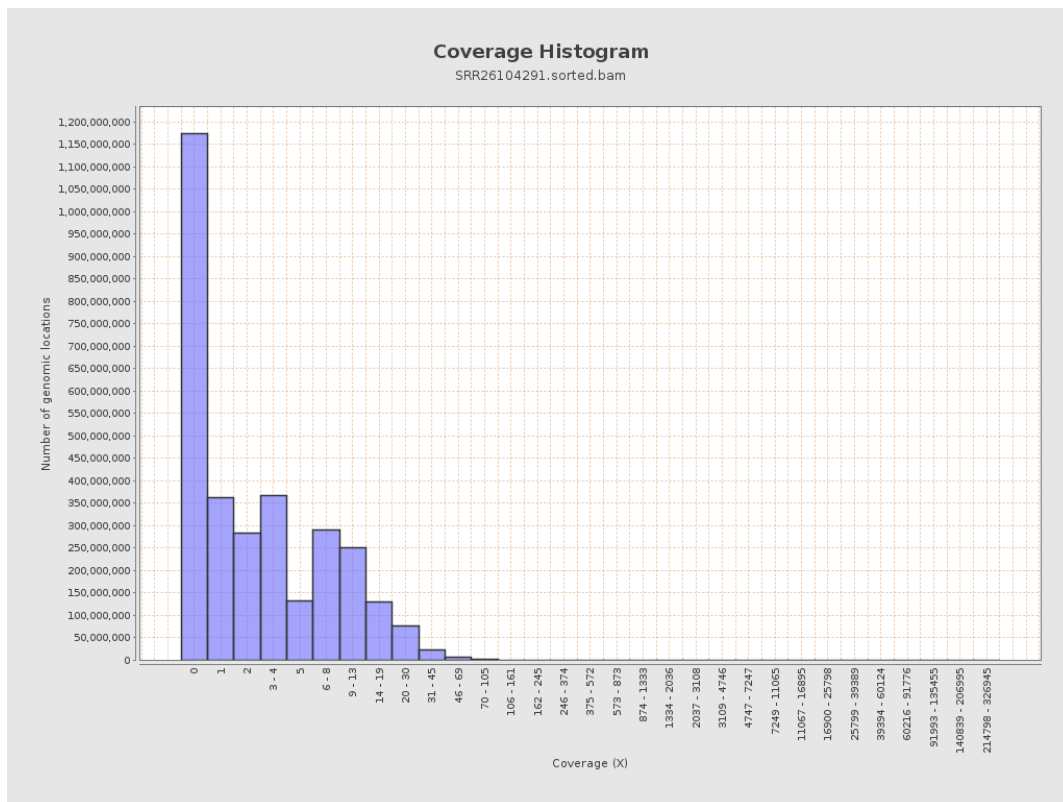
		bases	coverage	deviation
chr1	249250621	1158006925	4.646	62.1796
chr2	243199373	1386463299	5.7009	14.8025
chr3	198022430	978412077	4.9409	7.6377
chr4	191154276	1283670295	6.7154	13.1026
chr5	180915260	949639692	5.2491	10.3807
chr6	171115067	1054272713	6.1612	11.2269
chr7	159138663	1060847394	6.6662	40.0065
chr8	146364022	834872309	5.7041	206.1155
chr9	141213431	332424598	2.3541	16.9666
chr10	135534747	486940842	3.5927	32.4584
chr11	135006516	622195071	4.6086	12.5217
chr12	133851895	464980777	3.4738	6.1325
chr13	115169878	499446604	4.3366	13.9362
chr14	107349540	243791895	2.271	5.2139
chr15	102531392	208068413	2.0293	4.3243
chr16	90354753	169118664	1.8717	14.9689
chr17	81195210	102609259	1.2637	7.5773
chr18	78077248	276725884	3.5443	19.4526
chr19	59128983	63143822	1.0679	33.2591
chr20	63025520	119733162	1.8998	4.9033
chr21	48129895	122087971	2.5366	6.6343
chr22	51304566	35651252	0.6949	3.4794
chrMT	16571	535219331	32,298.5536	6,508.1117
chrX	155270560	566219547	3.6467	6.4501

chrY	59373566	15478024	0.2607	8.9212
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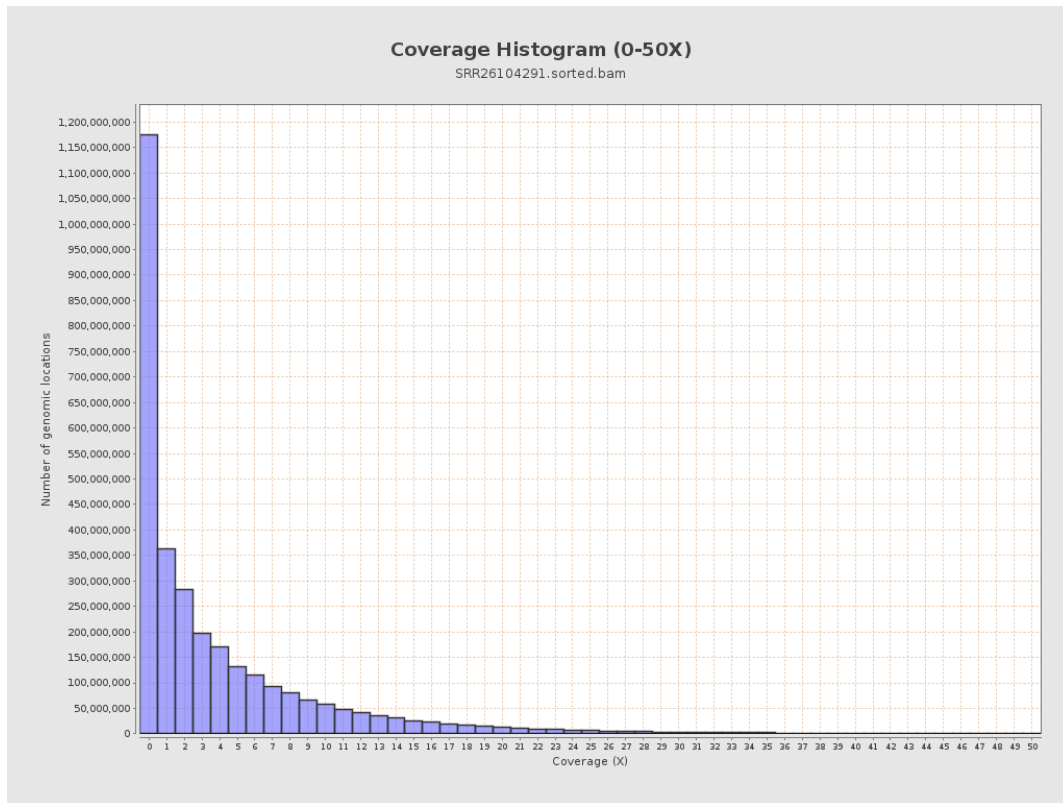
3. Results : Coverage across reference



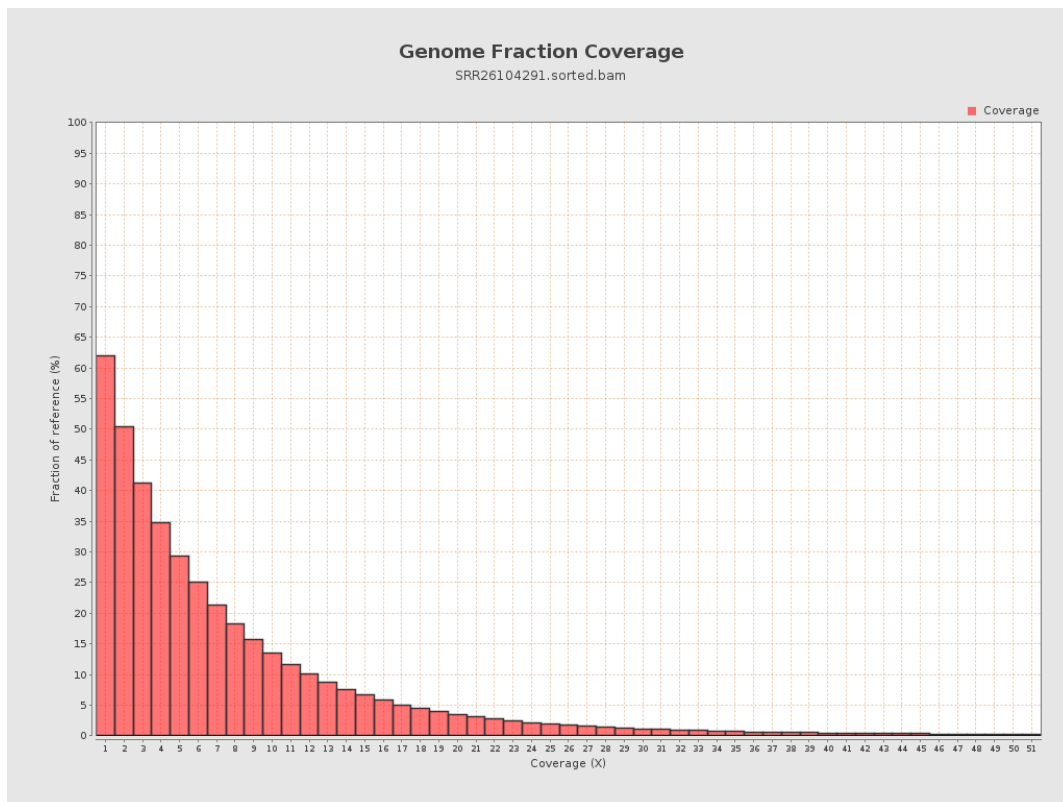
4. Results : Coverage Histogram



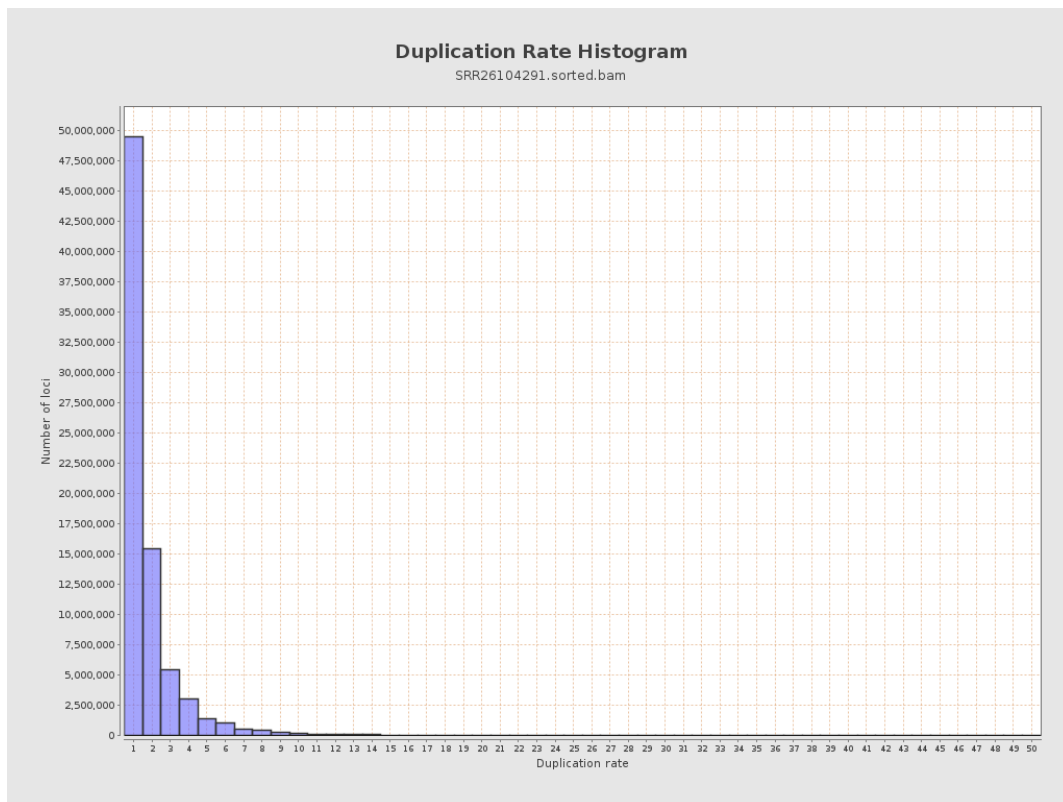
5. Results : Coverage Histogram (0-50X)



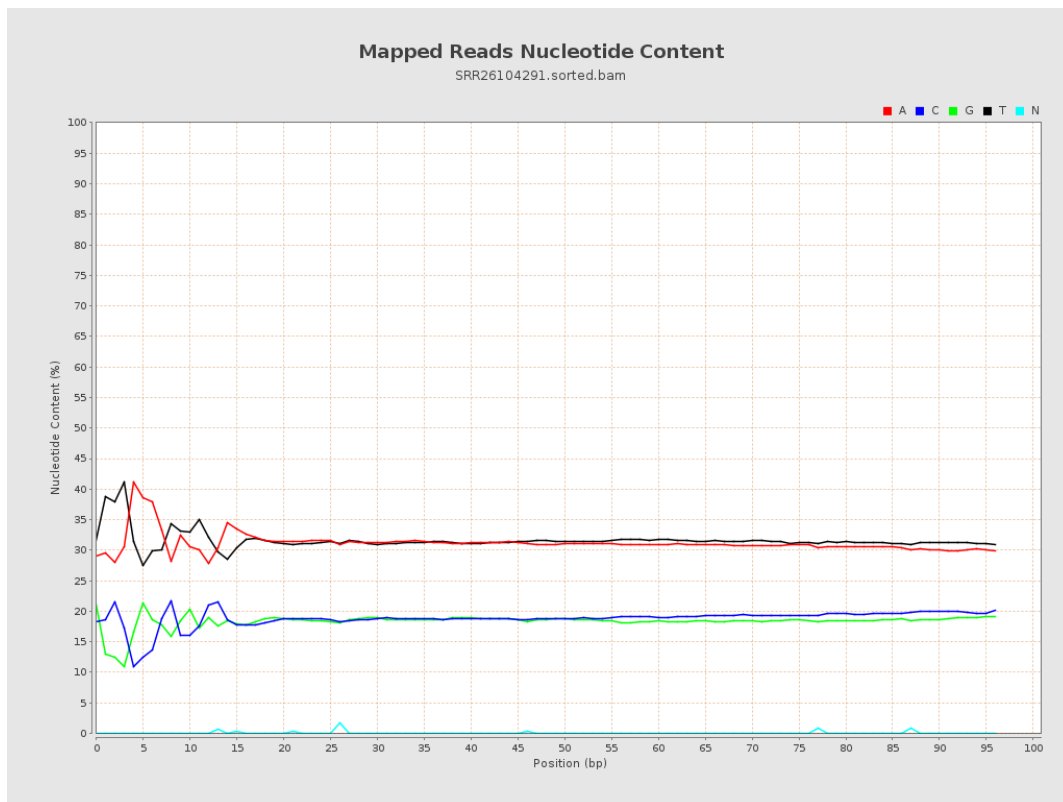
6. Results : Genome Fraction Coverage



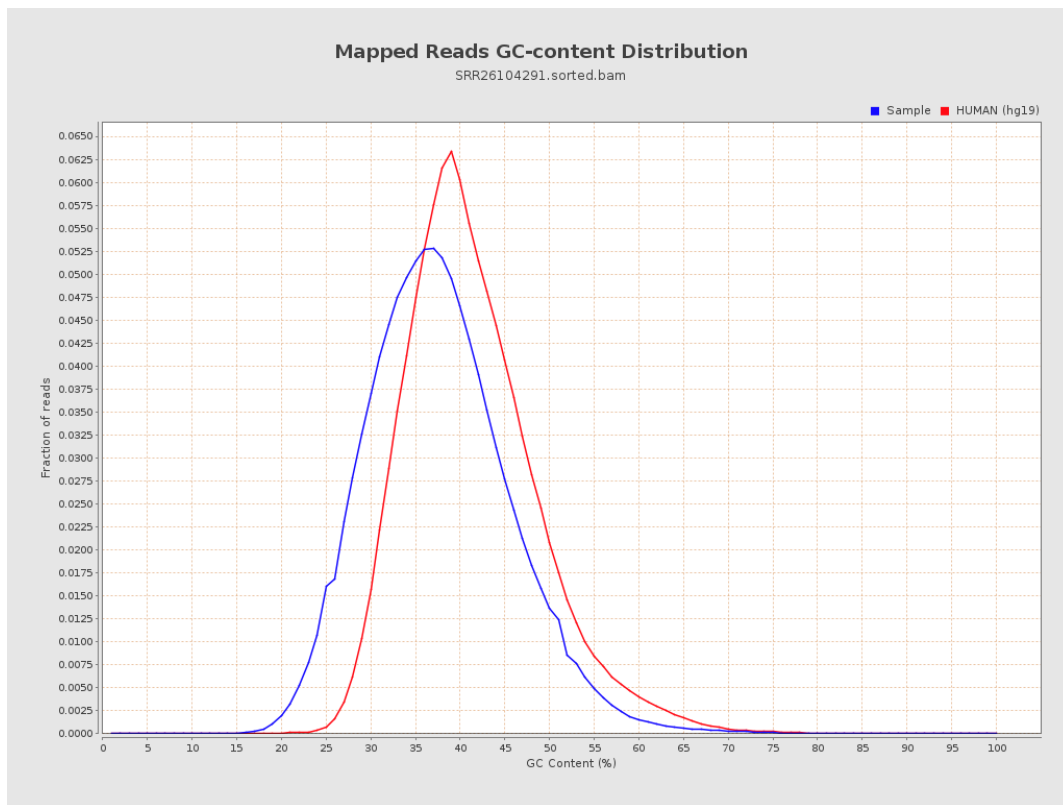
7. Results : Duplication Rate Histogram



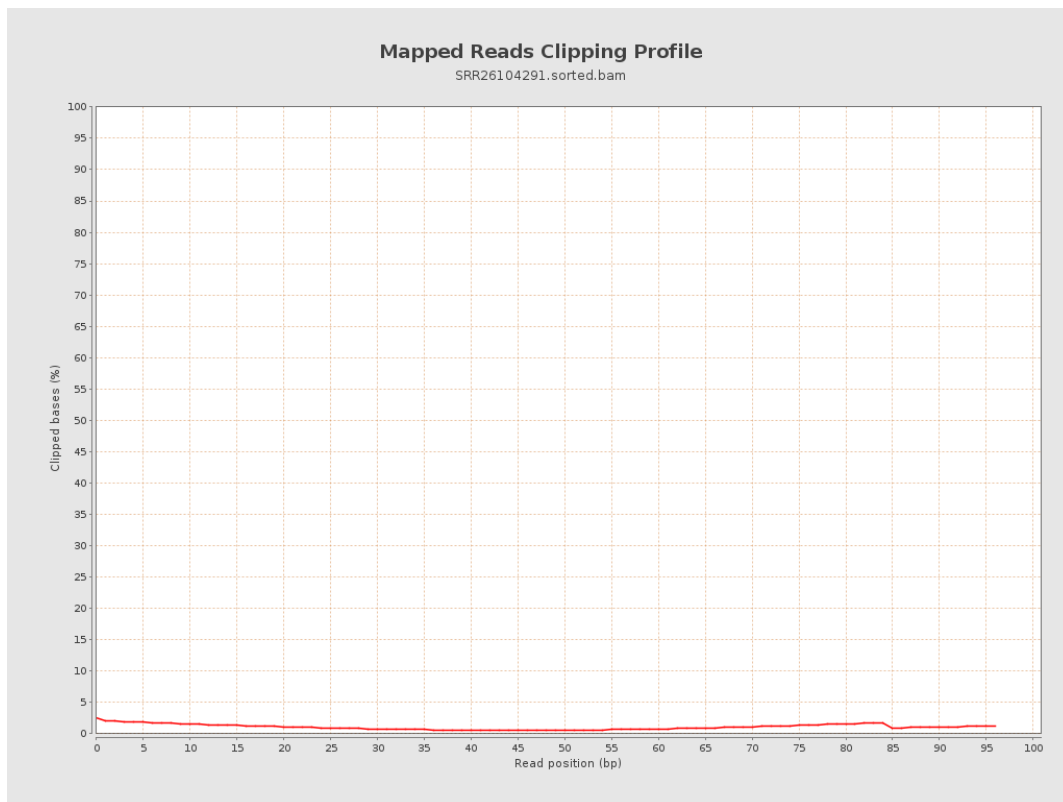
8. Results : Mapped Reads Nucleotide Content



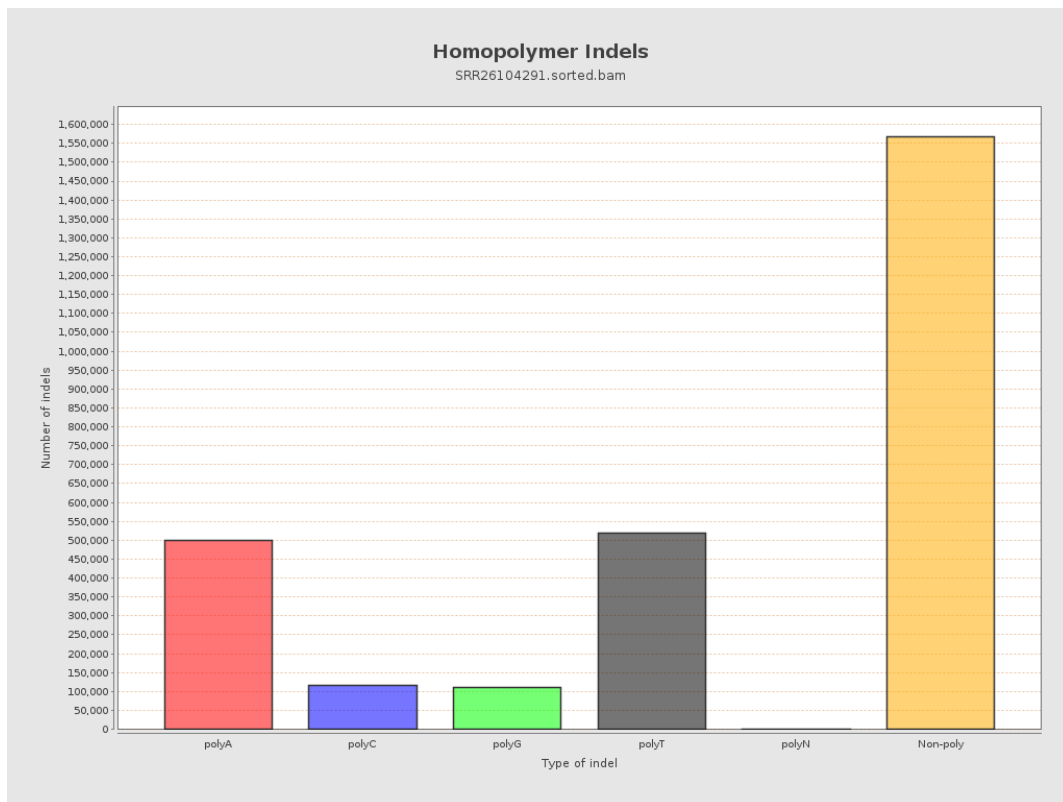
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



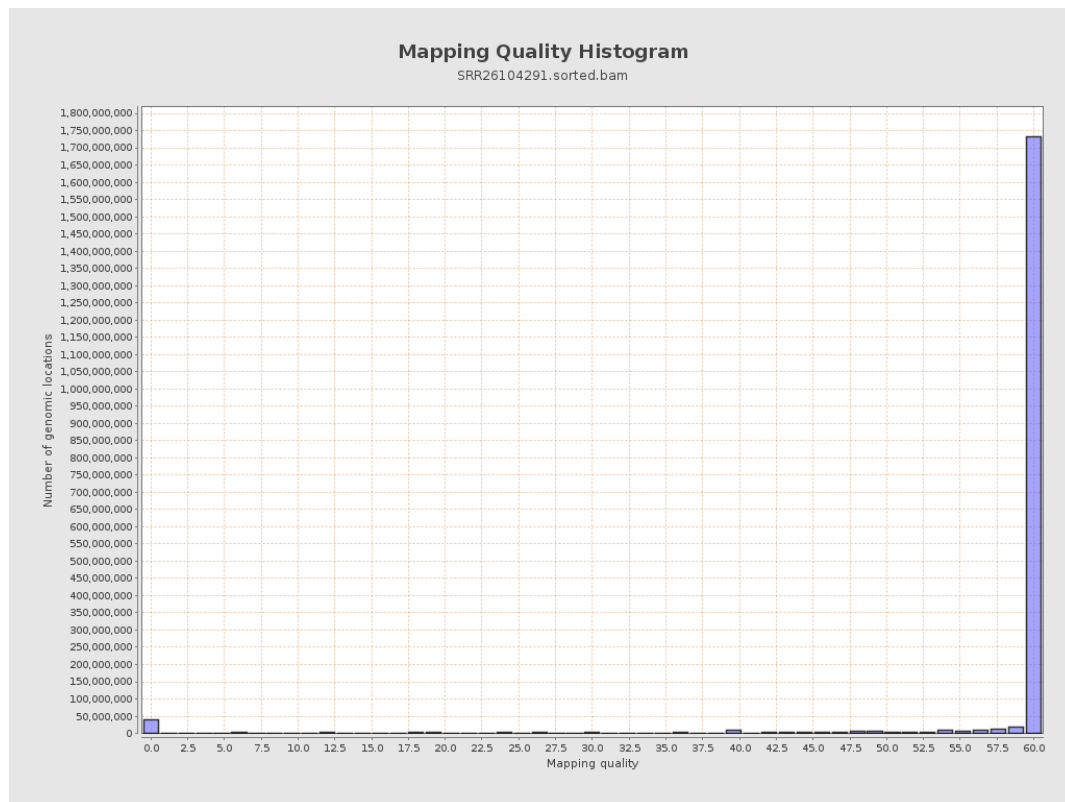
11. Results : Homopolymer Indels



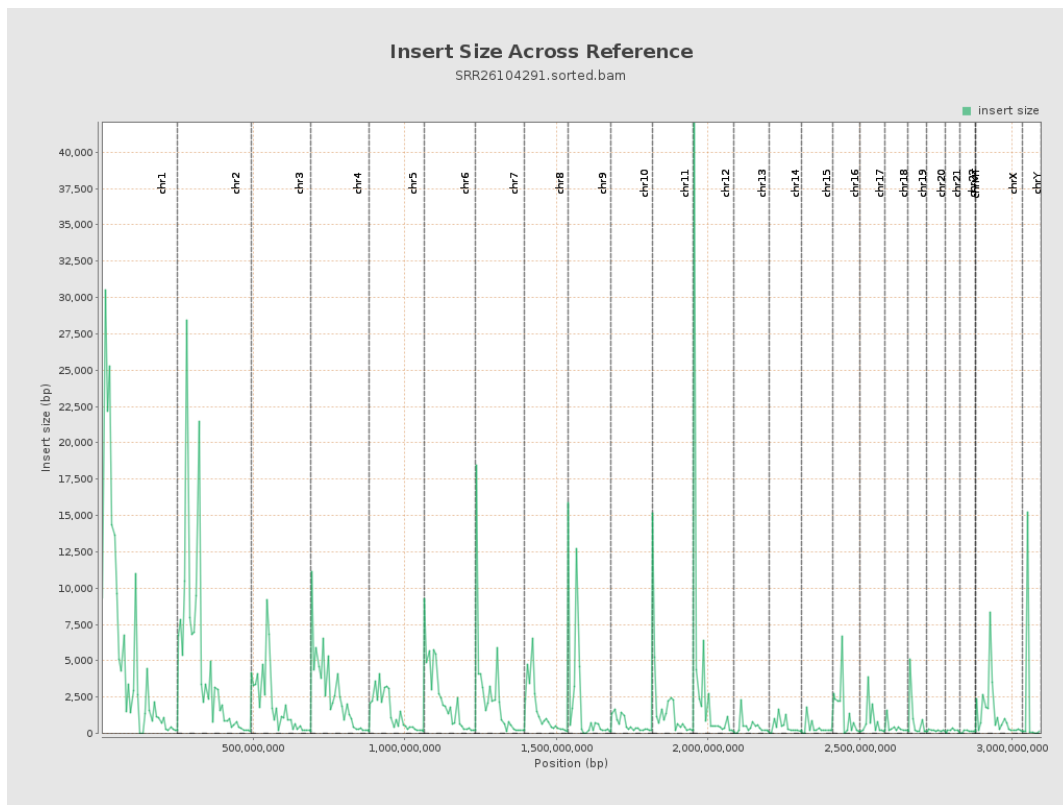
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

