

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/04 12:26:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365345.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_SRR5365345 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365345_1.fastq.gz SRR5365345_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Nov 04 12:26:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365345.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	560,350,488
Mapped reads	535,437,395 / 95.55%
Unmapped reads	24,913,093 / 4.45%
Mapped paired reads	535,437,395 / 95.55%
Mapped reads, first in pair	268,262,078 / 47.87%
Mapped reads, second in pair	267,175,317 / 47.68%
Mapped reads, both in pair	532,066,586 / 94.95%
Mapped reads, singletons	3,370,809 / 0.6%
Secondary alignments	0
Supplementary alignments	2,333,285 / 0.42%
Read min/max/mean length	30 / 125 / 125.17
Duplicated reads (estimated)	407,023,909 / 72.64%
Duplication rate	44.48%
Clipped reads	389,226,476 / 69.46%

2.2. ACGT Content

Number/percentage of A's	16,042,742,889 / 29.54%
Number/percentage of C's	10,852,718,111 / 19.98%
Number/percentage of T's	15,479,623,989 / 28.5%
Number/percentage of G's	11,910,617,980 / 21.93%
Number/percentage of N's	21,994,910 / 0.04%

GC Percentage	41.92%
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2.3. Coverage

Mean	17.5487
Standard Deviation	144.5366

2.4. Mapping Quality

Mean Mapping Quality	53.79
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2.5. Insert size

Mean	64,598.02
Standard Deviation	2,493,646.12
P25/Median/P75	122 / 190 / 290

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	337,940,098
Insertions	15,487,613
Mapped reads with at least one insertion	2.83%
Deletions	8,506,679
Mapped reads with at least one deletion	1.55%
Homopolymer indels	49.87%

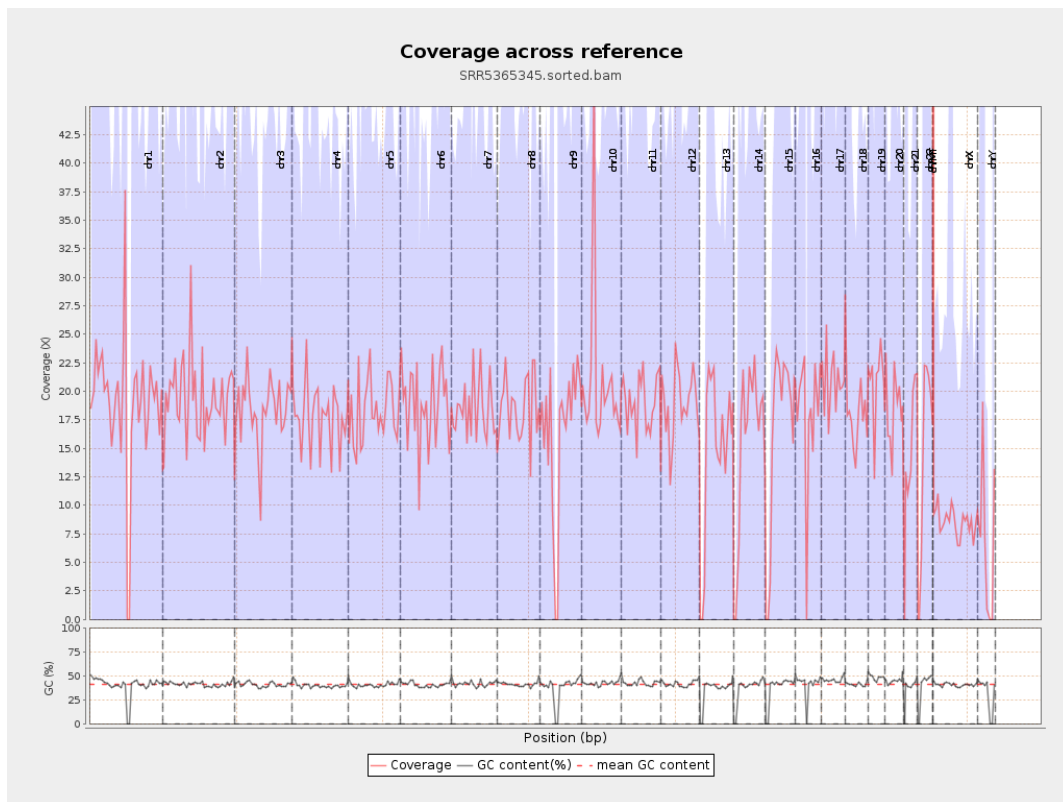
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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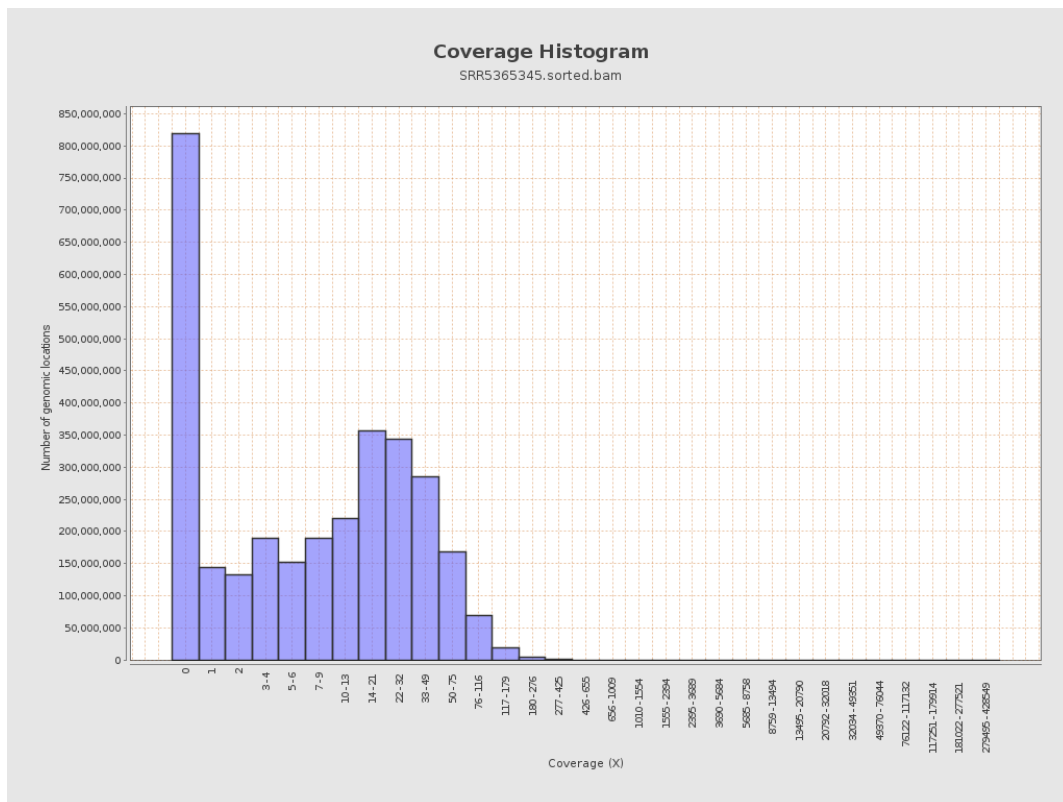
		bases	coverage	deviation
chr1	249250621	4731203470	18.9817	402.1292
chr2	243199373	4745743218	19.5138	95.6379
chr3	198022430	3626651588	18.3143	29.8366
chr4	191154276	3388343608	17.7257	78.4139
chr5	180915260	3323422614	18.3701	25.8652
chr6	171115067	3209894853	18.7587	52.1615
chr7	159138663	2929435423	18.4081	103.9222
chr8	146364022	2717613753	18.5675	44.1682
chr9	141213431	2316835583	16.4066	121.7986
chr10	135534747	2795077449	20.6226	249.305
chr11	135006516	2567005099	19.0139	78.4933
chr12	133851895	2568105792	19.1862	39.355
chr13	115169878	1697157739	14.7361	22.6944
chr14	107349540	1703892846	15.8724	26.2637
chr15	102531392	1652269614	16.1148	28.2749
chr16	90354753	1618680358	17.9147	53.4415
chr17	81195210	1695831601	20.8859	67.2566
chr18	78077248	1403232677	17.9724	146.8374
chr19	59128983	1221001065	20.6498	199.9607
chr20	63025520	1154468016	18.3175	32.2542
chr21	48129895	713937616	14.8336	49.9218
chr22	51304566	739250973	14.4091	38.7685
chrMT	16571	59668209	3,600.7609	804.6115
chrX	155270560	1336202935	8.6056	31.1828

chrY	59373566	410539246	6.9145	135.3956
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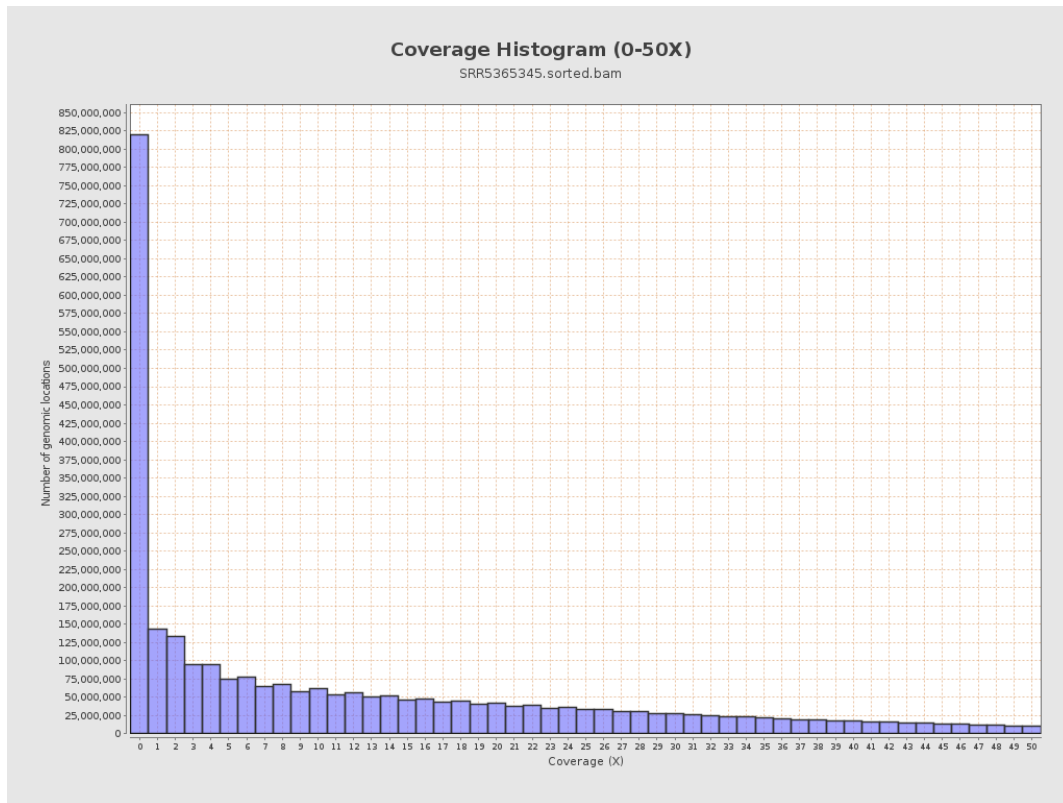
3. Results : Coverage across reference



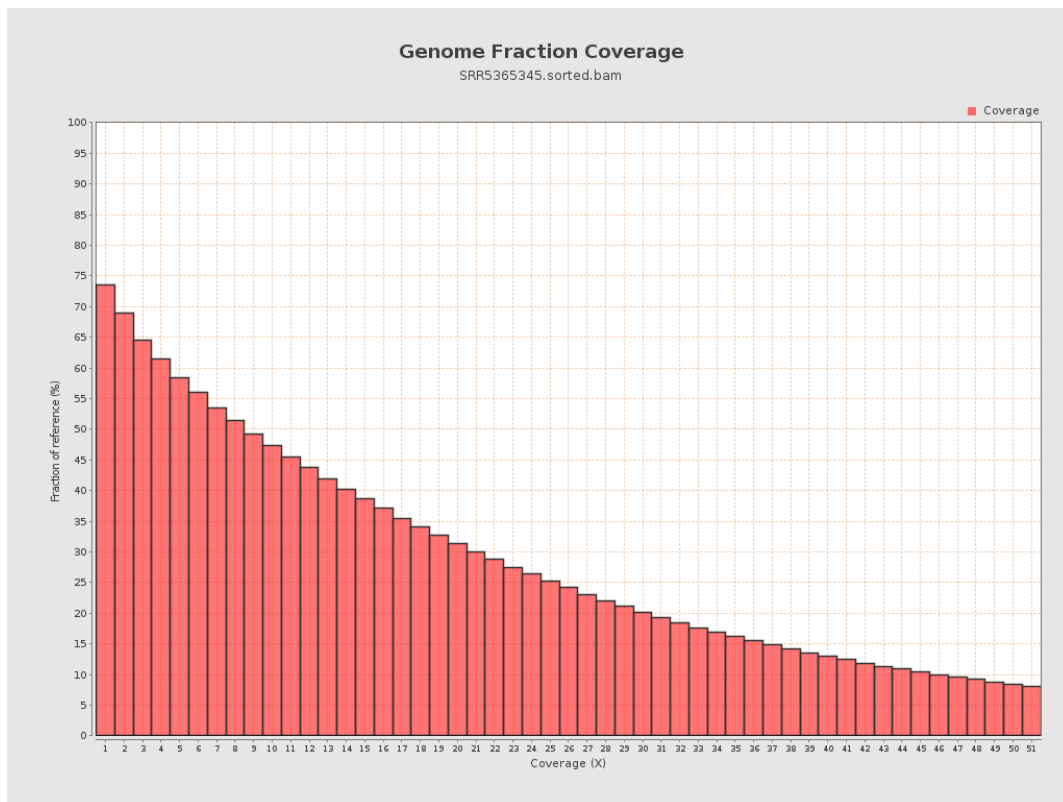
4. Results : Coverage Histogram



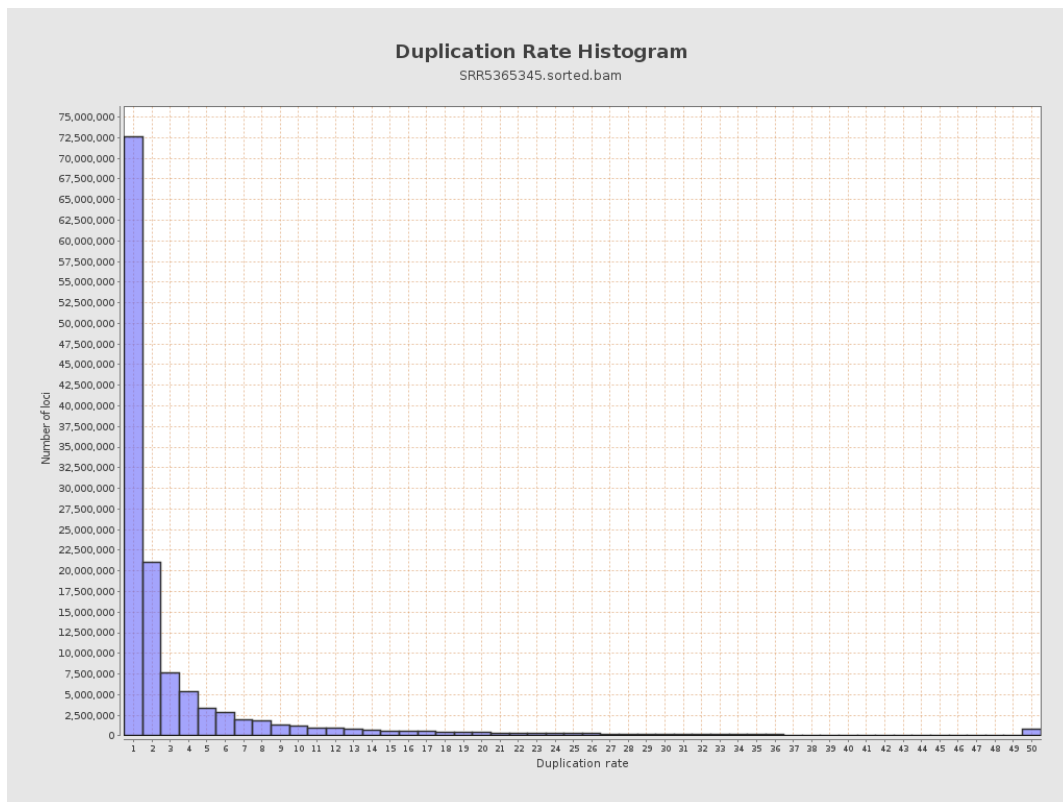
5. Results : Coverage Histogram (0-50X)



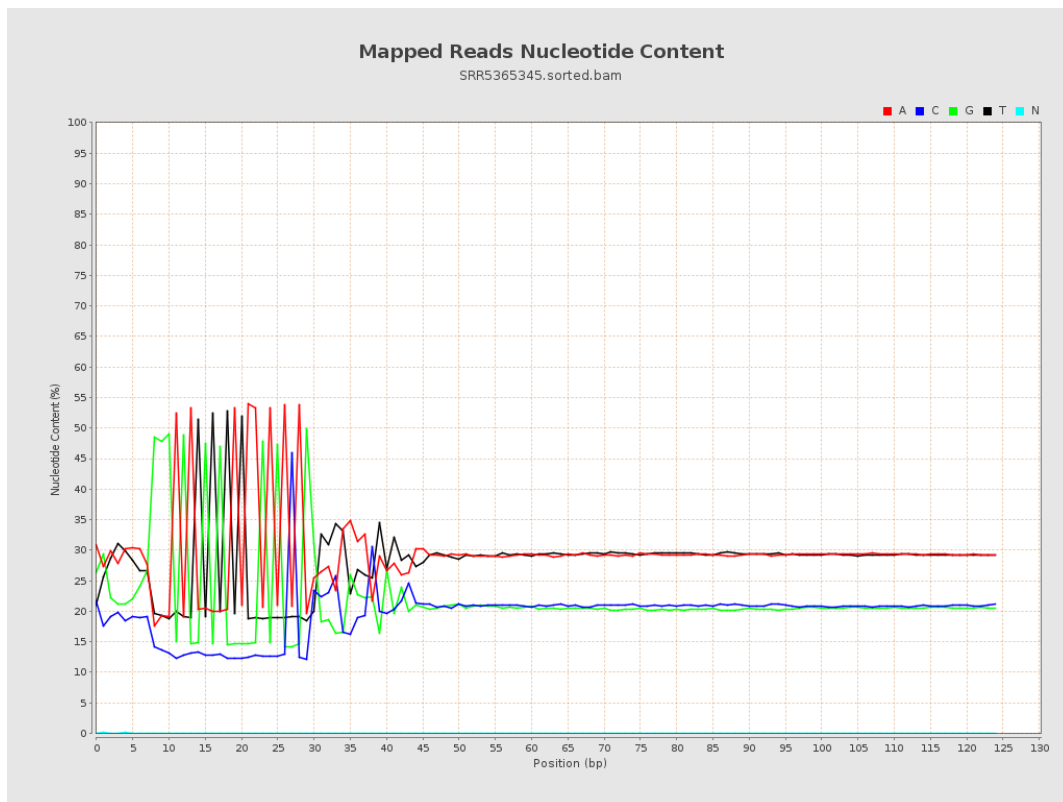
6. Results : Genome Fraction Coverage



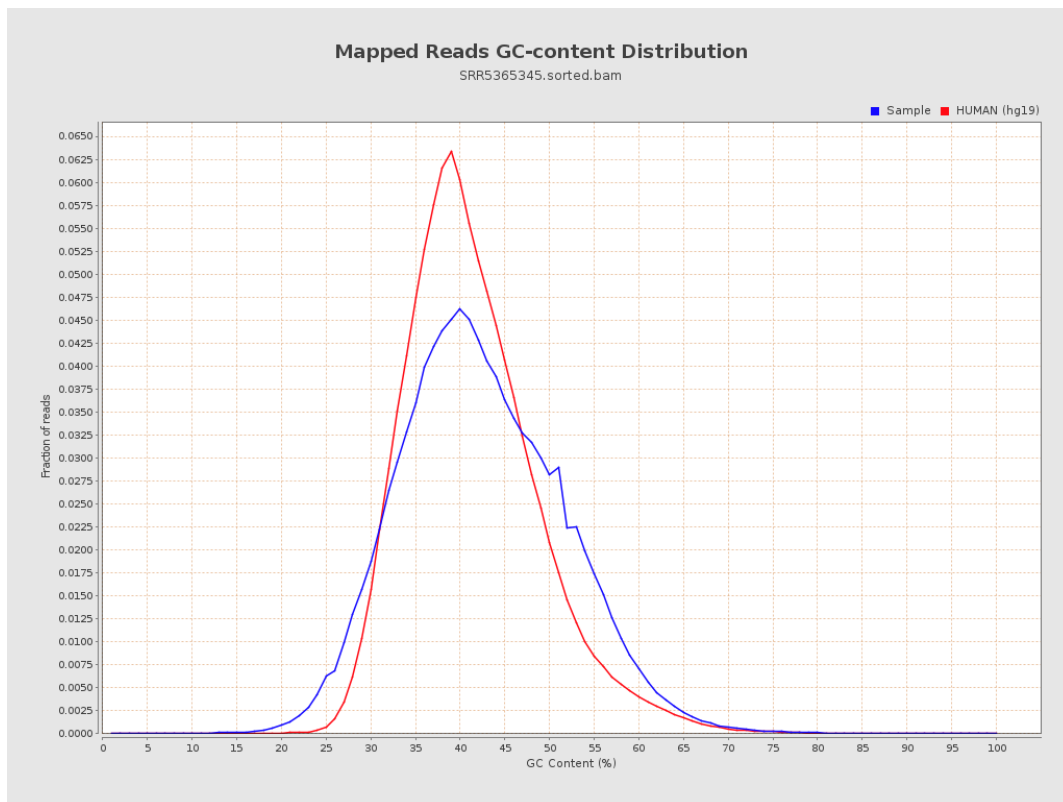
7. Results : Duplication Rate Histogram



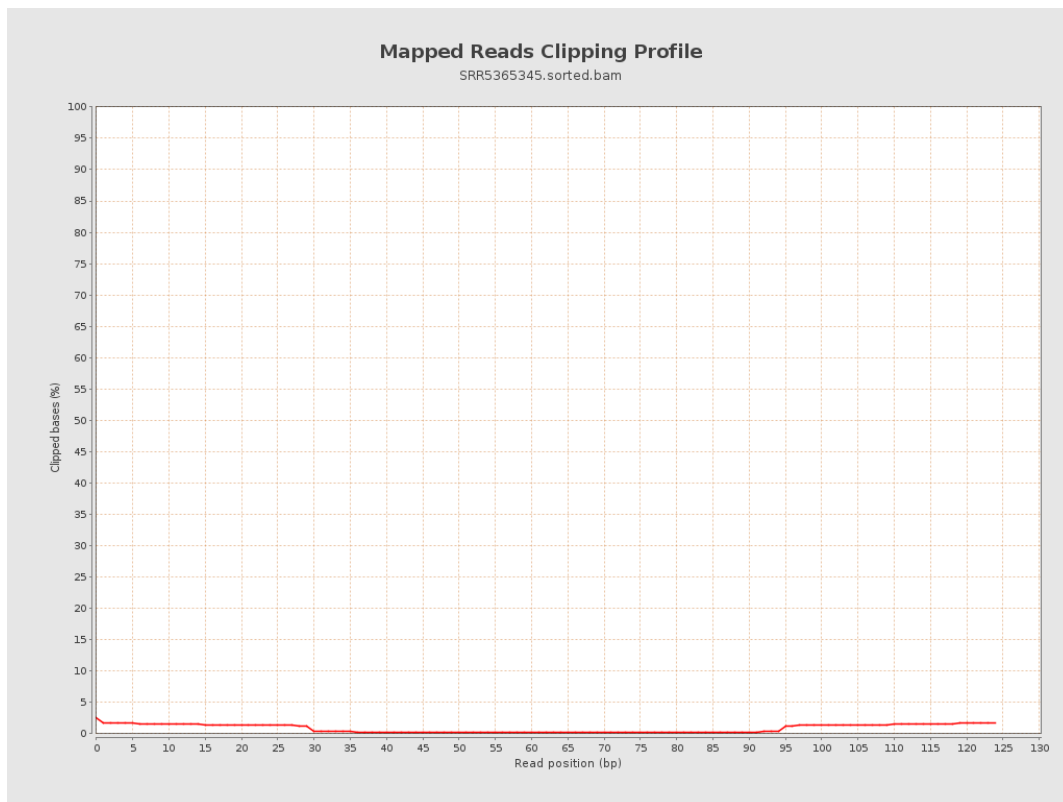
8. Results : Mapped Reads Nucleotide Content



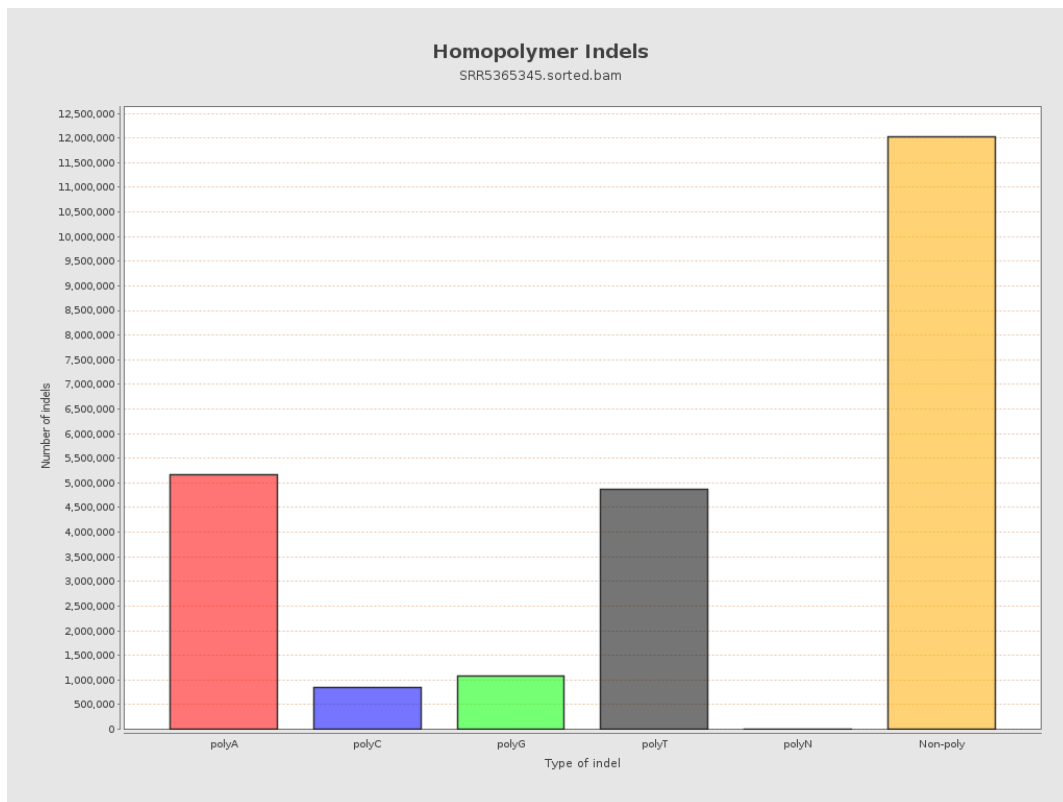
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



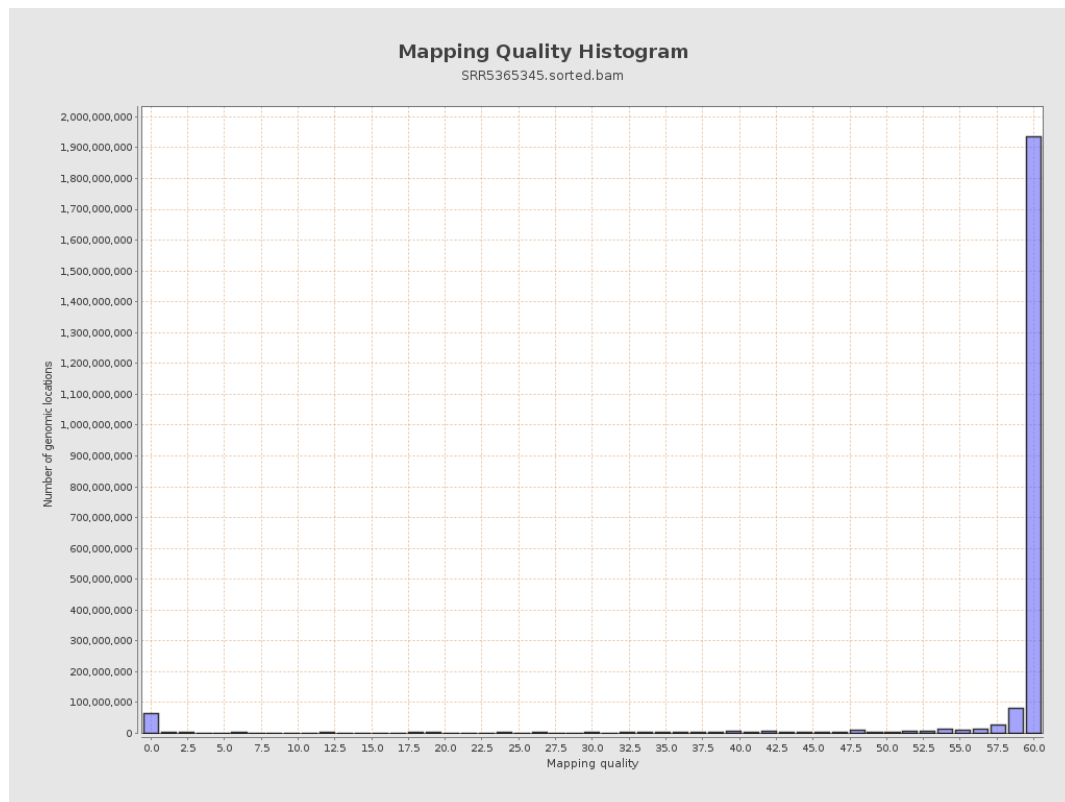
11. Results : Homopolymer Indels



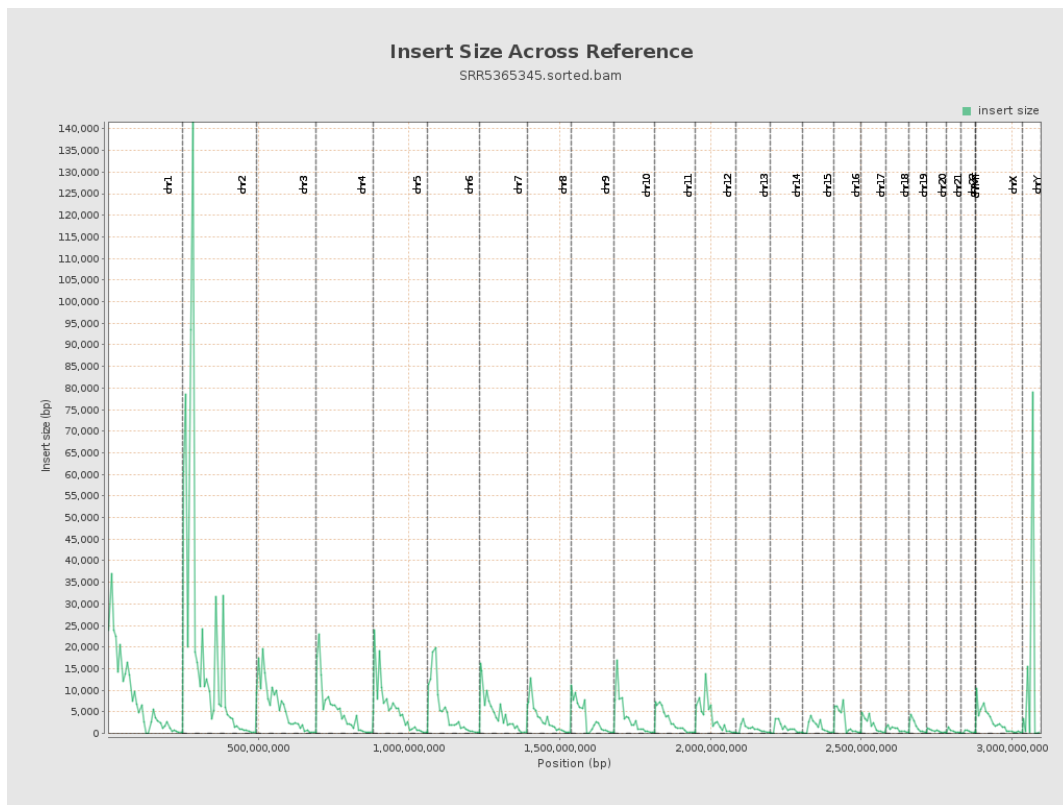
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

