Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/14 10:04:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365359.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_SRR5365359 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365359_1.fastq.gz SRR5365359_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Nov 14 10:04:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365359.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	572,714,332
Mapped reads	456,903,566 / 79.78%
Unmapped reads	115,810,766 / 20.22%
Mapped paired reads	456,903,566 / 79.78%
Mapped reads, first in pair	225,430,078 / 39.36%
Mapped reads, second in pair	231,473,488 / 40.42%
Mapped reads, both in pair	441,043,066 / 77.01%
Mapped reads, singletons	15,860,500 / 2.77%
Secondary alignments	0
Supplementary alignments	12,128,619 / 2.12%
Read min/max/mean length	30 / 150 / 151.02
Duplicated reads (estimated)	275,890,720 / 48.17%
Duplication rate	47.73%
Clipped reads	353,612,558 / 61.74%

2.2. ACGT Content

Number/percentage of A's	14,497,304,006 / 26.13%
Number/percentage of C's	12,929,910,506 / 23.3%
Number/percentage of T's	14,238,431,914 / 25.66%
Number/percentage of G's	13,816,337,545 / 24.9%
Number/percentage of N's	1,191,770 / 0%

GC Percentage	48.21%

2.3. Coverage

Mean	17.9318
Standard Deviation	139.65

2.4. Mapping Quality

Mean Mapping Quality	52.6

2.5. Insert size

Mean	122,773.5
Standard Deviation	3,517,023.44
P25/Median/P75	112 / 140 / 174

2.6. Mismatches and indels

General error rate	1.15%
Mismatches	619,075,600
Insertions	6,788,694
Mapped reads with at least one insertion	1.4%
Deletions	15,299,017
Mapped reads with at least one deletion	3.24%
Homopolymer indels	39.87%

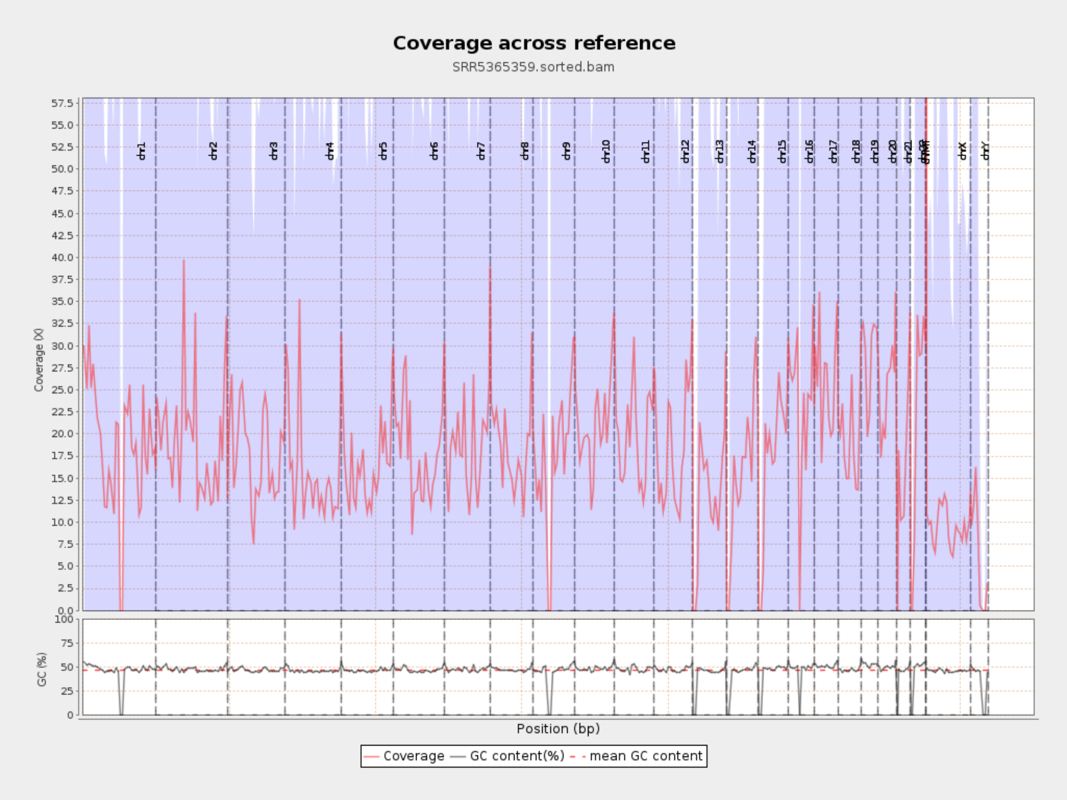
2.7. Chromosome stats

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

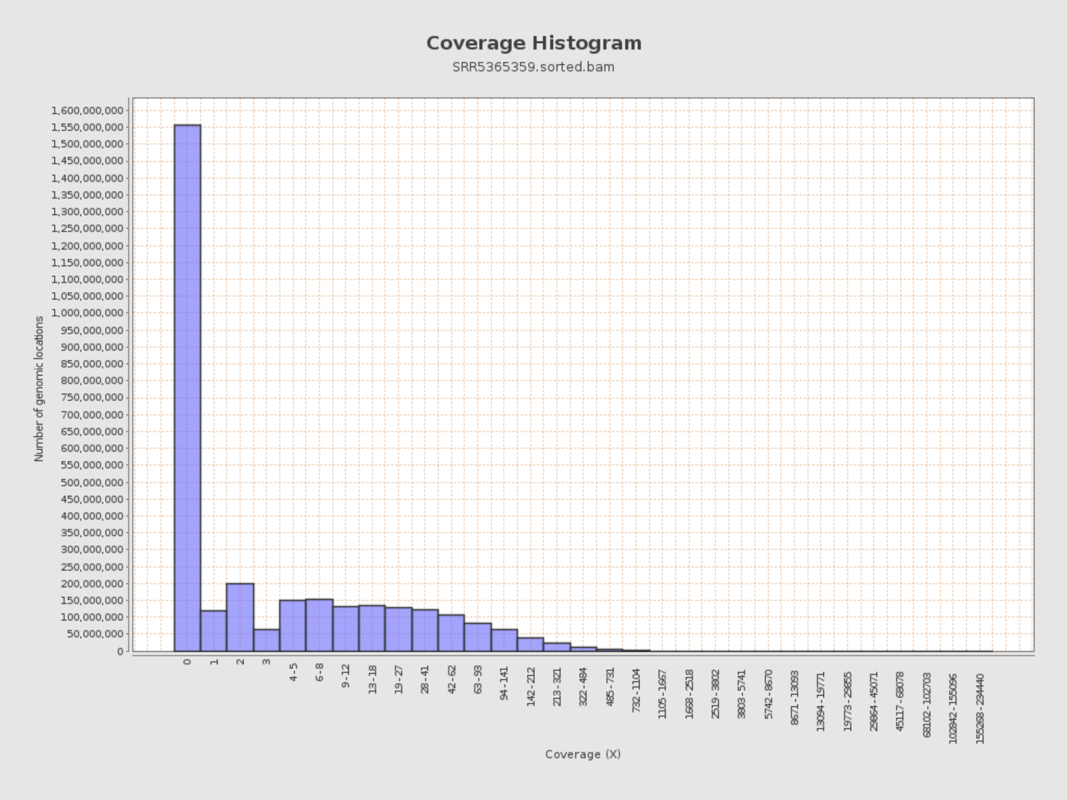
		bases	coverage	deviation
chr1	249250621	4640131937	18.6163	126.0074
chr2	243199373	4721546140	19.4143	260.9103
chr3	198022430	3500063544	17.6751	64.729
chr4	191154276	3000817342	15.6984	111.2329
chr5	180915260	3027881258	16.7365	76.8032
chr6	171115067	3041882011	17.7768	139.3809
chr7	159138663	2970351708	18.6652	118.7598
chr8	146364022	2676666743	18.2877	95.8795
chr9	141213431	2398642423	16.9859	169.4911
chr10	135534747	2820846359	20.8127	78.5024
chr11	135006516	2685832171	19.8941	223.8332
chr12	133851895	2465949616	18.423	60.2096
chr13	115169878	1481904521	12.8671	48.9545
chr14	107349540	1674451954	15.5981	64.3978
chr15	102531392	1706800856	16.6466	58.6257
chr16	90354753	2113027915	23.3859	119.1845
chr17	81195210	2112085680	26.0124	240.0556
chr18	78077248	1453741142	18.6193	247.3182
chr19	59128983	1698247112	28.7211	102.3453
chr20	63025520	1570902357	24.9249	93.1898
chr21	48129895	802152491	16.6664	168.6668
chr22	51304566	1086666339	21.1807	104.1865
chrMT	16571	13757940	830.242	2,550.0565
chrX	155270560	1475824224	9.5049	70.9044

chrY	59373566	371302522	6.2537	108.0392

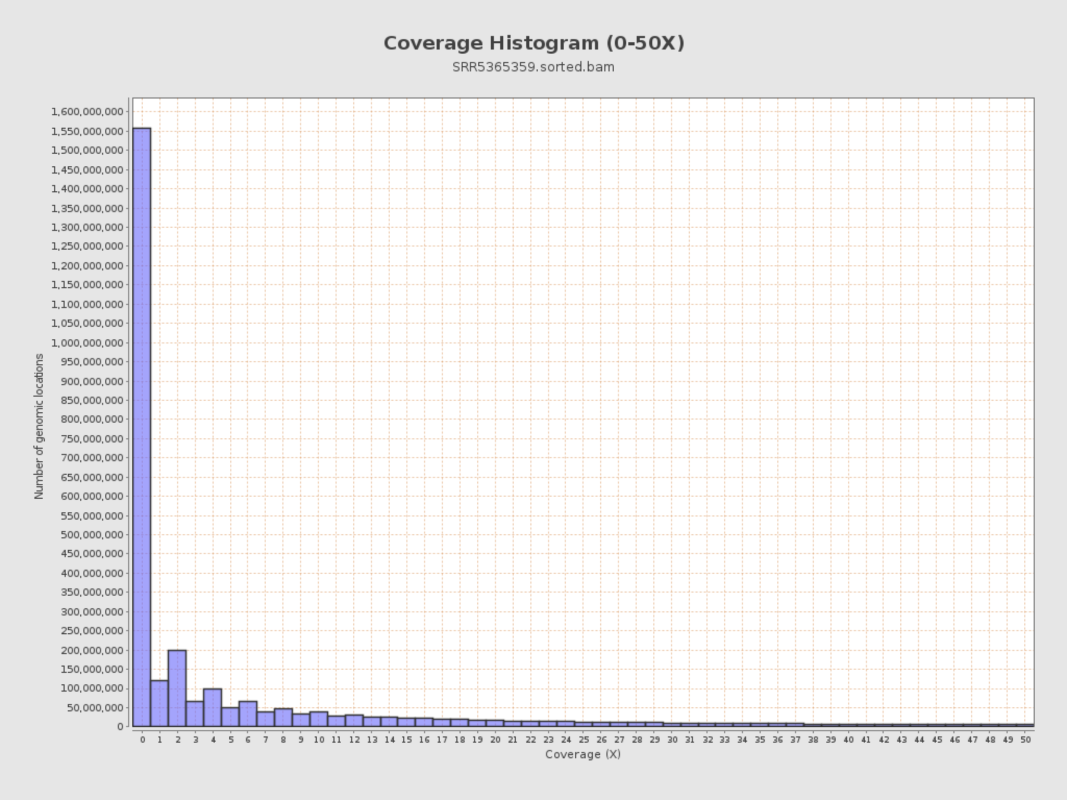
3. Results : Coverage across reference



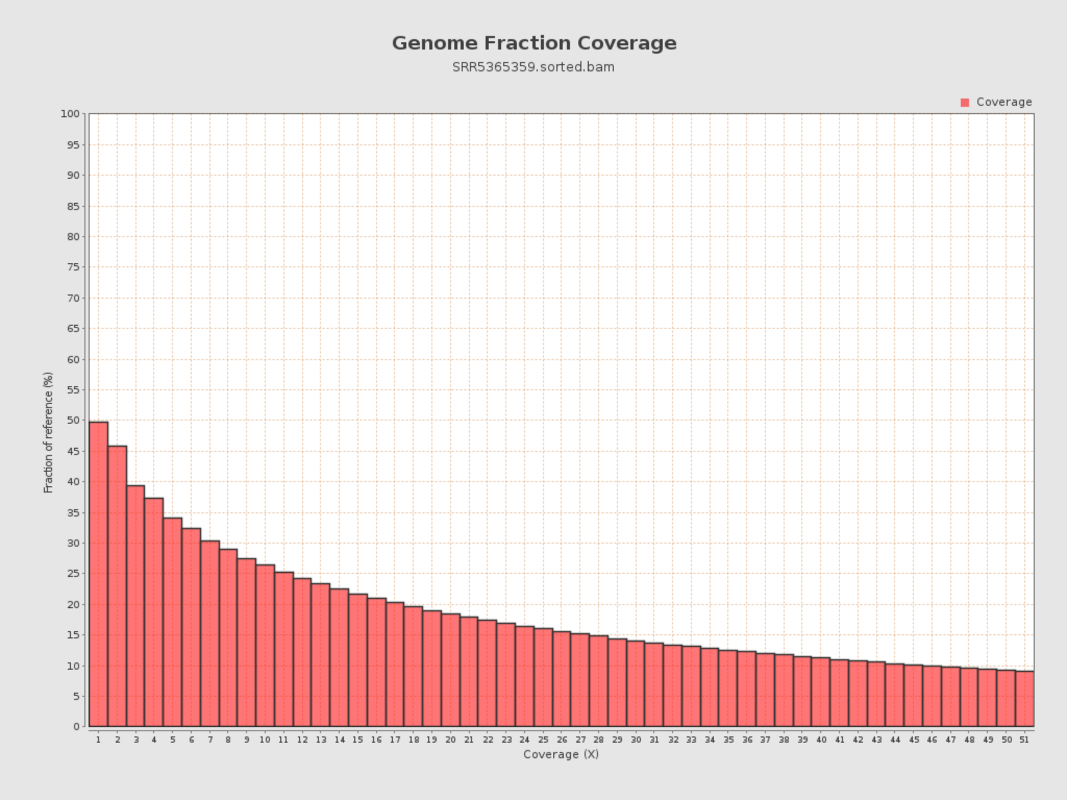
4. Results : Coverage Histogram



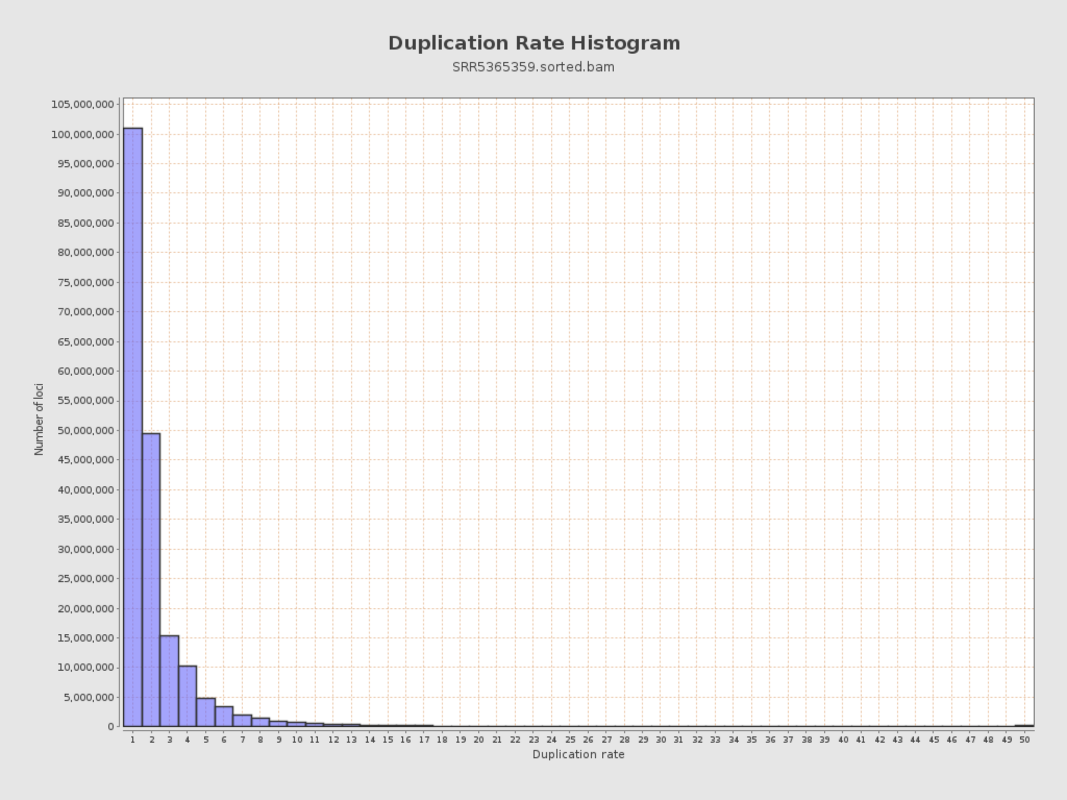
5. Results : Coverage Histogram (0-50X)



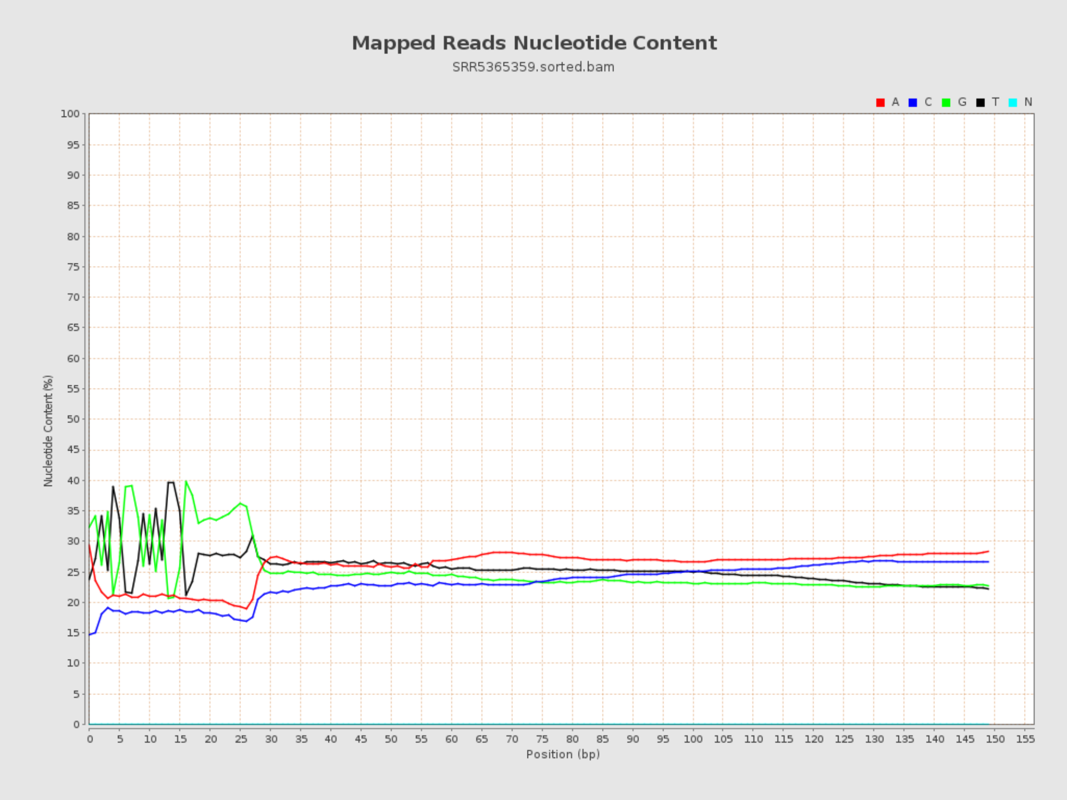
6. Results : Genome Fraction Coverage



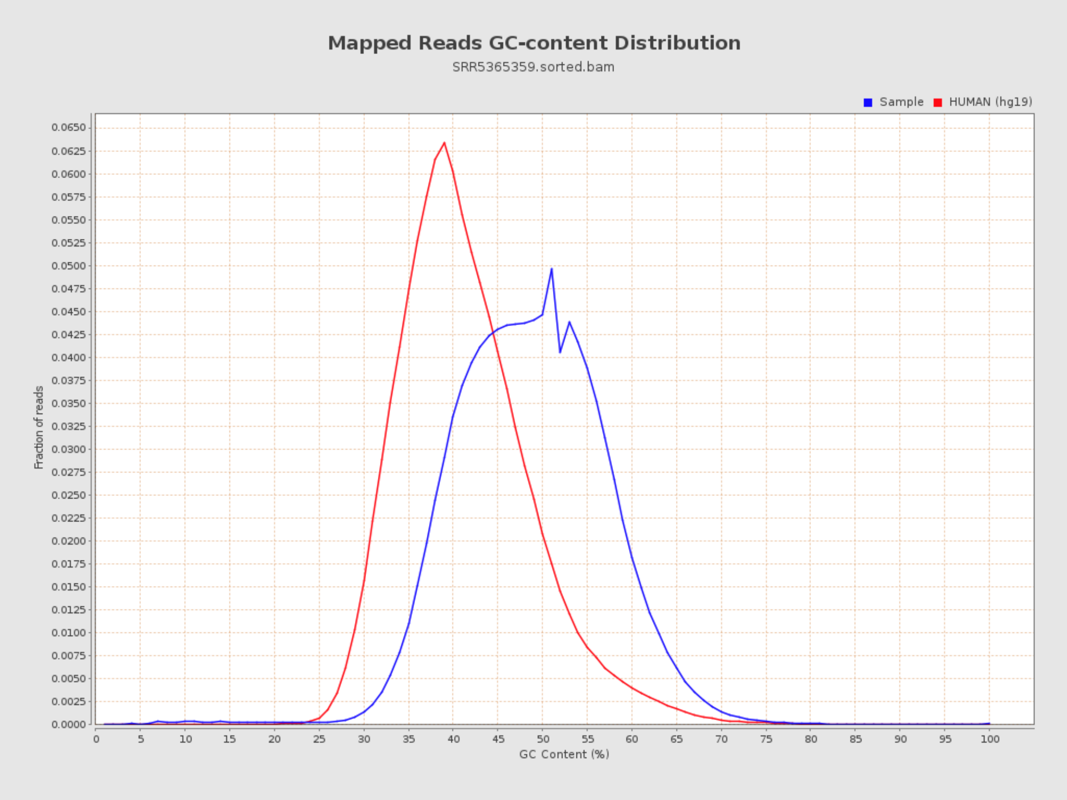
7. Results : Duplication Rate Histogram



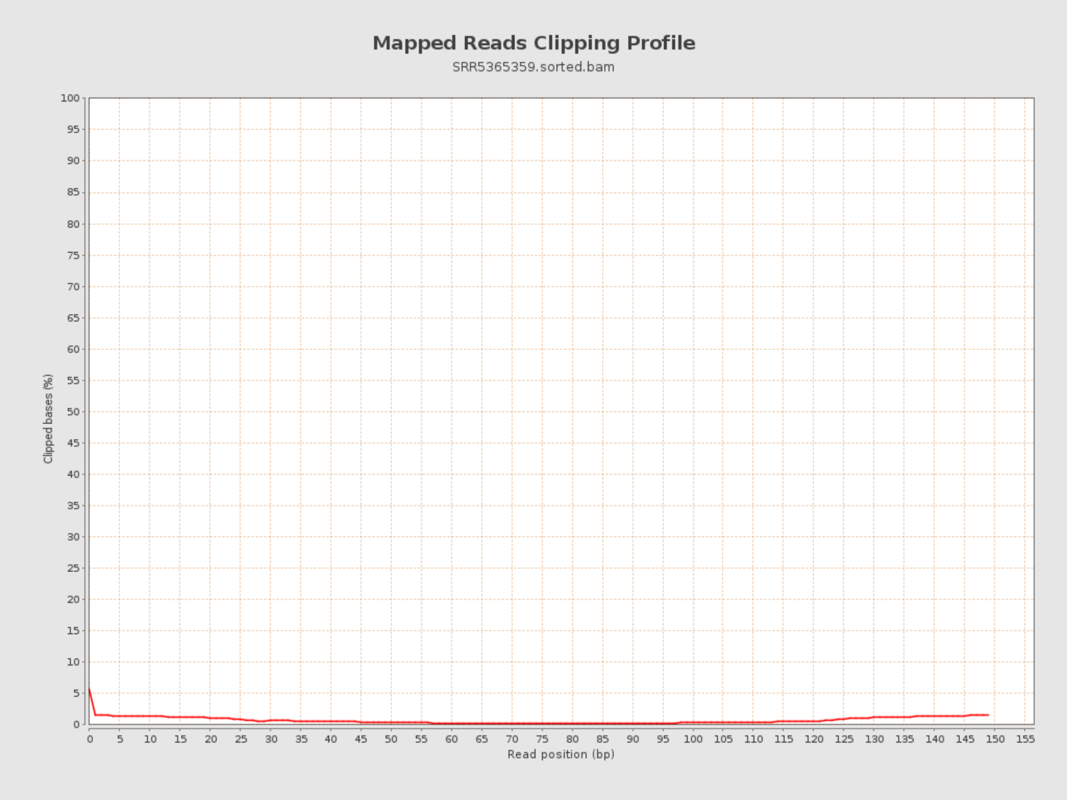
8. Results : Mapped Reads Nucleotide Content



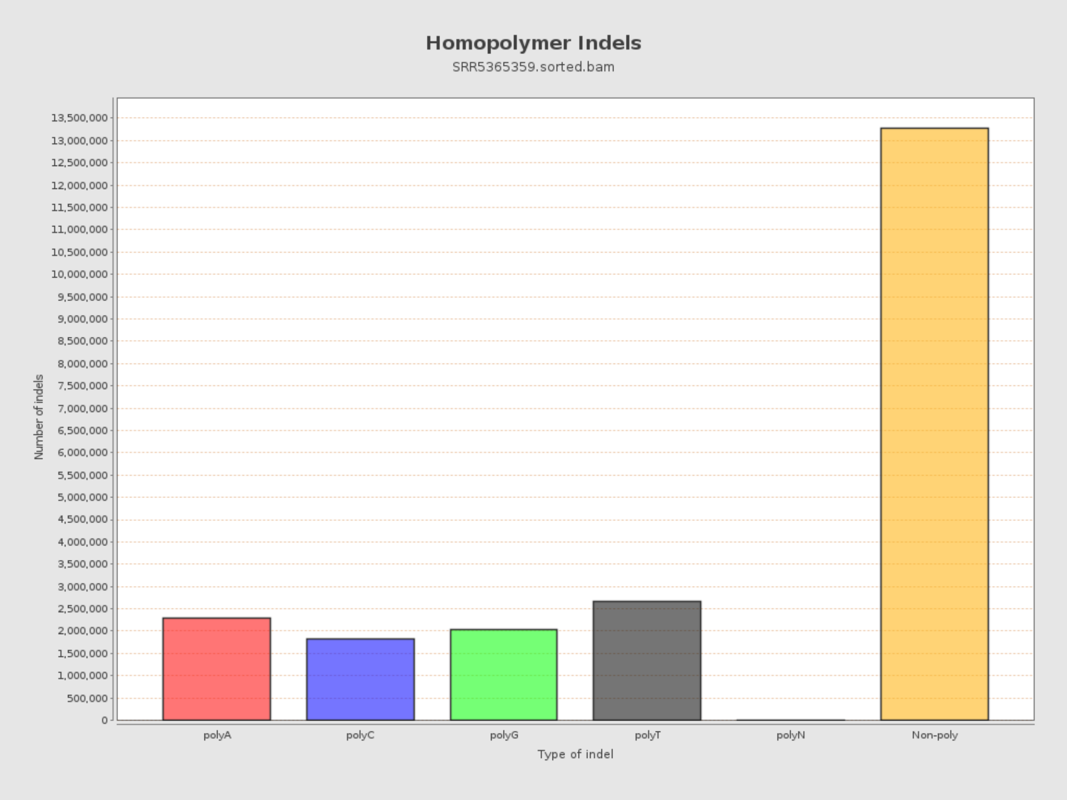
9. Results : Mapped Reads GC-content Distribution



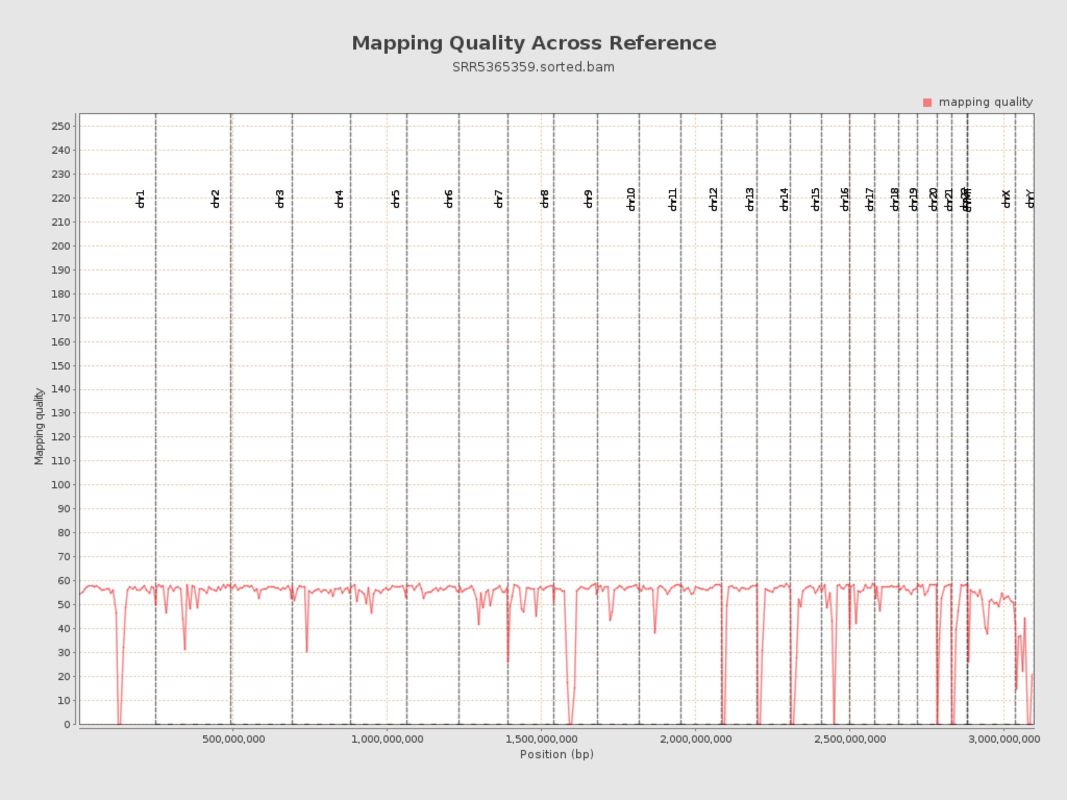
10. Results : Mapped Reads Clipping Profile



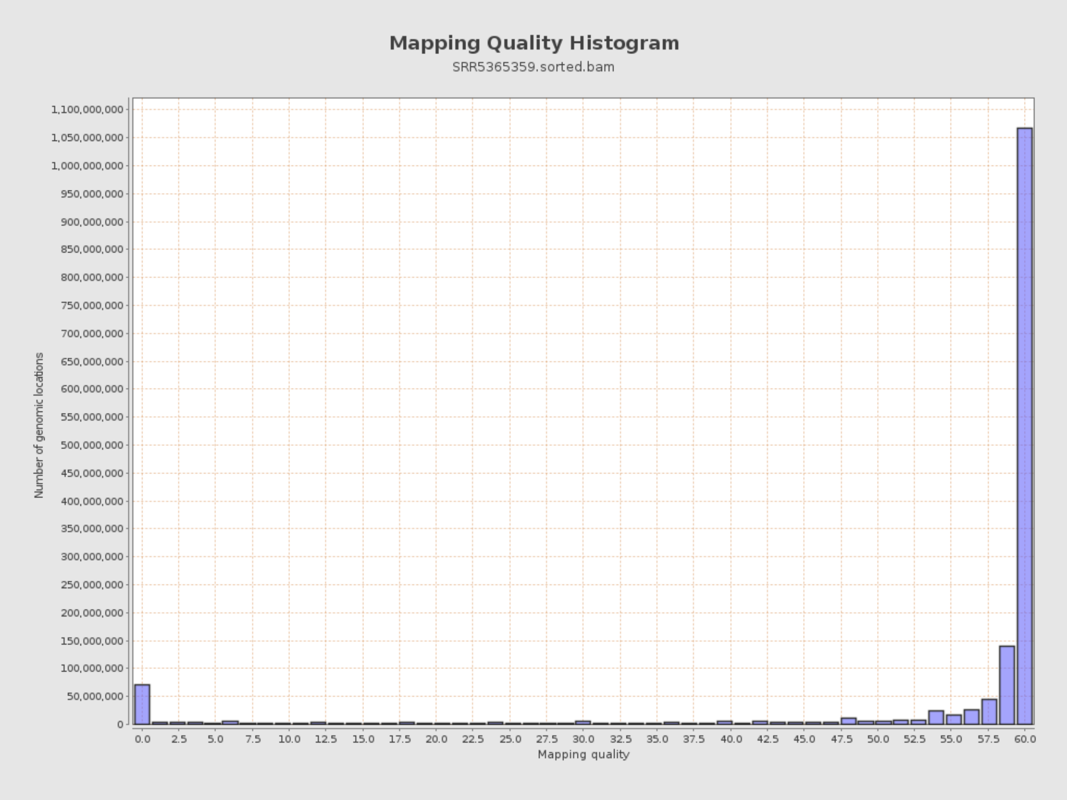
11. Results : Homopolymer Indels



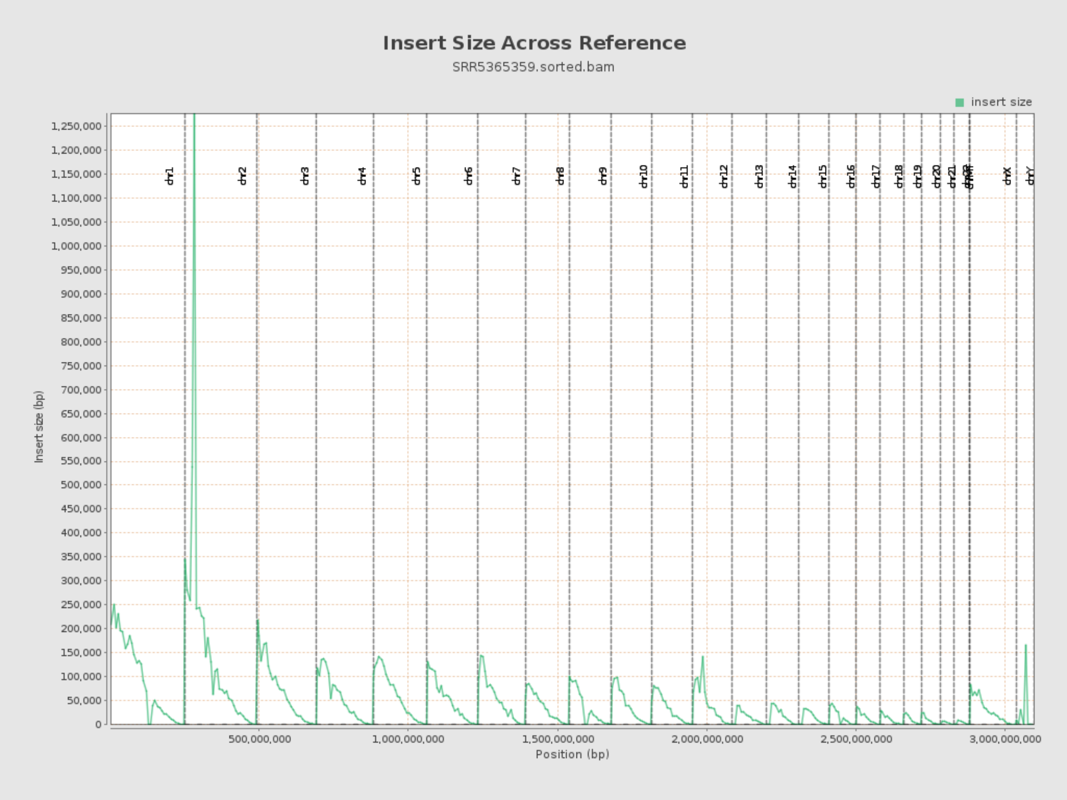
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram