Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/02 06:24:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365334.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_SRR5365334 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365334_1.fastq.gz SRR5365334_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Nov 02 06:24:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365334.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	118,053,232
Mapped reads	115,656,801 / 97.97%
Unmapped reads	2,396,431 / 2.03%
Mapped paired reads	115,656,801 / 97.97%
Mapped reads, first in pair	58,096,097 / 49.21%
Mapped reads, second in pair	57,560,704 / 48.76%
Mapped reads, both in pair	114,951,210 / 97.37%
Mapped reads, singletons	705,591 / 0.6%
Secondary alignments	0
Supplementary alignments	908,761 / 0.77%
Read min/max/mean length	30 / 151 / 151.34
Duplicated reads (estimated)	52,440,620 / 44.42%
Duplication rate	32.78%
Clipped reads	71,294,185 / 60.39%

2.2. ACGT Content

Number/percentage of A's	4,484,168,783 / 29.64%
Number/percentage of C's	3,034,081,154 / 20.06%
Number/percentage of T's	4,421,142,189 / 29.23%
Number/percentage of G's	3,187,421,241 / 21.07%
Number/percentage of N's	888,180 / 0.01%

GC Percentage	41.13%

2.3. Coverage

Mean	4.8885
Standard Deviation	41.277

2.4. Mapping Quality

Mean Mapping Quality	54.29

2.5. Insert size

Mean	80,760.67
Standard Deviation	2,813,922.21
P25/Median/P75	145 / 199 / 272

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	107,551,047
Insertions	4,452,666
Mapped reads with at least one insertion	3.74%
Deletions	2,302,272
Mapped reads with at least one deletion	1.93%
Homopolymer indels	50.51%

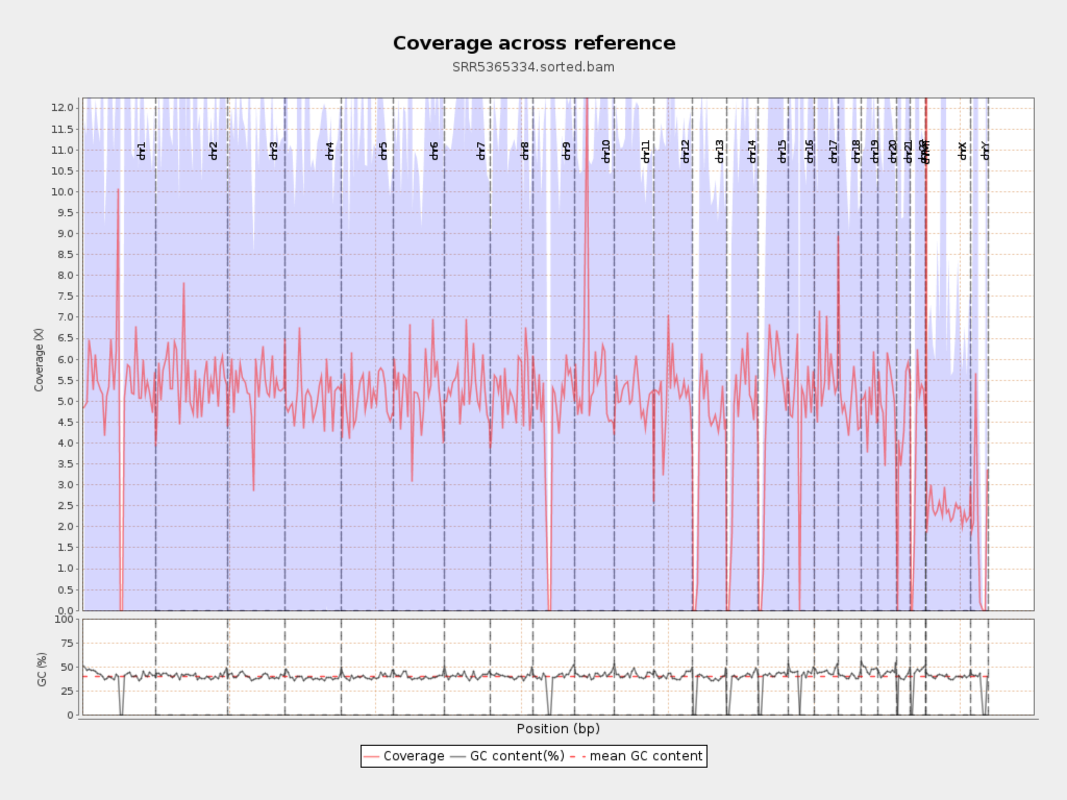
2.7. Chromosome stats

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

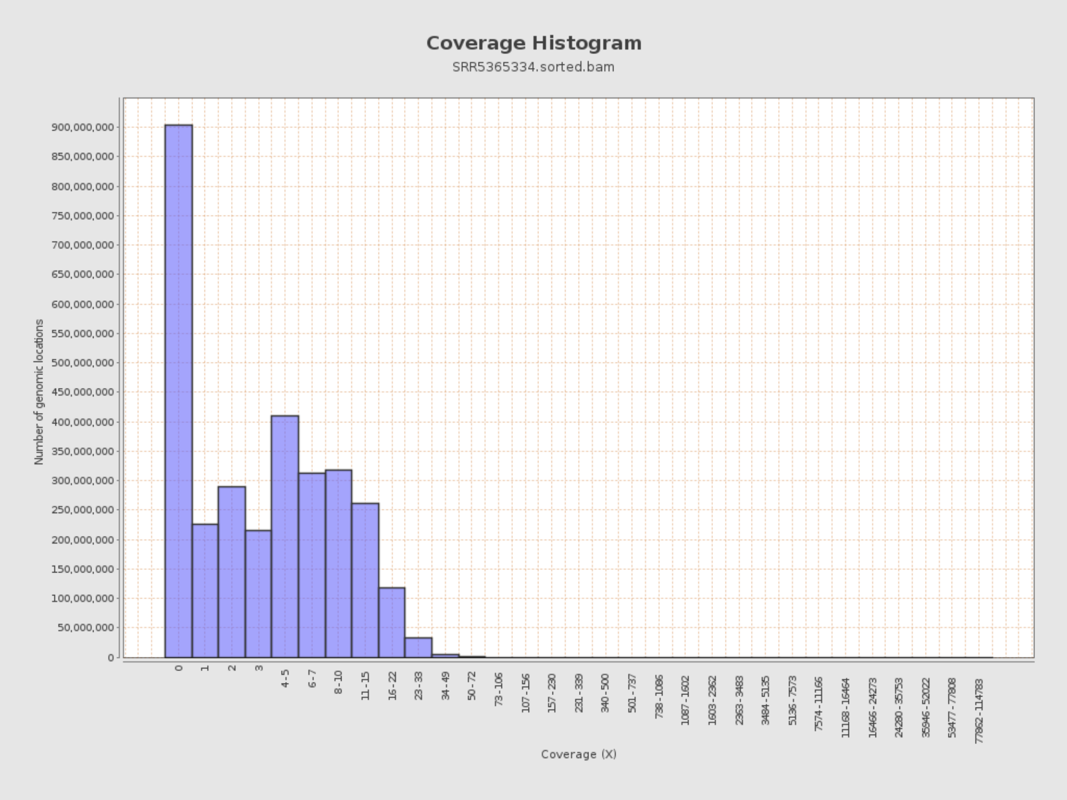
		bases	coverage	deviation
chr1	249250621	1311712526	5.2626	113.5697
chr2	243199373	1346555775	5.5368	25.6577
chr3	198022430	1052917122	5.3172	6.5809
chr4	191154276	975175449	5.1015	21.5562
chr5	180915260	920555331	5.0883	6.5794
chr6	171115067	899420922	5.2562	20.0605
chr7	159138663	844730152	5.3081	23.0249
chr8	146364022	762961937	5.2128	15.1998
chr9	141213431	641687655	4.5441	32.7
chr10	135534747	774461320	5.7141	69.4606
chr11	135006516	691912825	5.125	30.3223
chr12	133851895	704191517	5.261	27.2691
chr13	115169878	471118720	4.0906	5.2499
chr14	107349540	476493889	4.4387	5.7865
chr15	102531392	462835679	4.5141	13.6623
chr16	90354753	434864125	4.8129	14.4222
chr17	81195210	457983152	5.6405	24.5483
chr18	78077248	396142902	5.0737	38.781
chr19	59128983	292612629	4.9487	61.3473
chr20	63025520	319125701	5.0634	9.5656
chr21	48129895	208916617	4.3407	16.5671
chr22	51304566	191411364	3.7309	14.5938
chrMT	16571	8077401	487.442	120.0248
chrX	155270560	372373671	2.3982	10.3439

chrY	59373566	115013053	1.9371	39.4221

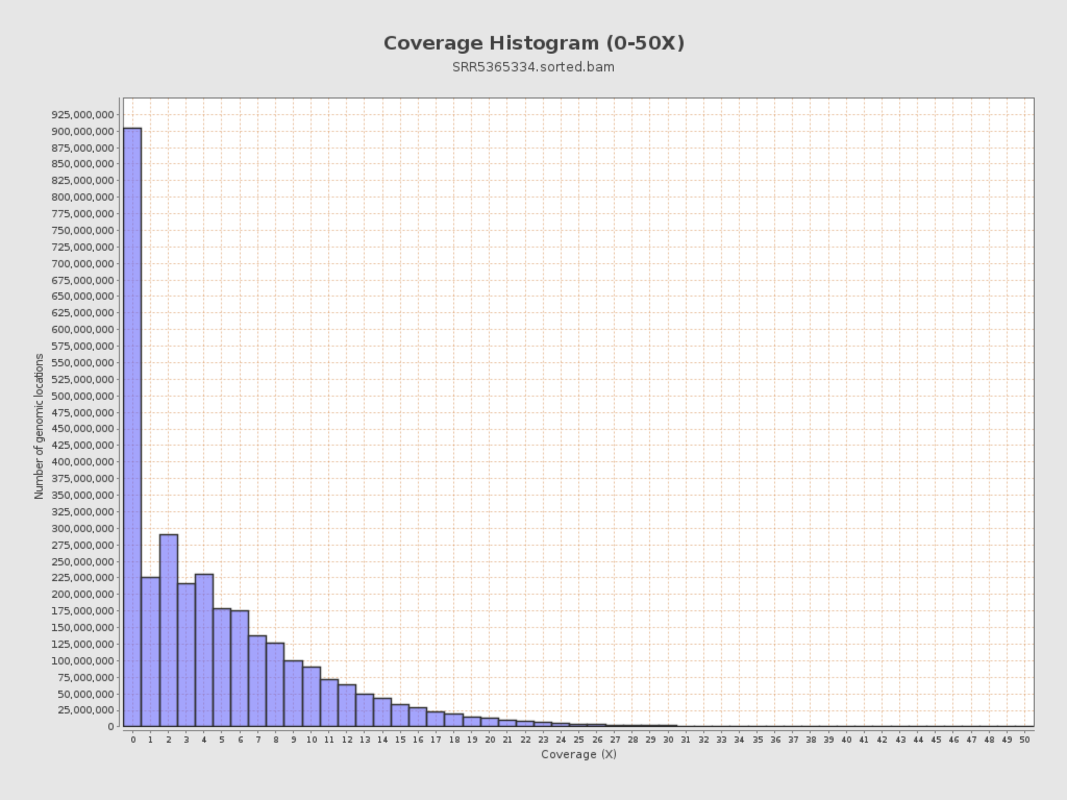
3. Results : Coverage across reference



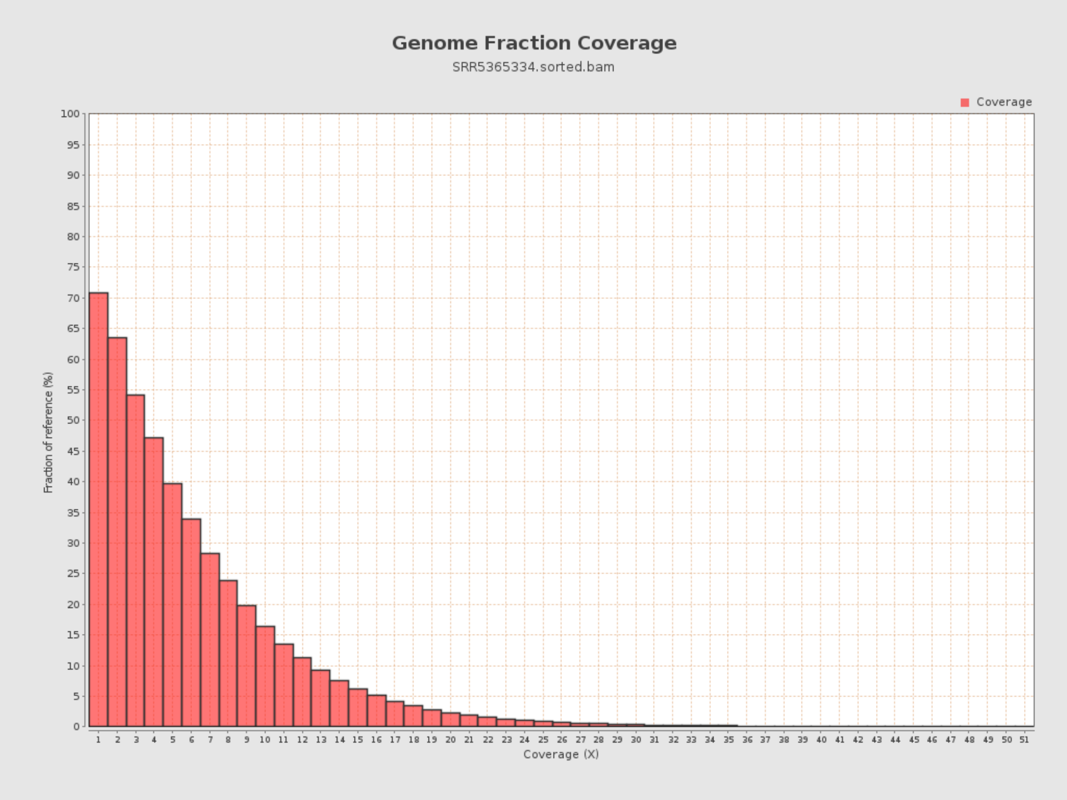
4. Results : Coverage Histogram



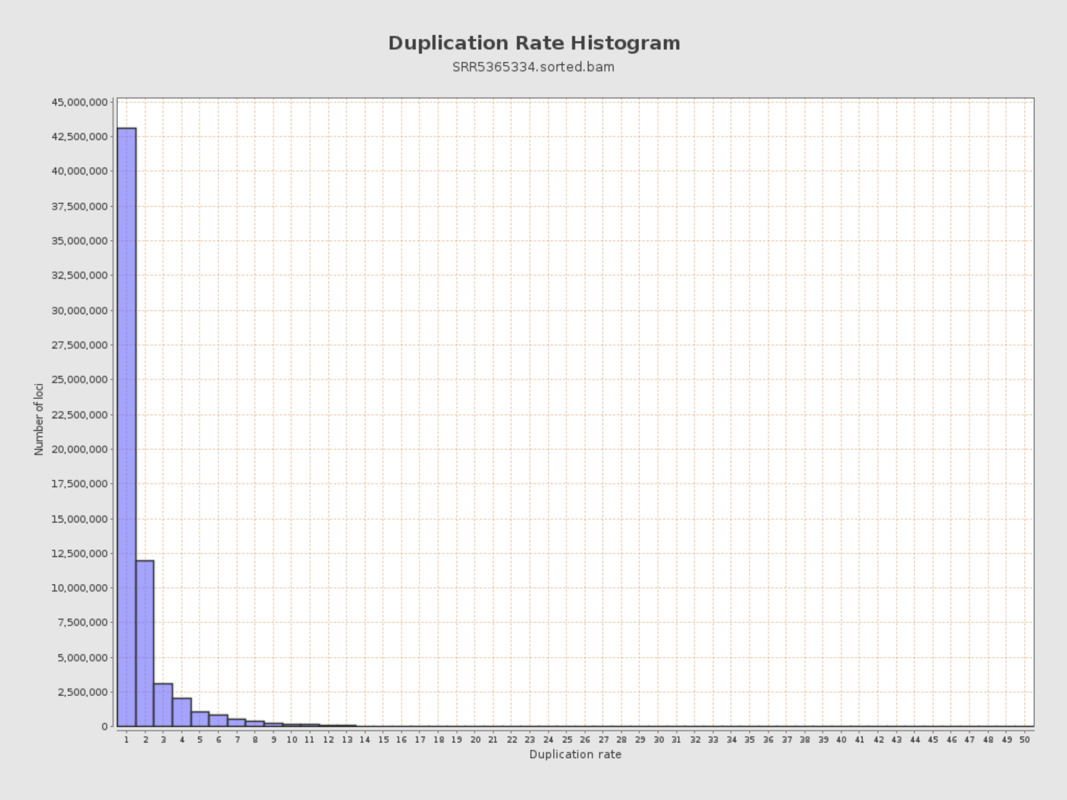
5. Results : Coverage Histogram (0-50X)



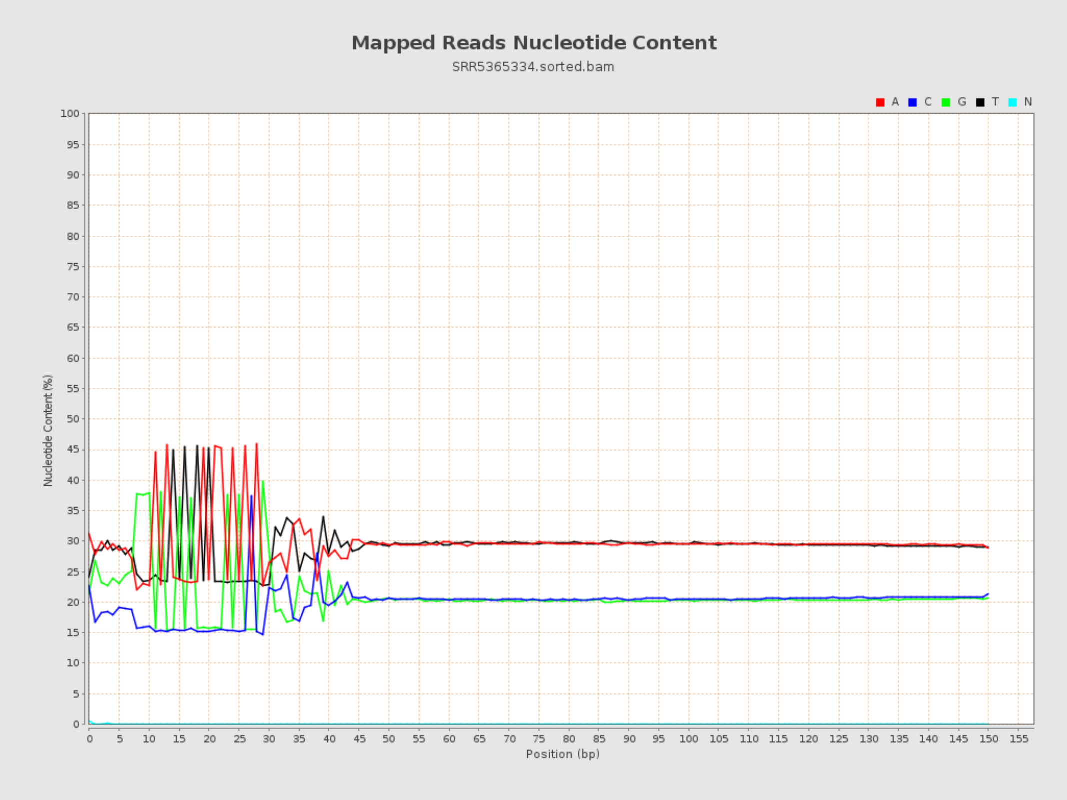
6. Results : Genome Fraction Coverage



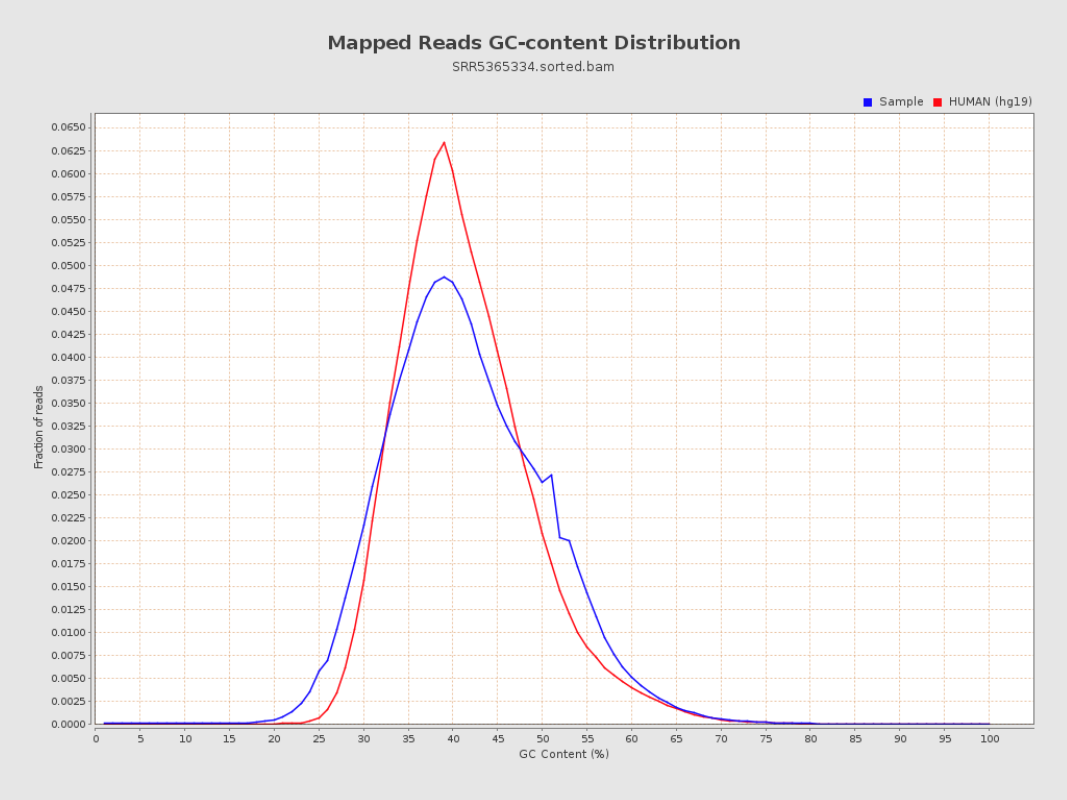
7. Results : Duplication Rate Histogram



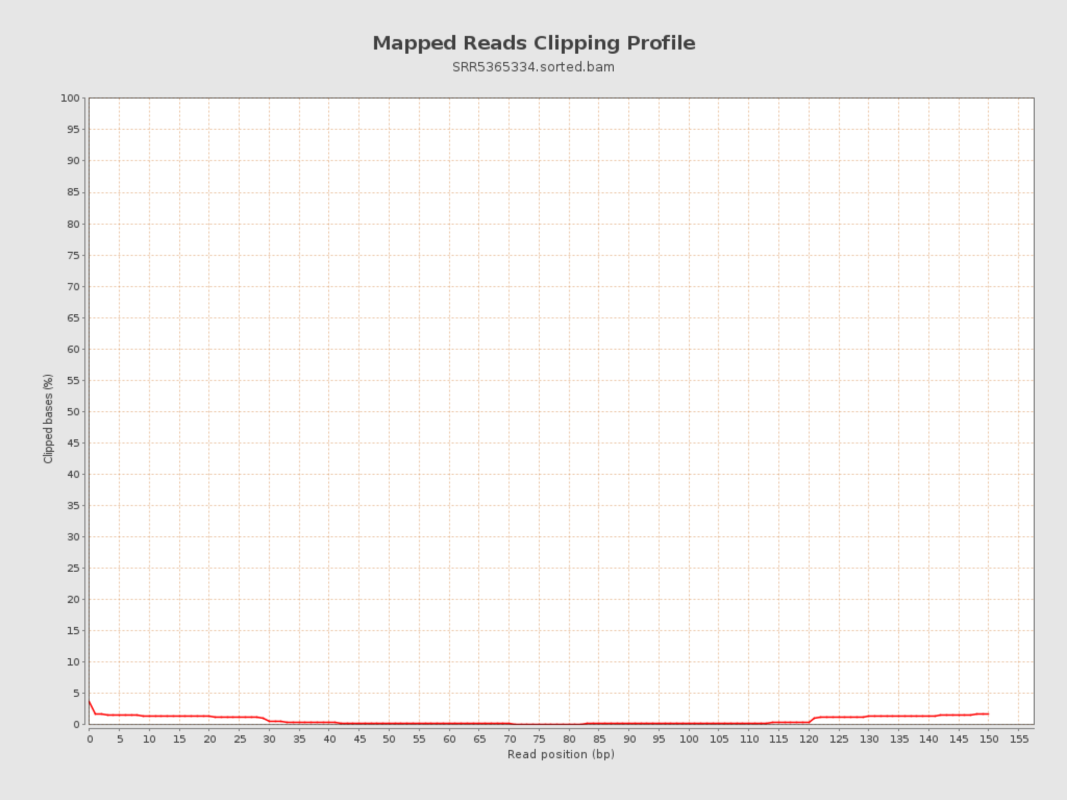
8. Results : Mapped Reads Nucleotide Content



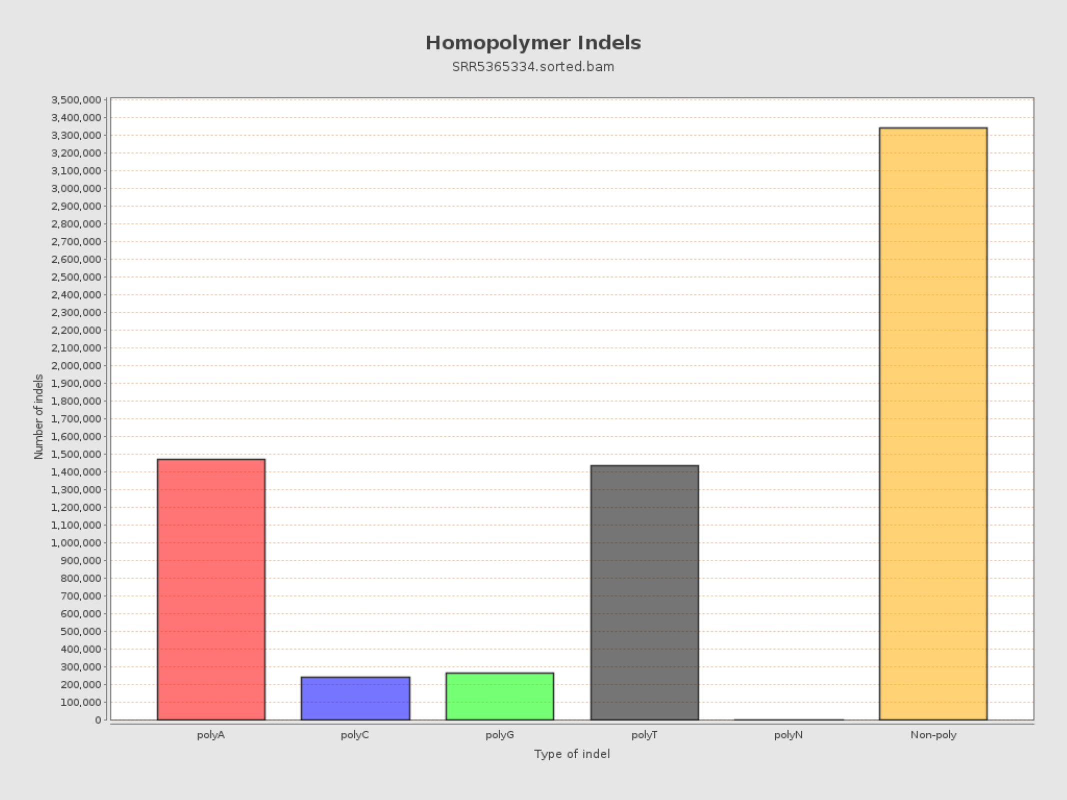
9. Results : Mapped Reads GC-content Distribution



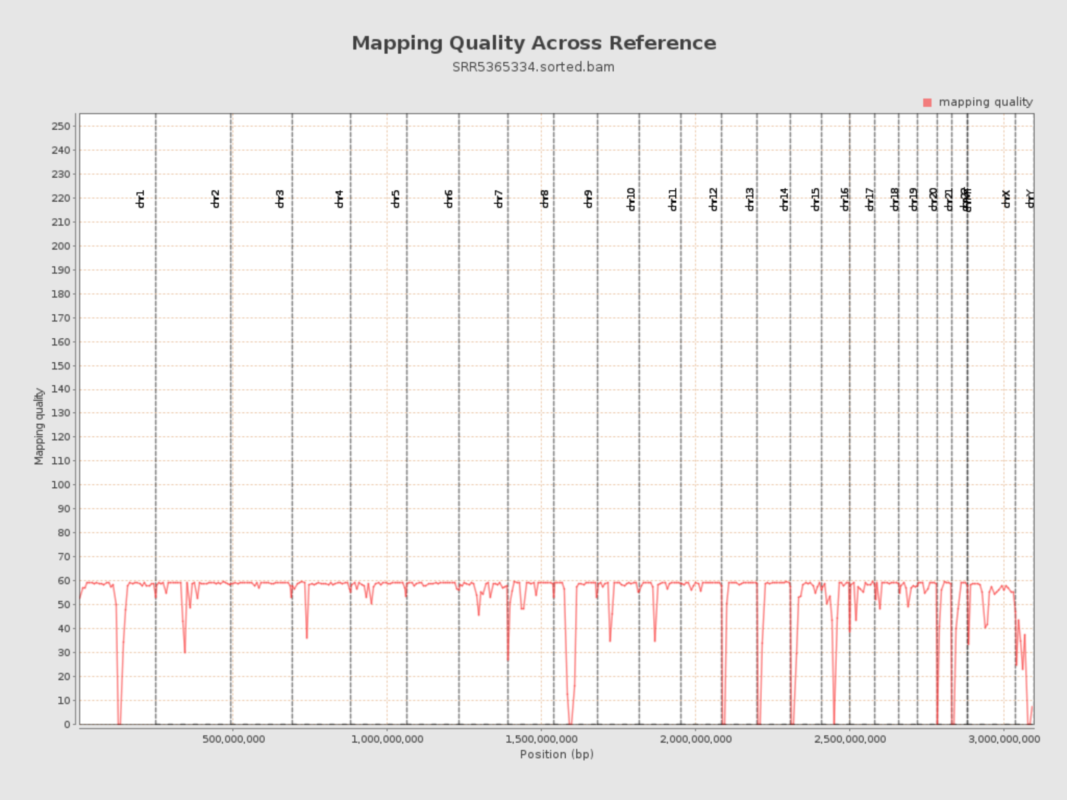
10. Results : Mapped Reads Clipping Profile



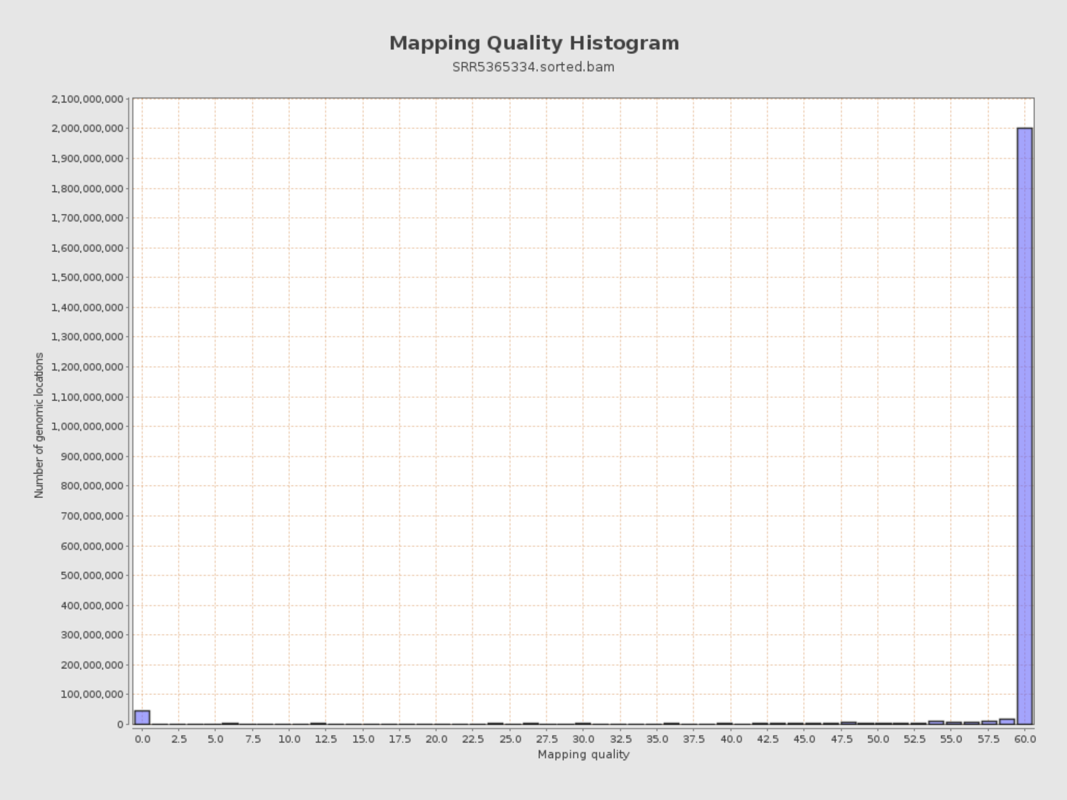
11. Results : Homopolymer Indels



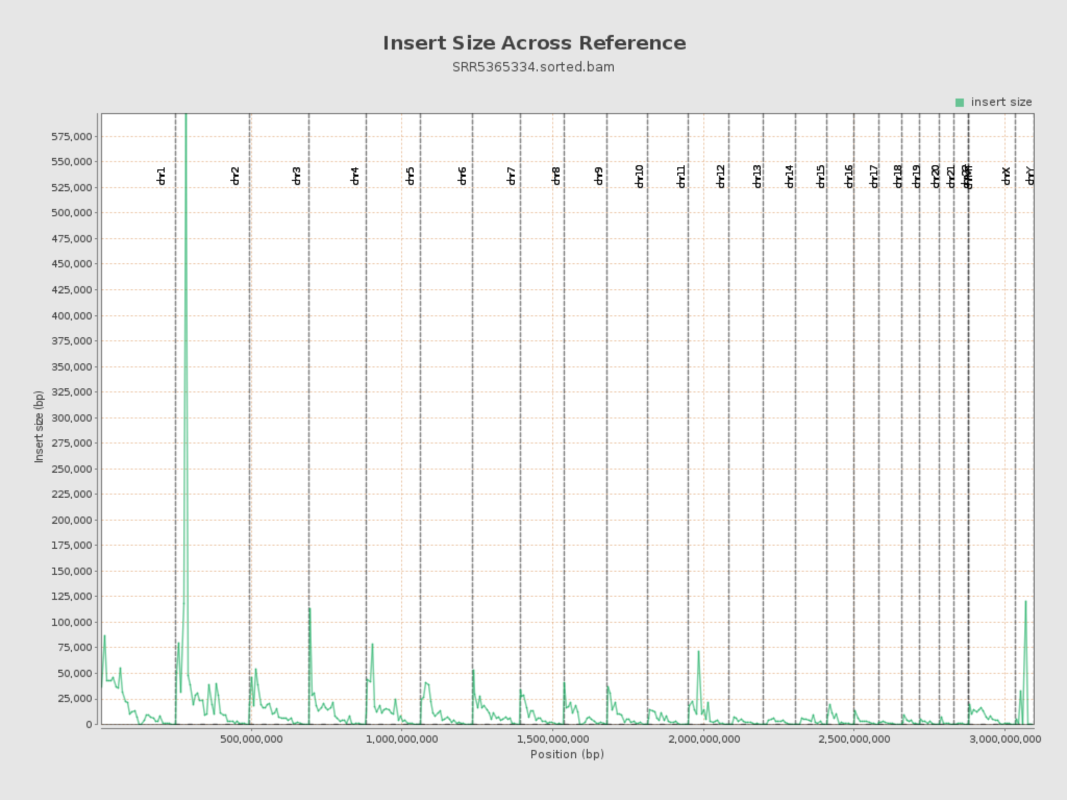
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram