

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/12 15:54:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365354.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_SRR5365354 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365354_1.fastq.gz SRR5365354_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Nov 12 15:54:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365354.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	582,080,132
Mapped reads	562,301,320 / 96.6%
Unmapped reads	19,778,812 / 3.4%
Mapped paired reads	562,301,320 / 96.6%
Mapped reads, first in pair	281,701,249 / 48.4%
Mapped reads, second in pair	280,600,071 / 48.21%
Mapped reads, both in pair	559,802,970 / 96.17%
Mapped reads, singletons	2,498,350 / 0.43%
Secondary alignments	0
Supplementary alignments	2,519,559 / 0.43%
Read min/max/mean length	30 / 125 / 125.18
Duplicated reads (estimated)	314,164,536 / 53.97%
Duplication rate	30.71%
Clipped reads	354,954,789 / 60.98%

2.2. ACGT Content

Number/percentage of A's	17,813,618,761 / 30.29%
Number/percentage of C's	11,413,601,045 / 19.41%
Number/percentage of T's	17,347,908,706 / 29.5%
Number/percentage of G's	12,233,005,111 / 20.8%
Number/percentage of N's	7,396,760 / 0.01%

GC Percentage	40.2%
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2.3. Coverage

Mean	19.0056
Standard Deviation	166.5791

2.4. Mapping Quality

Mean Mapping Quality	53.82
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2.5. Insert size

Mean	58,840.15
Standard Deviation	2,351,195.46
P25/Median/P75	114 / 162 / 229

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	305,741,260
Insertions	17,860,433
Mapped reads with at least one insertion	3.1%
Deletions	9,408,135
Mapped reads with at least one deletion	1.63%
Homopolymer indels	50.42%

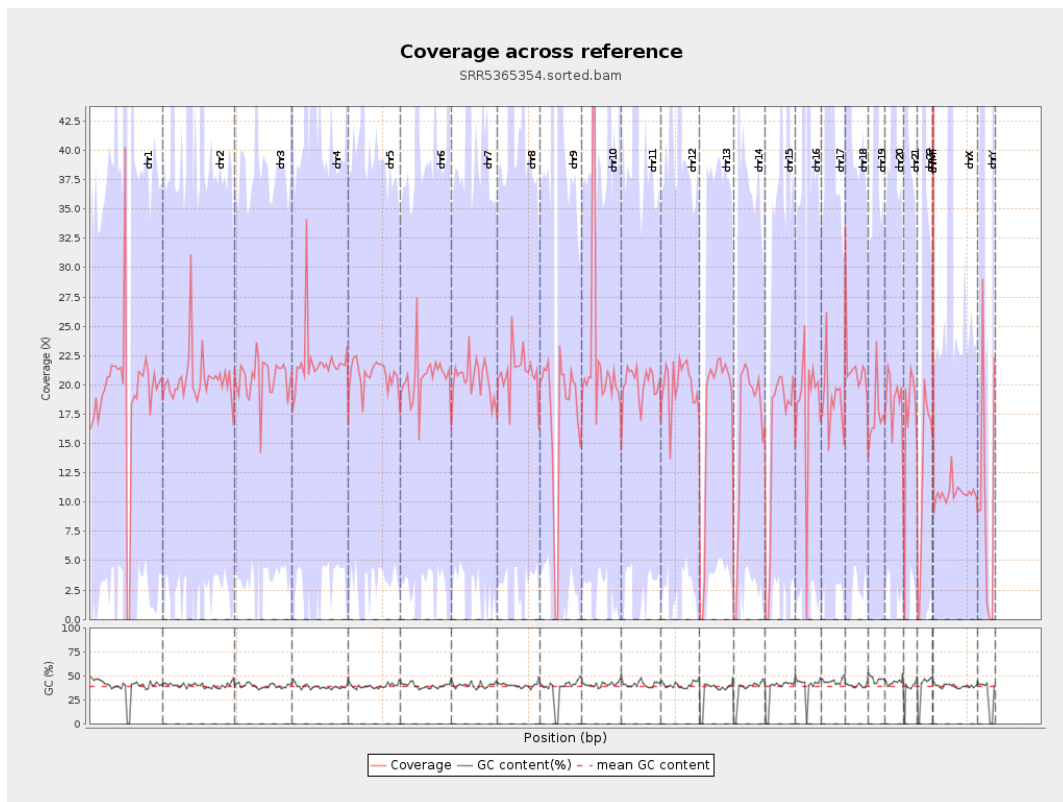
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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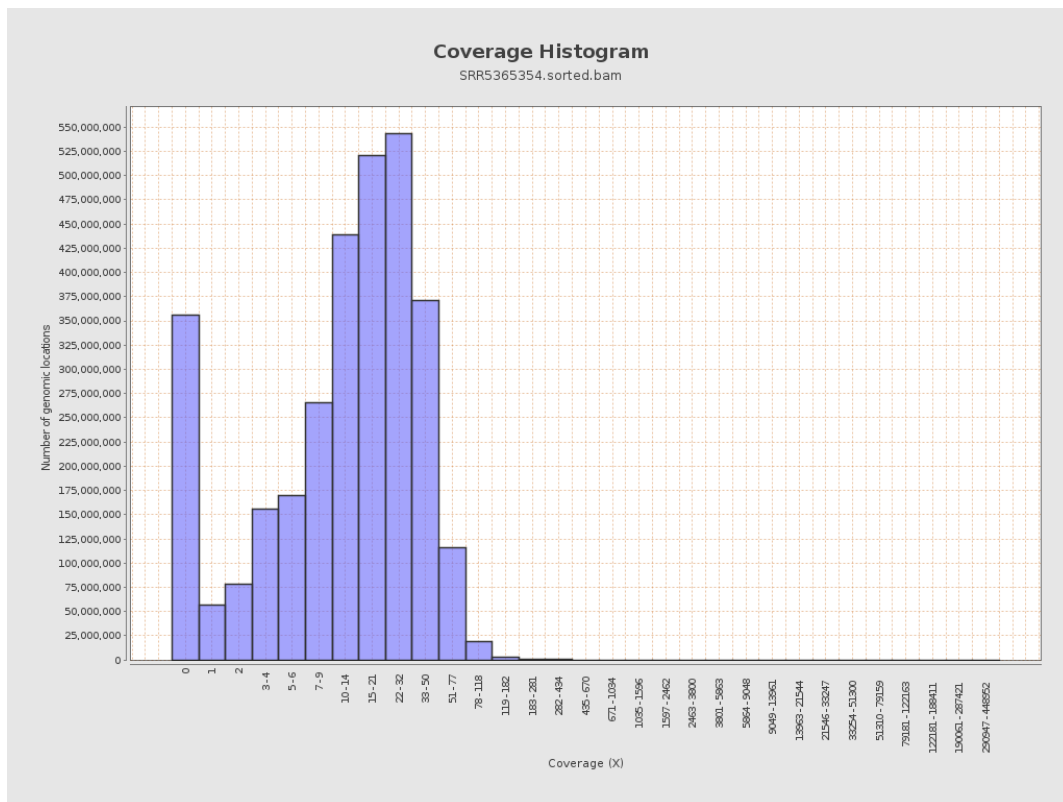
		bases	coverage	deviation
chr1	249250621	4804603764	19.2762	434.103
chr2	243199373	4989510567	20.5161	102.0142
chr3	198022430	4074057839	20.5737	27.6022
chr4	191154276	4197235556	21.9573	113.6496
chr5	180915260	3759950434	20.7829	20.516
chr6	171115067	3538781588	20.6807	81.6728
chr7	159138663	3246756396	20.4021	118.322
chr8	146364022	3075730843	21.0143	53.6638
chr9	141213431	2467327510	17.4723	134.9171
chr10	135534747	3035606062	22.3973	331.1441
chr11	135006516	2715655284	20.115	109.2039
chr12	133851895	2679491256	20.0183	36.6624
chr13	115169878	2008823718	17.4423	16.9548
chr14	107349540	1771056400	16.498	19.9522
chr15	102531392	1594951192	15.5557	22.6977
chr16	90354753	1636506133	18.112	58.5255
chr17	81195210	1533165207	18.8825	105.4528
chr18	78077248	1673948789	21.4396	175.2089
chr19	59128983	1036155776	17.5237	220.7277
chr20	63025520	1190145573	18.8836	35.6029
chr21	48129895	823281812	17.1054	70.6018
chr22	51304566	651935624	12.7072	60.4461
chrMT	16571	51361213	3,099.4637	543.5051
chrX	155270560	1666146355	10.7306	45.0176

chrY	59373566	613328728	10.33	227.0499
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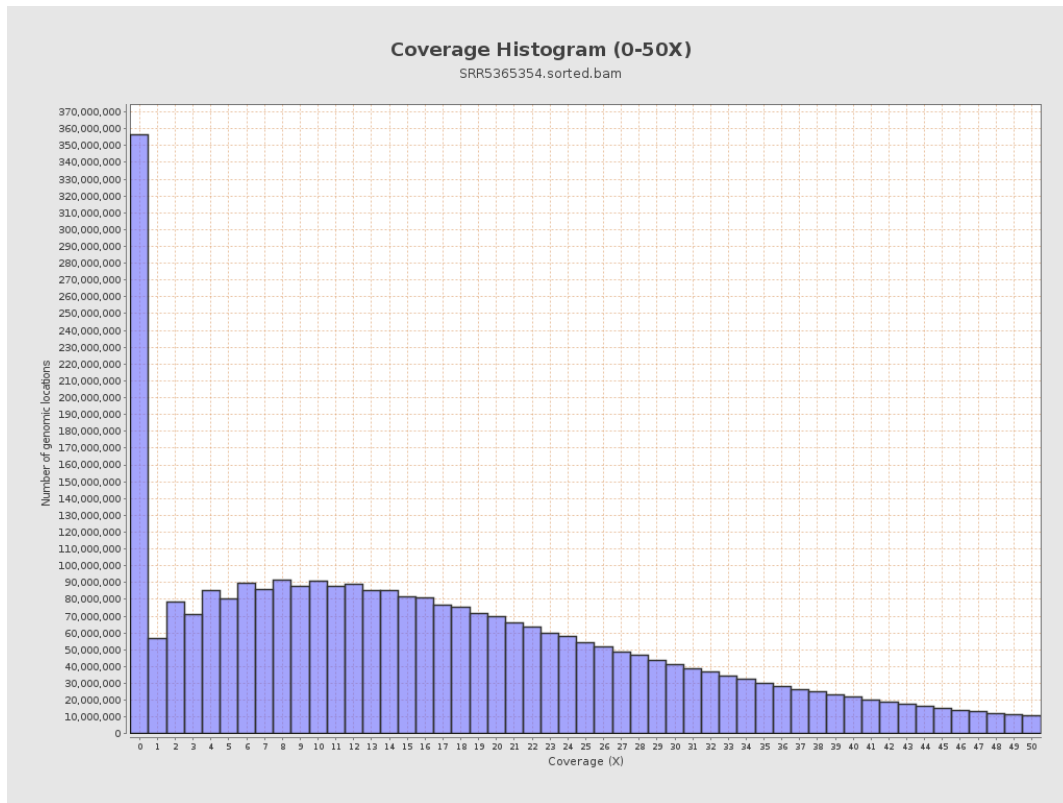
3. Results : Coverage across reference



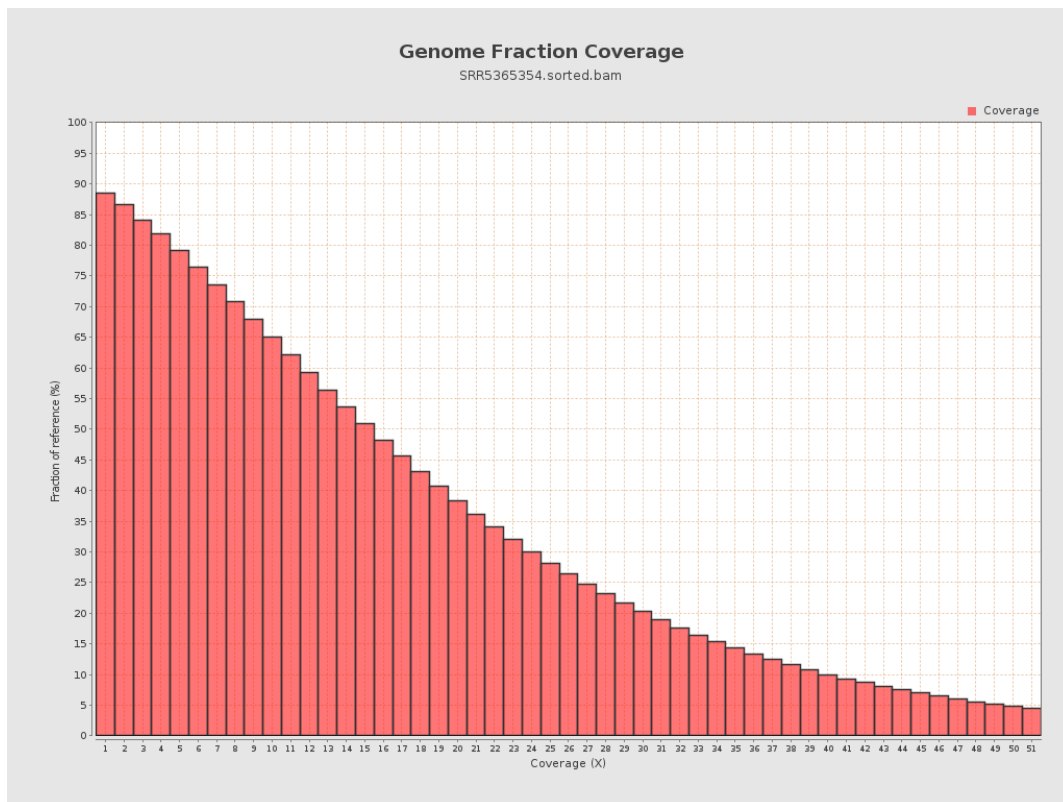
4. Results : Coverage Histogram



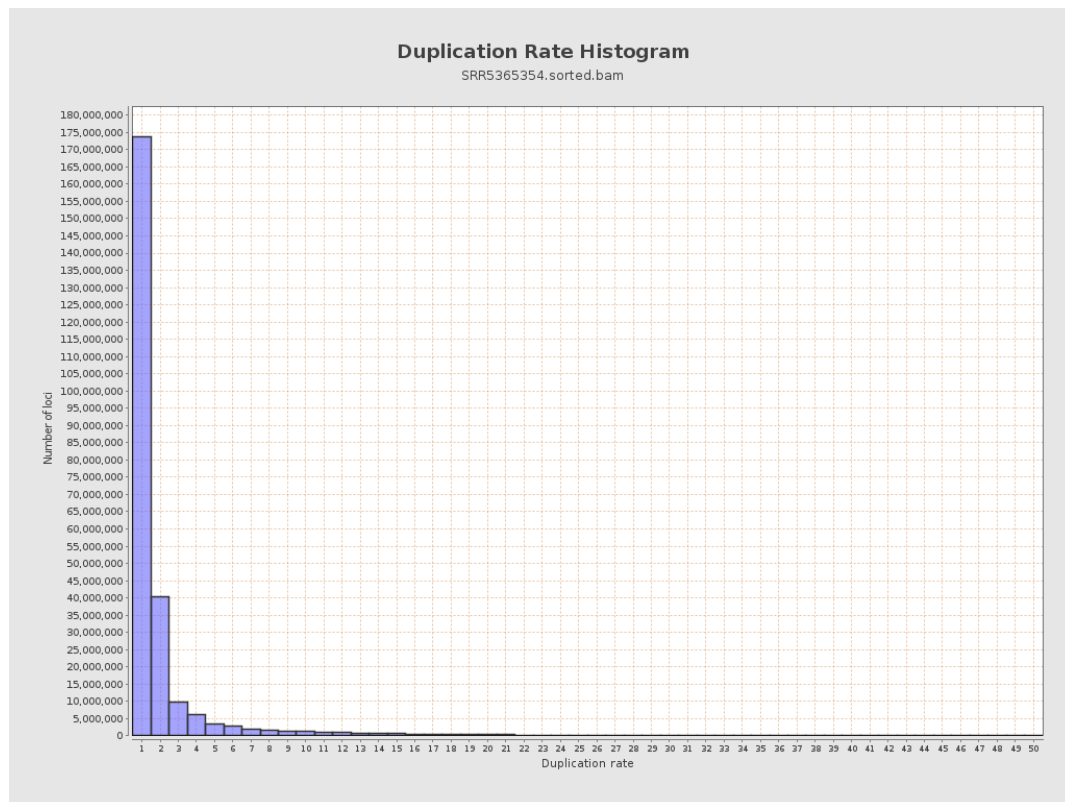
5. Results : Coverage Histogram (0-50X)



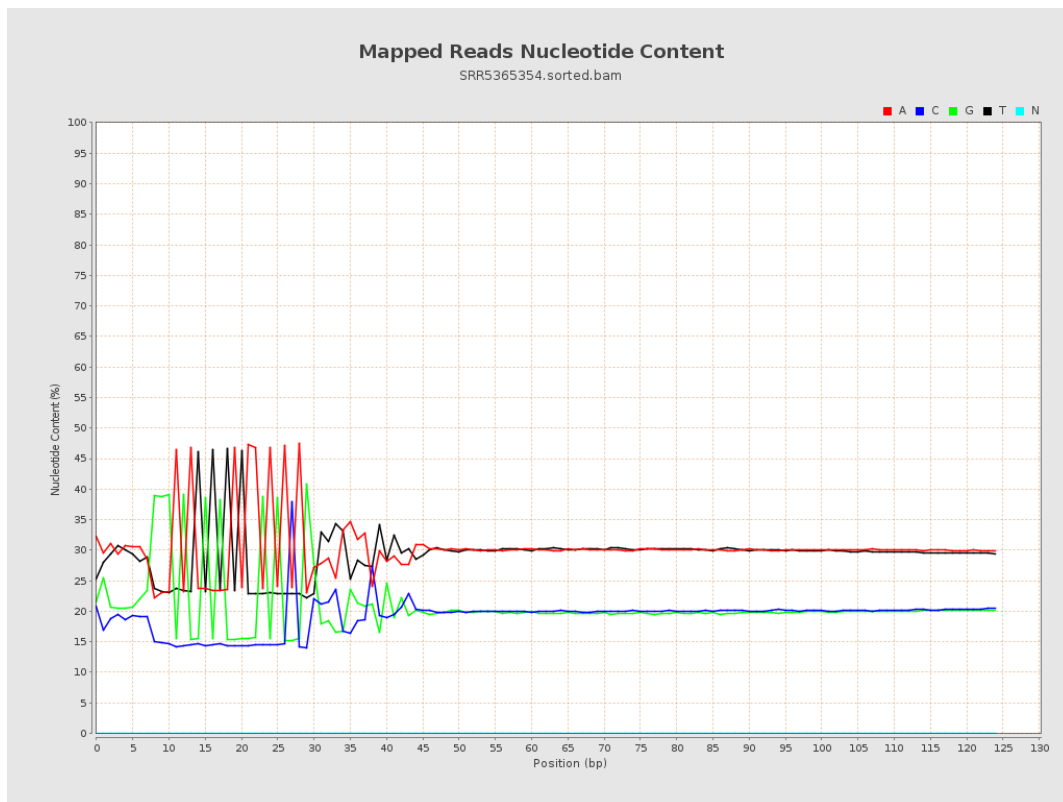
6. Results : Genome Fraction Coverage



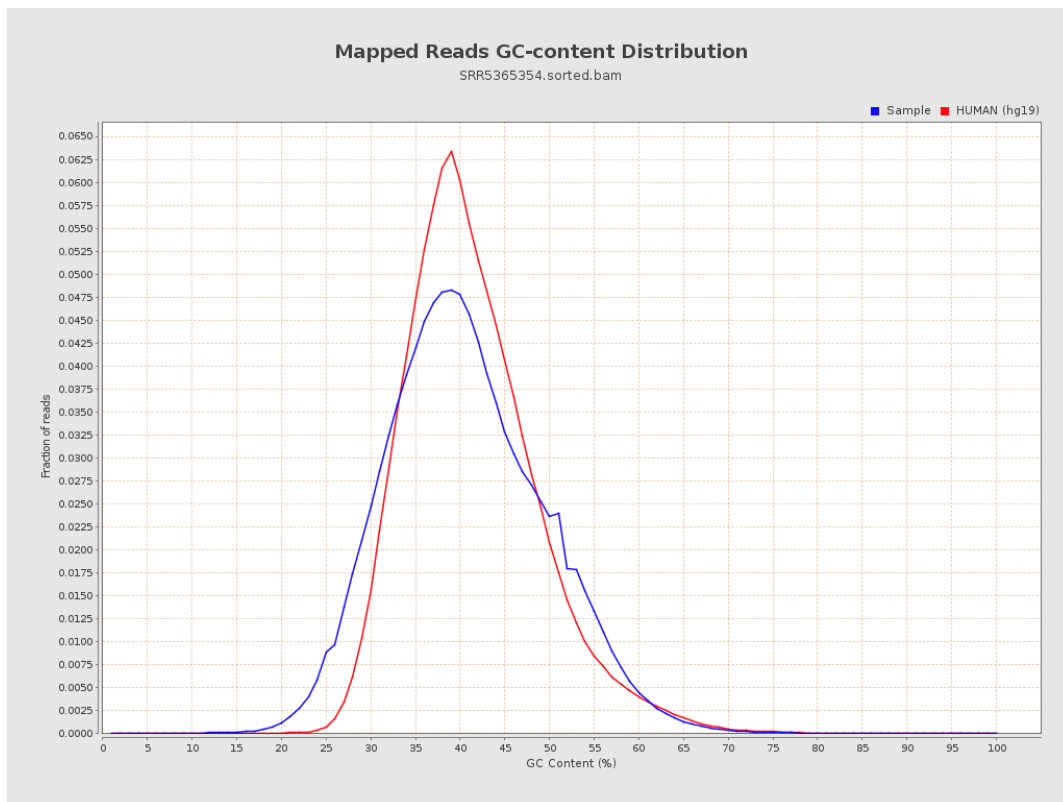
7. Results : Duplication Rate Histogram



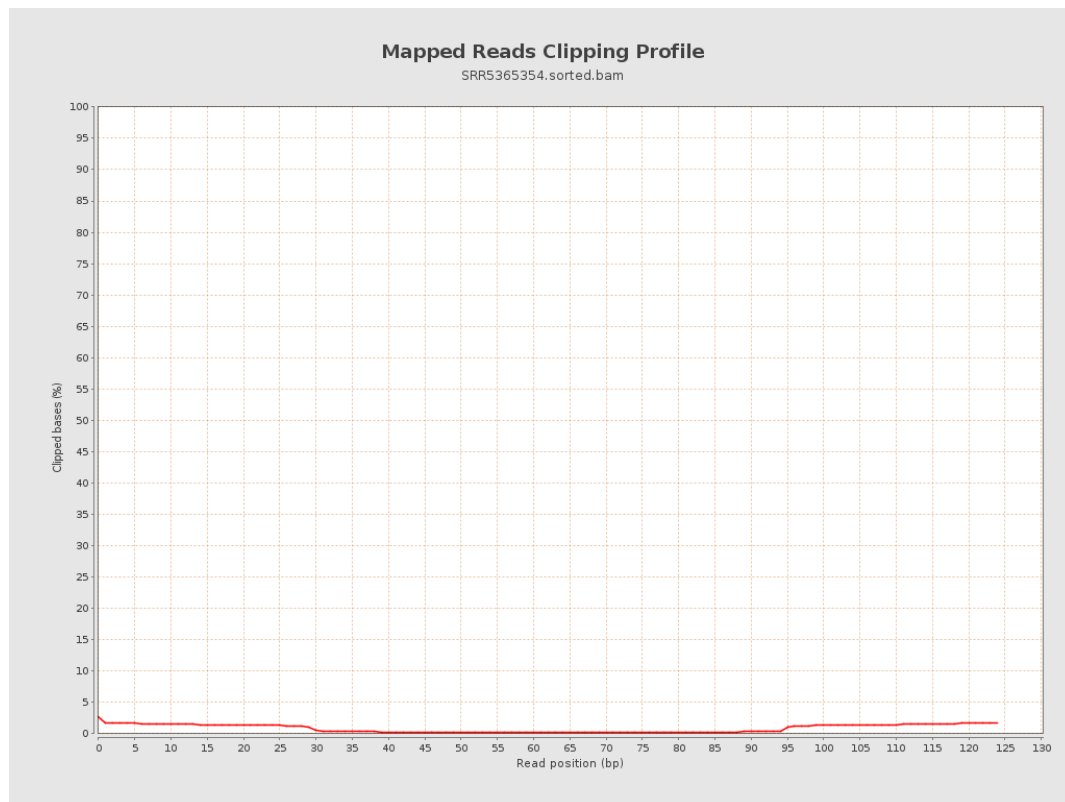
8. Results : Mapped Reads Nucleotide Content



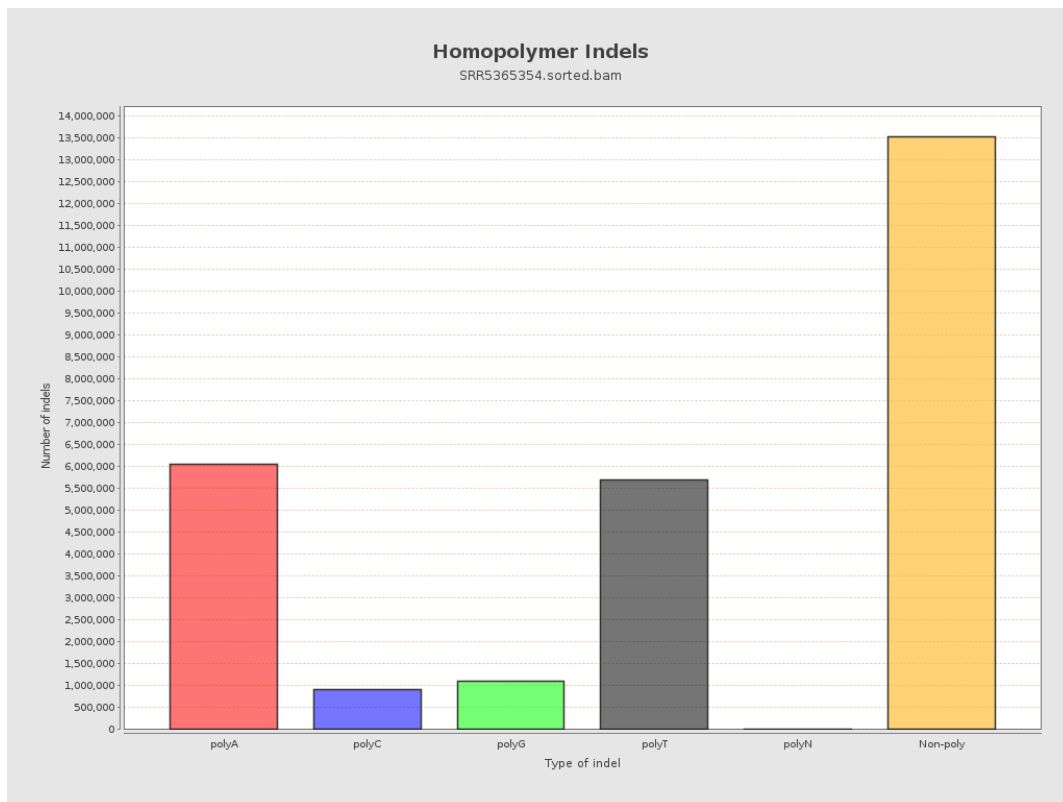
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



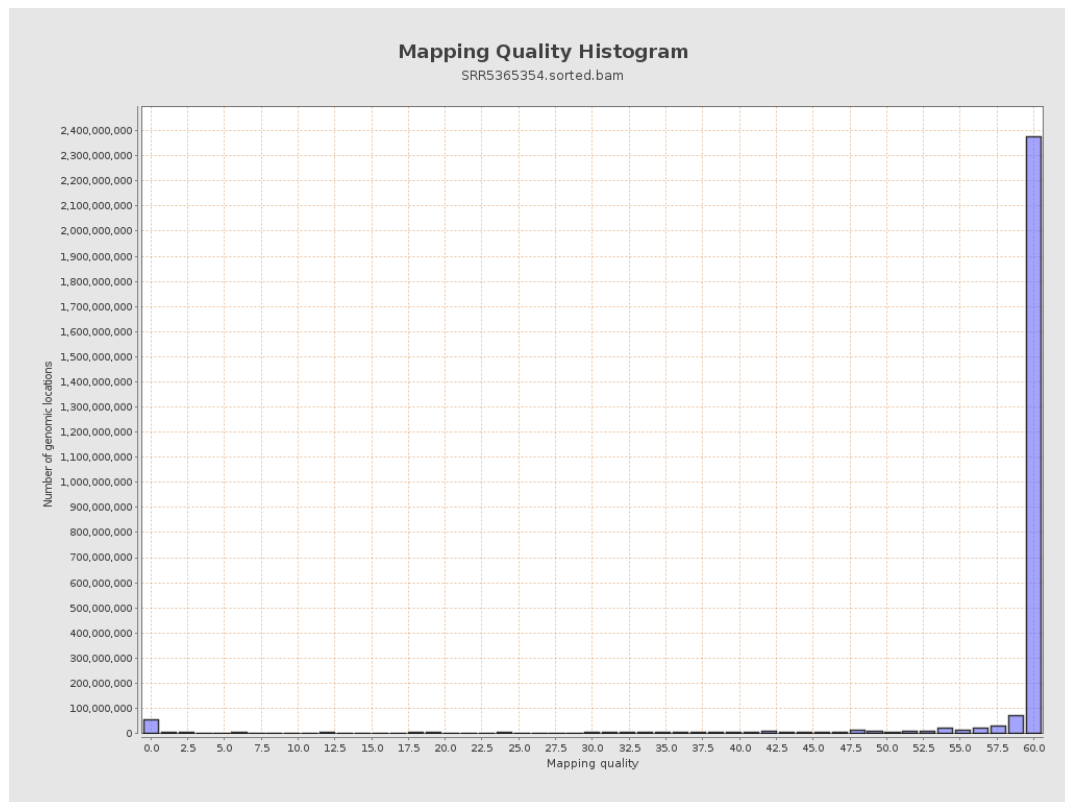
11. Results : Homopolymer Indels



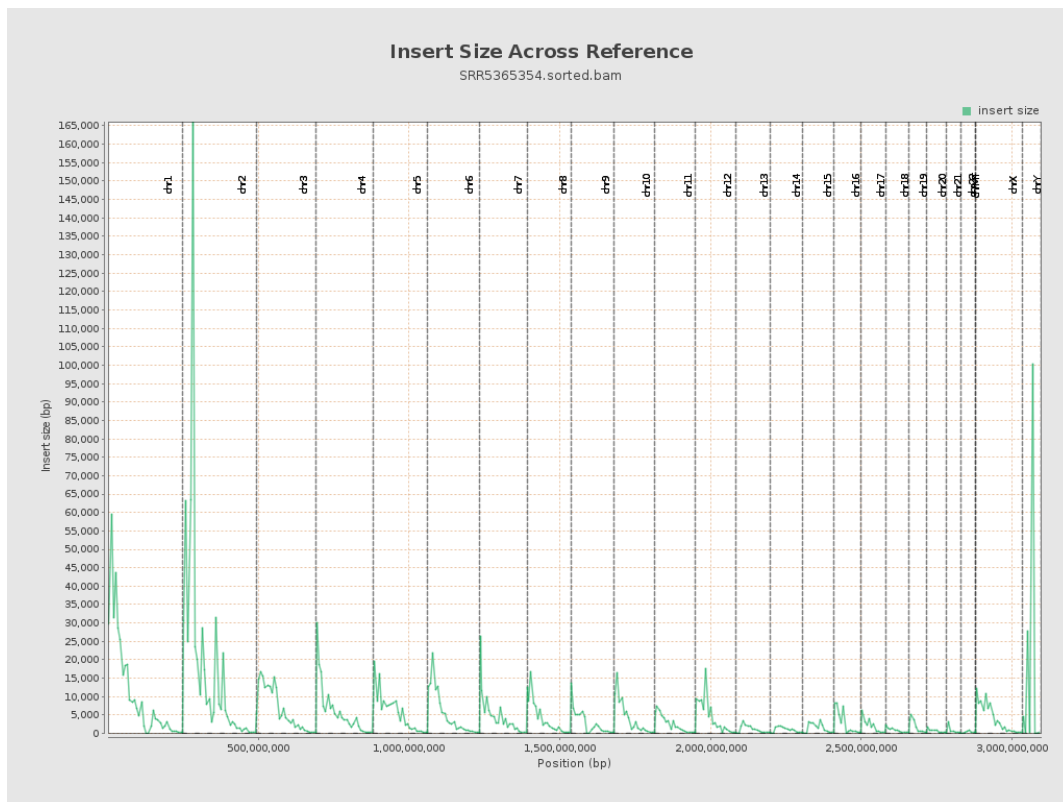
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

