Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/11 19:28:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365351.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_SRR5365351 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365351_1.fastq.gz SRR5365351_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Nov 11 19:28:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365351.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	557,871,970
Mapped reads	540,504,399 / 96.89%
Unmapped reads	17,367,571 / 3.11%
Mapped paired reads	540,504,399 / 96.89%
Mapped reads, first in pair	270,736,777 / 48.53%
Mapped reads, second in pair	269,767,622 / 48.36%
Mapped reads, both in pair	538,179,174 / 96.47%
Mapped reads, singletons	2,325,225 / 0.42%
Secondary alignments	0
Supplementary alignments	2,709,349 / 0.49%
Read min/max/mean length	30 / 125 / 125.2
Duplicated reads (estimated)	289,925,203 / 51.97%
Duplication rate	28.38%
Clipped reads	316,375,919 / 56.71%

2.2. ACGT Content

Number/percentage of A's	17,260,205,041 / 30.13%
Number/percentage of C's	11,224,359,794 / 19.6%
Number/percentage of T's	16,829,577,492 / 29.38%
Number/percentage of G's	11,959,428,756 / 20.88%
Number/percentage of N's	6,770,746 / 0.01%

GC Percentage	40.47%

2.3. Coverage

Mean	18.5099
Standard Deviation	226.4837

2.4. Mapping Quality

Mean Mapping Quality	53.61

2.5. Insert size

Mean	49,871.74
Standard Deviation	2,161,178.1
P25/Median/P75	115 / 165 / 235

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	312,136,719
Insertions	17,447,205
Mapped reads with at least one insertion	3.15%
Deletions	9,471,361
Mapped reads with at least one deletion	1.7%
Homopolymer indels	49.73%

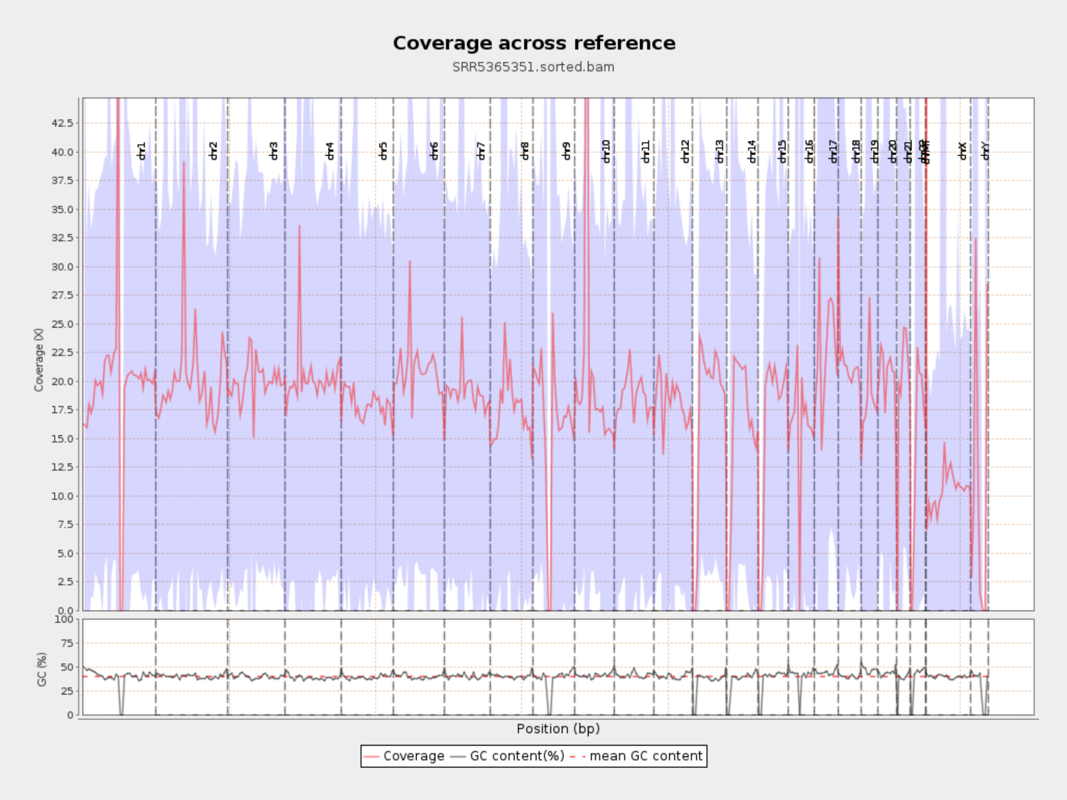
2.7. Chromosome stats

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

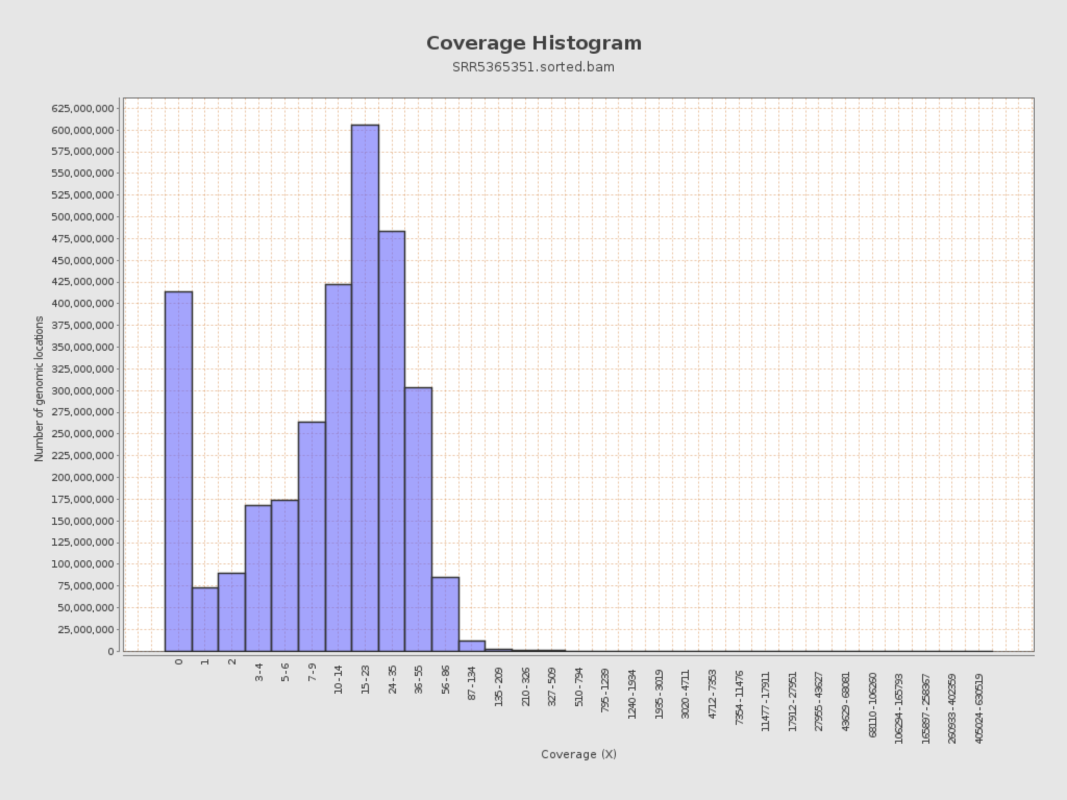
		bases	coverage	deviation
chr1	249250621	4923624934	19.7537	609.786
chr2	243199373	4906365792	20.1743	129.8247
chr3	198022430	3975536967	20.0762	35.8593
chr4	191154276	3898781591	20.396	116.8684
chr5	180915260	3245790348	17.9409	20.6029
chr6	171115067	3607553149	21.0826	86.2399
chr7	159138663	3034808803	19.0702	150.6587
chr8	146364022	2573331835	17.5817	85.3073
chr9	141213431	2320287457	16.4311	183.8339
chr10	135534747	2866283667	21.148	448.7132
chr11	135006516	2523686414	18.6931	135.7626
chr12	133851895	2452810166	18.3248	38.2739
chr13	115169878	2025009686	17.5828	17.8248
chr14	107349540	1715180206	15.9775	21.9958
chr15	102531392	1659224754	16.1826	23.2964
chr16	90354753	1438391286	15.9194	66.6266
chr17	81195210	1871578854	23.0504	119.9207
chr18	78077248	1694218245	21.6993	217.27
chr19	59128983	1112409905	18.8133	305.0371
chr20	63025520	1307634103	20.7477	37.3839
chr21	48129895	941377215	19.5591	82.9658
chr22	51304566	726133449	14.1534	78.3948
chrMT	16571	184873012	11,156.4186	1,969.4426
chrX	155270560	1630173574	10.4989	53.9892

chrY	59373566	665930186	11.2159	264.1884

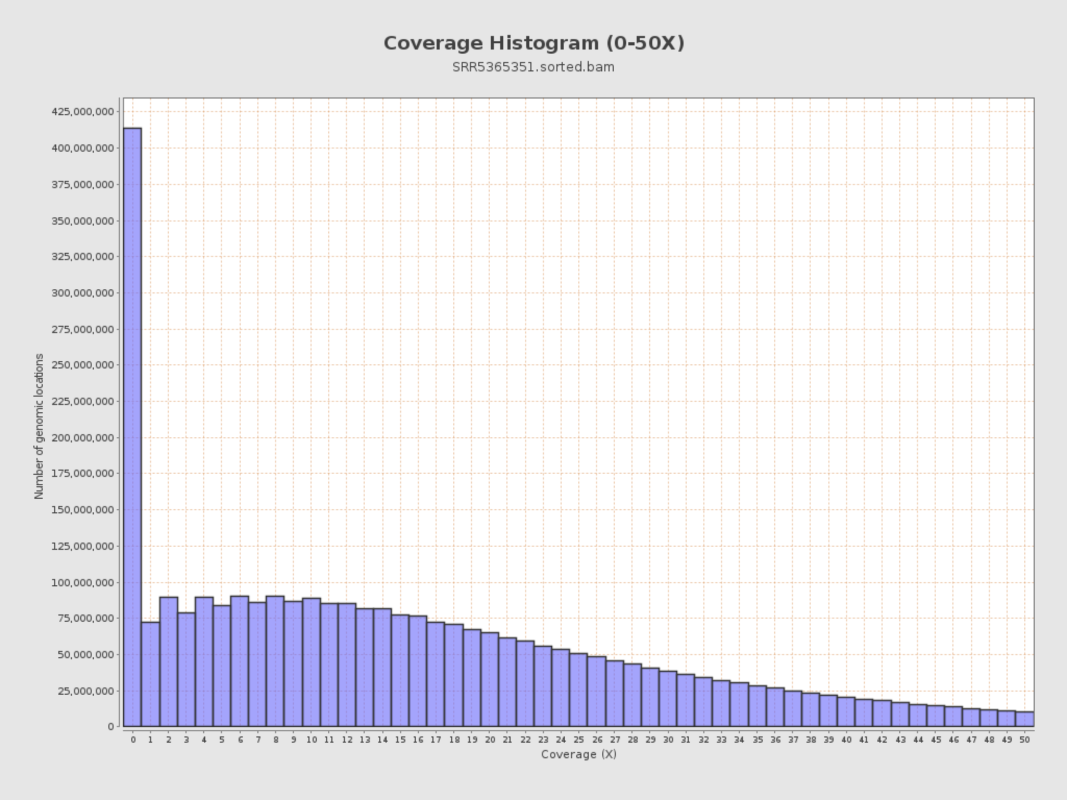
3. Results : Coverage across reference



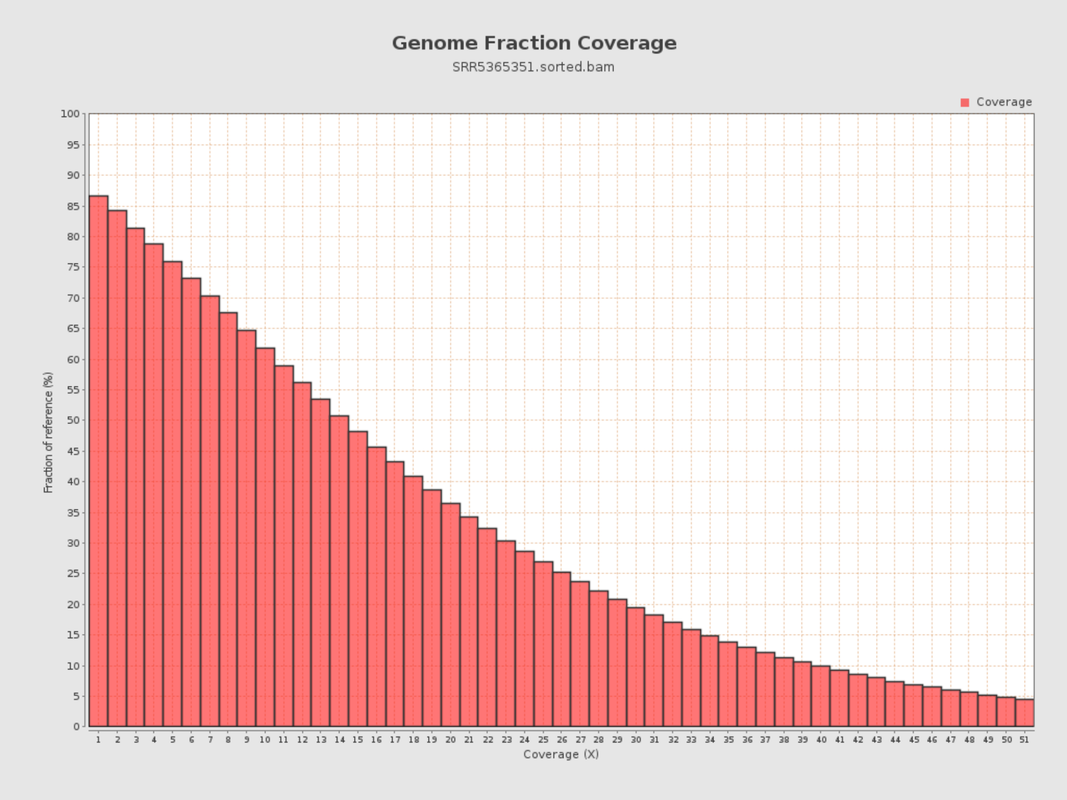
4. Results : Coverage Histogram



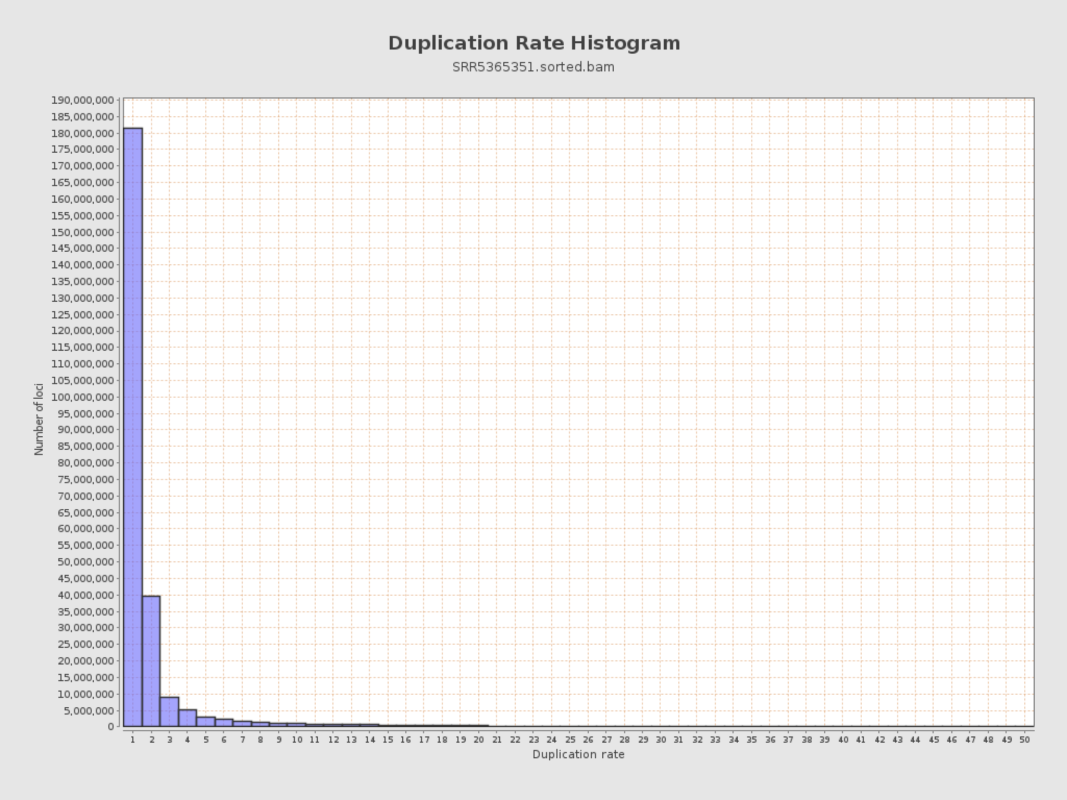
5. Results : Coverage Histogram (0-50X)



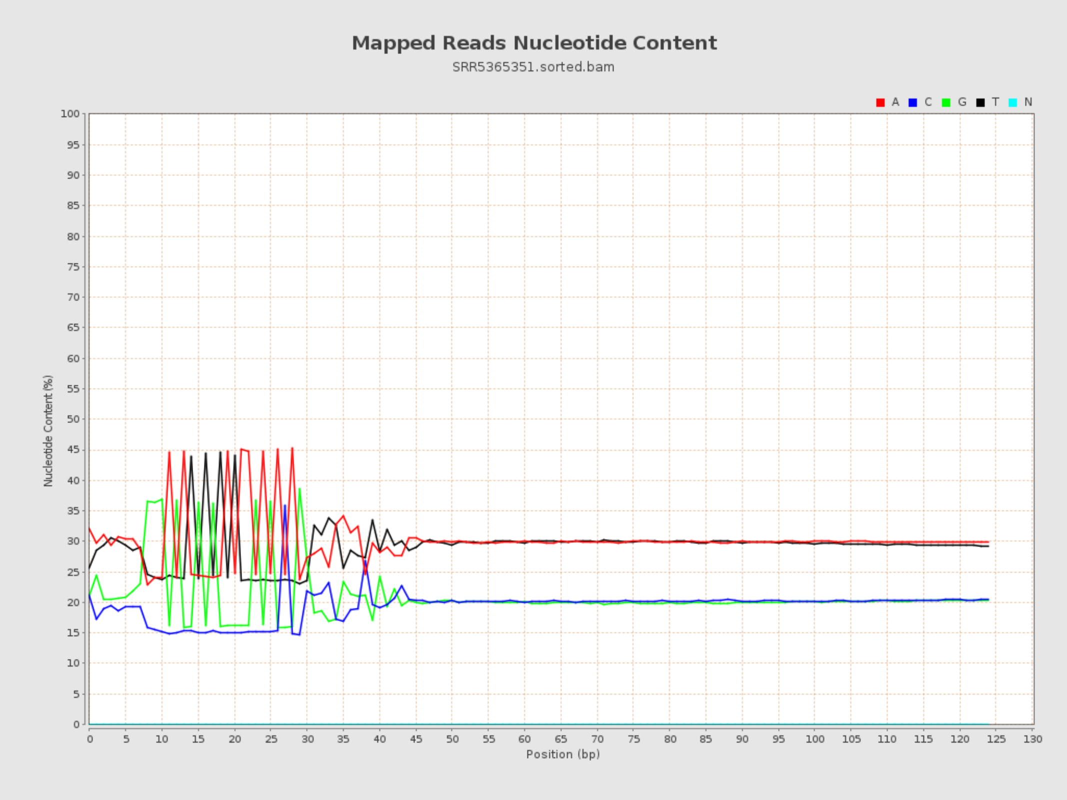
6. Results : Genome Fraction Coverage



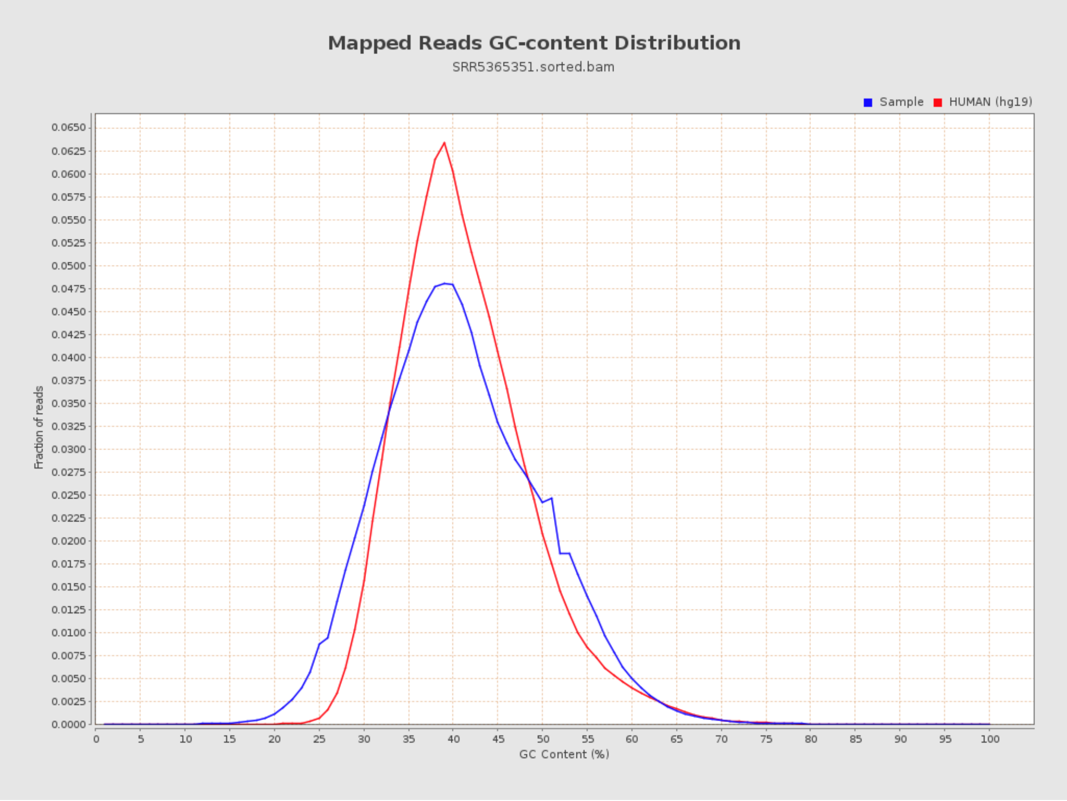
7. Results : Duplication Rate Histogram



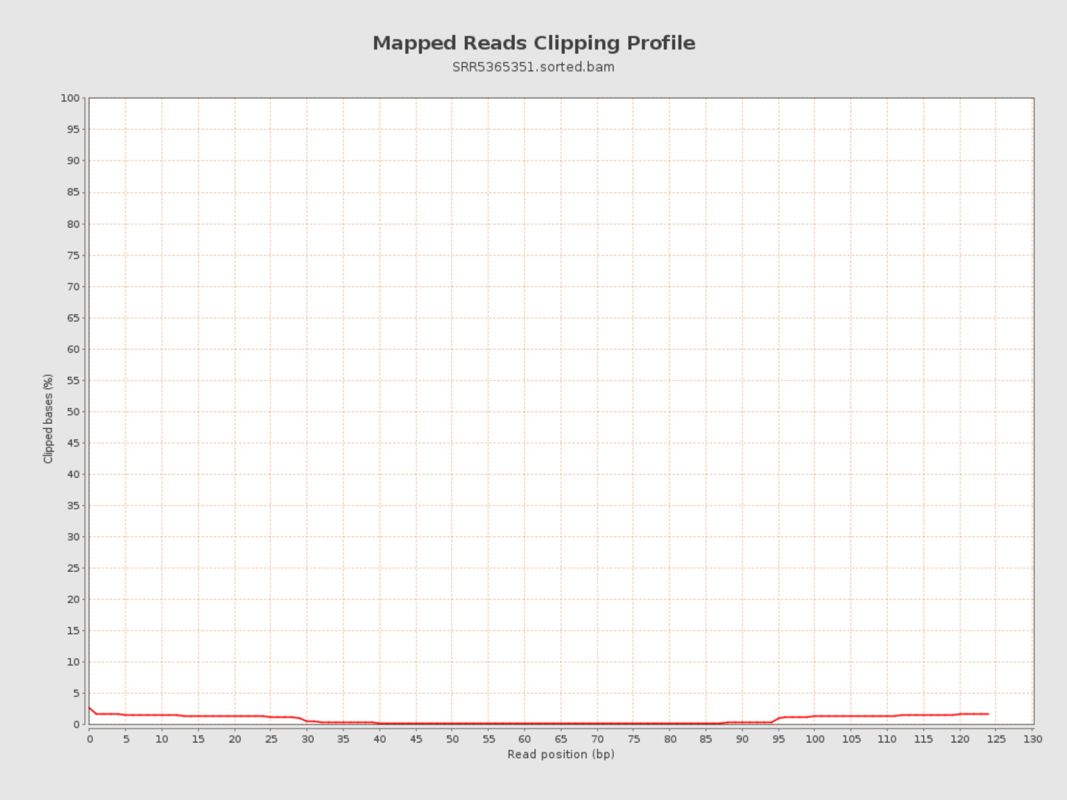
8. Results : Mapped Reads Nucleotide Content



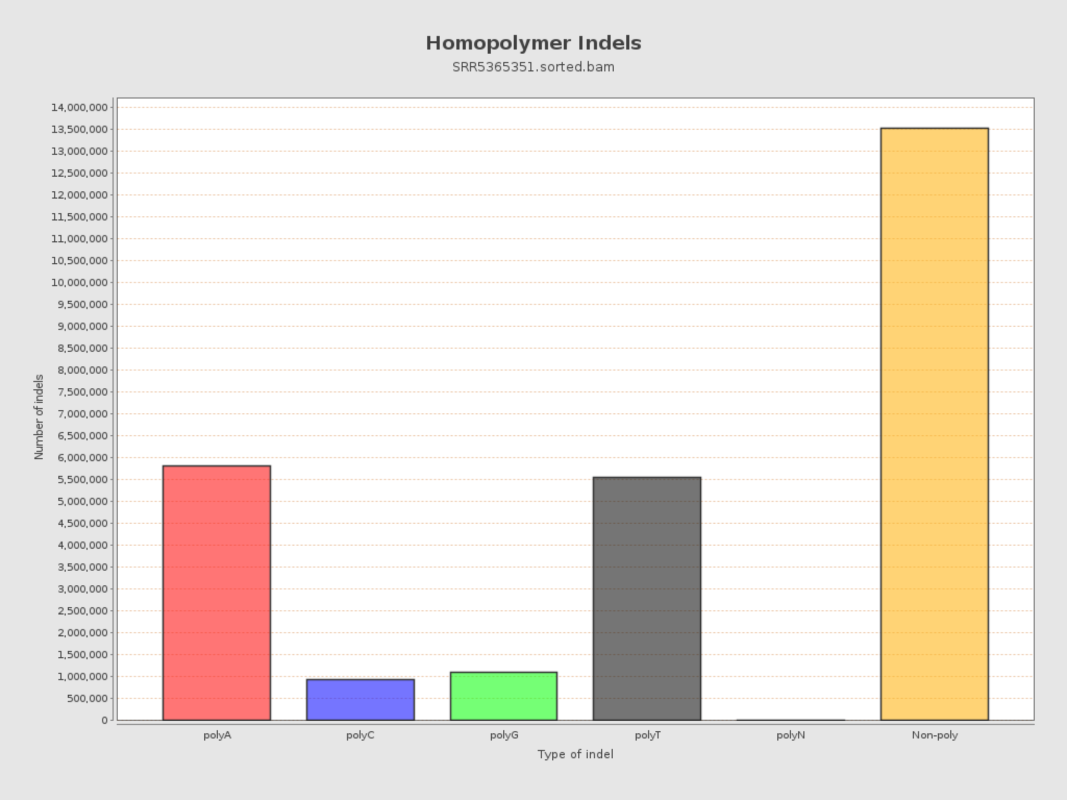
9. Results : Mapped Reads GC-content Distribution



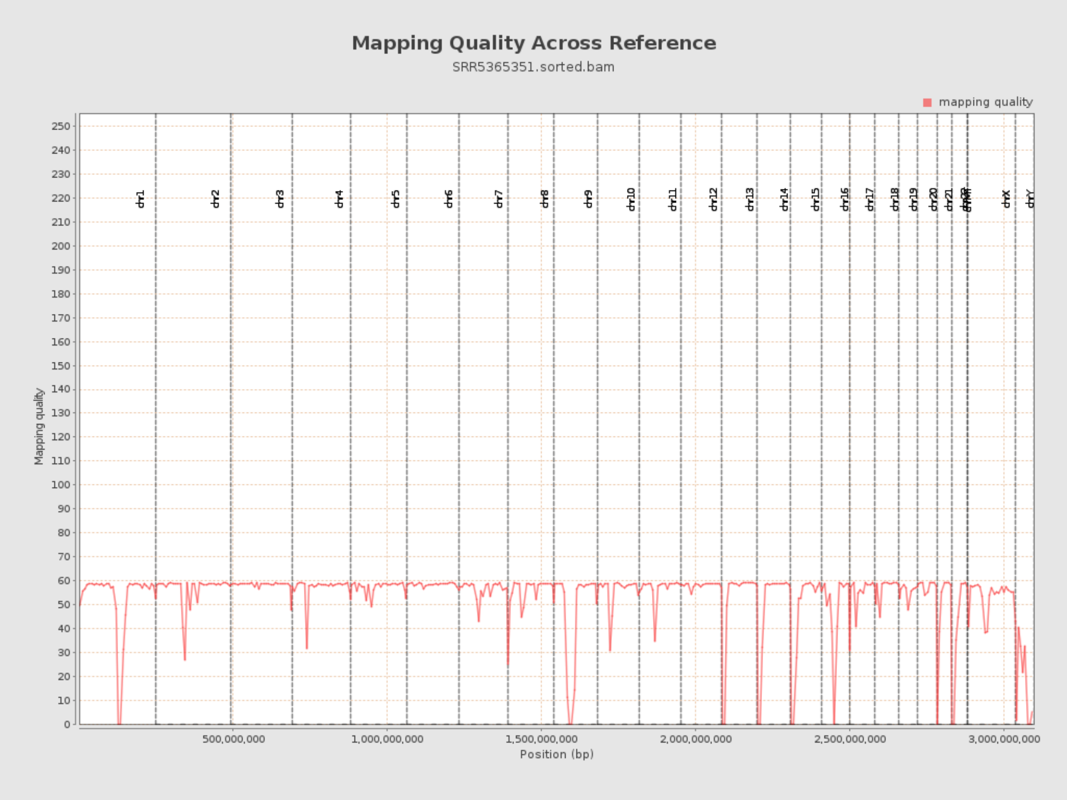
10. Results : Mapped Reads Clipping Profile



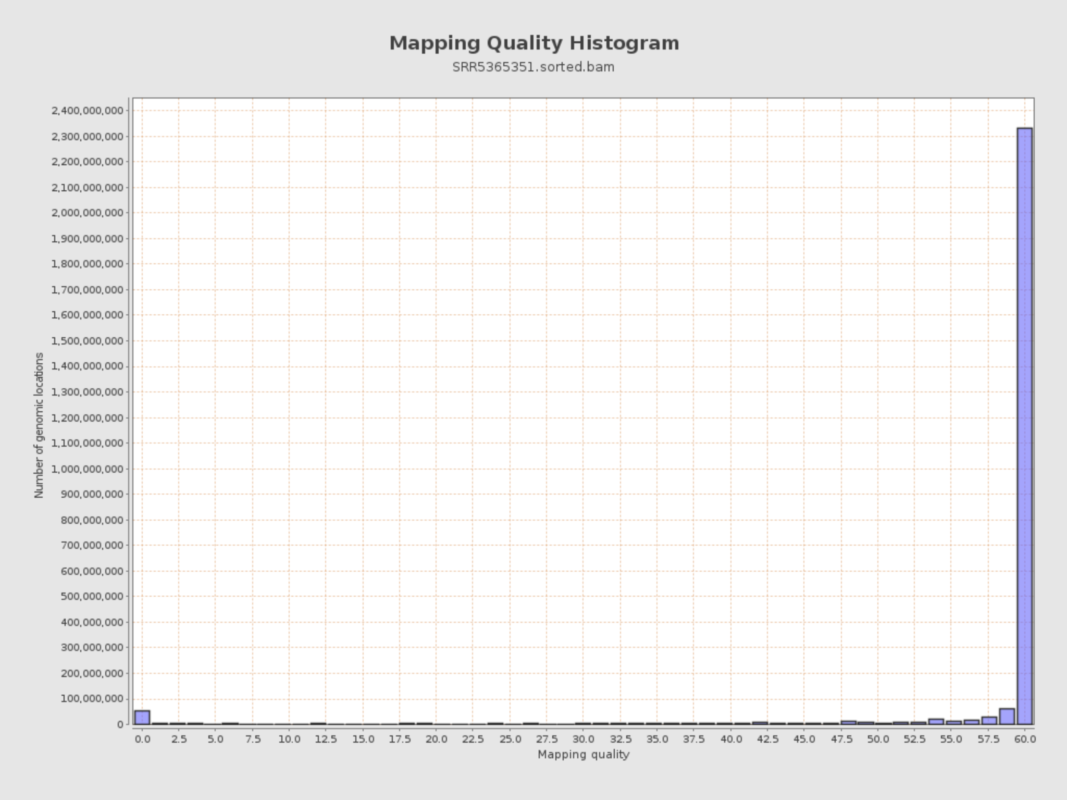
11. Results : Homopolymer Indels



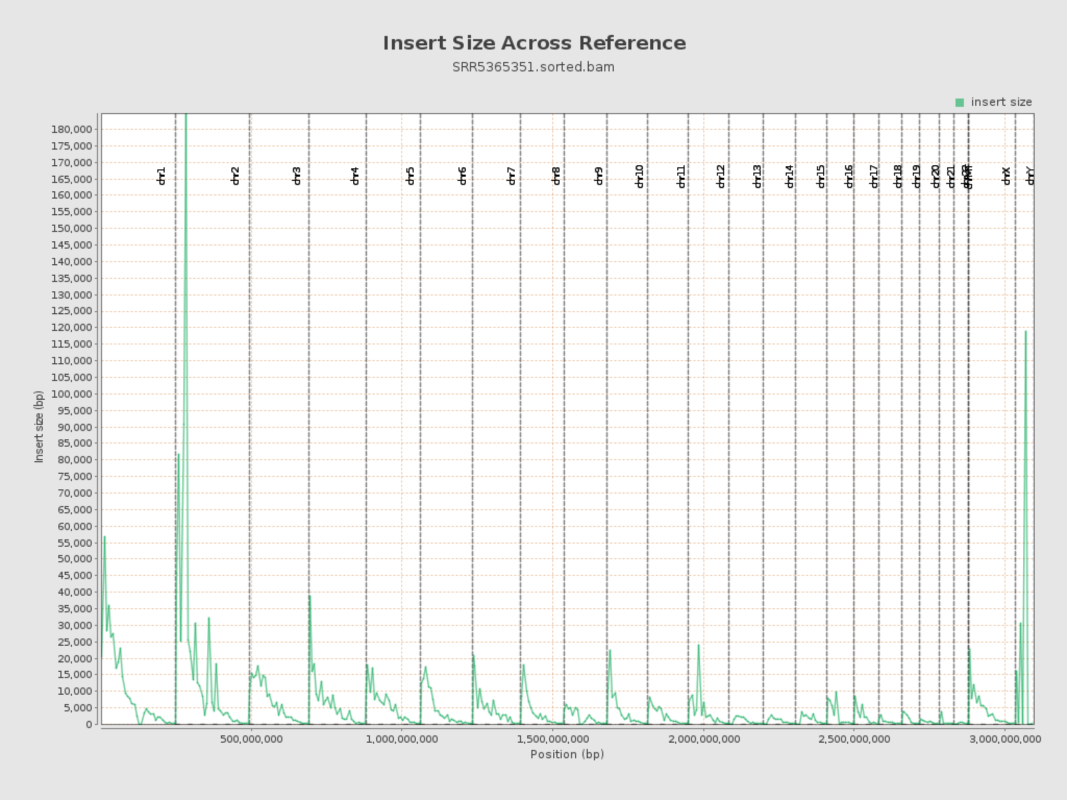
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram