

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 04:00:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR26104290.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_SRR26104290 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR26104290_1.fastq.gz SRR26104290_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 04:00:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR26104290.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	44,475,822
Mapped reads	42,849,406 / 96.34%
Unmapped reads	1,626,416 / 3.66%
Mapped paired reads	42,849,406 / 96.34%
Mapped reads, first in pair	21,715,758 / 48.83%
Mapped reads, second in pair	21,133,648 / 47.52%
Mapped reads, both in pair	42,212,052 / 94.91%
Mapped reads, singletons	637,354 / 1.43%
Secondary alignments	0
Supplementary alignments	42,069 / 0.09%
Read min/max/mean length	30 / 97 / 91.04
Duplicated reads (estimated)	27,170,559 / 61.09%
Duplication rate	40.27%
Clipped reads	21,064,582 / 47.36%

2.2. ACGT Content

Number/percentage of A's	815,433,445 / 25.53%
Number/percentage of C's	791,332,738 / 24.77%
Number/percentage of T's	831,983,552 / 26.05%
Number/percentage of G's	753,832,108 / 23.6%
Number/percentage of N's	1,677,606 / 0.05%

GC Percentage	48.37%
---------------	--------

2.3. Coverage

Mean	1.0321
Standard Deviation	59.9473

2.4. Mapping Quality

Mean Mapping Quality	52.84
----------------------	-------

2.5. Insert size

Mean	11,265.48
Standard Deviation	1,036,840.41
P25/Median/P75	55 / 94 / 184

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	18,035,643
Insertions	293,618
Mapped reads with at least one insertion	0.68%
Deletions	353,357
Mapped reads with at least one deletion	0.82%
Homopolymer indels	46.01%

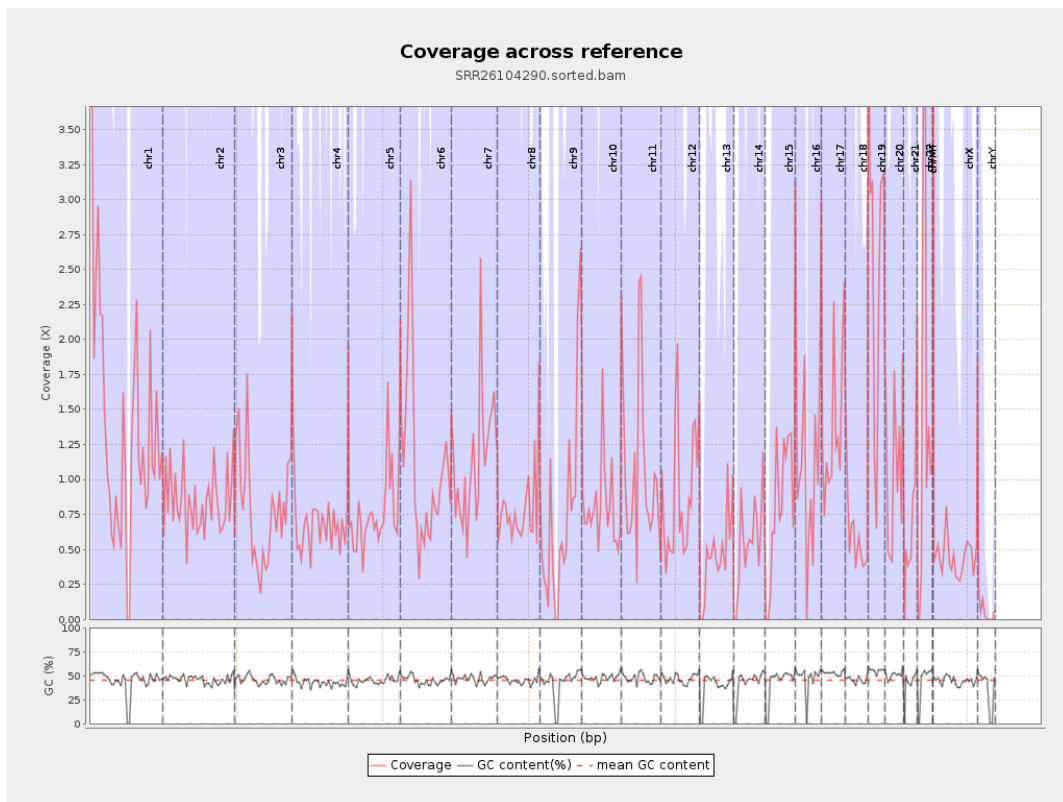
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

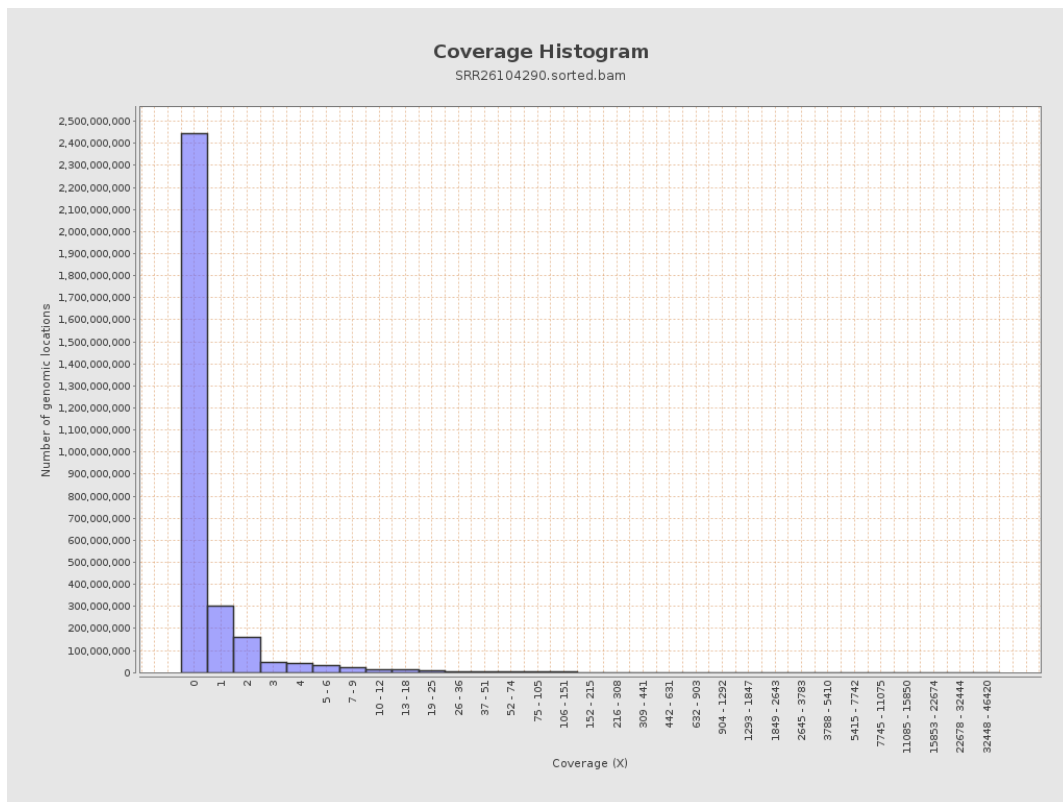
		bases	coverage	deviation
chr1	249250621	344038684	1.3803	28.3325
chr2	243199373	205863137	0.8465	7.6211
chr3	198022430	156594924	0.7908	5.3022
chr4	191154276	128684687	0.6732	4.2368
chr5	180915260	142688307	0.7887	8.8578
chr6	171115067	183206862	1.0707	6.7605
chr7	159138663	182546636	1.1471	8.0679
chr8	146364022	115206194	0.7871	8.9549
chr9	141213431	104190202	0.7378	6.0803
chr10	135534747	109138021	0.8052	5.8475
chr11	135006516	143243009	1.061	9.0687
chr12	133851895	120896588	0.9032	6.2866
chr13	115169878	52708594	0.4577	10.9566
chr14	107349540	59987484	0.5588	4.535
chr15	102531392	79976643	0.78	5.5037
chr16	90354753	103077082	1.1408	7.8919
chr17	81195210	109345588	1.3467	9.6255
chr18	78077248	46966332	0.6015	4.5862
chr19	59128983	144291496	2.4403	14.3174
chr20	63025520	62305588	0.9886	6.3339
chr21	48129895	35348741	0.7344	6.9661
chr22	51304566	76180622	1.4849	13.3013
chrMT	16571	412174559	24,873.246	5,611.3115
chrX	155270560	73035475	0.4704	3.4991

chrY	59373566	3351212	0.0564	2.3786
------	----------	---------	--------	--------

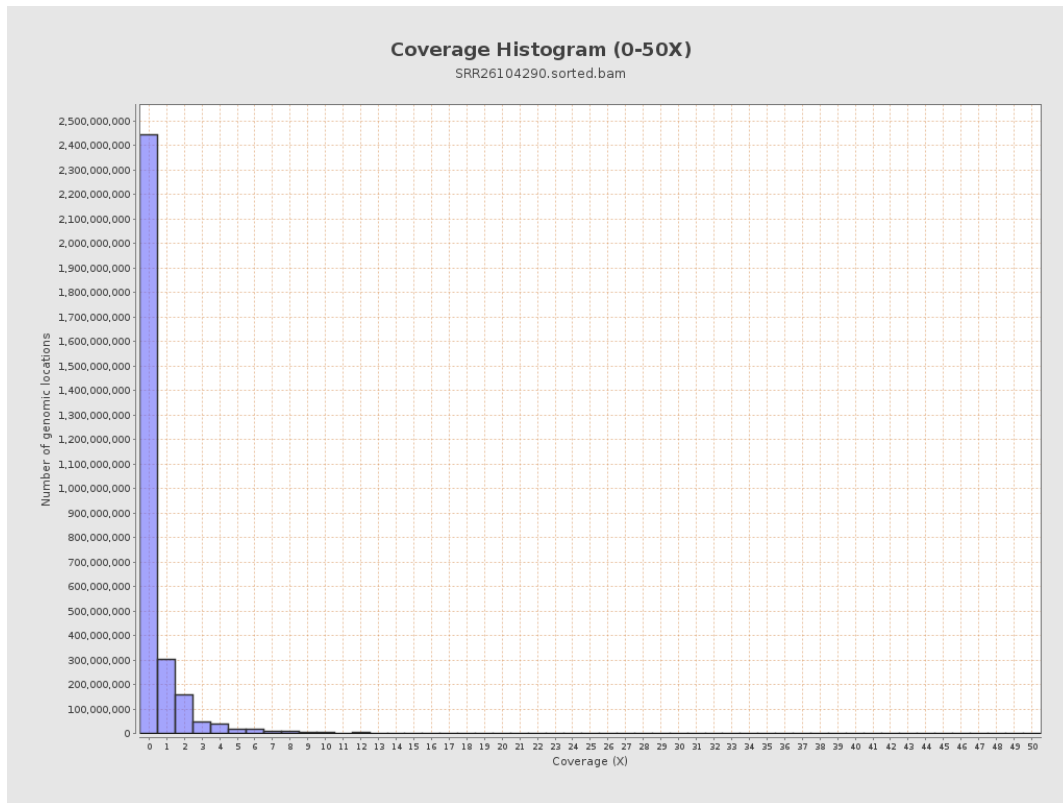
3. Results : Coverage across reference



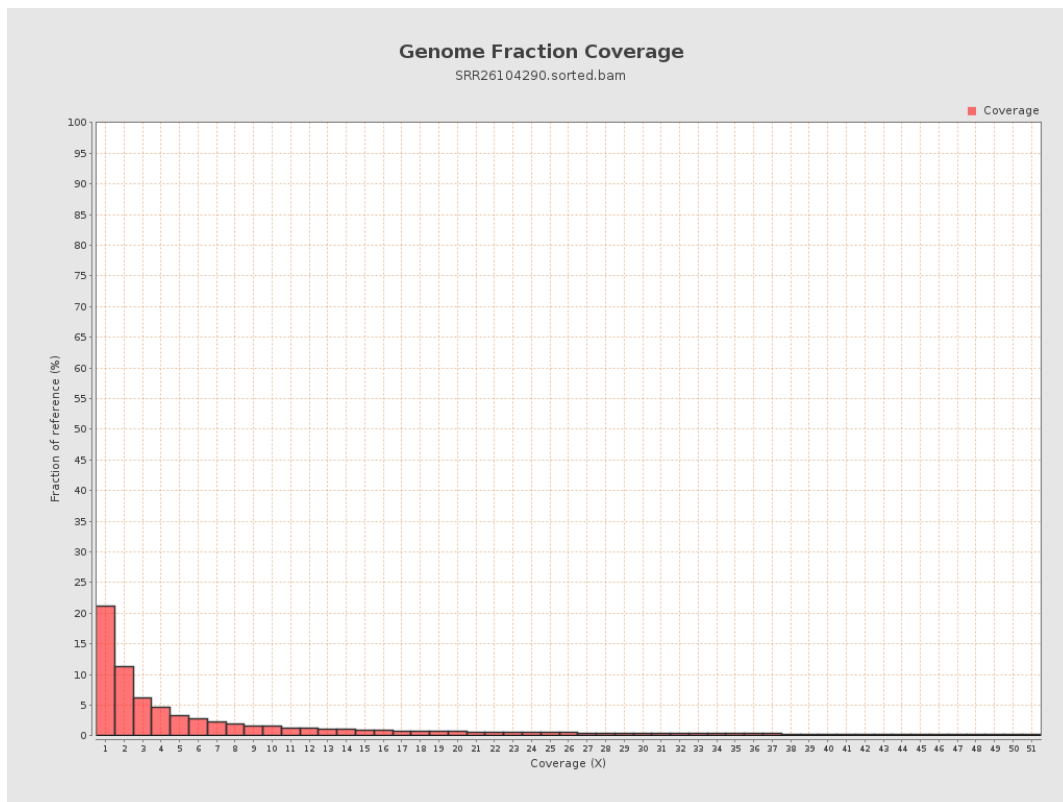
4. Results : Coverage Histogram



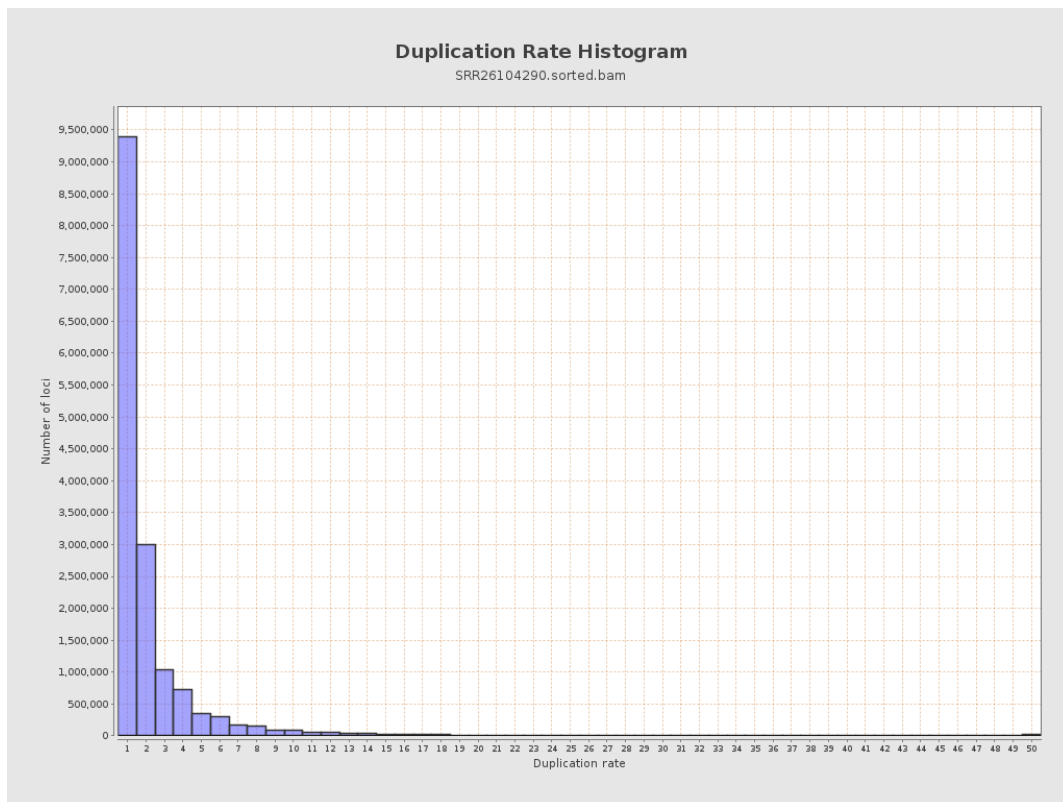
5. Results : Coverage Histogram (0-50X)



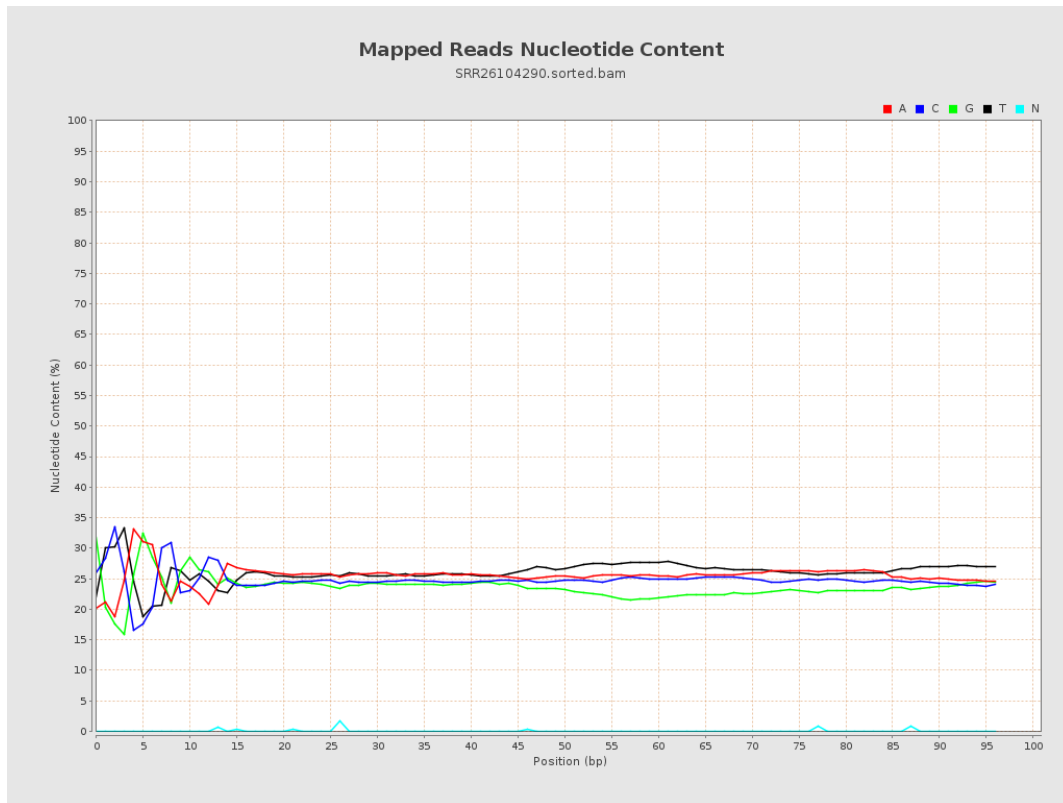
6. Results : Genome Fraction Coverage



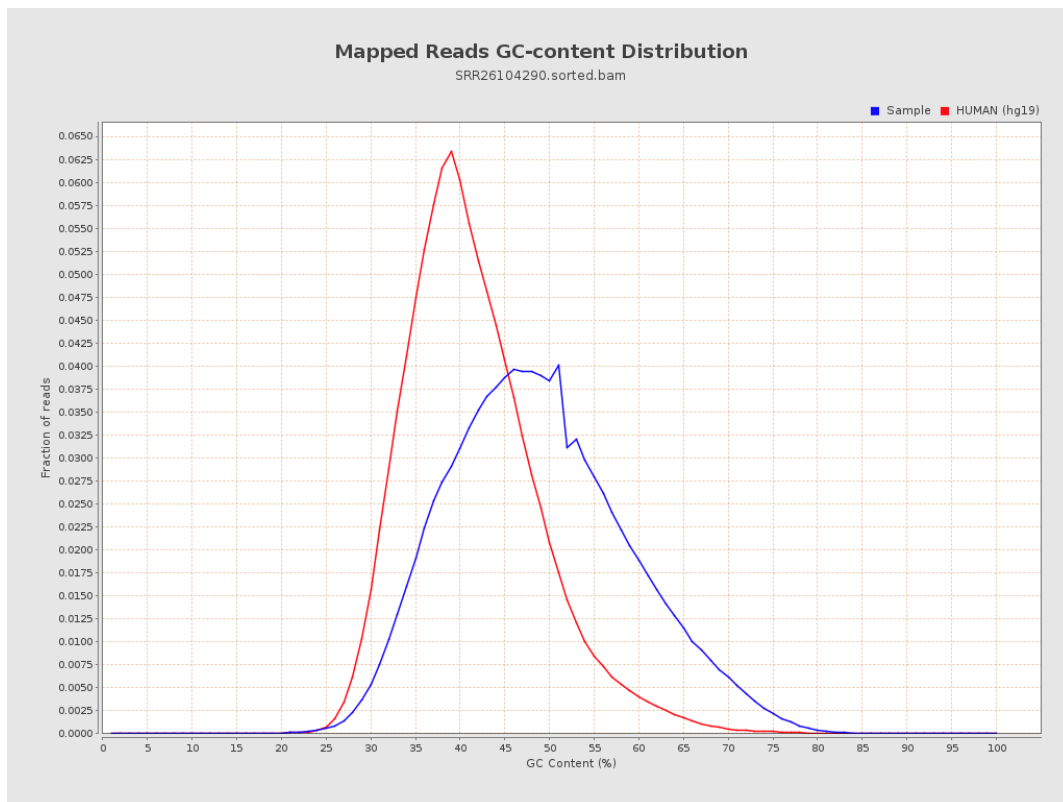
7. Results : Duplication Rate Histogram



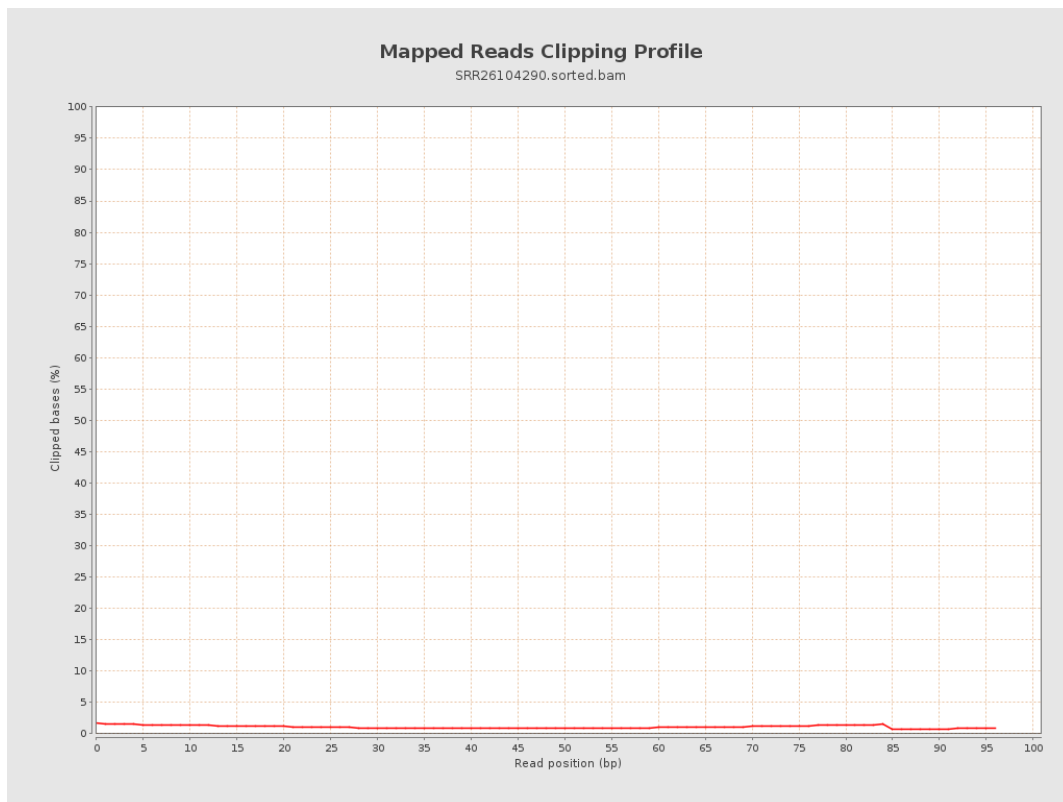
8. Results : Mapped Reads Nucleotide Content



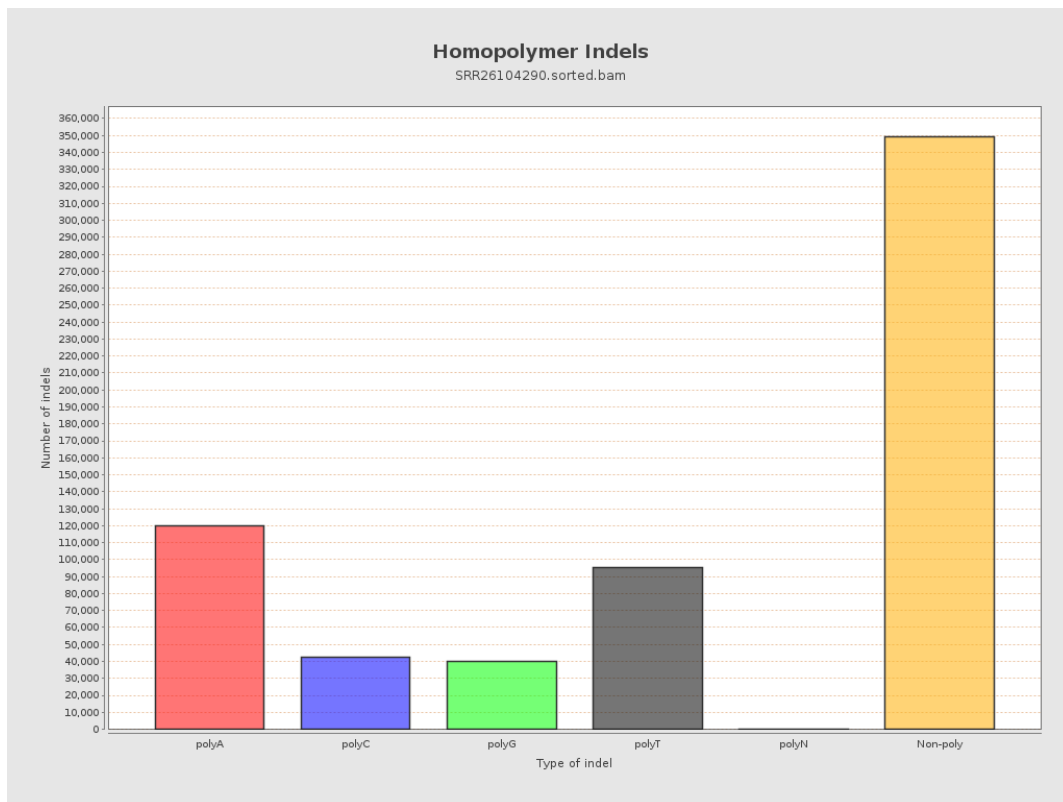
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



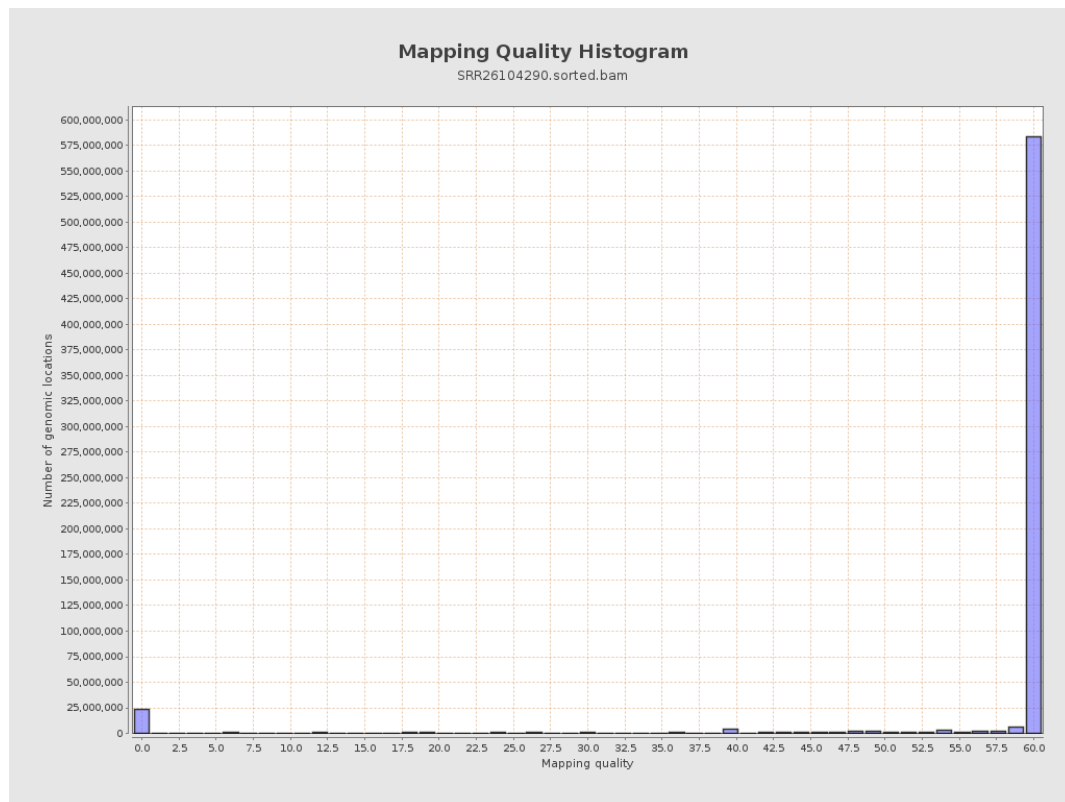
11. Results : Homopolymer Indels



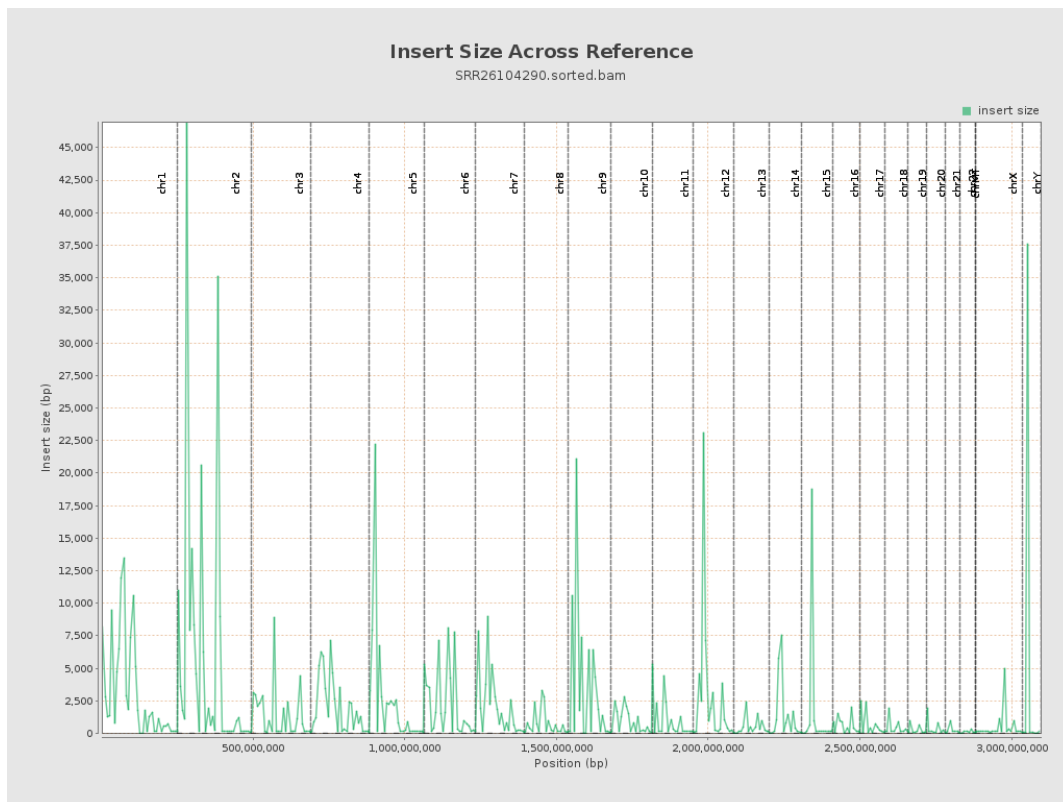
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

