

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:27:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354862.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_SRR22354862 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354862_1.fastq.gz SRR22354862_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:27:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354862.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,196,724
Mapped reads	20,981,743 / 98.99%
Unmapped reads	214,981 / 1.01%
Mapped paired reads	20,981,743 / 98.99%
Mapped reads, first in pair	10,511,825 / 49.59%
Mapped reads, second in pair	10,469,918 / 49.39%
Mapped reads, both in pair	20,899,202 / 98.6%
Mapped reads, singletons	82,541 / 0.39%
Secondary alignments	0
Supplementary alignments	378,913 / 1.79%
Read min/max/mean length	30 / 150 / 150.78
Duplicated reads (estimated)	6,914,059 / 32.62%
Duplication rate	28.08%
Clipped reads	5,672,385 / 26.76%

2.2. ACGT Content

Number/percentage of A's	832,475,329 / 28.64%
Number/percentage of C's	612,695,341 / 21.08%
Number/percentage of T's	838,305,340 / 28.84%
Number/percentage of G's	623,073,909 / 21.44%
Number/percentage of N's	49,111 / 0%

GC Percentage	42.52%
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2.3. Coverage

Mean	0.9395
Standard Deviation	18.832

2.4. Mapping Quality

Mean Mapping Quality	53.92
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2.5. Insert size

Mean	139,579.35
Standard Deviation	4,129,057.79
P25/Median/P75	168 / 267 / 396

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	24,306,131
Insertions	545,086
Mapped reads with at least one insertion	2.36%
Deletions	521,001
Mapped reads with at least one deletion	2.31%
Homopolymer indels	38.79%

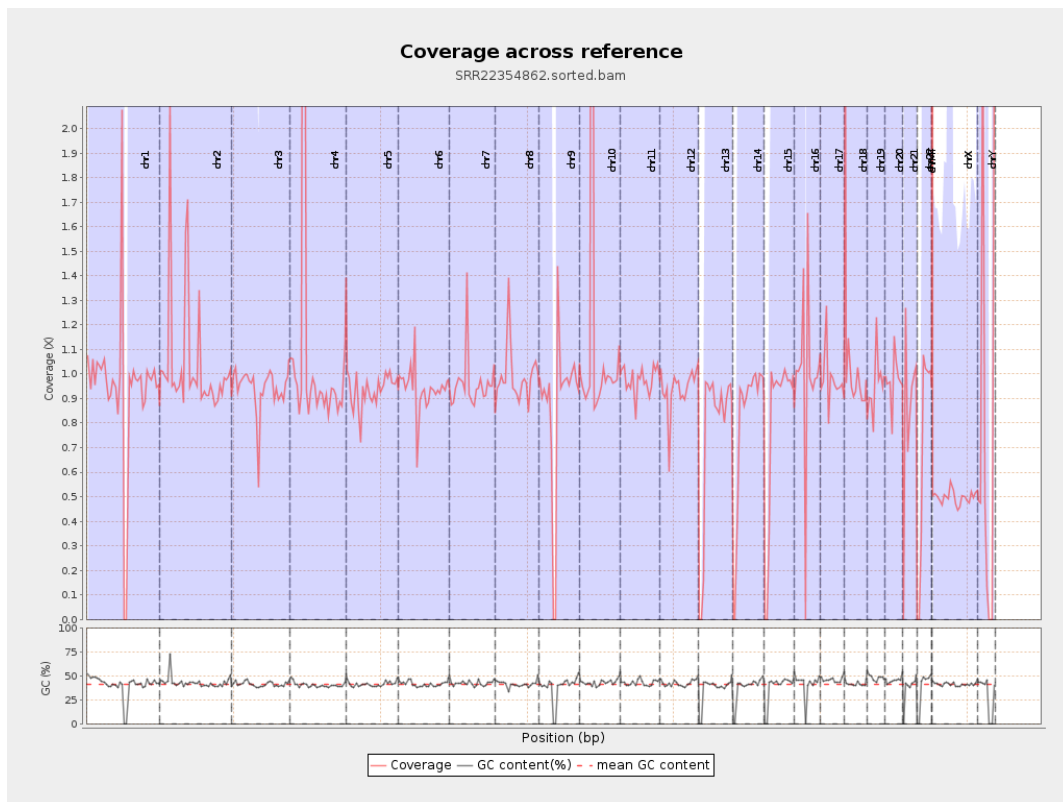
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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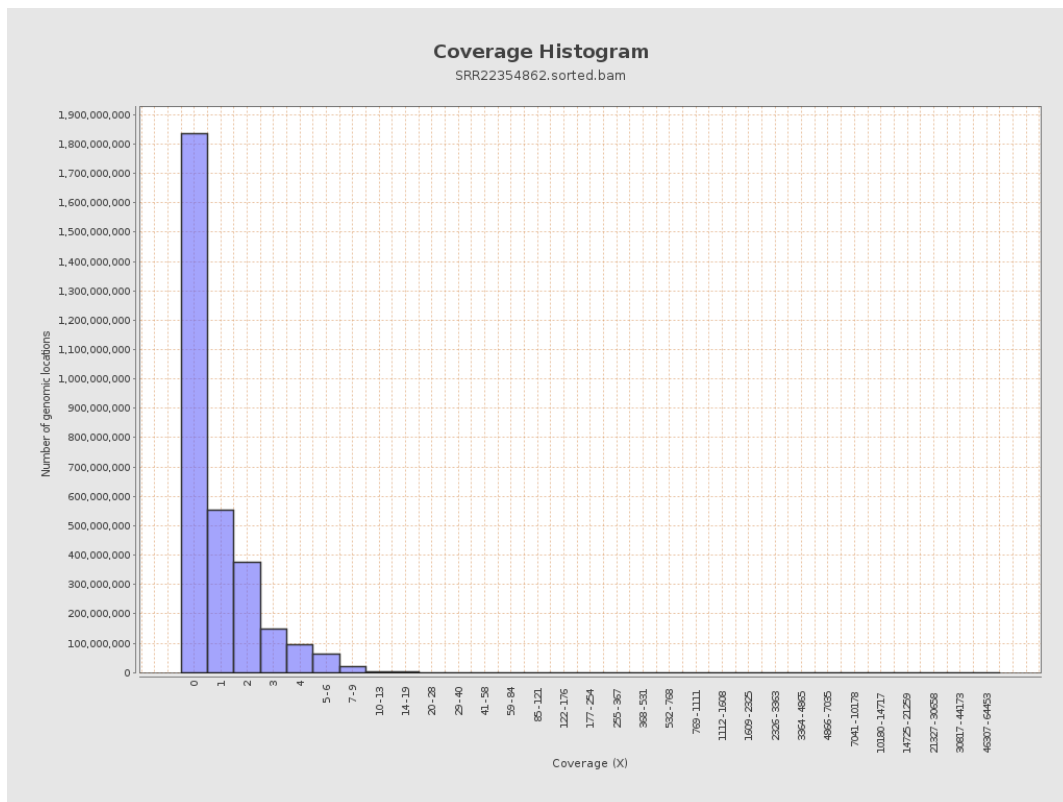
		bases	coverage	deviation
chr1	249250621	236158906	0.9475	26.3998
chr2	243199373	254071290	1.0447	38.6915
chr3	198022430	186028478	0.9394	1.7987
chr4	191154276	204425908	1.0694	26.1792
chr5	180915260	169258814	0.9356	1.6471
chr6	171115067	160847281	0.94	3.388
chr7	159138663	153023206	0.9616	11.6036
chr8	146364022	145060302	0.9911	22.7329
chr9	141213431	122406262	0.8668	12.8662
chr10	135534747	164358520	1.2127	32.5657
chr11	135006516	132009453	0.9778	3.8218
chr12	133851895	125440851	0.9372	1.6236
chr13	115169878	87556906	0.7602	1.3712
chr14	107349540	85655213	0.7979	2.427
chr15	102531392	80974903	0.7898	1.3964
chr16	90354753	90352347	1	6.784
chr17	81195210	79055030	0.9736	5.3575
chr18	78077248	81041747	1.038	16.8708
chr19	59128983	56441103	0.9545	14.6124
chr20	63025520	61571802	0.9769	8.5959
chr21	48129895	41805224	0.8686	13.3569
chr22	51304566	36467736	0.7108	2.6042
chrMT	16571	29237989	1,764.407	551.6216
chrX	155270560	77144368	0.4968	1.5904

chrY	59373566	47892366	0.8066	27.9769
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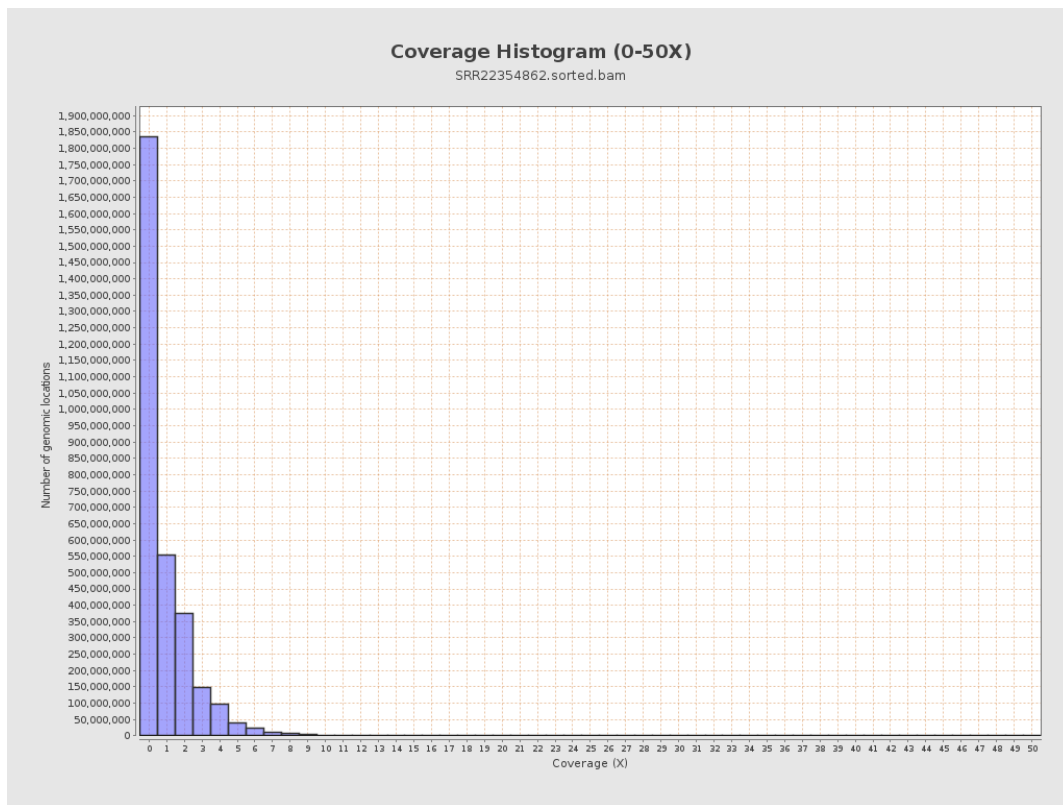
3. Results : Coverage across reference



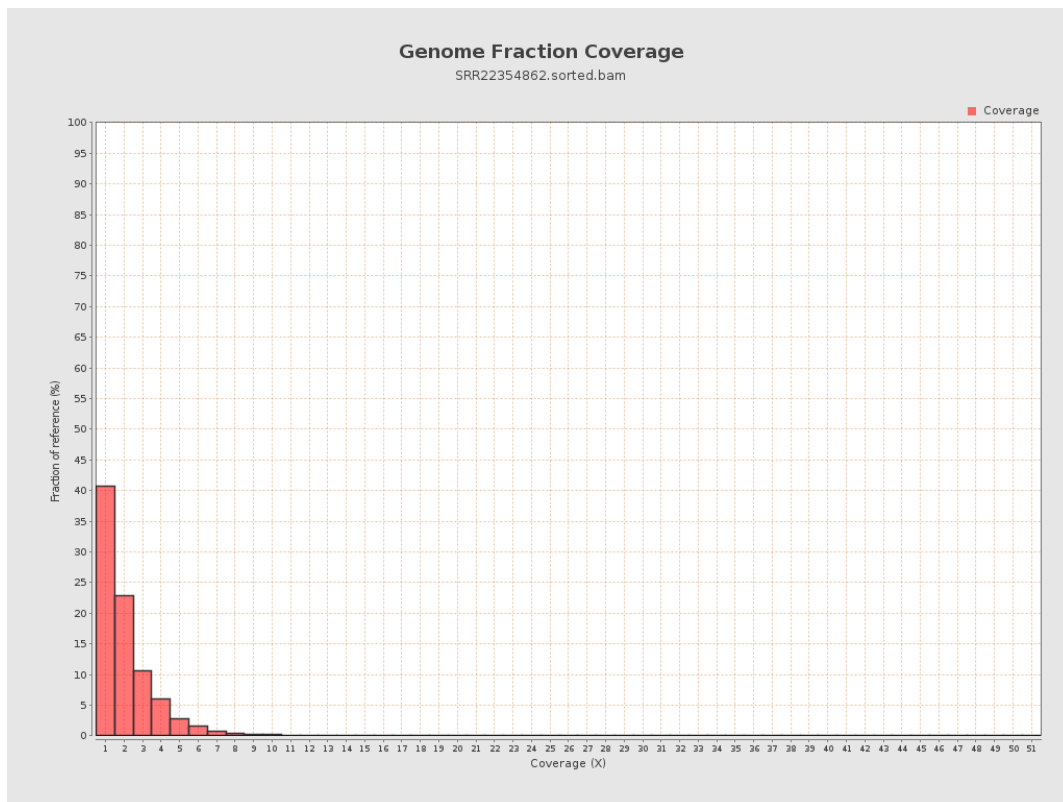
4. Results : Coverage Histogram



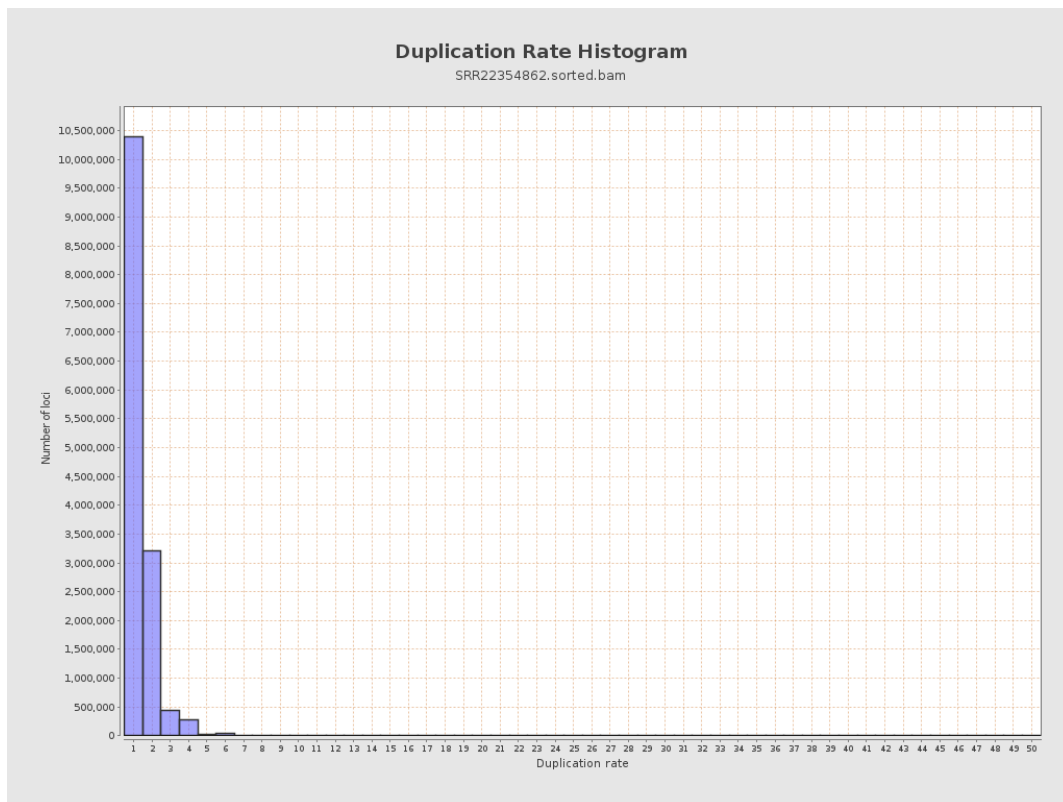
5. Results : Coverage Histogram (0-50X)



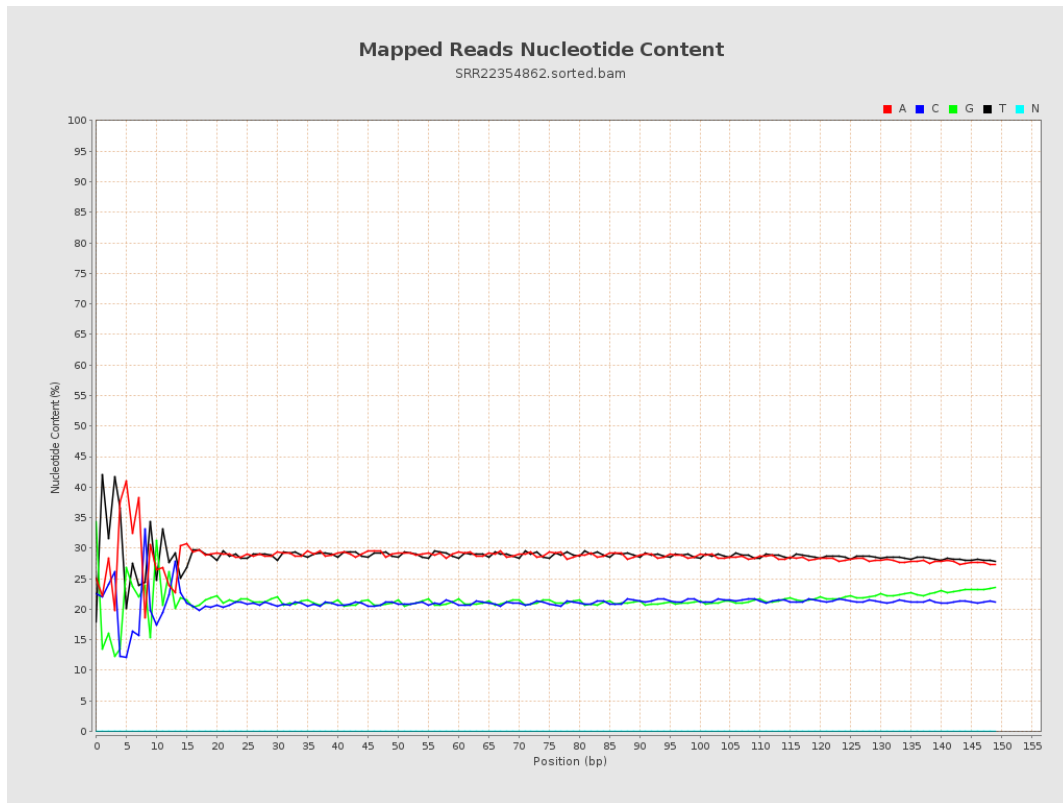
6. Results : Genome Fraction Coverage



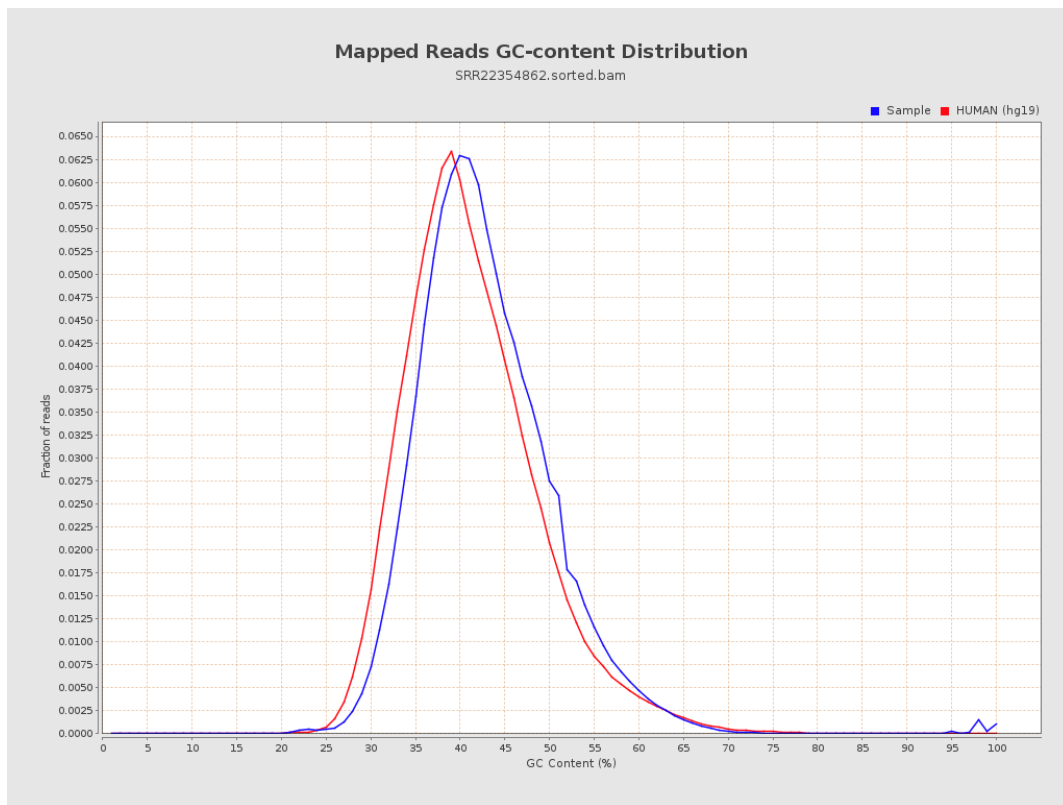
7. Results : Duplication Rate Histogram



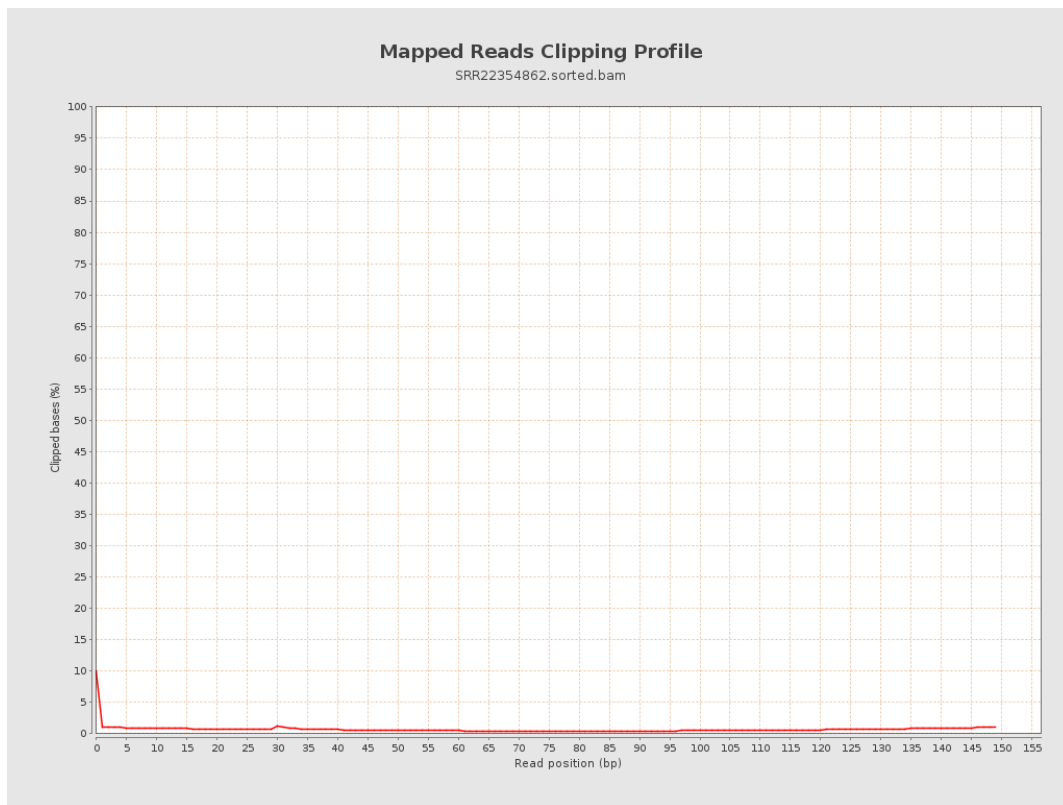
8. Results : Mapped Reads Nucleotide Content



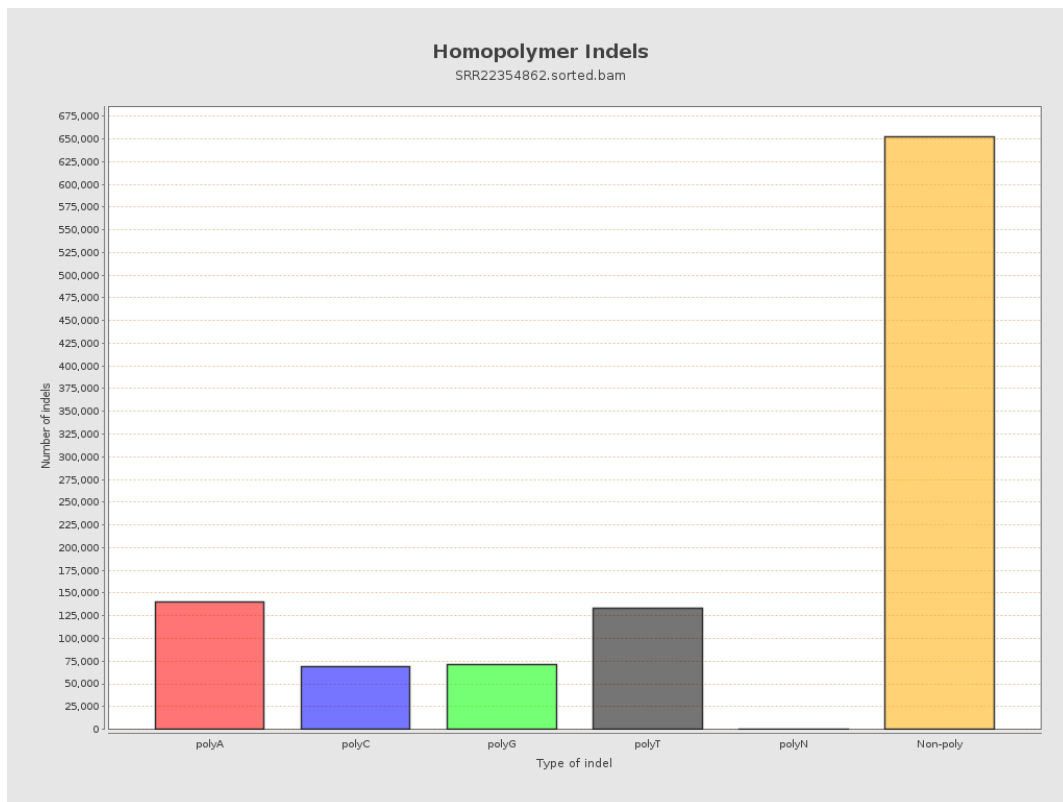
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



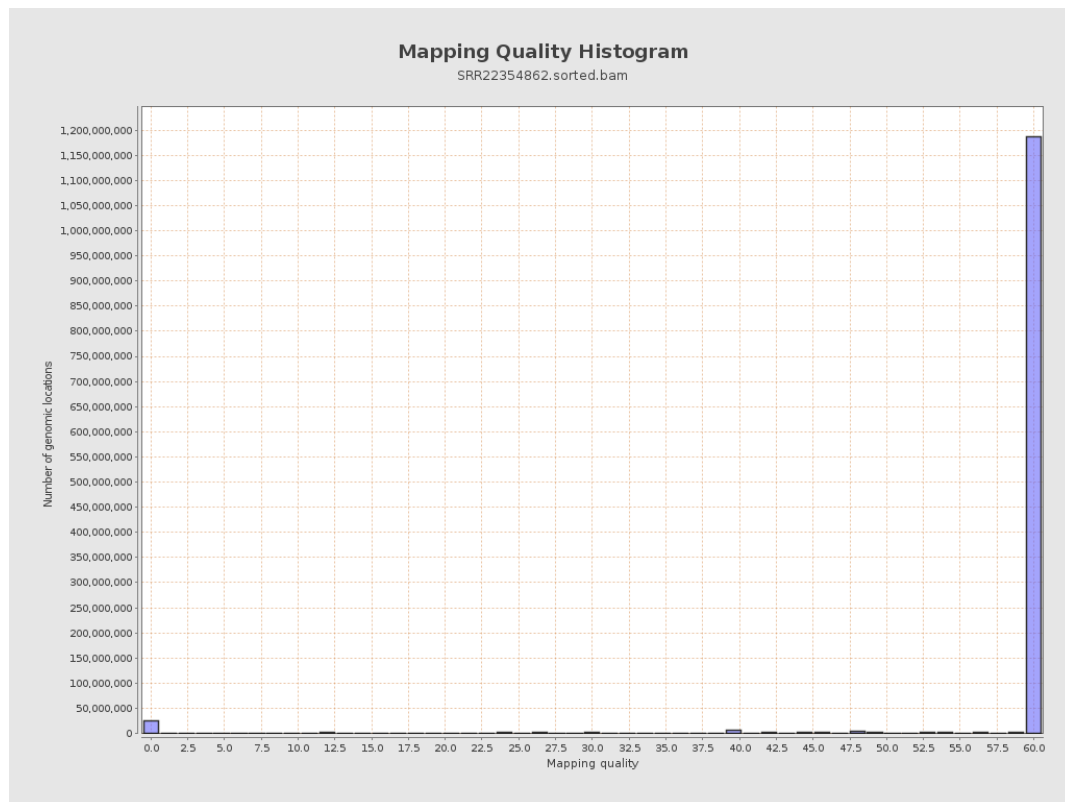
11. Results : Homopolymer Indels



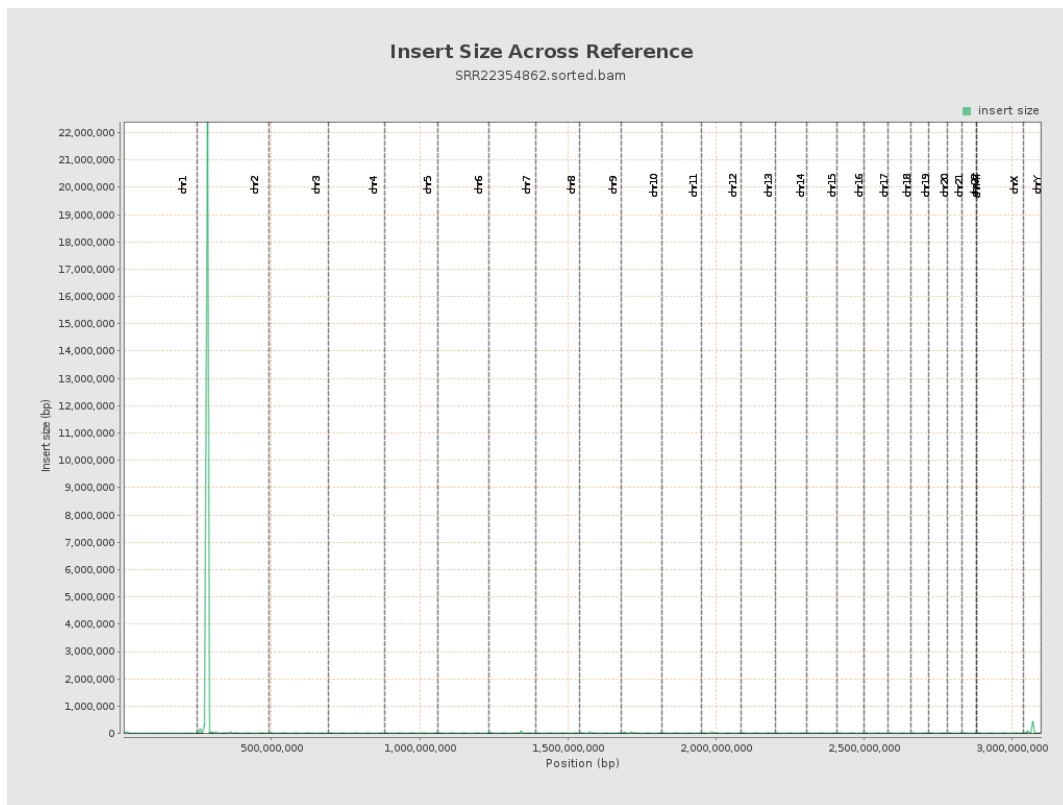
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

