

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 03:41:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10156415.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_SRR10156415 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10156415_1.fastq.gz SRR10156415_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 03:41:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10156415.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,608,694
Mapped reads	6,476,483 / 98%
Unmapped reads	132,211 / 2%
Mapped paired reads	6,476,483 / 98%
Mapped reads, first in pair	3,239,974 / 49.03%
Mapped reads, second in pair	3,236,509 / 48.97%
Mapped reads, both in pair	6,393,170 / 96.74%
Mapped reads, singletons	83,313 / 1.26%
Secondary alignments	0
Supplementary alignments	848,521 / 12.84%
Read min/max/mean length	30 / 133 / 125.13
Duplicated reads (estimated)	5,171,527 / 78.25%
Duplication rate	64.97%
Clipped reads	3,307,377 / 50.05%

2.2. ACGT Content

Number/percentage of A's	219,471,687 / 29.96%
Number/percentage of C's	144,815,047 / 19.77%
Number/percentage of T's	217,716,759 / 29.72%
Number/percentage of G's	150,437,488 / 20.54%
Number/percentage of N's	5,743 / 0%

GC Percentage	40.31%
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2.3. Coverage

Mean	0.2368
Standard Deviation	4.4423

2.4. Mapping Quality

Mean Mapping Quality	52.57
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2.5. Insert size

Mean	1,277,169.56
Standard Deviation	9,400,645.07
P25/Median/P75	106 / 155 / 243

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	6,173,658
Insertions	80,749
Mapped reads with at least one insertion	1.2%
Deletions	224,171
Mapped reads with at least one deletion	3.38%
Homopolymer indels	40.93%

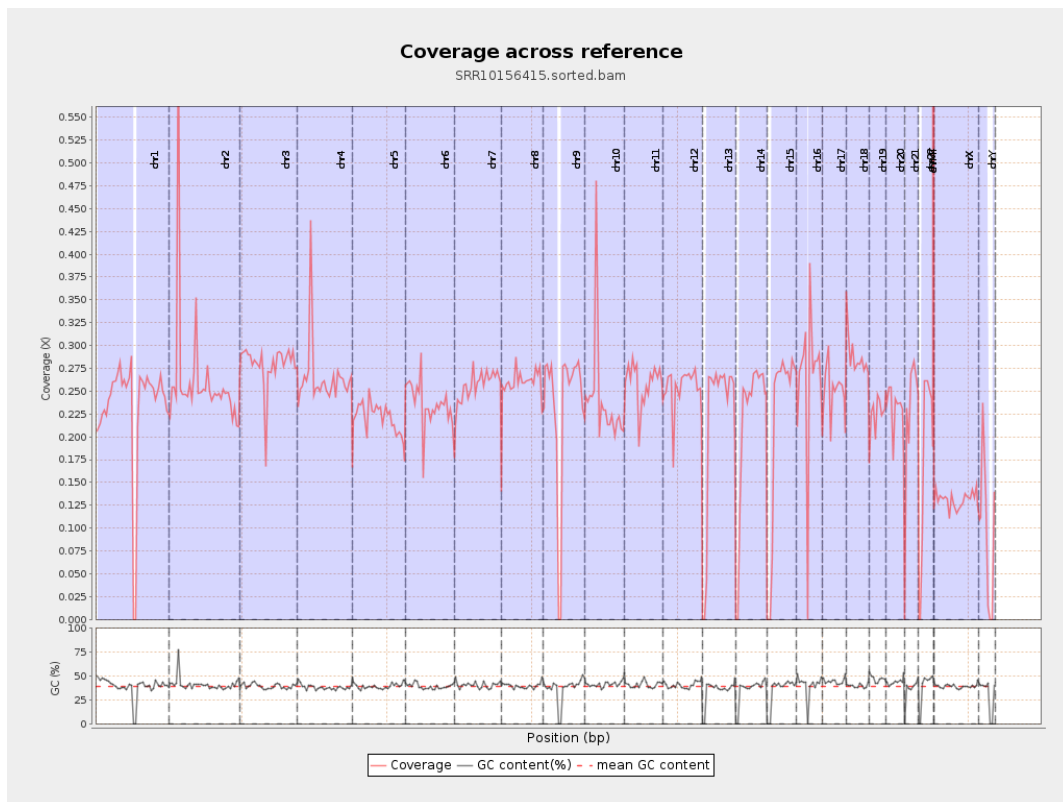
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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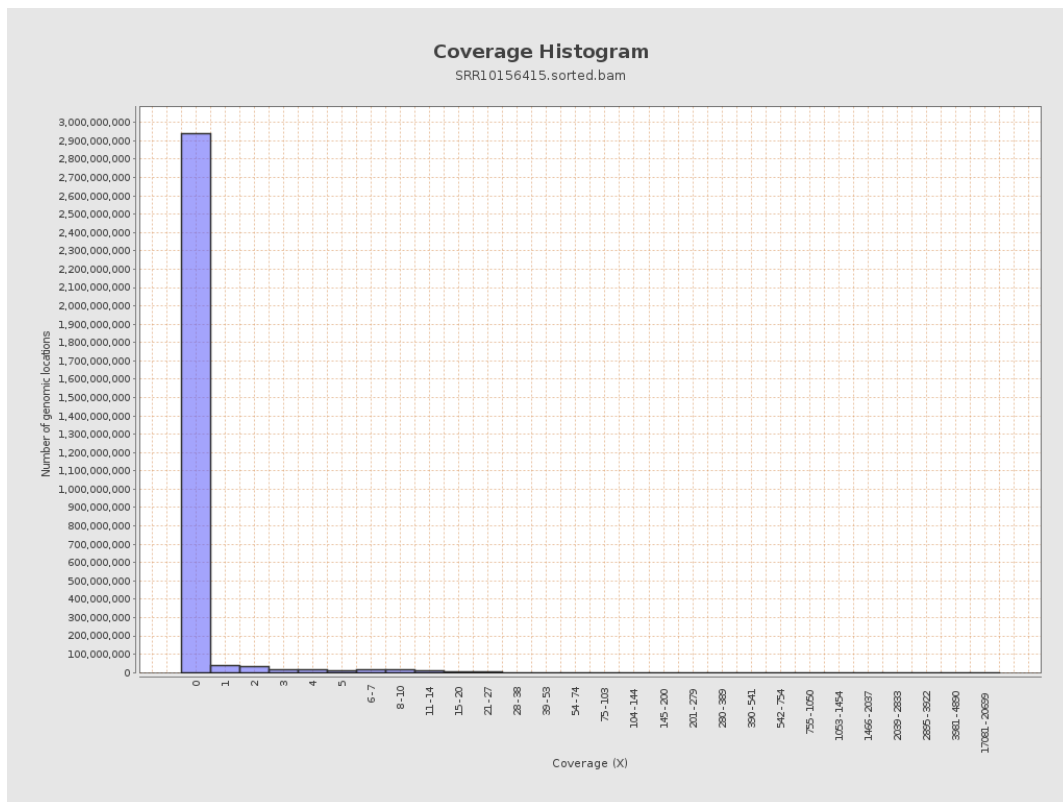
		bases	coverage	deviation
chr1	249250621	58392353	0.2343	2.0064
chr2	243199373	63646065	0.2617	14.5472
chr3	198022430	55272391	0.2791	1.5948
chr4	191154276	50473416	0.264	2.1329
chr5	180915260	40010311	0.2212	1.4107
chr6	171115067	40241144	0.2352	1.6474
chr7	159138663	40972667	0.2575	1.9174
chr8	146364022	38198034	0.261	2.4846
chr9	141213431	33165789	0.2349	1.9221
chr10	135534747	32495962	0.2398	2.6484
chr11	135006516	34991925	0.2592	1.5826
chr12	133851895	33994390	0.254	1.565
chr13	115169878	25054167	0.2175	1.4087
chr14	107349540	23069460	0.2149	1.3998
chr15	102531392	22361957	0.2181	1.4295
chr16	90354753	23673157	0.262	2.1047
chr17	81195210	20259007	0.2495	1.658
chr18	78077248	22445697	0.2875	2.6898
chr19	59128983	13404234	0.2267	1.6458
chr20	63025520	14526069	0.2305	1.5083
chr21	48129895	10831606	0.225	1.8117
chr22	51304566	8949296	0.1744	1.5285
chrMT	16571	750739	45.3044	46.8176
chrX	155270560	20331278	0.1309	1.0881

chrY	59373566	5474136	0.0922	1.4148
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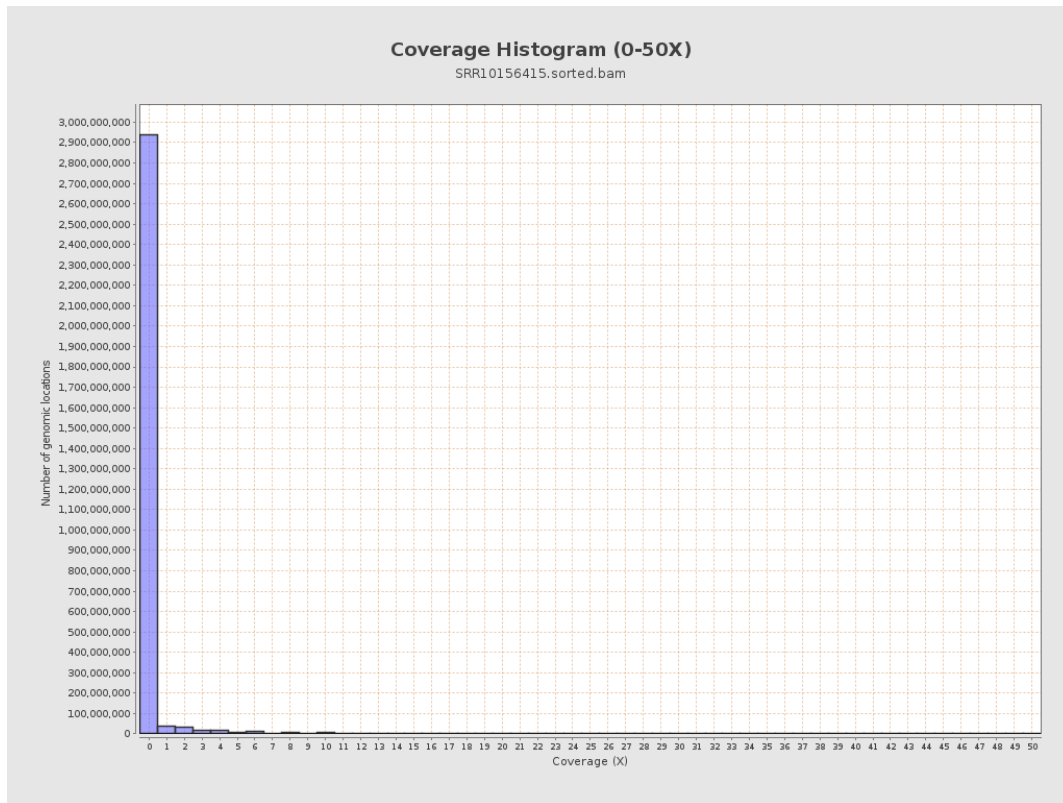
3. Results : Coverage across reference



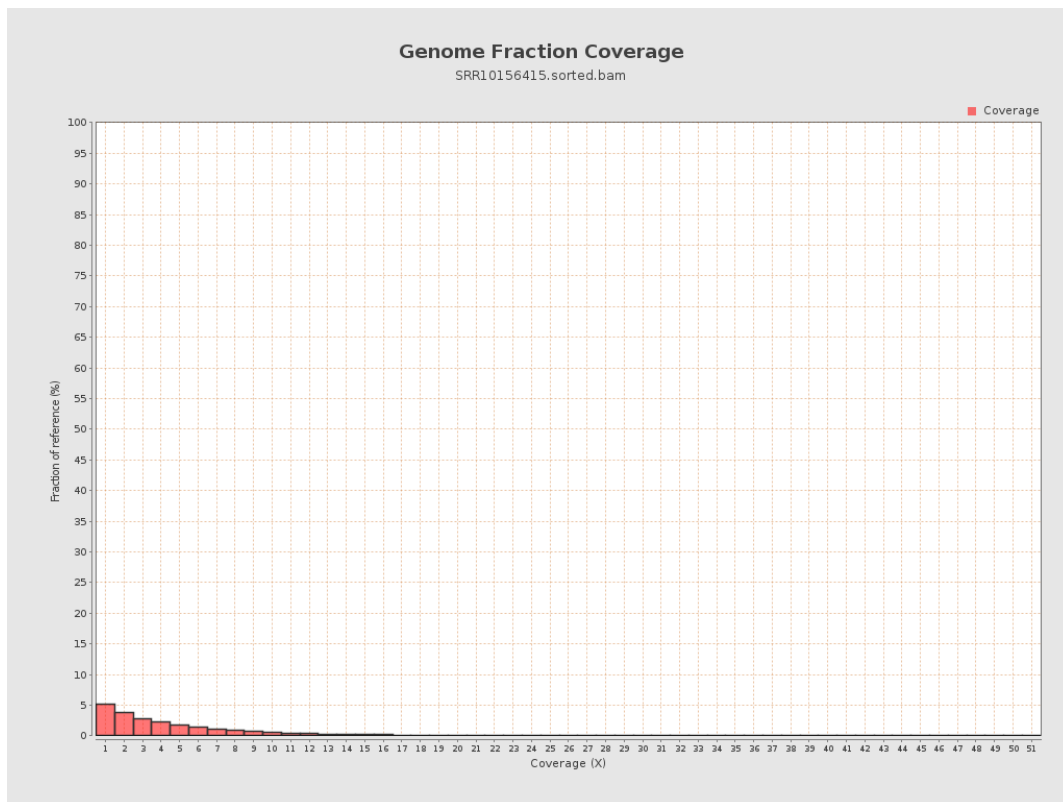
4. Results : Coverage Histogram



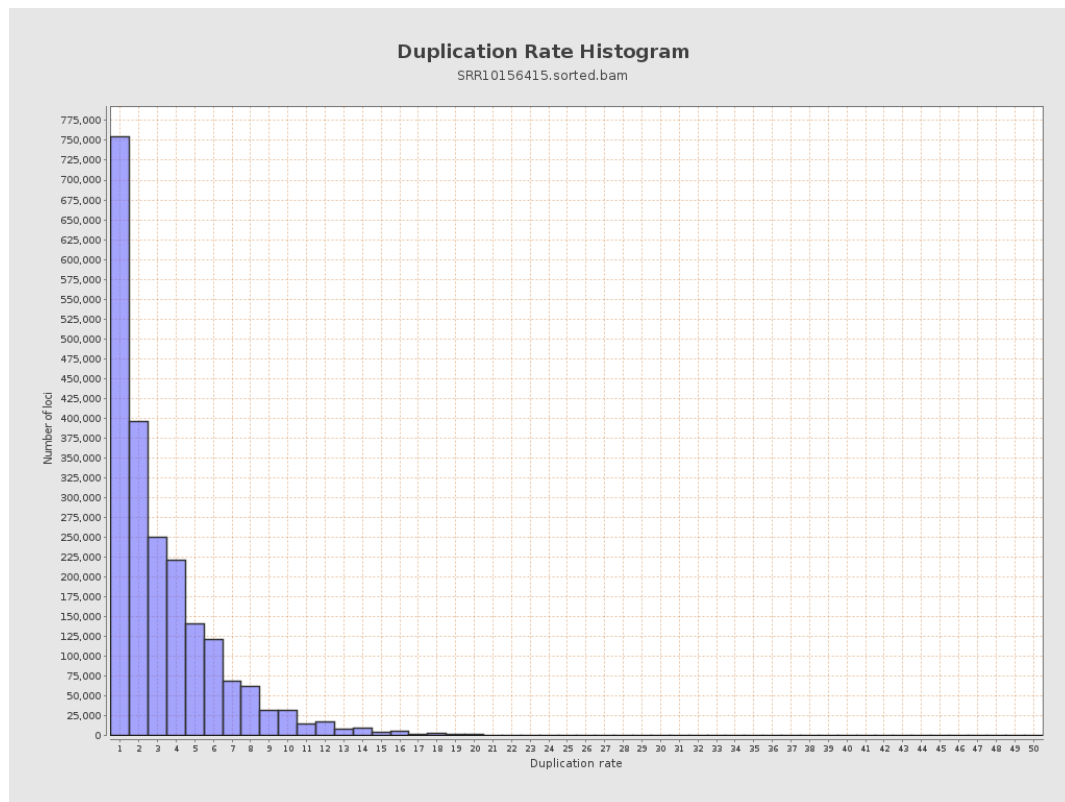
5. Results : Coverage Histogram (0-50X)



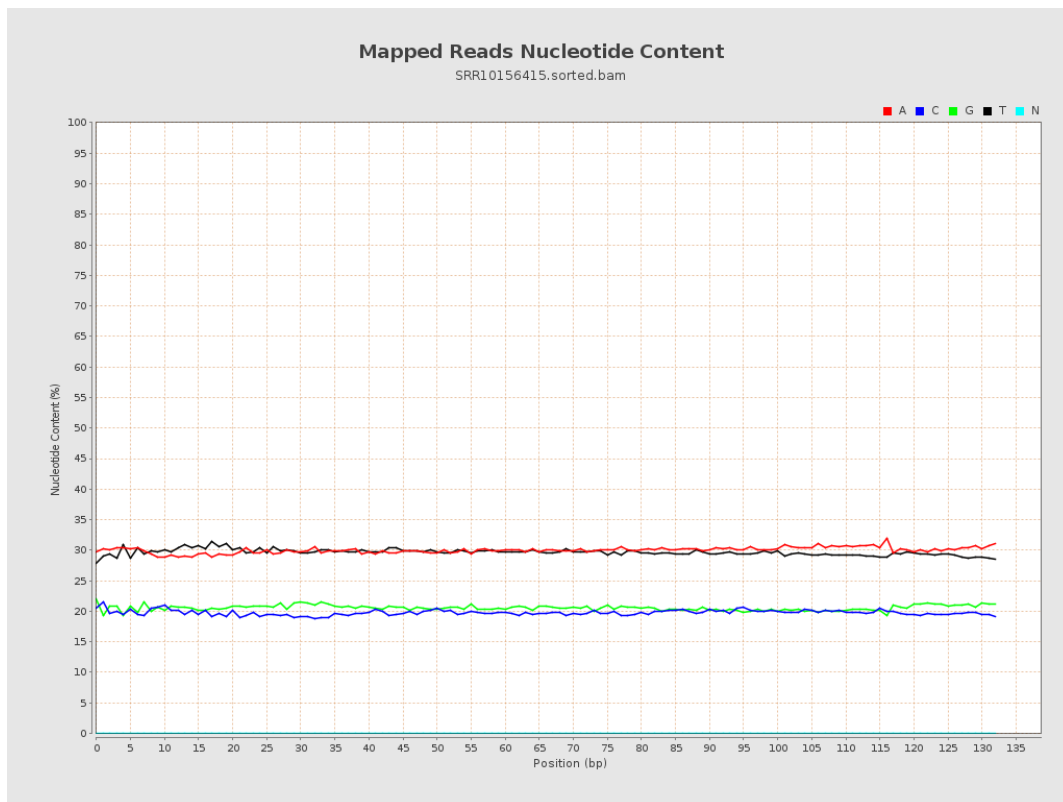
6. Results : Genome Fraction Coverage



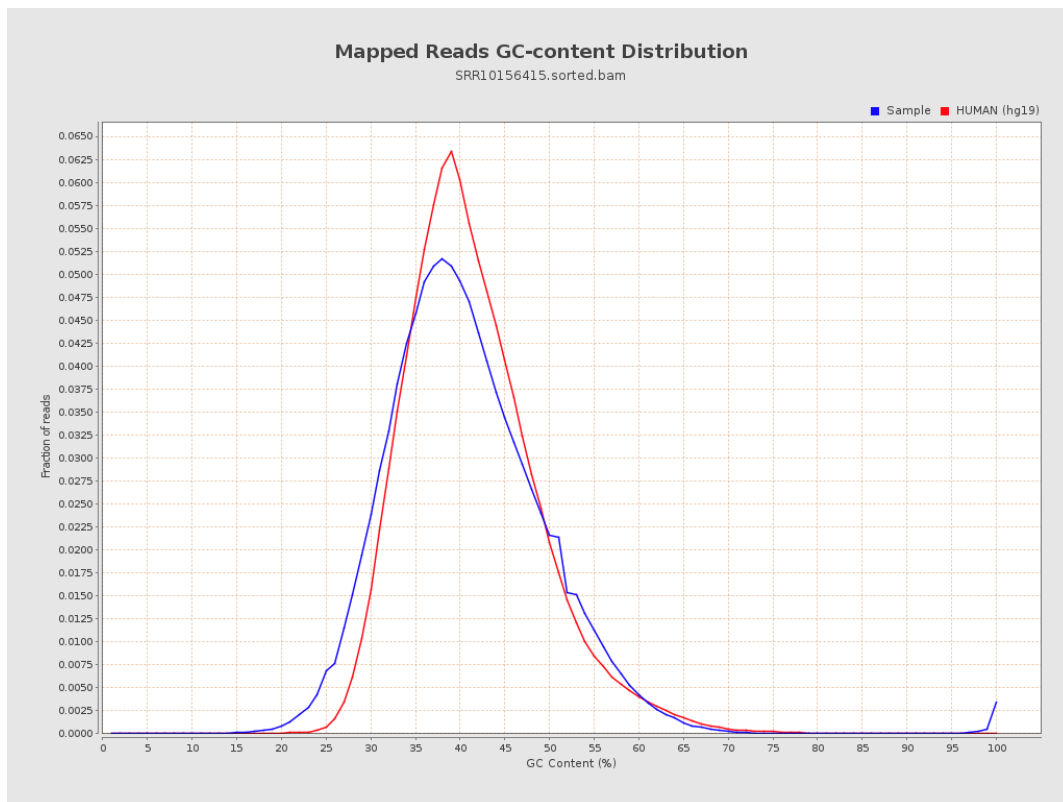
7. Results : Duplication Rate Histogram



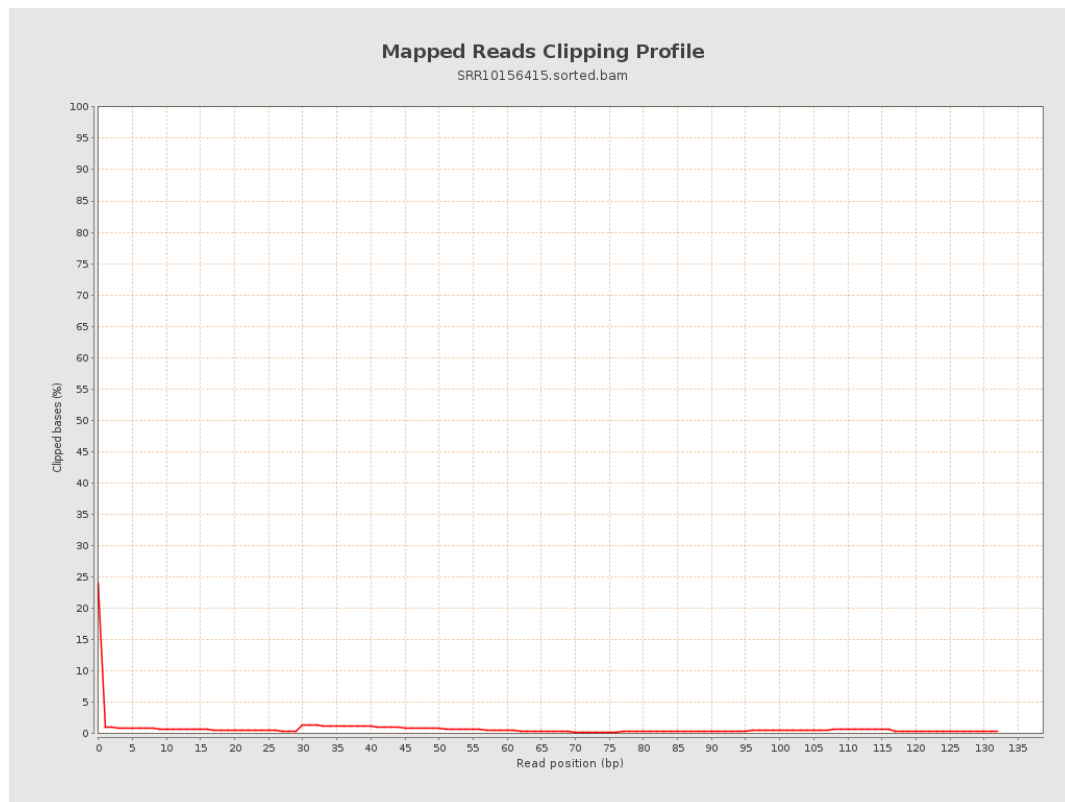
8. Results : Mapped Reads Nucleotide Content



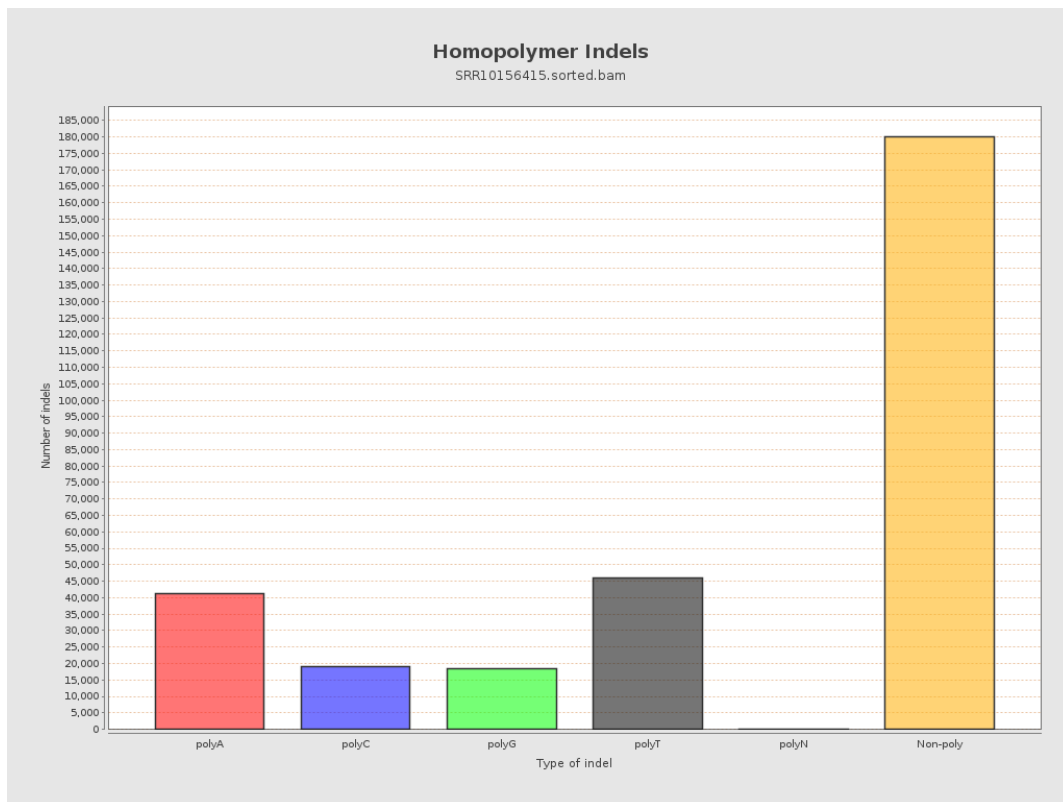
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



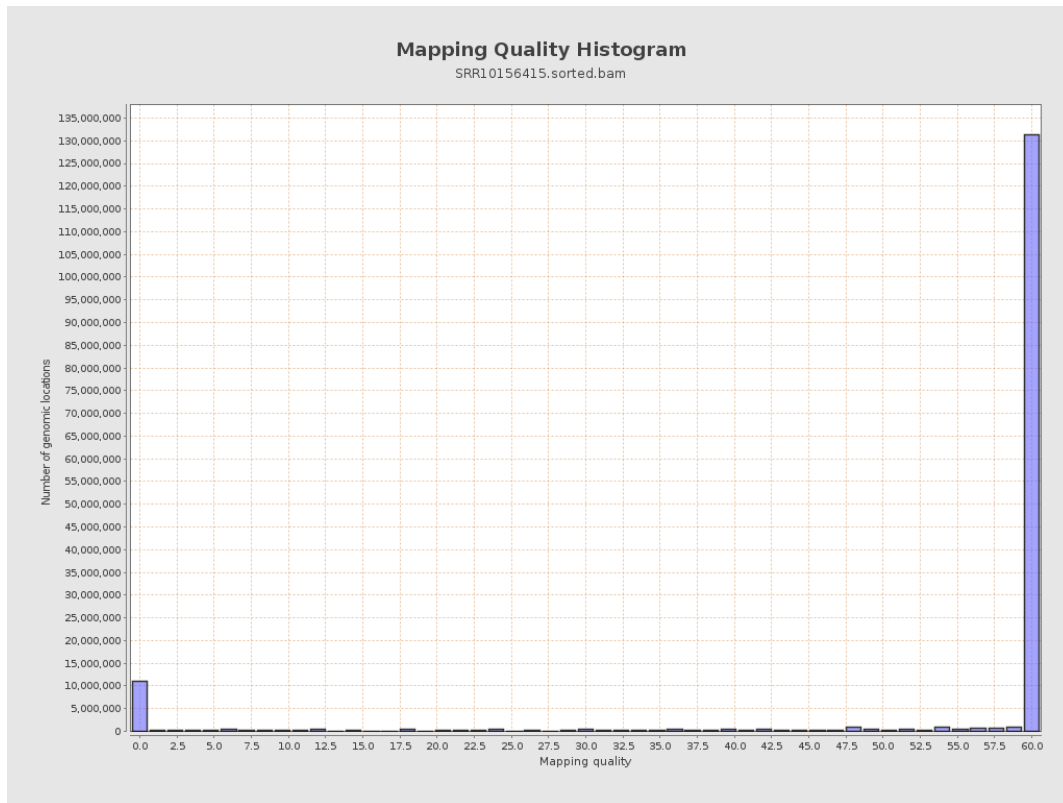
11. Results : Homopolymer Indels



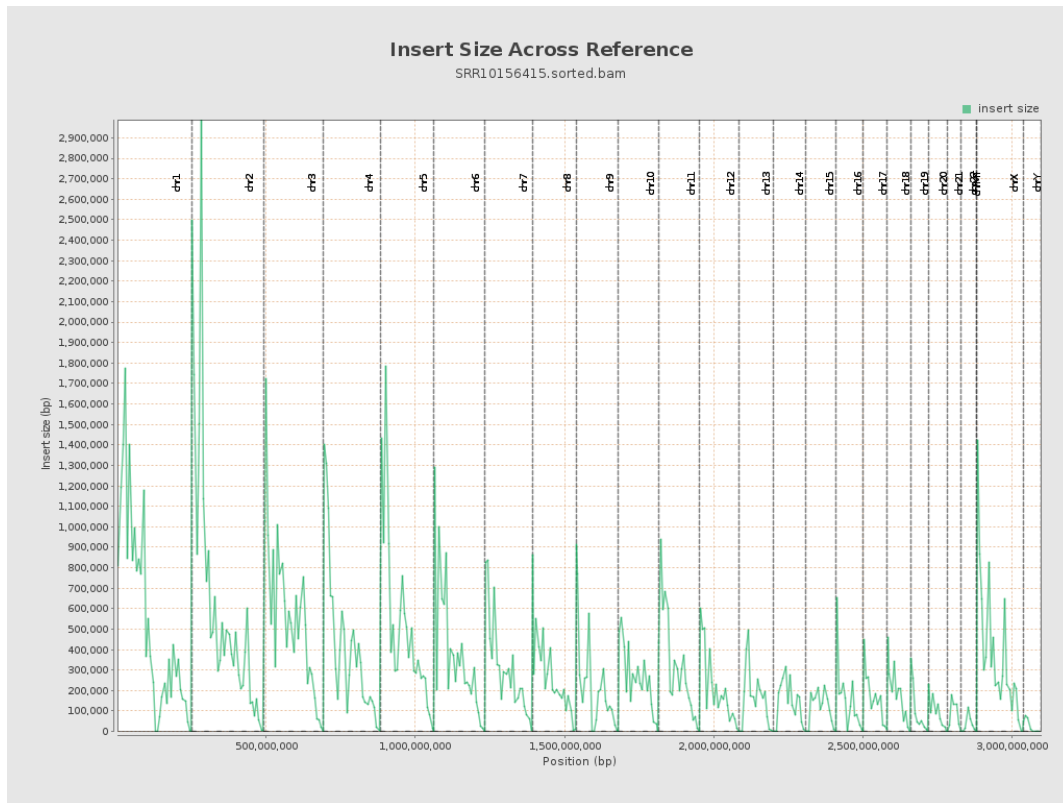
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

