

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/28 12:24:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365372.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_SRR5365372 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365372_1.fastq.gz SRR5365372_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Nov 28 12:24:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365372.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	558,021,958
Mapped reads	536,553,522 / 96.15%
Unmapped reads	21,468,436 / 3.85%
Mapped paired reads	536,553,522 / 96.15%
Mapped reads, first in pair	268,484,274 / 48.11%
Mapped reads, second in pair	268,069,248 / 48.04%
Mapped reads, both in pair	533,041,450 / 95.52%
Mapped reads, singletons	3,512,072 / 0.63%
Secondary alignments	0
Supplementary alignments	12,317,754 / 2.21%
Read min/max/mean length	30 / 150 / 151.16
Duplicated reads (estimated)	221,478,023 / 39.69%
Duplication rate	38.55%
Clipped reads	205,754,119 / 36.87%

2.2. ACGT Content

Number/percentage of A's	20,505,747,173 / 27.27%
Number/percentage of C's	17,137,232,367 / 22.79%
Number/percentage of T's	19,914,087,853 / 26.49%
Number/percentage of G's	17,621,922,403 / 23.44%
Number/percentage of N's	2,732,133 / 0%

GC Percentage	46.23%
---------------	--------

2.3. Coverage

Mean	24.2909
Standard Deviation	54.2649

2.4. Mapping Quality

Mean Mapping Quality	54.37
----------------------	-------

2.5. Insert size

Mean	82,691
Standard Deviation	2,838,544.87
P25/Median/P75	139 / 169 / 206

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	445,796,094
Insertions	6,981,092
Mapped reads with at least one insertion	1.27%
Deletions	5,449,245
Mapped reads with at least one deletion	0.98%
Homopolymer indels	42.42%

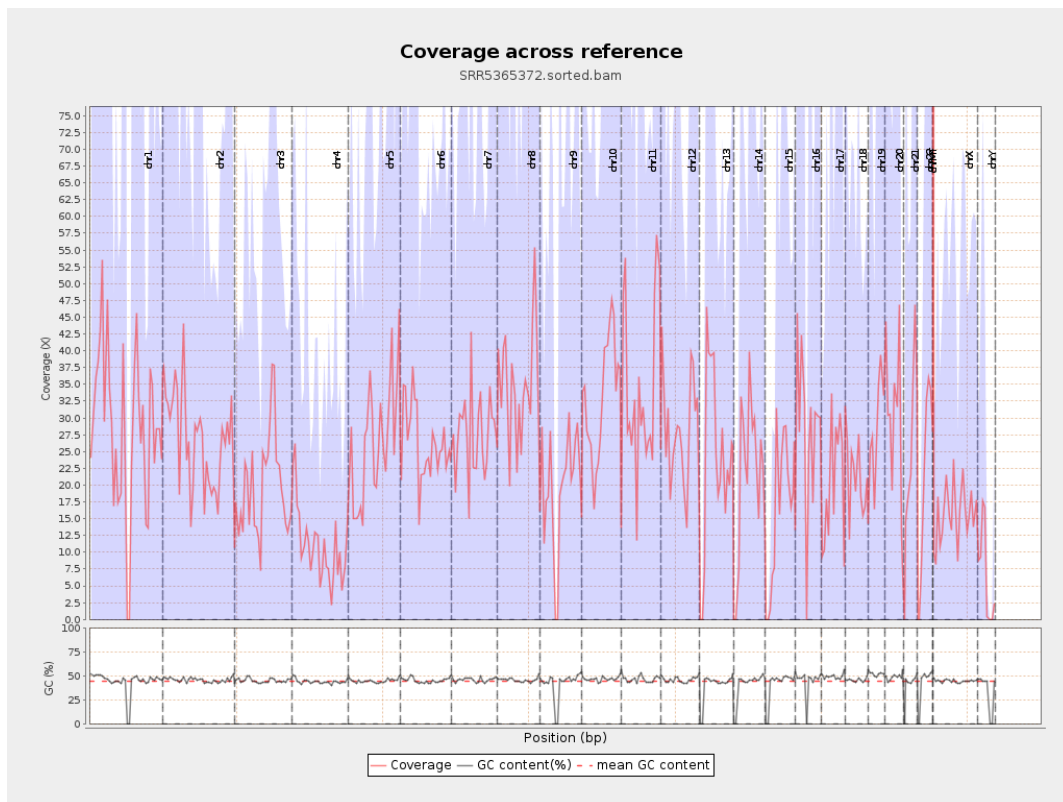
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

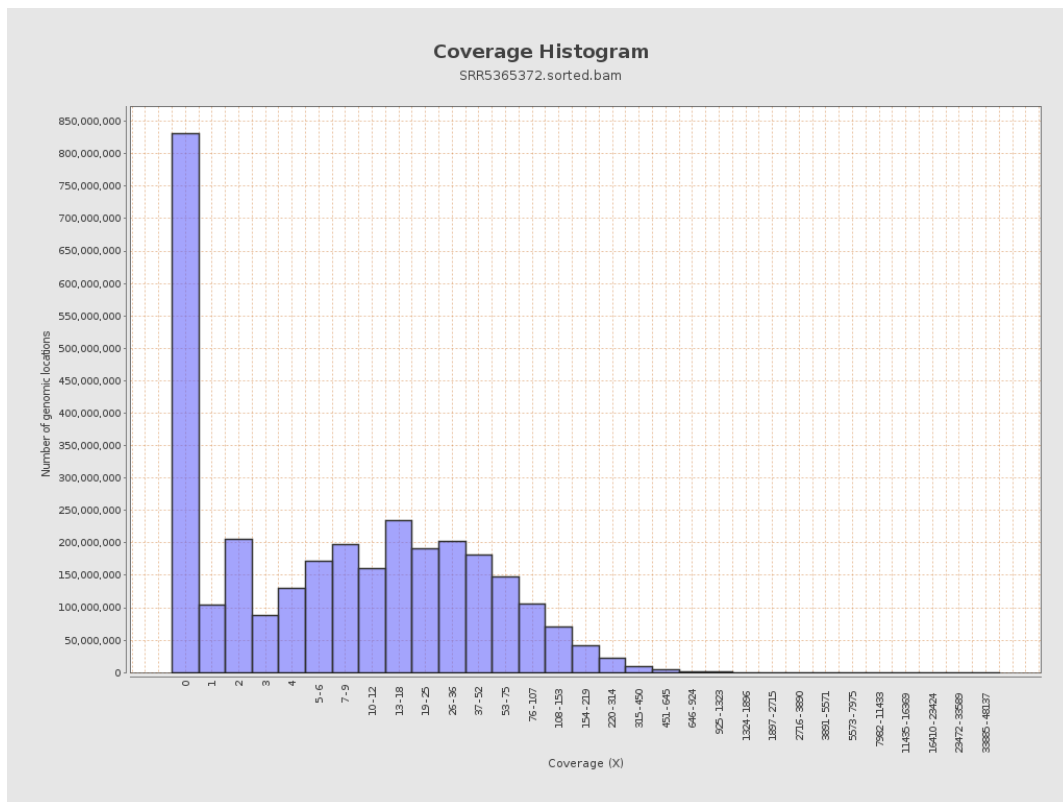
		bases	coverage	deviation
chr1	249250621	7106231263	28.5104	65.4258
chr2	243199373	6468568720	26.5978	67.3071
chr3	198022430	3886106413	19.6246	40.3174
chr4	191154276	2084883454	10.9068	33.0607
chr5	180915260	4771418122	26.3738	51.8856
chr6	171115067	4513428225	26.3766	49.6403
chr7	159138663	4375817914	27.4969	49.9127
chr8	146364022	5088295238	34.7647	65.3343
chr9	141213431	2765946658	19.587	48.128
chr10	135534747	4506489469	33.2497	61.2103
chr11	135006516	4593399446	34.0235	66.829
chr12	133851895	3796872143	28.3662	55.7095
chr13	115169878	2753879690	23.9115	48.3801
chr14	107349540	2335356070	21.7547	46.1277
chr15	102531392	1640261827	15.9977	39.084
chr16	90354753	2494565040	27.6086	59.2458
chr17	81195210	1663605664	20.489	50.6192
chr18	78077248	1639992998	21.0047	56.2961
chr19	59128983	1689530555	28.5736	63.0061
chr20	63025520	1875502353	29.7578	63.911
chr21	48129895	1219813433	25.3442	58.7068
chr22	51304566	1091353264	21.272	49.3619
chrMT	16571	10583576	638.6806	275.9142
chrX	155270560	2420342664	15.5879	38.2477

chrY	59373566	405042983	6.8219	29.47
------	----------	-----------	--------	-------

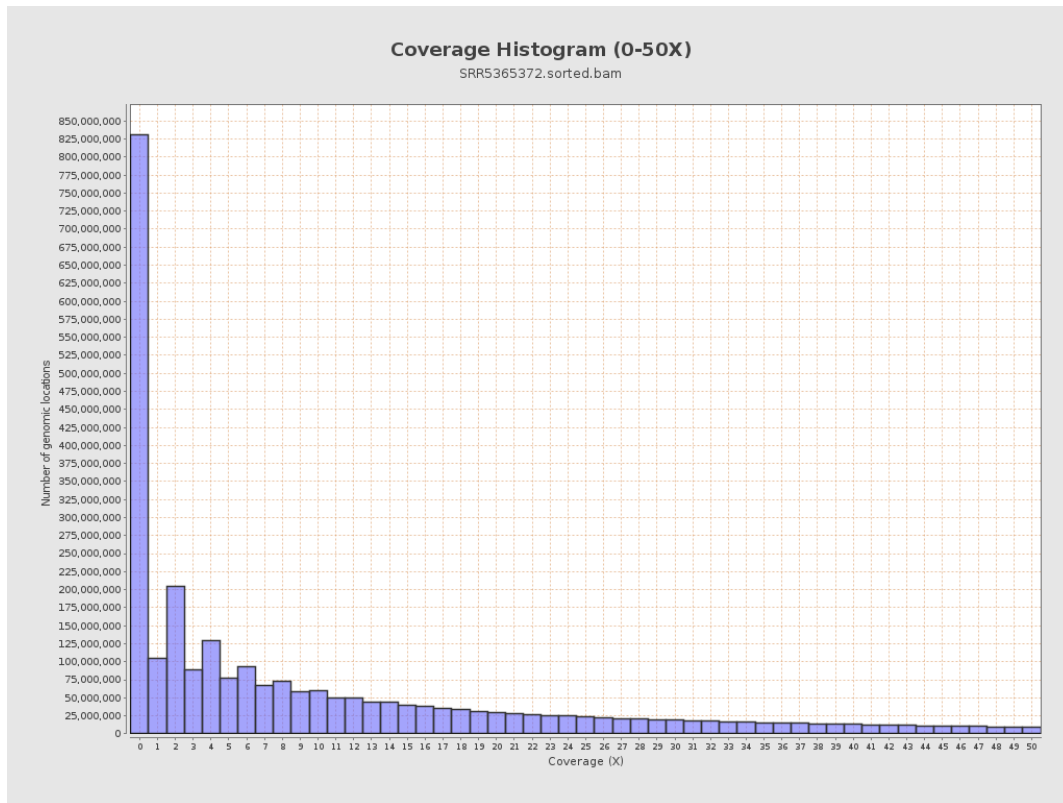
3. Results : Coverage across reference



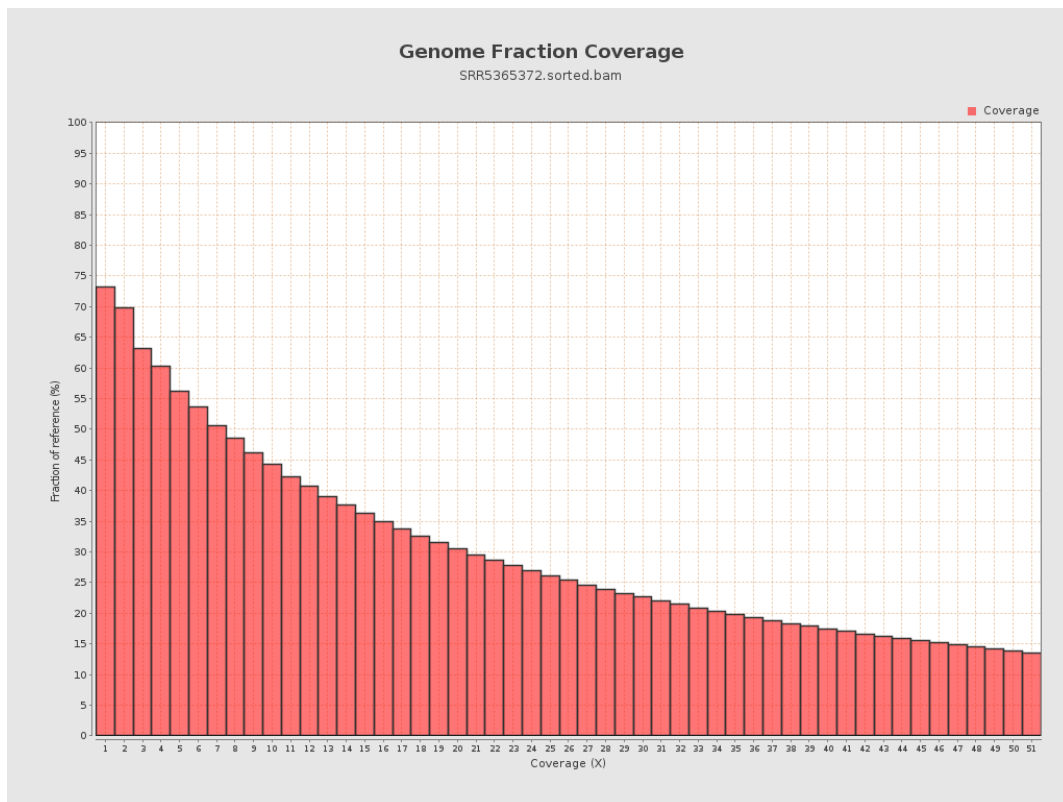
4. Results : Coverage Histogram



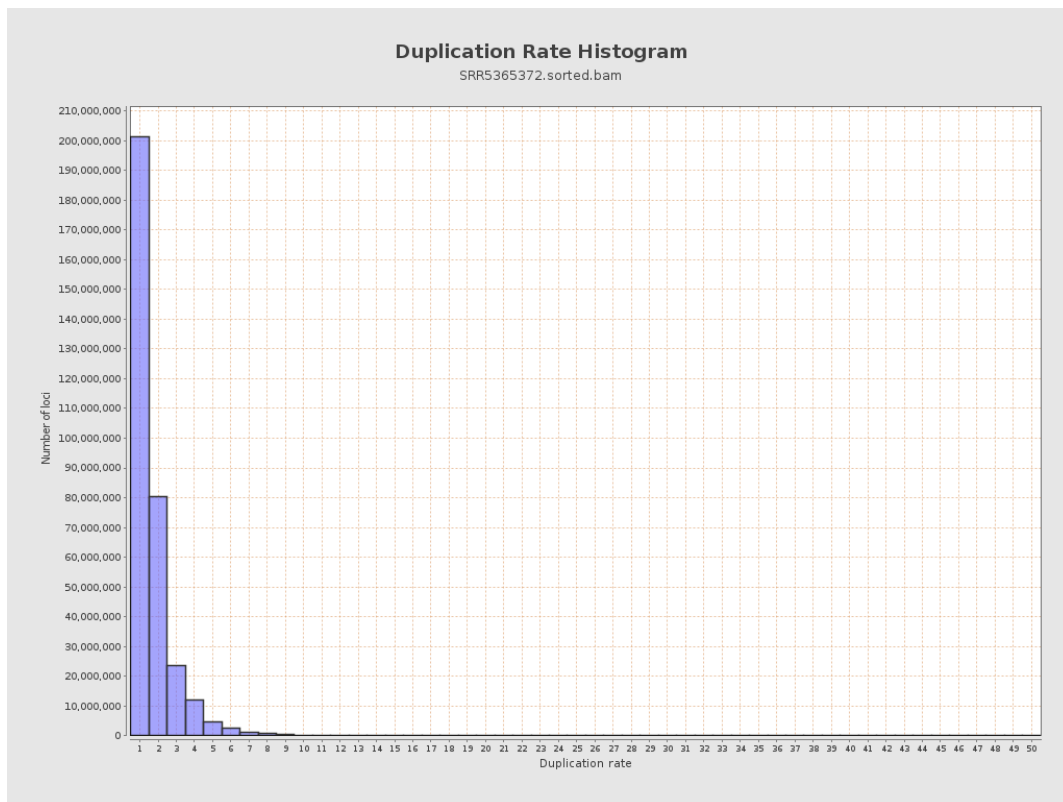
5. Results : Coverage Histogram (0-50X)



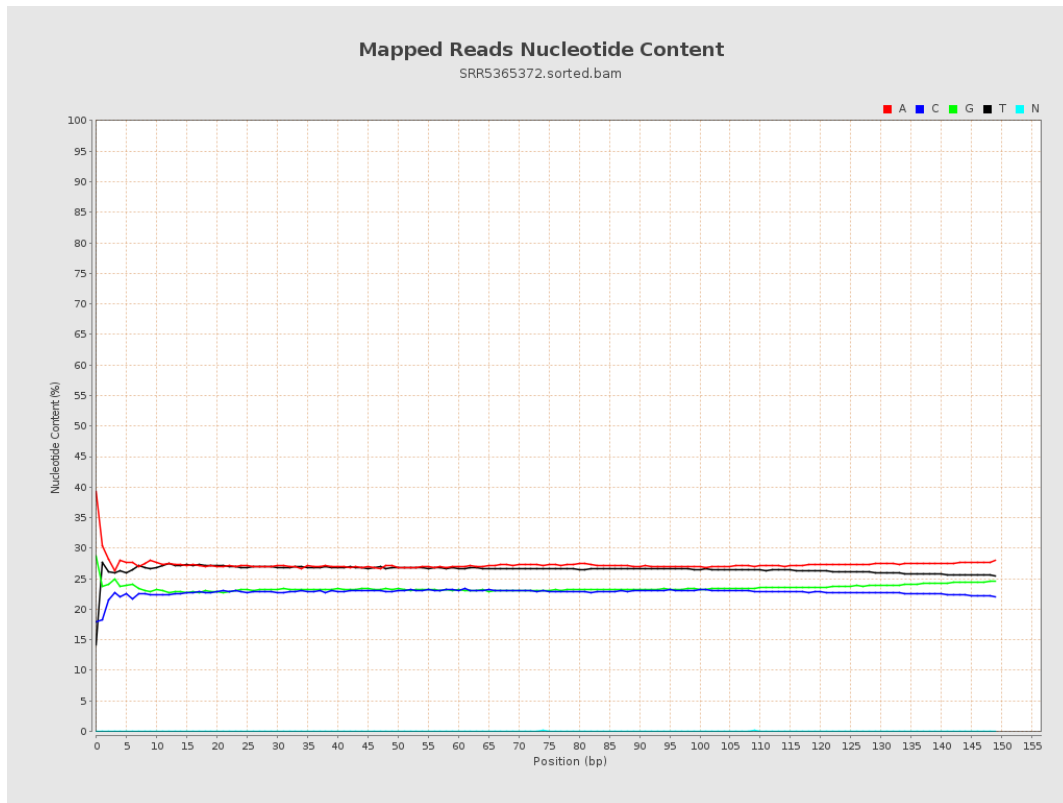
6. Results : Genome Fraction Coverage



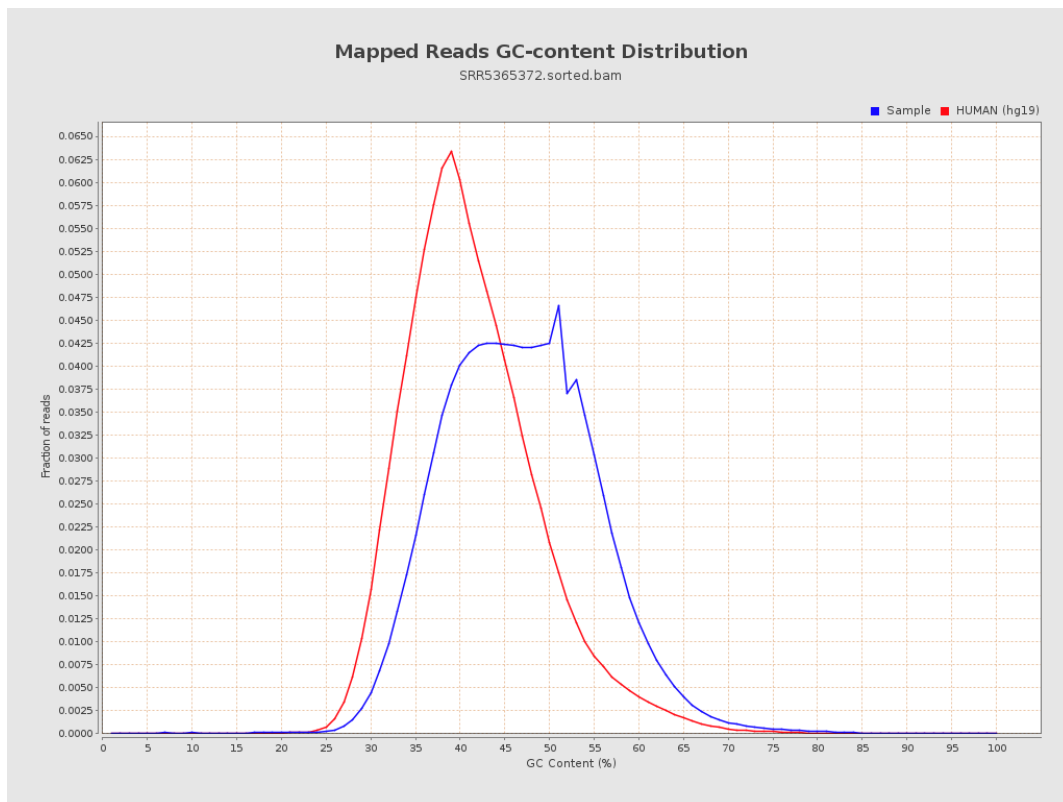
7. Results : Duplication Rate Histogram



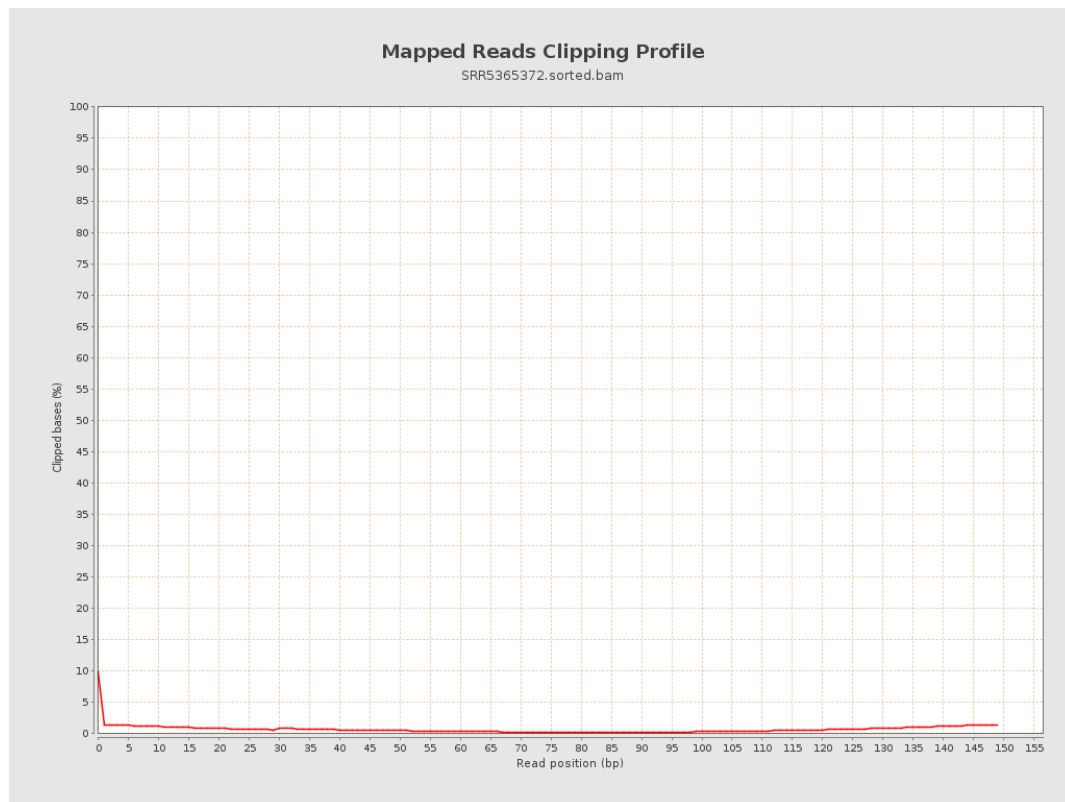
8. Results : Mapped Reads Nucleotide Content



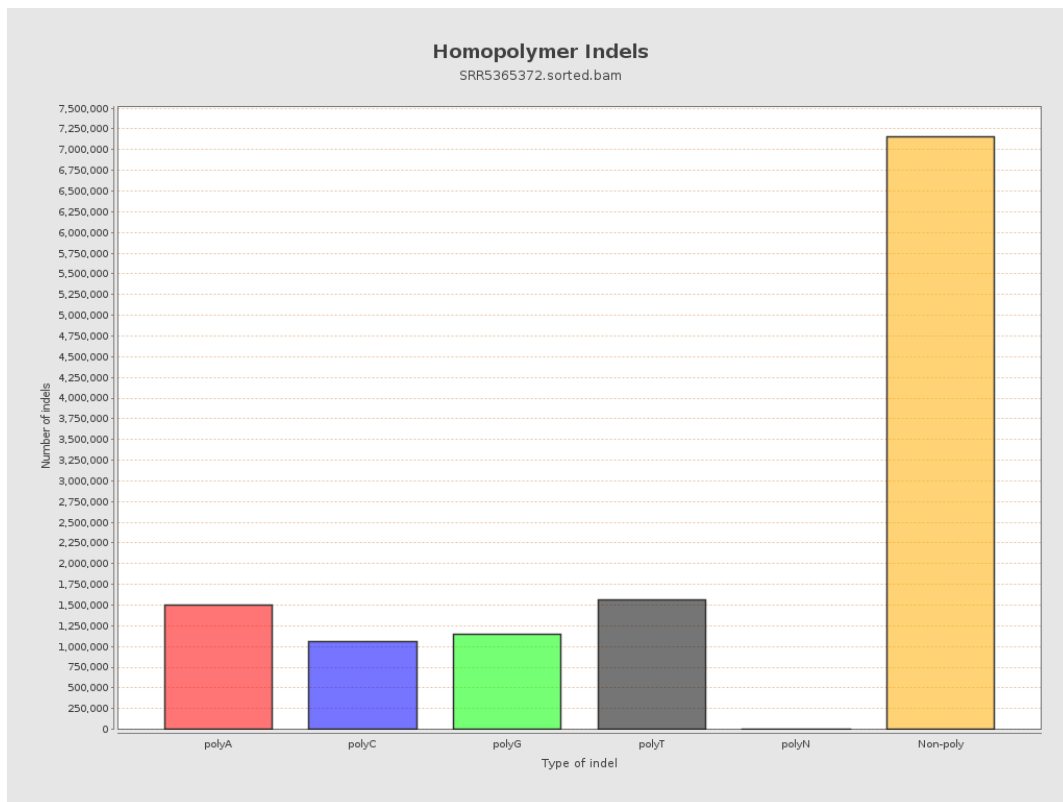
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



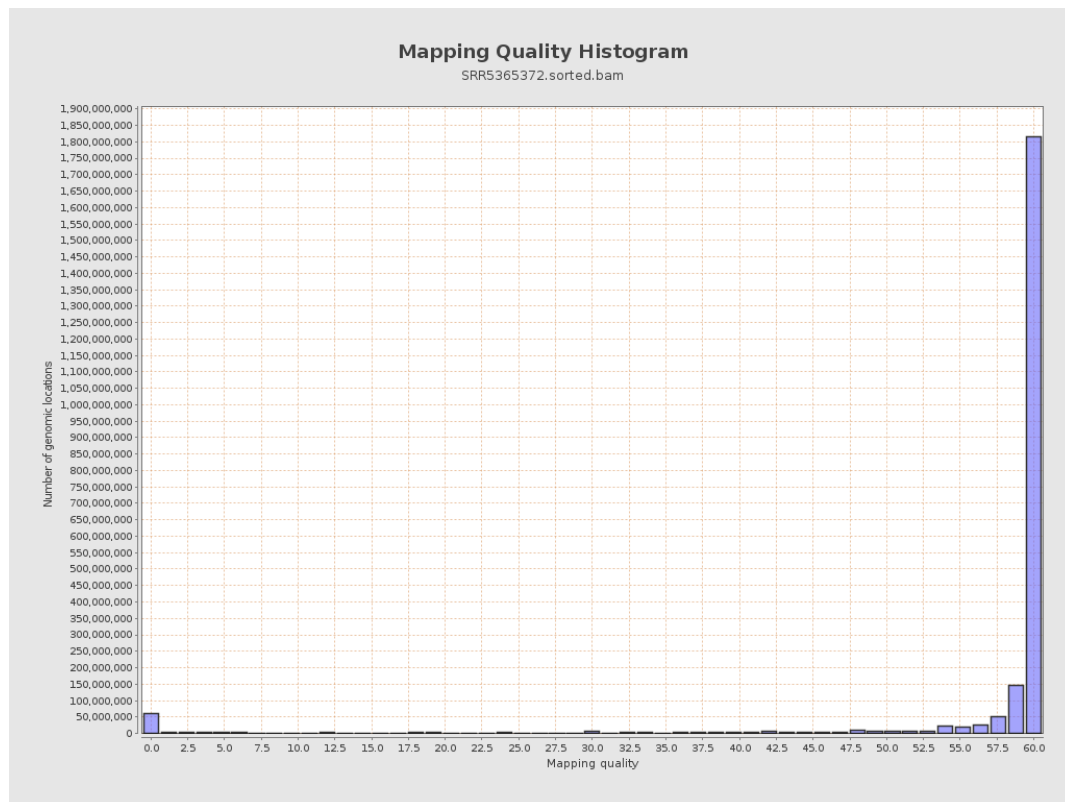
11. Results : Homopolymer Indels



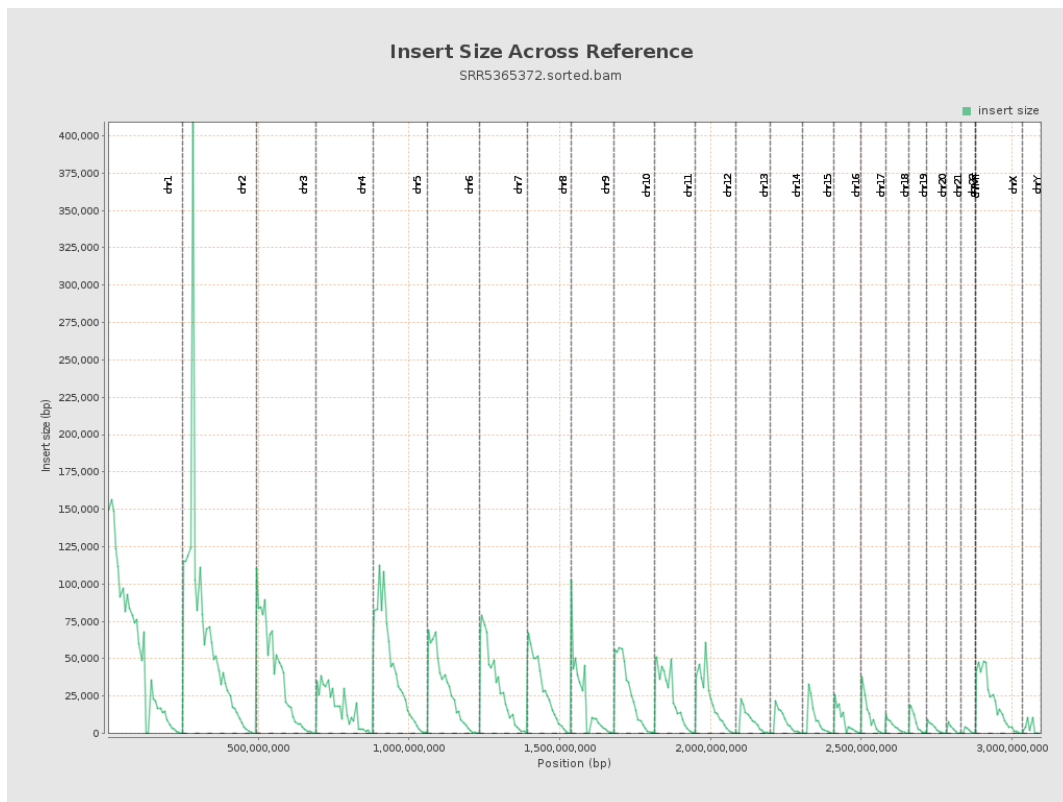
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

