

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/25 14:21:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365370.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_SRR5365370 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365370_1.fastq.gz SRR5365370_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Nov 25 14:21:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365370.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	608,316,104
Mapped reads	513,474,098 / 84.41%
Unmapped reads	94,842,006 / 15.59%
Mapped paired reads	513,474,098 / 84.41%
Mapped reads, first in pair	254,194,314 / 41.79%
Mapped reads, second in pair	259,279,784 / 42.62%
Mapped reads, both in pair	503,688,392 / 82.8%
Mapped reads, singletons	9,785,706 / 1.61%
Secondary alignments	0
Supplementary alignments	4,575,720 / 0.75%
Read min/max/mean length	30 / 150 / 150.37
Duplicated reads (estimated)	243,069,702 / 39.96%
Duplication rate	41.87%
Clipped reads	255,482,385 / 42%

2.2. ACGT Content

Number/percentage of A's	17,979,883,466 / 26.39%
Number/percentage of C's	15,981,596,722 / 23.46%
Number/percentage of T's	17,426,123,873 / 25.58%
Number/percentage of G's	16,735,434,733 / 24.57%
Number/percentage of N's	2,091,335 / 0%

GC Percentage	48.02%
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2.3. Coverage

Mean	22.022
Standard Deviation	82.7997

2.4. Mapping Quality

Mean Mapping Quality	54.23
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2.5. Insert size

Mean	46,126.43
Standard Deviation	2,187,368.83
P25/Median/P75	129 / 161 / 202

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	685,155,159
Insertions	9,759,383
Mapped reads with at least one insertion	1.84%
Deletions	33,094,333
Mapped reads with at least one deletion	6.21%
Homopolymer indels	51.34%

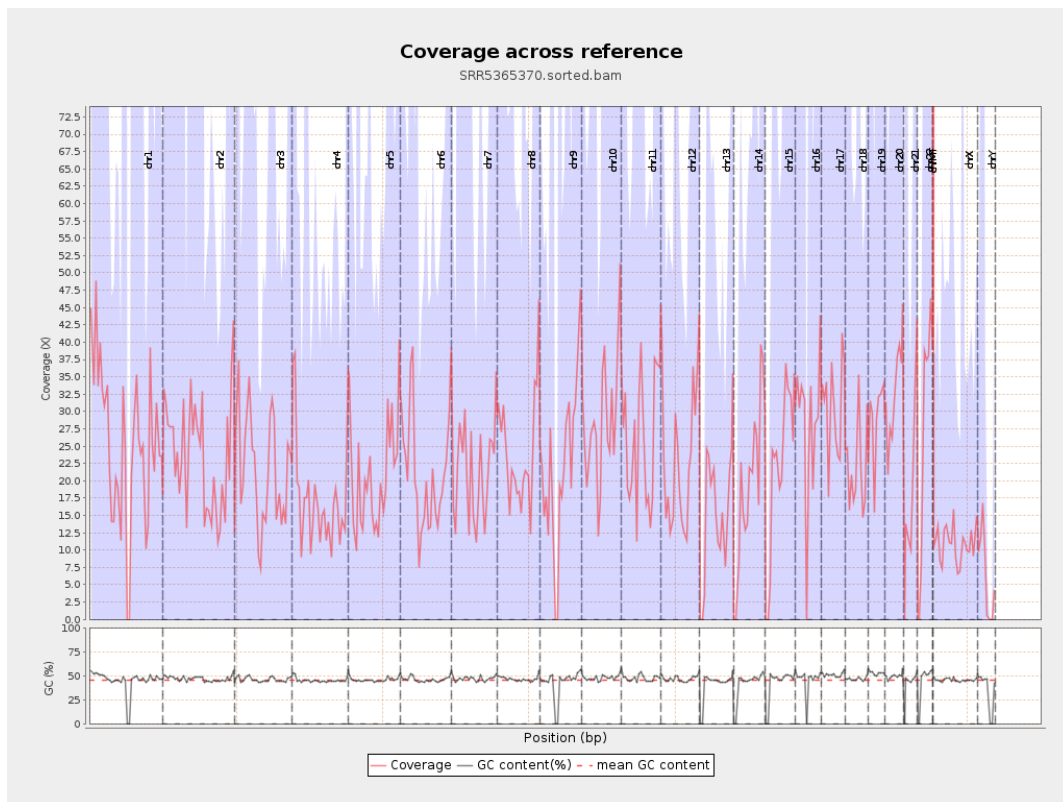
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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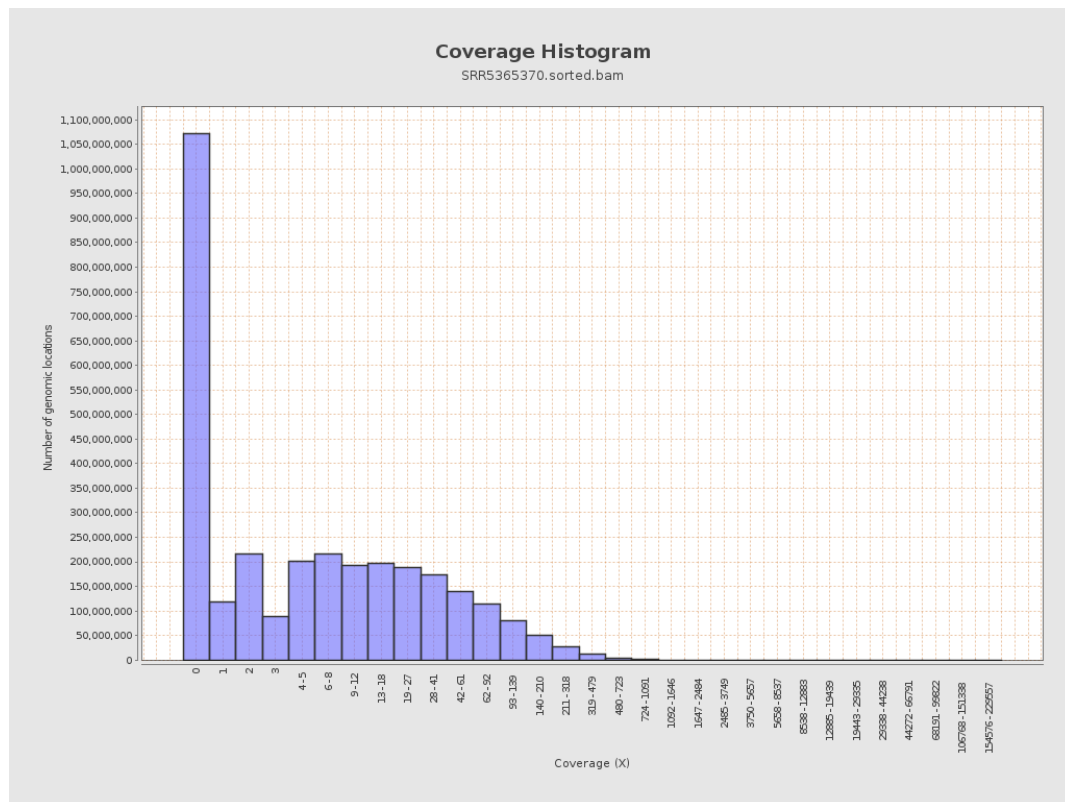
		bases	coverage	deviation
chr1	249250621	6271343170	25.1608	92.8406
chr2	243199373	5741684764	23.609	164.7361
chr3	198022430	4255499459	21.49	51.6458
chr4	191154276	3261159148	17.0604	55.5807
chr5	180915260	3808715681	21.0525	64.0885
chr6	171115067	3554718093	20.7738	51.0741
chr7	159138663	3444088526	21.6421	69.4796
chr8	146364022	3503422824	23.9364	61.6257
chr9	141213431	3104879759	21.9871	84.3327
chr10	135534747	3819186584	28.1787	100.4589
chr11	135006516	3492339186	25.8679	72.0938
chr12	133851895	3071739396	22.9488	55.6292
chr13	115169878	1718731401	14.9234	40.3807
chr14	107349540	2079840087	19.3745	54.7406
chr15	102531392	2215088108	21.604	57.3209
chr16	90354753	2547099110	28.19	107.7743
chr17	81195210	2468790682	30.4056	90.3228
chr18	78077248	1680263825	21.5205	89.8375
chr19	59128983	1704155347	28.821	80.2909
chr20	63025520	2029585641	32.2026	83.3842
chr21	48129895	917580527	19.0647	87.9643
chr22	51304566	1383461992	26.9657	74.7055
chrMT	16571	11026070	665.3835	541.1127
chrX	155270560	1701845589	10.9605	38.8063

chrY	59373566	387007108	6.5182	78.6052
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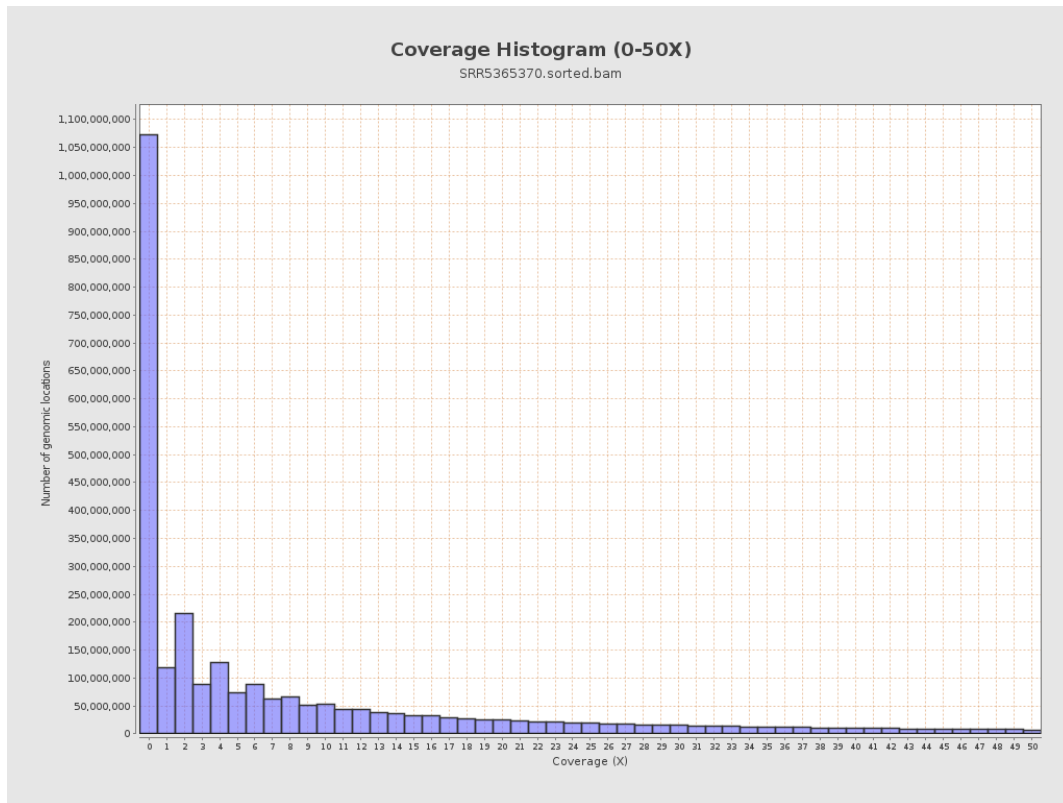
3. Results : Coverage across reference



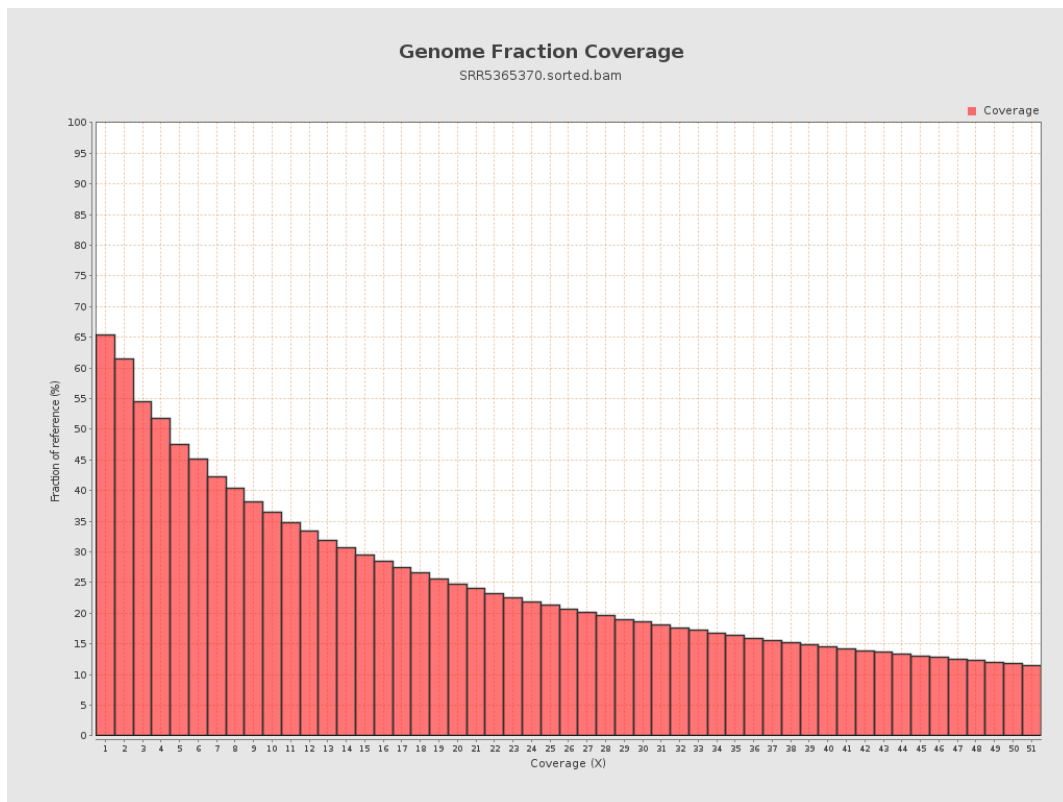
4. Results : Coverage Histogram



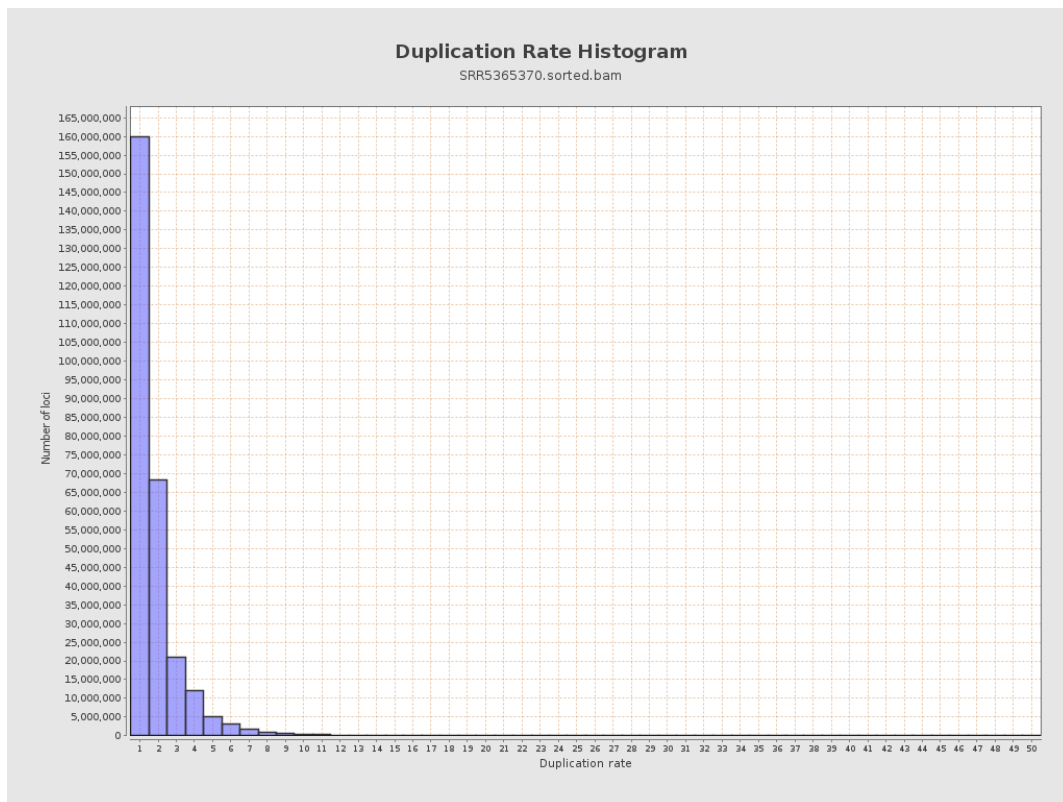
5. Results : Coverage Histogram (0-50X)



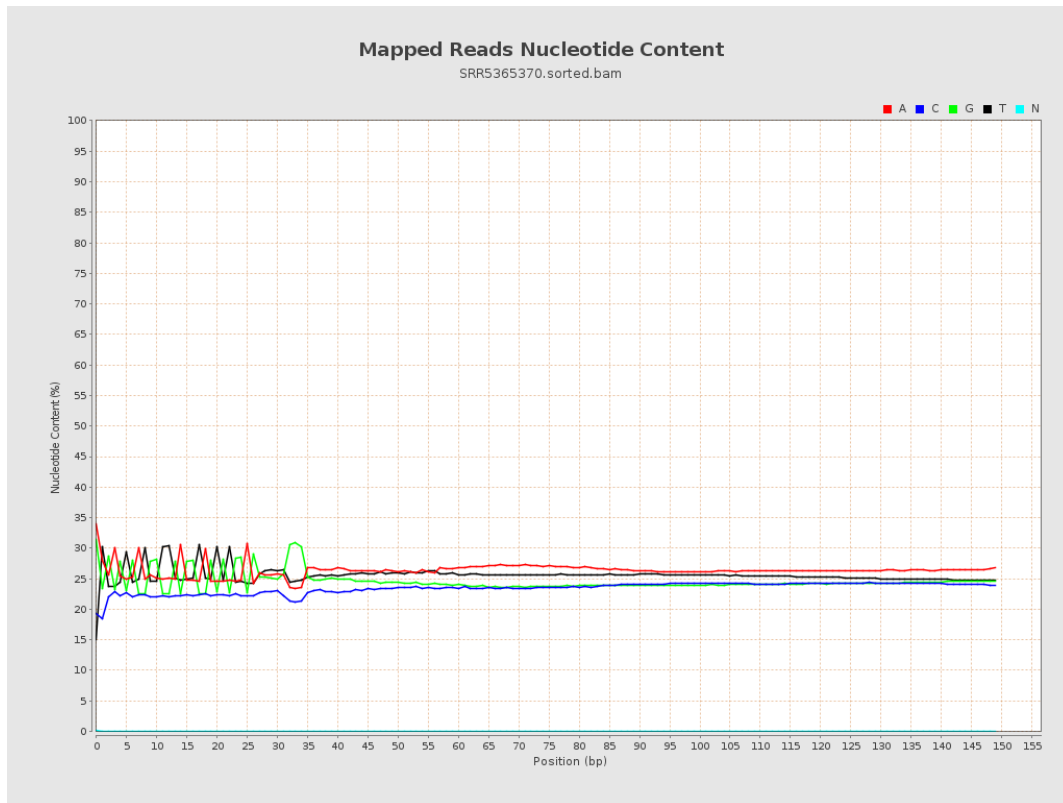
6. Results : Genome Fraction Coverage



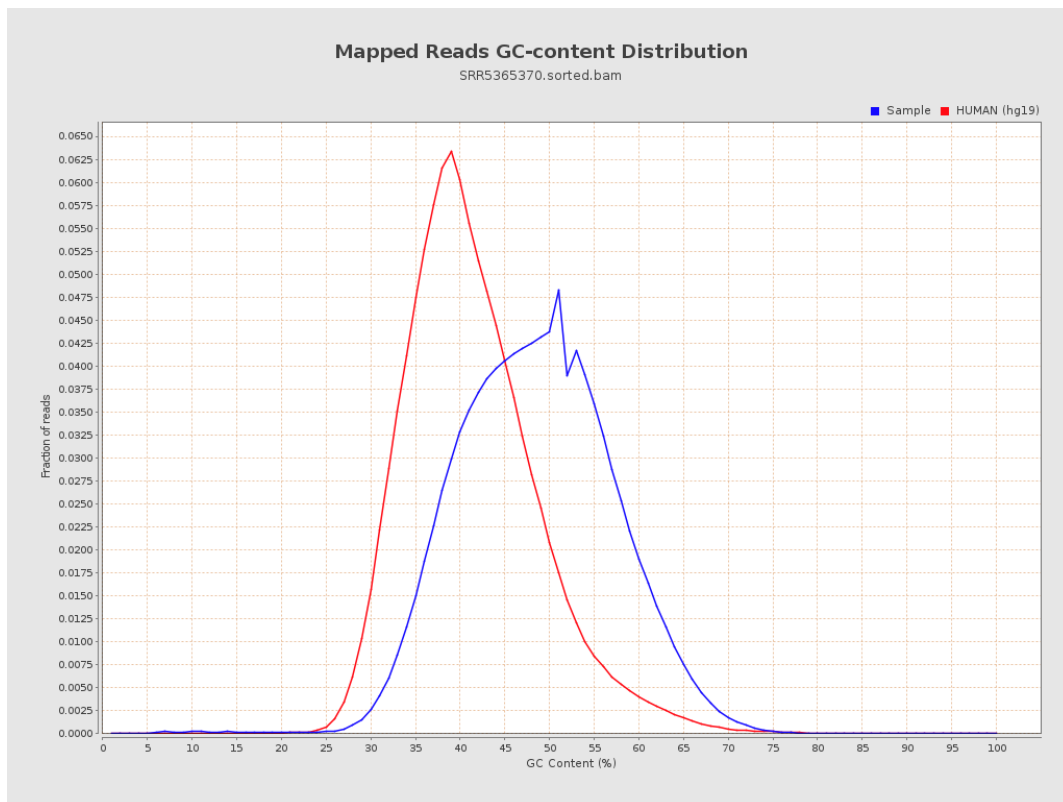
7. Results : Duplication Rate Histogram



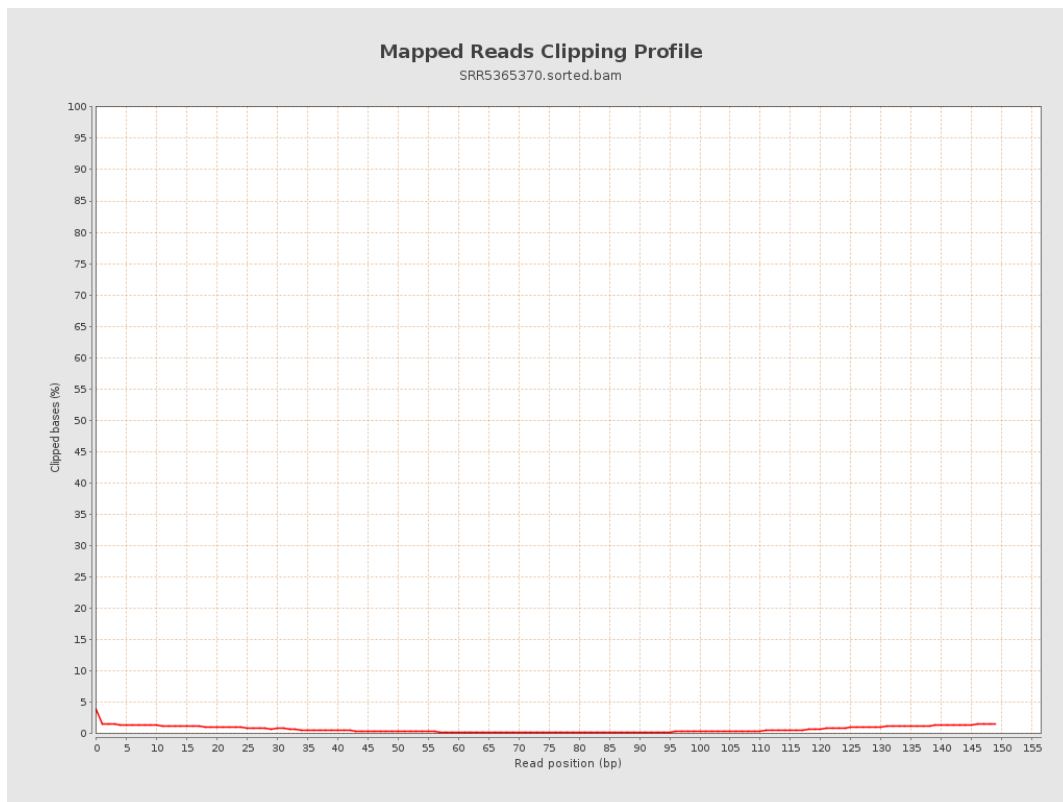
8. Results : Mapped Reads Nucleotide Content



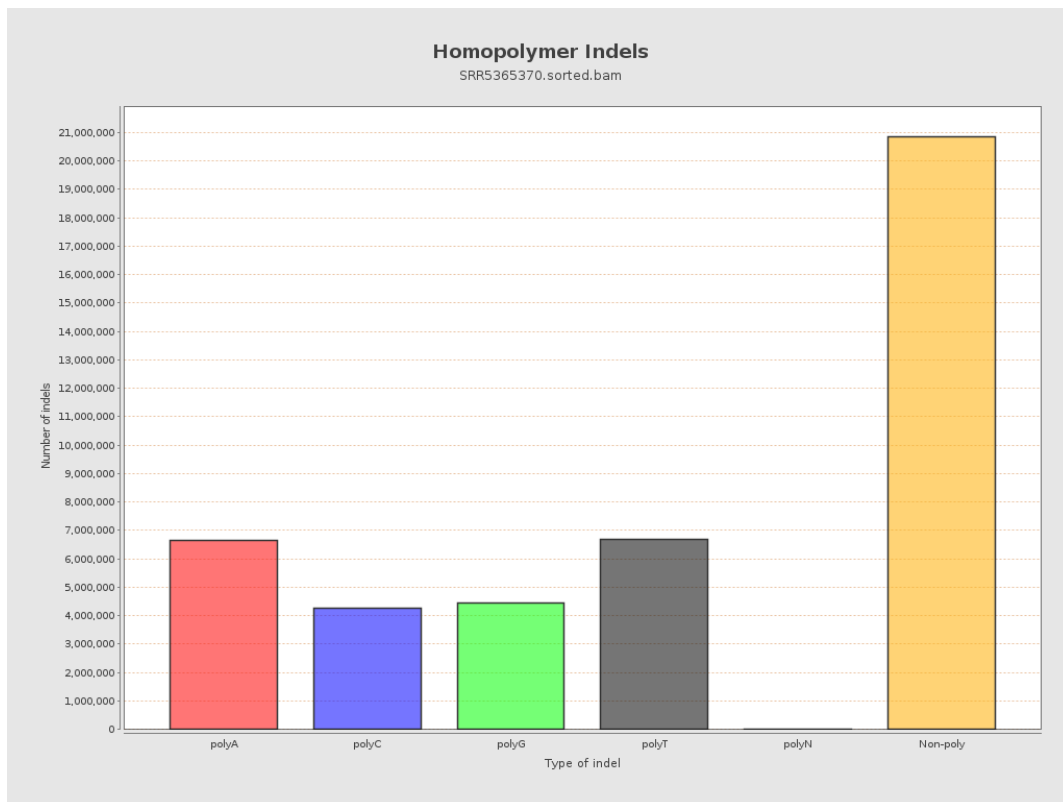
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



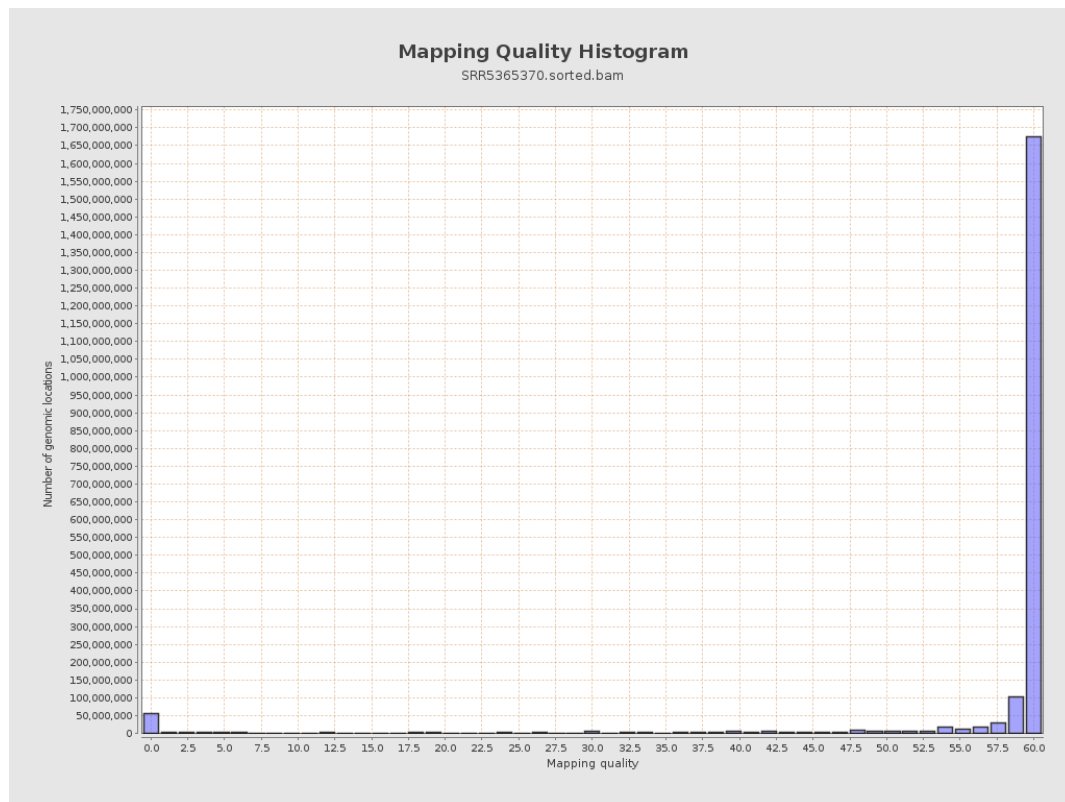
11. Results : Homopolymer Indels



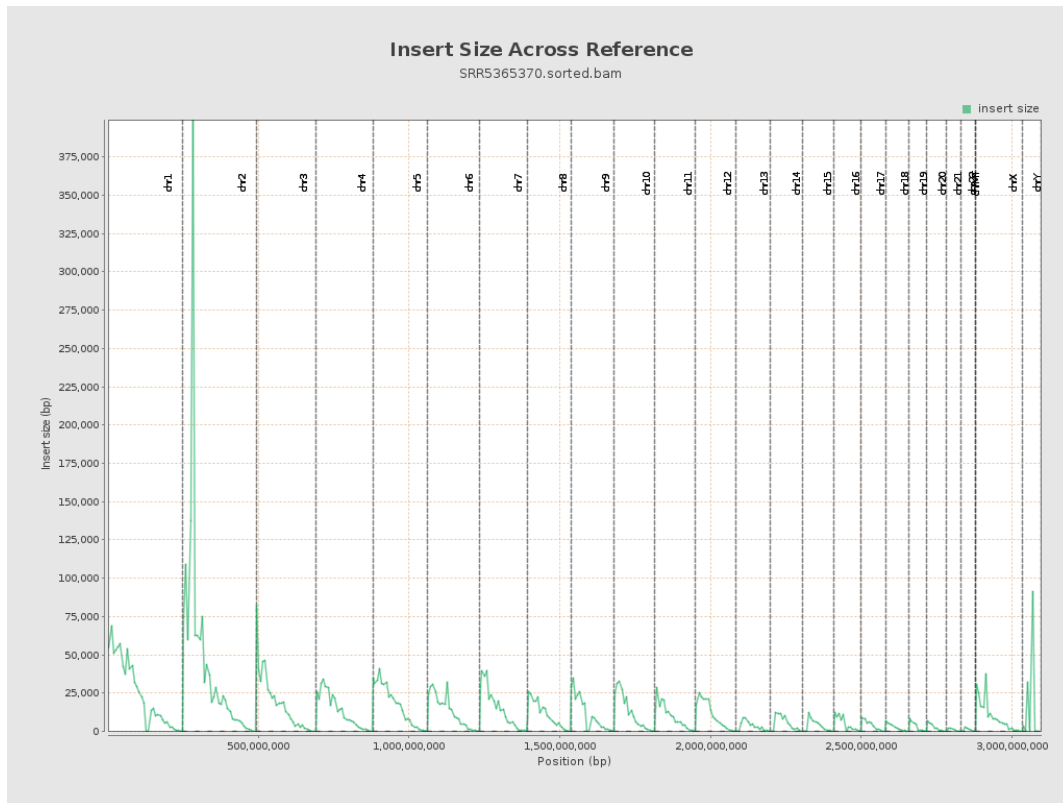
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

