

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 10:54:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251058.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_SRR10251058 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251058_1.fastq.gz SRR10251058_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 10:54:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251058.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,748,530
Mapped reads	1,425,077 / 81.5%
Unmapped reads	323,453 / 18.5%
Mapped paired reads	1,425,077 / 81.5%
Mapped reads, first in pair	713,828 / 40.82%
Mapped reads, second in pair	711,249 / 40.68%
Mapped reads, both in pair	1,415,314 / 80.94%
Mapped reads, singletons	9,763 / 0.56%
Secondary alignments	0
Supplementary alignments	40,100 / 2.29%
Read min/max/mean length	30 / 127 / 128.03
Duplicated reads (estimated)	233,513 / 13.35%
Duplication rate	14.73%
Clipped reads	411,509 / 23.53%

2.2. ACGT Content

Number/percentage of A's	50,728,126 / 29.33%
Number/percentage of C's	35,228,415 / 20.37%
Number/percentage of T's	50,709,600 / 29.32%
Number/percentage of G's	36,262,332 / 20.97%
Number/percentage of N's	5,753 / 0%

GC Percentage	41.34%
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2.3. Coverage

Mean	0.0559
Standard Deviation	0.7005

2.4. Mapping Quality

Mean Mapping Quality	52.92
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2.5. Insert size

Mean	96,563.27
Standard Deviation	2,987,141.46
P25/Median/P75	139 / 177 / 237

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	1,261,146
Insertions	30,222
Mapped reads with at least one insertion	1.97%
Deletions	72,494
Mapped reads with at least one deletion	4.88%
Homopolymer indels	42.82%

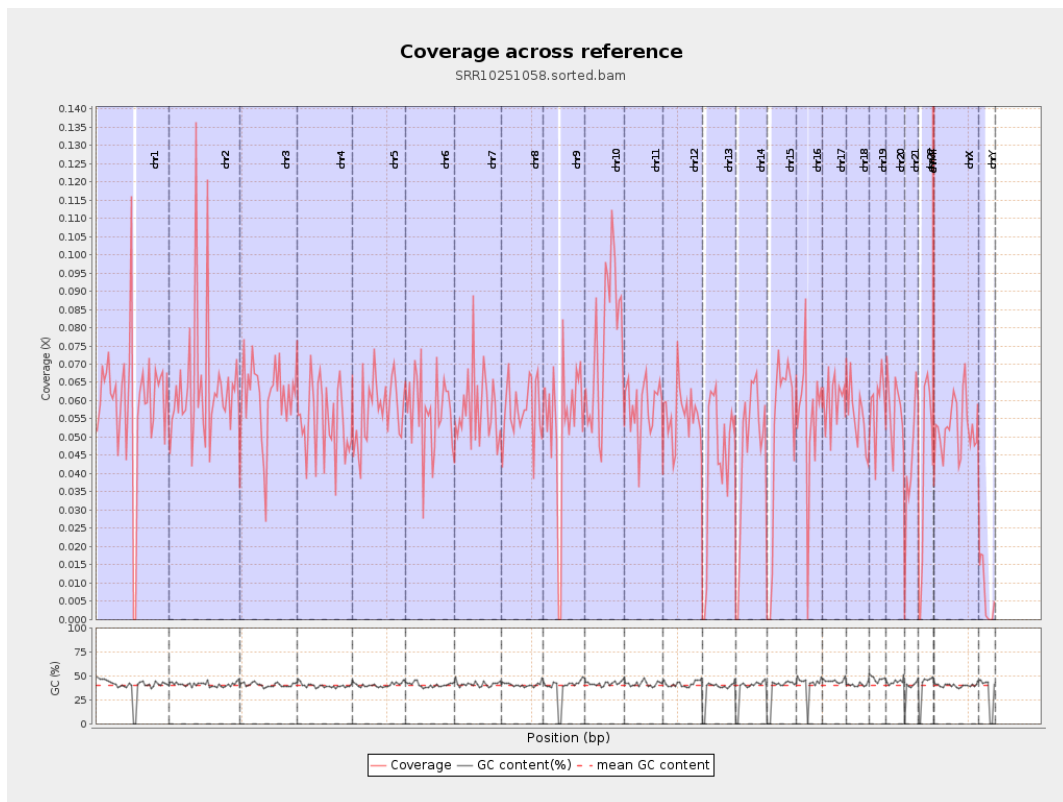
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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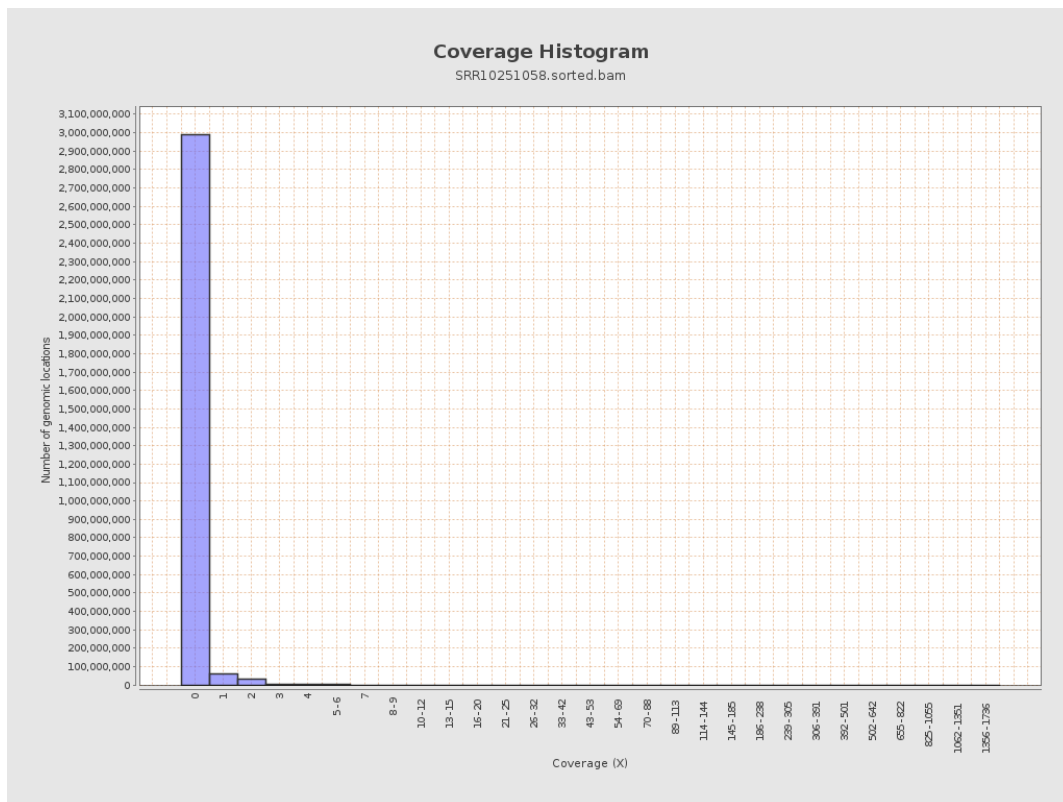
		bases	coverage	deviation
chr1	249250621	14799932	0.0594	1.4421
chr2	243199373	15478163	0.0636	1.0466
chr3	198022430	12019775	0.0607	0.3579
chr4	191154276	10295486	0.0539	0.4073
chr5	180915260	10414529	0.0576	0.3592
chr6	171115067	9746787	0.057	0.3961
chr7	159138663	9222820	0.058	0.9448
chr8	146364022	8389646	0.0573	0.4118
chr9	141213431	7534040	0.0534	0.8326
chr10	135534747	10223594	0.0754	0.8627
chr11	135006516	7891744	0.0585	0.4502
chr12	133851895	7530807	0.0563	0.356
chr13	115169878	4952080	0.043	0.3087
chr14	107349540	5017833	0.0467	0.3301
chr15	102531392	5198003	0.0507	0.3258
chr16	90354753	5050372	0.0559	0.6564
chr17	81195210	4878655	0.0601	0.4276
chr18	78077248	4375485	0.056	0.7202
chr19	59128983	3467853	0.0586	0.7385
chr20	63025520	3609592	0.0573	0.3673
chr21	48129895	2098858	0.0436	0.3291
chr22	51304566	2117239	0.0413	0.3077
chrMT	16571	225896	13.632	8.5503
chrX	155270560	8150527	0.0525	0.3473

chrY	59373566	397205	0.0067	0.5019
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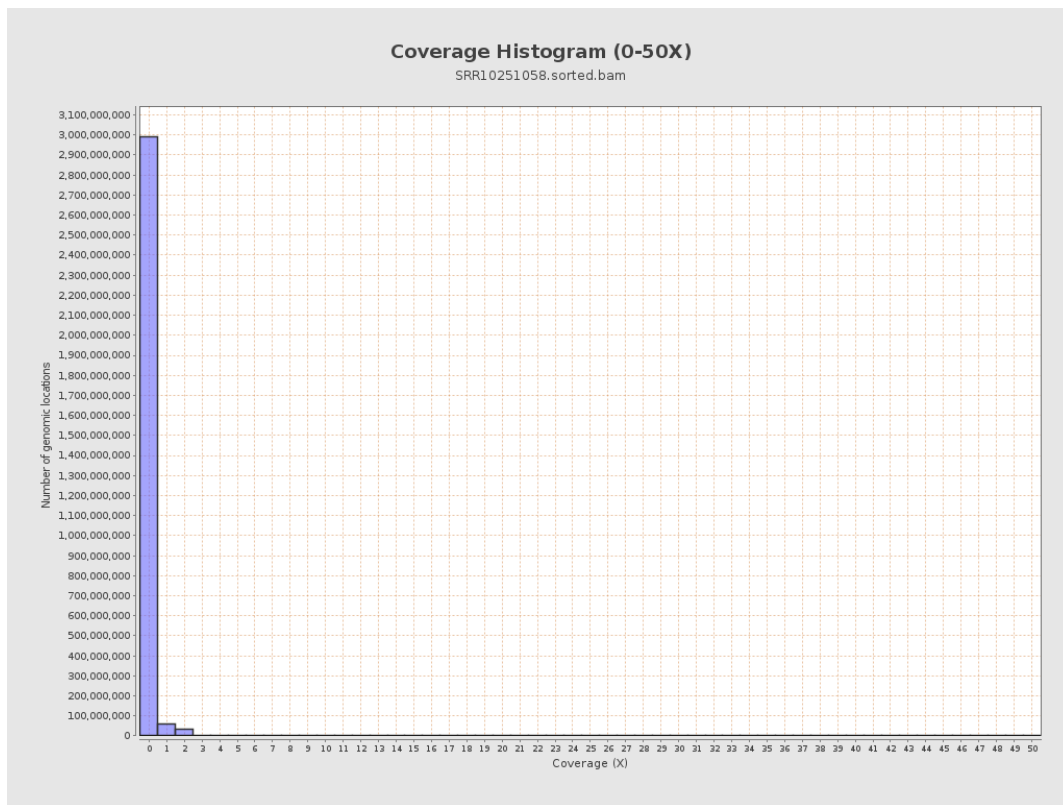
3. Results : Coverage across reference



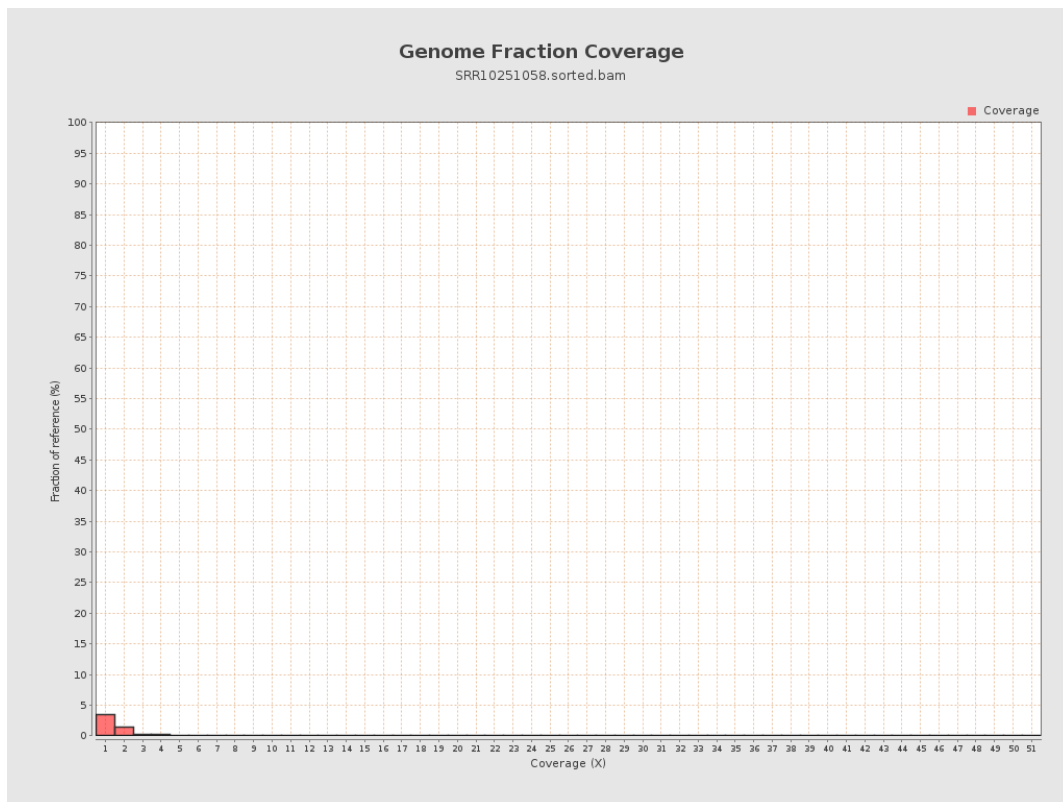
4. Results : Coverage Histogram



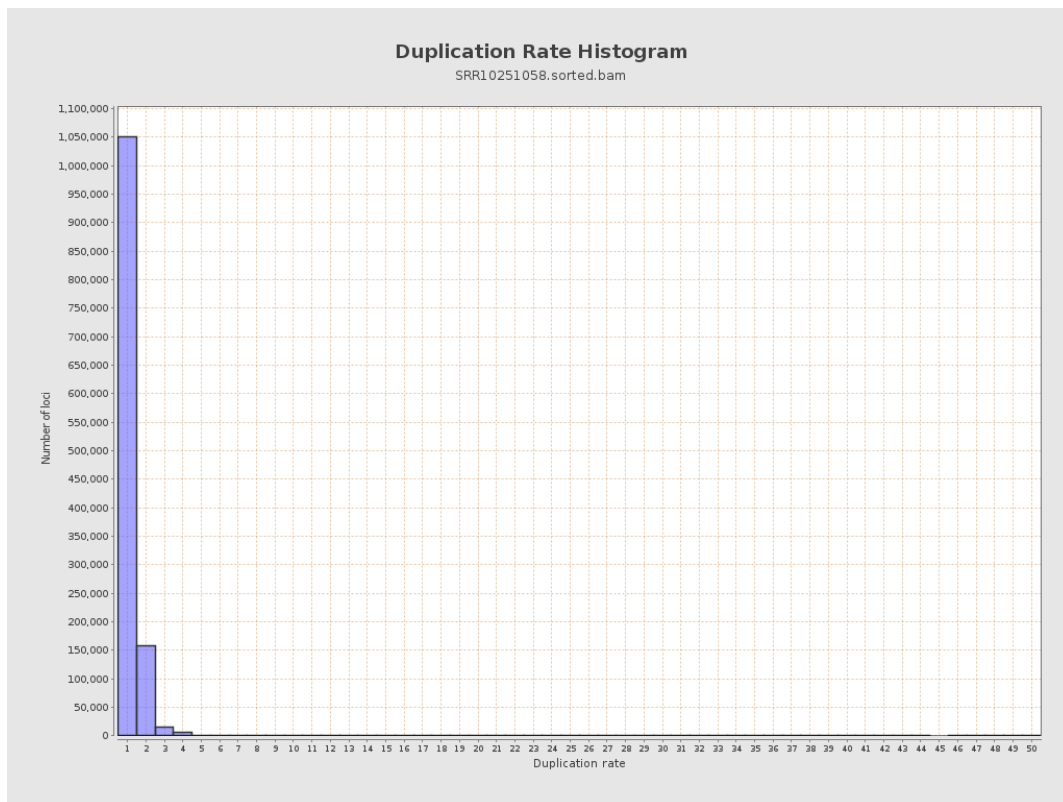
5. Results : Coverage Histogram (0-50X)



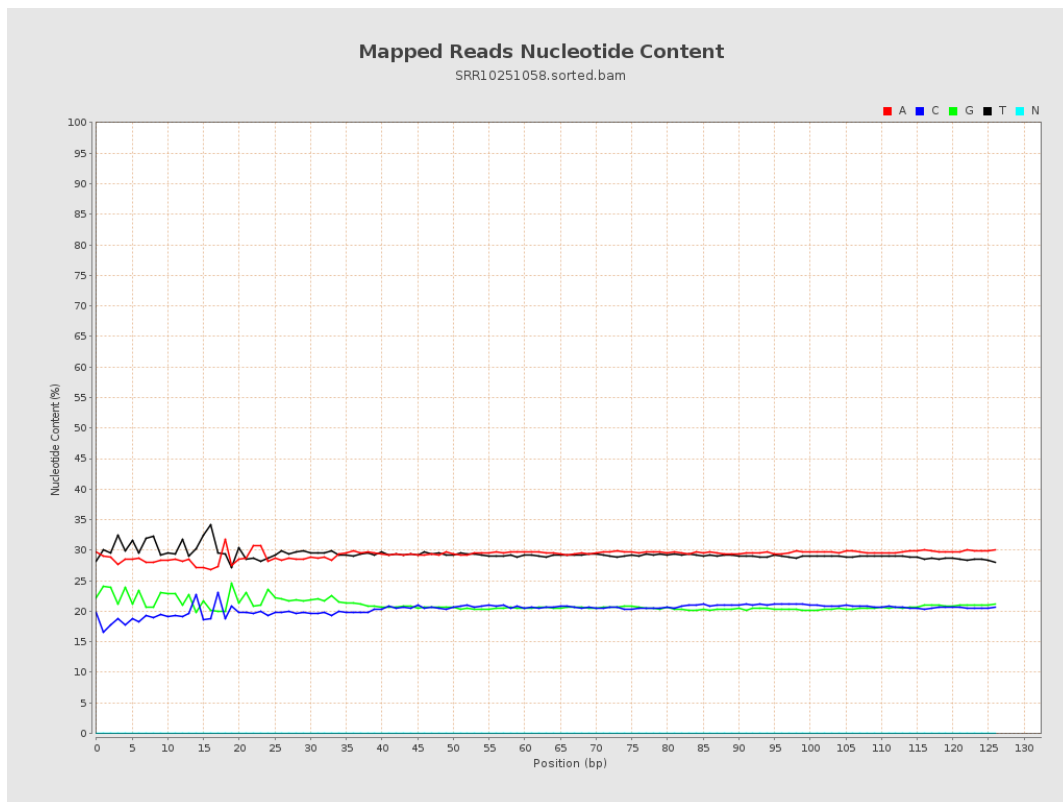
6. Results : Genome Fraction Coverage



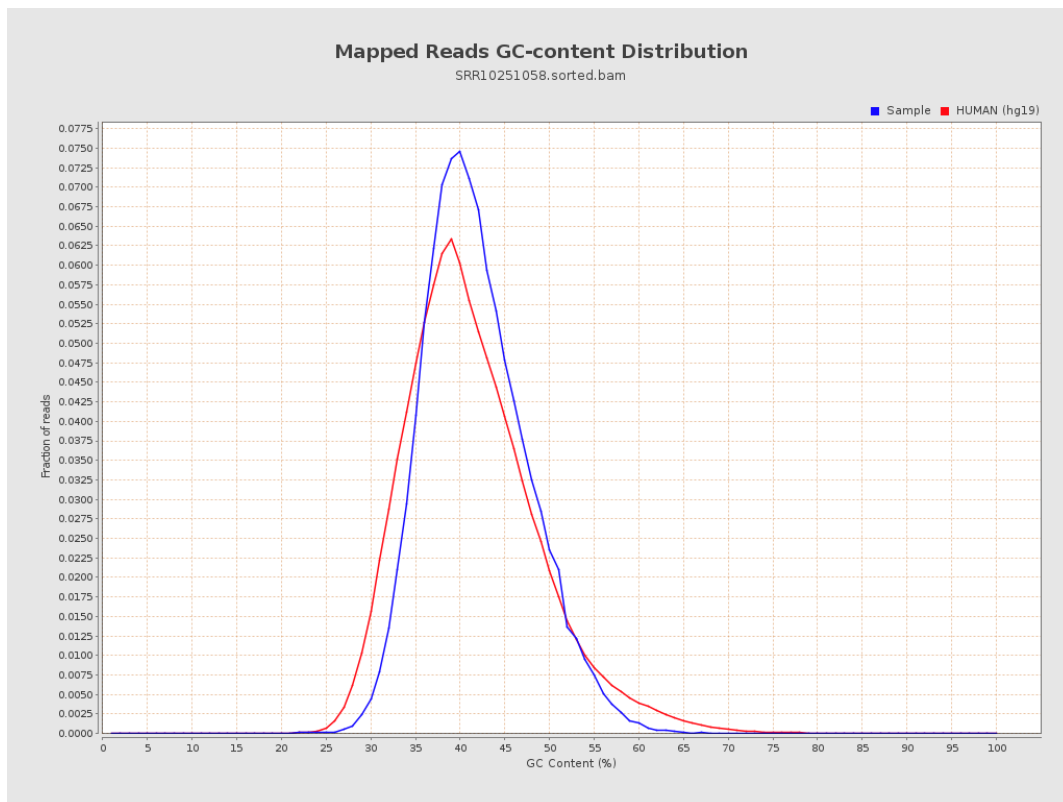
7. Results : Duplication Rate Histogram



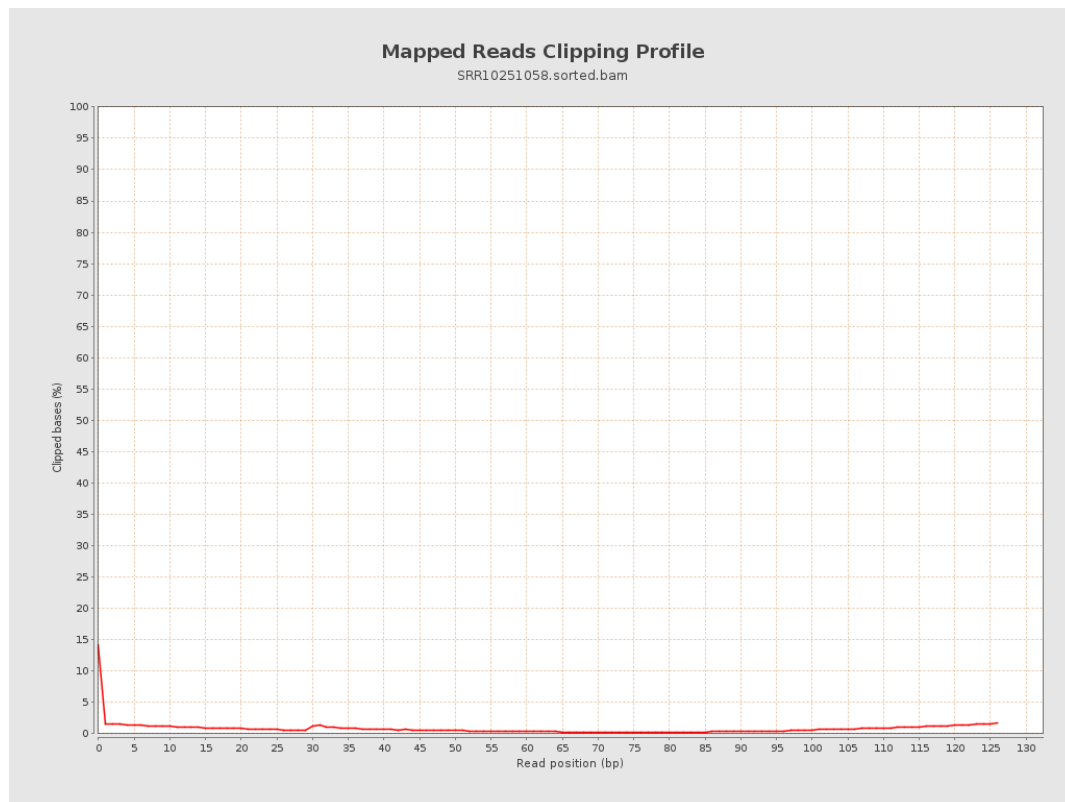
8. Results : Mapped Reads Nucleotide Content



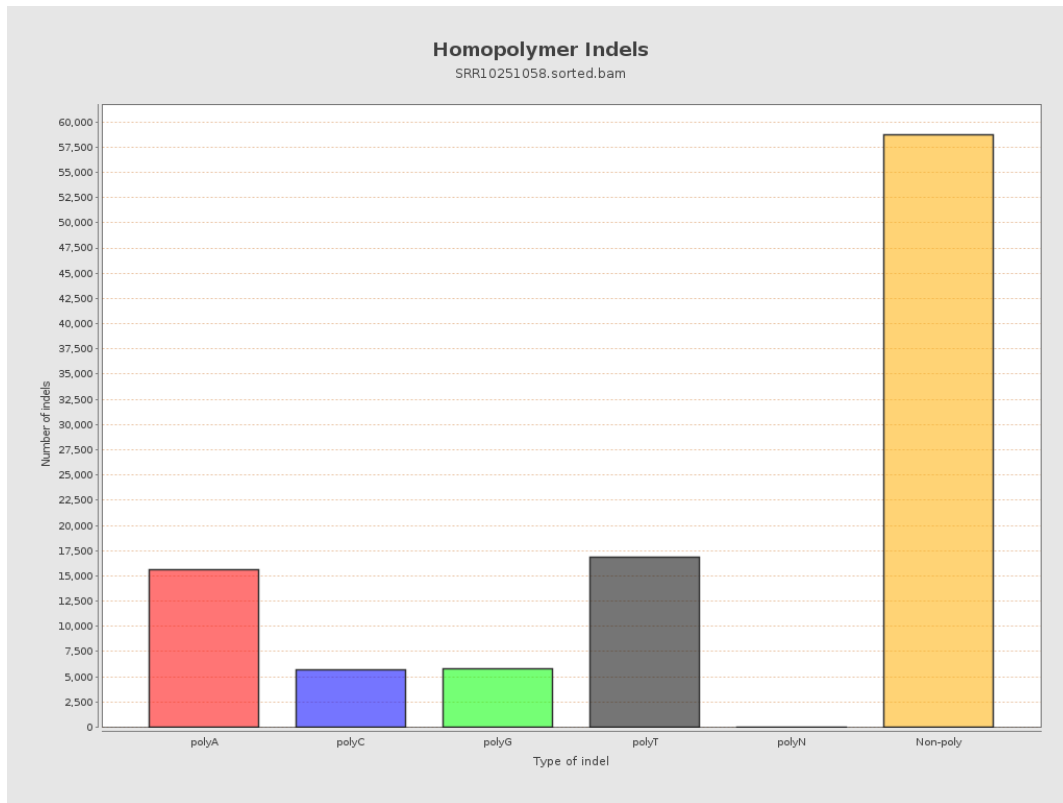
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



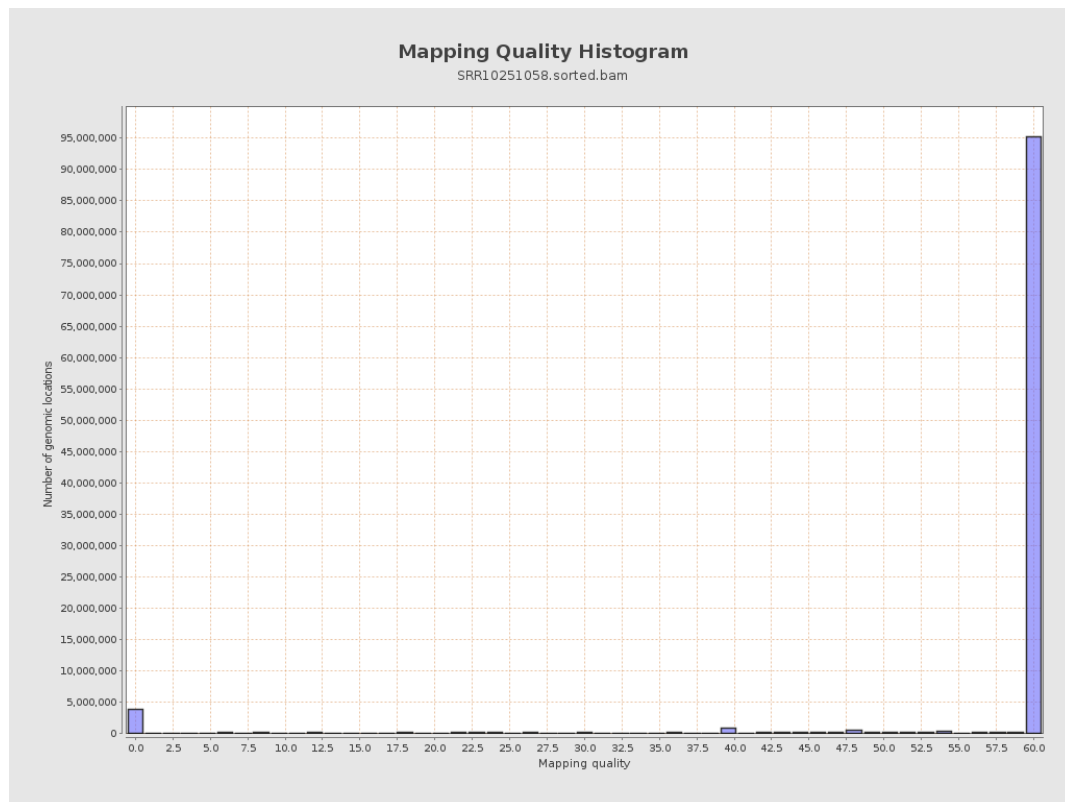
11. Results : Homopolymer Indels



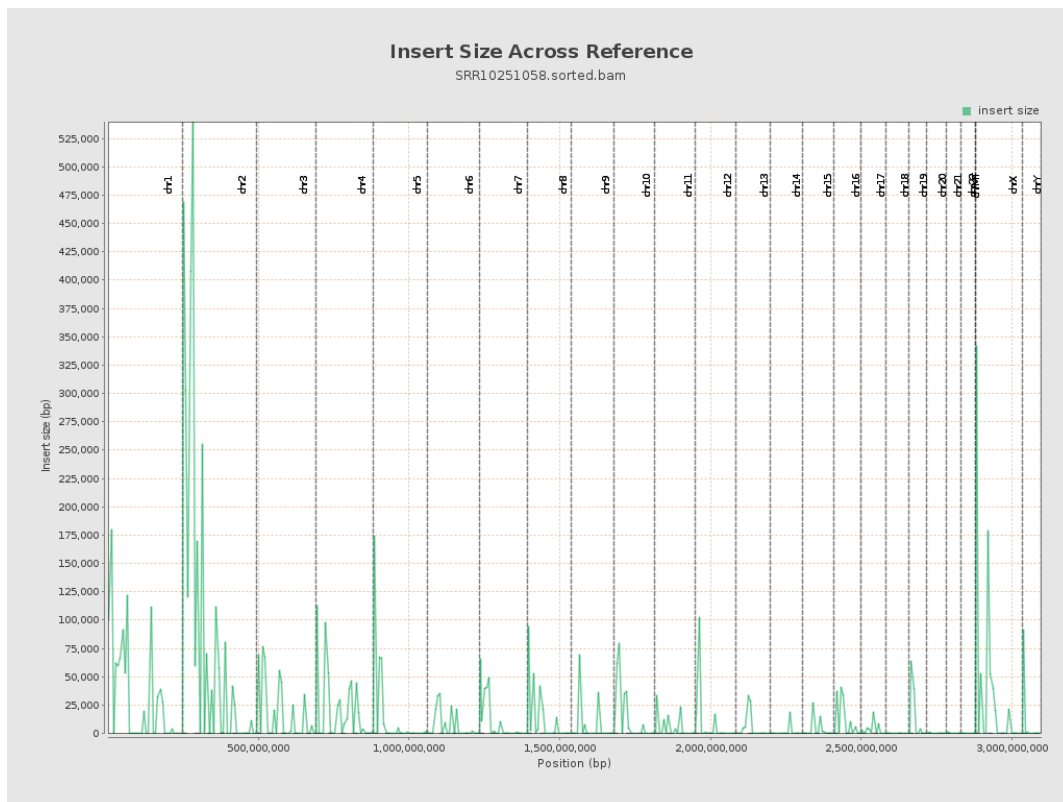
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

