

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:42:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173847.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_SRR10173847 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173847_1.fastq.gz SRR10173847_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:42:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173847.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,373,816
Mapped reads	10,111,526 / 97.47%
Unmapped reads	262,290 / 2.53%
Mapped paired reads	10,111,526 / 97.47%
Mapped reads, first in pair	5,063,451 / 48.81%
Mapped reads, second in pair	5,048,075 / 48.66%
Mapped reads, both in pair	9,932,260 / 95.74%
Mapped reads, singletons	179,266 / 1.73%
Secondary alignments	0
Supplementary alignments	1,069,947 / 10.31%
Read min/max/mean length	30 / 133 / 128.68
Duplicated reads (estimated)	8,038,399 / 77.49%
Duplication rate	65.71%
Clipped reads	4,096,354 / 39.49%

2.2. ACGT Content

Number/percentage of A's	359,210,176 / 29.95%
Number/percentage of C's	235,963,903 / 19.68%
Number/percentage of T's	358,963,435 / 29.93%
Number/percentage of G's	245,121,122 / 20.44%
Number/percentage of N's	13,579 / 0%

GC Percentage	40.11%
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2.3. Coverage

Mean	0.3876
Standard Deviation	5.1731

2.4. Mapping Quality

Mean Mapping Quality	52.63
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2.5. Insert size

Mean	984,661.63
Standard Deviation	9,093,557.81
P25/Median/P75	151 / 211 / 306

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	12,444,436
Insertions	125,469
Mapped reads with at least one insertion	1.2%
Deletions	289,105
Mapped reads with at least one deletion	2.79%
Homopolymer indels	42.72%

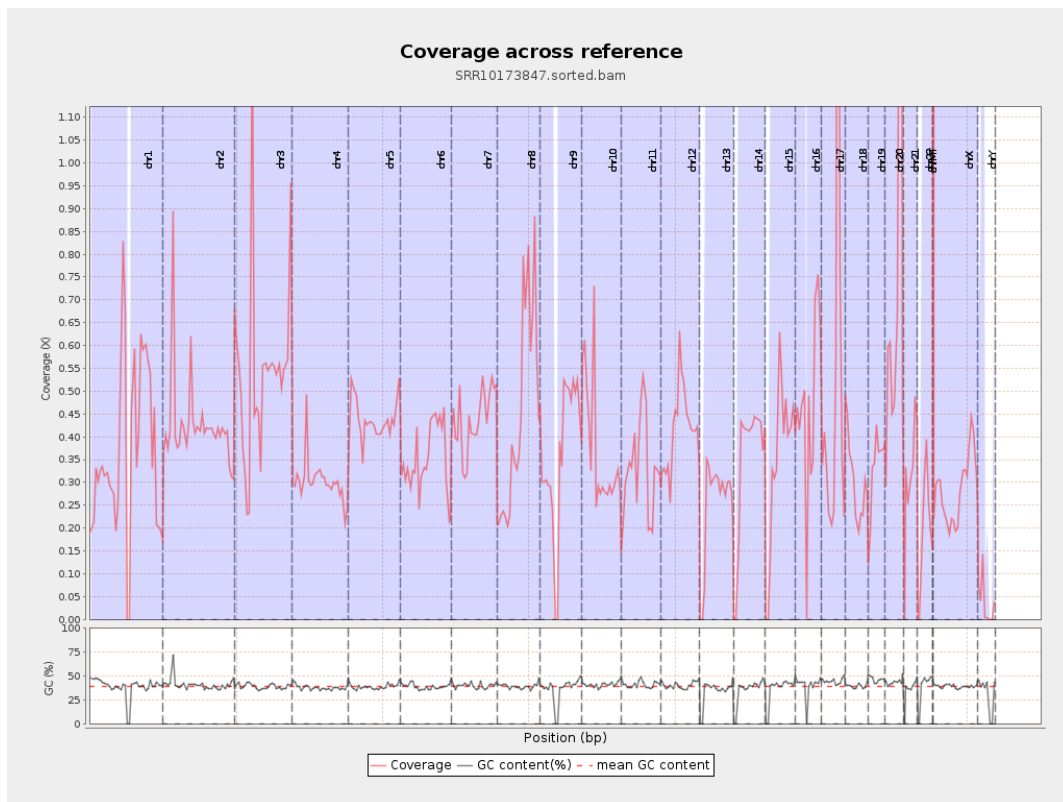
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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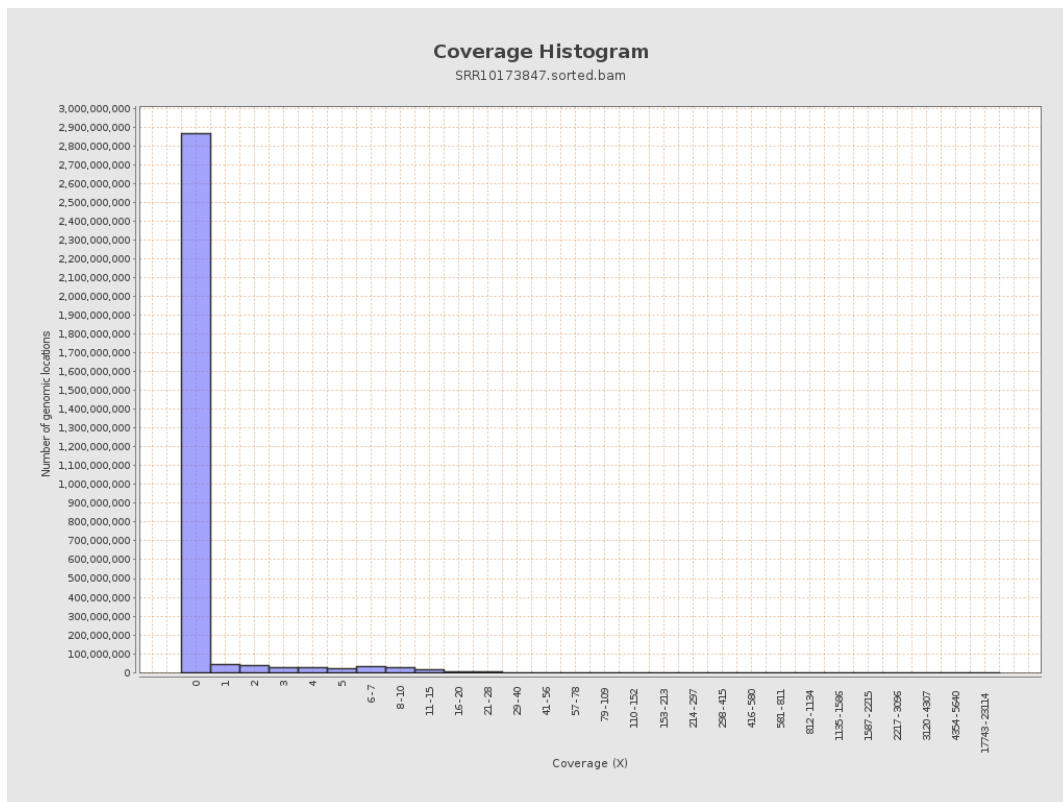
		bases	coverage	deviation
chr1	249250621	91929723	0.3688	3.7016
chr2	243199373	103076859	0.4238	16.1512
chr3	198022430	106810670	0.5394	2.2292
chr4	191154276	57917771	0.303	2.2411
chr5	180915260	79152398	0.4375	1.9467
chr6	171115067	60594566	0.3541	2.0412
chr7	159138663	69791503	0.4386	2.9461
chr8	146364022	66458414	0.4541	2.6297
chr9	141213431	50684963	0.3589	2.4694
chr10	135534747	49940763	0.3685	4.3949
chr11	135006516	44225364	0.3276	1.7698
chr12	133851895	56134718	0.4194	1.9049
chr13	115169878	29258697	0.254	1.4775
chr14	107349540	37739131	0.3516	1.7497
chr15	102531392	35617123	0.3474	1.7308
chr16	90354753	41679247	0.4613	2.8176
chr17	81195210	45981400	0.5663	2.6566
chr18	78077248	23762015	0.3043	4.2438
chr19	59128983	19711628	0.3334	2.7229
chr20	63025520	55708053	0.8839	3.2454
chr21	48129895	15461522	0.3212	1.8829
chr22	51304566	10148626	0.1978	1.2357
chrMT	16571	2064997	124.6151	94.924
chrX	155270560	43974864	0.2832	1.5524

chrY	59373566	2148119	0.0362	1.3499
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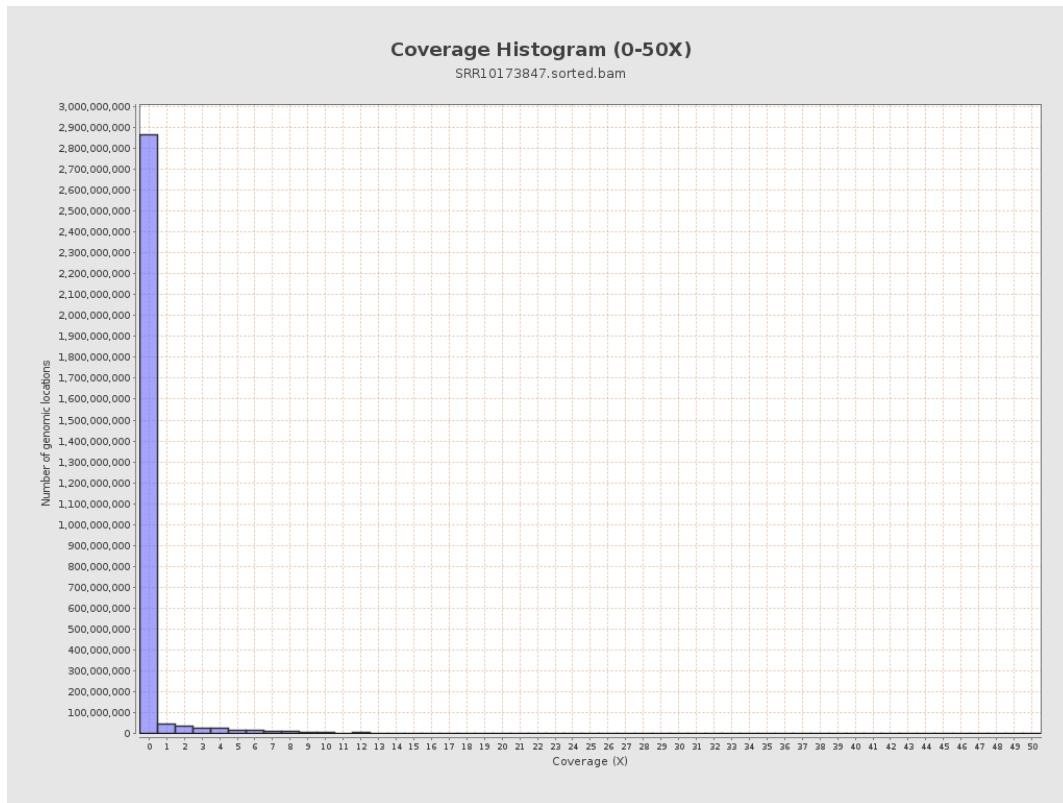
3. Results : Coverage across reference



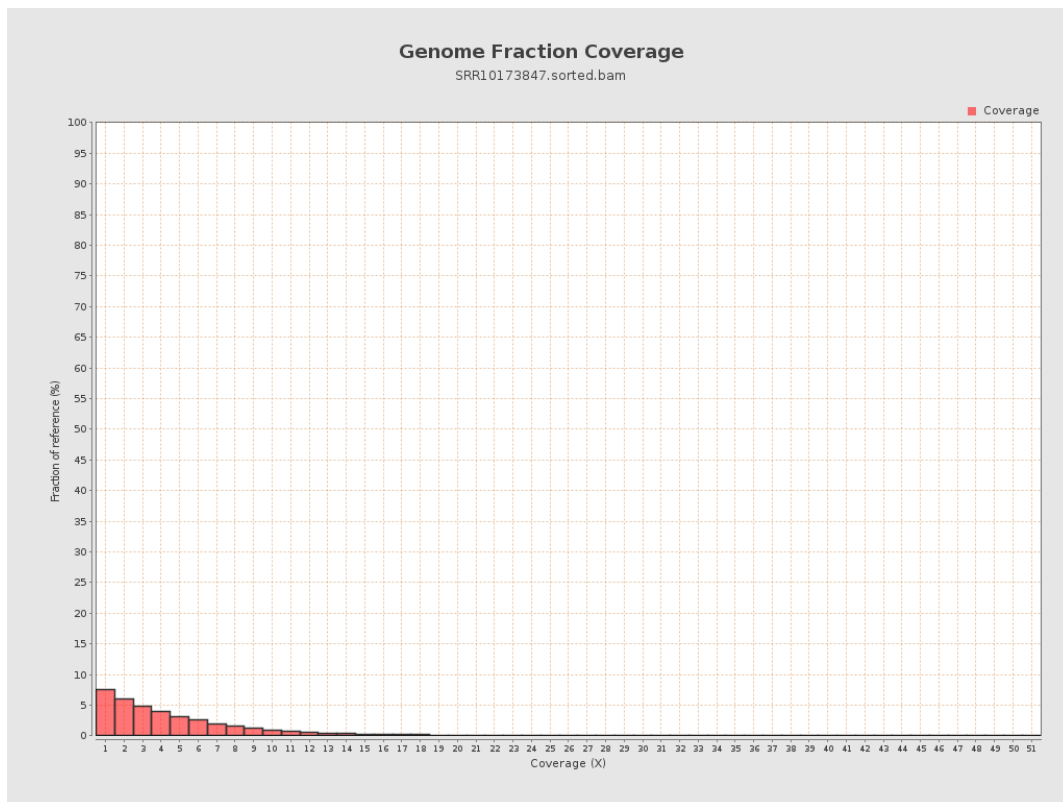
4. Results : Coverage Histogram



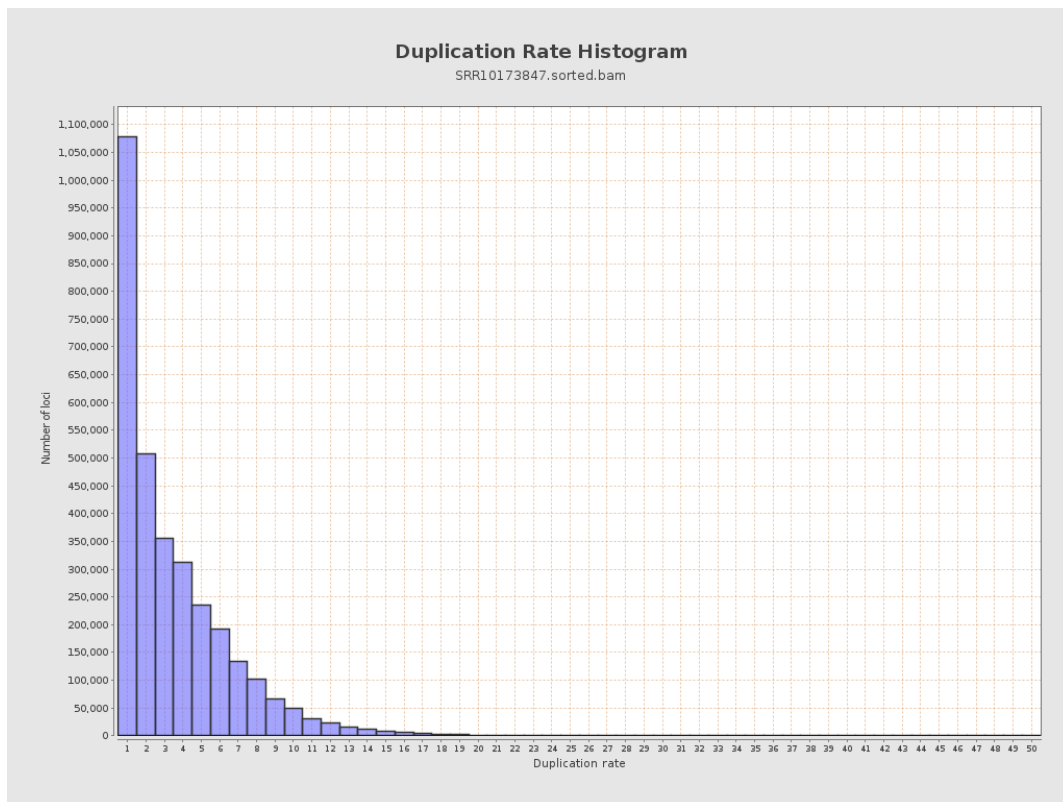
5. Results : Coverage Histogram (0-50X)



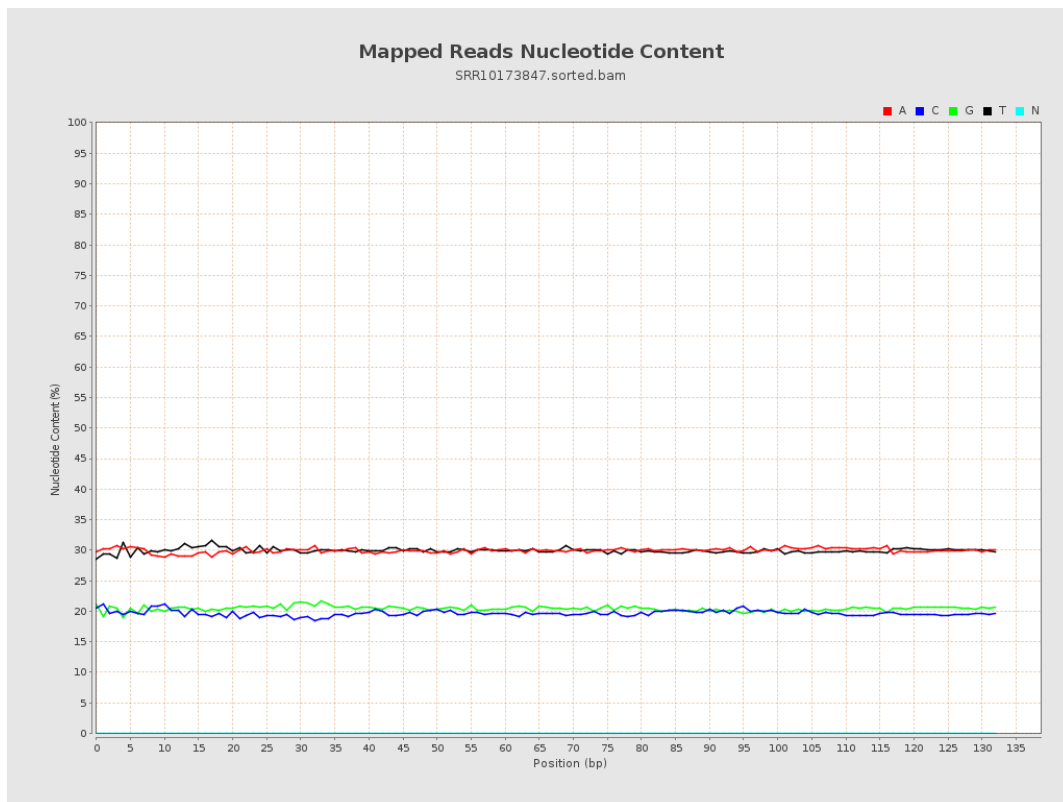
6. Results : Genome Fraction Coverage



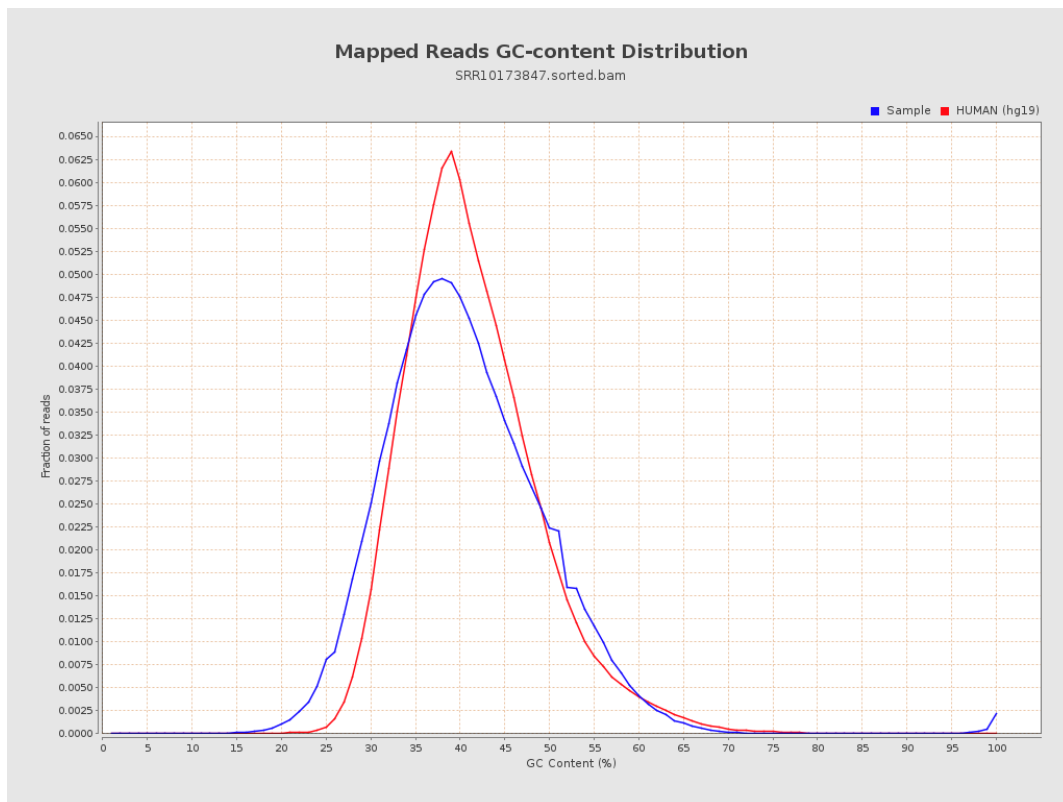
7. Results : Duplication Rate Histogram



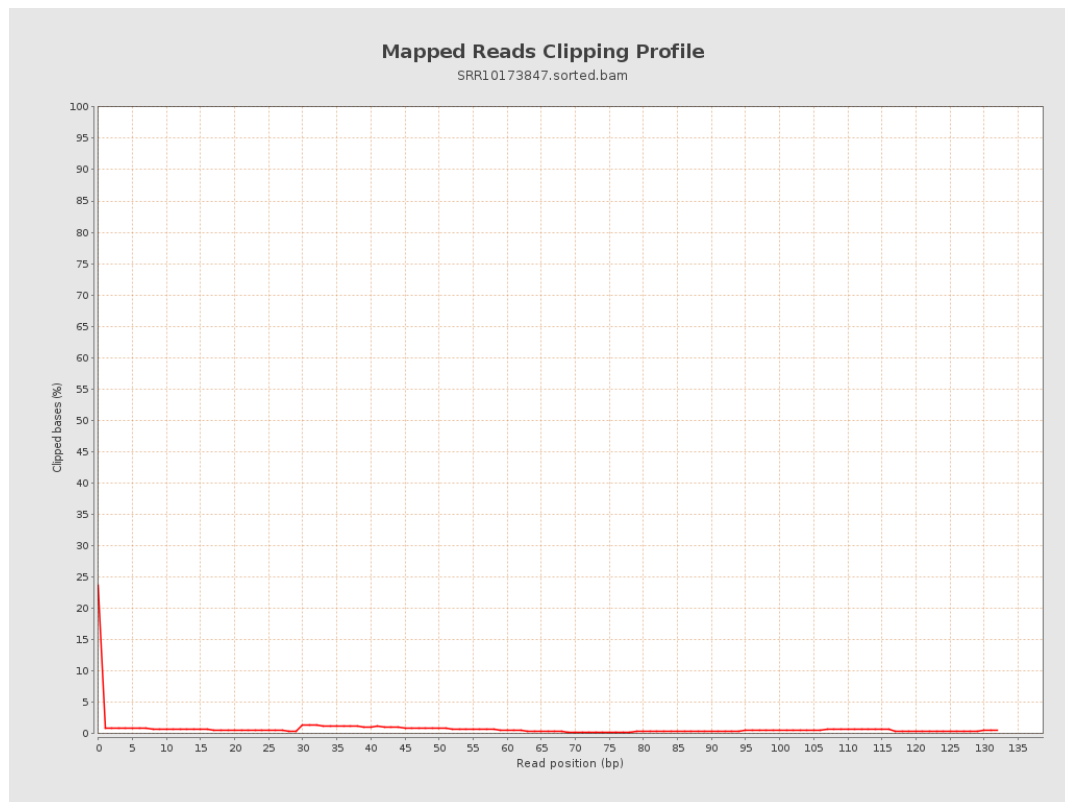
8. Results : Mapped Reads Nucleotide Content



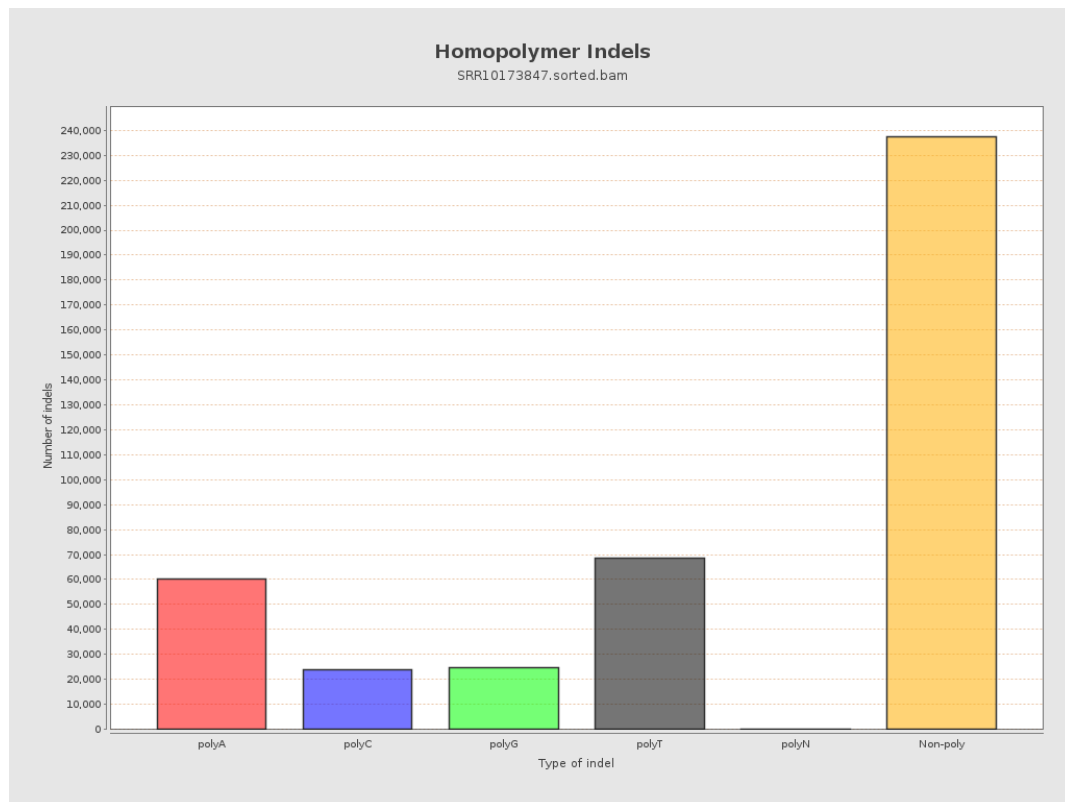
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



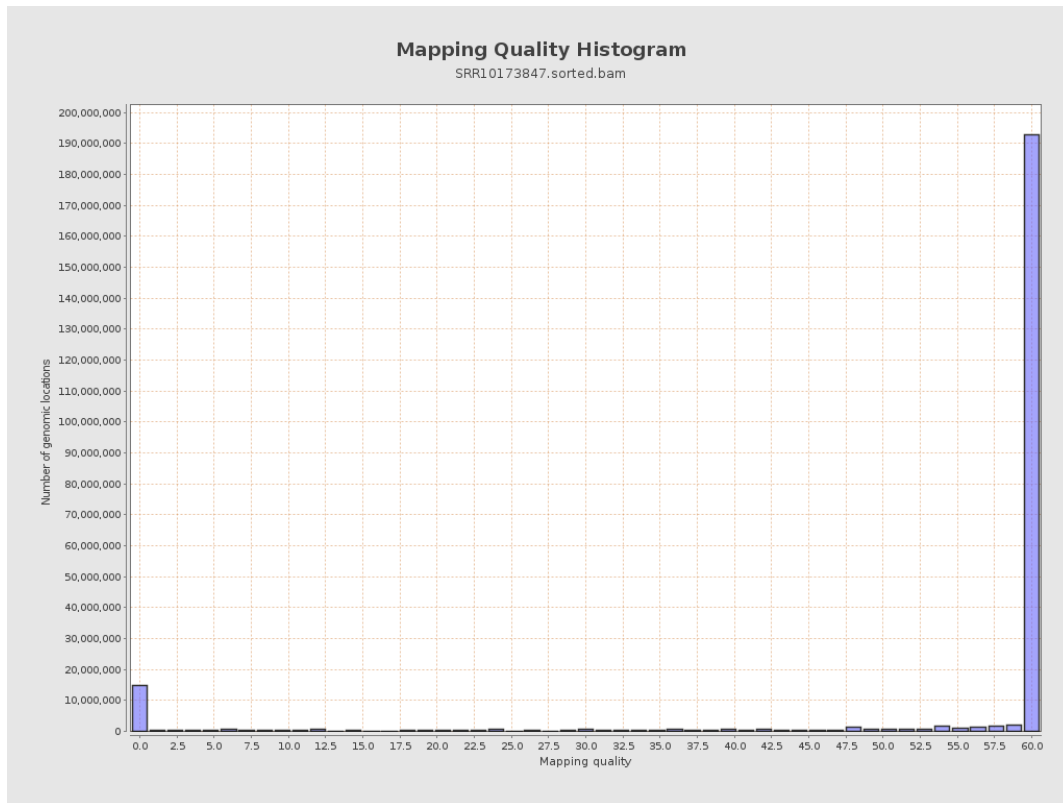
11. Results : Homopolymer Indels



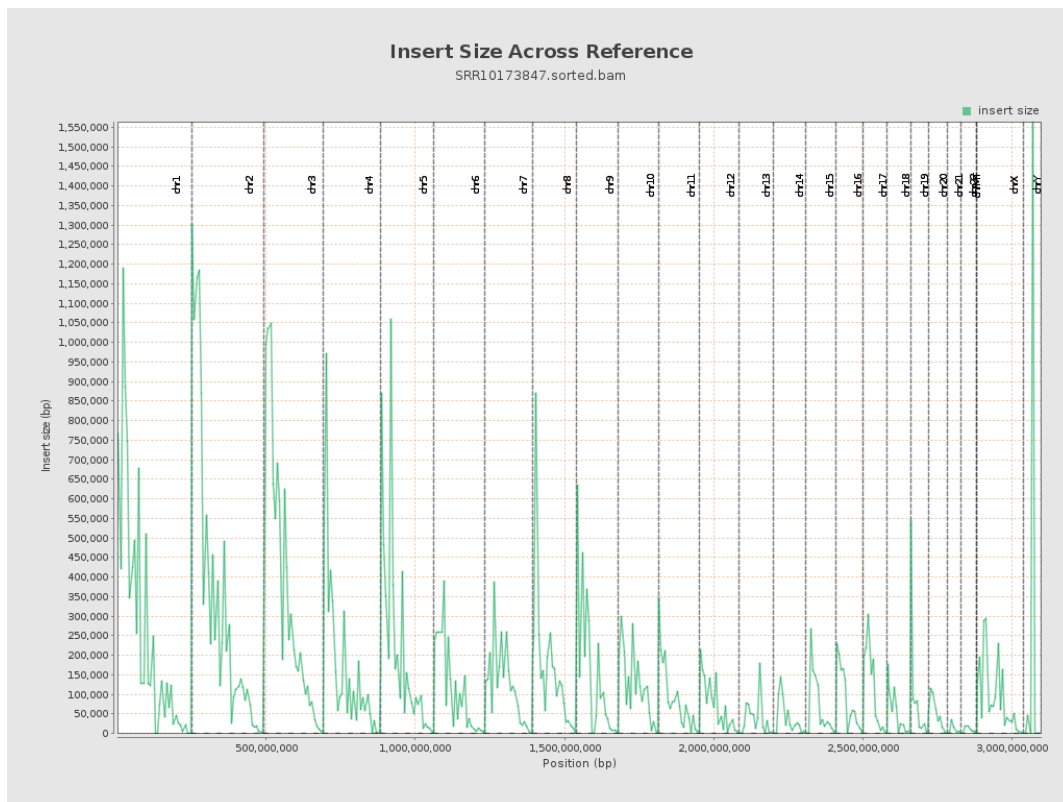
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

