

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/12 05:17:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365352.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_SRR5365352 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365352_1.fastq.gz SRR5365352_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Nov 12 05:17:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365352.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	570,379,364
Mapped reads	551,413,701 / 96.67%
Unmapped reads	18,965,663 / 3.33%
Mapped paired reads	551,413,701 / 96.67%
Mapped reads, first in pair	276,236,200 / 48.43%
Mapped reads, second in pair	275,177,501 / 48.24%
Mapped reads, both in pair	548,996,588 / 96.25%
Mapped reads, singletons	2,417,113 / 0.42%
Secondary alignments	0
Supplementary alignments	2,357,407 / 0.41%
Read min/max/mean length	30 / 125 / 125.17
Duplicated reads (estimated)	326,912,468 / 57.31%
Duplication rate	32.82%
Clipped reads	358,599,156 / 62.87%

2.2. ACGT Content

Number/percentage of A's	17,208,381,329 / 30.04%
Number/percentage of C's	11,258,796,638 / 19.66%
Number/percentage of T's	16,727,985,396 / 29.2%
Number/percentage of G's	12,080,770,398 / 21.09%
Number/percentage of N's	6,128,311 / 0.01%

GC Percentage	40.74%
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2.3. Coverage

Mean	18.5099
Standard Deviation	127.9371

2.4. Mapping Quality

Mean Mapping Quality	53.85
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2.5. Insert size

Mean	62,618.59
Standard Deviation	2,438,586.21
P25/Median/P75	111 / 159 / 225

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	286,949,886
Insertions	17,079,760
Mapped reads with at least one insertion	3.03%
Deletions	8,962,287
Mapped reads with at least one deletion	1.58%
Homopolymer indels	50.6%

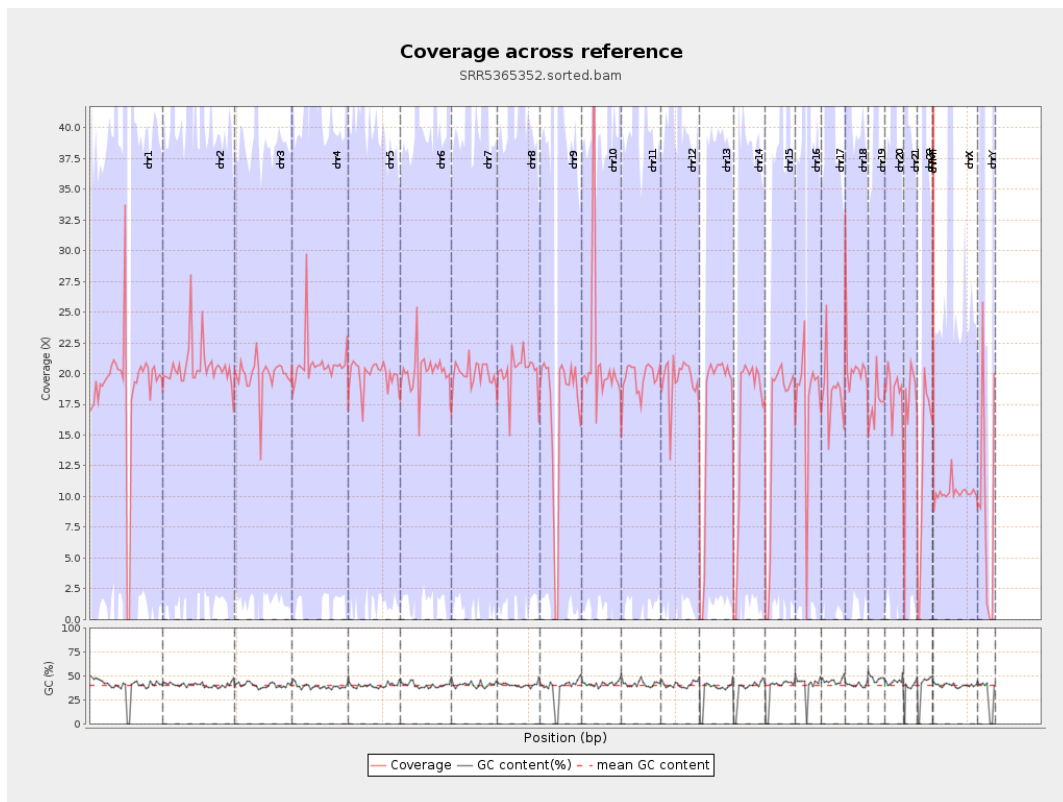
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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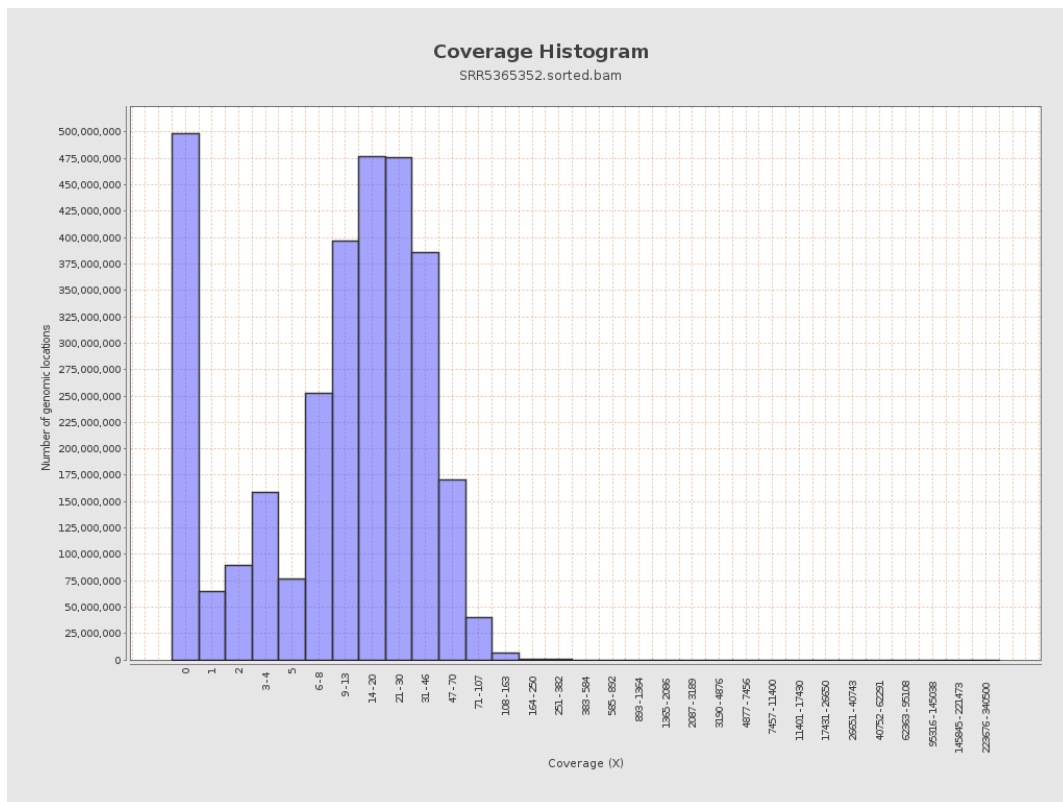
		bases	coverage	deviation
chr1	249250621	4688955324	18.8122	327.203
chr2	243199373	5001895052	20.5671	81.9819
chr3	198022430	3933441069	19.8636	25.592
chr4	191154276	3990375341	20.8752	93.3006
chr5	180915260	3588296085	19.8341	21.0376
chr6	171115067	3448884090	20.1554	57.8577
chr7	159138663	3178517859	19.9733	98.1043
chr8	146364022	2950557150	20.159	35.8963
chr9	141213431	2418297928	17.1251	94.0804
chr10	135534747	2863873192	21.1302	248.4615
chr11	135006516	2656109278	19.6739	79.6106
chr12	133851895	2611592945	19.5111	34.4979
chr13	115169878	1937872479	16.8262	18.2035
chr14	107349540	1767603865	16.4659	19.9728
chr15	102531392	1605100352	15.6547	23.3074
chr16	90354753	1603890612	17.751	45.8095
chr17	81195210	1514087786	18.6475	92.6185
chr18	78077248	1609762974	20.6176	152.8816
chr19	59128983	1040368542	17.5949	162.7699
chr20	63025520	1172766375	18.6078	32.1119
chr21	48129895	817986497	16.9954	66.0404
chr22	51304566	656210101	12.7905	59.1481
chrMT	16571	78631224	4,745.1104	782.0457
chrX	155270560	1601395630	10.3136	37.7052

chrY	59373566	564410620	9.5061	186.1489
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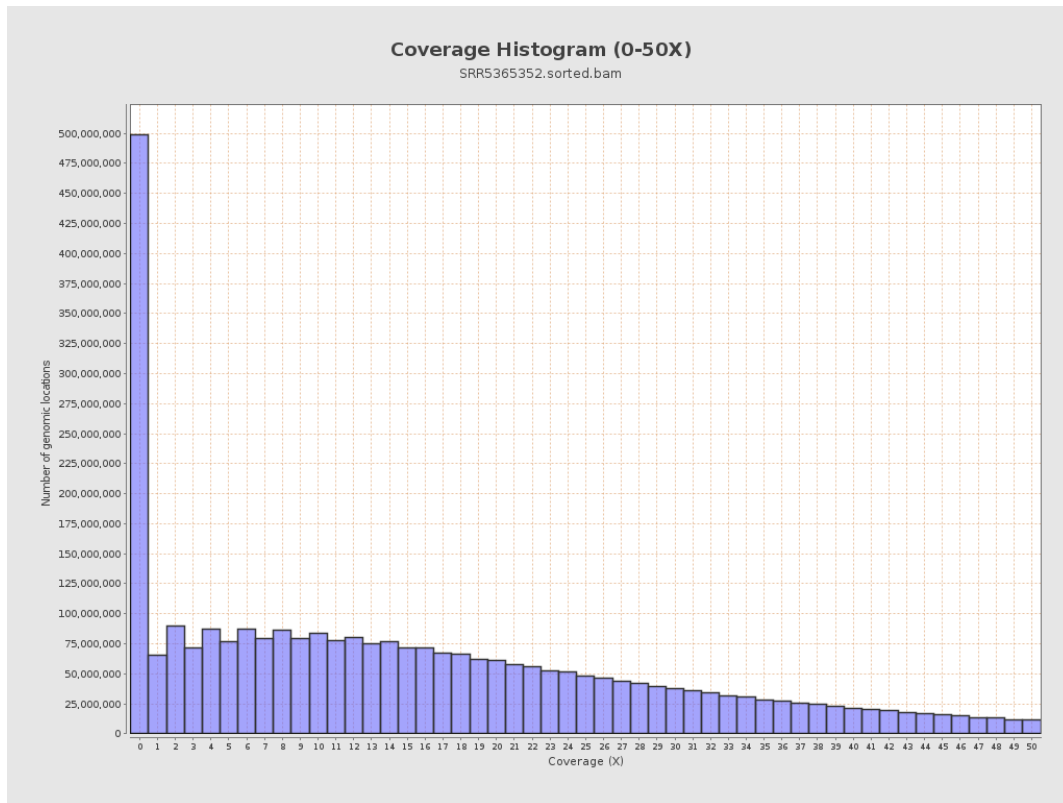
3. Results : Coverage across reference



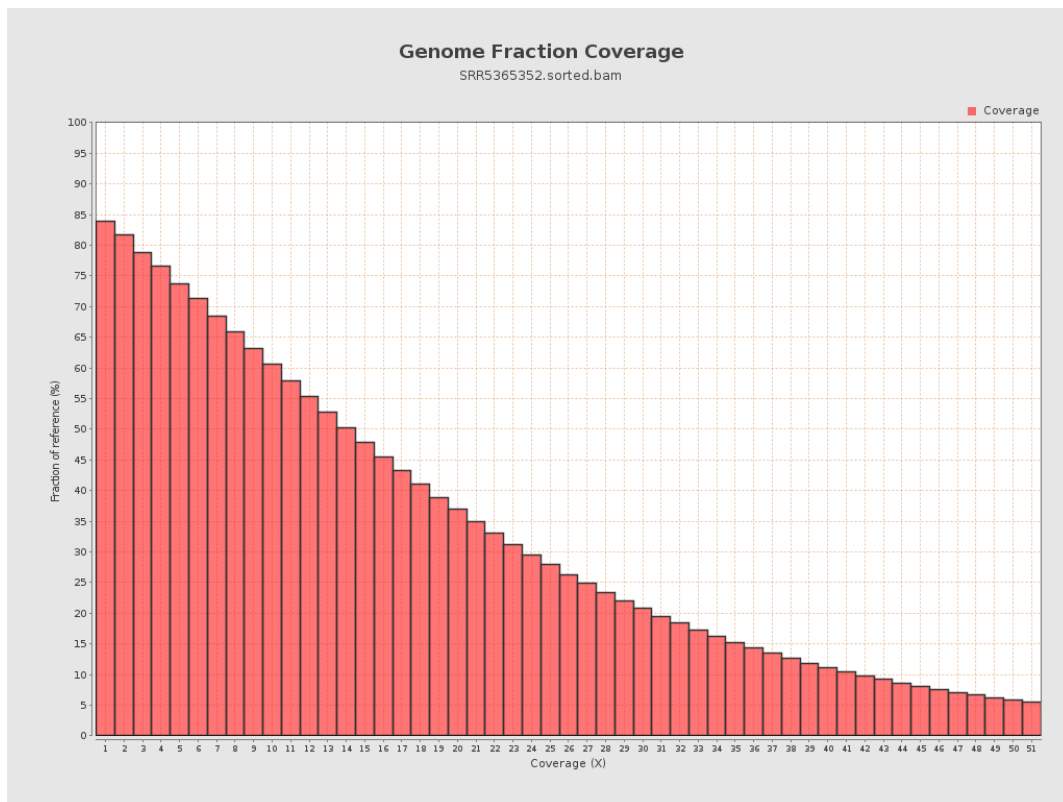
4. Results : Coverage Histogram



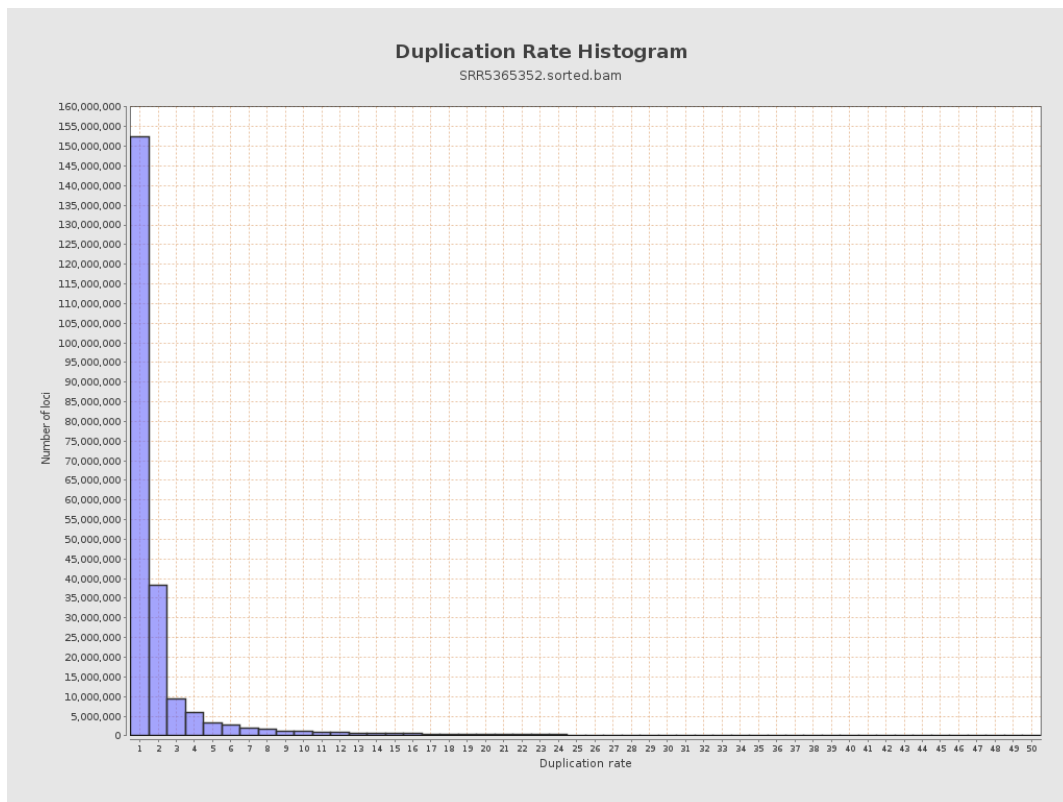
5. Results : Coverage Histogram (0-50X)



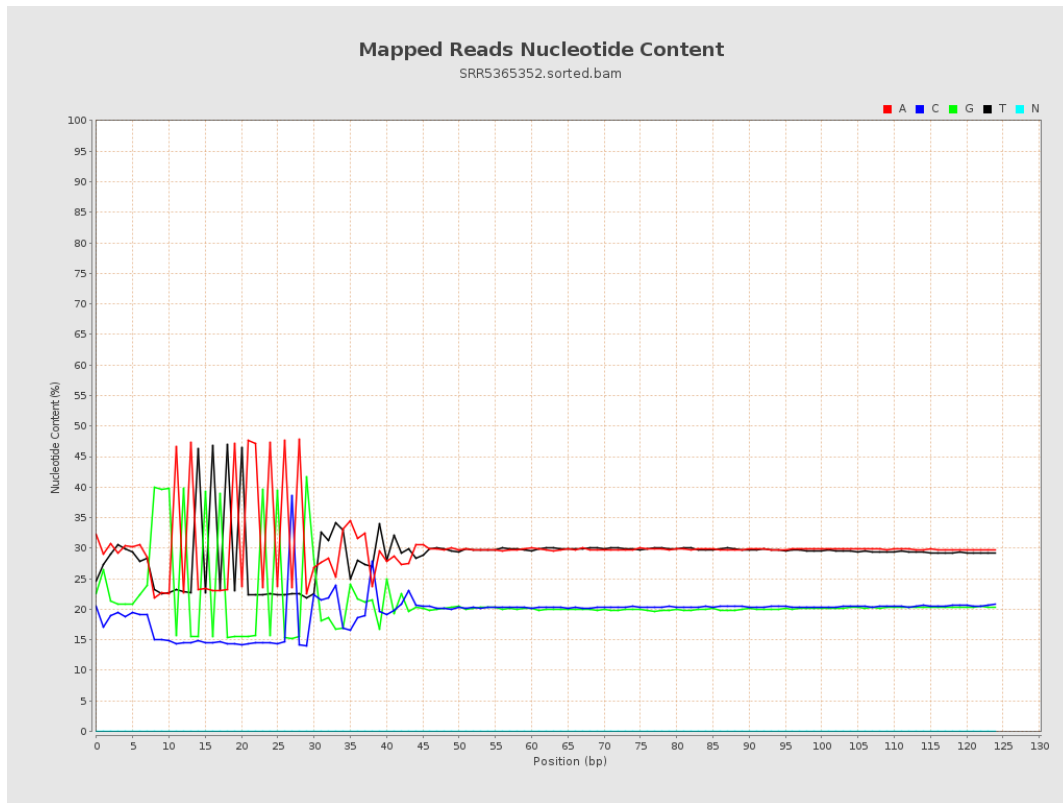
6. Results : Genome Fraction Coverage



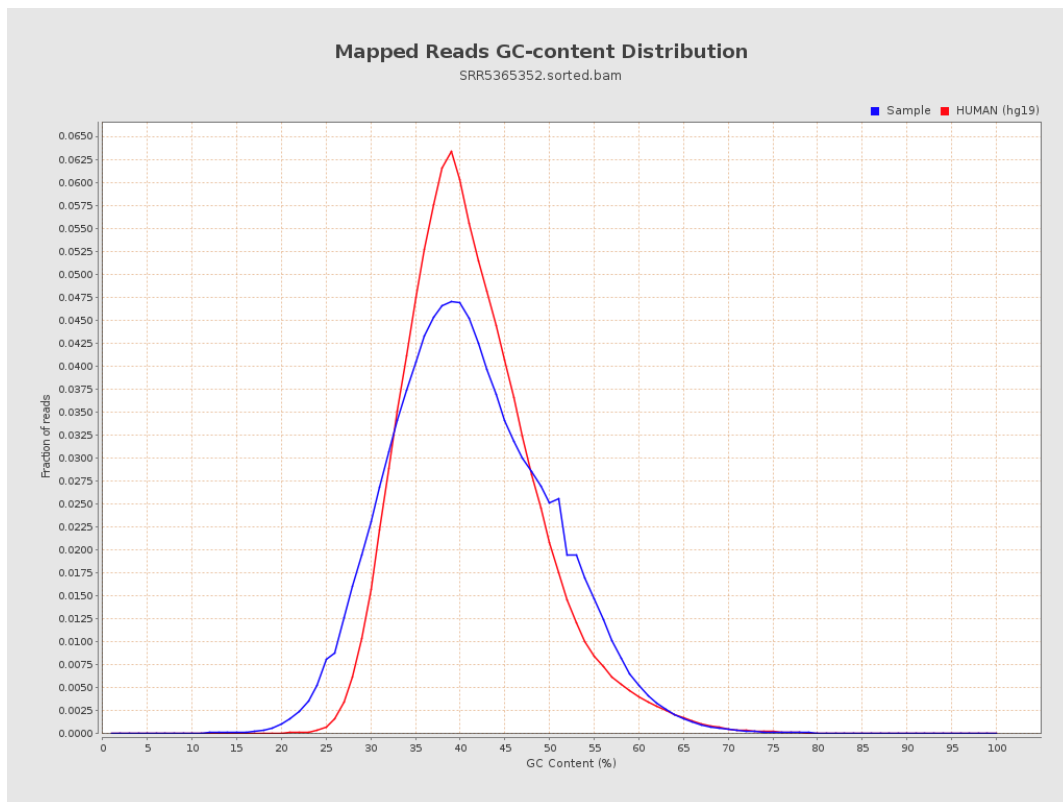
7. Results : Duplication Rate Histogram



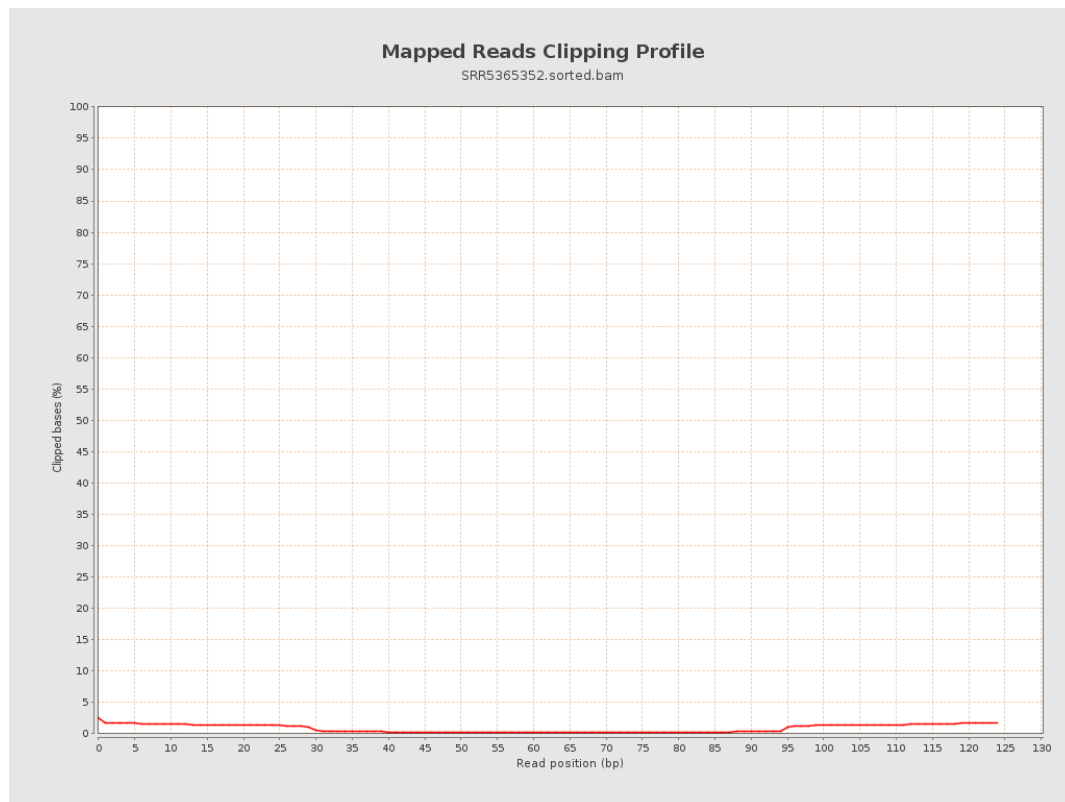
8. Results : Mapped Reads Nucleotide Content



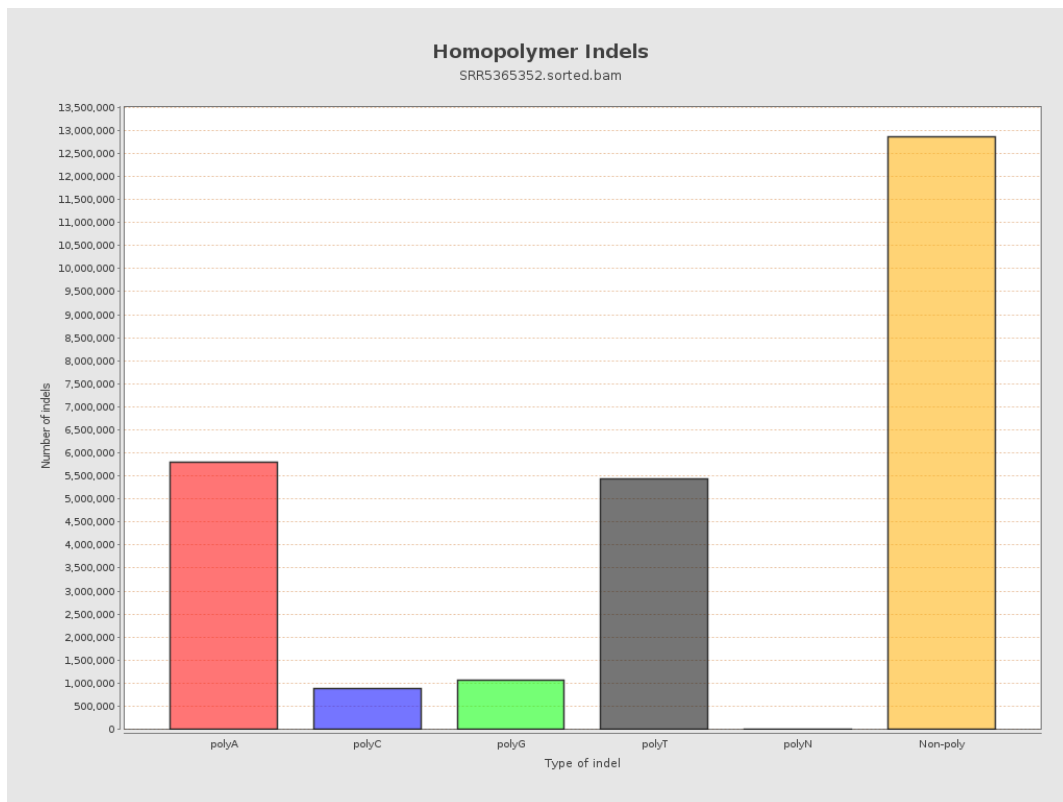
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



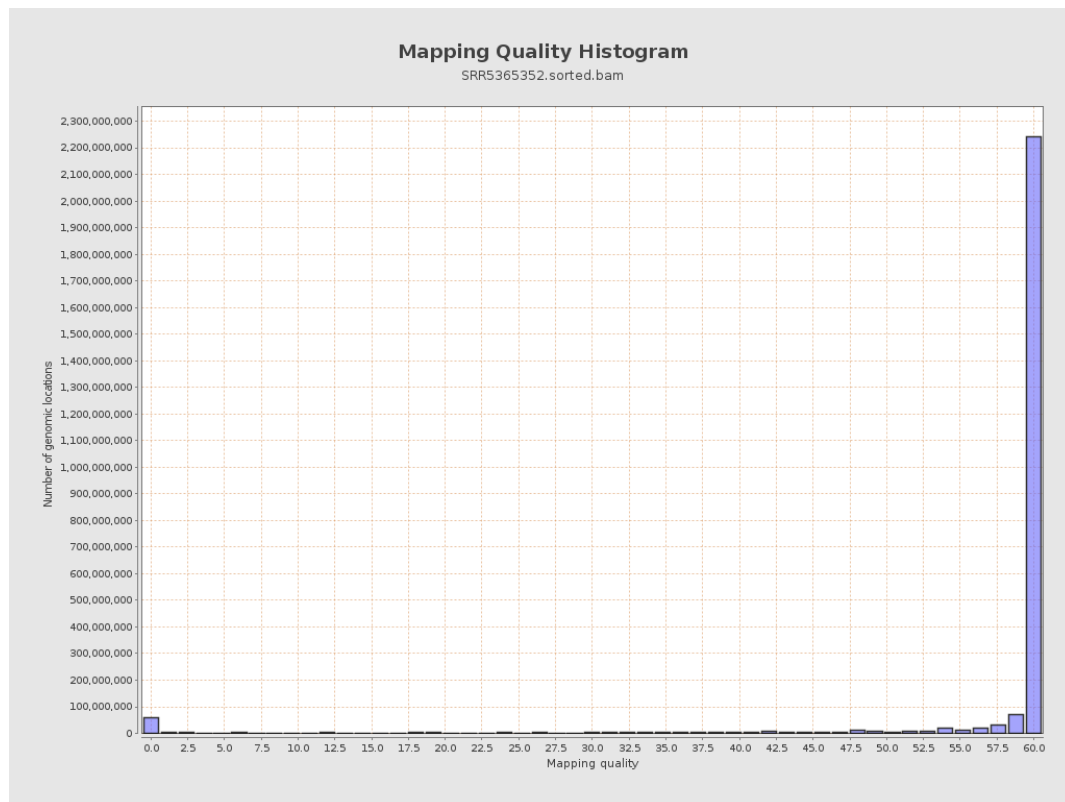
11. Results : Homopolymer Indels



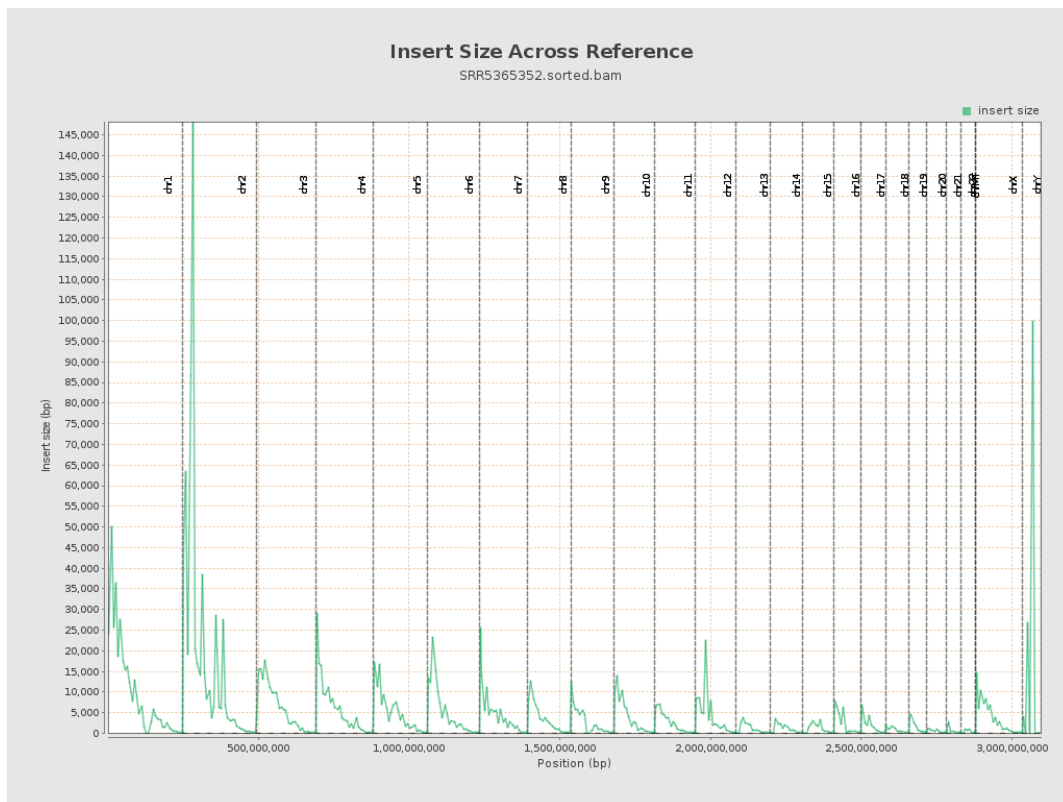
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

