

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/23 00:06:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365368.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_SRR5365368 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365368_1.fastq.gz SRR5365368_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Nov 23 00:06:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365368.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	642,069,020
Mapped reads	607,829,124 / 94.67%
Unmapped reads	34,239,896 / 5.33%
Mapped paired reads	607,829,124 / 94.67%
Mapped reads, first in pair	303,631,137 / 47.29%
Mapped reads, second in pair	304,197,987 / 47.38%
Mapped reads, both in pair	605,274,036 / 94.27%
Mapped reads, singletons	2,555,088 / 0.4%
Secondary alignments	0
Supplementary alignments	5,229,325 / 0.81%
Read min/max/mean length	30 / 150 / 150.41
Duplicated reads (estimated)	298,279,112 / 46.46%
Duplication rate	43.66%
Clipped reads	255,450,175 / 39.79%

2.2. ACGT Content

Number/percentage of A's	22,399,931,254 / 26.76%
Number/percentage of C's	19,263,598,765 / 23.01%
Number/percentage of T's	21,913,246,234 / 26.18%
Number/percentage of G's	20,131,688,792 / 24.05%
Number/percentage of N's	2,877,847 / 0%

GC Percentage	47.06%
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2.3. Coverage

Mean	27.0607
Standard Deviation	80.6614

2.4. Mapping Quality

Mean Mapping Quality	54.64
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2.5. Insert size

Mean	45,647.61
Standard Deviation	2,177,293.24
P25/Median/P75	138 / 170 / 213

2.6. Mismatches and indels

General error rate	0.93%
Mismatches	754,971,836
Insertions	12,454,997
Mapped reads with at least one insertion	1.99%
Deletions	42,375,910
Mapped reads with at least one deletion	6.71%
Homopolymer indels	52.32%

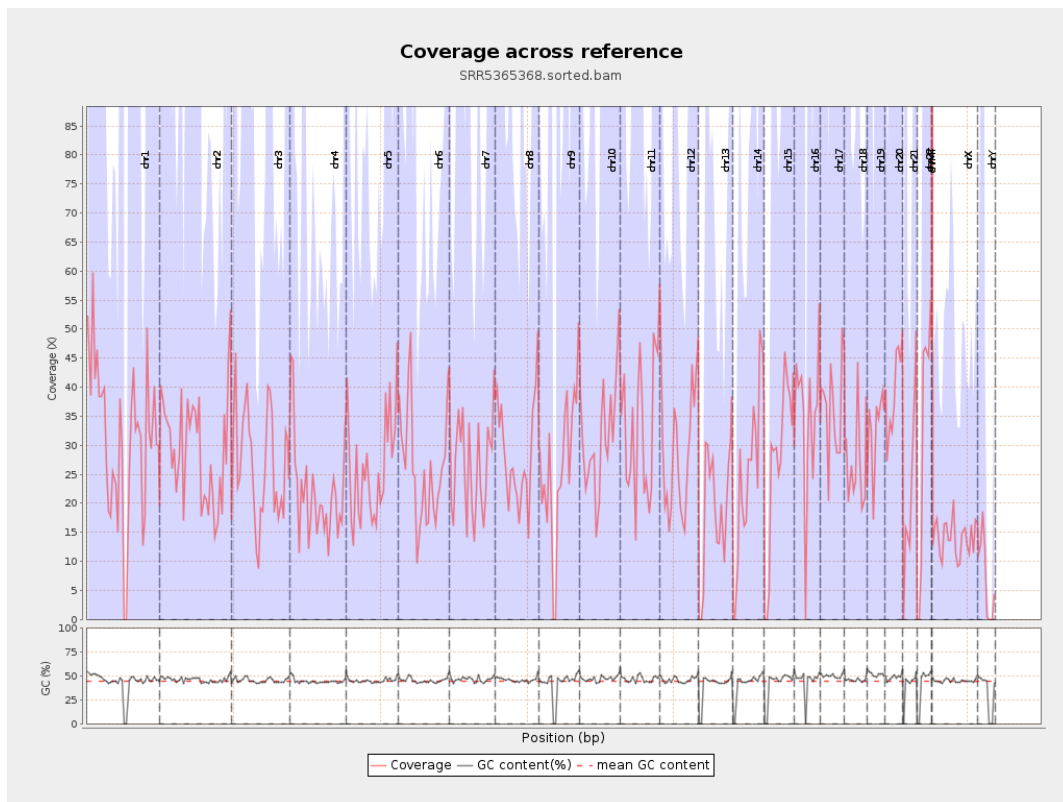
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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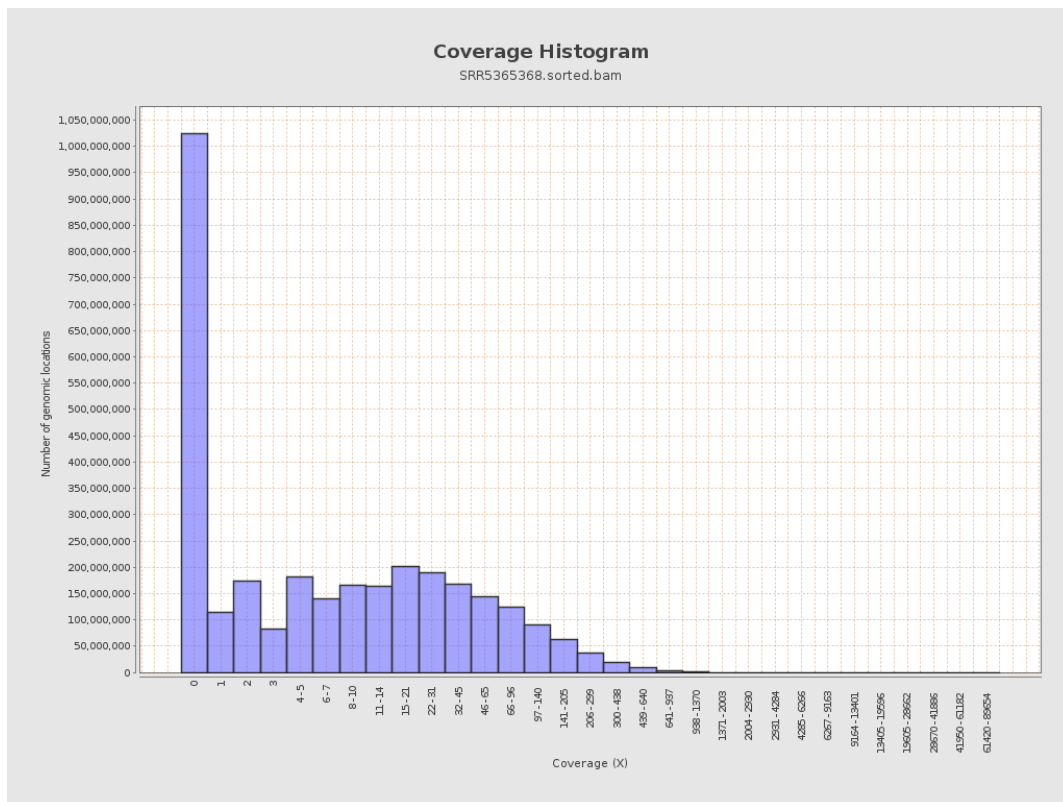
		bases	coverage	deviation
chr1	249250621	7738722187	31.048	97.8483
chr2	243199373	7105327409	29.2161	125.3644
chr3	198022430	5366215222	27.099	61.0658
chr4	191154276	4139136817	21.6534	60.4711
chr5	180915260	4750488963	26.2581	59.6796
chr6	171115067	4461207977	26.0714	60.2904
chr7	159138663	4237497222	26.6277	63.0582
chr8	146364022	4125762725	28.1884	68.2808
chr9	141213431	3743330760	26.5083	91.1976
chr10	135534747	4260481190	31.4346	91.7208
chr11	135006516	4447211778	32.9407	84.9576
chr12	133851895	3850303715	28.7654	65.1506
chr13	115169878	2165567827	18.8032	48.0804
chr14	107349540	2626423553	24.4661	61.8315
chr15	102531392	2750884049	26.8297	64.674
chr16	90354753	3134866849	34.6951	124.8146
chr17	81195210	2965707459	36.5256	83.6308
chr18	78077248	2116646958	27.1097	96.3589
chr19	59128983	1953657860	33.0406	85.3213
chr20	63025520	2460741850	39.0436	83.8992
chr21	48129895	1100464901	22.8645	93.5298
chr22	51304566	1665277151	32.4587	81.098
chrMT	16571	9613109	580.1164	470.3169
chrX	155270560	2160216963	13.9126	36.0533

chrY	59373566	435746620	7.3391	71.5804
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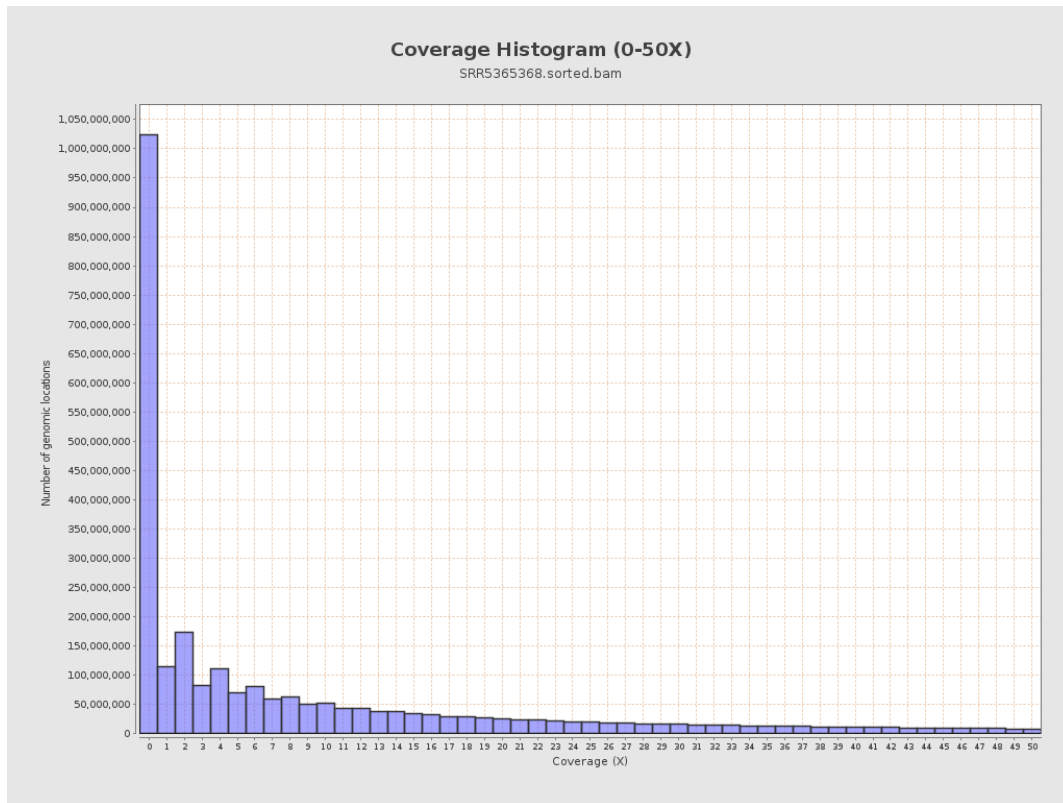
3. Results : Coverage across reference



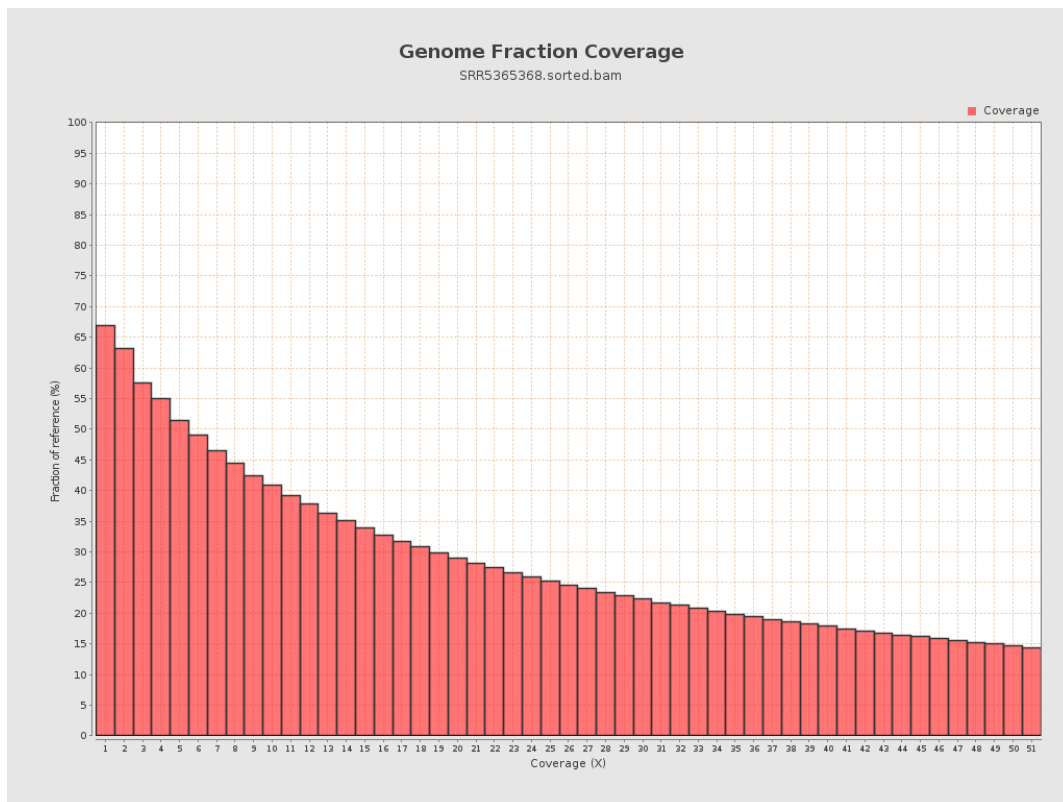
4. Results : Coverage Histogram



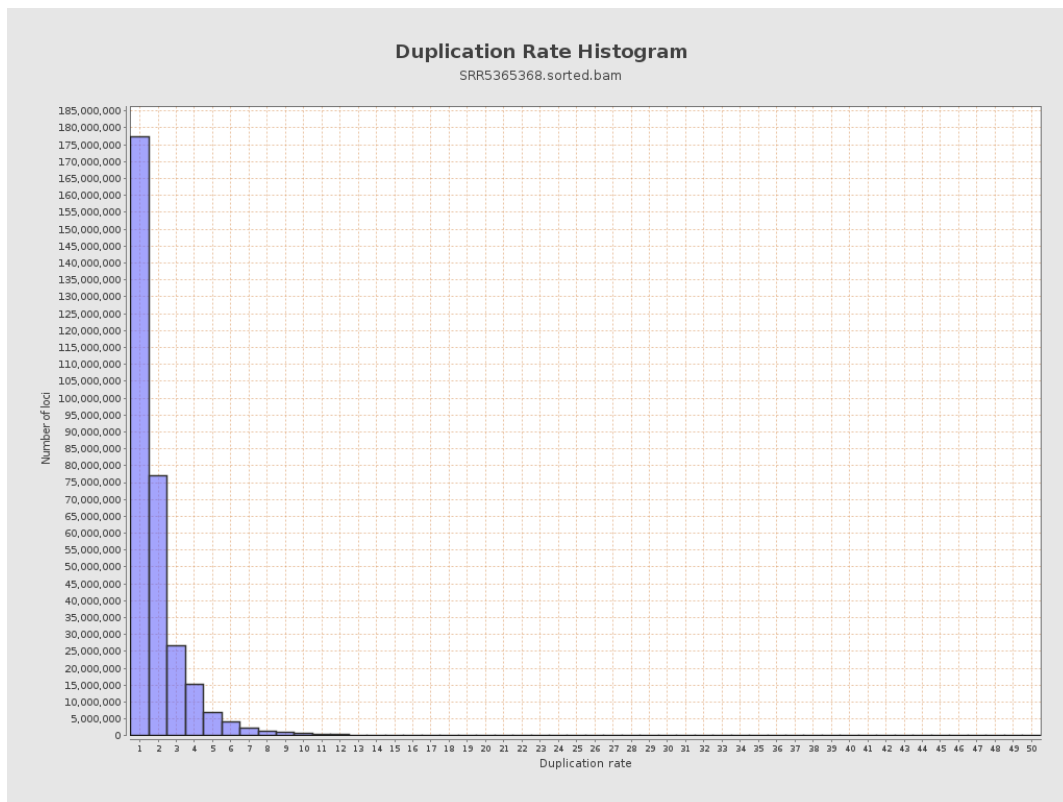
5. Results : Coverage Histogram (0-50X)



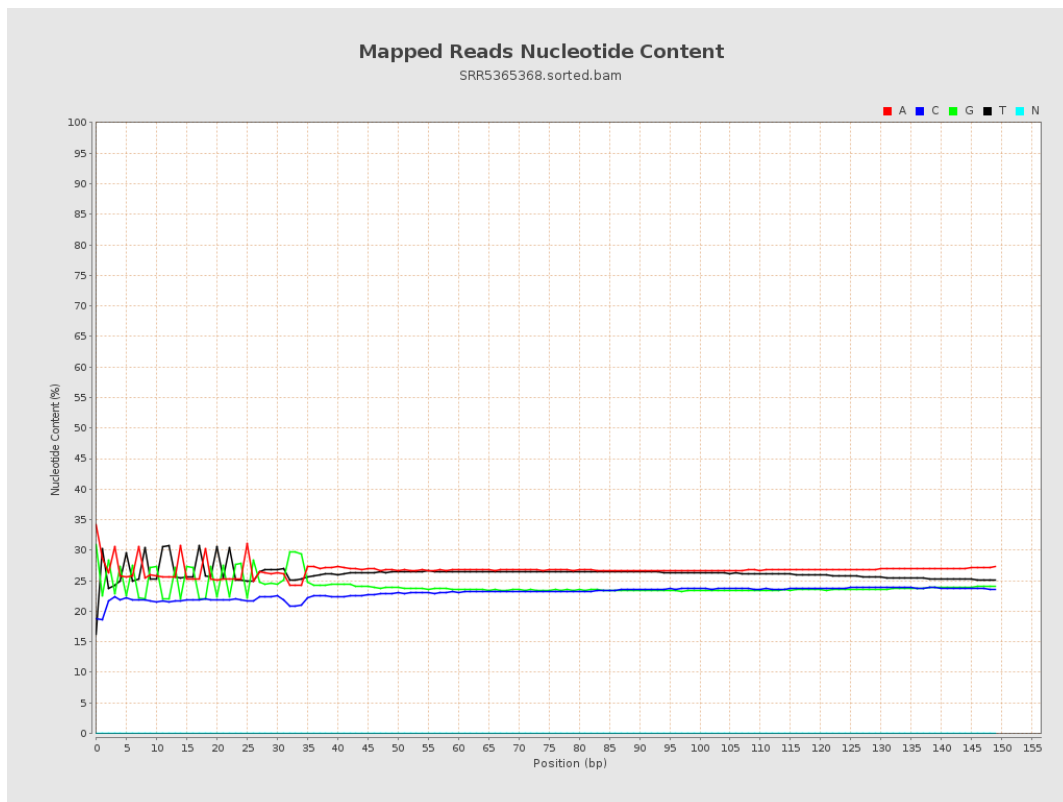
6. Results : Genome Fraction Coverage



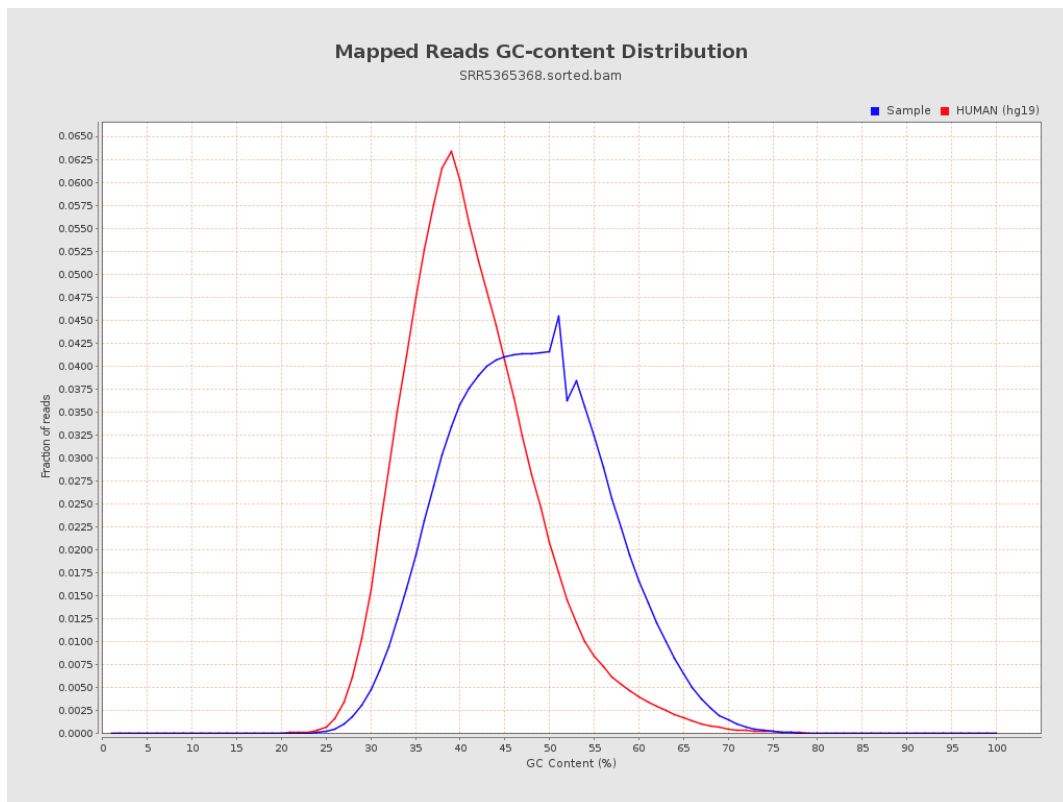
7. Results : Duplication Rate Histogram



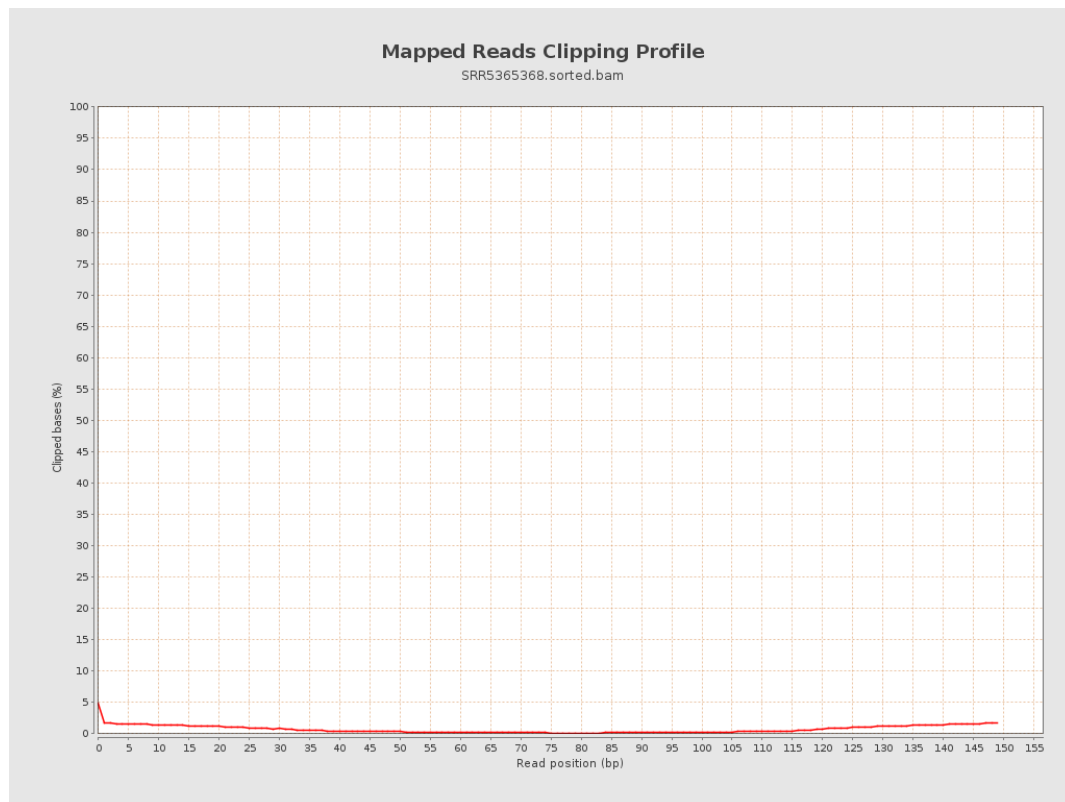
8. Results : Mapped Reads Nucleotide Content



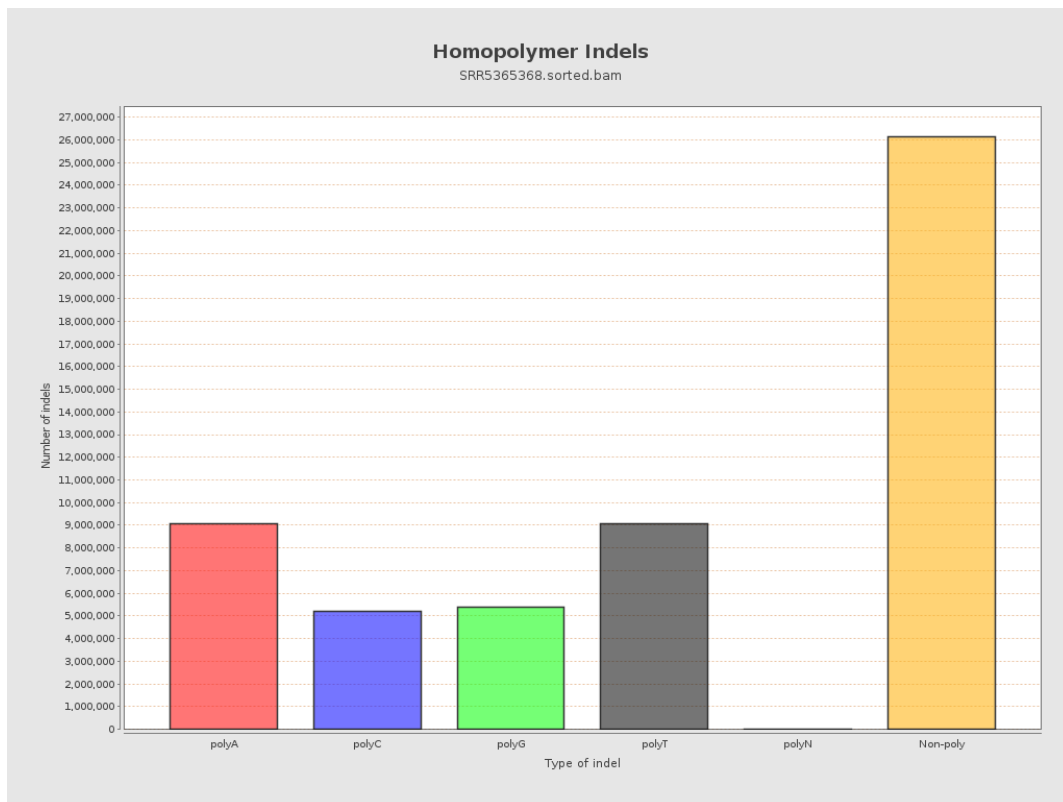
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



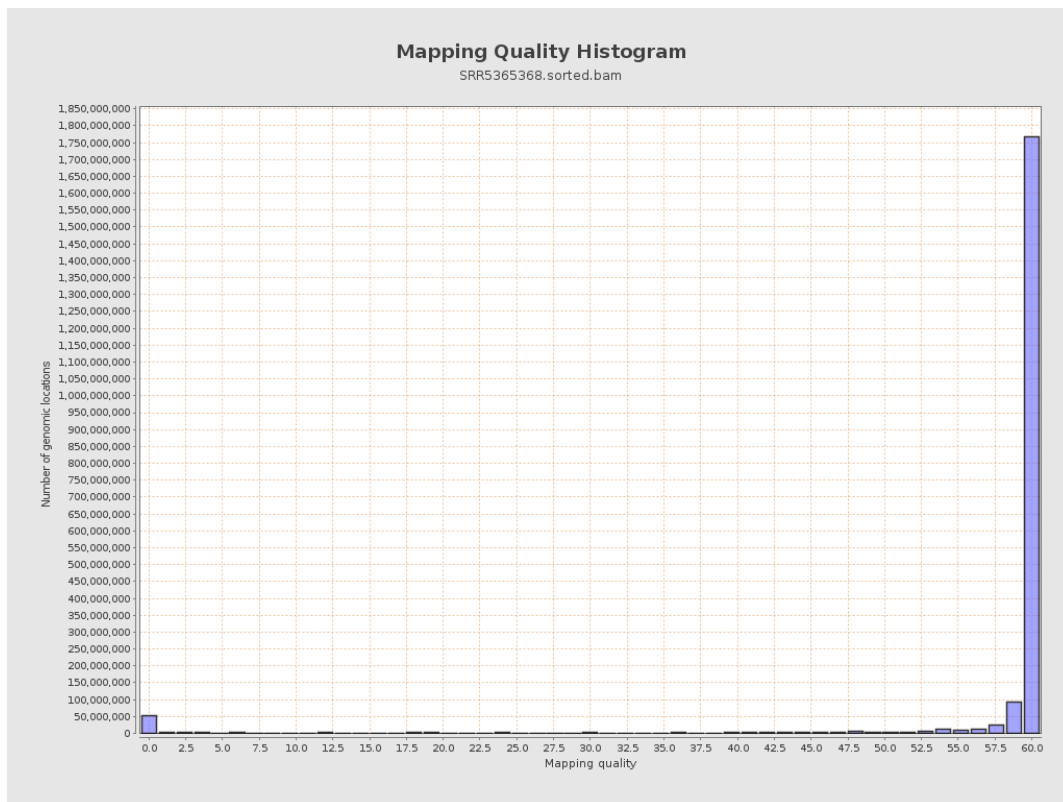
11. Results : Homopolymer Indels



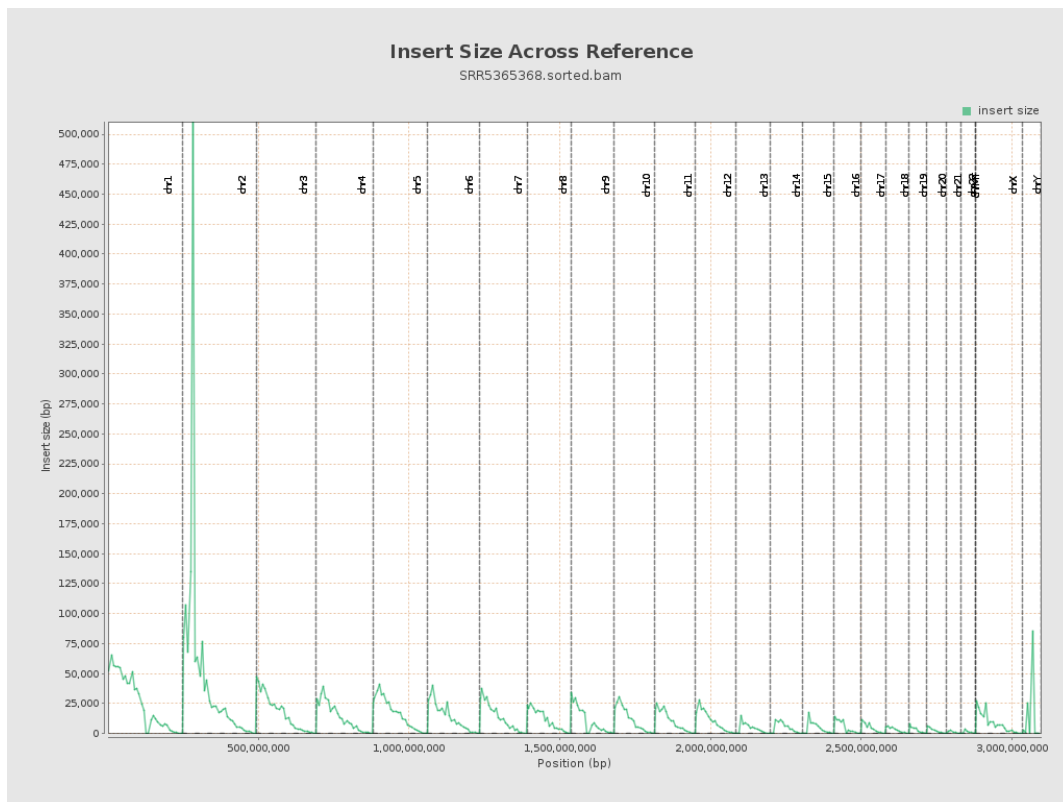
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

