

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/05/08 03:32:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365366.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_SRR5365366 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365366_1.fastq.gz SRR5365366_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun May 08 03:32:25 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365366.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	548,656,868
Mapped reads	461,117,606 / 84.04%
Unmapped reads	87,539,262 / 15.96%
Mapped paired reads	461,117,606 / 84.04%
Mapped reads, first in pair	229,163,420 / 41.77%
Mapped reads, second in pair	231,954,186 / 42.28%
Mapped reads, both in pair	445,530,460 / 81.2%
Mapped reads, singletons	15,587,146 / 2.84%
Secondary alignments	0
Supplementary alignments	17,902,456 / 3.26%
Read min/max/mean length	30 / 150 / 151.54
Duplicated reads (estimated)	326,923,724 / 59.59%
Duplication rate	45.96%
Clipped reads	362,857,486 / 66.14%

2.2. ACGT Content

Number/percentage of A's	15,867,823,998 / 27.95%
Number/percentage of C's	11,913,352,330 / 20.99%
Number/percentage of T's	16,103,443,736 / 28.37%
Number/percentage of G's	12,883,526,812 / 22.69%
Number/percentage of N's	1,582,533 / 0%

GC Percentage	43.68%
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2.3. Coverage

Mean	18.349
Standard Deviation	182.2477

2.4. Mapping Quality

Mean Mapping Quality	52.98
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2.5. Insert size

Mean	131,670.07
Standard Deviation	3,548,907.66
P25/Median/P75	116 / 147 / 185

2.6. Mismatches and indels

General error rate	1.09%
Mismatches	601,527,652
Insertions	5,779,982
Mapped reads with at least one insertion	1.19%
Deletions	15,700,557
Mapped reads with at least one deletion	3.3%
Homopolymer indels	42.77%

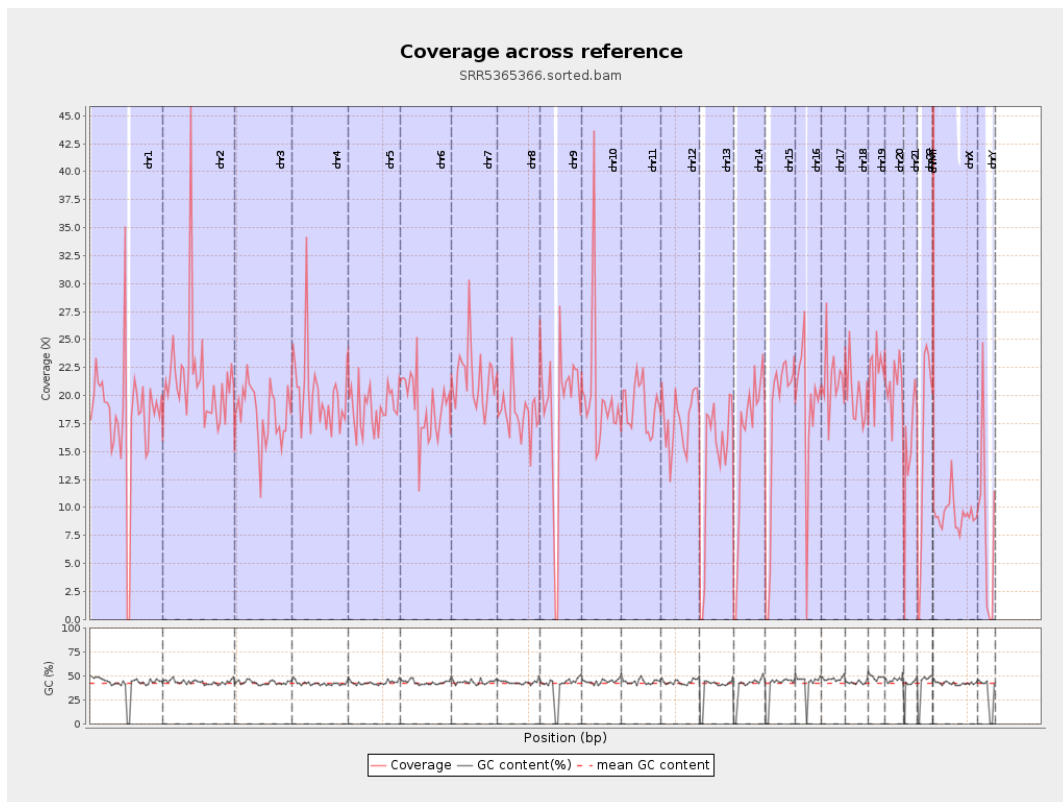
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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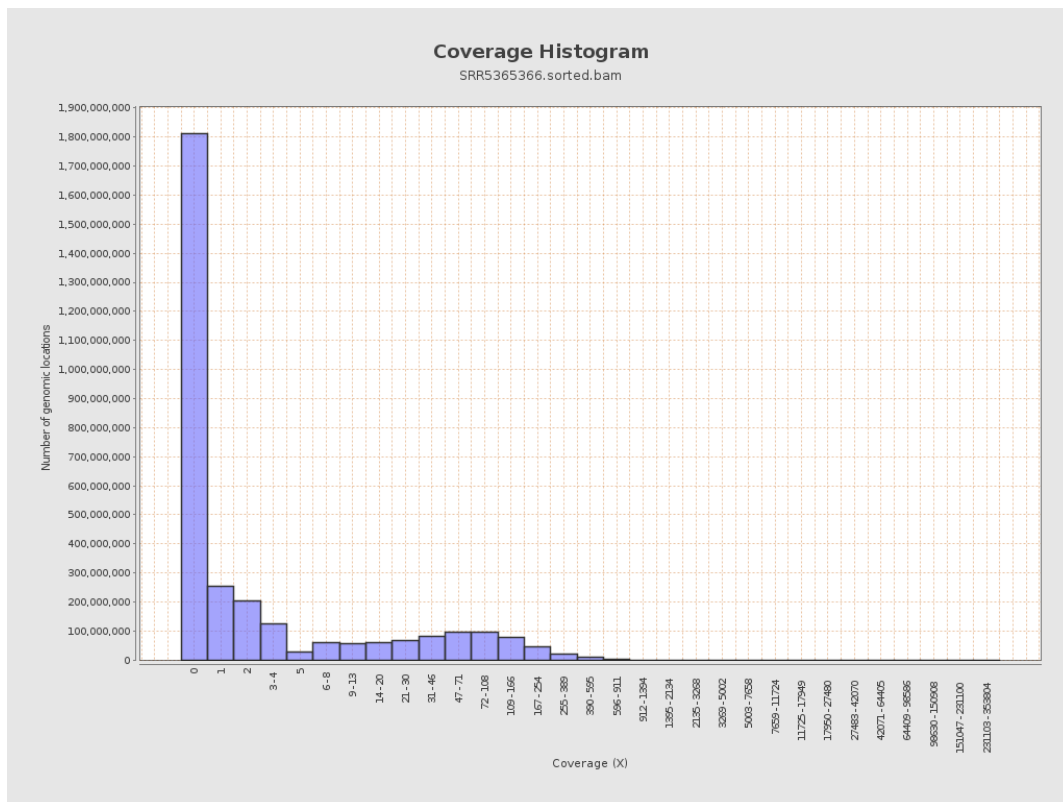
		bases	coverage	deviation
chr1	249250621	4514081453	18.1106	364.0174
chr2	243199373	5220758292	21.467	227.8894
chr3	198022430	3633969200	18.3513	57.0791
chr4	191154276	3863118747	20.2094	116.849
chr5	180915260	3434014011	18.9813	73.2257
chr6	171115067	3245199402	18.965	98.4246
chr7	159138663	3434055267	21.579	220.2667
chr8	146364022	2679791042	18.3091	99.5323
chr9	141213431	2627478049	18.6064	236.5069
chr10	135534747	2672830057	19.7206	242.8808
chr11	135006516	2568018105	19.0214	230.0734
chr12	133851895	2397976282	17.9151	58.5062
chr13	115169878	1632696625	14.1764	50.3262
chr14	107349540	1756345639	16.361	154.2095
chr15	102531392	1762507936	17.1899	57.5722
chr16	90354753	1721213271	19.0495	78.3807
chr17	81195210	1743199745	21.4692	150.1433
chr18	78077248	1568609811	20.0905	262.0033
chr19	59128983	1315462712	22.2473	203.7405
chr20	63025520	1317795336	20.9089	80.3162
chr21	48129895	753466845	15.6549	93.3271
chr22	51304566	813048428	15.8475	78.1433
chrMT	16571	147304820	8,889.3139	5,734.738
chrX	155270560	1464250167	9.4303	72.2734

chrY	59373566	515614097	8.6842	153.539
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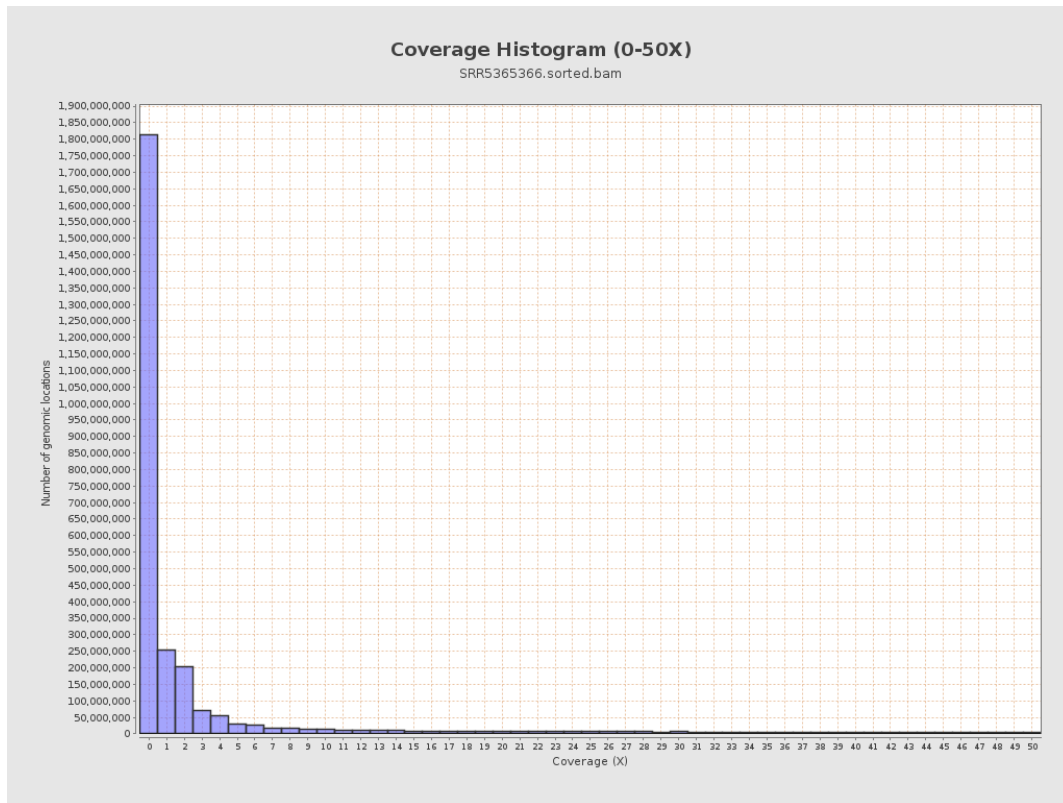
3. Results : Coverage across reference



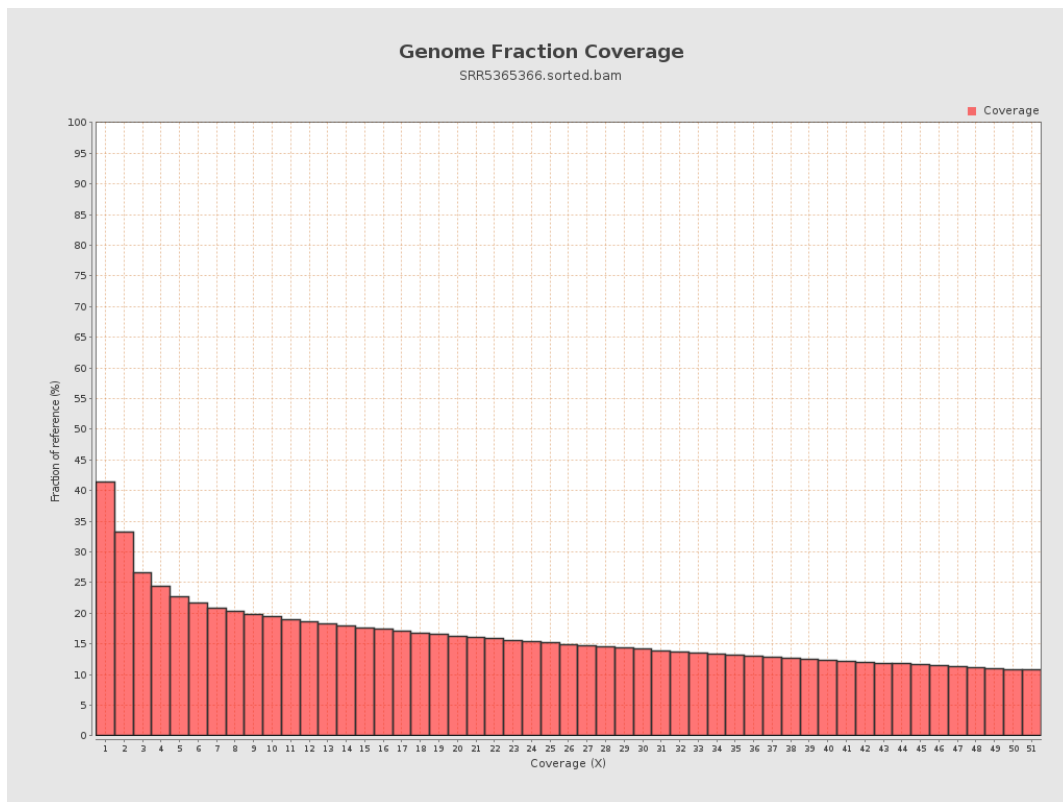
4. Results : Coverage Histogram



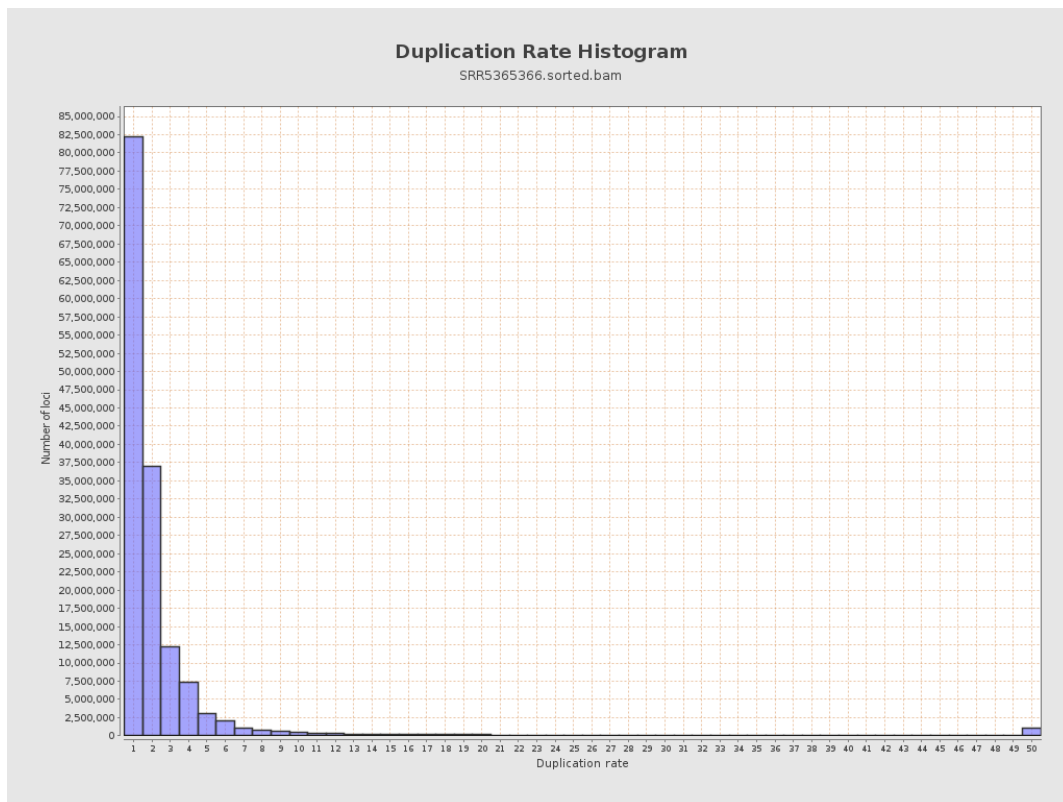
5. Results : Coverage Histogram (0-50X)



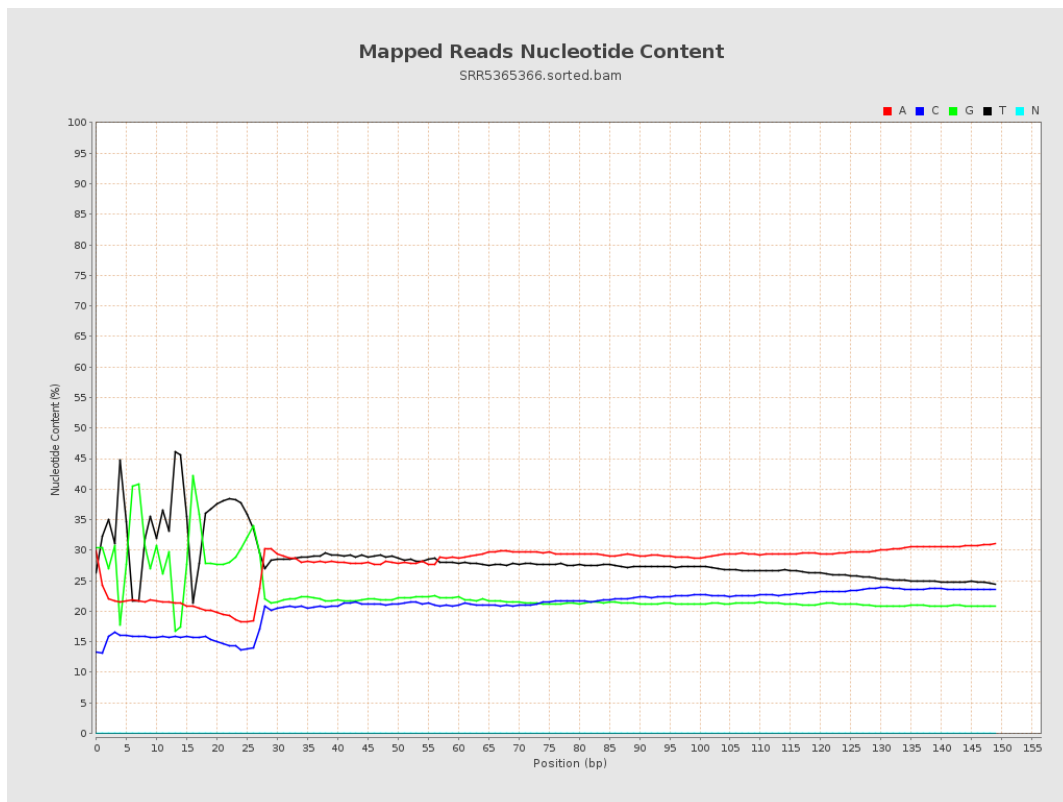
6. Results : Genome Fraction Coverage



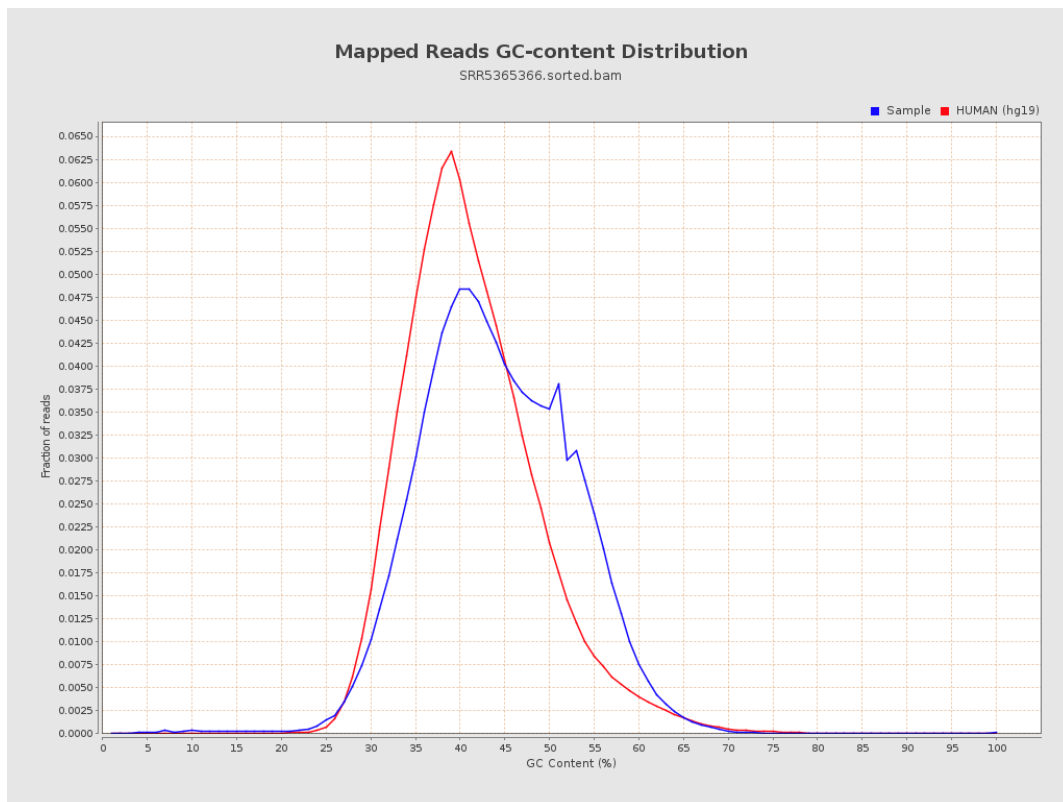
7. Results : Duplication Rate Histogram



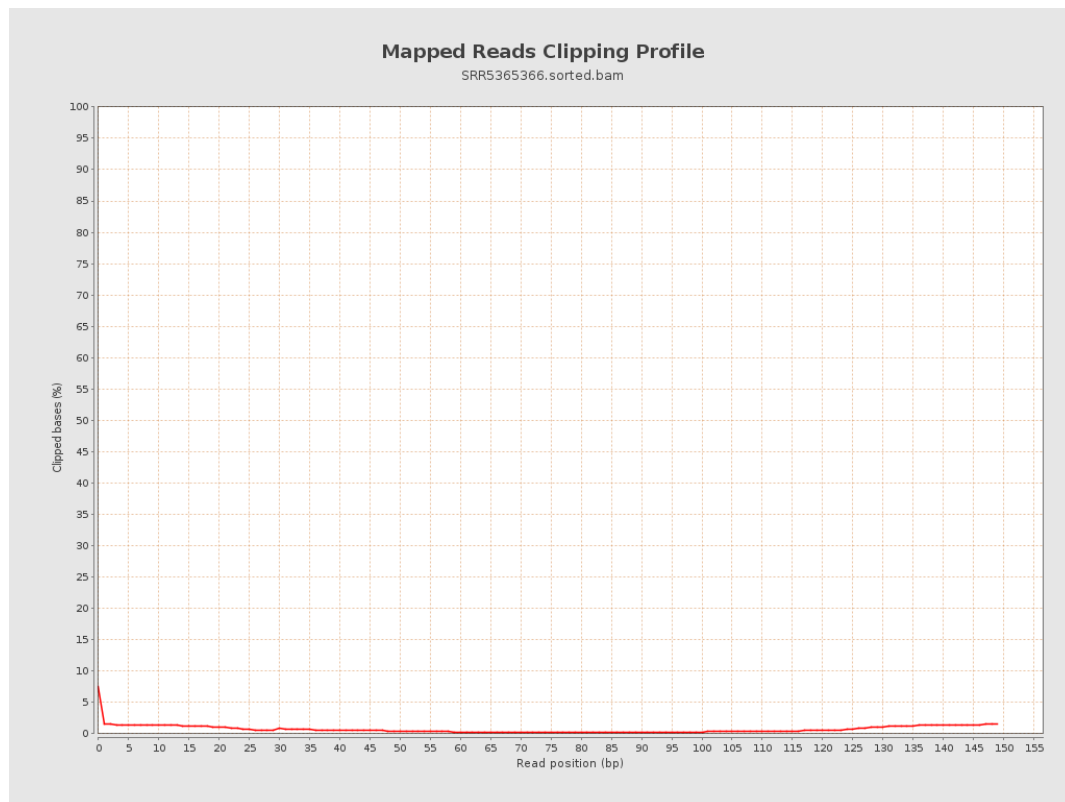
8. Results : Mapped Reads Nucleotide Content



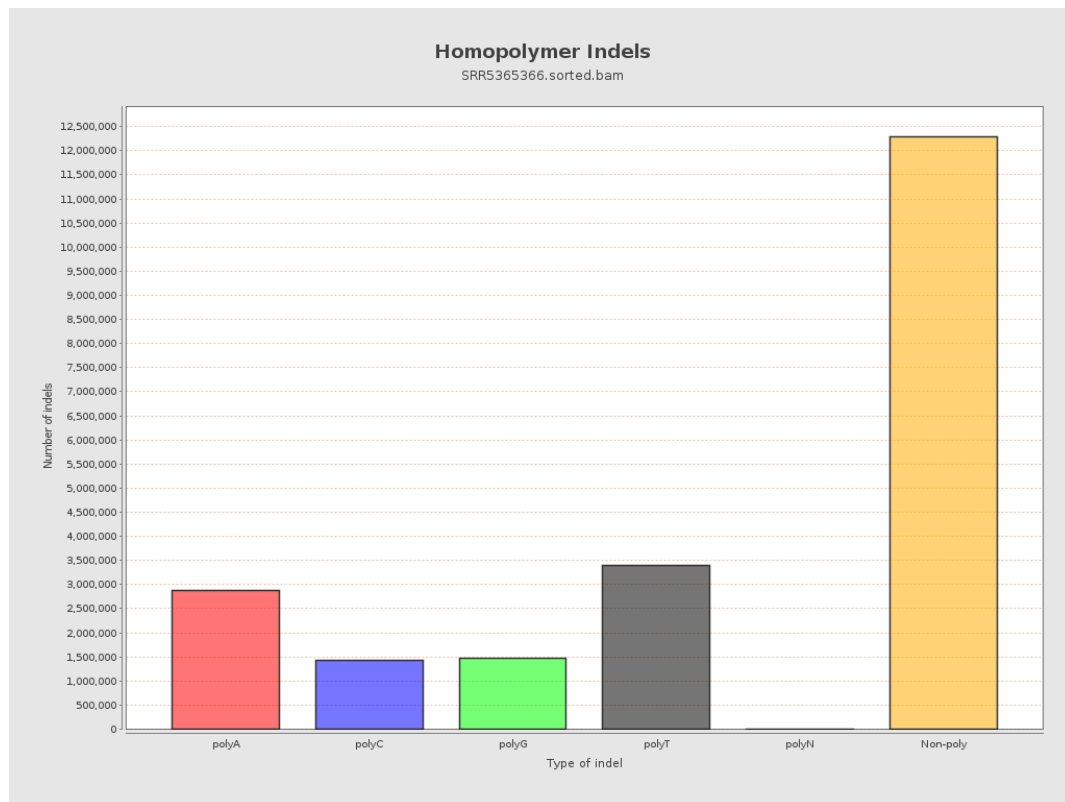
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



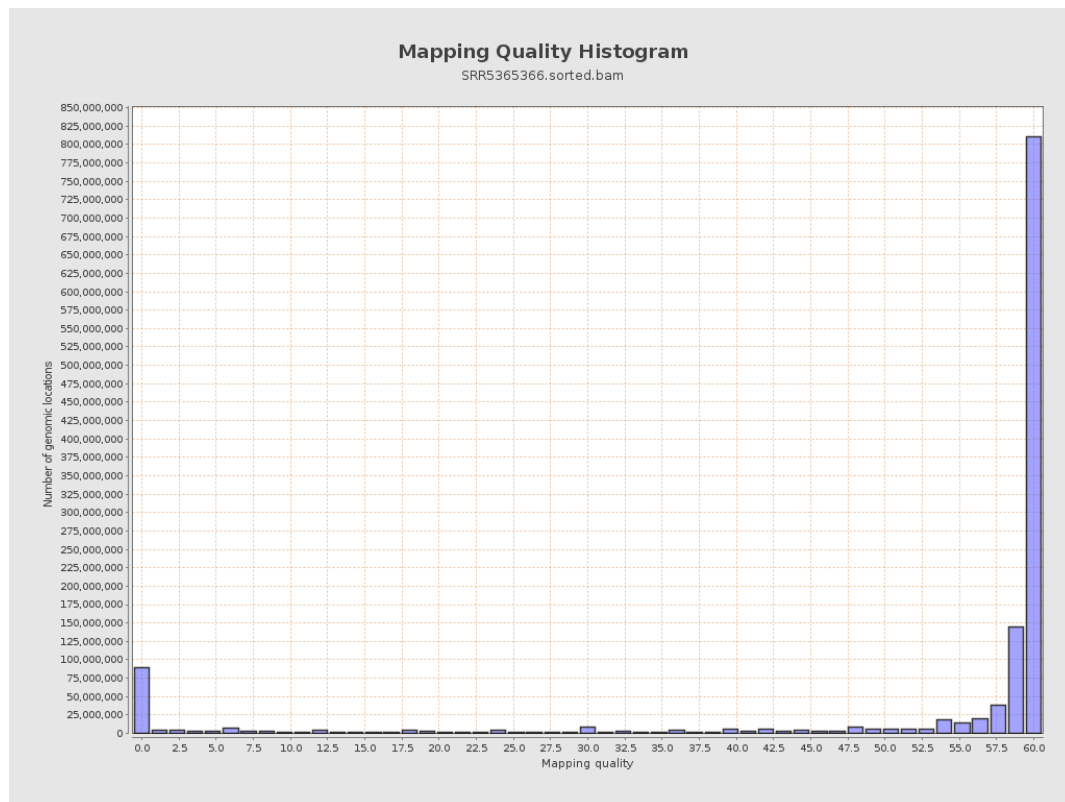
11. Results : Homopolymer Indels



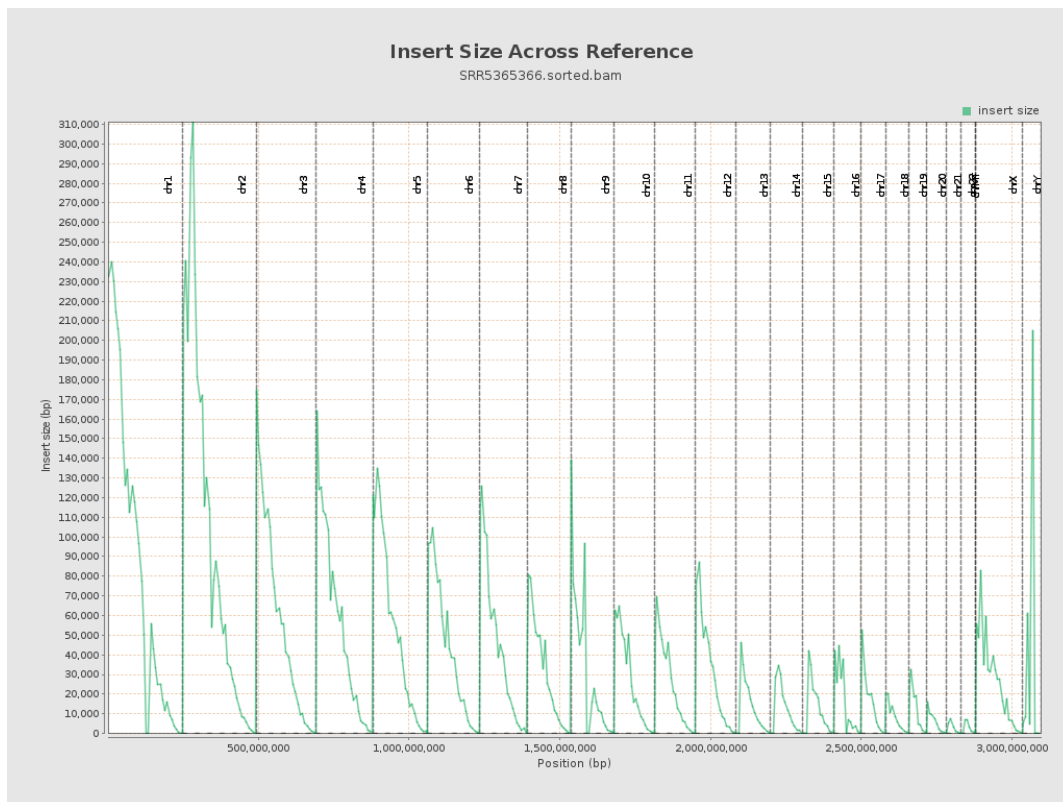
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

