

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 22:32:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124862.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_SRR3124862 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124862_1.fastq.gz SRR3124862_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 22:32:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124862.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,780,112
Mapped reads	3,751,576 / 99.25%
Unmapped reads	28,536 / 0.75%
Mapped paired reads	3,751,576 / 99.25%
Mapped reads, first in pair	1,880,248 / 49.74%
Mapped reads, second in pair	1,871,328 / 49.5%
Mapped reads, both in pair	3,739,752 / 98.93%
Mapped reads, singletons	11,824 / 0.31%
Secondary alignments	0
Supplementary alignments	53,512 / 1.42%
Read min/max/mean length	30 / 151 / 151.73
Duplicated reads (estimated)	510,358 / 13.5%
Duplication rate	11.39%
Clipped reads	1,526,181 / 40.37%

2.2. ACGT Content

Number/percentage of A's	157,822,572 / 29.58%
Number/percentage of C's	107,353,213 / 20.12%
Number/percentage of T's	157,288,782 / 29.48%
Number/percentage of G's	111,129,838 / 20.83%
Number/percentage of N's	32,532 / 0.01%

GC Percentage	40.94%
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2.3. Coverage

Mean	0.1725
Standard Deviation	2.1682

2.4. Mapping Quality

Mean Mapping Quality	53.66
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2.5. Insert size

Mean	61,672.62
Standard Deviation	2,330,262.73
P25/Median/P75	148 / 181 / 237

2.6. Mismatches and indels

General error rate	1.17%
Mismatches	5,966,709
Insertions	99,987
Mapped reads with at least one insertion	2.54%
Deletions	214,685
Mapped reads with at least one deletion	5.51%
Homopolymer indels	48.54%

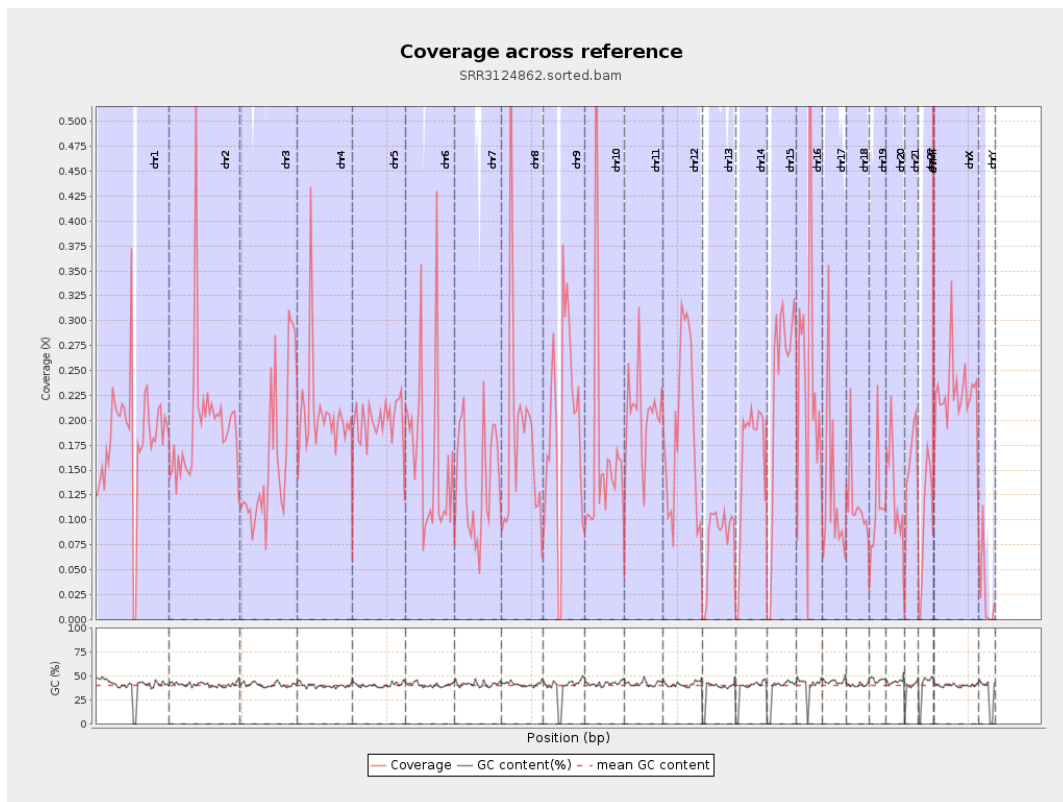
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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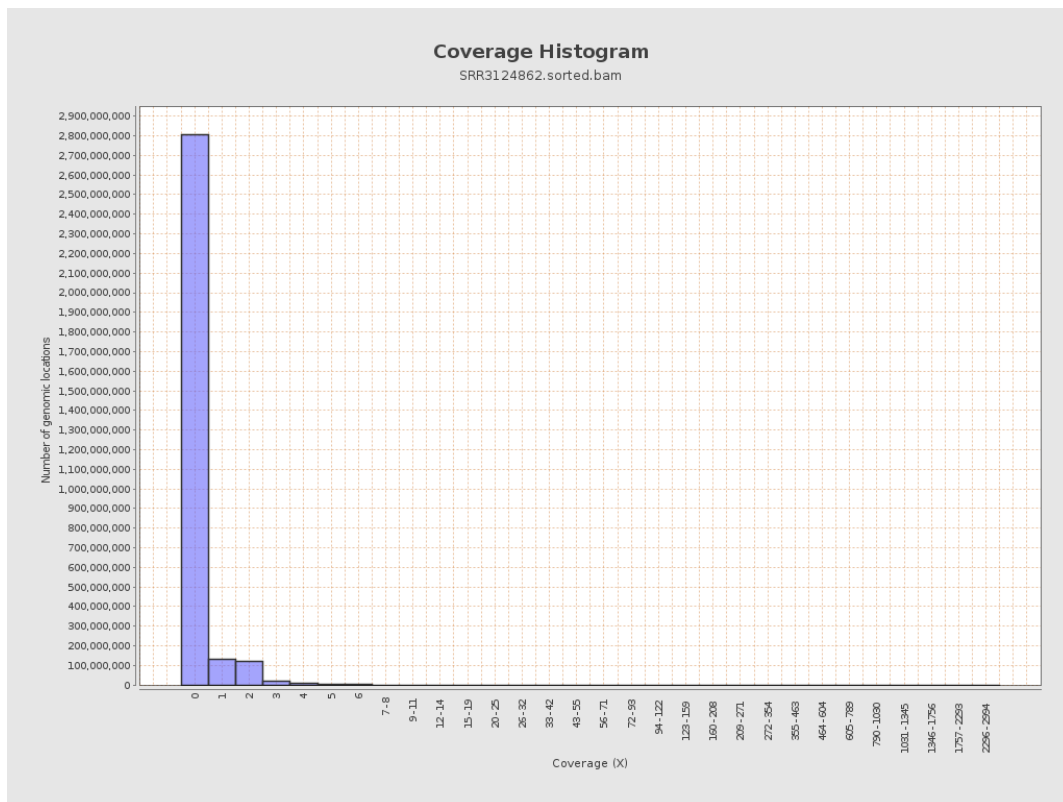
		bases	coverage	deviation
chr1	249250621	45298788	0.1817	3.0316
chr2	243199373	47757326	0.1964	2.1508
chr3	198022430	32035890	0.1618	0.6127
chr4	191154276	39338661	0.2058	1.8109
chr5	180915260	35887696	0.1984	0.64
chr6	171115067	28068952	0.164	1.9614
chr7	159138663	22362938	0.1405	0.8272
chr8	146364022	25776246	0.1761	0.8385
chr9	141213431	27994261	0.1982	3.6406
chr10	135534747	22015439	0.1624	4.6262
chr11	135006516	27456816	0.2034	2.4588
chr12	133851895	25514177	0.1906	0.634
chr13	115169878	9233933	0.0802	0.3889
chr14	107349540	17139100	0.1597	0.5987
chr15	102531392	23755367	0.2317	0.7122
chr16	90354753	21484879	0.2378	3.2459
chr17	81195210	9854851	0.1214	4.1407
chr18	78077248	9204222	0.1179	2.9604
chr19	59128983	6658324	0.1126	1.6435
chr20	63025520	8235667	0.1307	0.8548
chr21	48129895	7146783	0.1485	1.1621
chr22	51304566	5112636	0.0997	0.4545
chrMT	16571	37984	2.2922	2.0868
chrX	155270560	35252583	0.227	1.1953

chrY	59373566	1399129	0.0236	1.8549
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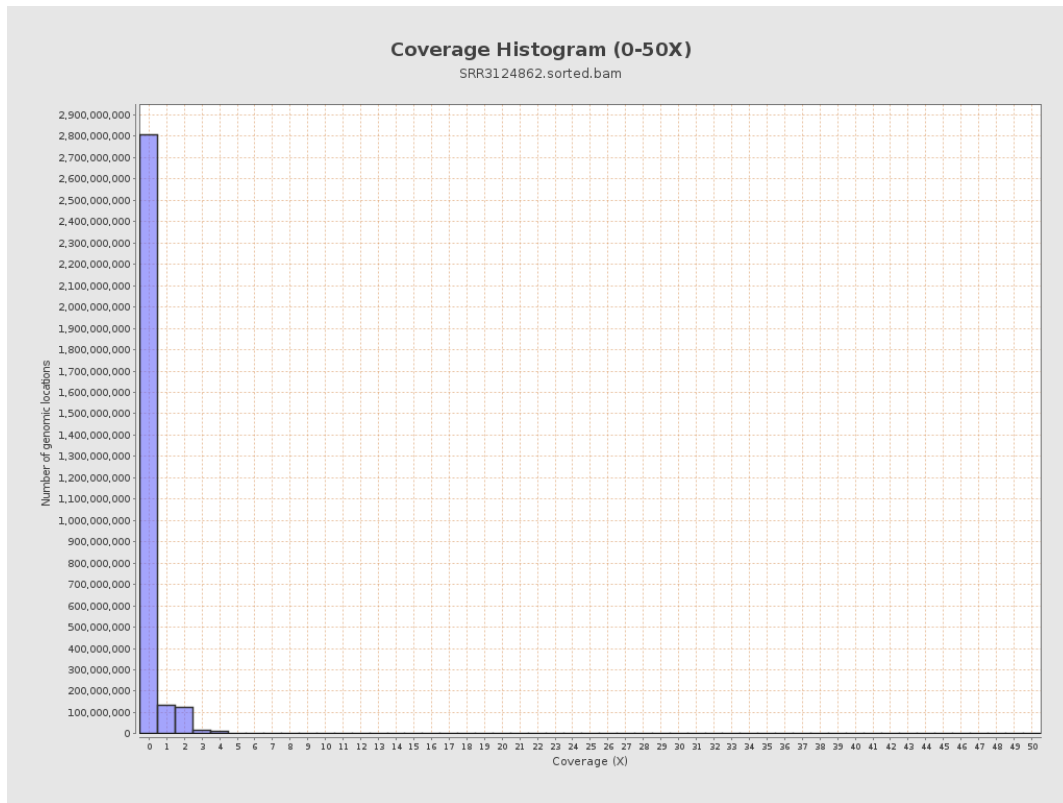
3. Results : Coverage across reference



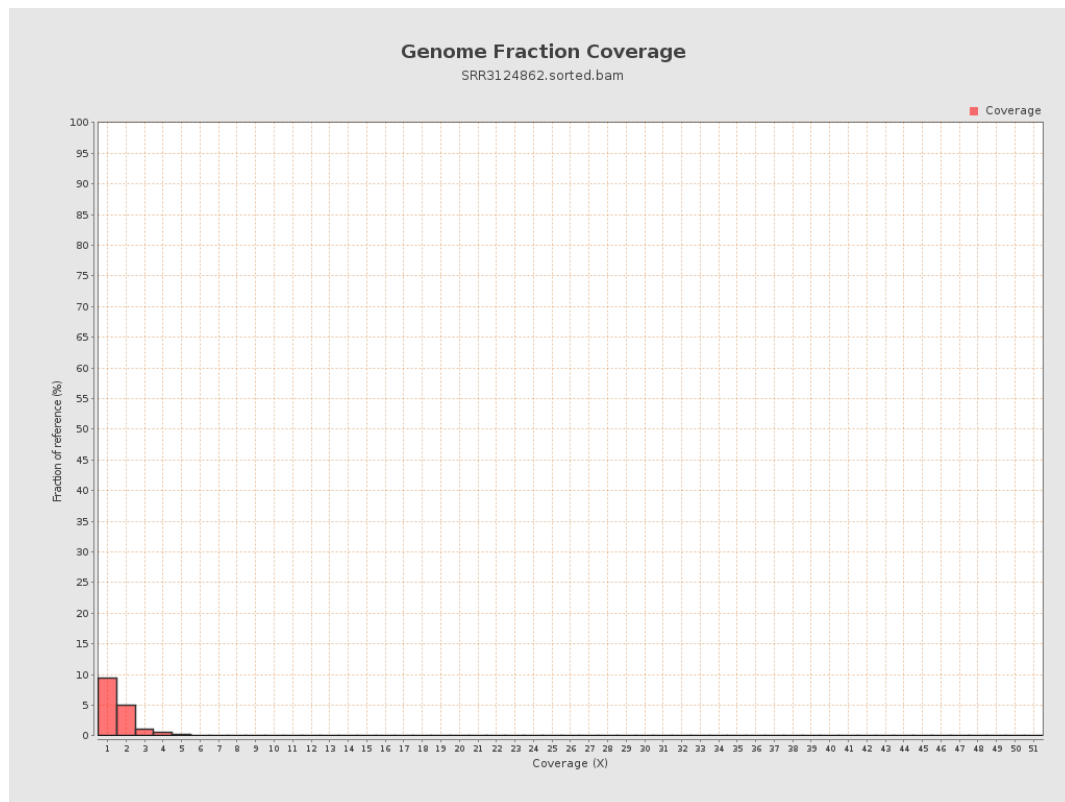
4. Results : Coverage Histogram



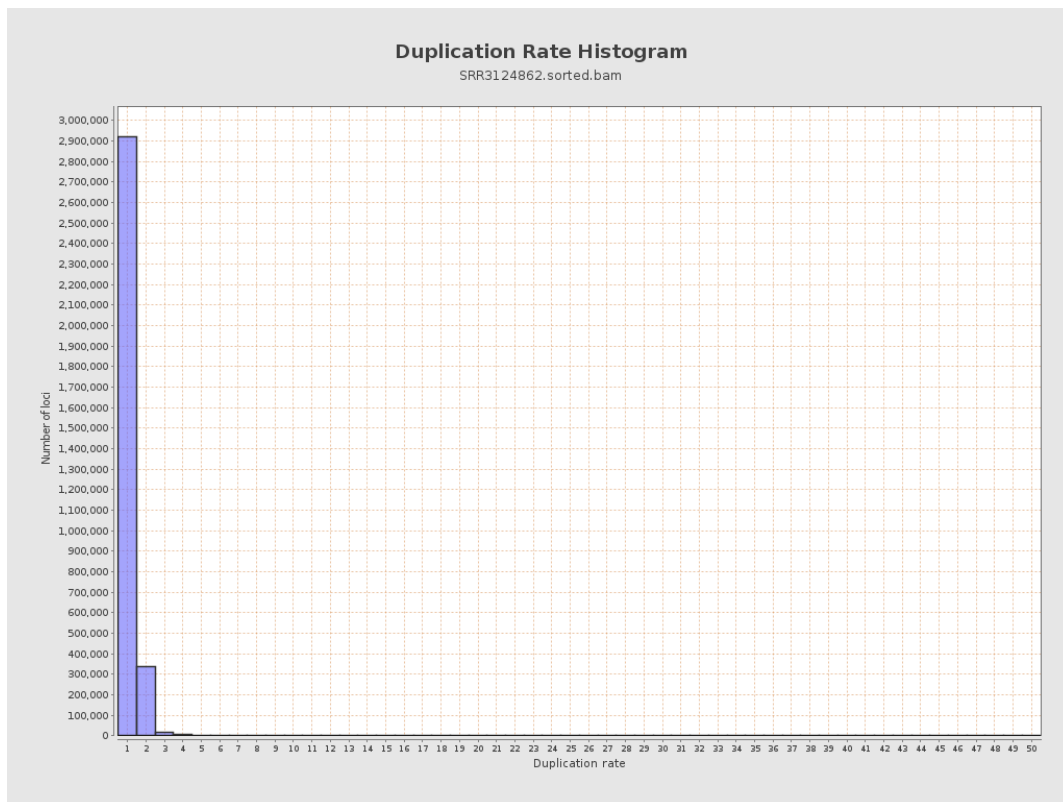
5. Results : Coverage Histogram (0-50X)



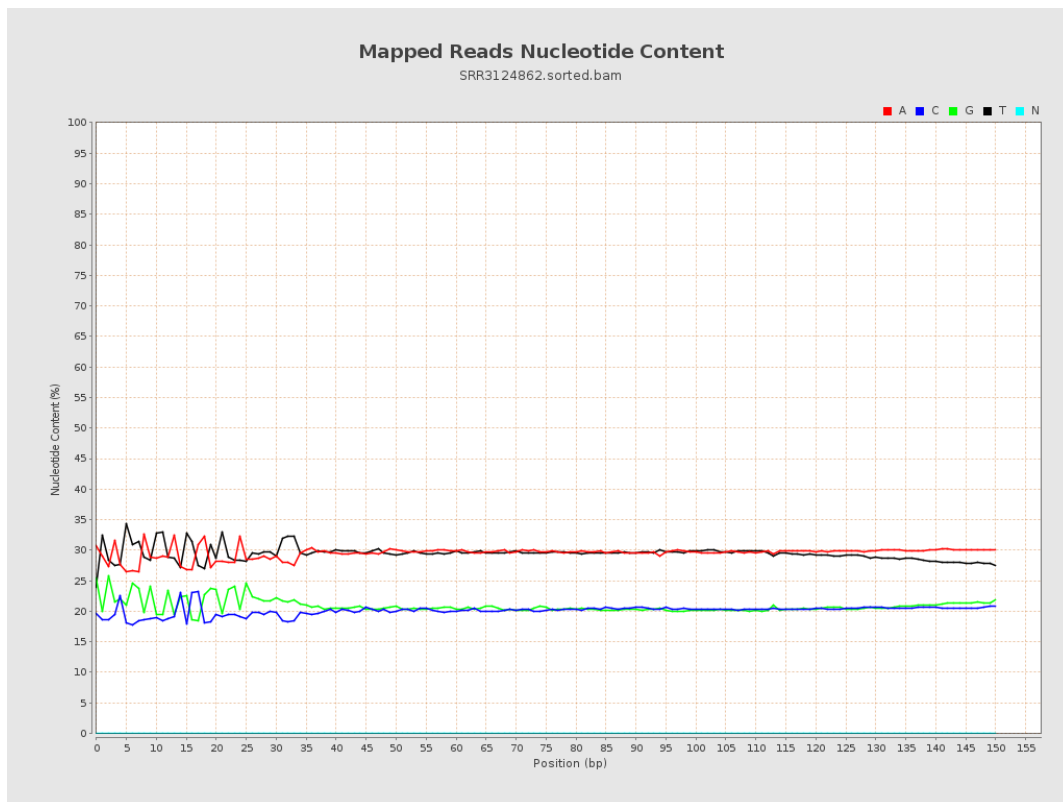
6. Results : Genome Fraction Coverage



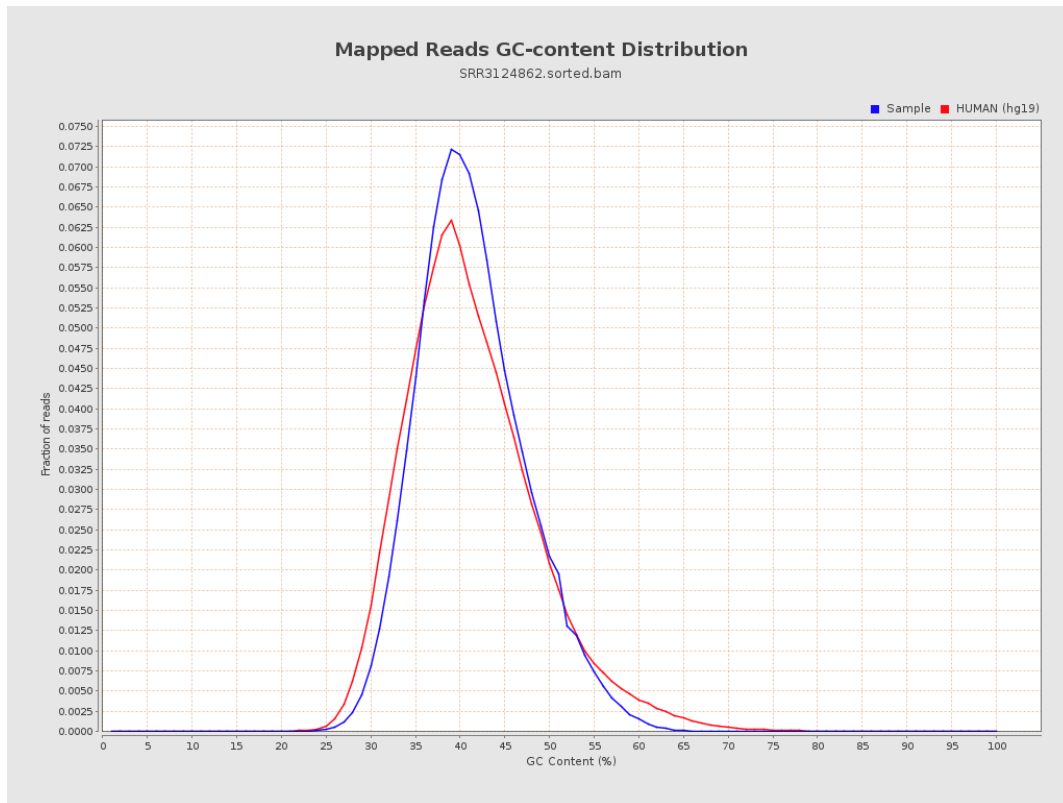
7. Results : Duplication Rate Histogram



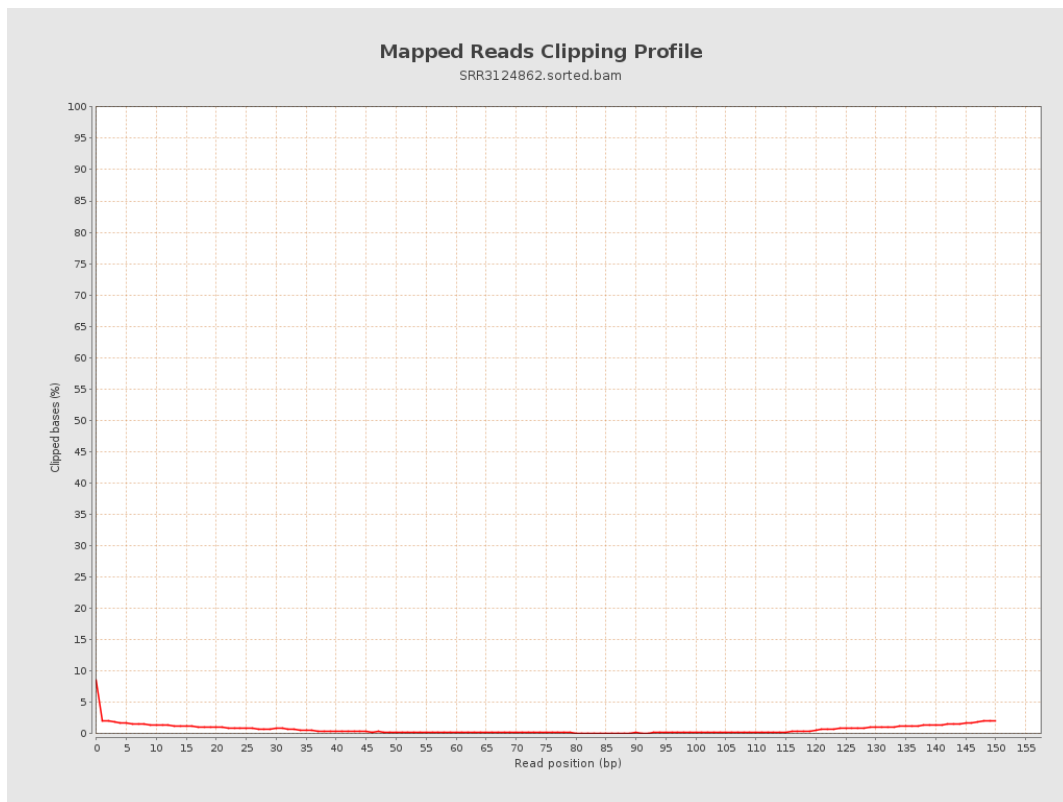
8. Results : Mapped Reads Nucleotide Content



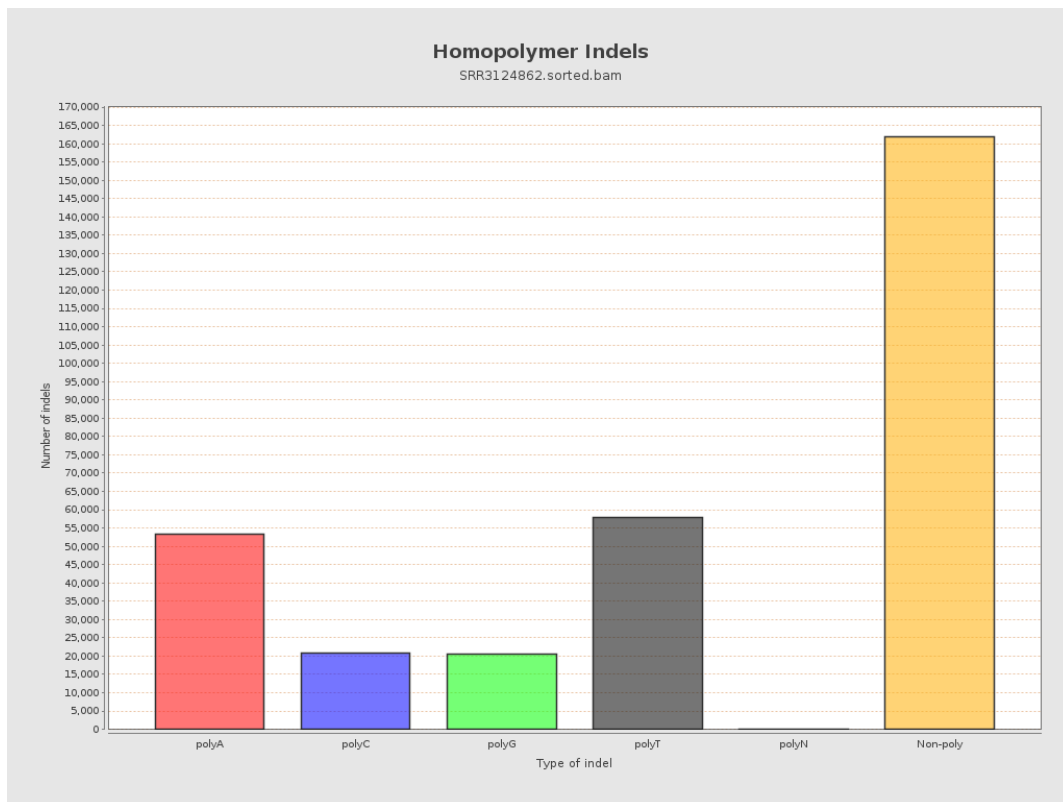
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



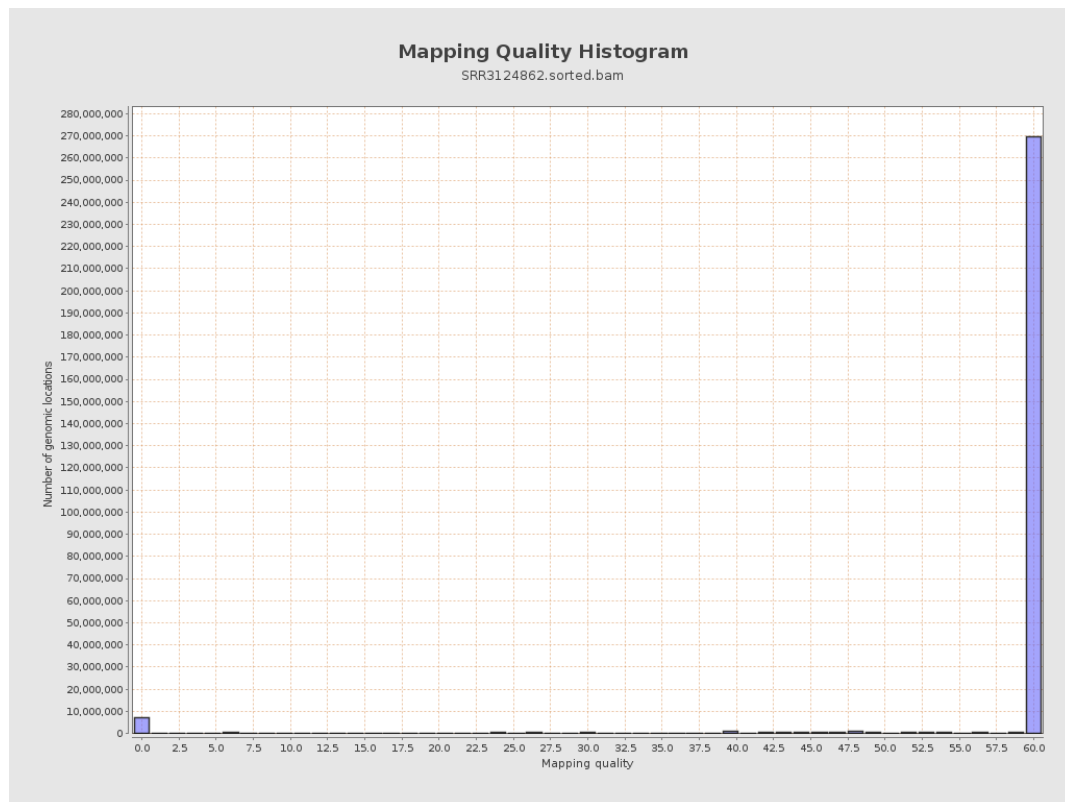
11. Results : Homopolymer Indels



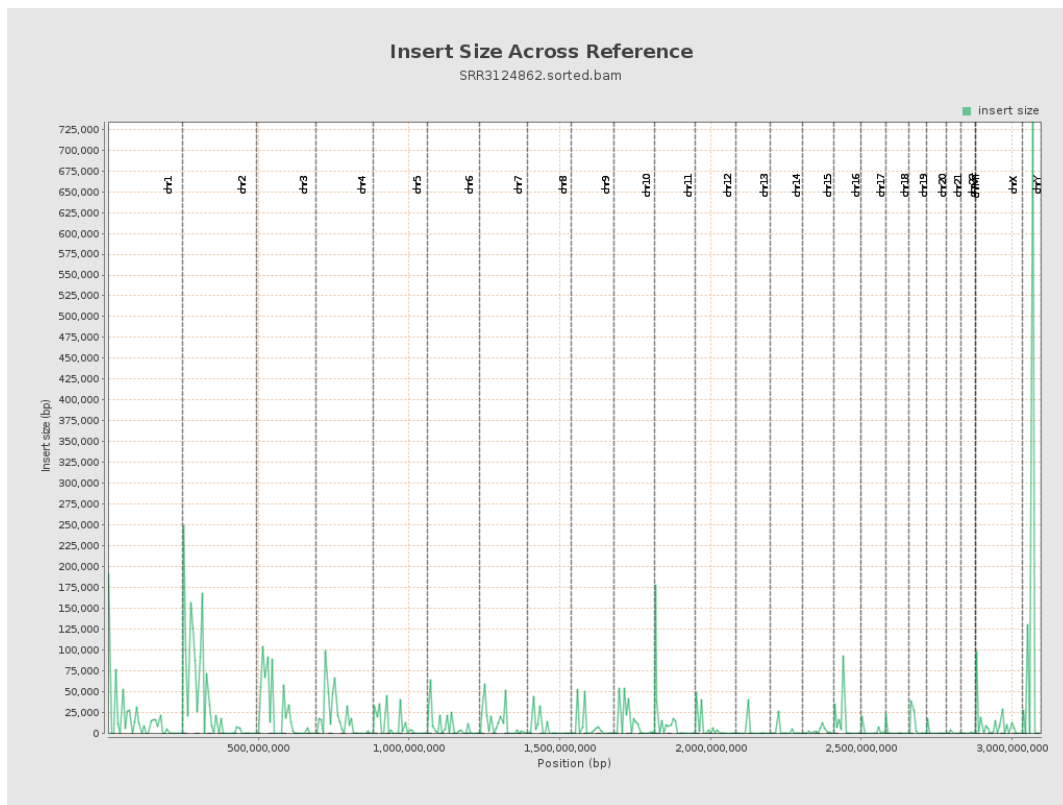
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

