

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 00:56:05

1. Input data & parameters

1.1. QualiMap command line

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qualimap bamqc -bam SRR10173875.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_SRR10173875 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173875_1.fastq.gz SRR10173875_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 00:56:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173875.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,353,276
Mapped reads	1,316,763 / 97.3%
Unmapped reads	36,513 / 2.7%
Mapped paired reads	1,316,763 / 97.3%
Mapped reads, first in pair	659,882 / 48.76%
Mapped reads, second in pair	656,881 / 48.54%
Mapped reads, both in pair	1,293,814 / 95.61%
Mapped reads, singletons	22,949 / 1.7%
Secondary alignments	0
Supplementary alignments	136,488 / 10.09%
Read min/max/mean length	30 / 133 / 127.82
Duplicated reads (estimated)	956,531 / 70.68%
Duplication rate	60.49%
Clipped reads	600,053 / 44.34%

2.2. ACGT Content

Number/percentage of A's	46,640,428 / 30.34%
Number/percentage of C's	29,772,490 / 19.37%
Number/percentage of T's	46,481,341 / 30.24%
Number/percentage of G's	30,818,189 / 20.05%
Number/percentage of N's	1,617 / 0%

GC Percentage	39.42%
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2.3. Coverage

Mean	0.0497
Standard Deviation	0.9374

2.4. Mapping Quality

Mean Mapping Quality	52.89
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2.5. Insert size

Mean	1,049,074.26
Standard Deviation	9,357,953.88
P25/Median/P75	135 / 189 / 267

2.6. Mismatches and indels

General error rate	1.09%
Mismatches	1,616,660
Insertions	19,138
Mapped reads with at least one insertion	1.39%
Deletions	39,352
Mapped reads with at least one deletion	2.9%
Homopolymer indels	41.46%

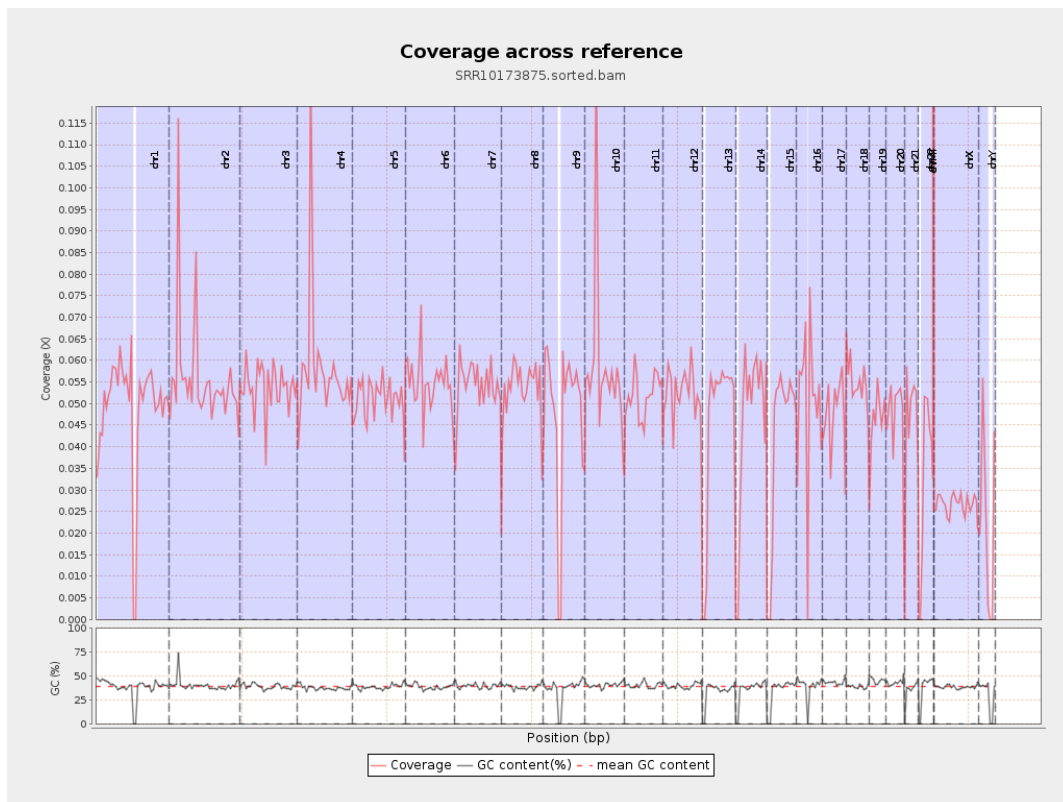
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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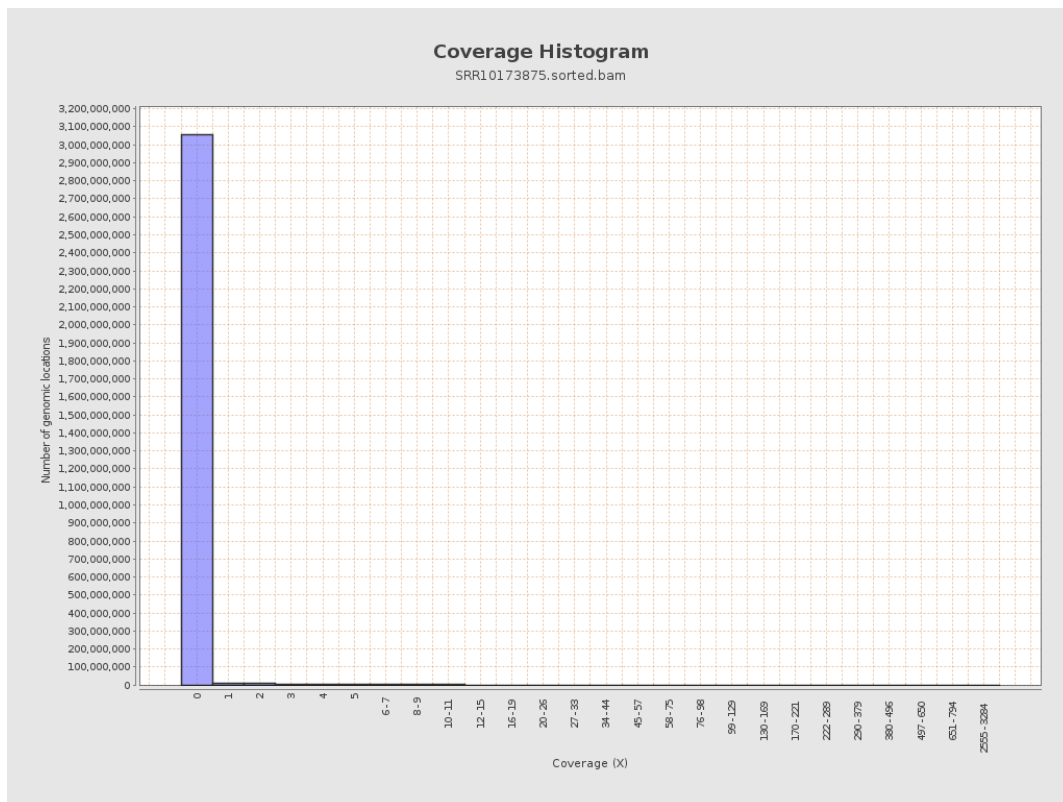
		bases	coverage	deviation
chr1	249250621	12262400	0.0492	0.7676
chr2	243199373	13627276	0.056	2.3696
chr3	198022430	10666610	0.0539	0.6281
chr4	191154276	11053442	0.0578	0.8391
chr5	180915260	9252220	0.0511	0.6091
chr6	171115067	9363610	0.0547	0.6735
chr7	159138663	8685502	0.0546	0.7005
chr8	146364022	7827823	0.0535	0.8596
chr9	141213431	6814446	0.0483	0.7049
chr10	135534747	7911157	0.0584	0.9654
chr11	135006516	6970540	0.0516	0.628
chr12	133851895	7008741	0.0524	0.6114
chr13	115169878	5203877	0.0452	0.5808
chr14	107349540	4893756	0.0456	0.579
chr15	102531392	4341361	0.0423	0.551
chr16	90354753	4529357	0.0501	0.6348
chr17	81195210	3821027	0.0471	0.5725
chr18	78077248	4297680	0.055	0.8574
chr19	59128983	2773281	0.0469	0.6594
chr20	63025520	3017522	0.0479	0.5993
chr21	48129895	2174769	0.0452	0.6467
chr22	51304566	1657303	0.0323	0.4804
chrMT	16571	239471	14.4512	13.7423
chrX	155270560	4142950	0.0267	0.4377

chrY	59373566	1277241	0.0215	0.6009
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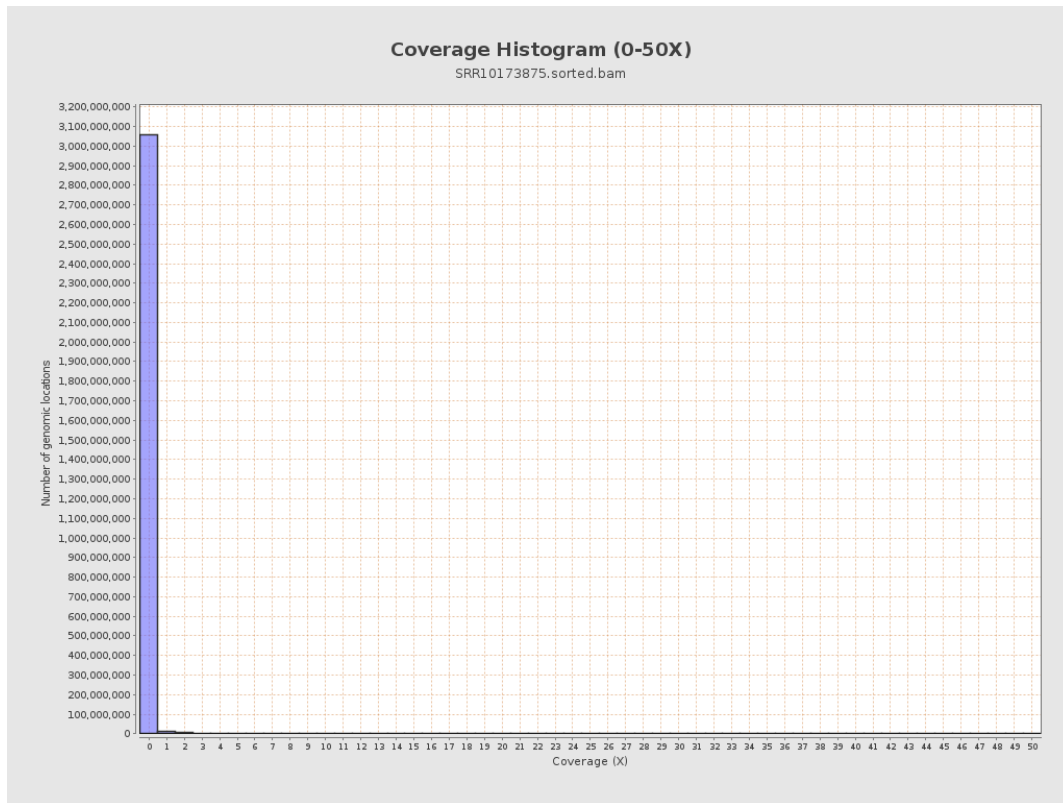
3. Results : Coverage across reference



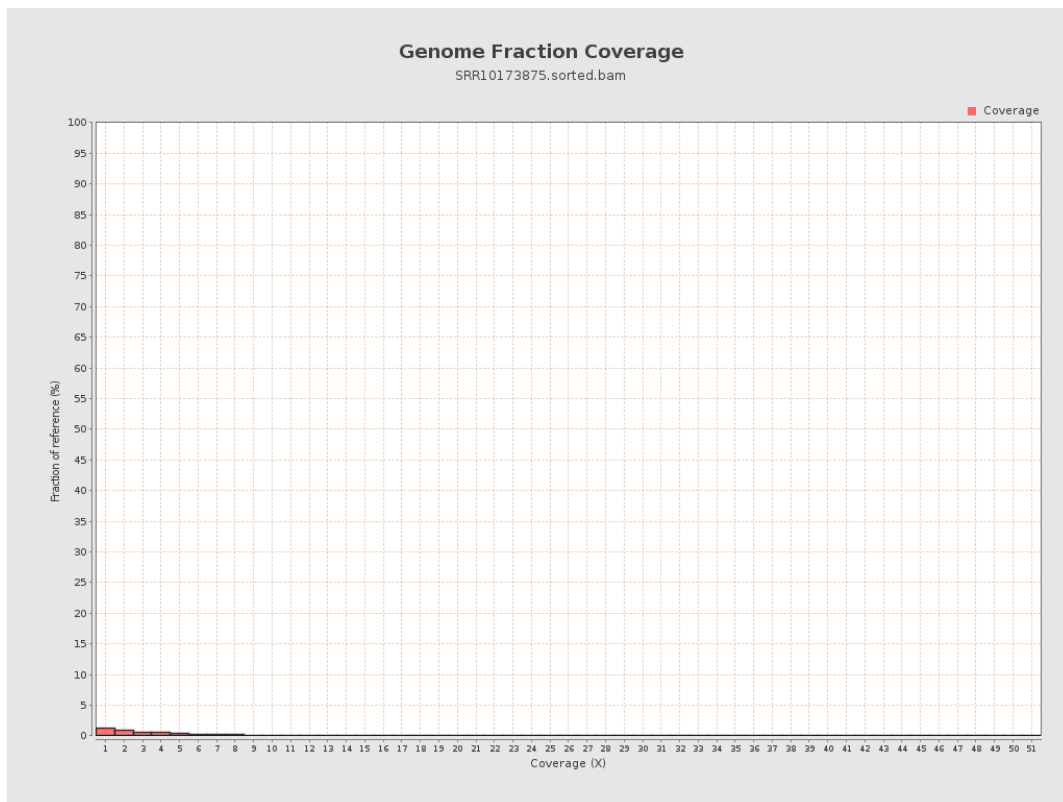
4. Results : Coverage Histogram



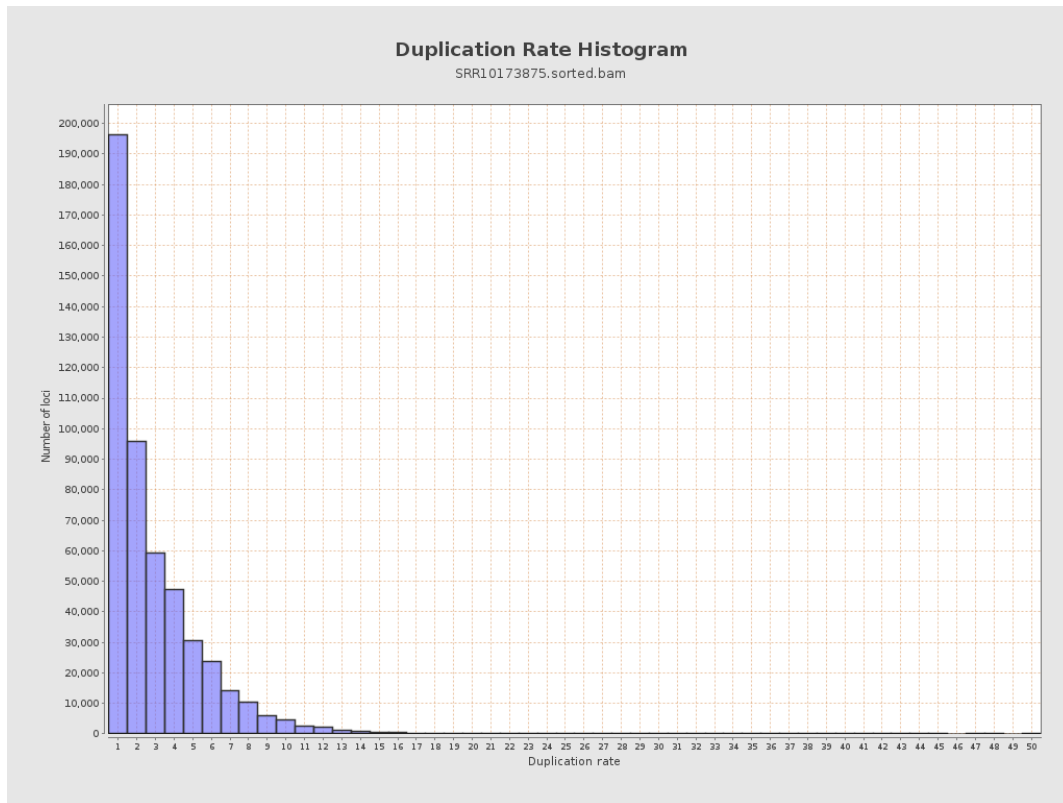
5. Results : Coverage Histogram (0-50X)



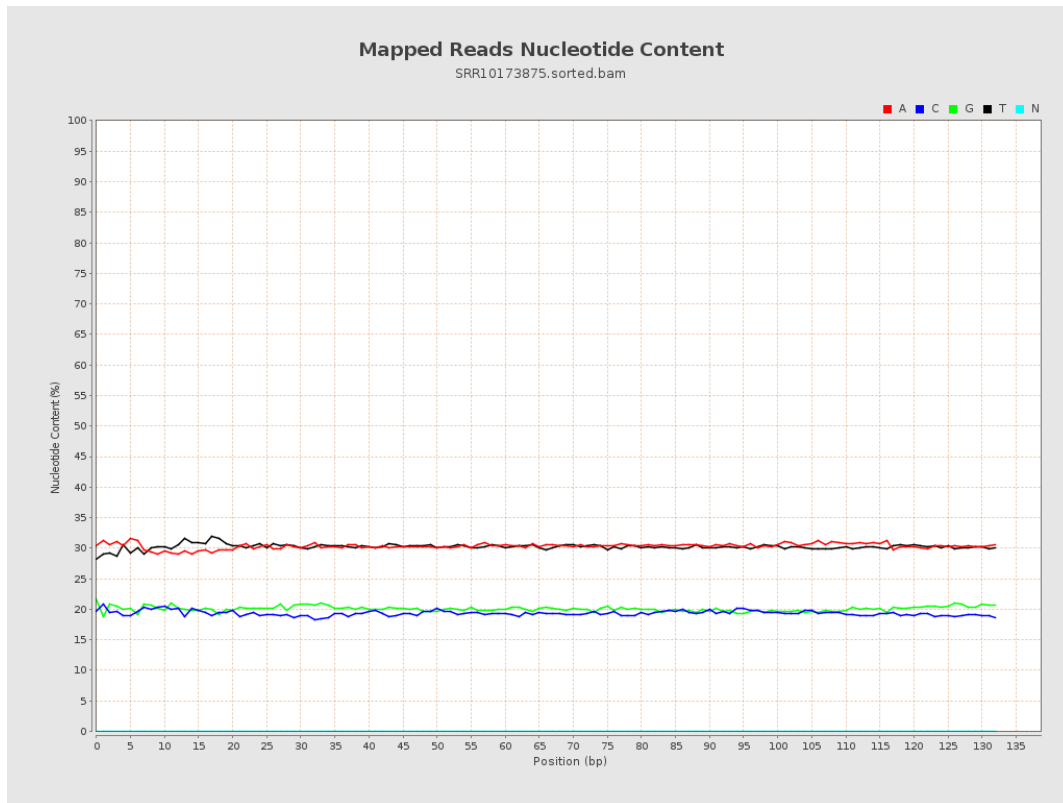
6. Results : Genome Fraction Coverage



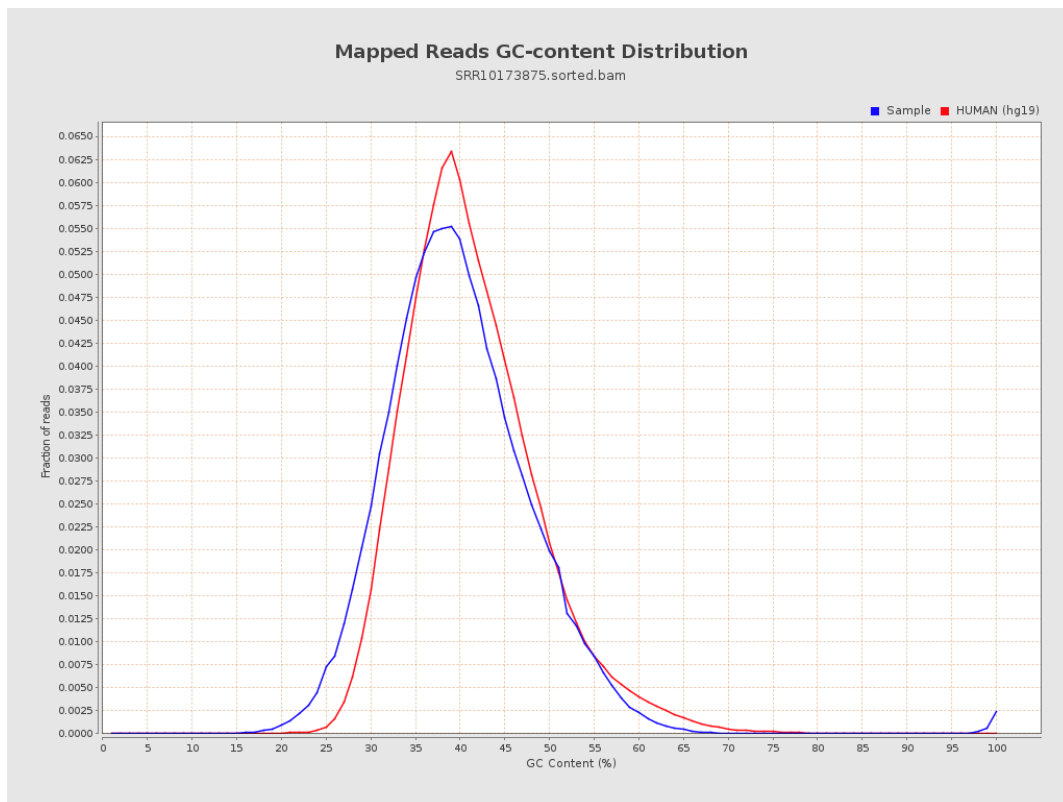
7. Results : Duplication Rate Histogram



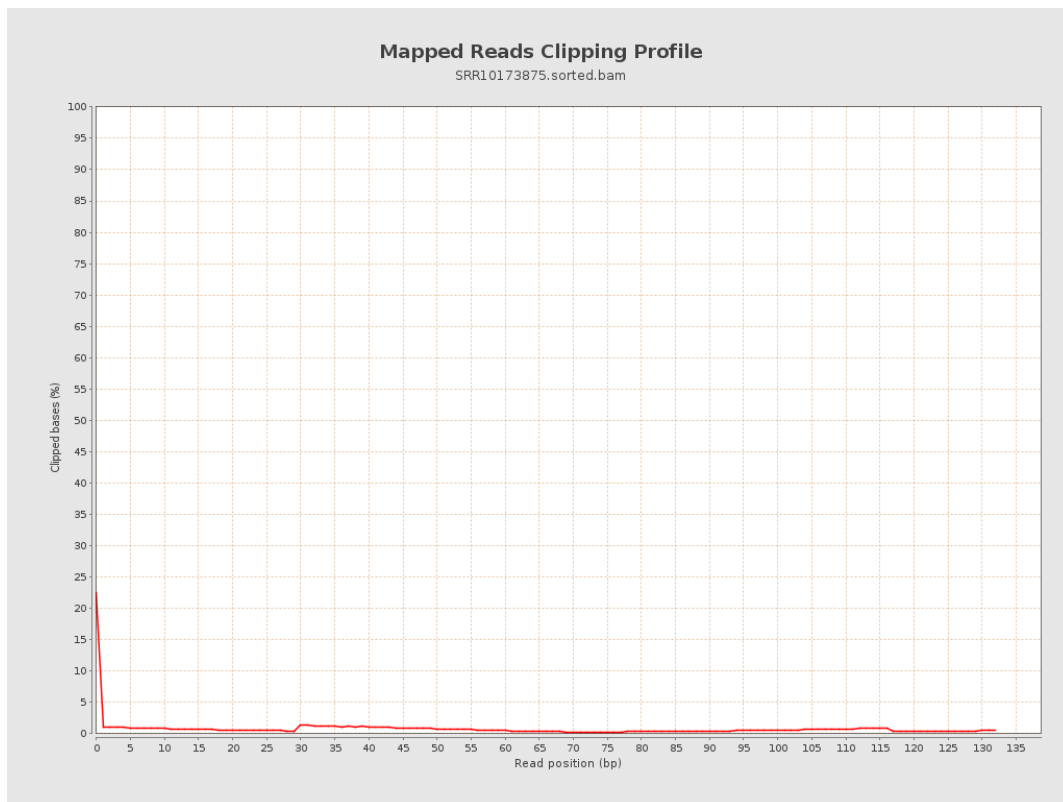
8. Results : Mapped Reads Nucleotide Content



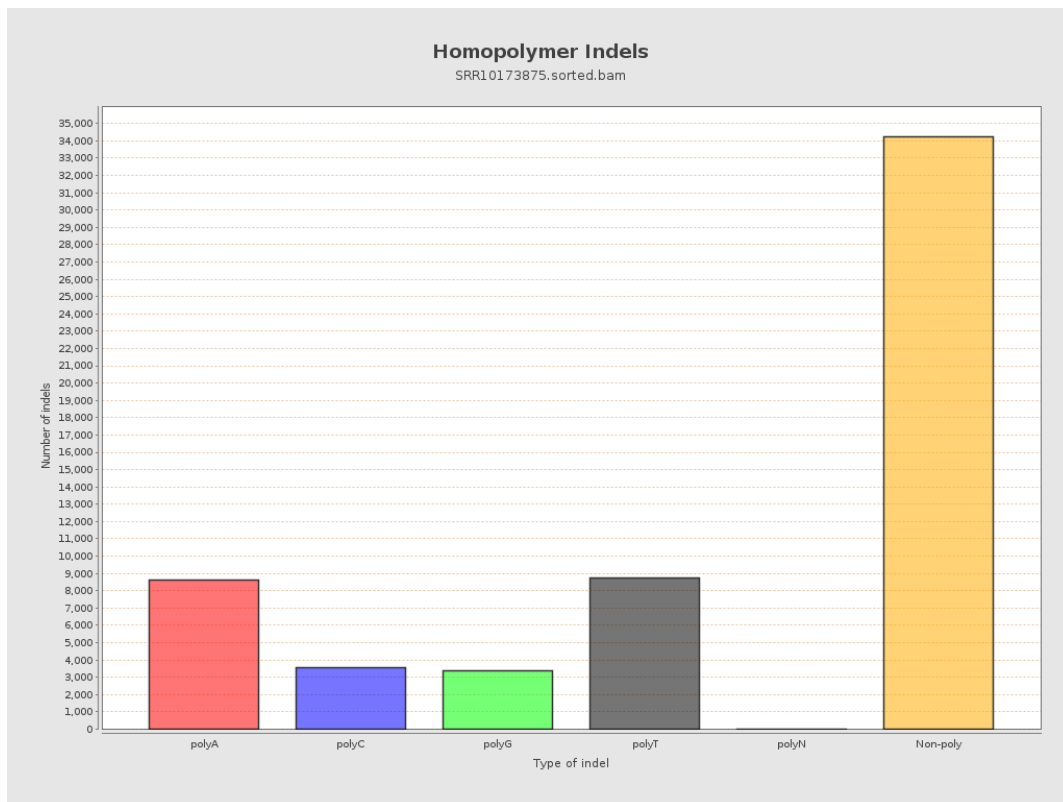
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



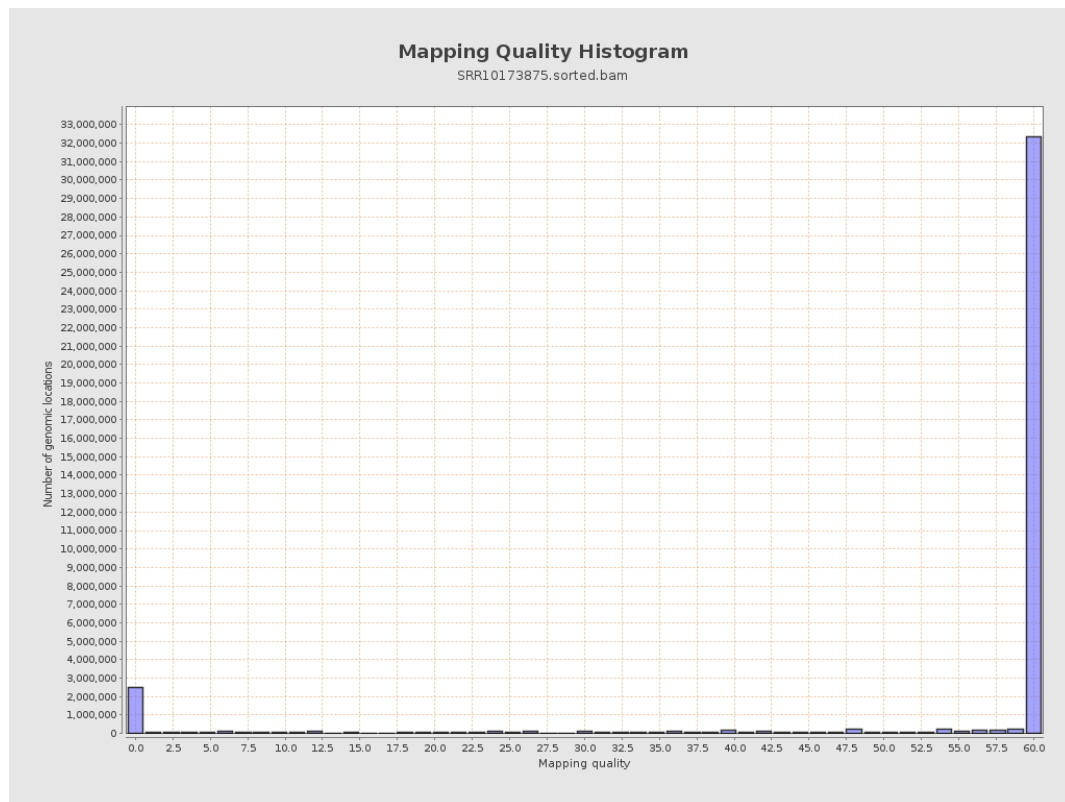
11. Results : Homopolymer Indels



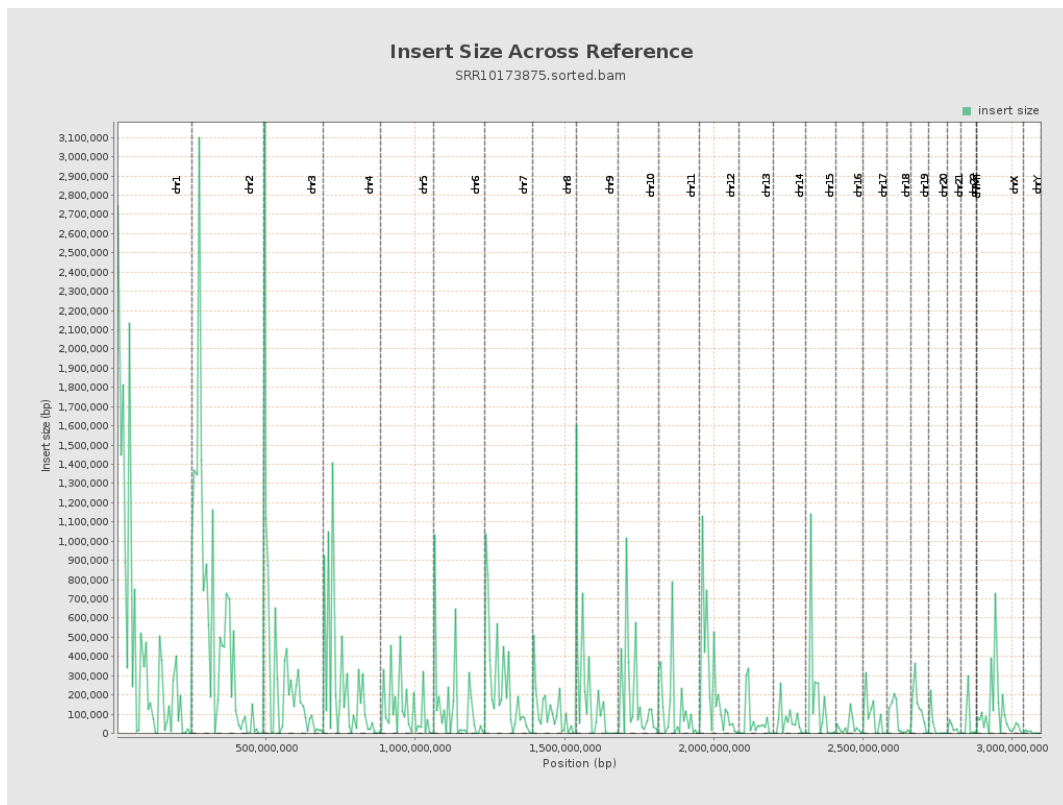
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

