Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/03 00:15:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365341.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_SRR5365341 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365341_1.fastq.gz SRR5365341_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Nov 03 00:15:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365341.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	103,530,222
Mapped reads	100,991,294 / 97.55%
Unmapped reads	2,538,928 / 2.45%
Mapped paired reads	100,991,294 / 97.55%
Mapped reads, first in pair	50,723,193 / 48.99%
Mapped reads, second in pair	50,268,101 / 48.55%
Mapped reads, both in pair	100,381,830 / 96.96%
Mapped reads, singletons	609,464 / 0.59%
Secondary alignments	0
Supplementary alignments	801,143 / 0.77%
Read min/max/mean length	30 / 151 / 151.35
Duplicated reads (estimated)	41,906,652 / 40.48%
Duplication rate	28.14%
Clipped reads	54,849,452 / 52.98%

2.2. ACGT Content

Number/percentage of A's	4,051,911,854 / 30.03%
Number/percentage of C's	2,654,991,968 / 19.68%
Number/percentage of T's	4,009,791,906 / 29.72%
Number/percentage of G's	2,776,972,010 / 20.58%
Number/percentage of N's	497,629 / 0%

GC Percentage	40.25%

2.3. Coverage

Mean	4.3608
Standard Deviation	56.3406

2.4. Mapping Quality

Mean Mapping Quality	54.23

2.5. Insert size

Mean	64,432
Standard Deviation	2,487,796.53
P25/Median/P75	155 / 213 / 292

2.6. Mismatches and indels

General error rate	0.82%
Mismatches	102,119,030
Insertions	4,314,208
Mapped reads with at least one insertion	4.13%
Deletions	2,194,870
Mapped reads with at least one deletion	2.1%
Homopolymer indels	49.96%

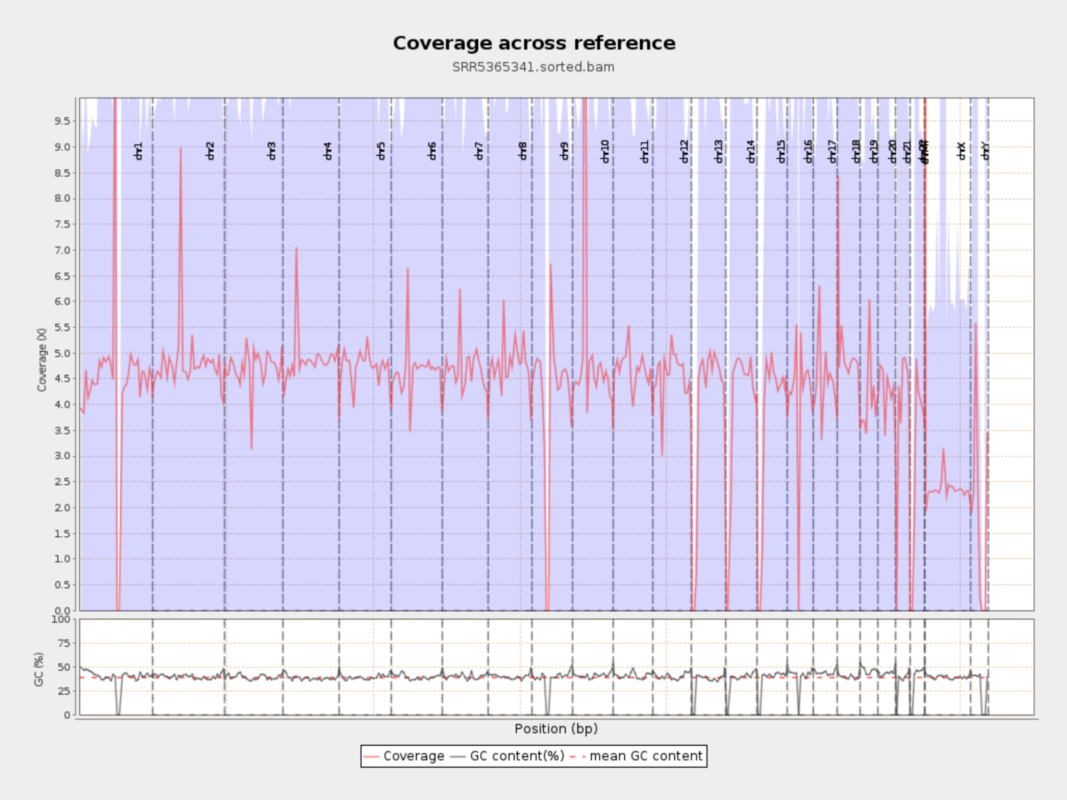
2.7. Chromosome stats

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

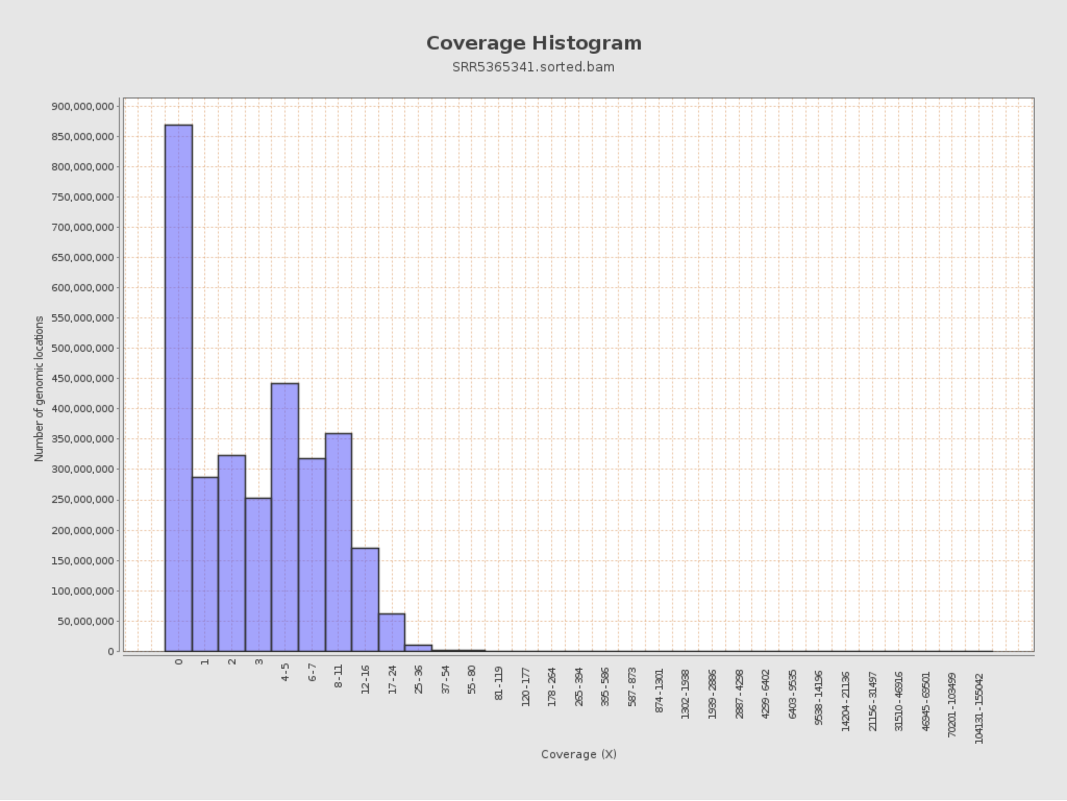
		bases	coverage	deviation
chr1	249250621	1115288103	4.4746	154.7782
chr2	243199373	1180761467	4.8551	31.0386
chr3	198022430	930543134	4.6992	6.396
chr4	191154276	932393037	4.8777	25.1251
chr5	180915260	853444214	4.7174	6.1602
chr6	171115067	801908471	4.6864	22.7813
chr7	159138663	745143851	4.6824	40.3319
chr8	146364022	704154684	4.811	19.5122
chr9	141213431	573298180	4.0598	55.5132
chr10	135534747	707407055	5.2194	107.3981
chr11	135006516	630360961	4.6691	33.9848
chr12	133851895	610641376	4.5621	23.116
chr13	115169878	449524113	3.9031	4.7161
chr14	107349540	416031017	3.8755	5.2846
chr15	102531392	370776526	3.6162	11.0558
chr16	90354753	374817042	4.1483	16.8276
chr17	81195210	361018467	4.4463	28.3185
chr18	78077248	389062636	4.983	54.5865
chr19	59128983	242440248	4.1002	78.1605
chr20	63025520	268180229	4.2551	9.9108
chr21	48129895	192609354	4.0019	18.856
chr22	51304566	150597446	2.9354	16.3141
chrMT	16571	15087270	910.4623	221.6093
chrX	155270560	366377260	2.3596	11.2542

chrY	59373566	117691830	1.9822	36.9115

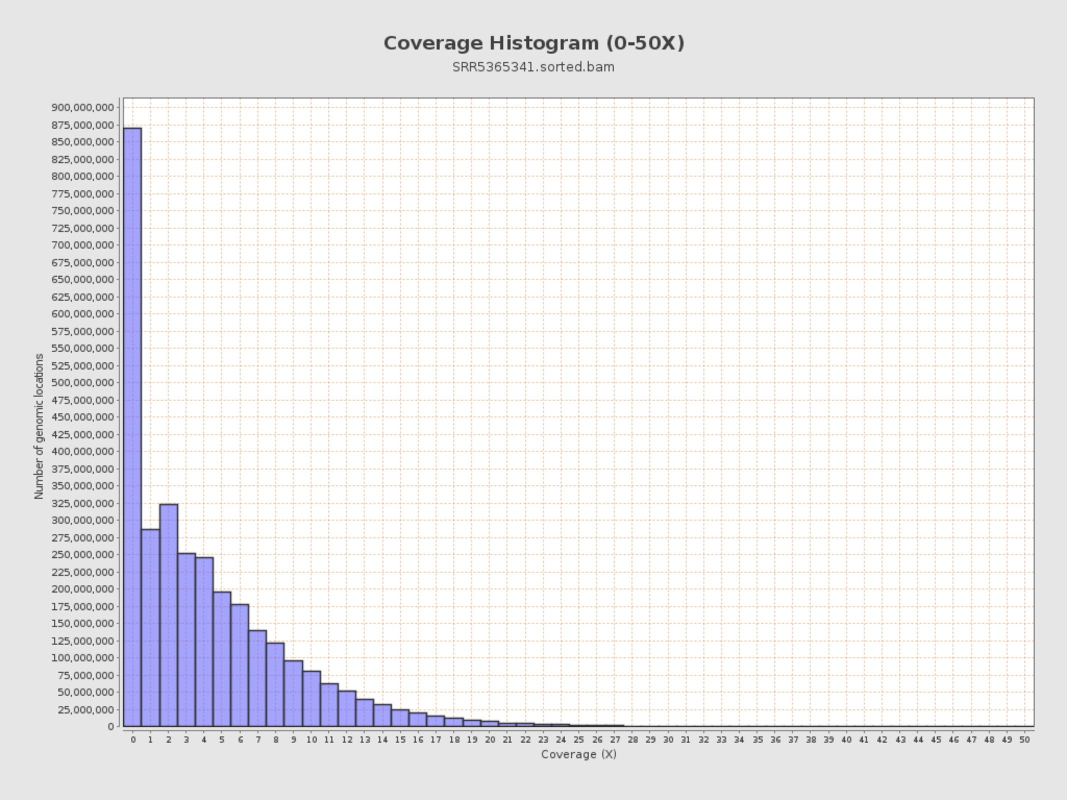
3. Results : Coverage across reference



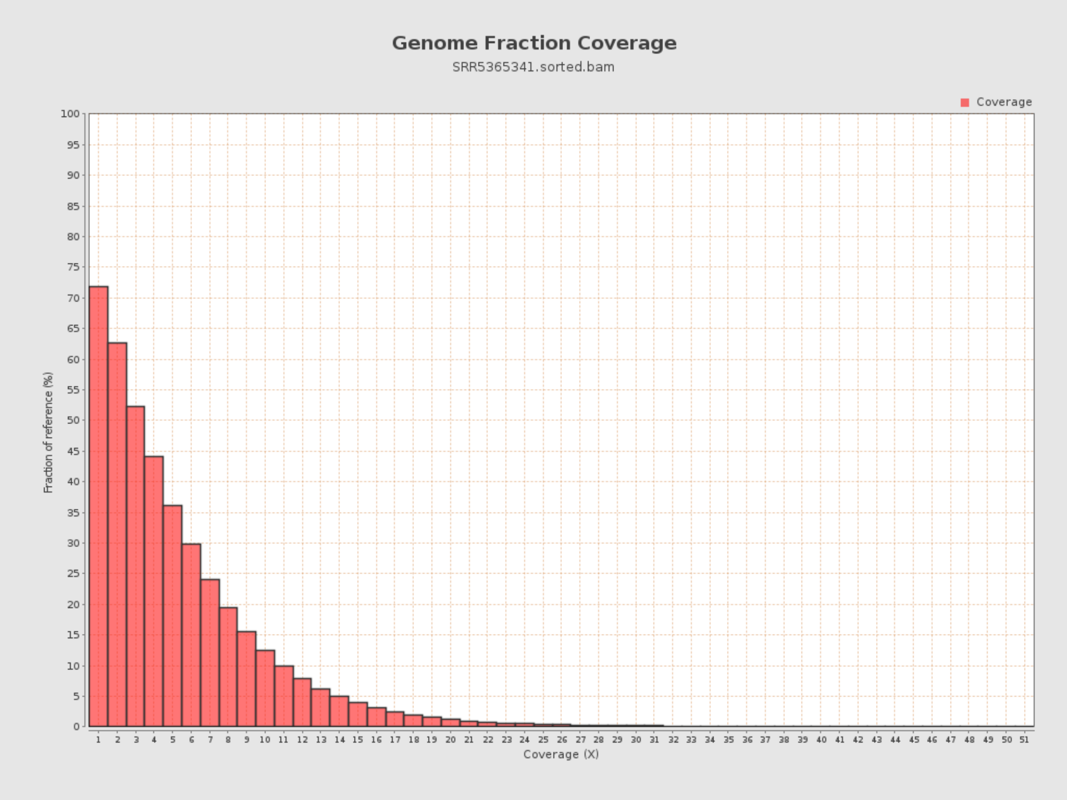
4. Results : Coverage Histogram



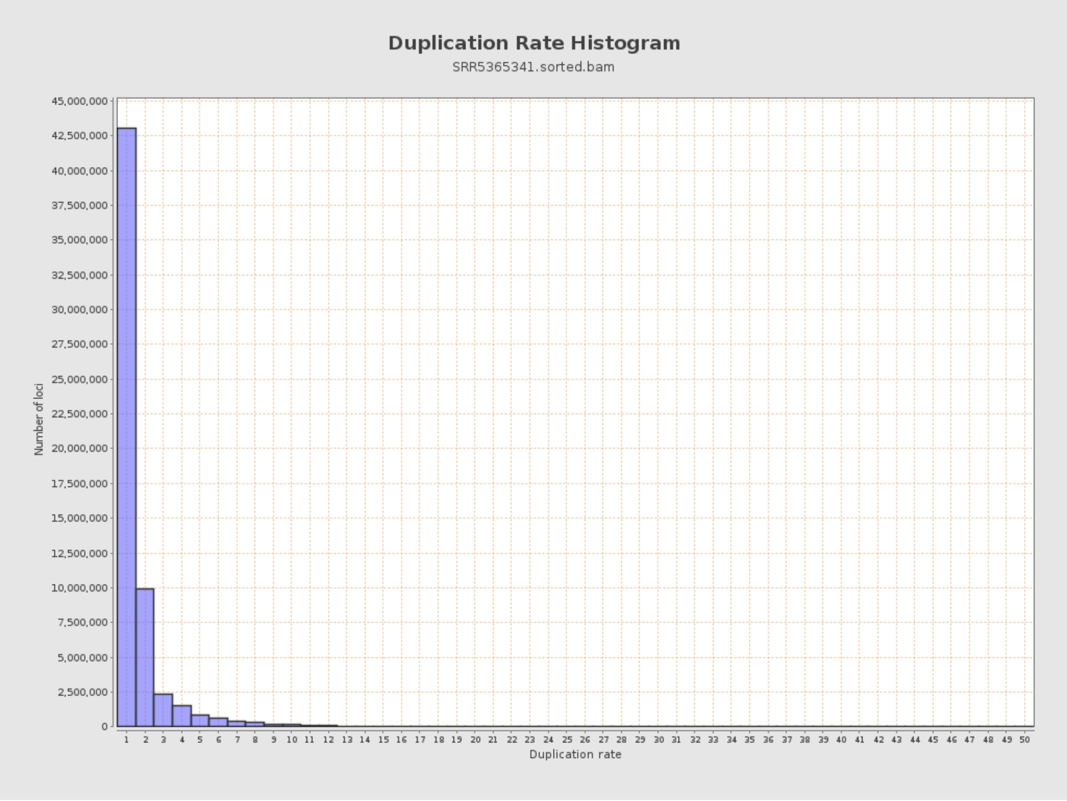
5. Results : Coverage Histogram (0-50X)



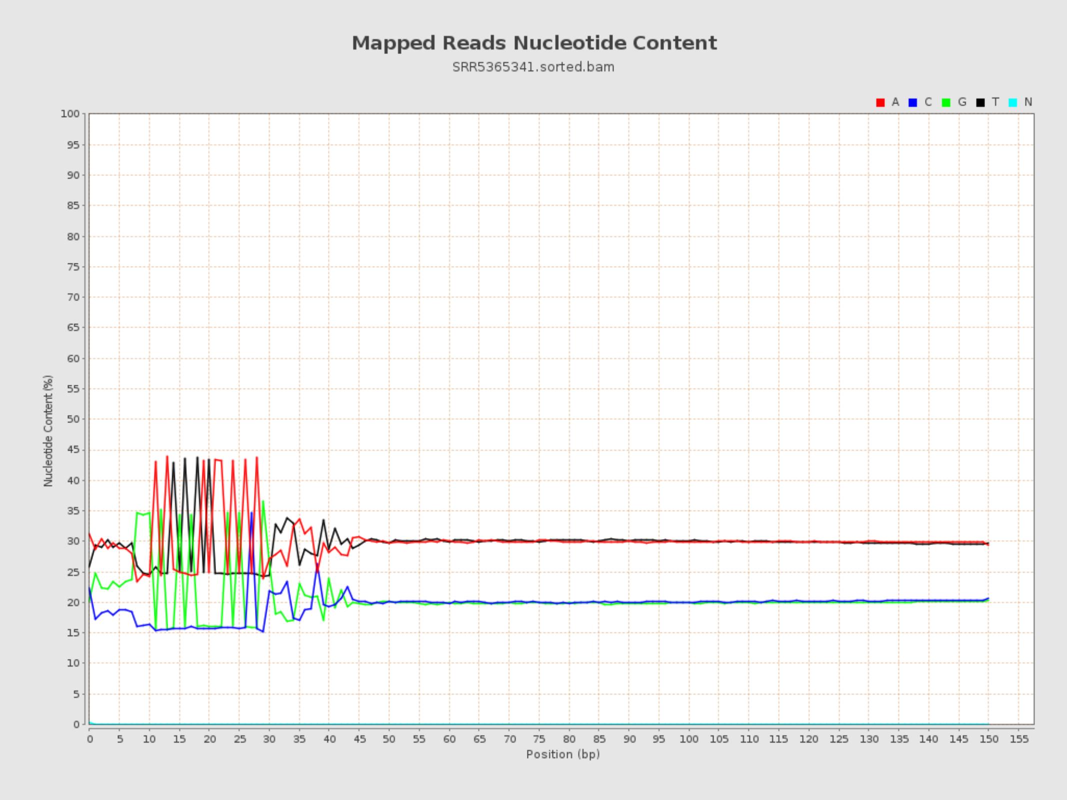
6. Results : Genome Fraction Coverage



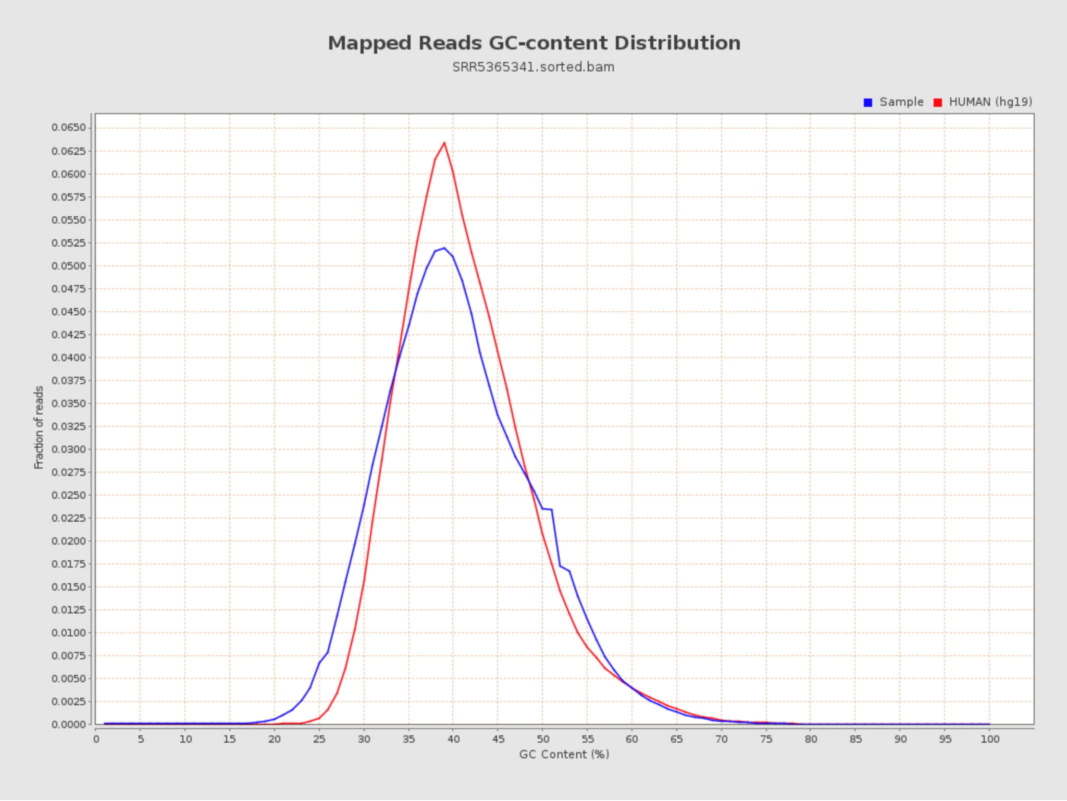
7. Results : Duplication Rate Histogram



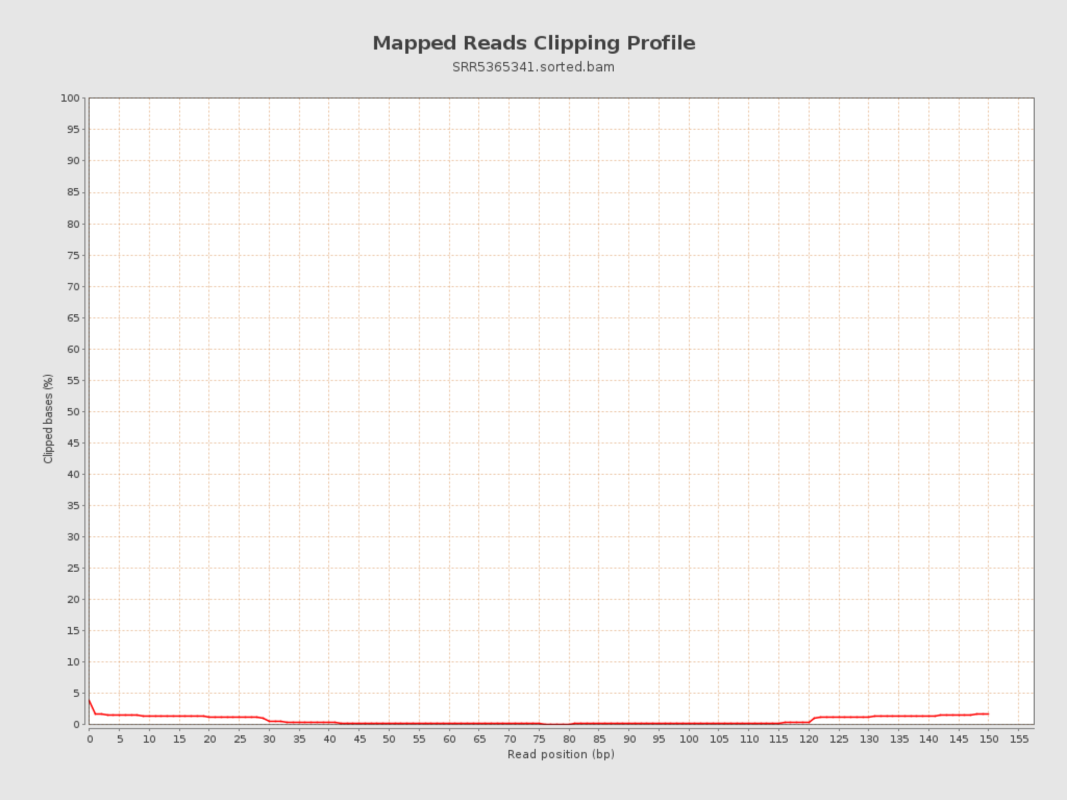
8. Results : Mapped Reads Nucleotide Content



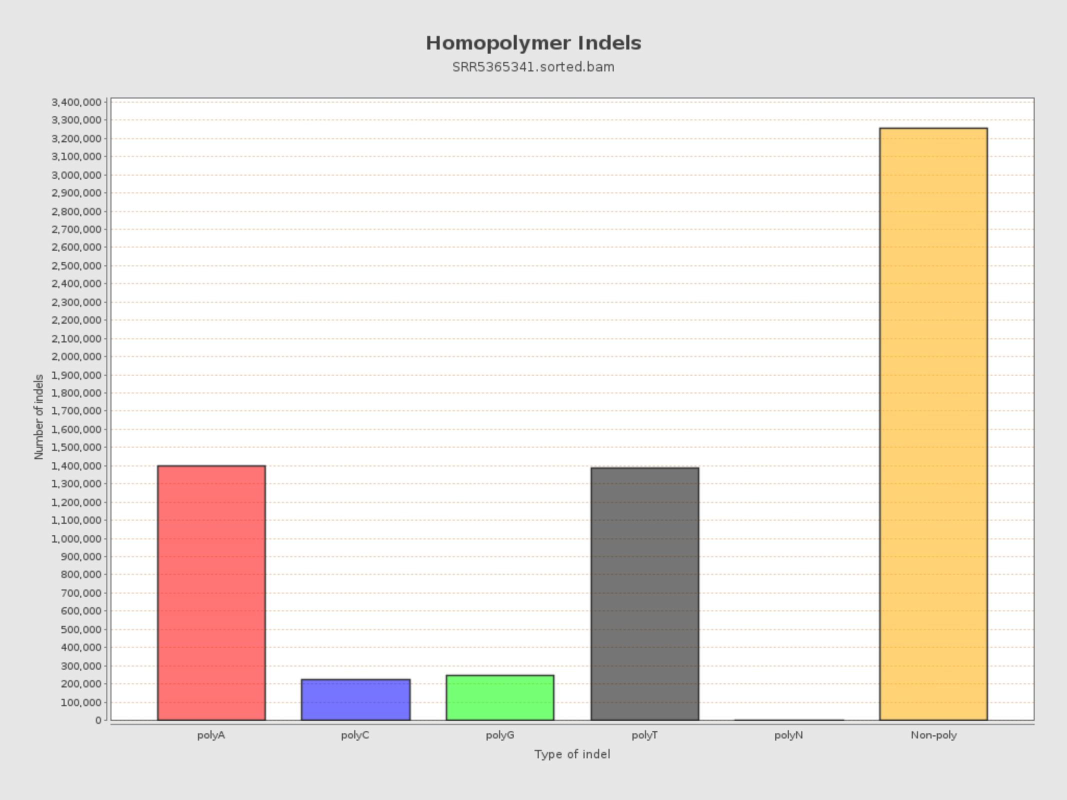
9. Results : Mapped Reads GC-content Distribution



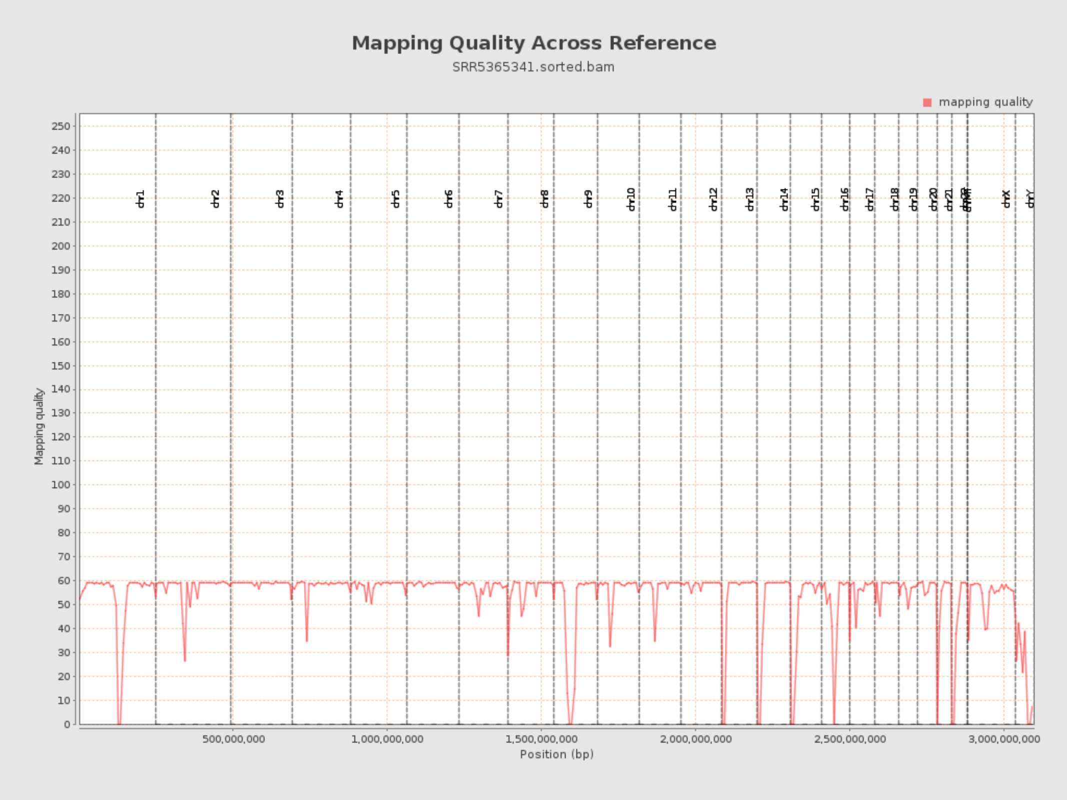
10. Results : Mapped Reads Clipping Profile



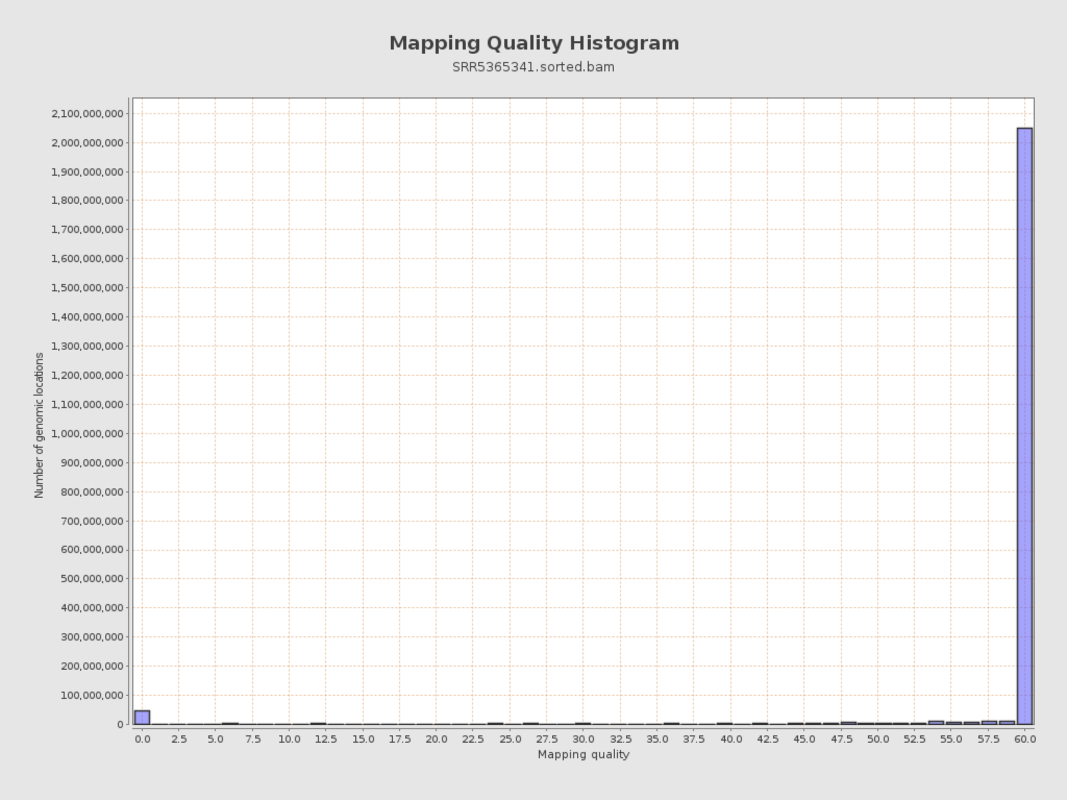
11. Results : Homopolymer Indels



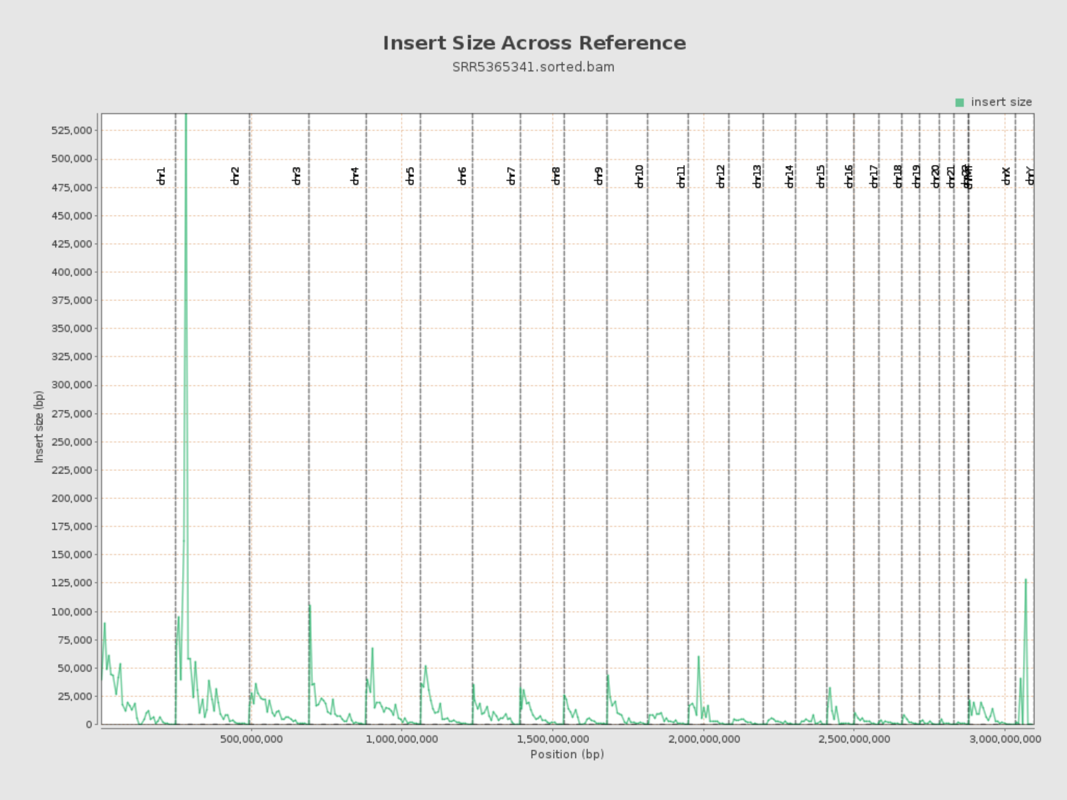
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram