Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/02 08:49:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365335.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_SRR5365335 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365335_1.fastq.gz SRR5365335_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Nov 02 08:49:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365335.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	108,727,676
Mapped reads	106,299,756 / 97.77%
Unmapped reads	2,427,920 / 2.23%
Mapped paired reads	106,299,756 / 97.77%
Mapped reads, first in pair	53,373,048 / 49.09%
Mapped reads, second in pair	52,926,708 / 48.68%
Mapped reads, both in pair	105,691,026 / 97.21%
Mapped reads, singletons	608,730 / 0.56%
Secondary alignments	0
Supplementary alignments	872,770 / 0.8%
Read min/max/mean length	30 / 151 / 151.36
Duplicated reads (estimated)	43,965,837 / 40.44%
Duplication rate	31.05%
Clipped reads	65,800,574 / 60.52%

2.2. ACGT Content

Number/percentage of A's	4,140,589,689 / 29.77%
Number/percentage of C's	2,765,422,333 / 19.89%
Number/percentage of T's	4,089,662,427 / 29.41%
Number/percentage of G's	2,910,320,362 / 20.93%
Number/percentage of N's	497,299 / 0%

GC Percentage	40.81%

2.3. Coverage

Mean	4.4938
Standard Deviation	29.8353

2.4. Mapping Quality

Mean Mapping Quality	54.35

2.5. Insert size

Mean	92,442.95
Standard Deviation	3,006,800.64
P25/Median/P75	145 / 196 / 265

2.6. Mismatches and indels

General error rate	0.71%
Mismatches	90,785,366
Insertions	4,326,675
Mapped reads with at least one insertion	3.95%
Deletions	2,079,453
Mapped reads with at least one deletion	1.89%
Homopolymer indels	50.98%

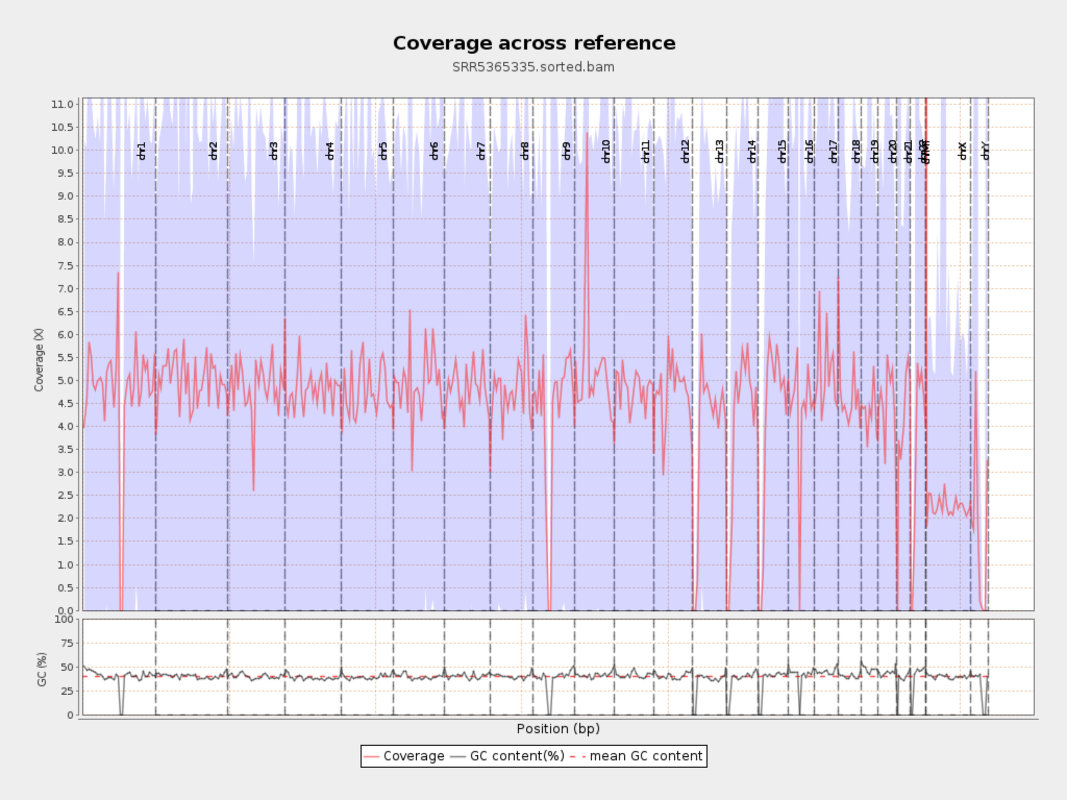
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

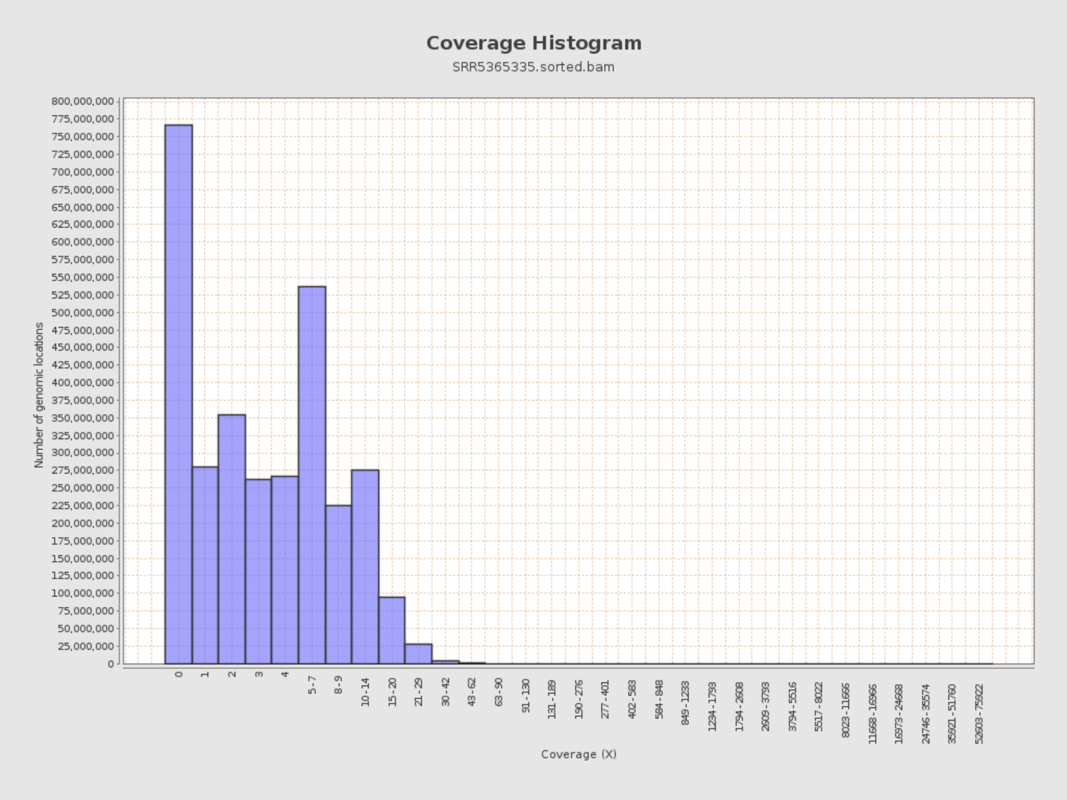
		bases	coverage	deviation
chr1	249250621	1182989415	4.7462	74.6114
chr2	243199373	1225228445	5.038	20.1242
chr3	198022430	957938147	4.8375	5.4944
chr4	191154276	916672311	4.7955	20.29
chr5	180915260	863093346	4.7707	5.5974
chr6	171115067	843717291	4.9307	16.9363
chr7	159138663	766447490	4.8162	17.5871
chr8	146364022	701014268	4.7895	10.5741
chr9	141213431	602880261	4.2693	27.28
chr10	135534747	710235592	5.2402	54.8117
chr11	135006516	646791249	4.7908	21.5194
chr12	133851895	640278170	4.7835	27.3564
chr13	115169878	445283148	3.8663	4.6044
chr14	107349540	439160400	4.0909	5.0338
chr15	102531392	414462184	4.0423	13.0772
chr16	90354753	388990324	4.3051	11.3454
chr17	81195210	421238495	5.188	22.5111
chr18	78077248	363721282	4.6585	33.7964
chr19	59128983	253132074	4.281	38.0561
chr20	63025520	286510319	4.5459	8.7444
chr21	48129895	192490803	3.9994	15.6549
chr22	51304566	175662593	3.4239	13.1853
chrMT	16571	16037632	967.8132	203.6755
chrX	155270560	351951495	2.2667	8.239

chrY	59373566	105641228	1.7793	37.9386

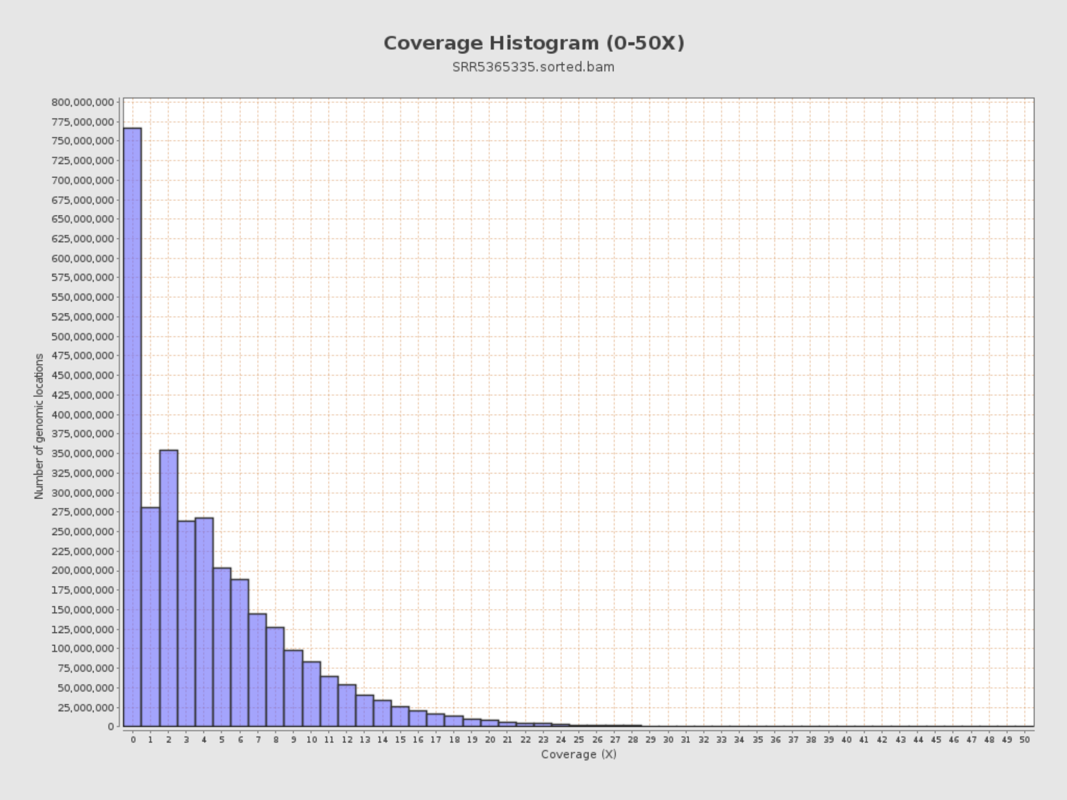
3. Results : Coverage across reference



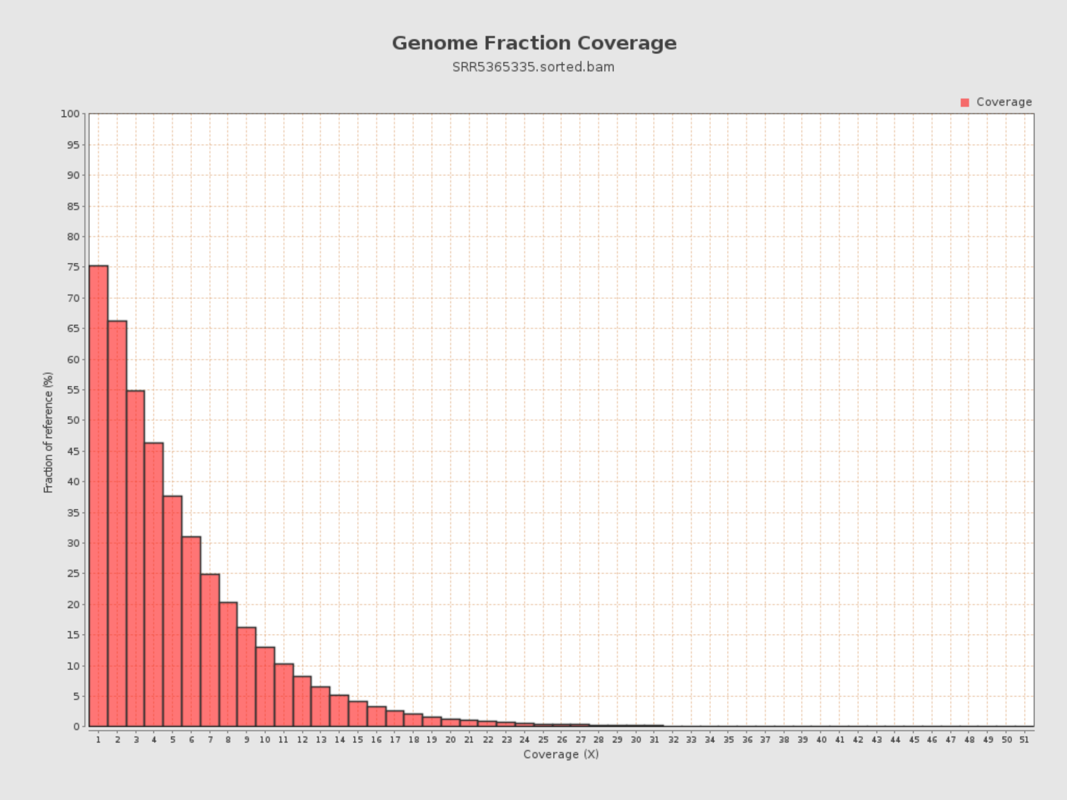
4. Results : Coverage Histogram



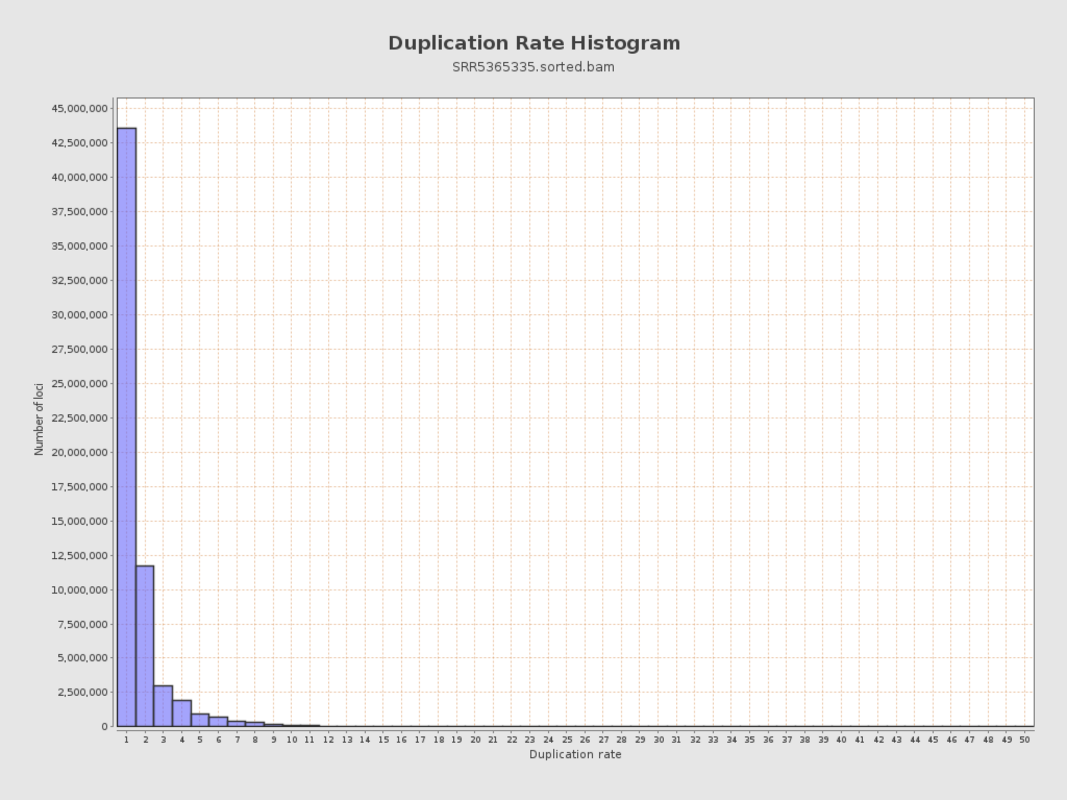
5. Results : Coverage Histogram (0-50X)



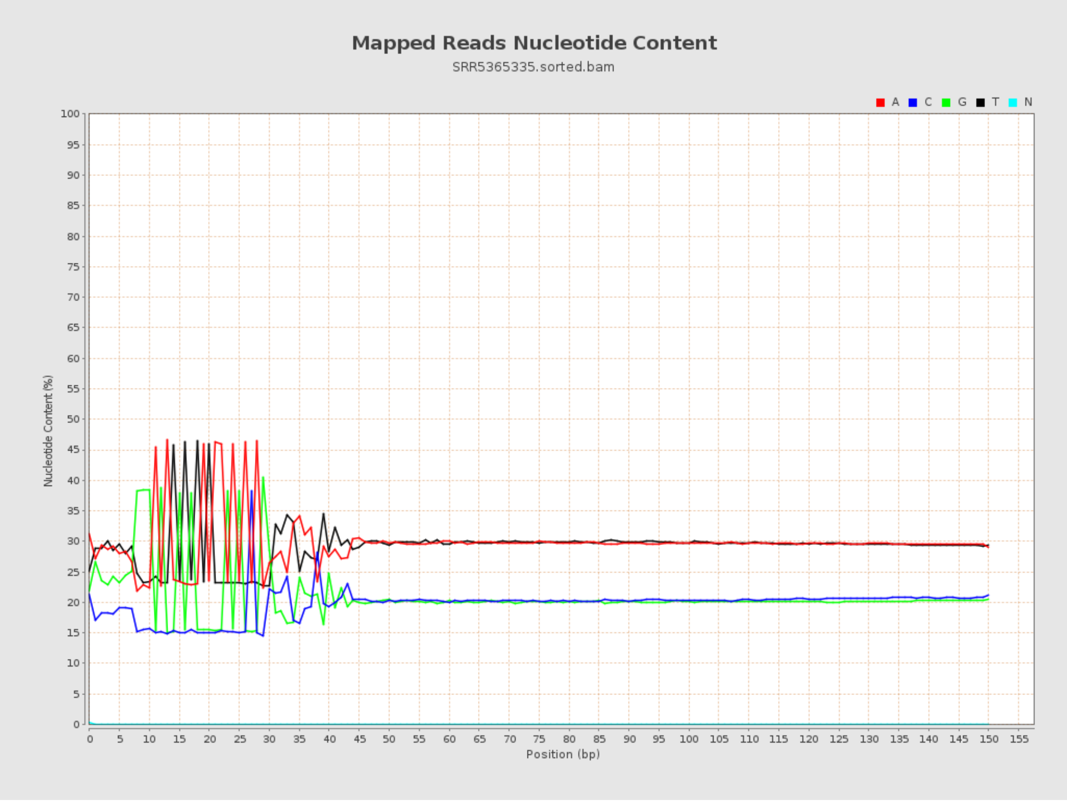
6. Results : Genome Fraction Coverage



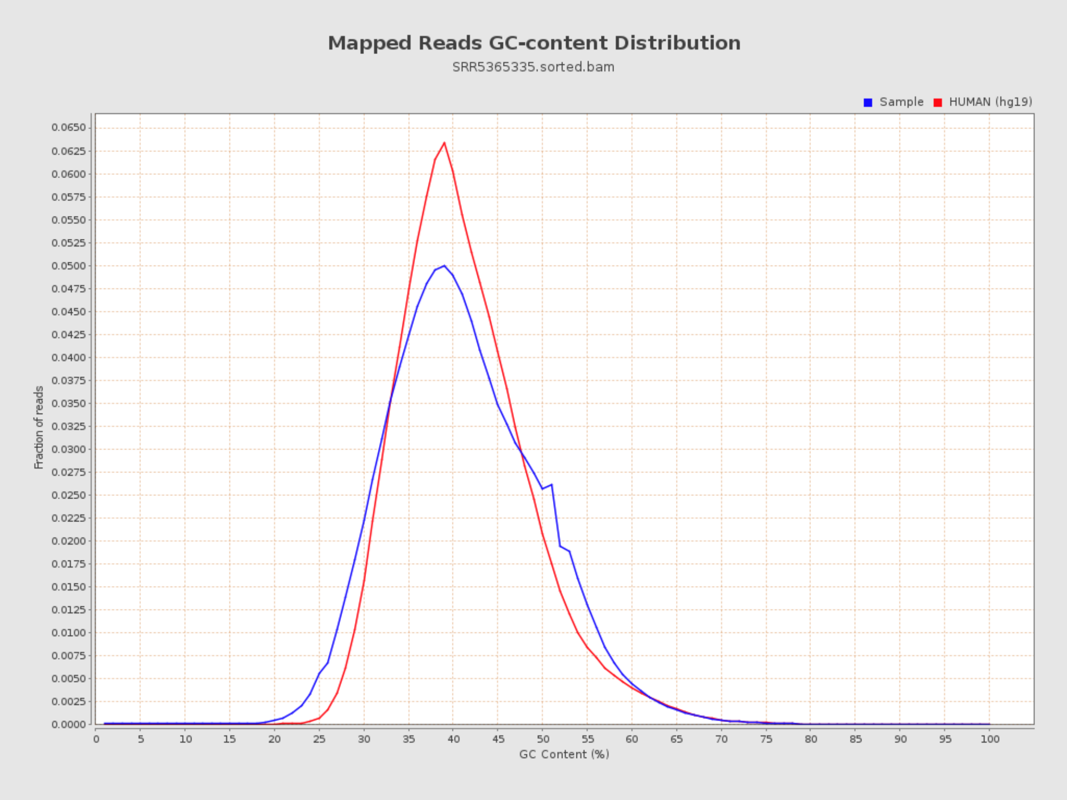
7. Results : Duplication Rate Histogram



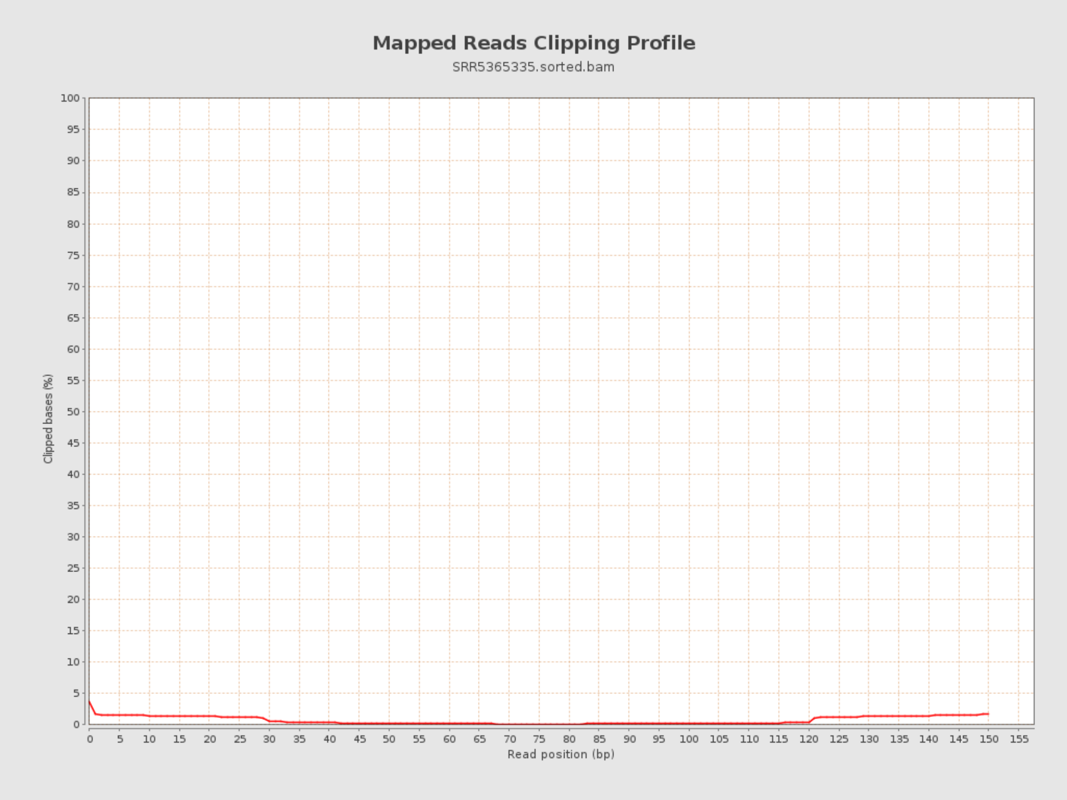
8. Results : Mapped Reads Nucleotide Content



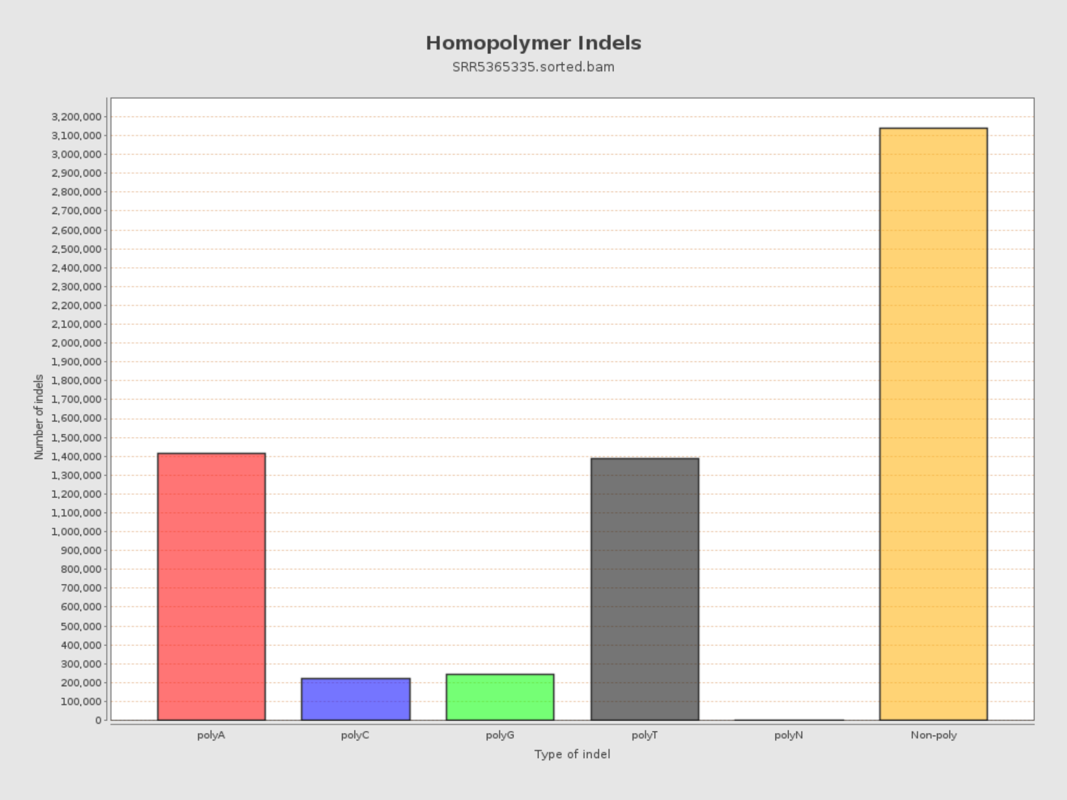
9. Results : Mapped Reads GC-content Distribution



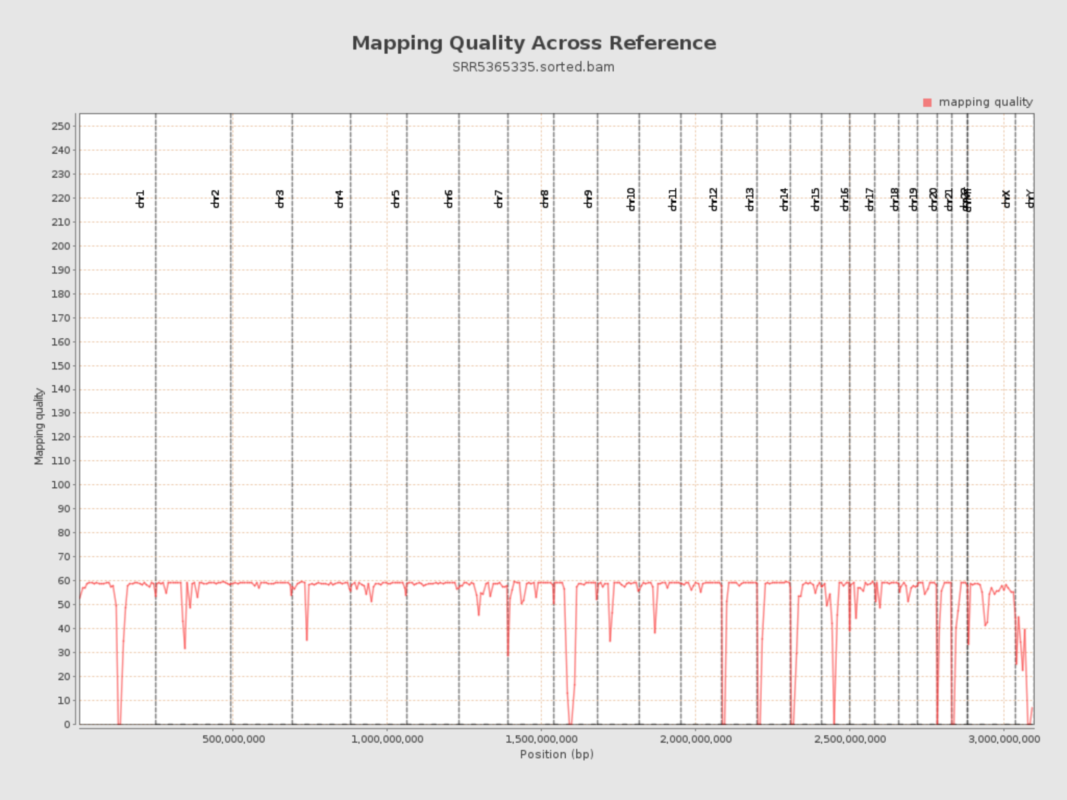
10. Results : Mapped Reads Clipping Profile



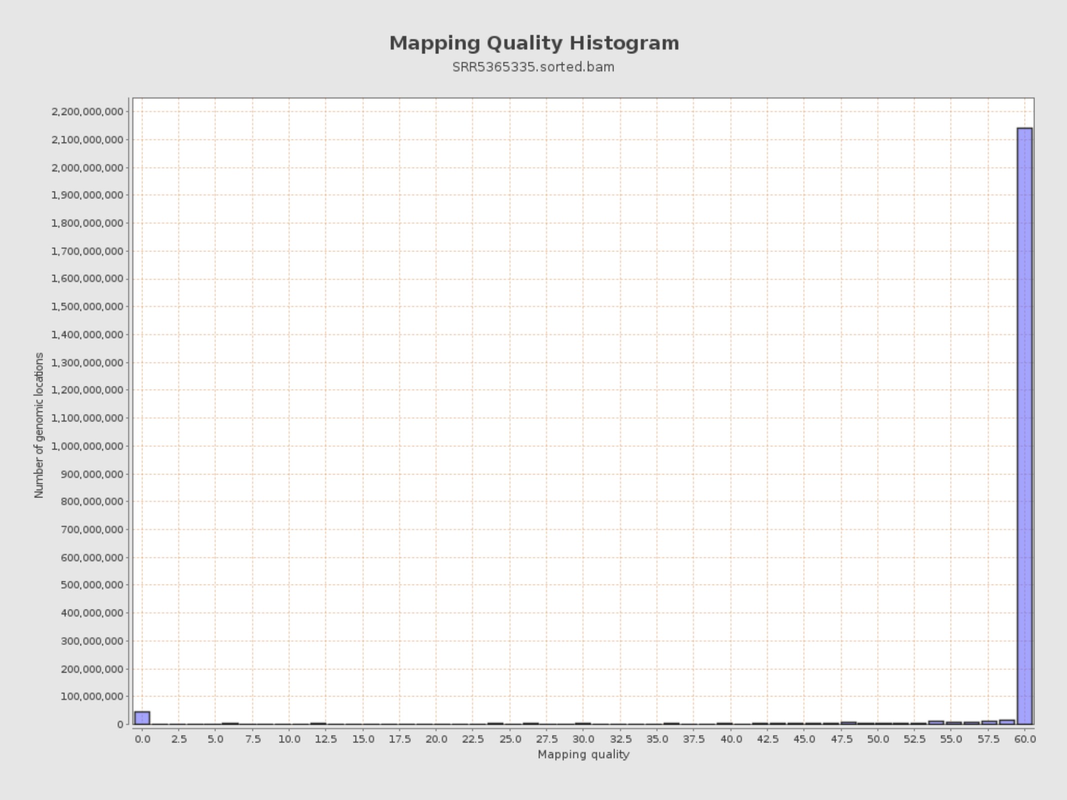
11. Results : Homopolymer Indels



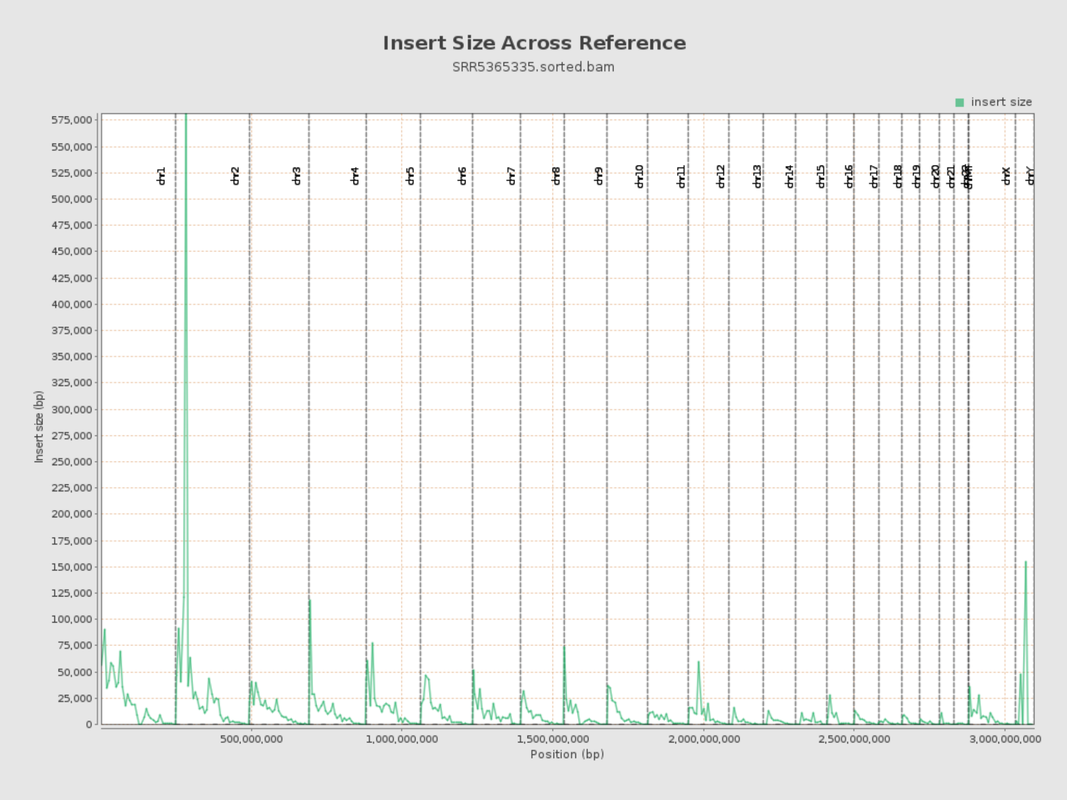
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram