

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 22:02:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173850.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_SRR10173850 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173850_1.fastq.gz SRR10173850_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 22:02:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173850.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,793,108
Mapped reads	6,642,407 / 97.78%
Unmapped reads	150,701 / 2.22%
Mapped paired reads	6,642,407 / 97.78%
Mapped reads, first in pair	3,323,163 / 48.92%
Mapped reads, second in pair	3,319,244 / 48.86%
Mapped reads, both in pair	6,540,896 / 96.29%
Mapped reads, singletons	101,511 / 1.49%
Secondary alignments	0
Supplementary alignments	638,055 / 9.39%
Read min/max/mean length	30 / 133 / 127.74
Duplicated reads (estimated)	5,106,500 / 75.17%
Duplication rate	65.7%
Clipped reads	2,539,574 / 37.38%

2.2. ACGT Content

Number/percentage of A's	233,027,717 / 29.64%
Number/percentage of C's	157,542,752 / 20.04%
Number/percentage of T's	232,606,386 / 29.58%
Number/percentage of G's	163,076,164 / 20.74%
Number/percentage of N's	9,683 / 0%

GC Percentage	40.78%
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2.3. Coverage

Mean	0.2541
Standard Deviation	3.506

2.4. Mapping Quality

Mean Mapping Quality	52.96
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2.5. Insert size

Mean	761,586.96
Standard Deviation	8,297,151.75
P25/Median/P75	141 / 194 / 274

2.6. Mismatches and indels

General error rate	0.96%
Mismatches	7,388,388
Insertions	77,707
Mapped reads with at least one insertion	1.13%
Deletions	184,690
Mapped reads with at least one deletion	2.71%
Homopolymer indels	42.77%

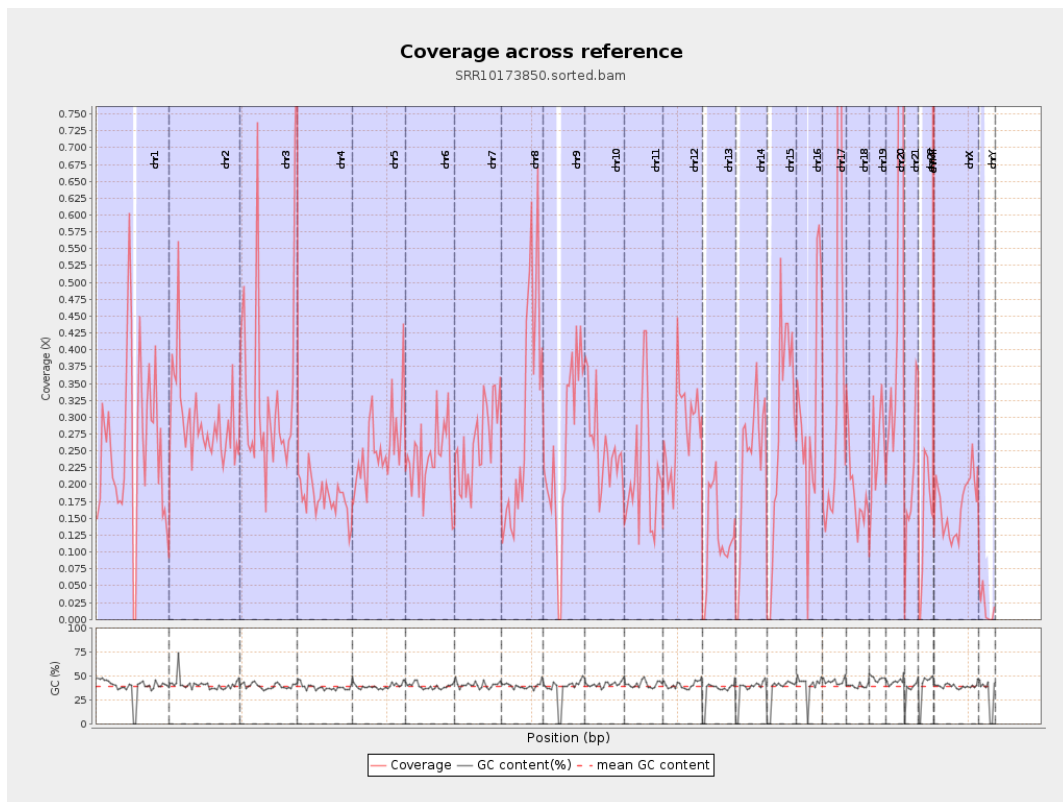
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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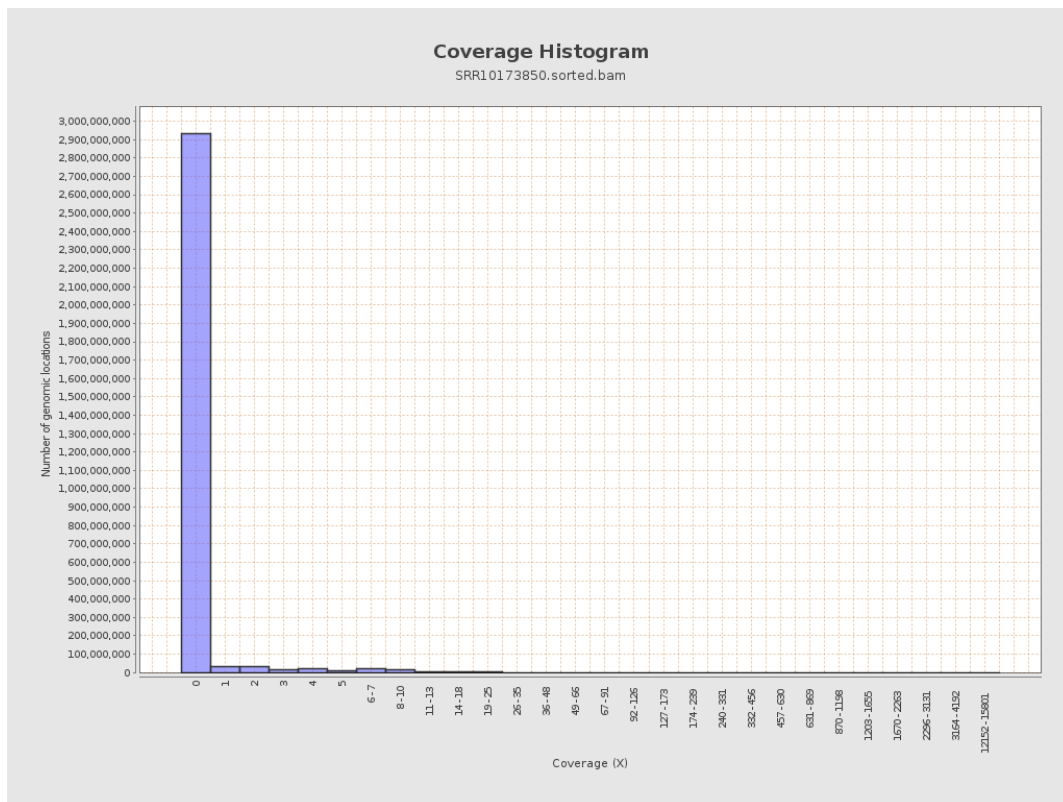
		bases	coverage	deviation
chr1	249250621	63205657	0.2536	2.0431
chr2	243199373	71725344	0.2949	11.0373
chr3	198022430	65215625	0.3293	1.6657
chr4	191154276	34504021	0.1805	1.3774
chr5	180915260	46257225	0.2557	1.4387
chr6	171115067	40509763	0.2367	1.532
chr7	159138663	41907495	0.2633	2.0097
chr8	146364022	43688972	0.2985	1.8083
chr9	141213431	35138753	0.2488	1.6173
chr10	135534747	34880534	0.2574	2.5878
chr11	135006516	29951658	0.2219	1.3579
chr12	133851895	38146798	0.285	1.5328
chr13	115169878	13763258	0.1195	0.9846
chr14	107349540	25154101	0.2343	1.3865
chr15	102531392	28400582	0.277	1.5144
chr16	90354753	28495561	0.3154	1.9097
chr17	81195210	31013529	0.382	2.0167
chr18	78077248	14865170	0.1904	1.975
chr19	59128983	14697051	0.2486	1.6311
chr20	63025520	39227680	0.6224	2.6816
chr21	48129895	10177476	0.2115	1.3635
chr22	51304566	7361023	0.1435	1.0373
chrMT	16571	1376144	83.0453	76.0832
chrX	155270560	25987087	0.1674	1.16

chrY	59373566	1065835	0.018	0.6101
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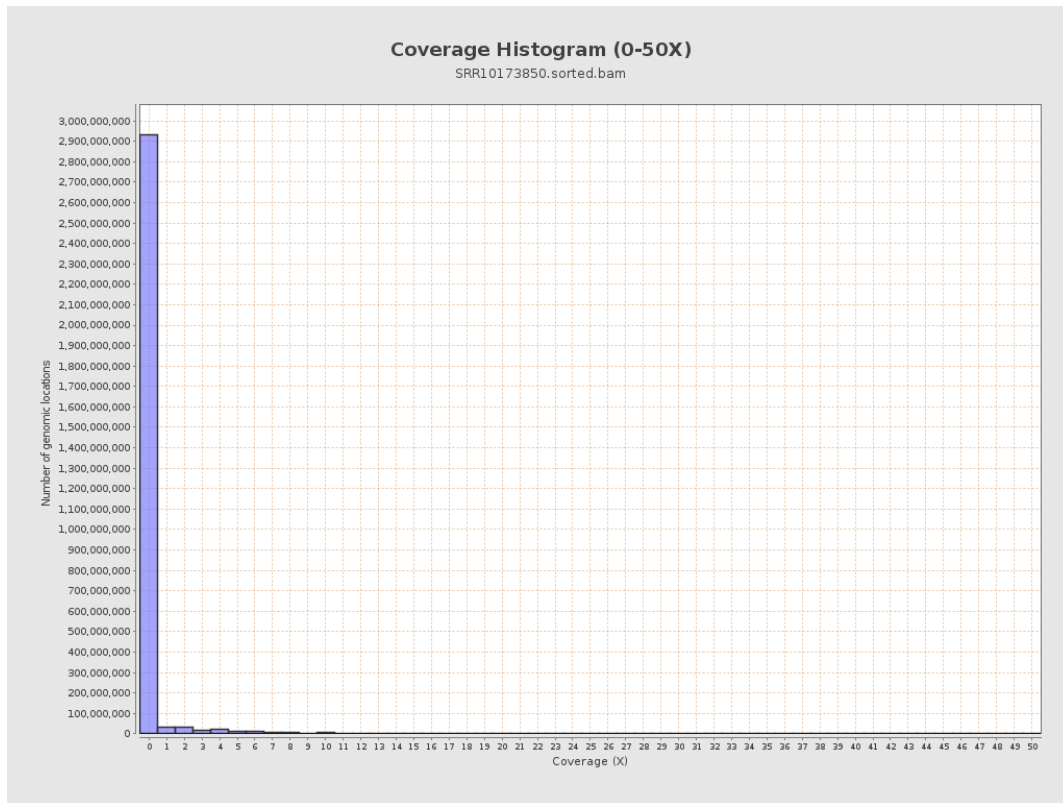
3. Results : Coverage across reference



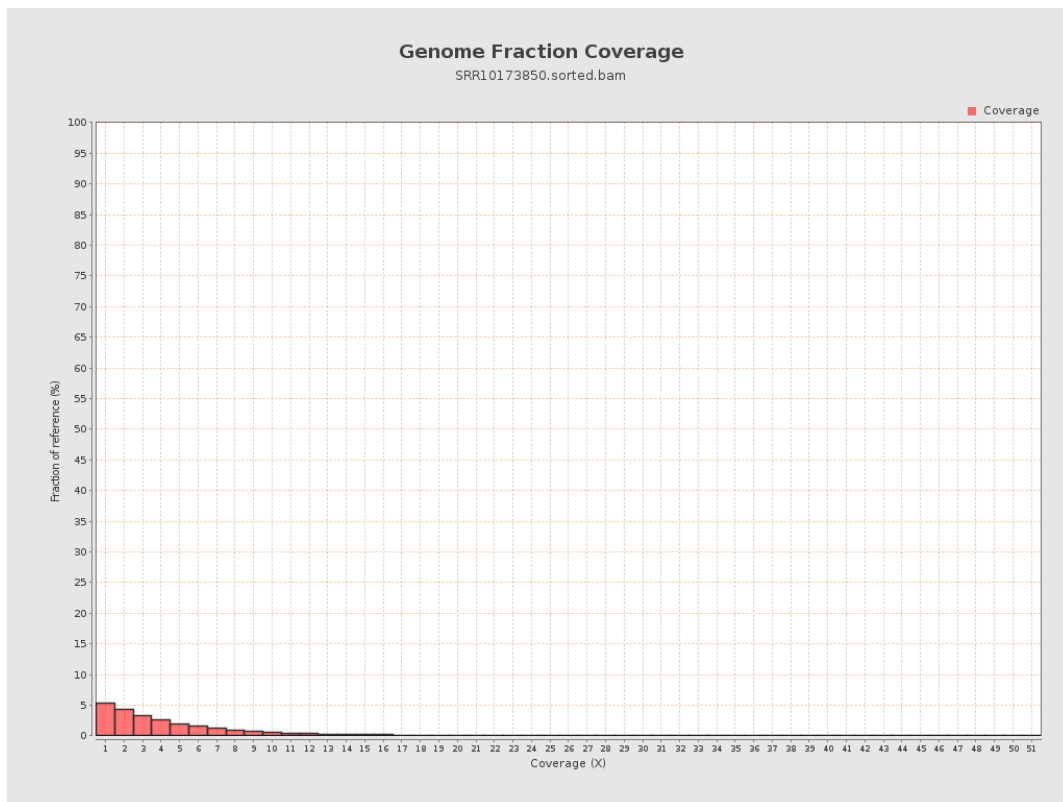
4. Results : Coverage Histogram



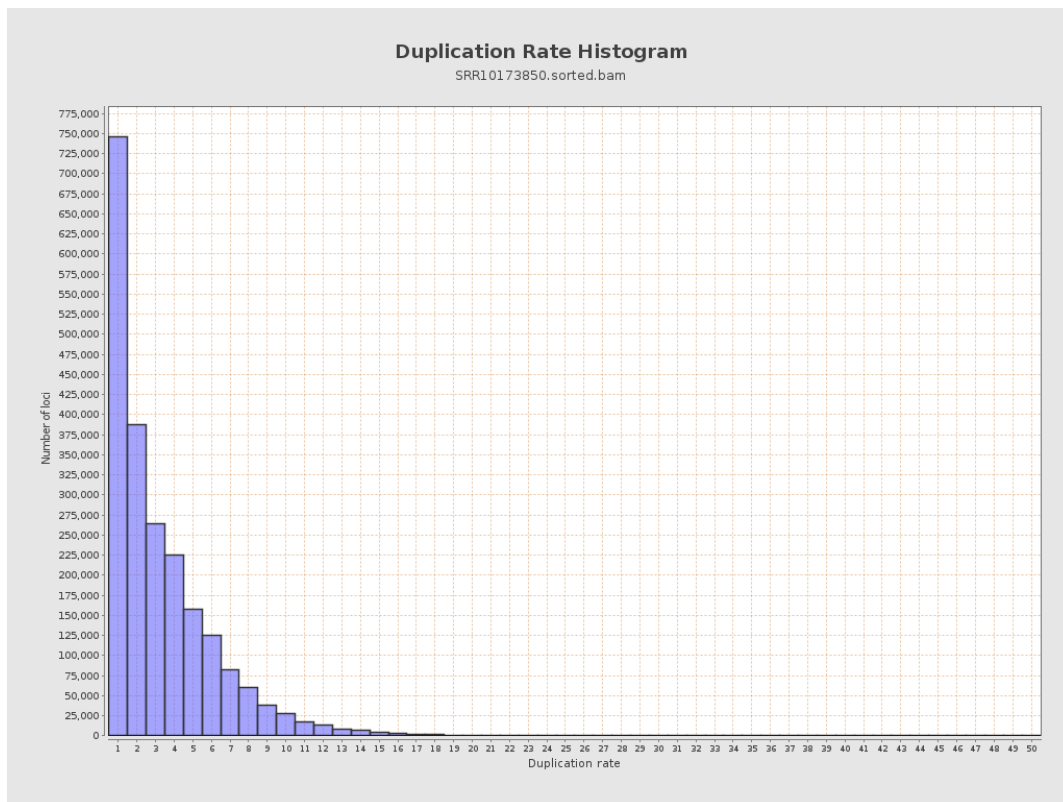
5. Results : Coverage Histogram (0-50X)



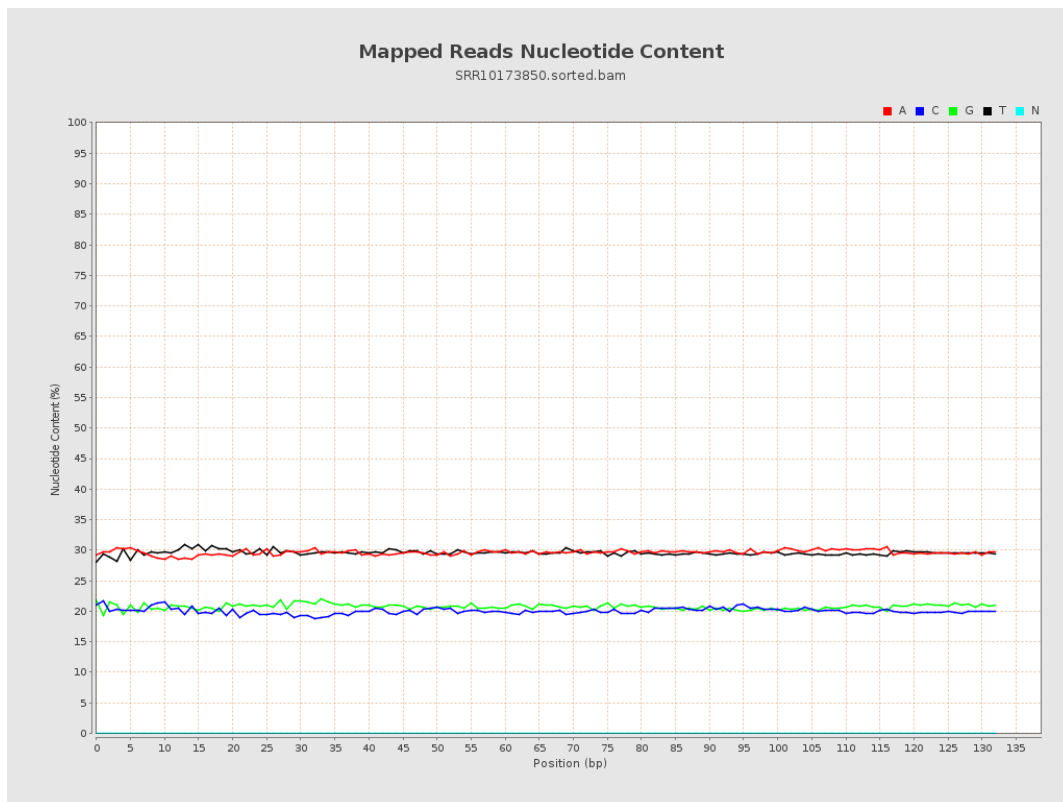
6. Results : Genome Fraction Coverage



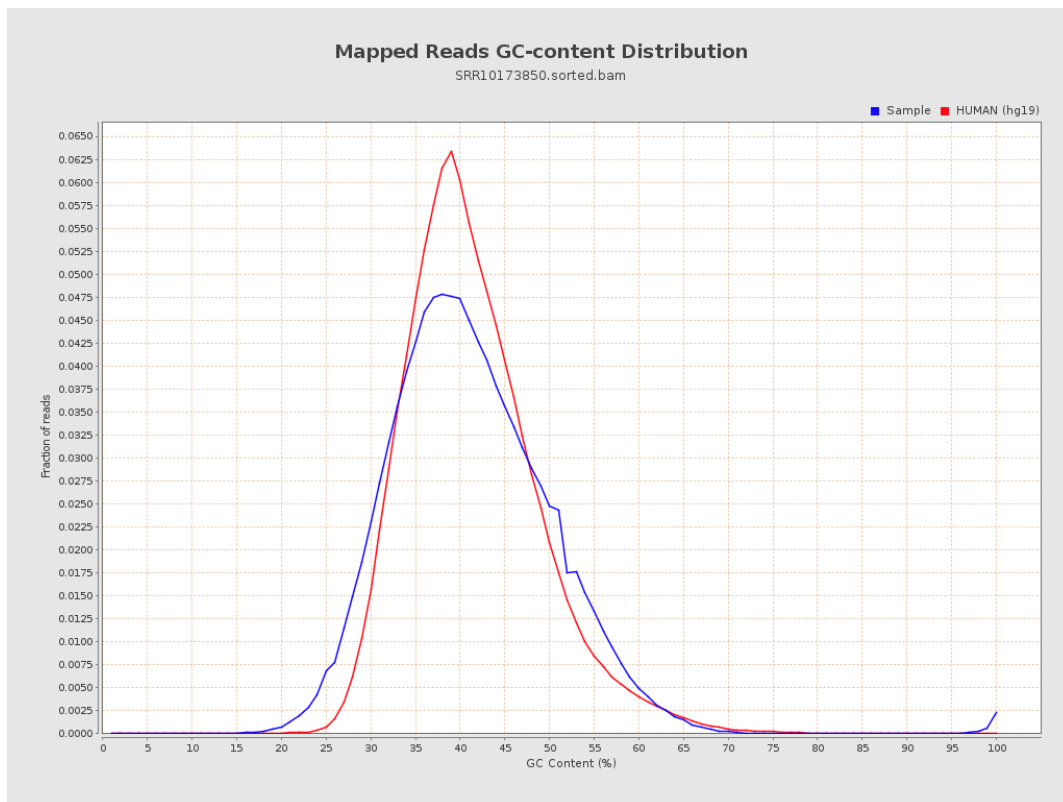
7. Results : Duplication Rate Histogram



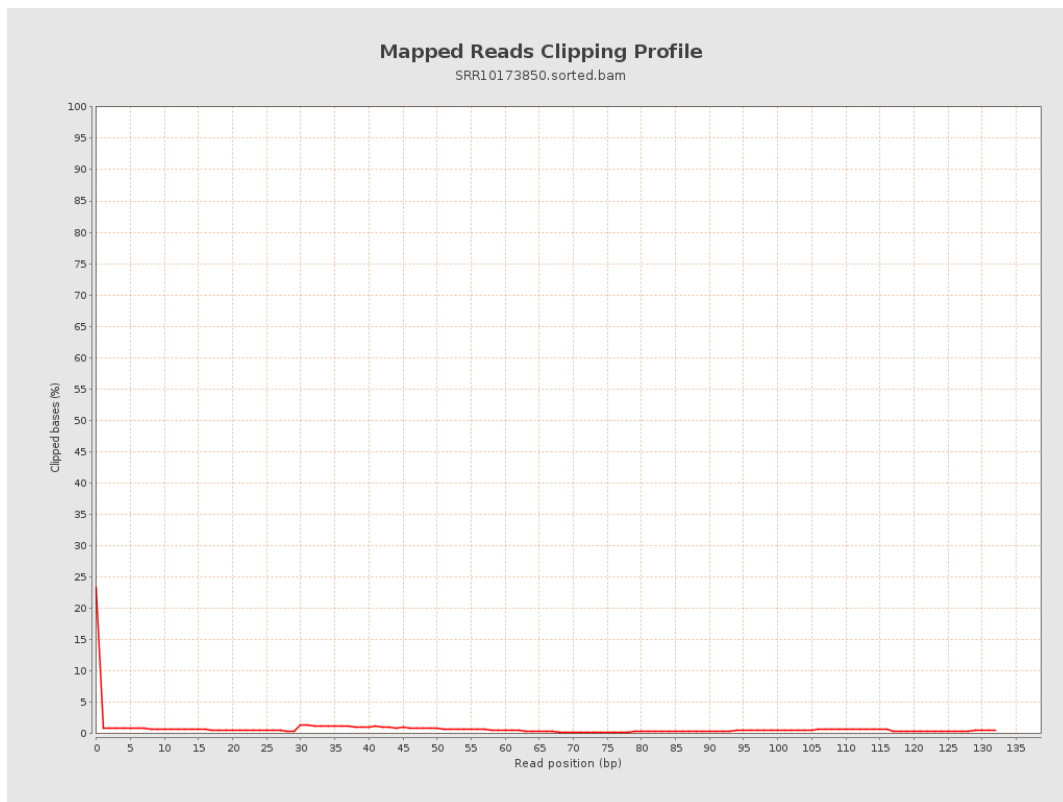
8. Results : Mapped Reads Nucleotide Content



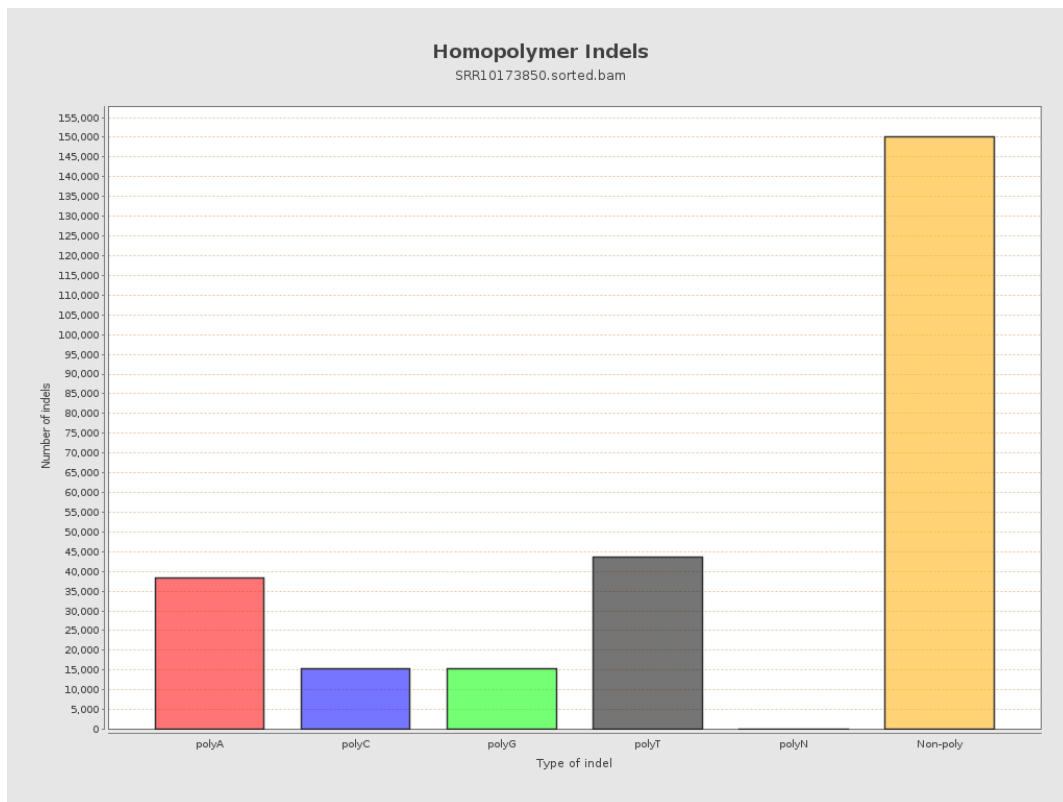
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



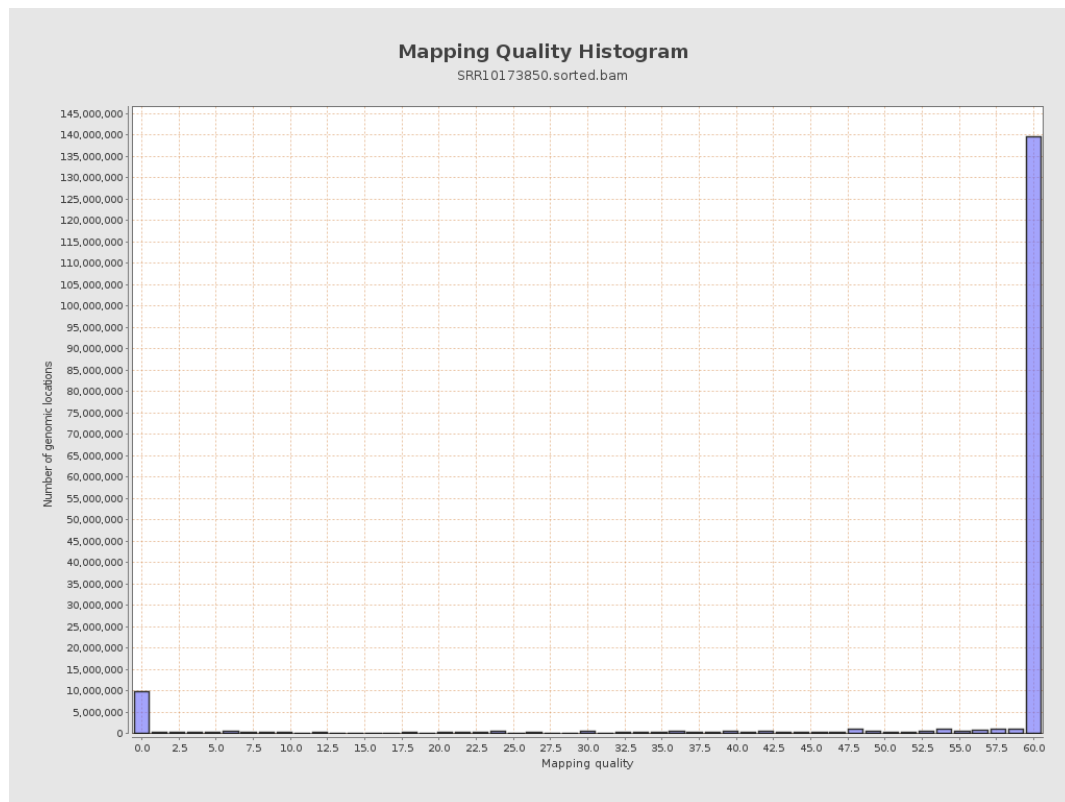
11. Results : Homopolymer Indels



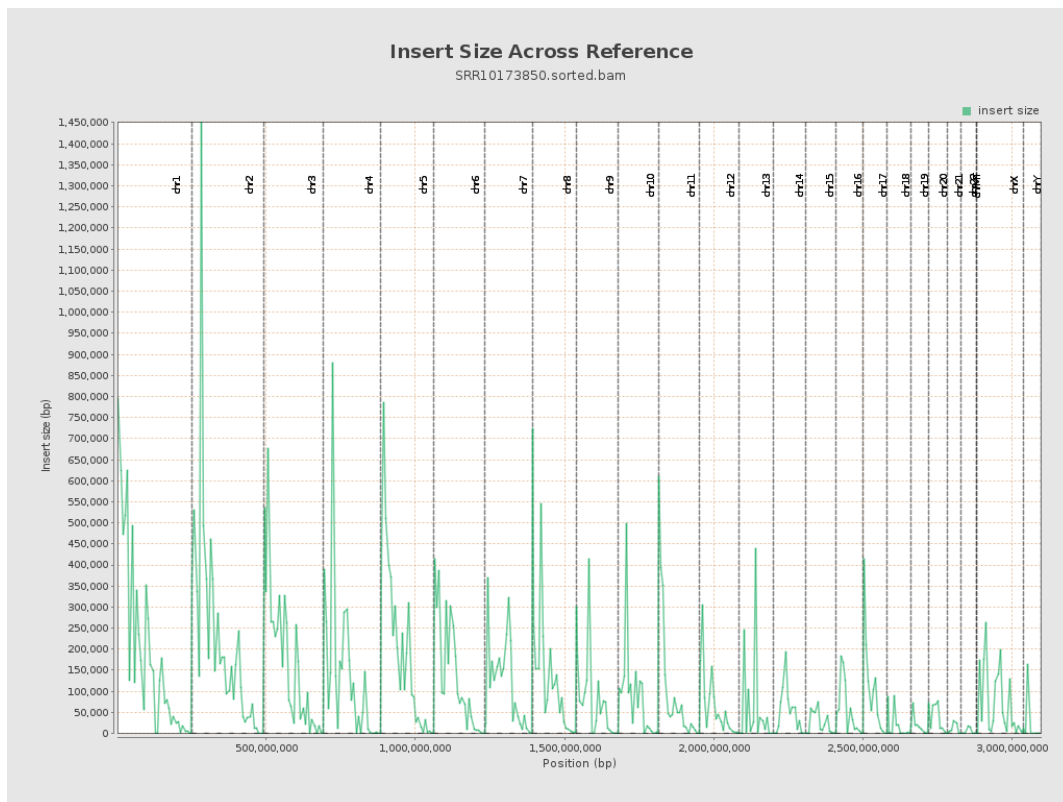
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

