

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 02:37:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10156410.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_SRR10156410 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10156410_1.fastq.gz SRR10156410_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 02:37:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10156410.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,270,332
Mapped reads	2,225,315 / 98.02%
Unmapped reads	45,017 / 1.98%
Mapped paired reads	2,225,315 / 98.02%
Mapped reads, first in pair	1,112,674 / 49.01%
Mapped reads, second in pair	1,112,641 / 49.01%
Mapped reads, both in pair	2,198,986 / 96.86%
Mapped reads, singletons	26,329 / 1.16%
Secondary alignments	0
Supplementary alignments	300,161 / 13.22%
Read min/max/mean length	30 / 133 / 124.41
Duplicated reads (estimated)	1,679,140 / 73.96%
Duplication rate	59.97%
Clipped reads	1,159,750 / 51.08%

2.2. ACGT Content

Number/percentage of A's	75,145,434 / 30.06%
Number/percentage of C's	49,308,826 / 19.72%
Number/percentage of T's	74,524,050 / 29.81%
Number/percentage of G's	51,018,729 / 20.41%
Number/percentage of N's	2,021 / 0%

GC Percentage	40.13%
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2.3. Coverage

Mean	0.0808
Standard Deviation	1.5918

2.4. Mapping Quality

Mean Mapping Quality	52.67
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2.5. Insert size

Mean	900,021.88
Standard Deviation	8,658,779.19
P25/Median/P75	99 / 141 / 210

2.6. Mismatches and indels

General error rate	0.85%
Mismatches	2,058,876
Insertions	27,963
Mapped reads with at least one insertion	1.21%
Deletions	70,542
Mapped reads with at least one deletion	3.1%
Homopolymer indels	41.16%

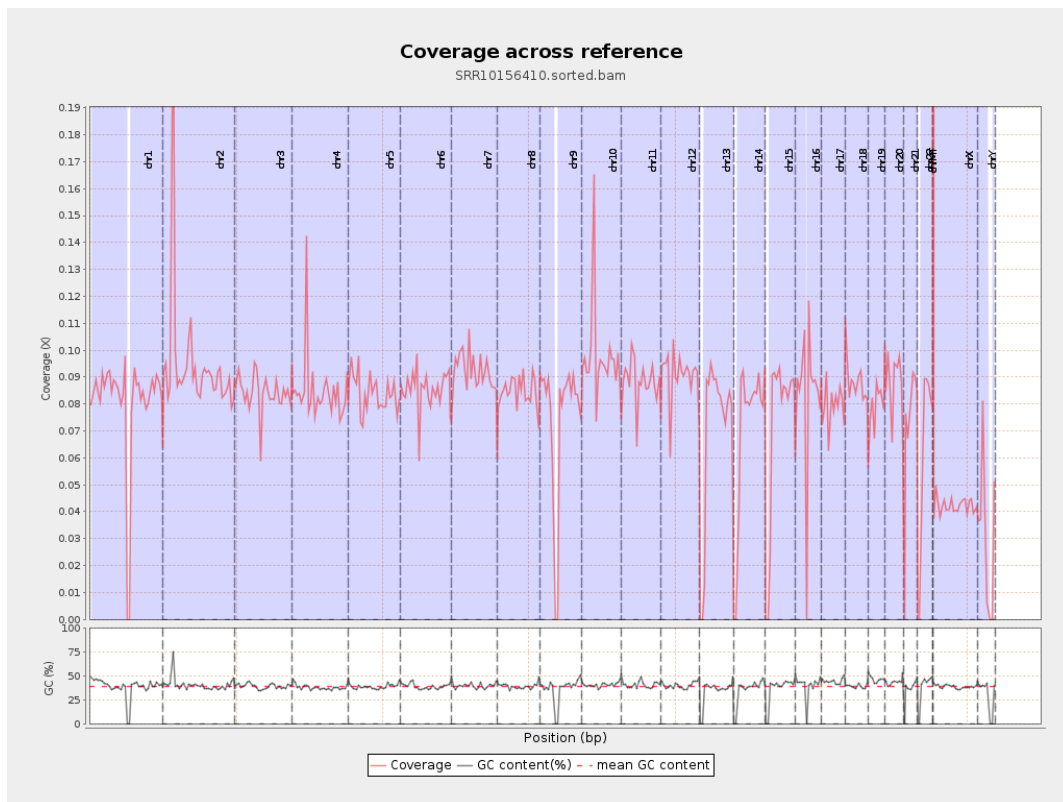
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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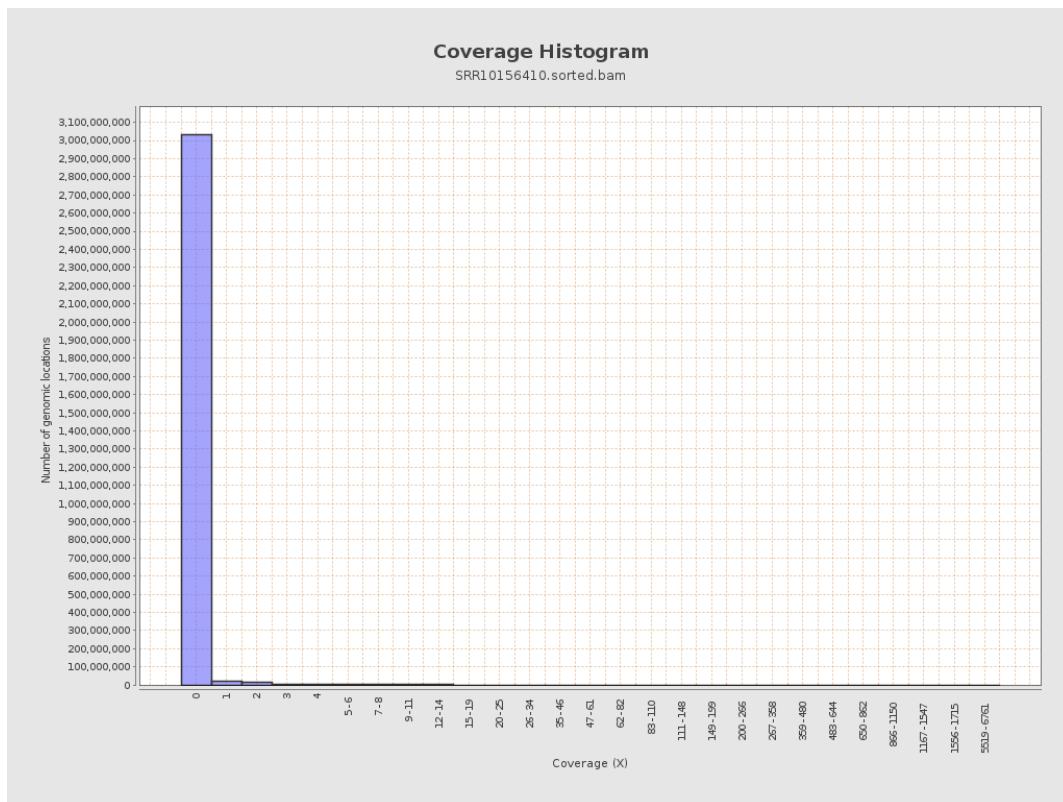
		bases	coverage	deviation
chr1	249250621	20066520	0.0805	1.0107
chr2	243199373	22945692	0.0943	4.7901
chr3	198022430	16676849	0.0842	0.8212
chr4	191154276	16256506	0.085	0.9354
chr5	180915260	15213655	0.0841	0.8245
chr6	171115067	14627251	0.0855	0.8671
chr7	159138663	14636182	0.092	1.0234
chr8	146364022	12380410	0.0846	1.0724
chr9	141213431	10490918	0.0743	0.8658
chr10	135534747	13218200	0.0975	1.1381
chr11	135006516	11916036	0.0883	0.8539
chr12	133851895	12185575	0.091	0.8679
chr13	115169878	8043716	0.0698	0.7556
chr14	107349540	7585891	0.0707	0.7516
chr15	102531392	7248483	0.0707	0.7475
chr16	90354753	7466287	0.0826	0.8759
chr17	81195210	6451843	0.0795	0.7928
chr18	78077248	6884578	0.0882	1.0474
chr19	59128983	4713518	0.0797	0.8408
chr20	63025520	5547238	0.088	0.8487
chr21	48129895	3565649	0.0741	0.8722
chr22	51304566	3118795	0.0608	0.7195
chrMT	16571	519709	31.3626	23.905
chrX	155270560	6548598	0.0422	0.5806

chrY	59373566	1860210	0.0313	0.6181
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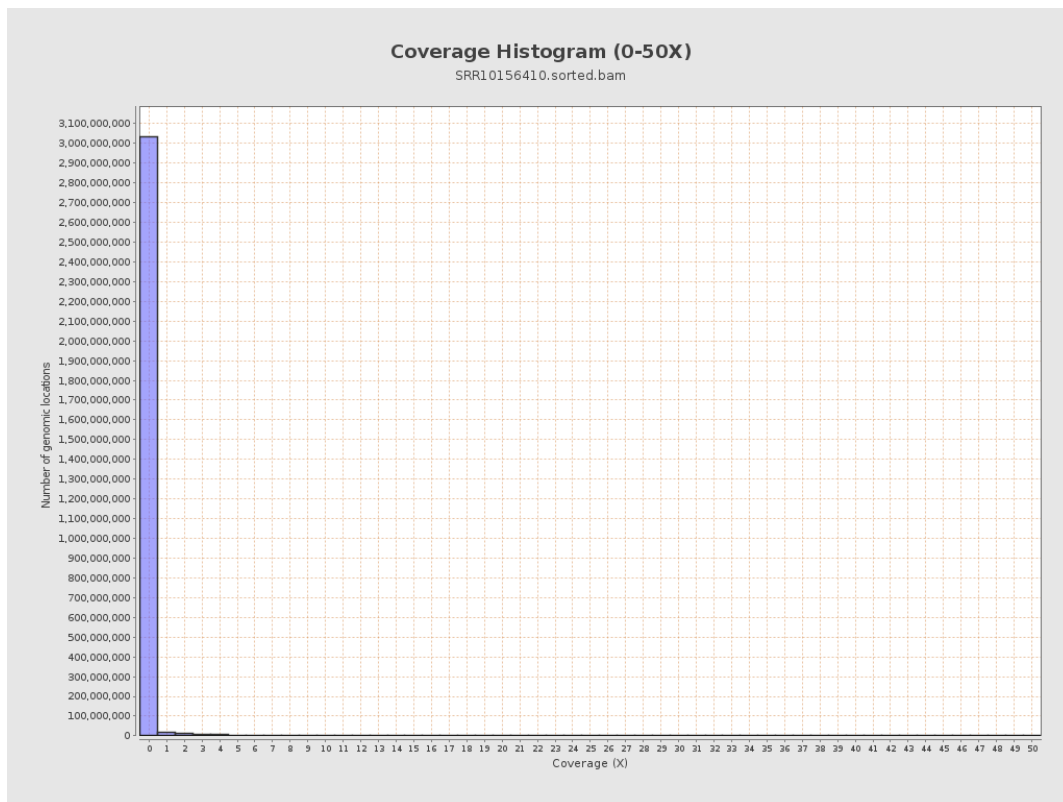
3. Results : Coverage across reference



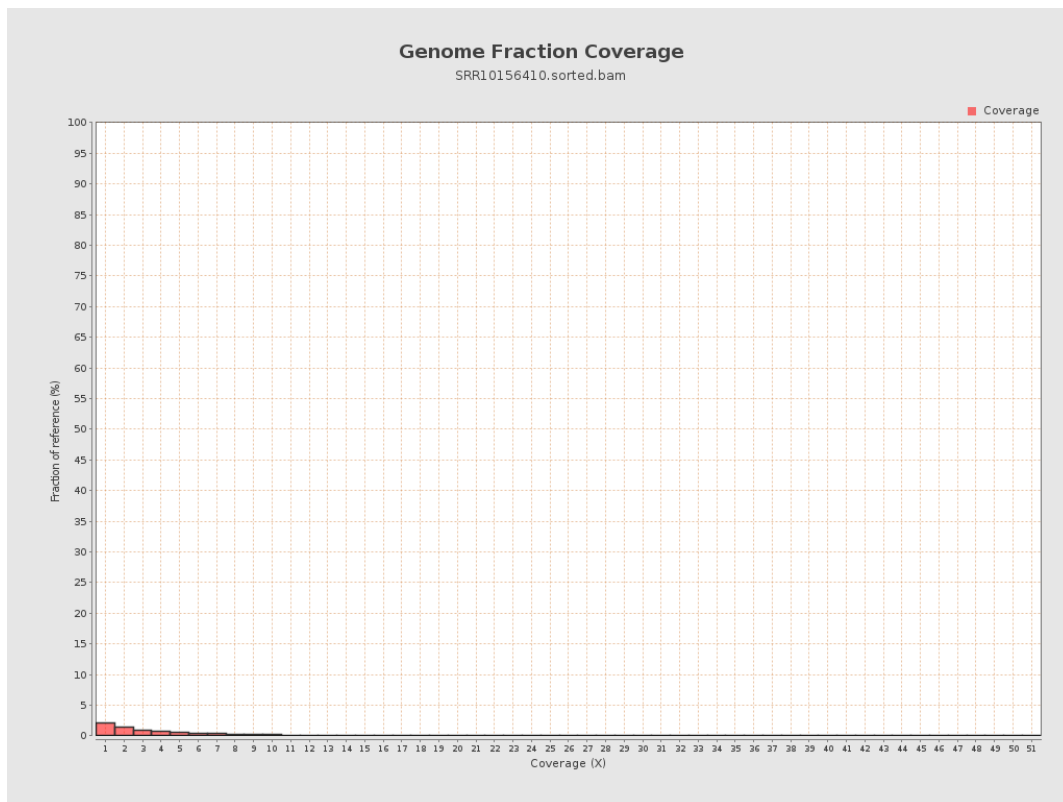
4. Results : Coverage Histogram



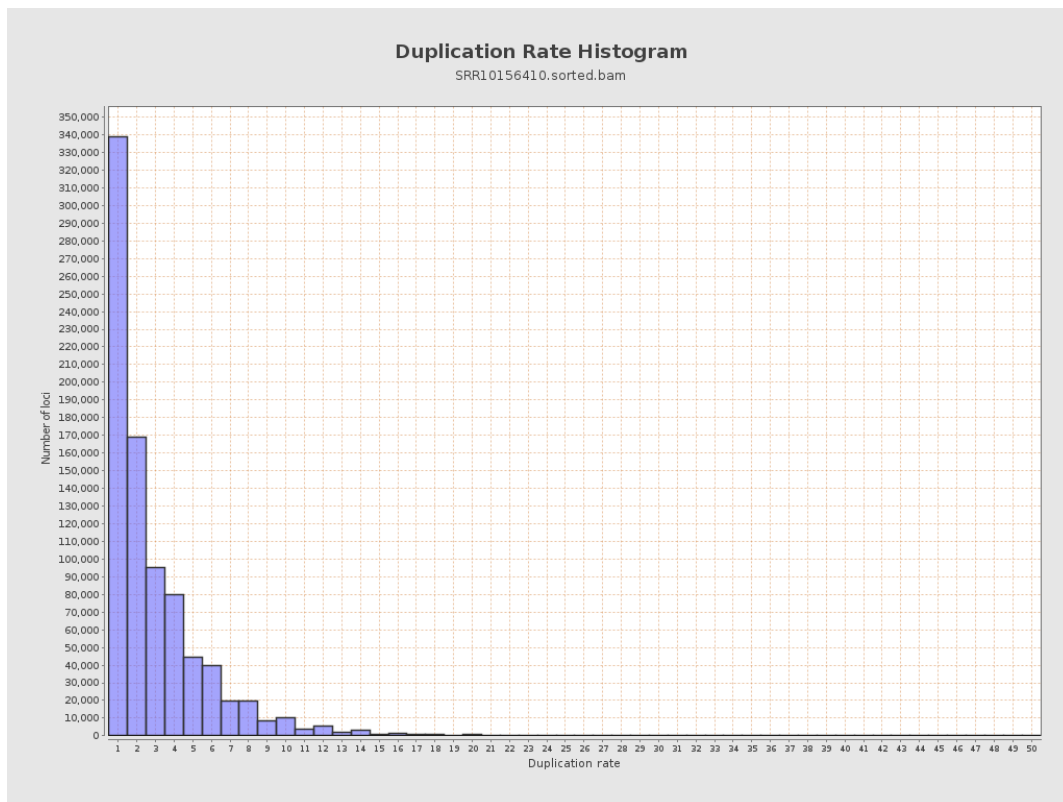
5. Results : Coverage Histogram (0-50X)



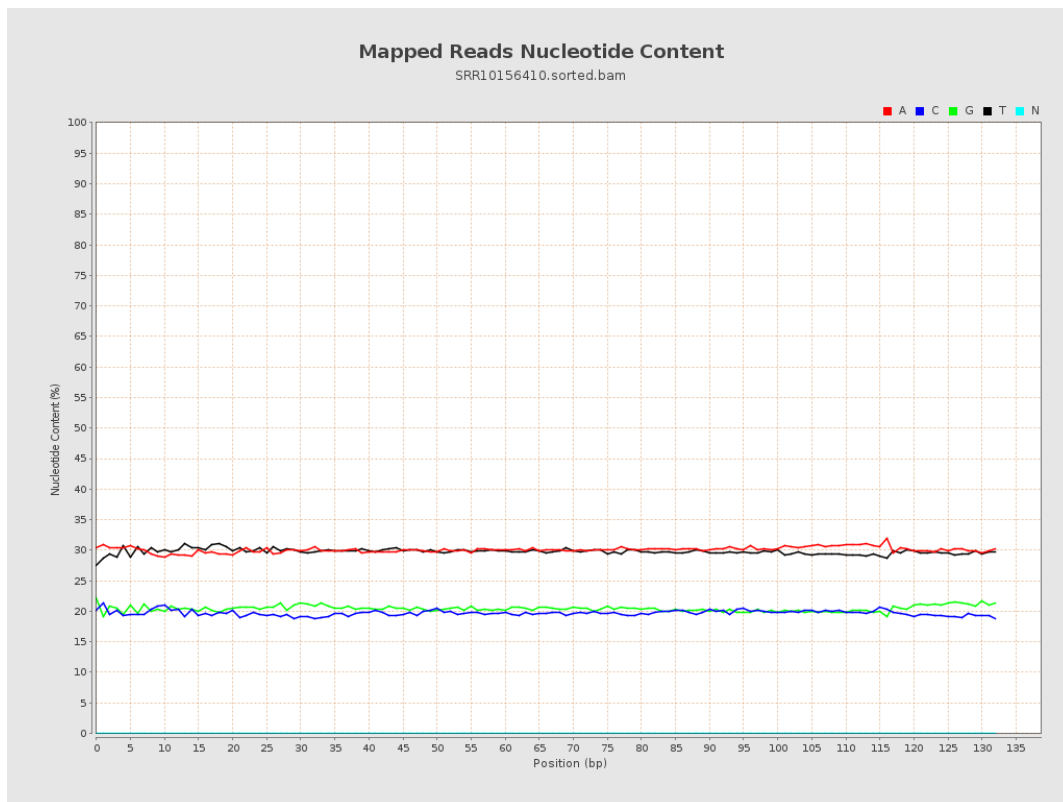
6. Results : Genome Fraction Coverage



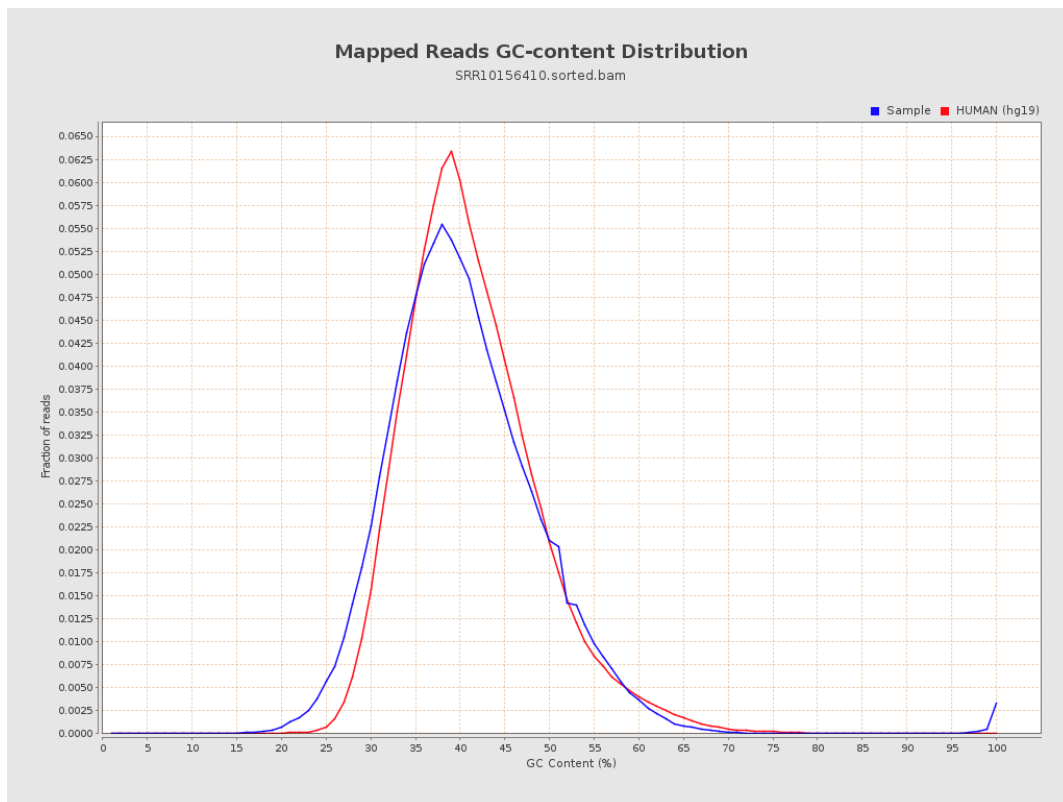
7. Results : Duplication Rate Histogram



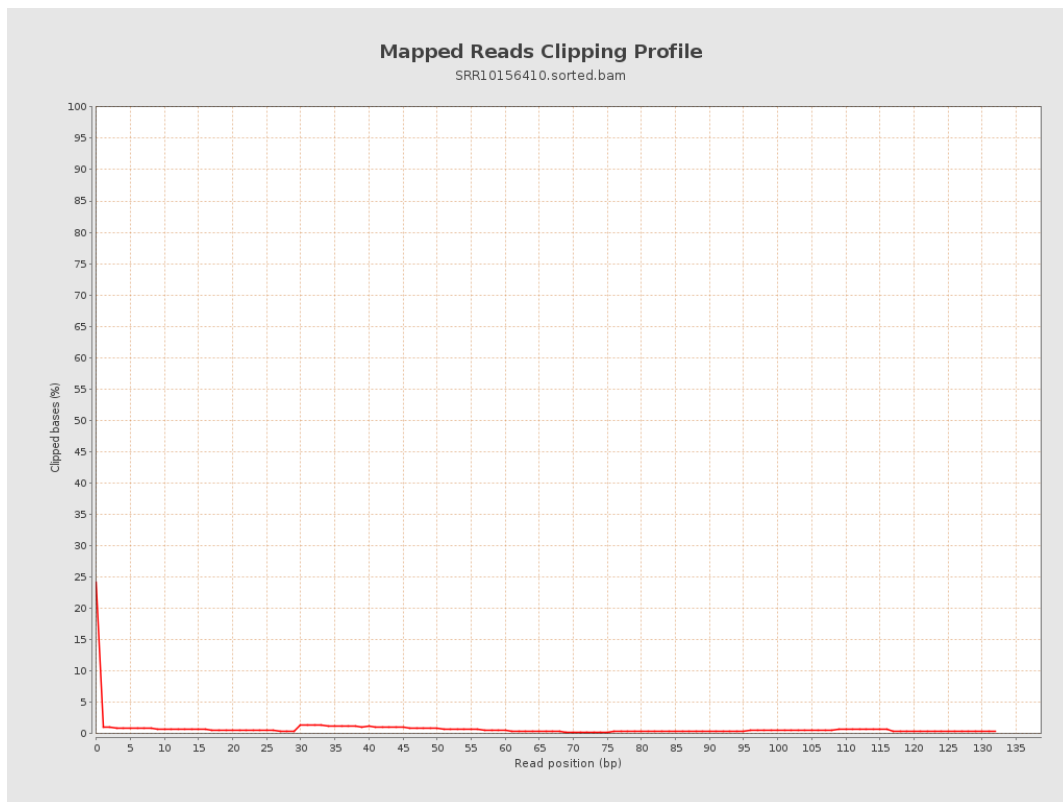
8. Results : Mapped Reads Nucleotide Content



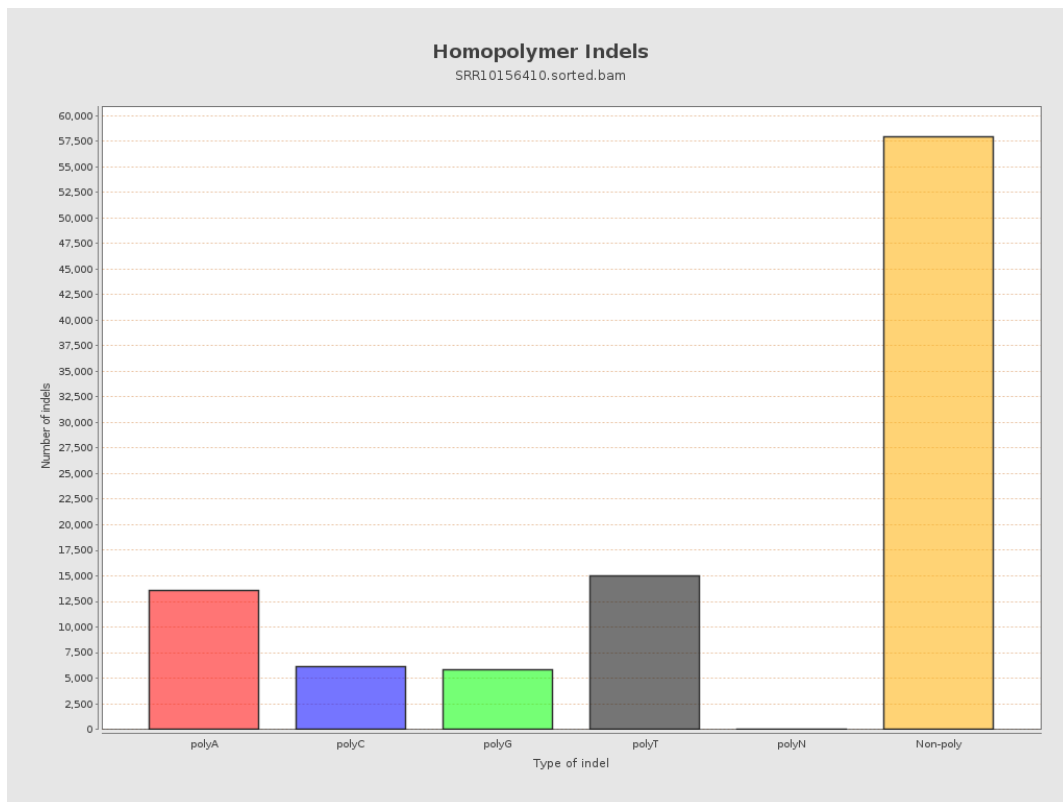
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



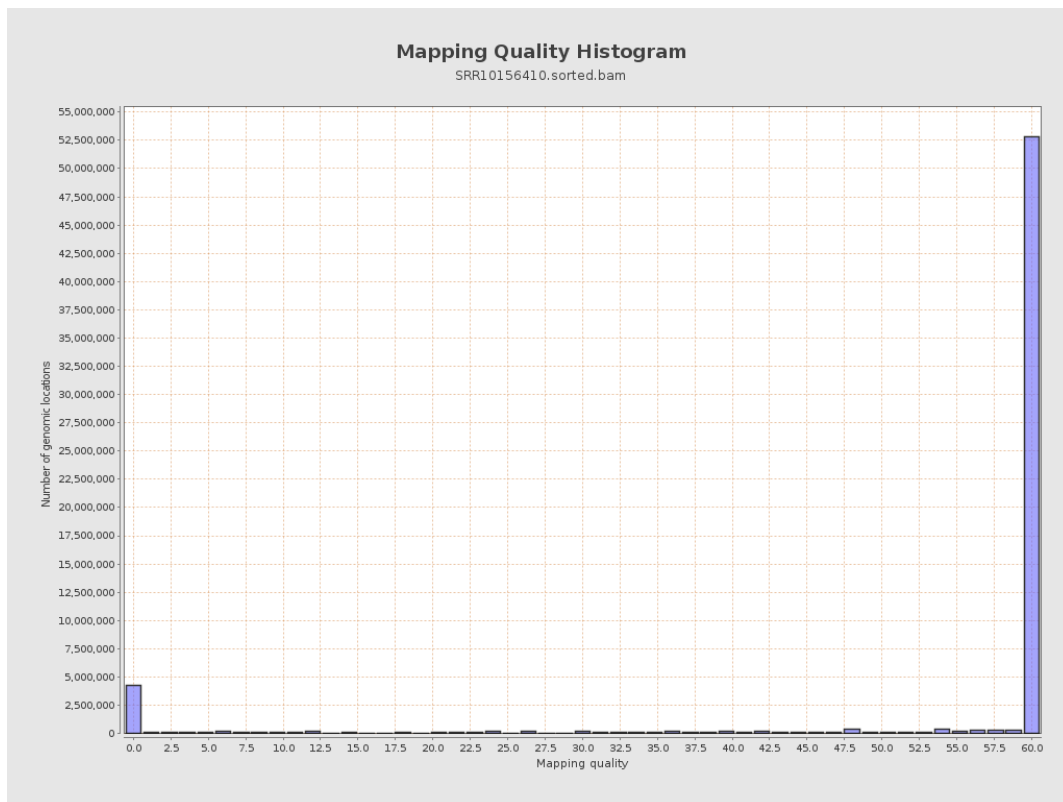
11. Results : Homopolymer Indels



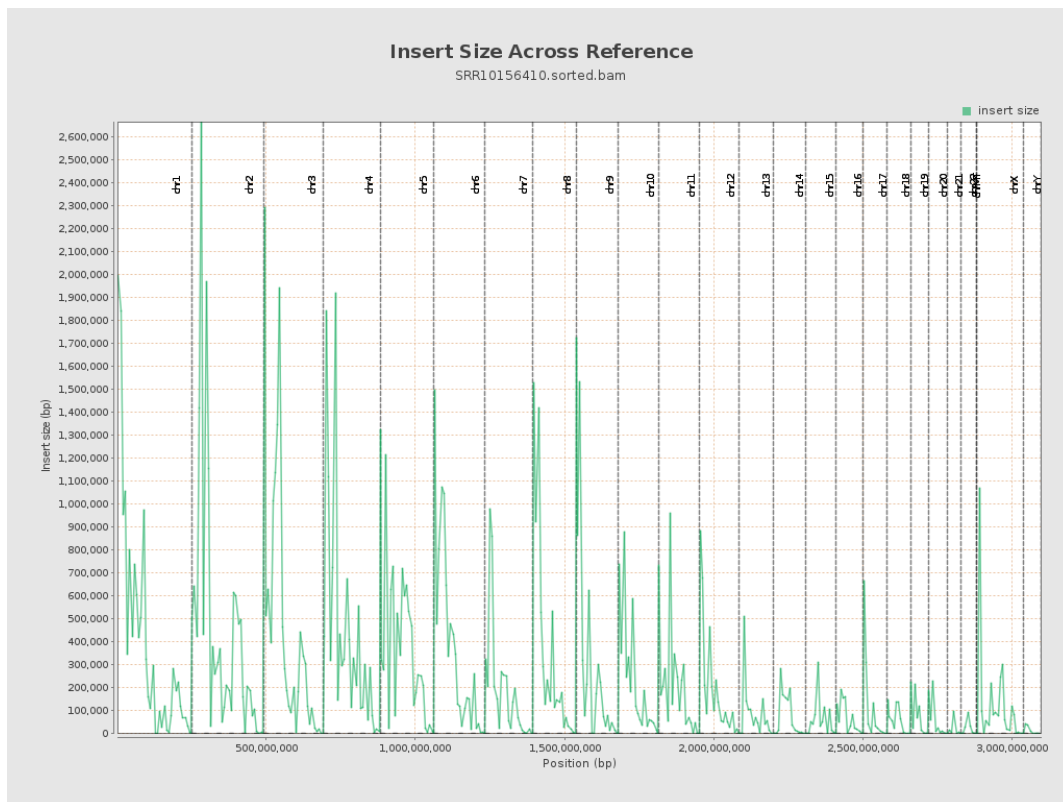
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

