Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/02 01:30:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365332.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_SRR5365332 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365332_1.fastq.gz SRR5365332_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Nov 02 01:29:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365332.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	96,559,960
Mapped reads	94,152,541 / 97.51%
Unmapped reads	2,407,419 / 2.49%
Mapped paired reads	94,152,541 / 97.51%
Mapped reads, first in pair	47,356,125 / 49.04%
Mapped reads, second in pair	46,796,416 / 48.46%
Mapped reads, both in pair	93,446,546 / 96.78%
Mapped reads, singletons	705,995 / 0.73%
Secondary alignments	0
Supplementary alignments	782,373 / 0.81%
Read min/max/mean length	30 / 151 / 151.36
Duplicated reads (estimated)	39,715,049 / 41.13%
Duplication rate	30.8%
Clipped reads	57,138,084 / 59.17%

2.2. ACGT Content

Number/percentage of A's	3,654,944,973 / 29.58%
Number/percentage of C's	2,485,233,223 / 20.11%
Number/percentage of T's	3,604,091,279 / 29.17%
Number/percentage of G's	2,612,030,270 / 21.14%
Number/percentage of N's	723,609 / 0.01%

GC Percentage	41.25%

2.3. Coverage

Mean	3.9931
Standard Deviation	38.484

2.4. Mapping Quality

Mean Mapping Quality	54.19

2.5. Insert size

Mean	97,127.16
Standard Deviation	3,082,814.4
P25/Median/P75	148 / 203 / 279

2.6. Mismatches and indels

General error rate	0.8%
Mismatches	92,132,270
Insertions	3,631,631
Mapped reads with at least one insertion	3.74%
Deletions	1,873,302
Mapped reads with at least one deletion	1.93%
Homopolymer indels	50.28%

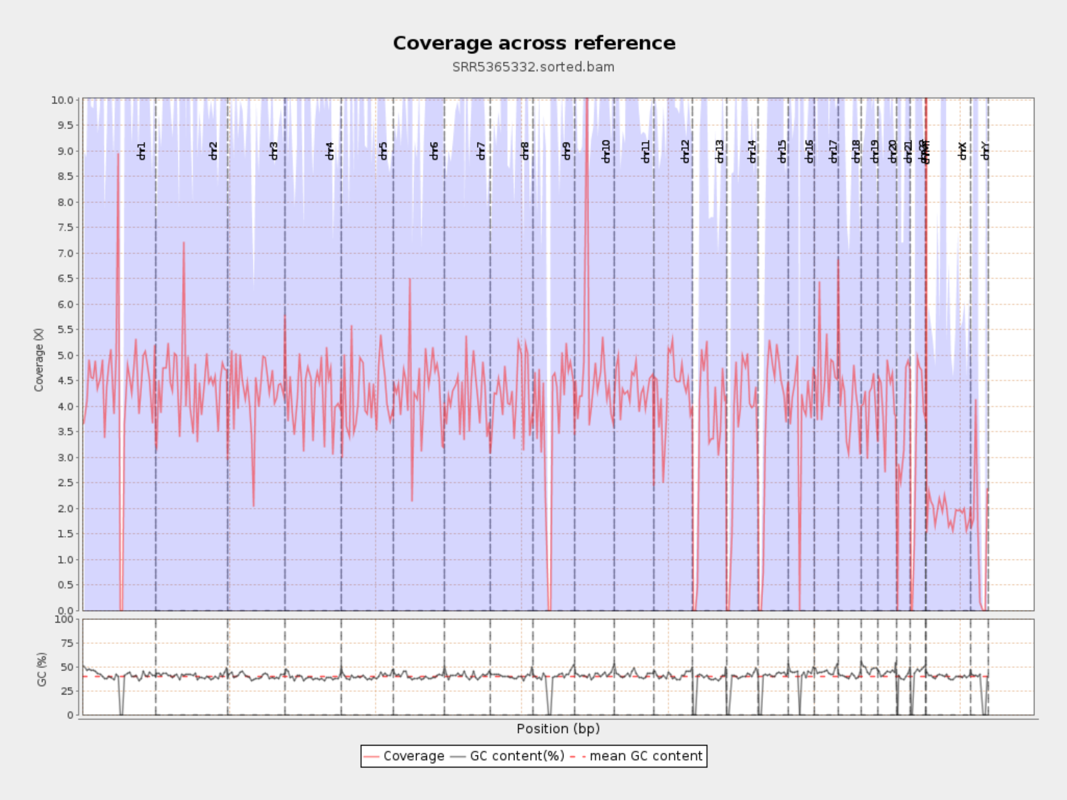
2.7. Chromosome stats

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

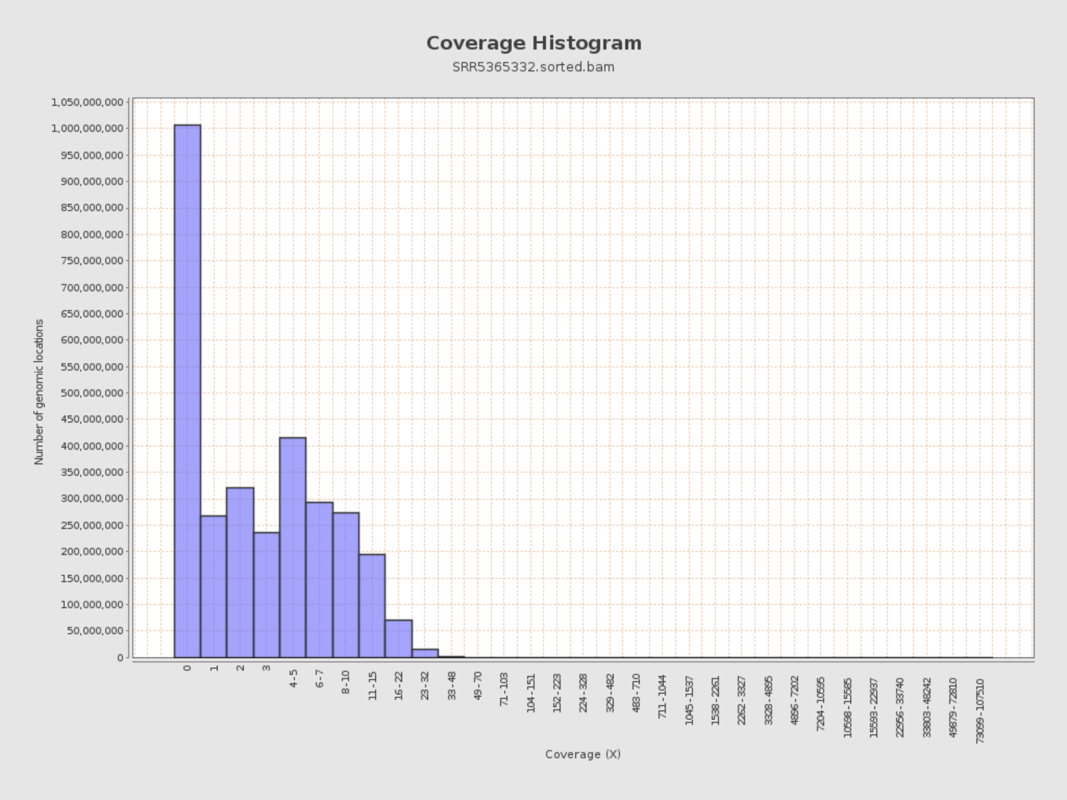
		bases	**coverage**	**deviation**
chr1	249250621	1087339889	4.3624	105.9131
chr2	243199373	1088512249	4.4758	25.2256
chr3	198022430	846134517	4.2729	5.5227
chr4	191154276	806398361	4.2186	16.2406
chr5	180915260	761579934	4.2096	5.4634
chr6	171115067	740297370	4.3263	21.5441
chr7	159138663	666181399	4.1862	24.2162
chr8	146364022	616661369	4.2132	13.9868
chr9	141213431	534387557	3.7843	37.5706
chr10	135534747	636624775	4.6971	63.3927
chr11	135006516	589925006	4.3696	27.4497
chr12	133851895	581305053	4.3429	24.0431
chr13	115169878	391826215	3.4022	4.5109
chr14	107349540	382817375	3.5661	4.9544
chr15	102531392	369468689	3.6035	11.8452
chr16	90354753	351003674	3.8847	12.1547
chr17	81195210	378853812	4.666	24.2286
chr18	78077248	319408567	4.0909	38.1397
chr19	59128983	236455466	3.999	53.7829
chr20	63025520	261190615	4.1442	7.5918
chr21	48129895	163882085	3.405	12.1263
chr22	51304566	159292603	3.1048	10.5771
chrMT	16571	7939867	479.1423	109.0718
chrX	155270560	297403909	1.9154	8.8539

chrY	59373566	86674149	1.4598	28.6286

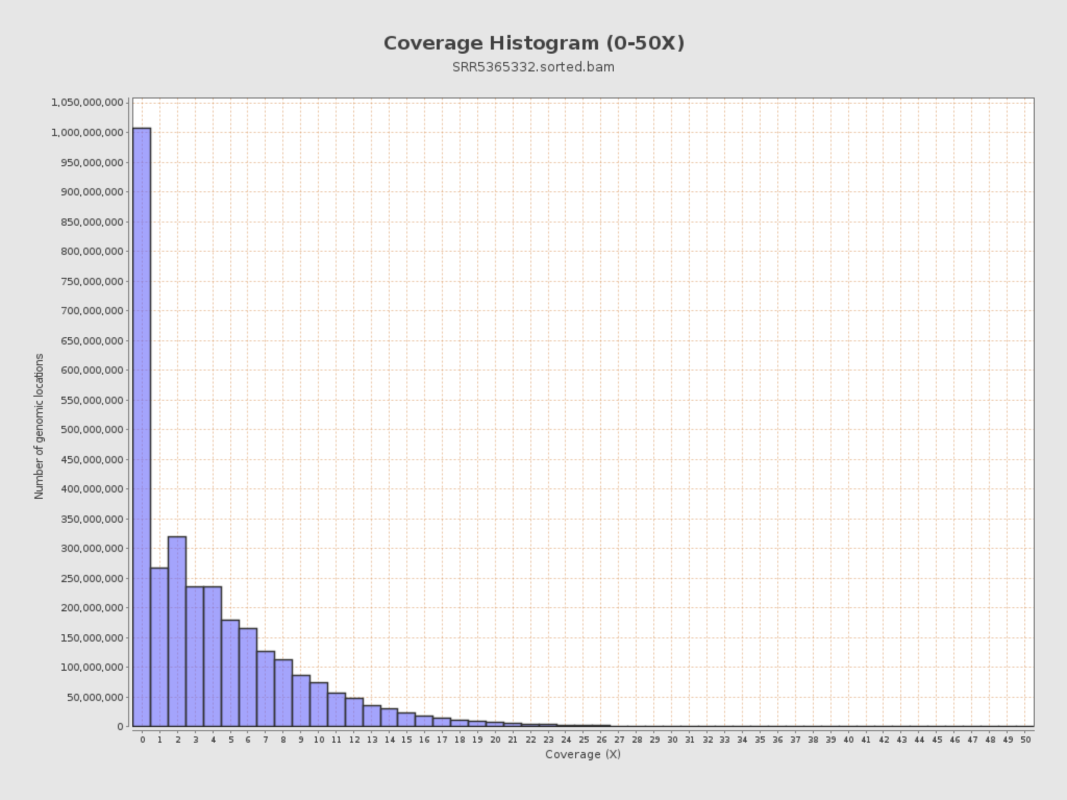
3. Results : Coverage across reference



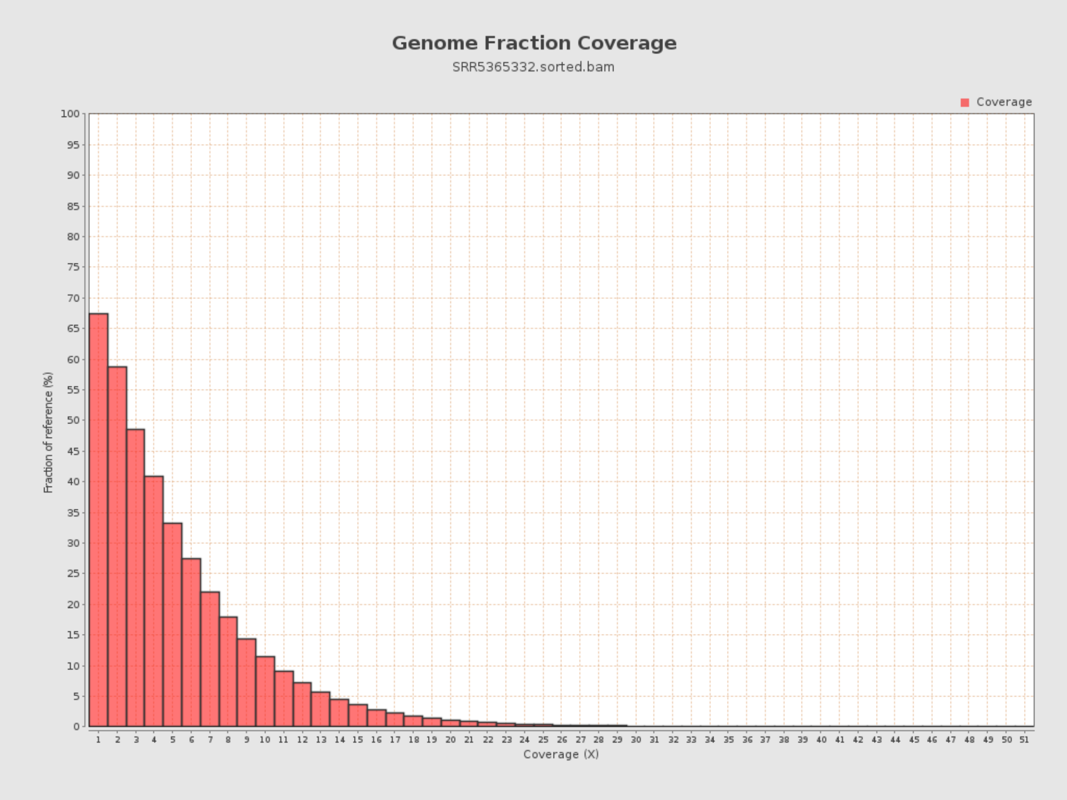
4. Results : Coverage Histogram



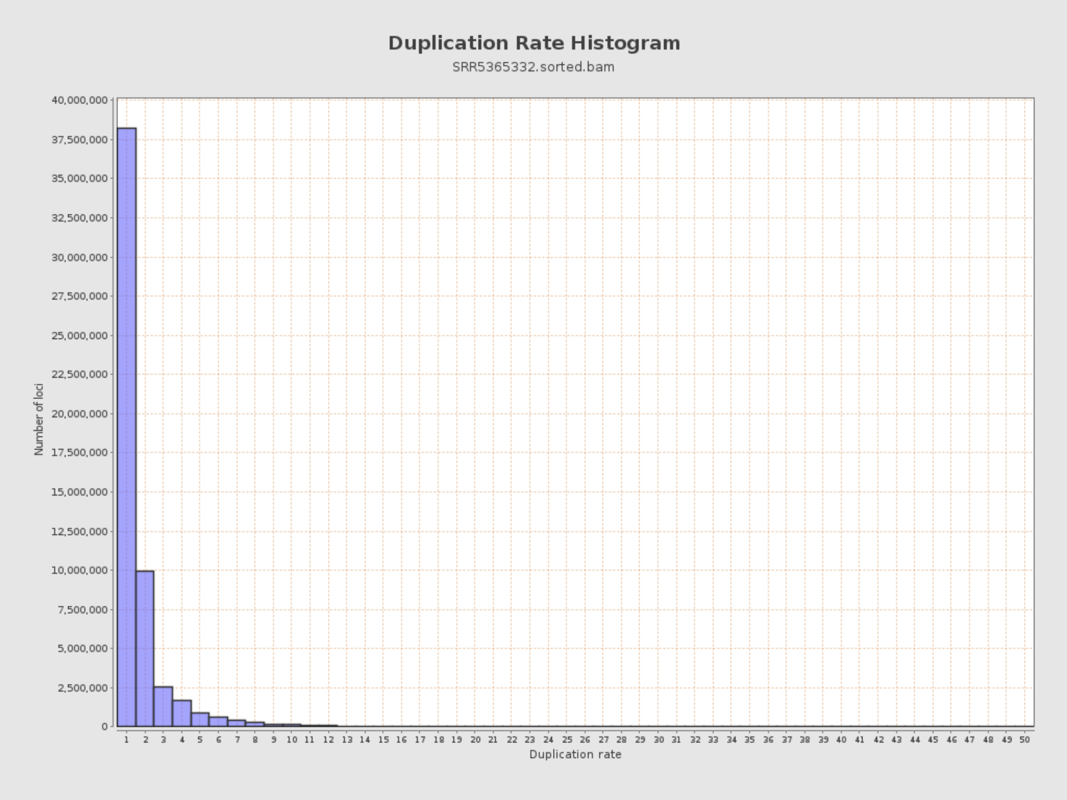
5. Results : Coverage Histogram (0-50X)



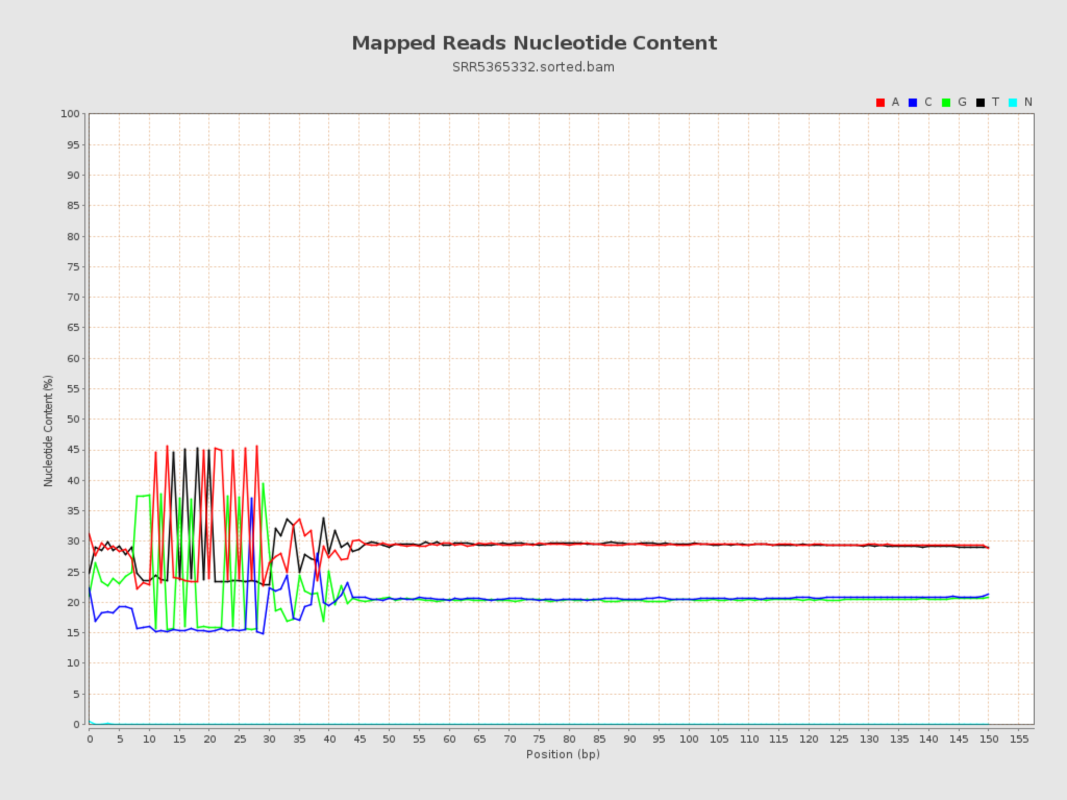
6. Results : Genome Fraction Coverage



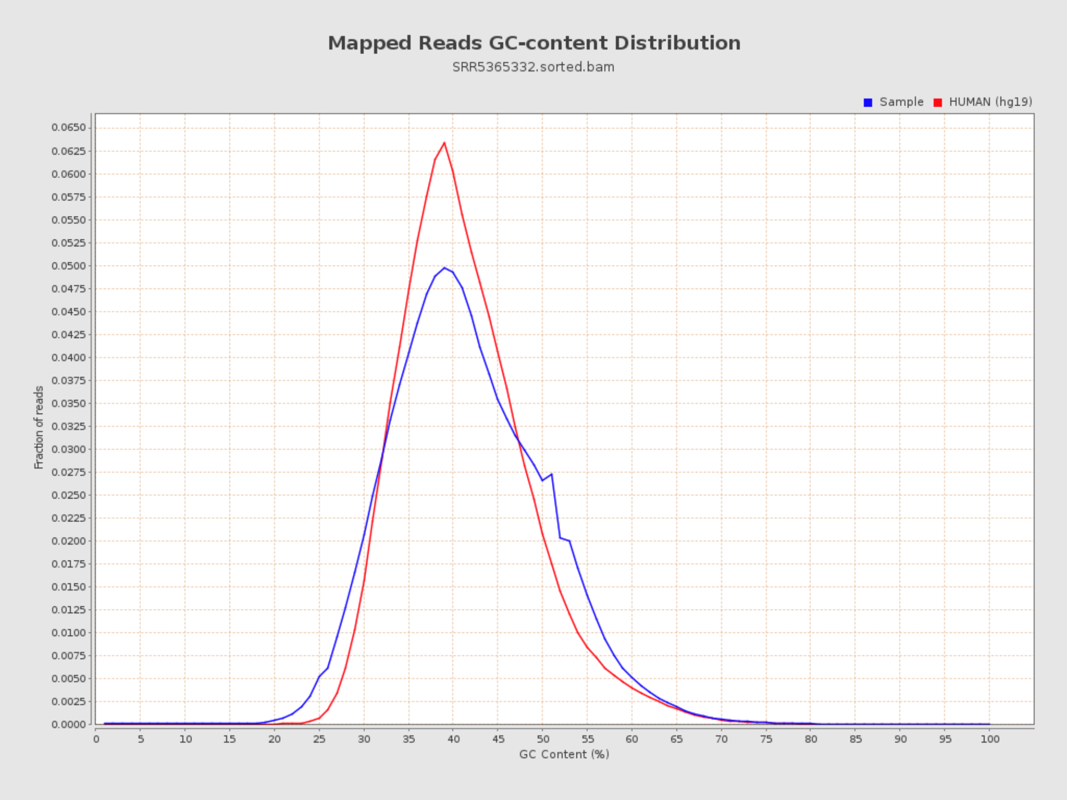
7. Results : Duplication Rate Histogram



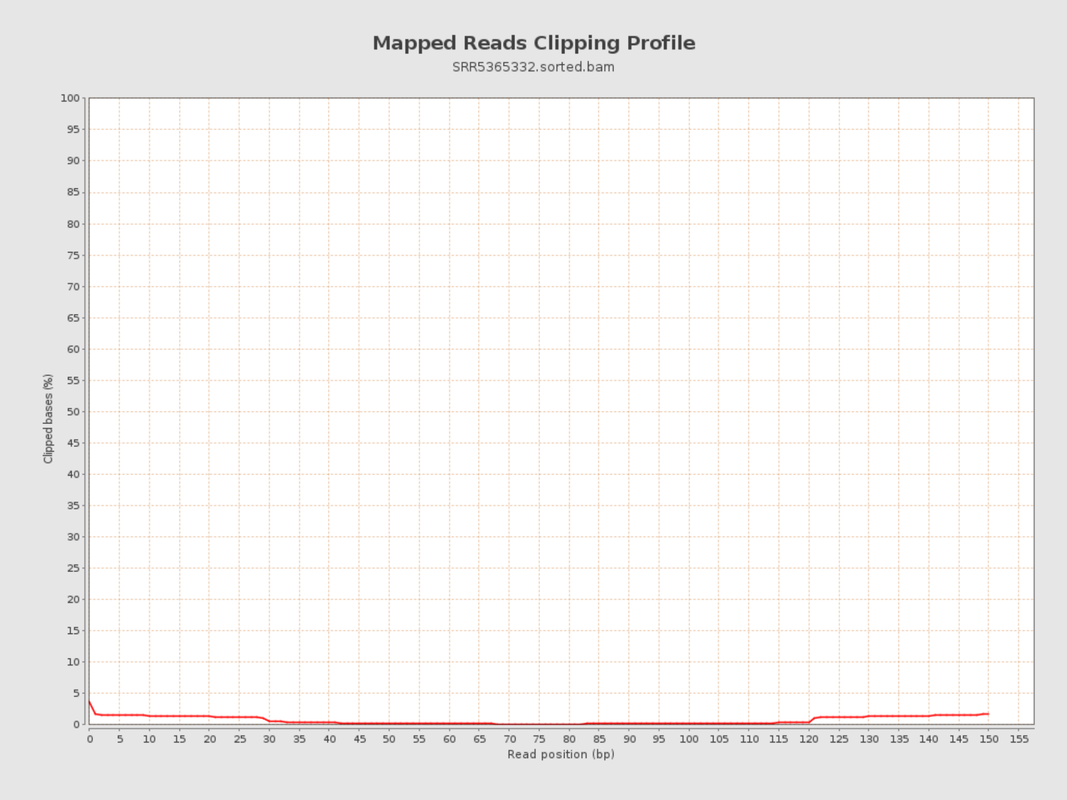
8. Results : Mapped Reads Nucleotide Content



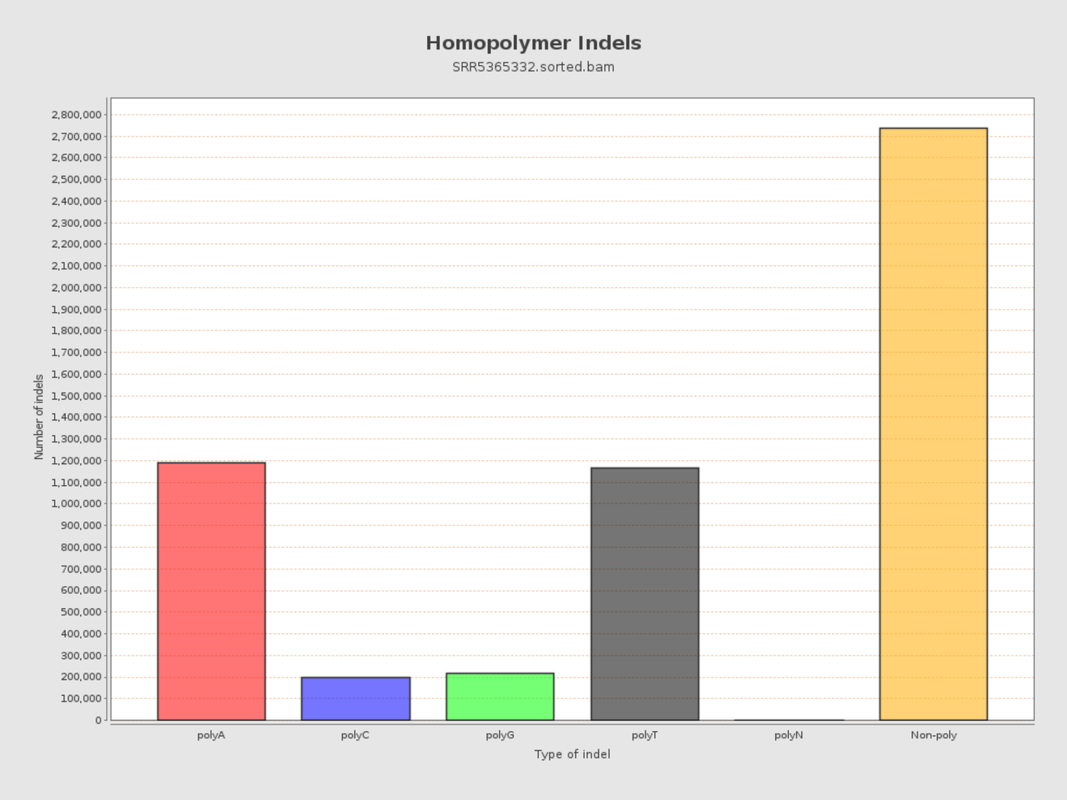
9. Results : Mapped Reads GC-content Distribution



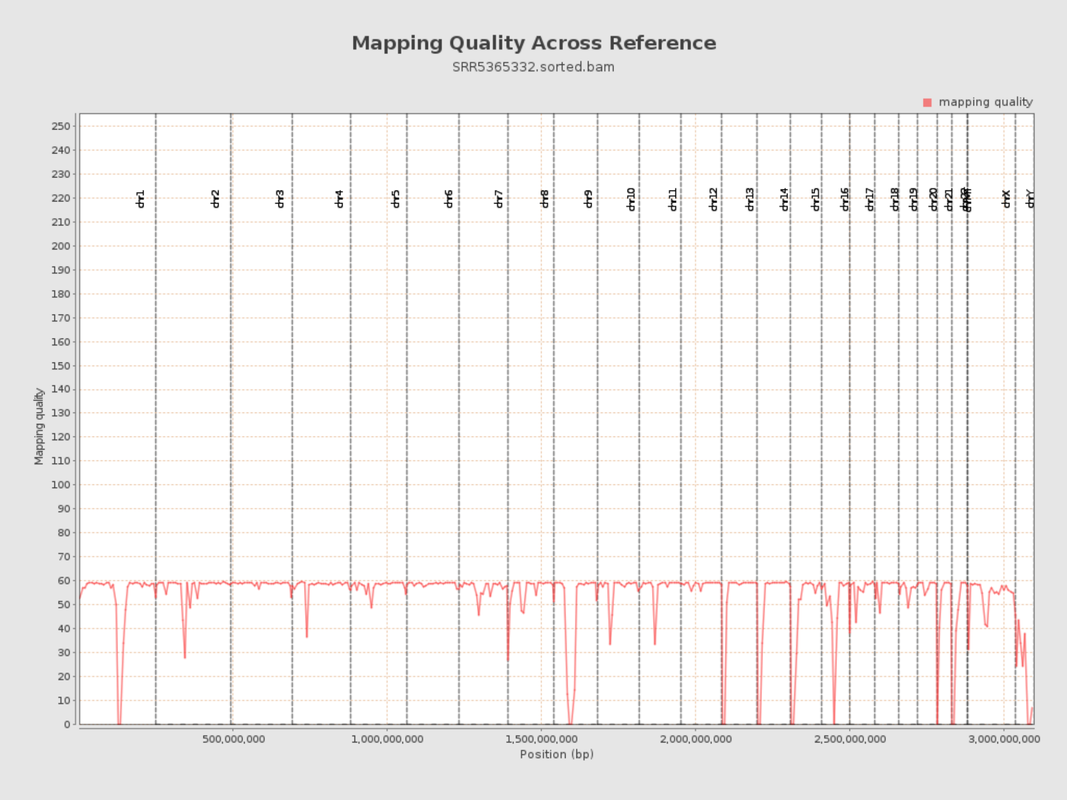
10. Results : Mapped Reads Clipping Profile



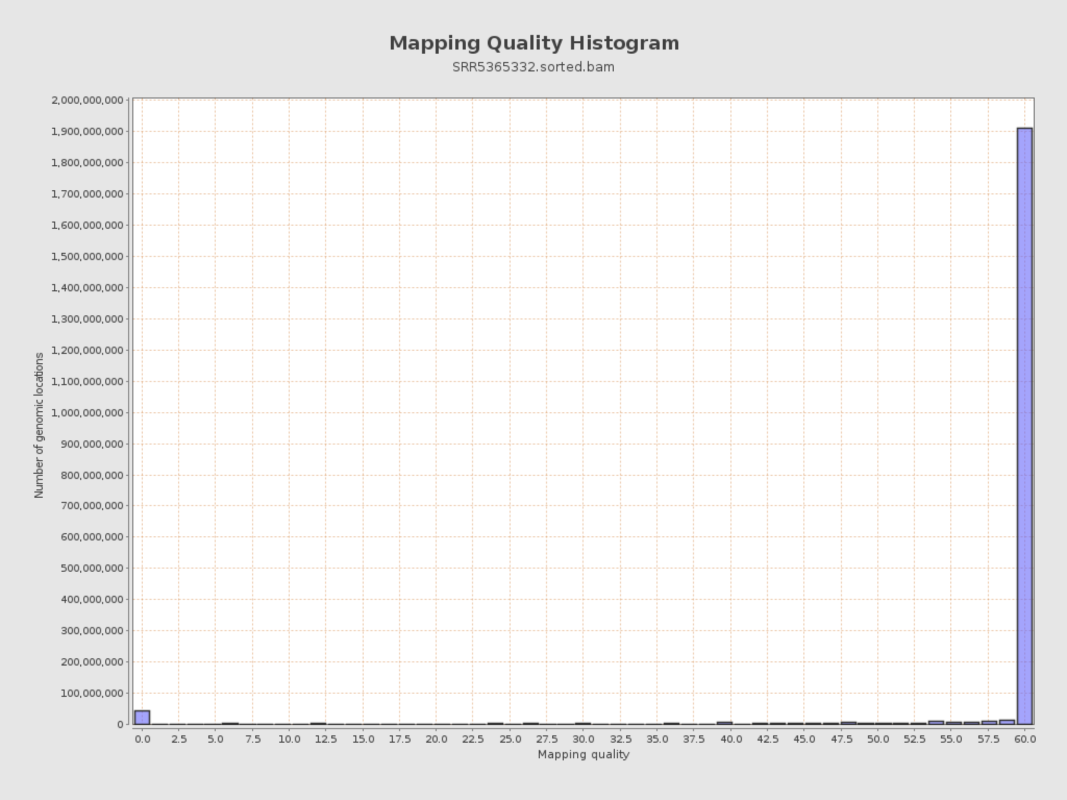
11. Results : Homopolymer Indels



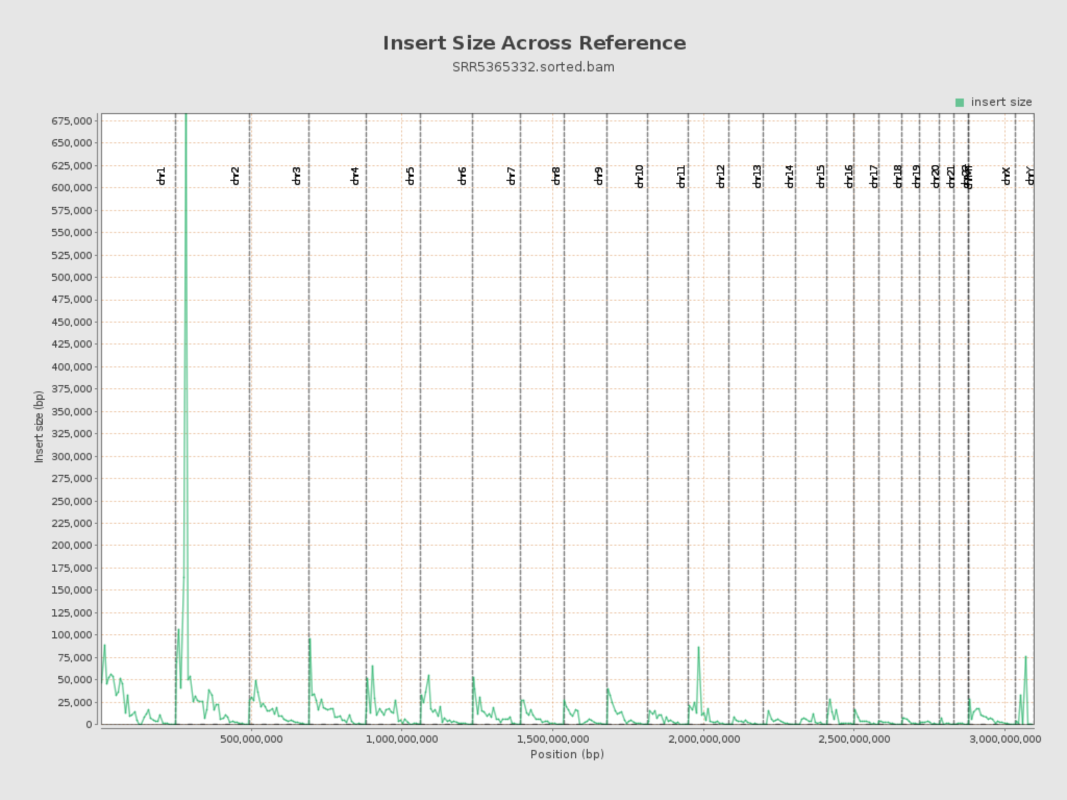
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram