

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 04:41:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10156418.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_SRR10156418 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10156418_1.fastq.gz SRR10156418_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 04:41:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10156418.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,982,874
Mapped reads	1,939,197 / 97.8%
Unmapped reads	43,677 / 2.2%
Mapped paired reads	1,939,197 / 97.8%
Mapped reads, first in pair	968,113 / 48.82%
Mapped reads, second in pair	971,084 / 48.97%
Mapped reads, both in pair	1,912,314 / 96.44%
Mapped reads, singletons	26,883 / 1.36%
Secondary alignments	0
Supplementary alignments	256,605 / 12.94%
Read min/max/mean length	30 / 133 / 124.23
Duplicated reads (estimated)	1,484,468 / 74.86%
Duplication rate	64.12%
Clipped reads	1,044,644 / 52.68%

2.2. ACGT Content

Number/percentage of A's	64,974,123 / 29.96%
Number/percentage of C's	42,939,785 / 19.8%
Number/percentage of T's	64,424,318 / 29.7%
Number/percentage of G's	44,555,291 / 20.54%
Number/percentage of N's	1,718 / 0%

GC Percentage	40.34%
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2.3. Coverage

Mean	0.0701
Standard Deviation	1.4431

2.4. Mapping Quality

Mean Mapping Quality	52.66
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2.5. Insert size

Mean	909,882.72
Standard Deviation	8,917,412.7
P25/Median/P75	98 / 138 / 202

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	1,821,584
Insertions	22,561
Mapped reads with at least one insertion	1.13%
Deletions	62,469
Mapped reads with at least one deletion	3.15%
Homopolymer indels	40.98%

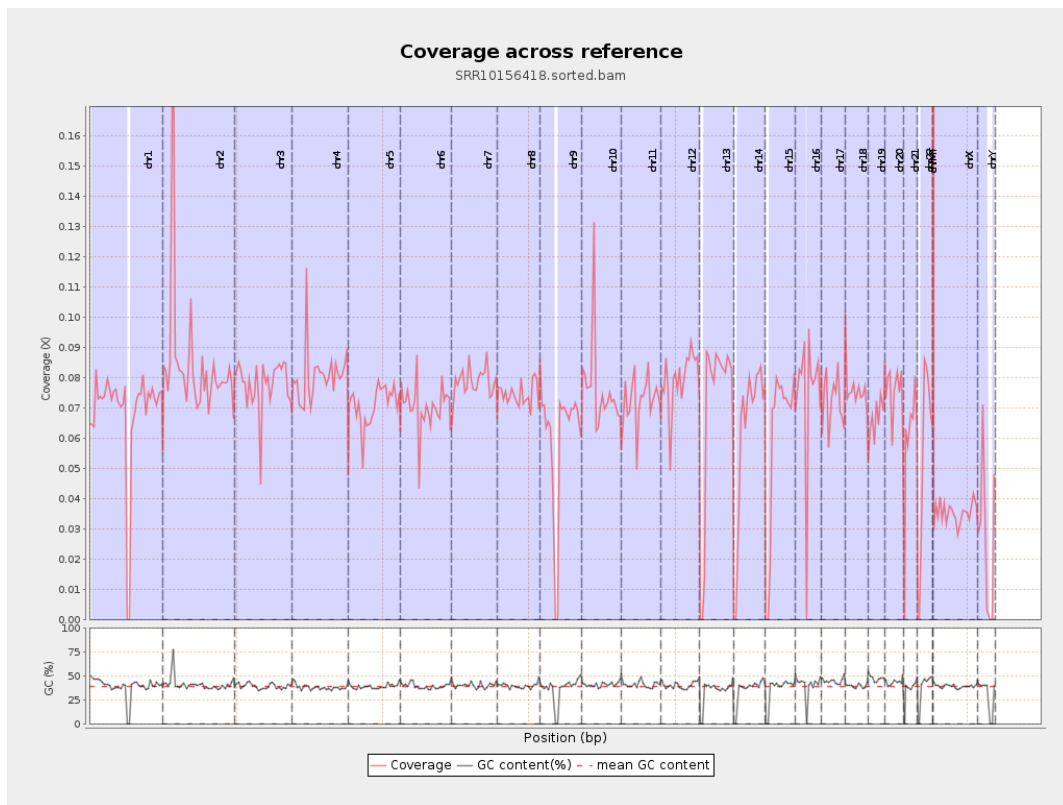
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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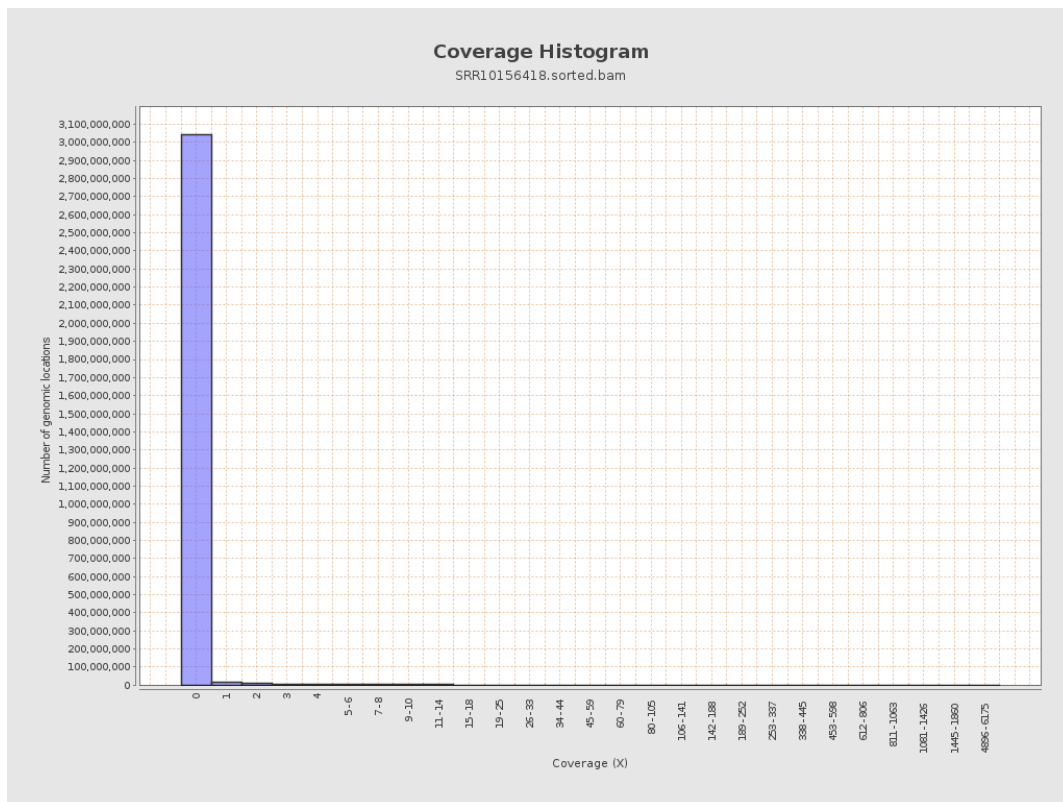
		bases	coverage	deviation
chr1	249250621	17092462	0.0686	0.8073
chr2	243199373	20443872	0.0841	4.3821
chr3	198022430	15400316	0.0778	0.7831
chr4	191154276	15407840	0.0806	0.8616
chr5	180915260	12829758	0.0709	0.7413
chr6	171115067	12045796	0.0704	0.7713
chr7	159138663	12502486	0.0786	0.8917
chr8	146364022	10901050	0.0745	0.9262
chr9	141213431	8427618	0.0597	0.7397
chr10	135534747	10279139	0.0758	0.9632
chr11	135006516	9750234	0.0722	0.7537
chr12	133851895	10701474	0.08	0.7996
chr13	115169878	8106662	0.0704	0.7369
chr14	107349540	6735241	0.0627	0.6994
chr15	102531392	6082205	0.0593	0.6798
chr16	90354753	6708188	0.0742	0.8073
chr17	81195210	5864233	0.0722	0.7528
chr18	78077248	5917061	0.0758	0.9722
chr19	59128983	3962614	0.067	0.7523
chr20	63025520	4765035	0.0756	0.758
chr21	48129895	2900034	0.0603	0.7264
chr22	51304566	2784553	0.0543	0.6674
chrMT	16571	337426	20.3624	22.0699
chrX	155270560	5464185	0.0352	0.5142

chrY	59373566	1631344	0.0275	0.5326
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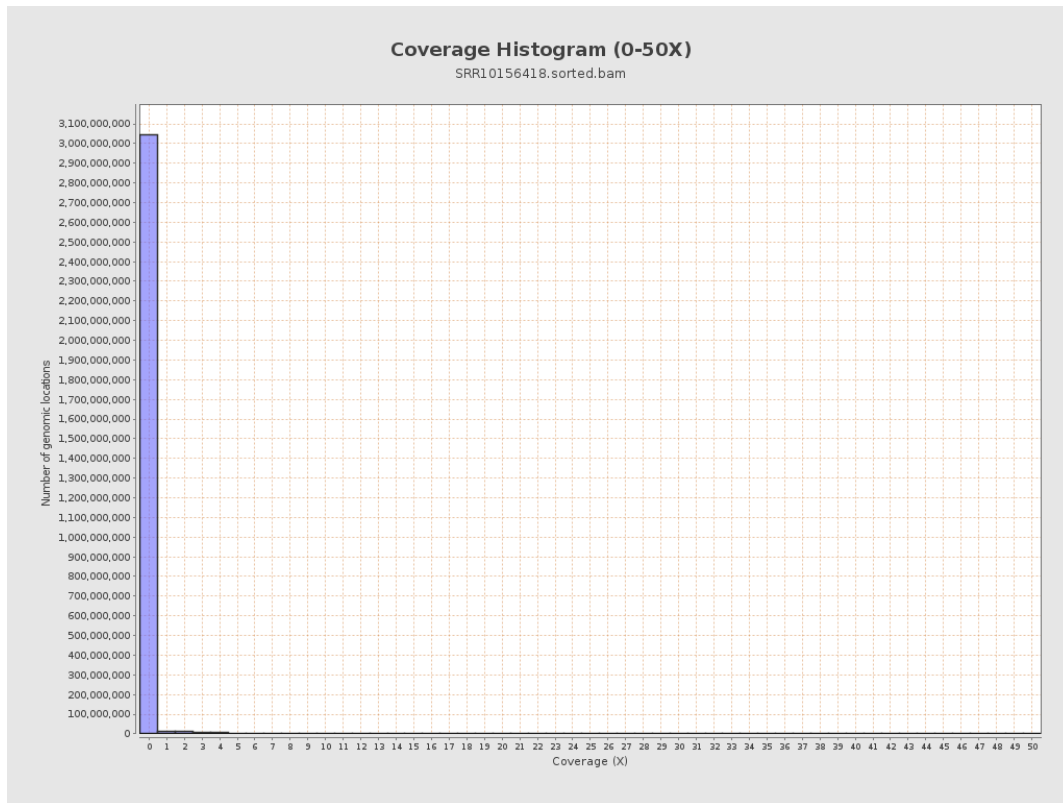
3. Results : Coverage across reference



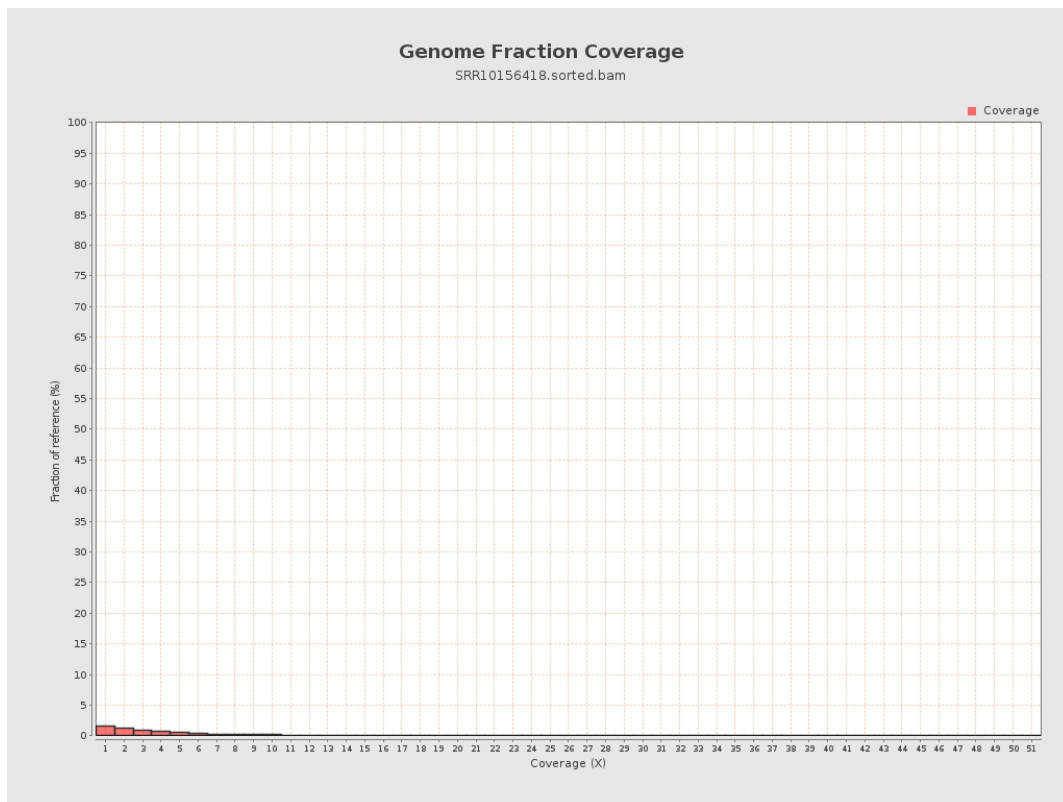
4. Results : Coverage Histogram



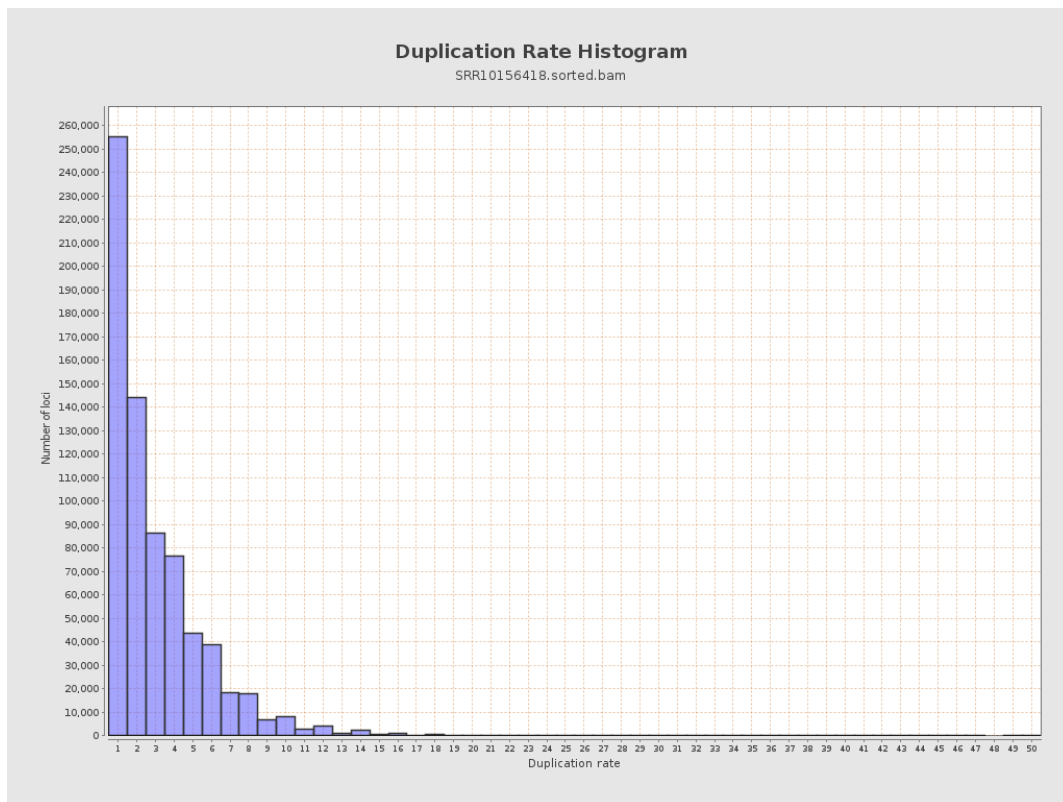
5. Results : Coverage Histogram (0-50X)



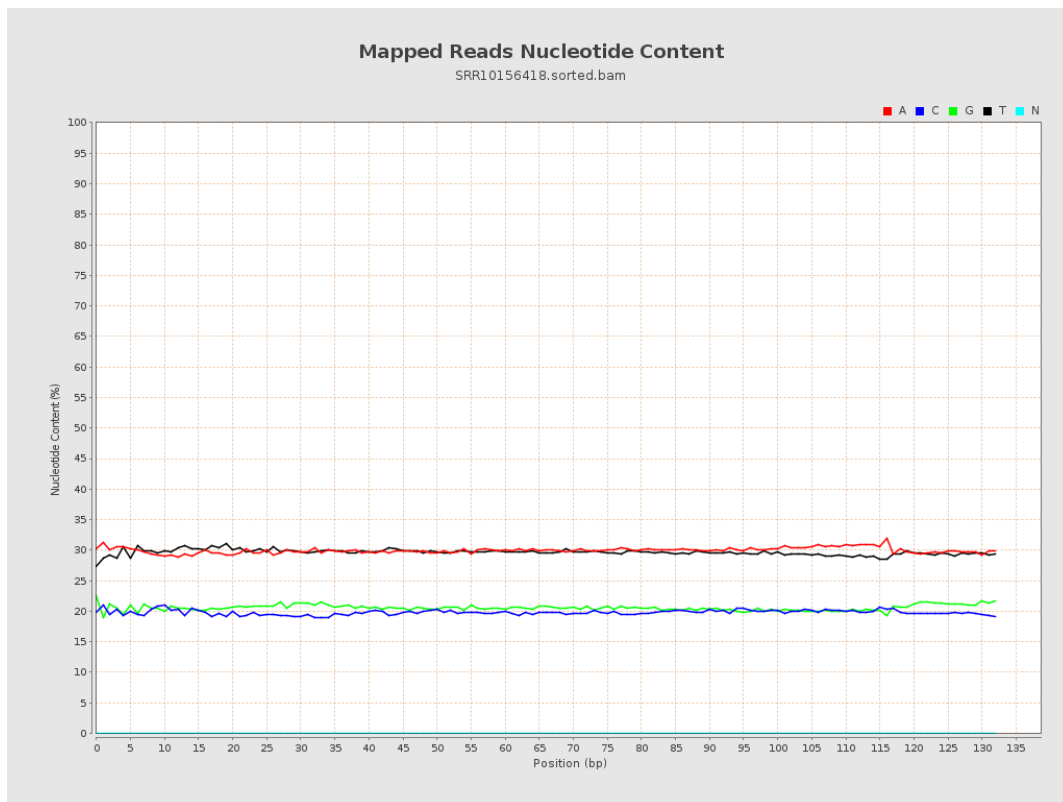
6. Results : Genome Fraction Coverage



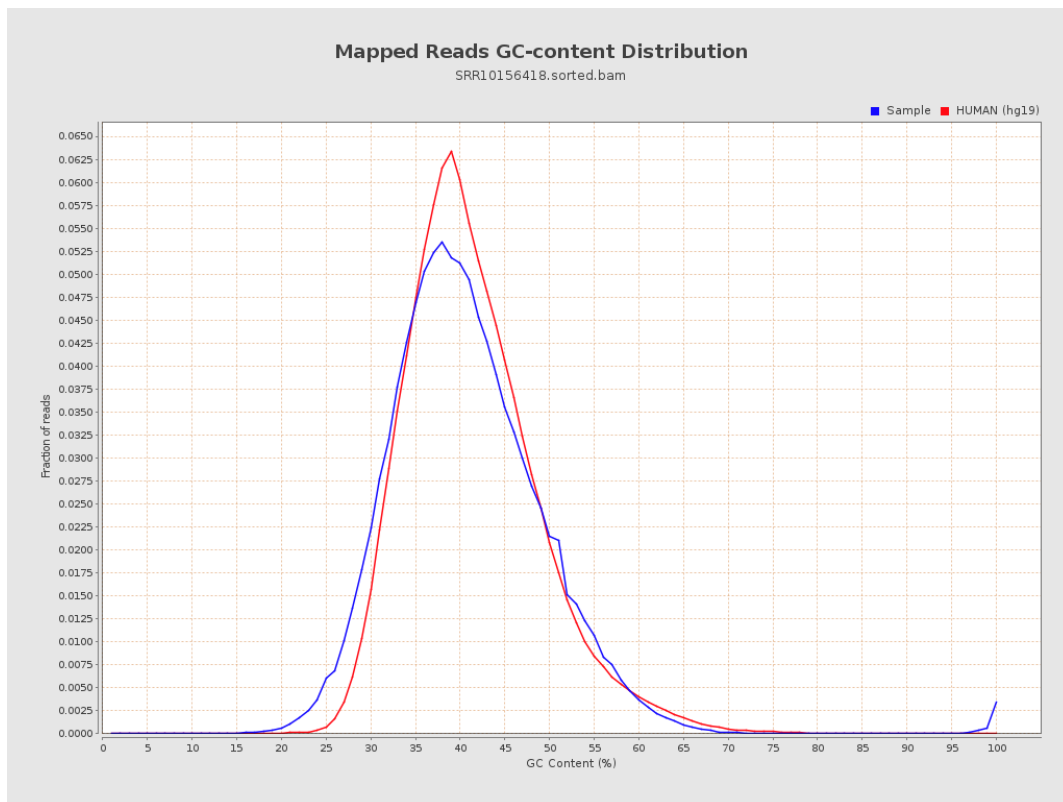
7. Results : Duplication Rate Histogram



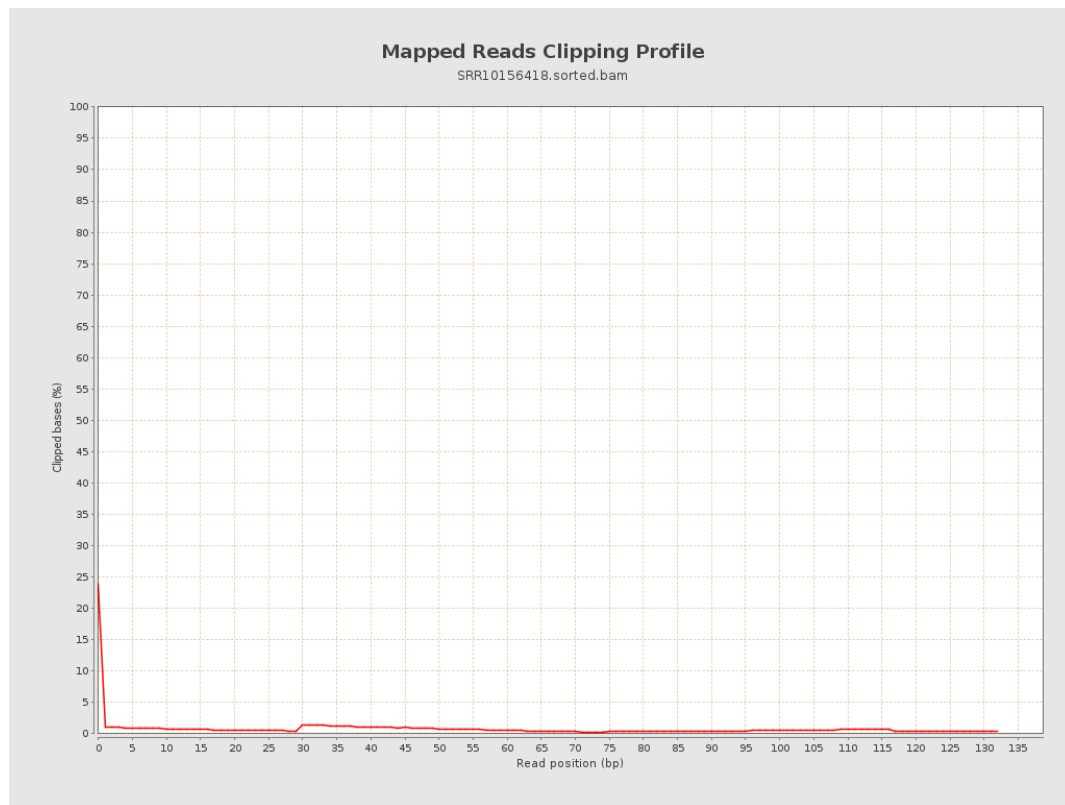
8. Results : Mapped Reads Nucleotide Content



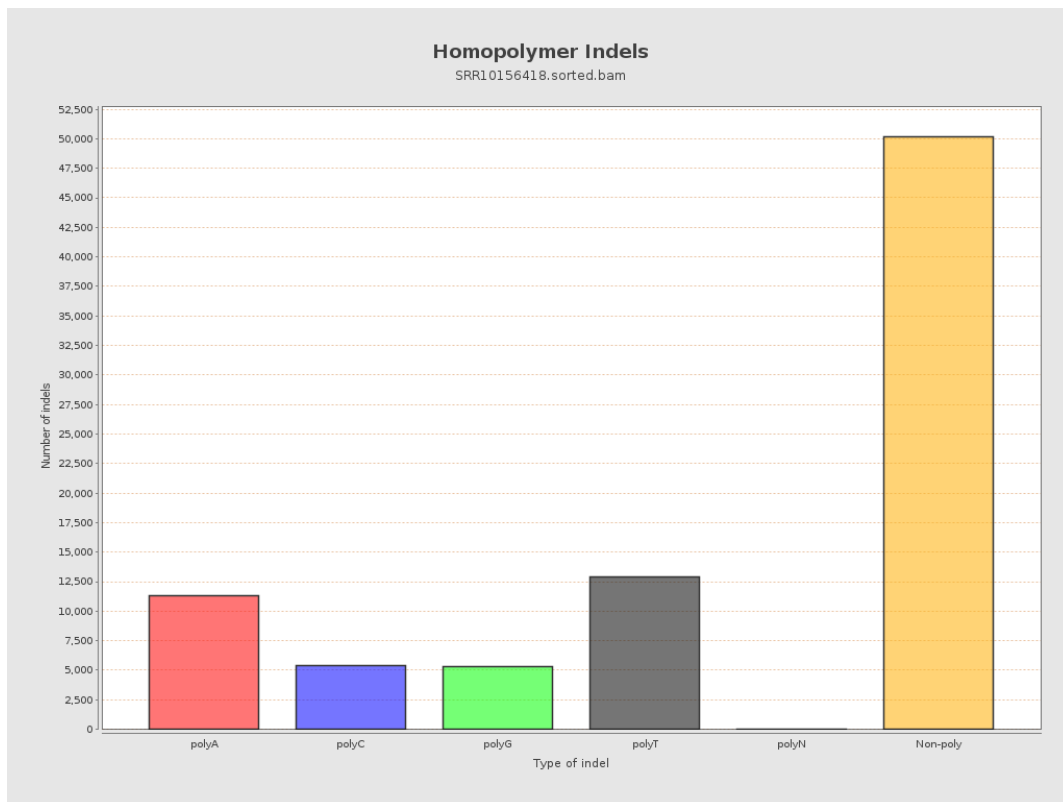
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



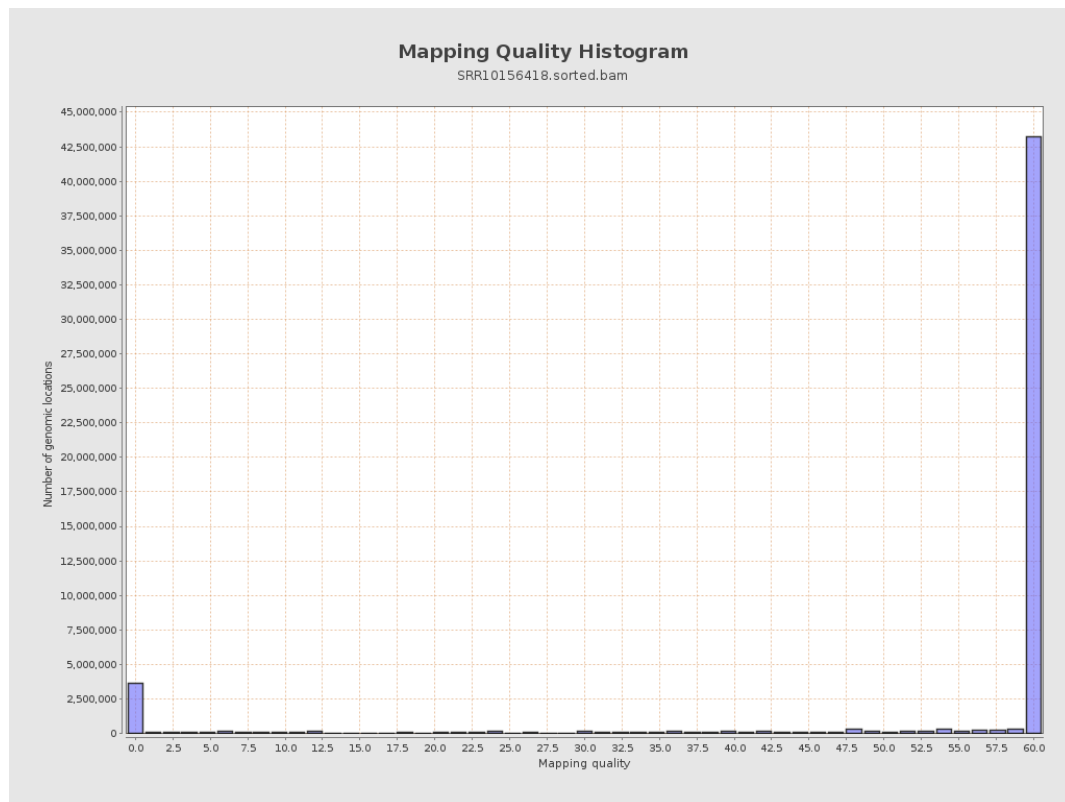
11. Results : Homopolymer Indels



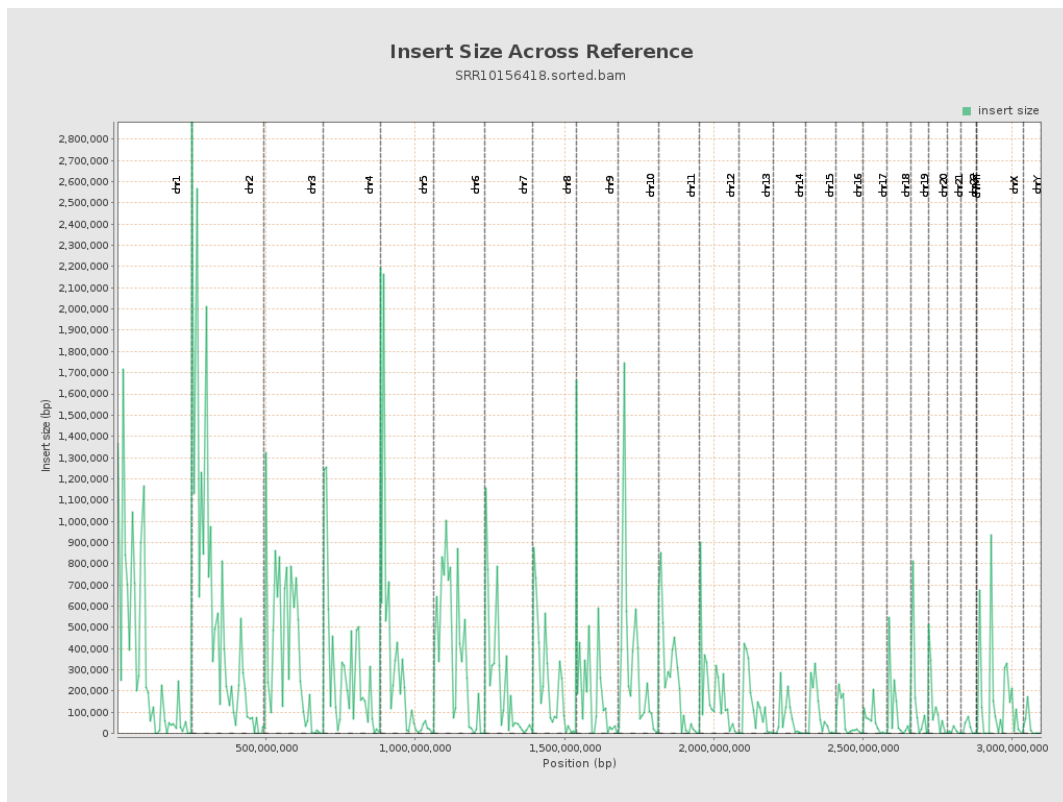
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

