

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/04 01:58:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365344.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_SRR5365344 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365344_1.fastq.gz SRR5365344_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Nov 04 01:58:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365344.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	548,091,404
Mapped reads	525,533,184 / 95.88%
Unmapped reads	22,558,220 / 4.12%
Mapped paired reads	525,533,184 / 95.88%
Mapped reads, first in pair	263,320,653 / 48.04%
Mapped reads, second in pair	262,212,531 / 47.84%
Mapped reads, both in pair	522,054,680 / 95.25%
Mapped reads, singletons	3,478,504 / 0.63%
Secondary alignments	0
Supplementary alignments	2,218,482 / 0.4%
Read min/max/mean length	30 / 125 / 125.16
Duplicated reads (estimated)	386,402,590 / 70.5%
Duplication rate	45.31%
Clipped reads	384,573,639 / 70.17%

2.2. ACGT Content

Number/percentage of A's	15,855,979,201 / 29.74%
Number/percentage of C's	10,556,104,041 / 19.8%
Number/percentage of T's	15,327,690,101 / 28.75%
Number/percentage of G's	11,556,772,996 / 21.67%
Number/percentage of N's	25,926,319 / 0.05%

GC Percentage	41.47%
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2.3. Coverage

Mean	17.2304
Standard Deviation	113.9044

2.4. Mapping Quality

Mean Mapping Quality	53.78
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2.5. Insert size

Mean	67,323.18
Standard Deviation	2,524,997.14
P25/Median/P75	121 / 186 / 283

2.6. Mismatches and indels

General error rate	0.74%
Mismatches	365,302,595
Insertions	15,599,423
Mapped reads with at least one insertion	2.9%
Deletions	8,445,606
Mapped reads with at least one deletion	1.57%
Homopolymer indels	49.72%

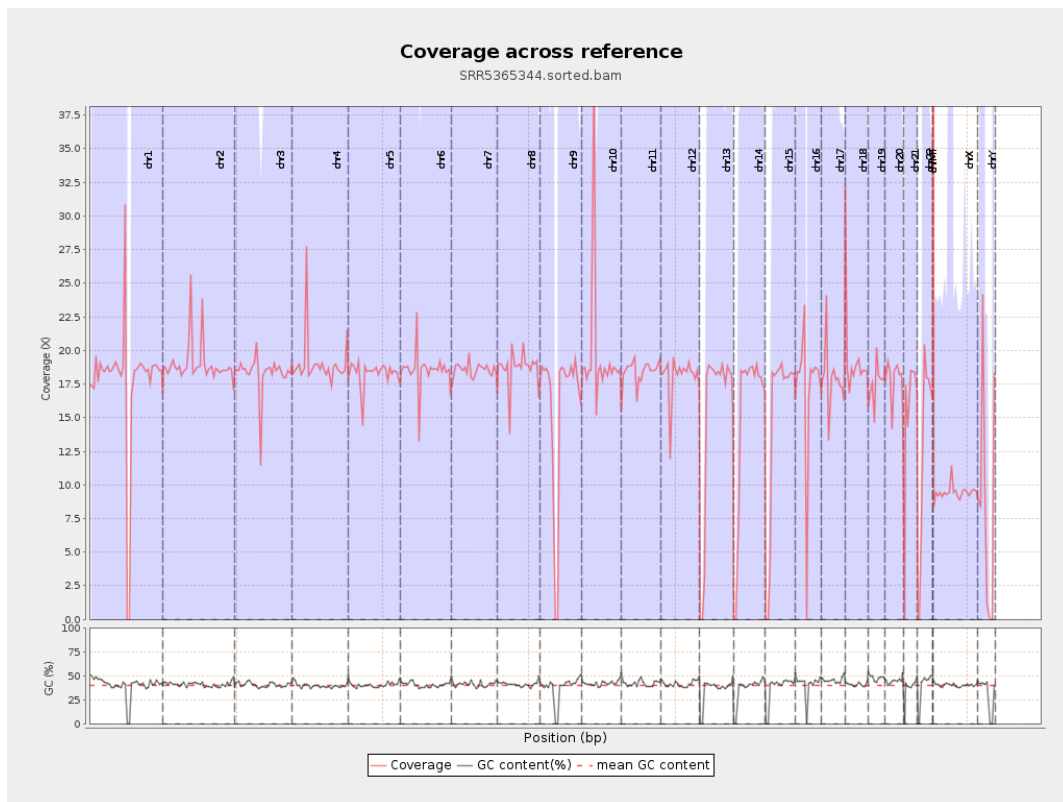
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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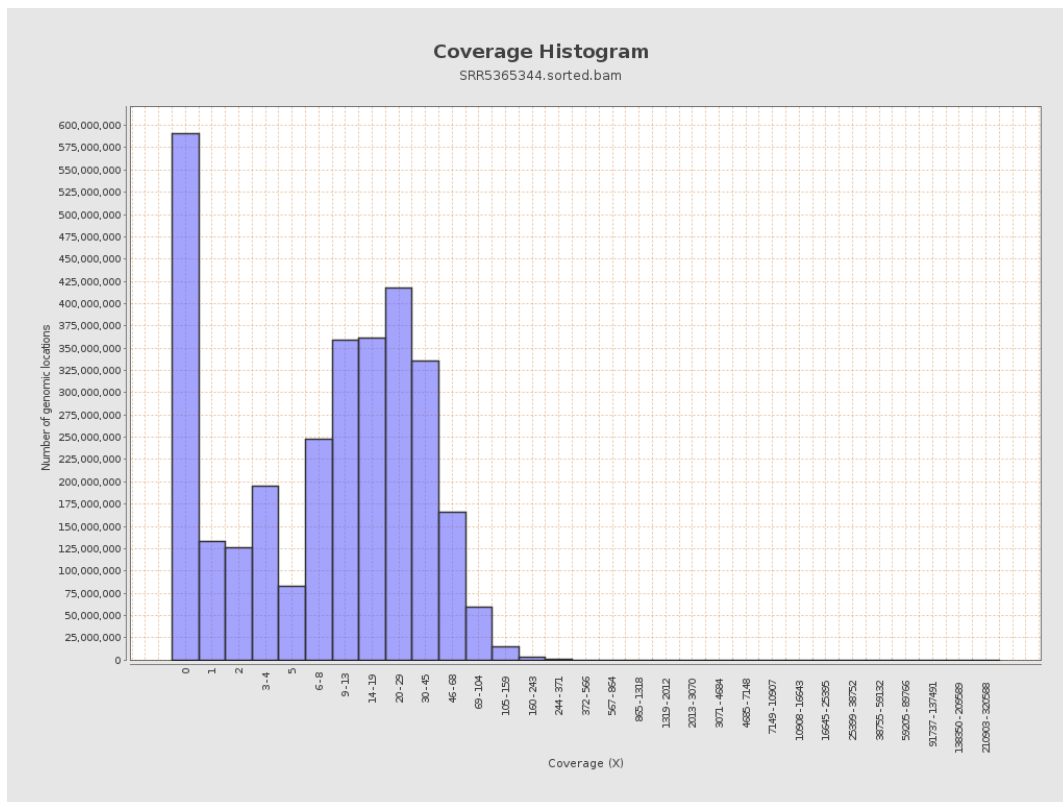
		bases	coverage	deviation
chr1	249250621	4413389852	17.7066	297.5789
chr2	243199373	4623996705	19.0132	74.9396
chr3	198022430	3627961682	18.321	24.4469
chr4	191154276	3637772537	19.0306	87.2908
chr5	180915260	3304381213	18.2648	22.3391
chr6	171115067	3175010548	18.5548	52.8066
chr7	159138663	2951461859	18.5465	87.4914
chr8	146364022	2734844158	18.6852	34.739
chr9	141213431	2254549548	15.9655	82.951
chr10	135534747	2655950199	19.5961	192.975
chr11	135006516	2490399187	18.4465	67.637
chr12	133851895	2429836561	18.1532	36.3562
chr13	115169878	1767563050	15.3474	19.7382
chr14	107349540	1642478850	15.3003	21.2594
chr15	102531392	1503919857	14.6679	24.5623
chr16	90354753	1538248828	17.0245	43.4082
chr17	81195210	1459234818	17.9719	81.6633
chr18	78077248	1486922375	19.0442	150.197
chr19	59128983	1038041957	17.5556	143.551
chr20	63025520	1126291382	17.8704	30.7362
chr21	48129895	756959118	15.7274	59.6852
chr22	51304566	651348898	12.6957	50.9618
chrMT	16571	77896571	4,700.7767	869.9315
chrX	155270560	1466968196	9.4478	31.3295

chrY	59373566	524464973	8.8333	164.9703
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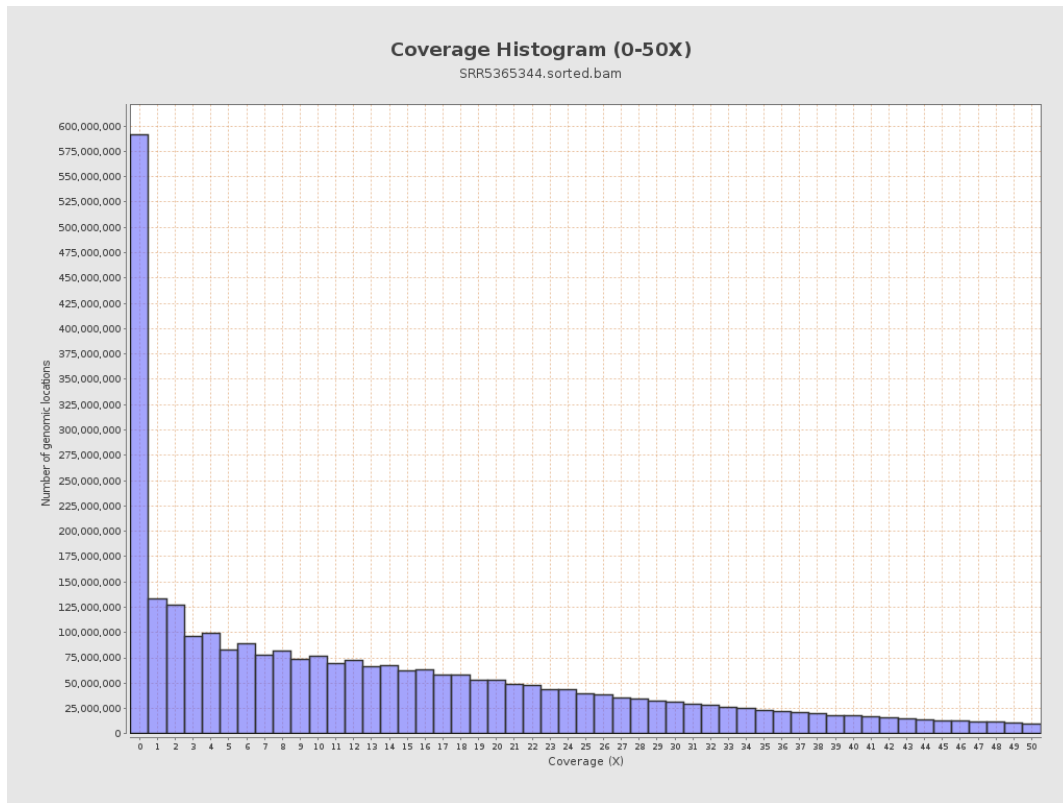
3. Results : Coverage across reference



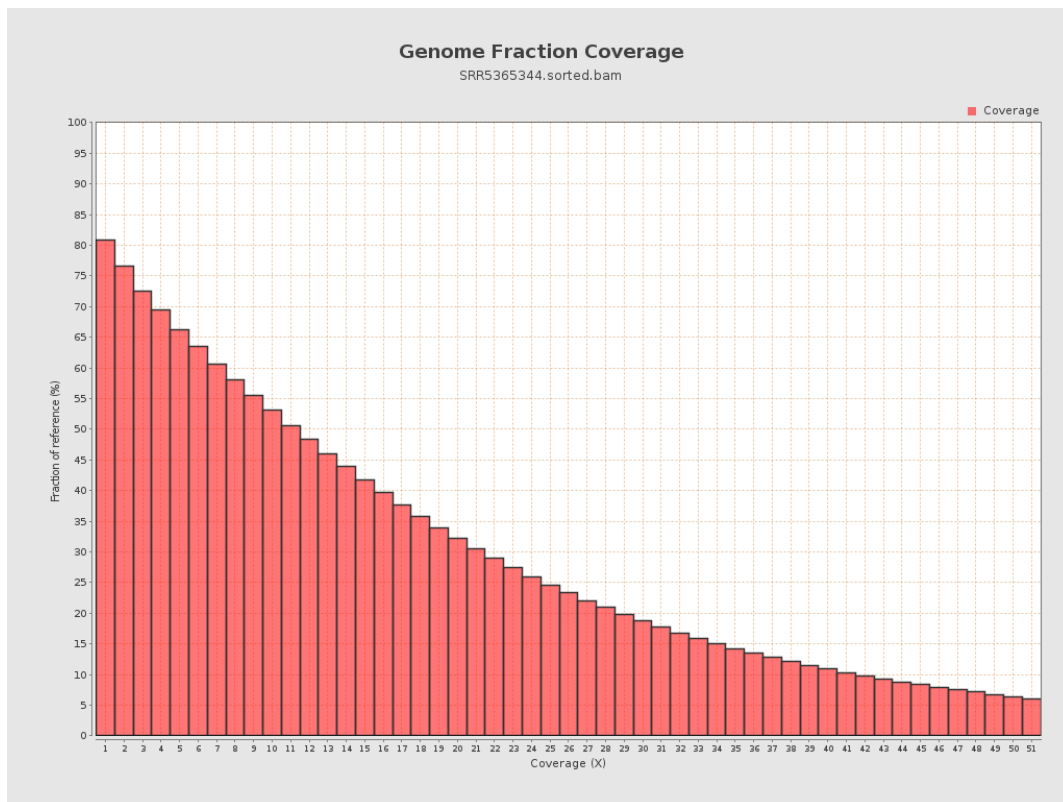
4. Results : Coverage Histogram



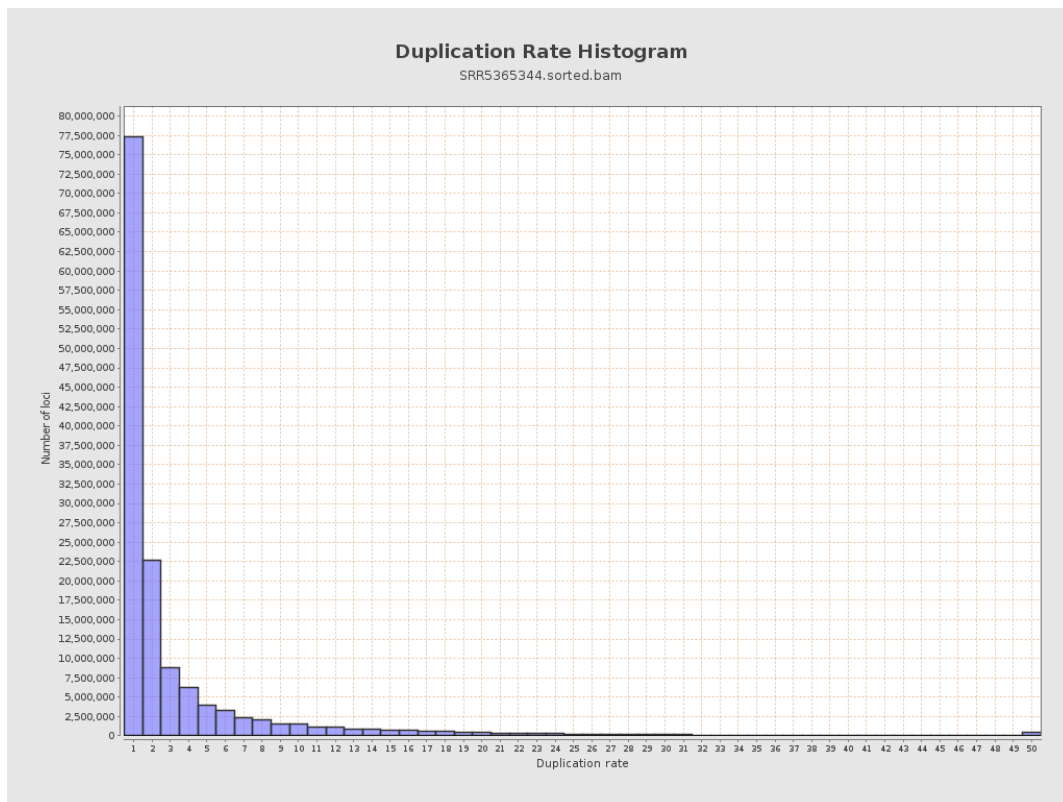
5. Results : Coverage Histogram (0-50X)



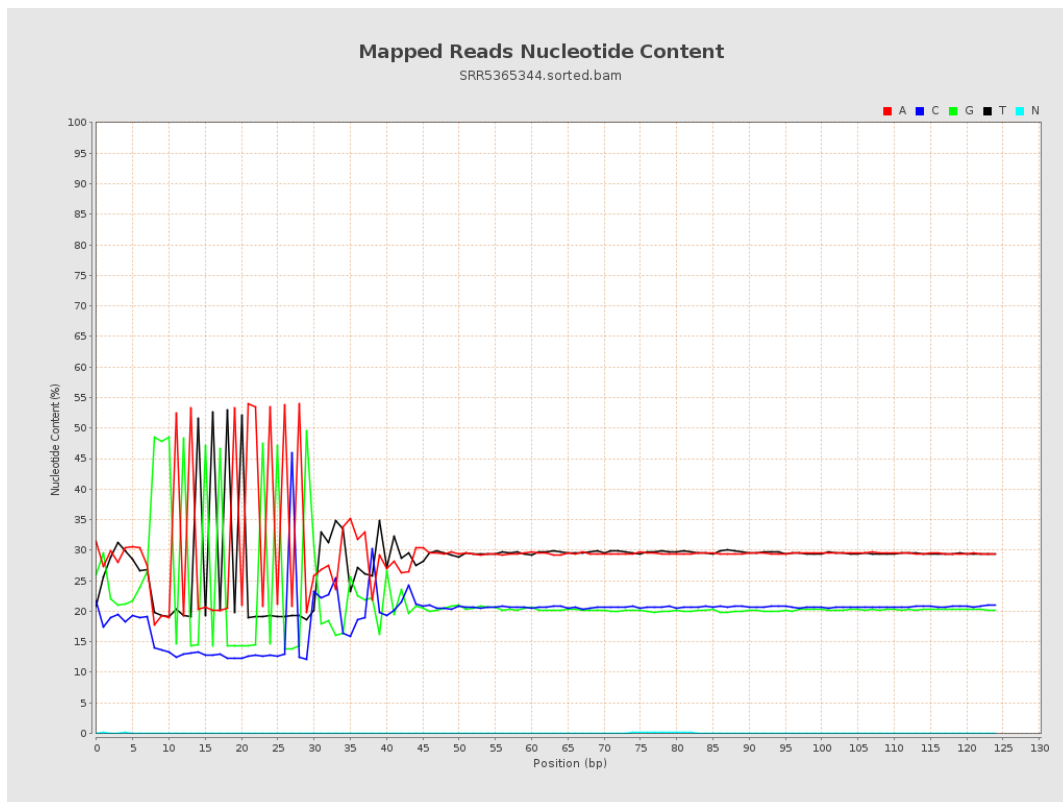
6. Results : Genome Fraction Coverage



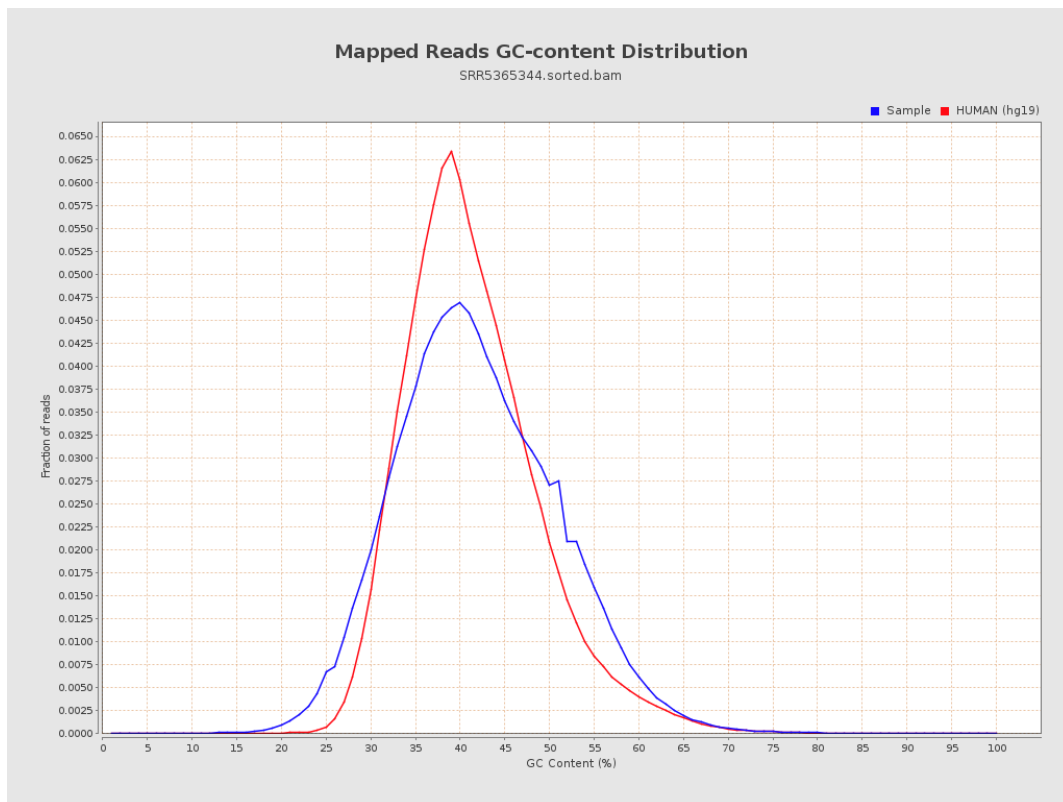
7. Results : Duplication Rate Histogram



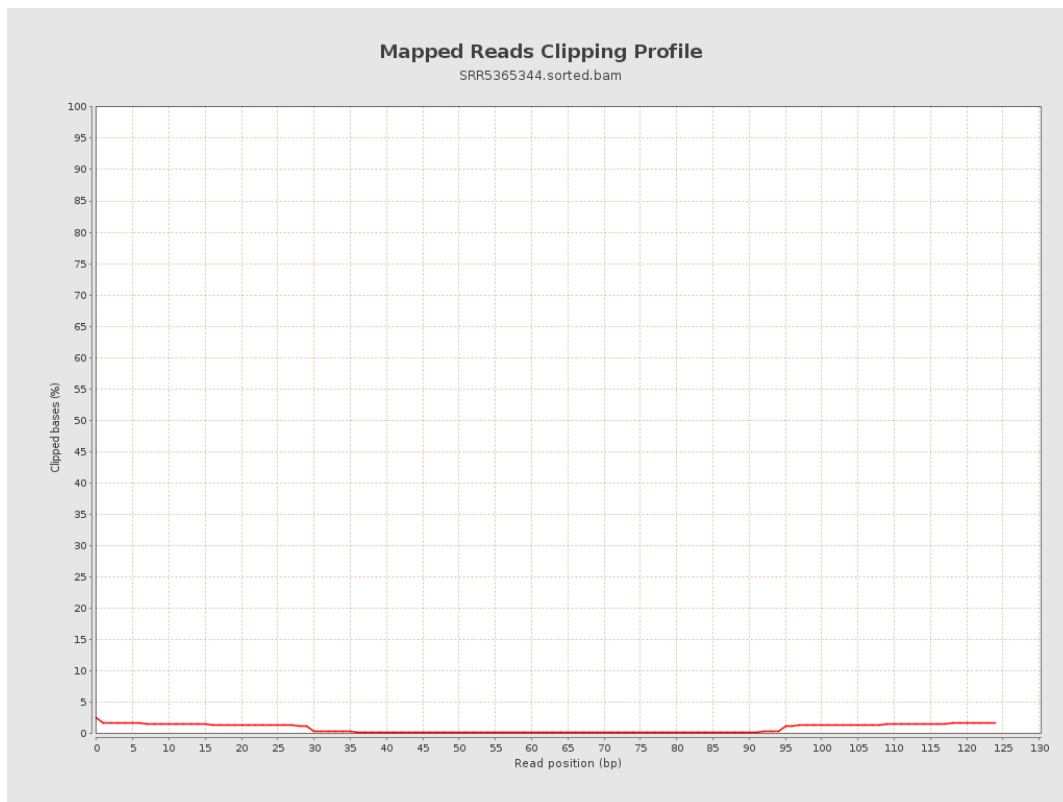
8. Results : Mapped Reads Nucleotide Content



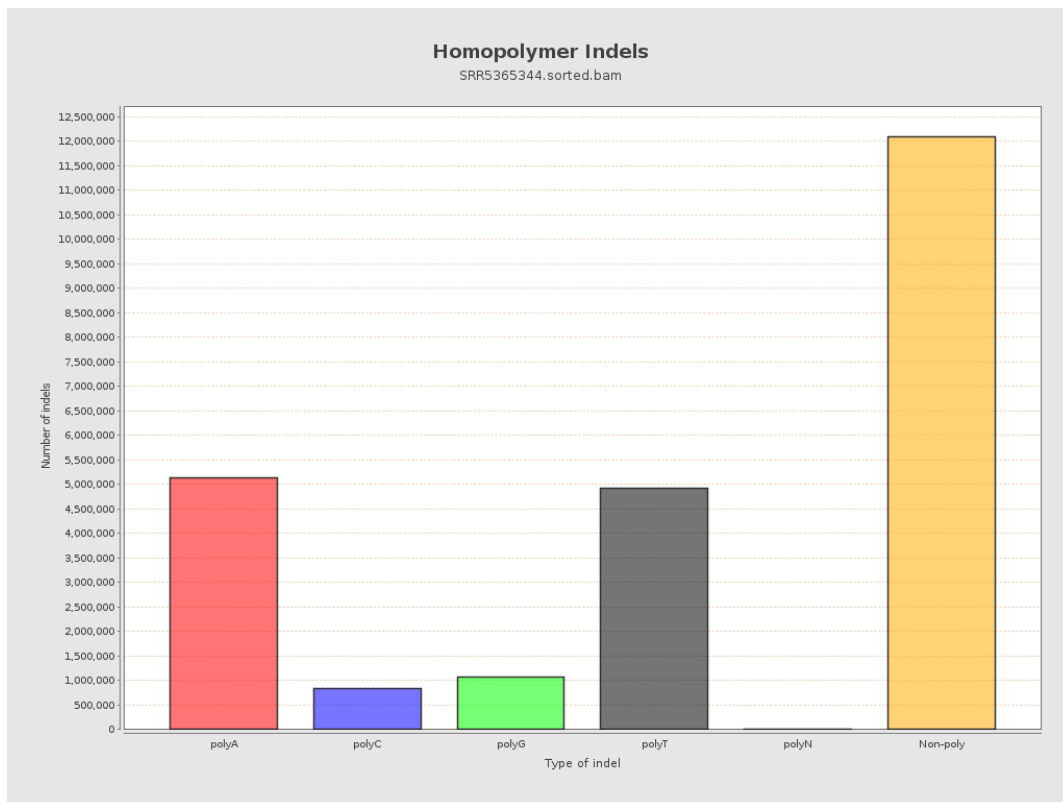
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



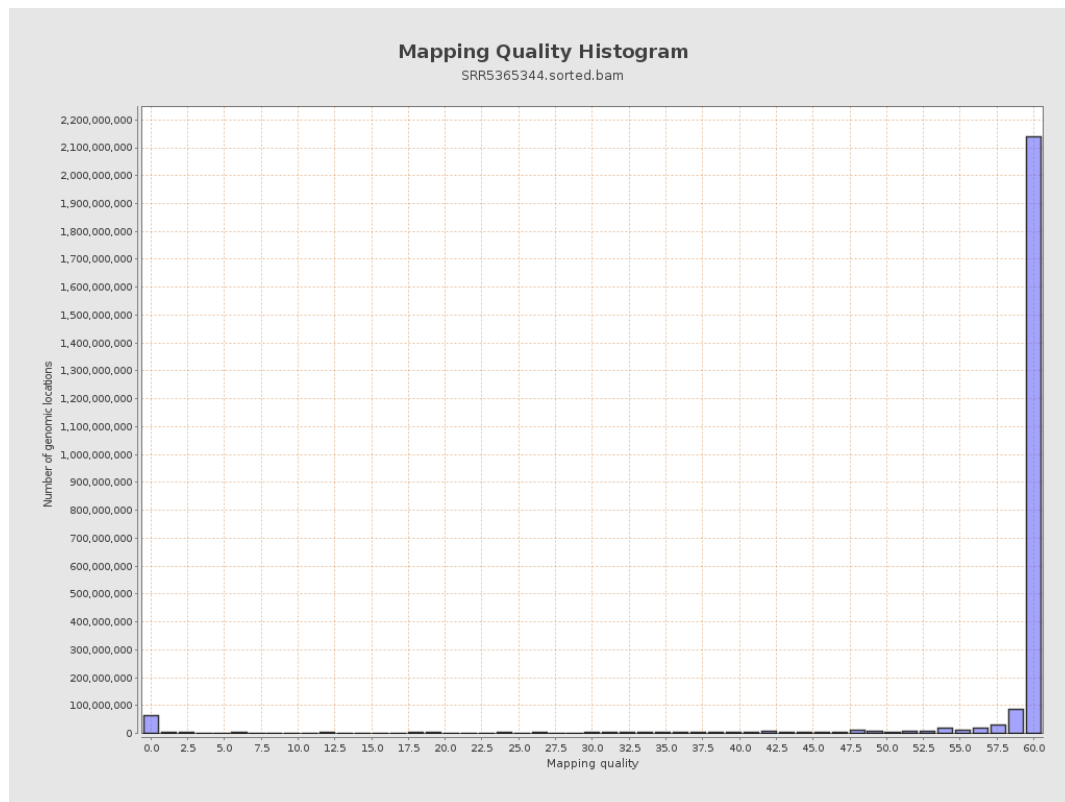
11. Results : Homopolymer Indels



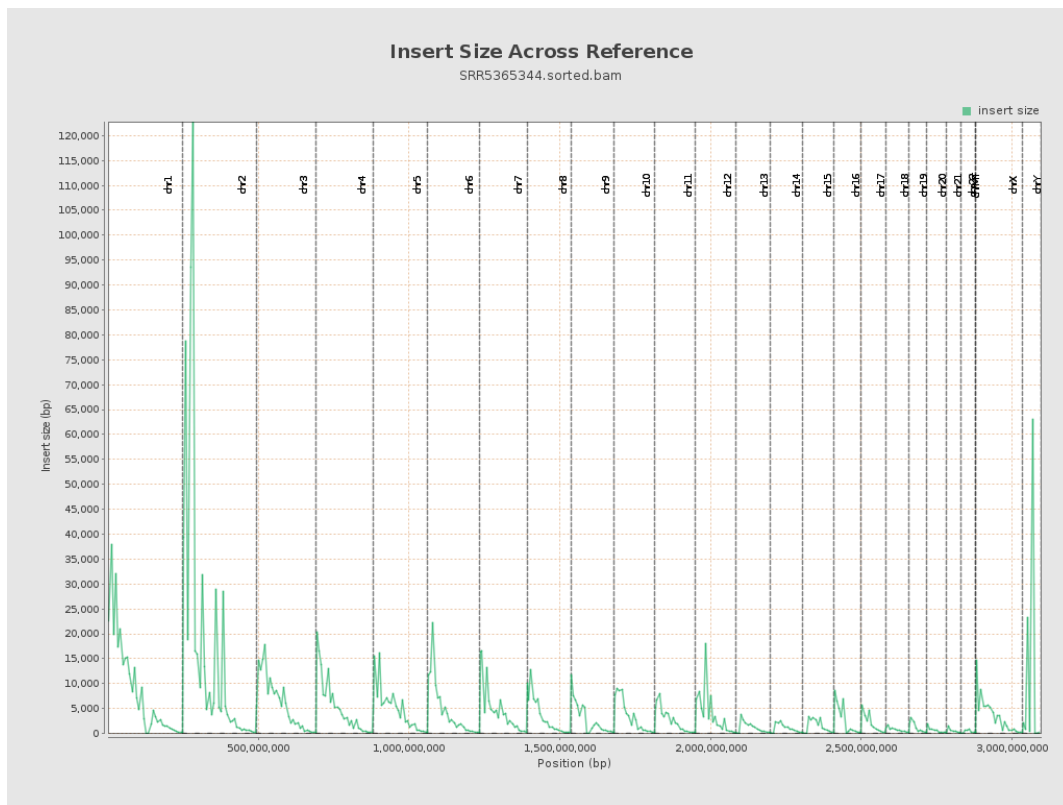
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

