Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/07 00:00:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365347.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_SRR5365347 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365347_1.fastq.gz SRR5365347_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Nov 07 00:00:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365347.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	296,349,006
Mapped reads	291,182,840 / 98.26%
Unmapped reads	5,166,166 / 1.74%
Mapped paired reads	291,182,840 / 98.26%
Mapped reads, first in pair	145,617,959 / 49.14%
Mapped reads, second in pair	145,564,881 / 49.12%
Mapped reads, both in pair	290,249,974 / 97.94%
Mapped reads, singletons	932,866 / 0.31%
Secondary alignments	0
Supplementary alignments	1,226,730 / 0.41%
Read min/max/mean length	30 / 125 / 125.17
Duplicated reads (estimated)	178,272,272 / 60.16%
Duplication rate	39.79%
Clipped reads	200,966,722 / 67.81%

2.2. ACGT Content

Number/percentage of A's	9,291,988,268 / 30.26%
Number/percentage of C's	5,887,414,146 / 19.18%
Number/percentage of T's	9,019,451,670 / 29.38%
Number/percentage of G's	6,503,787,071 / 21.18%
Number/percentage of N's	72,627 / 0%

GC Percentage	40.36%

2.3. Coverage

Mean	9.9212
Standard Deviation	63.036

2.4. Mapping Quality

Mean Mapping Quality	54.01

2.5. Insert size

Mean	83,246.53
Standard Deviation	2,800,632.69
P25/Median/P75	137 / 199 / 297

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	142,640,734
Insertions	9,535,699
Mapped reads with at least one insertion	3.2%
Deletions	4,801,842
Mapped reads with at least one deletion	1.61%
Homopolymer indels	50.57%

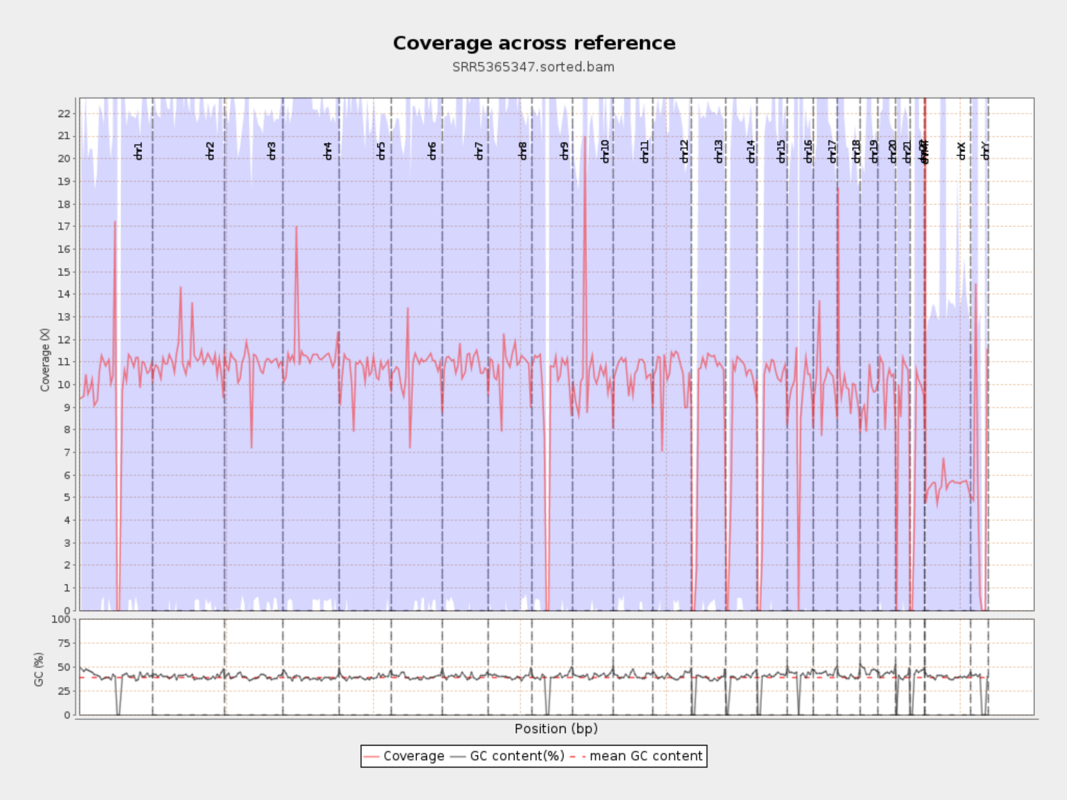
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

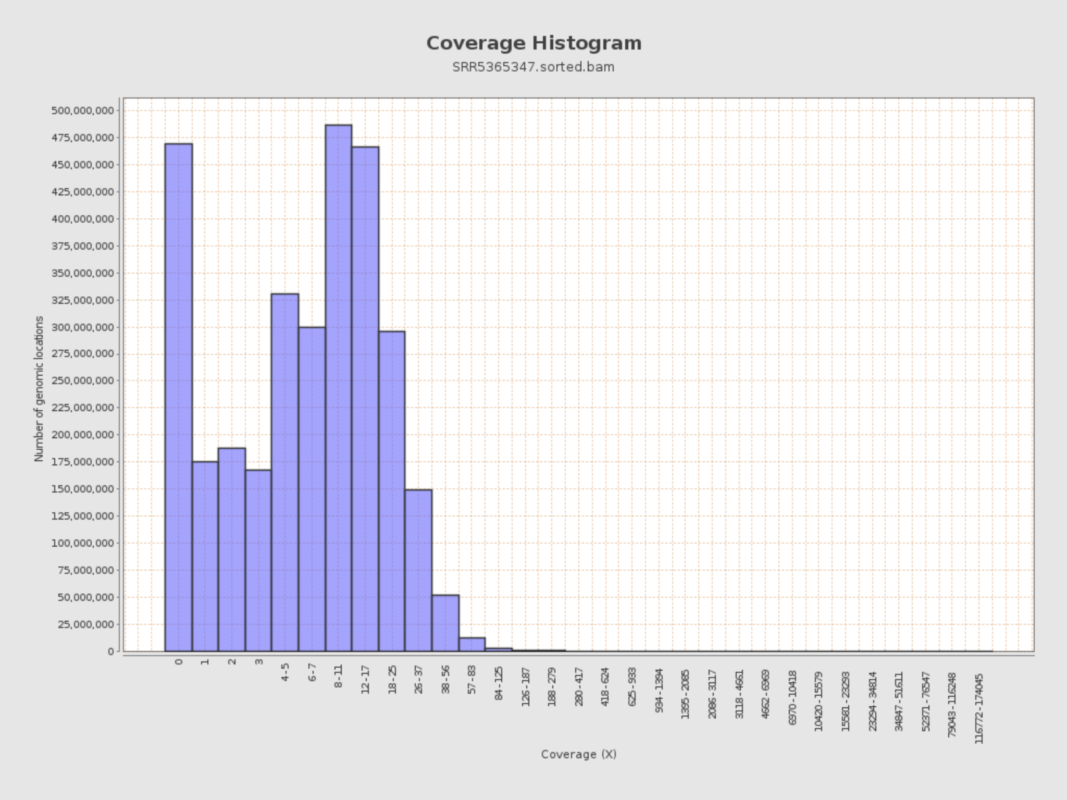
		bases	coverage	deviation
chr1	249250621	2494246169	10.007	161.9712
chr2	243199373	2712345381	11.1528	43.1804
chr3	198022430	2147609649	10.8453	11.7818
chr4	191154276	2179001678	11.3992	56.1896
chr5	180915260	1906505322	10.5381	11.4771
chr6	171115067	1839691213	10.7512	34.2651
chr7	159138663	1733244382	10.8914	57.8066
chr8	146364022	1584078418	10.8229	21.07
chr9	141213431	1316610337	9.3235	45.8813
chr10	135534747	1450440721	10.7016	95.9667
chr11	135006516	1424173993	10.5489	38.0687
chr12	133851895	1397240783	10.4387	18.6087
chr13	115169878	1050398891	9.1204	10.4342
chr14	107349540	956494333	8.9101	11.0007
chr15	102531392	875103569	8.535	12.5209
chr16	90354753	820704500	9.0831	24.1089
chr17	81195210	827711367	10.1941	50.8885
chr18	78077248	792637092	10.152	80.8803
chr19	59128983	555643845	9.3971	77.8269
chr20	63025520	640107390	10.1563	17.7519
chr21	48129895	443414733	9.2129	33.2531
chr22	51304566	356511024	6.9489	26.537
chrMT	16571	32055838	1,934.454	366.3961
chrX	155270560	863123282	5.5588	17.3642

chrY	59373566	313840571	5.2859	106.1236

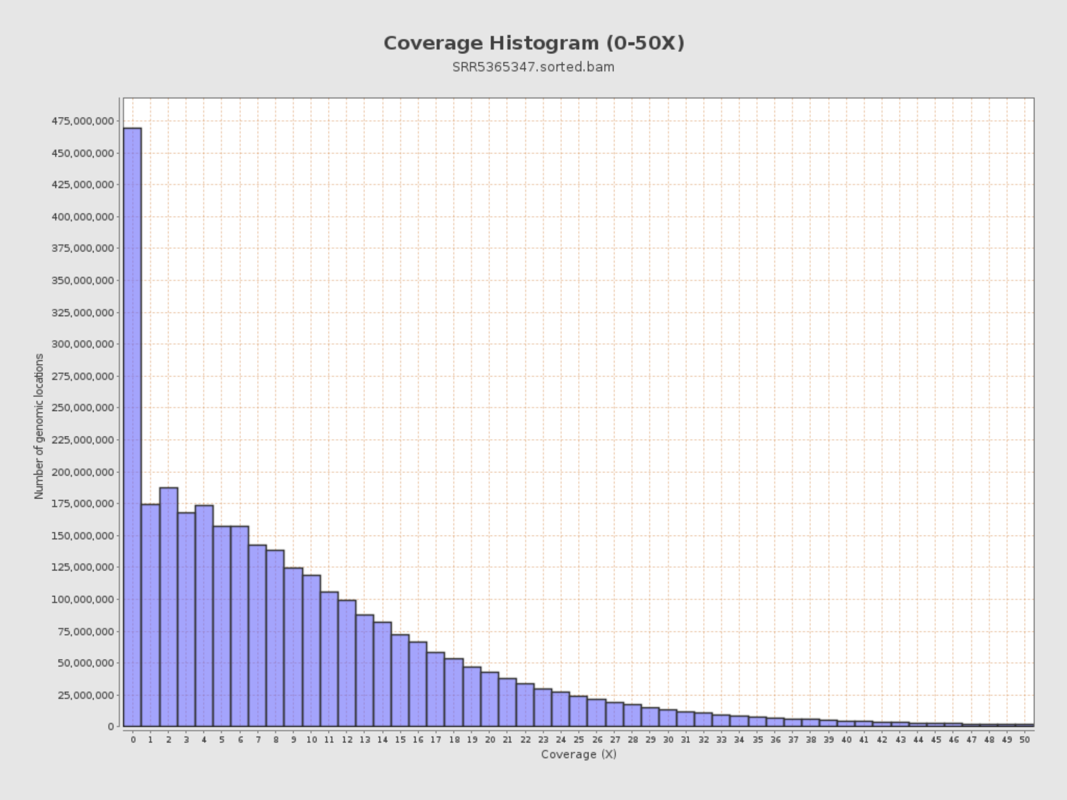
3. Results : Coverage across reference



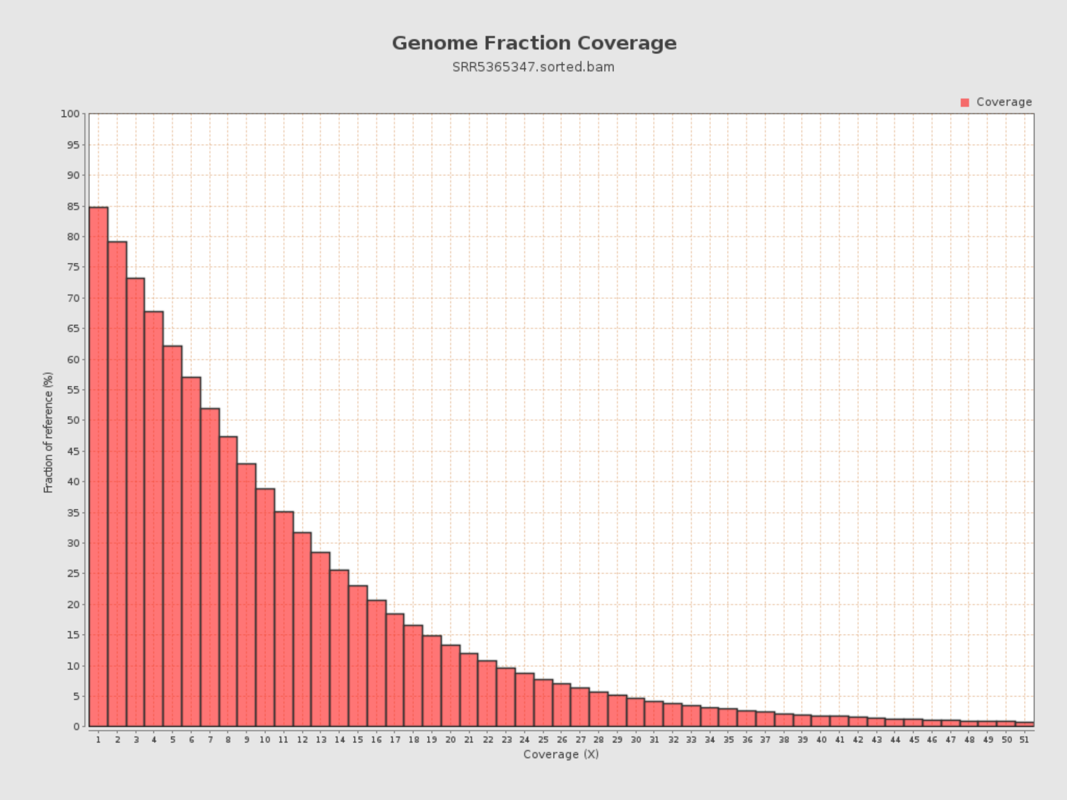
4. Results : Coverage Histogram



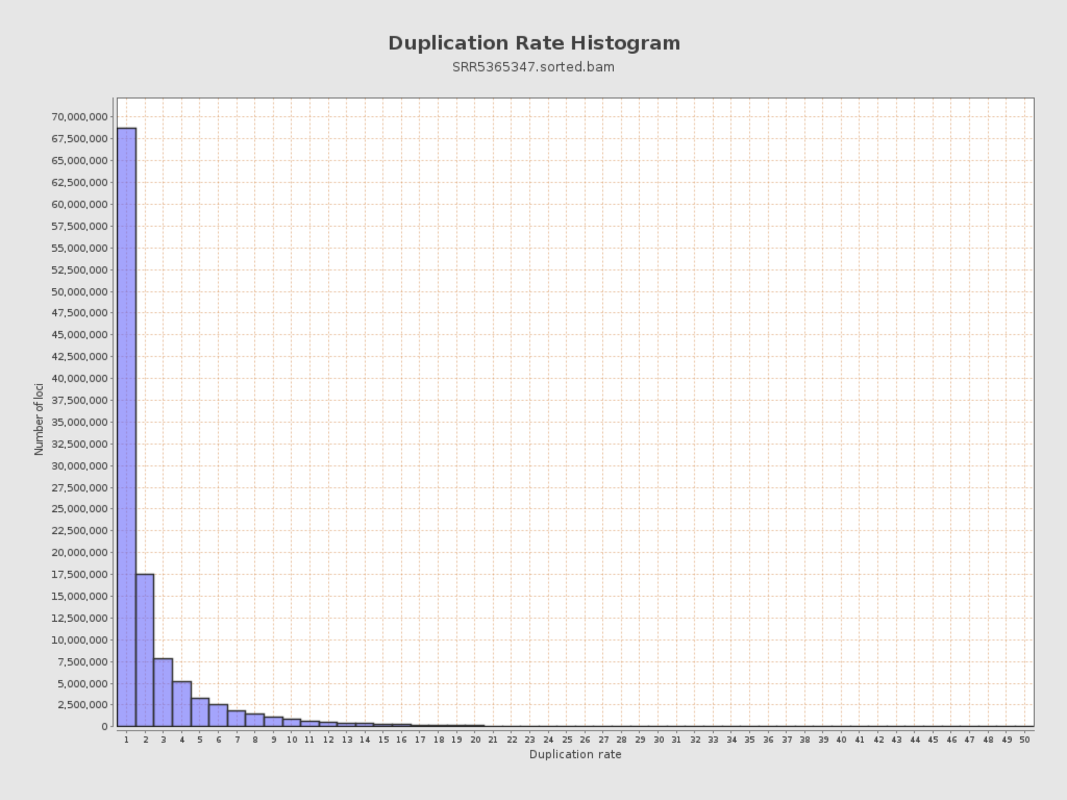
5. Results : Coverage Histogram (0-50X)



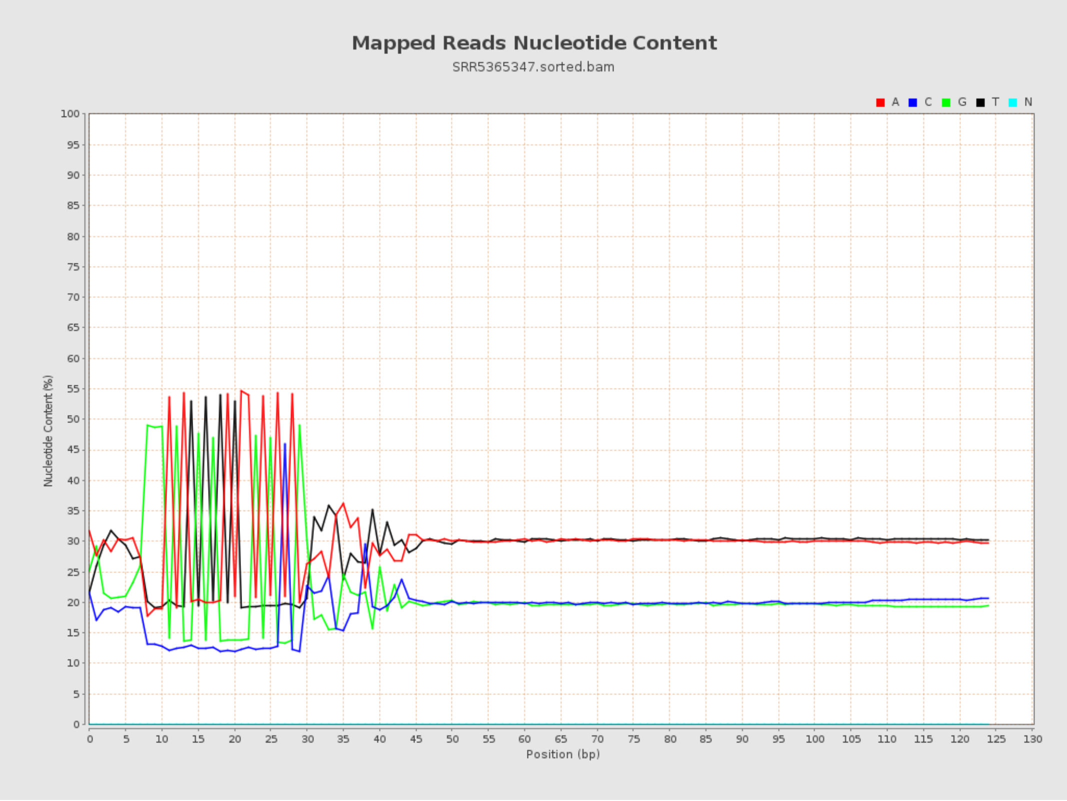
6. Results : Genome Fraction Coverage



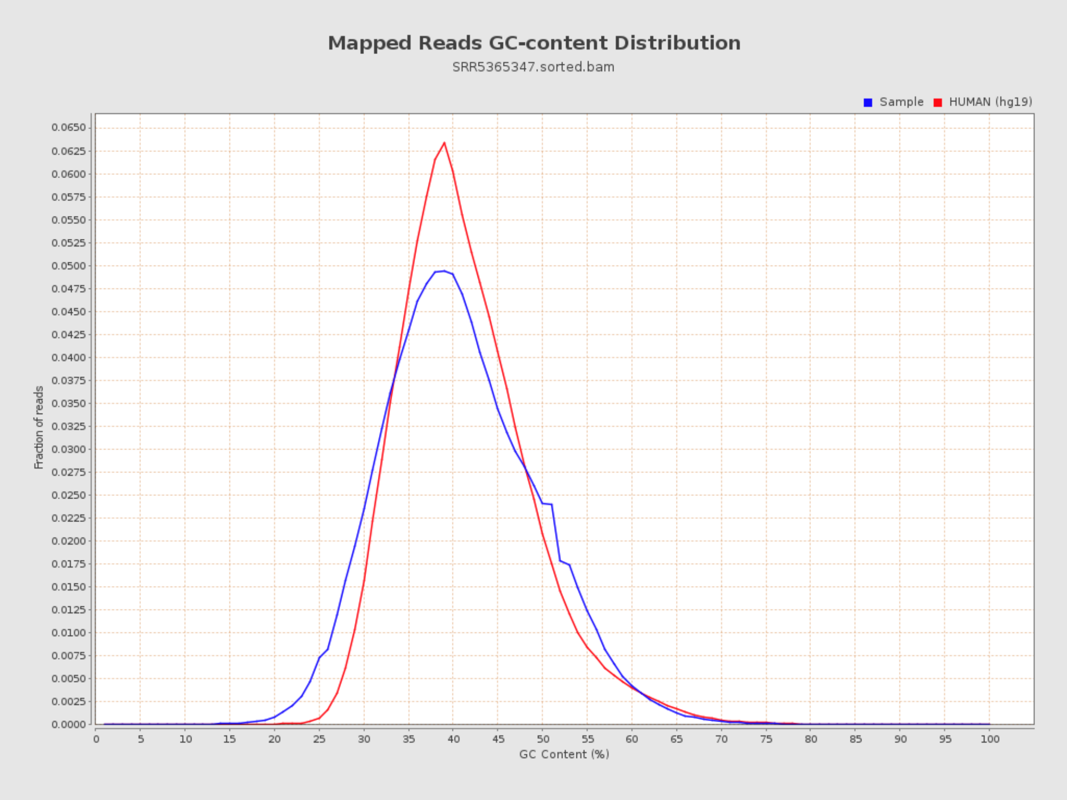
7. Results : Duplication Rate Histogram



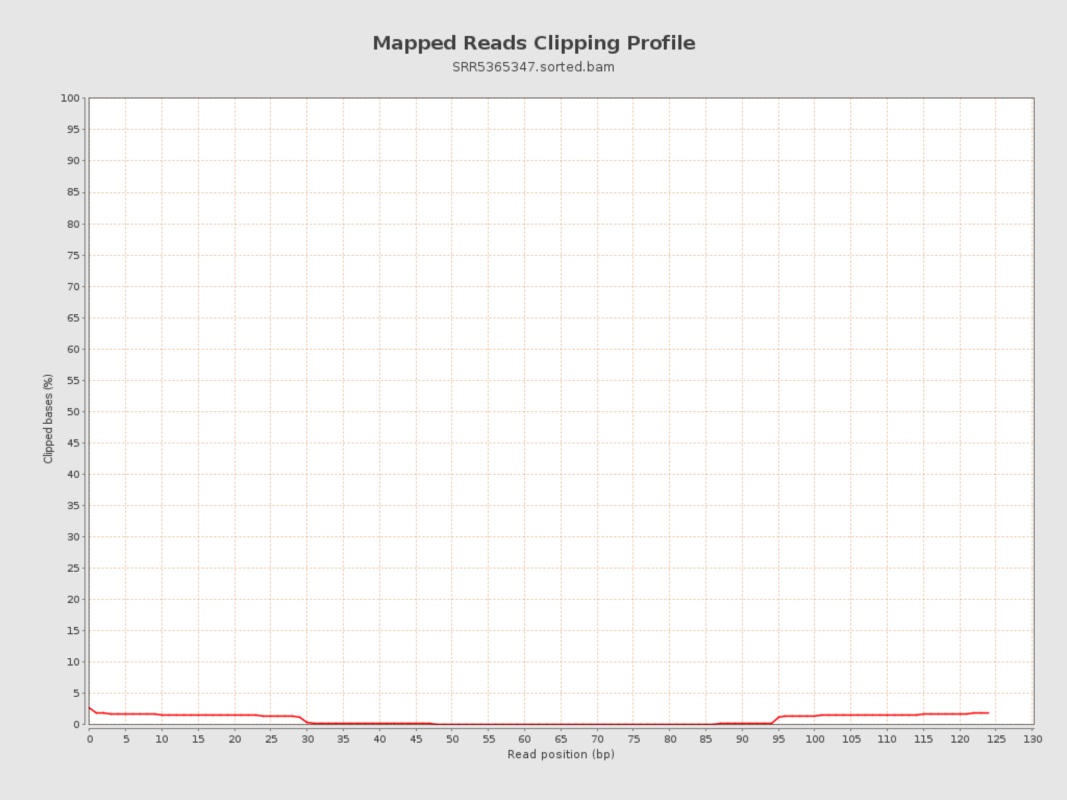
8. Results : Mapped Reads Nucleotide Content



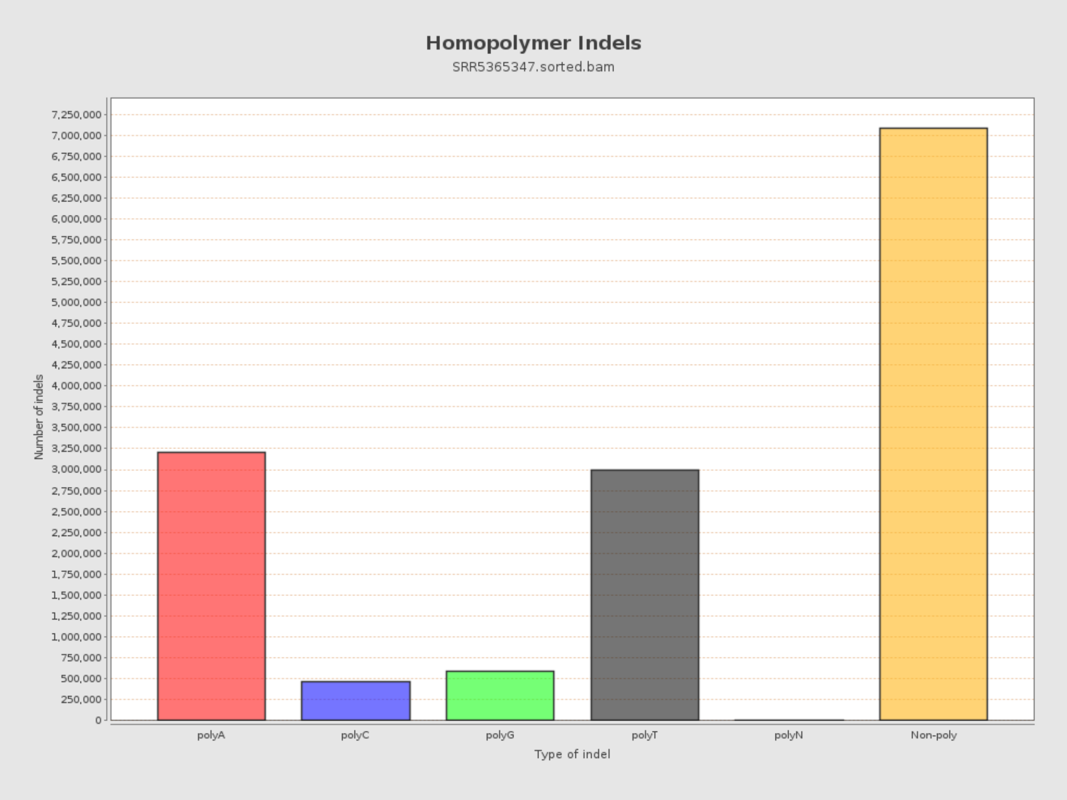
9. Results : Mapped Reads GC-content Distribution



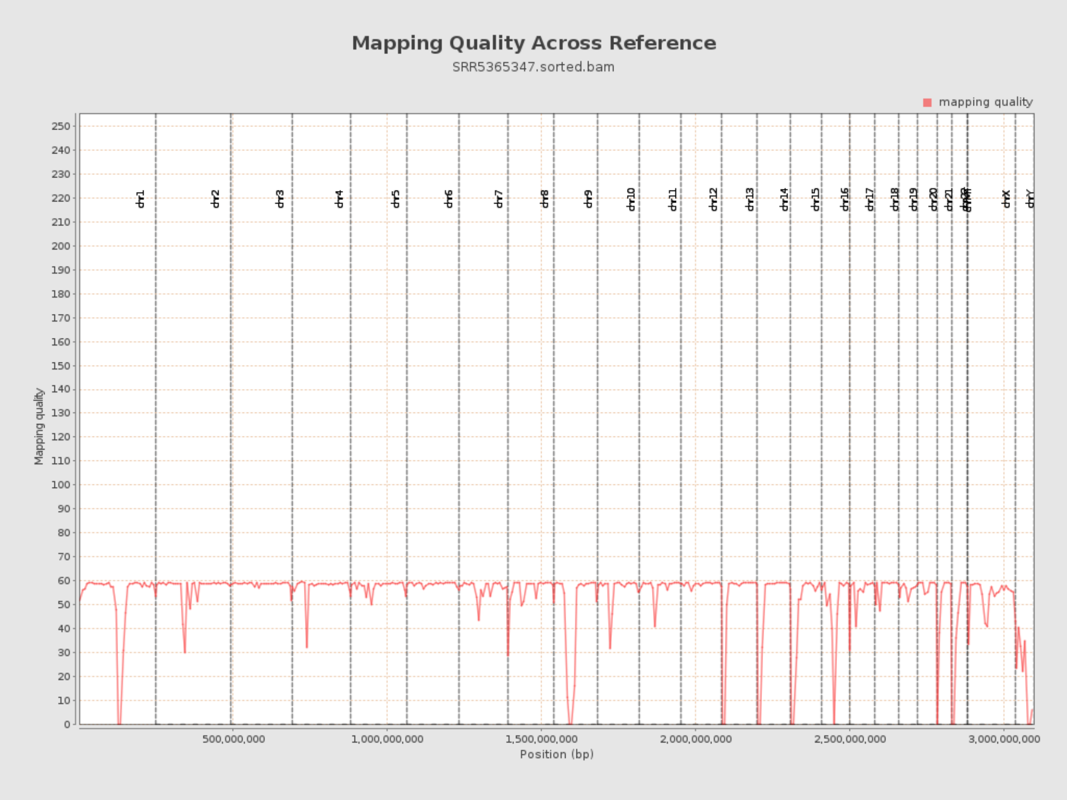
10. Results : Mapped Reads Clipping Profile



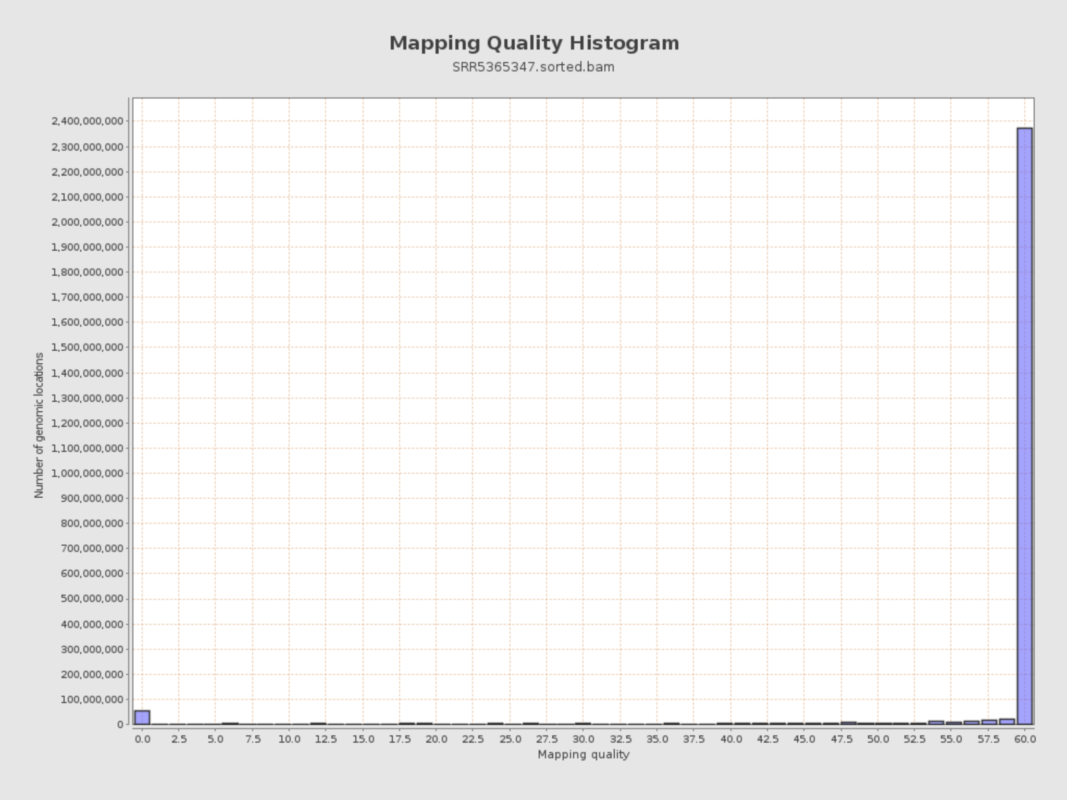
11. Results : Homopolymer Indels



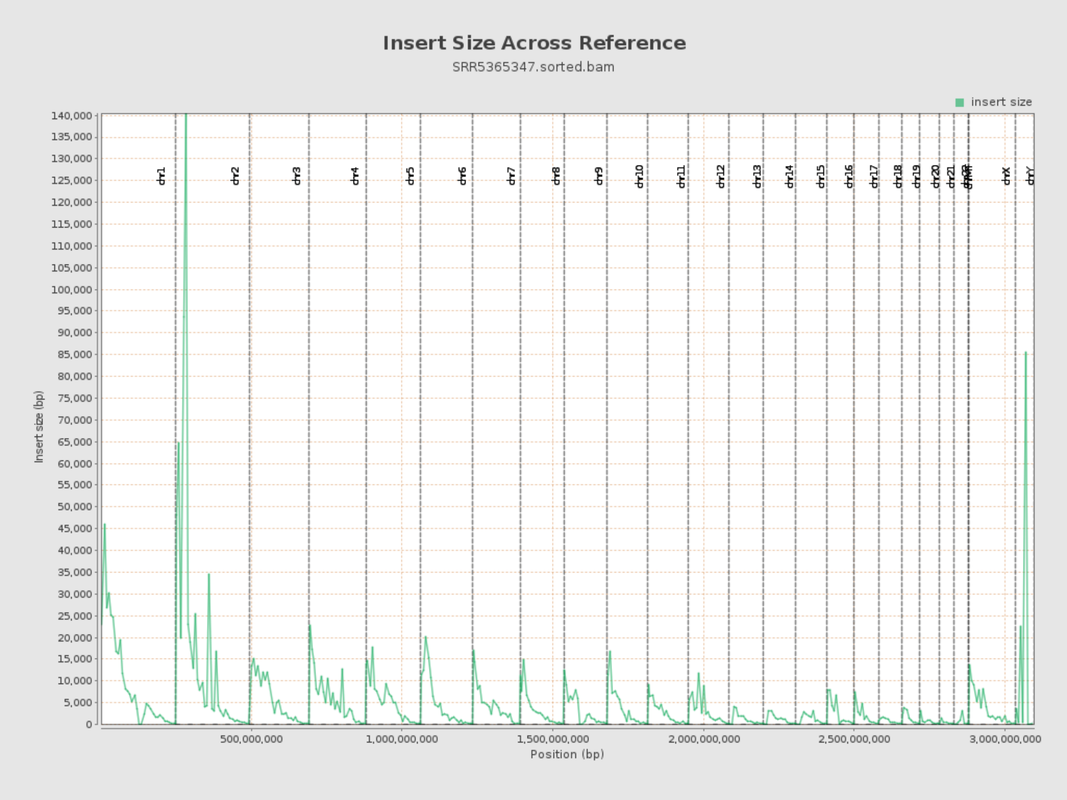
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram