Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/02 17:16:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365338.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_SRR5365338 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365338_1.fastq.gz SRR5365338_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Nov 02 17:16:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365338.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	122,090,618
Mapped reads	119,096,413 / 97.55%
Unmapped reads	2,994,205 / 2.45%
Mapped paired reads	119,096,413 / 97.55%
Mapped reads, first in pair	59,833,932 / 49.01%
Mapped reads, second in pair	59,262,481 / 48.54%
Mapped reads, both in pair	118,345,500 / 96.93%
Mapped reads, singletons	750,913 / 0.62%
Secondary alignments	0
Supplementary alignments	903,554 / 0.74%
Read min/max/mean length	30 / 151 / 151.33
Duplicated reads (estimated)	57,621,804 / 47.2%
Duplication rate	34.37%
Clipped reads	72,214,602 / 59.15%

2.2. ACGT Content

Number/percentage of A's	4,616,944,590 / 29.57%
Number/percentage of C's	3,144,763,779 / 20.14%
Number/percentage of T's	4,548,053,178 / 29.13%
Number/percentage of G's	3,303,139,308 / 21.16%
Number/percentage of N's	907,988 / 0.01%

GC Percentage	41.3%

2.3. Coverage

Mean	5.0456
Standard Deviation	46.8898

2.4. Mapping Quality

Mean Mapping Quality	54.23

2.5. Insert size

Mean	73,078.46
Standard Deviation	2,672,574.81
P25/Median/P75	147 / 201 / 274

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	113,540,133
Insertions	4,529,215
Mapped reads with at least one insertion	3.69%
Deletions	2,363,573
Mapped reads with at least one deletion	1.92%
Homopolymer indels	50.24%

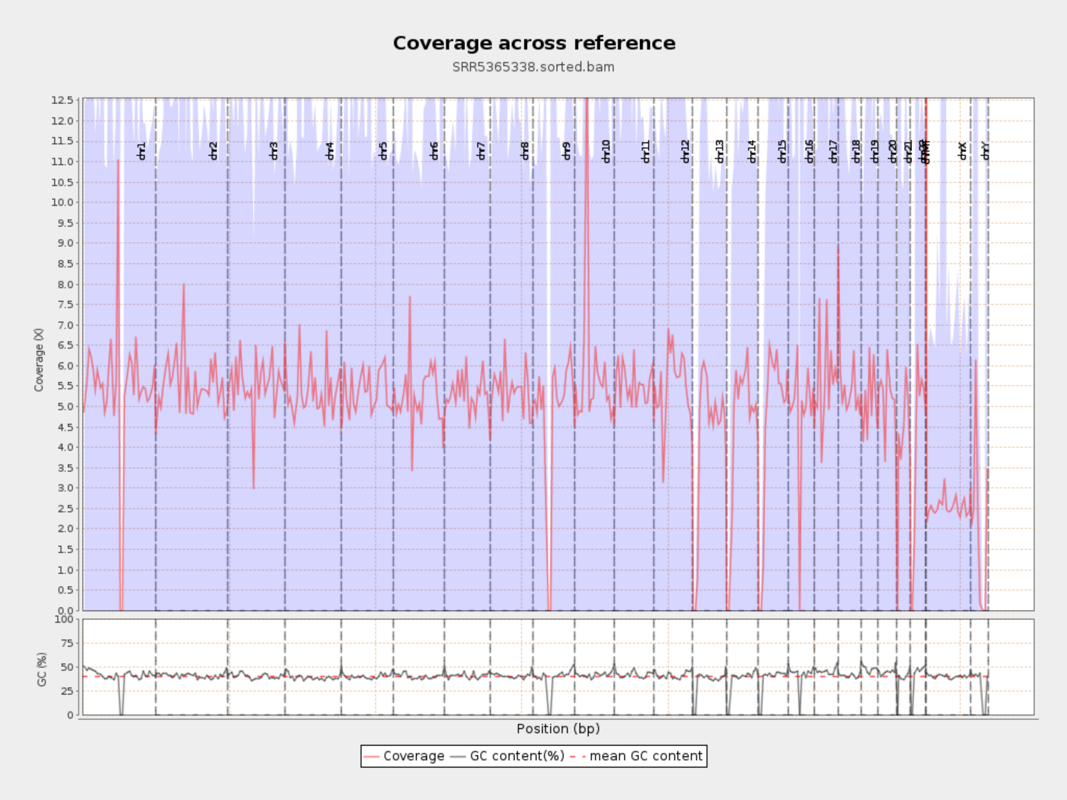
2.7. Chromosome stats

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

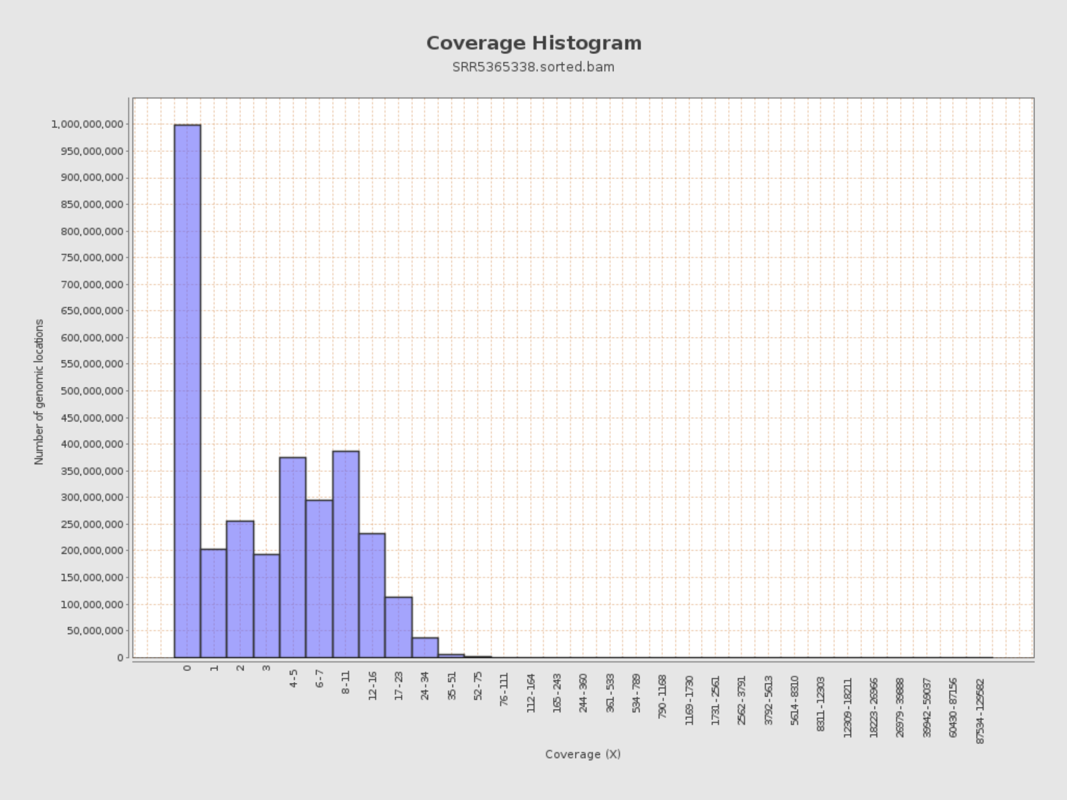
		bases	coverage	deviation
chr1	249250621	1353428020	5.43	128.5565
chr2	243199373	1353612234	5.5659	28.0389
chr3	198022430	1093024366	5.5197	7.1947
chr4	191154276	1028553334	5.3807	23.6602
chr5	180915260	974766999	5.388	7.2674
chr6	171115067	904342352	5.285	23.1589
chr7	159138663	842885075	5.2965	31.0027
chr8	146364022	789141147	5.3916	16.748
chr9	141213431	669215234	4.739	39.6062
chr10	135534747	795806445	5.8716	80.085
chr11	135006516	748918521	5.5473	35.2163
chr12	133851895	742856488	5.5498	26.7657
chr13	115169878	487130740	4.2297	5.6324
chr14	107349540	480917637	4.4799	6.169
chr15	102531392	459649265	4.483	13.7092
chr16	90354753	435545144	4.8204	14.6422
chr17	81195210	463352388	5.7066	27.0684
chr18	78077248	429242528	5.4977	47.755
chr19	59128983	302333862	5.1131	67.5295
chr20	63025520	329915134	5.2346	10.3083
chr21	48129895	202121662	4.1995	18.2764
chr22	51304566	199725429	3.8929	16.4495
chrMT	16571	14026153	846.4277	212.5649
chrX	155270560	394562316	2.5411	11.6733

chrY	59373566	124416706	2.0955	41.6672

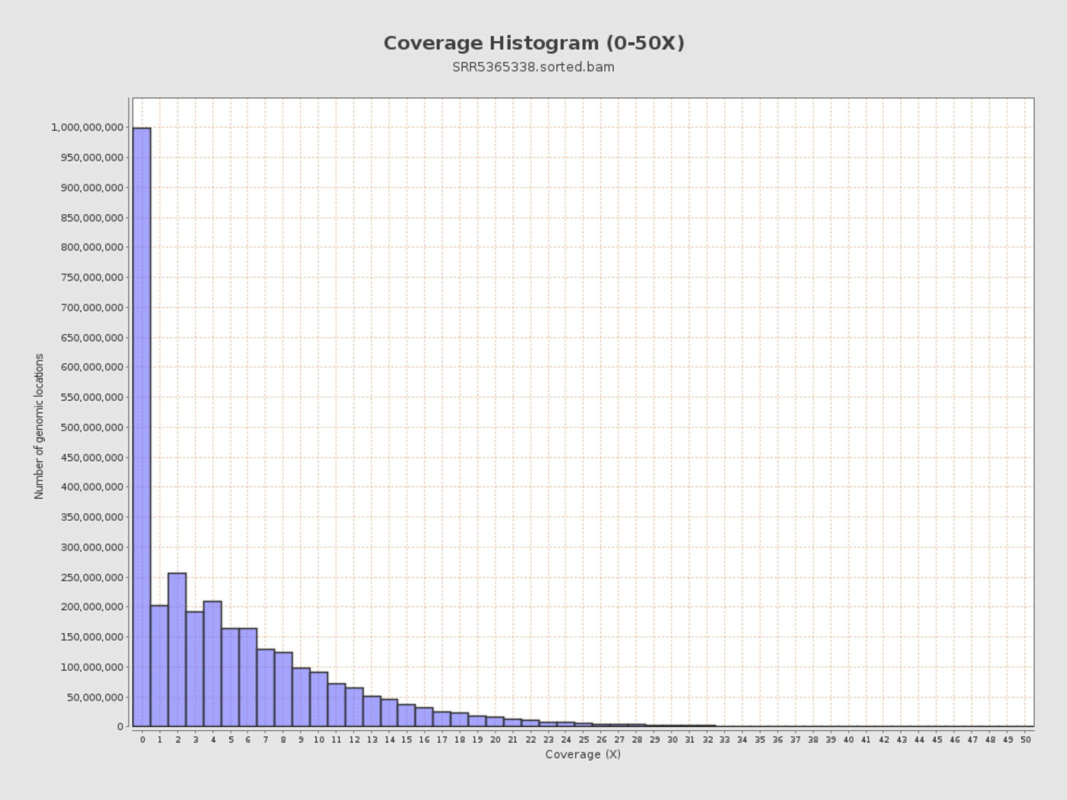
3. Results : Coverage across reference



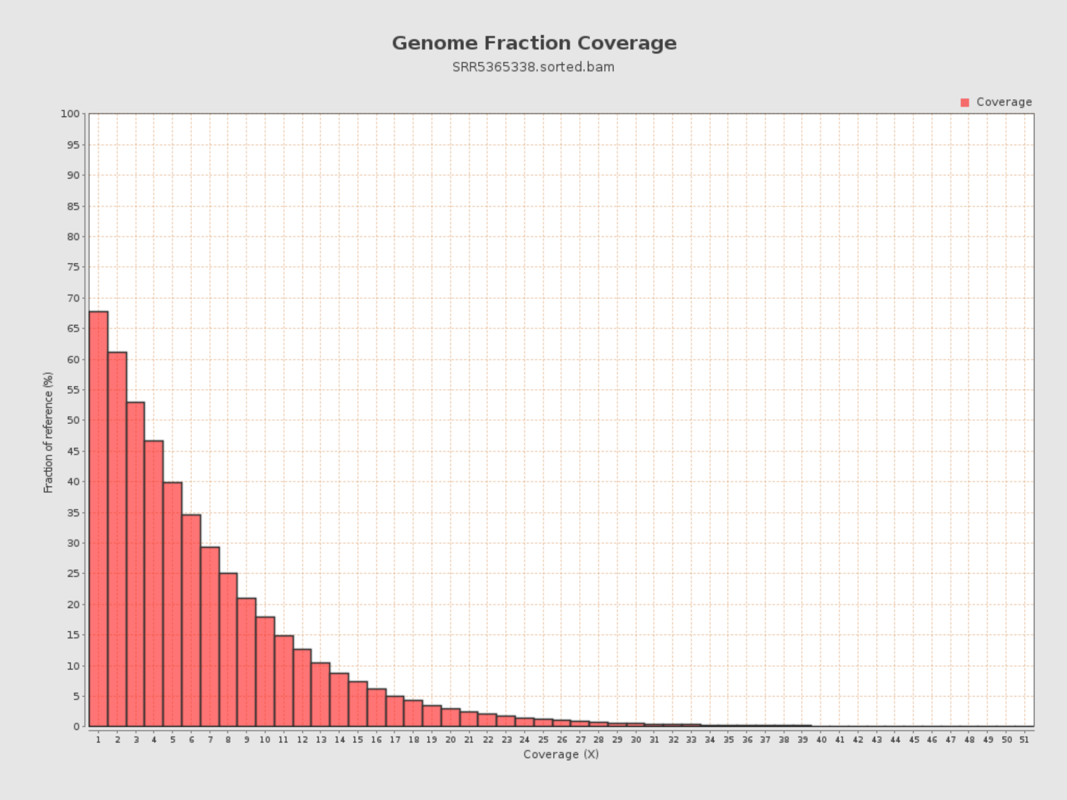
4. Results : Coverage Histogram



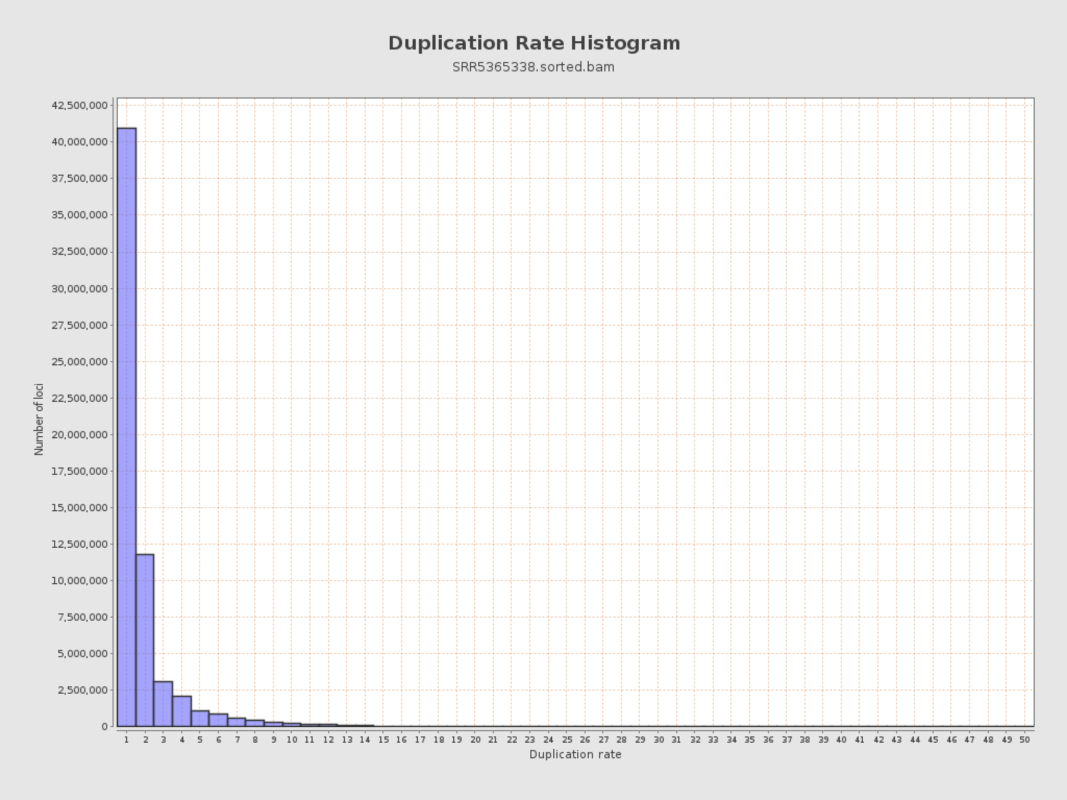
5. Results : Coverage Histogram (0-50X)



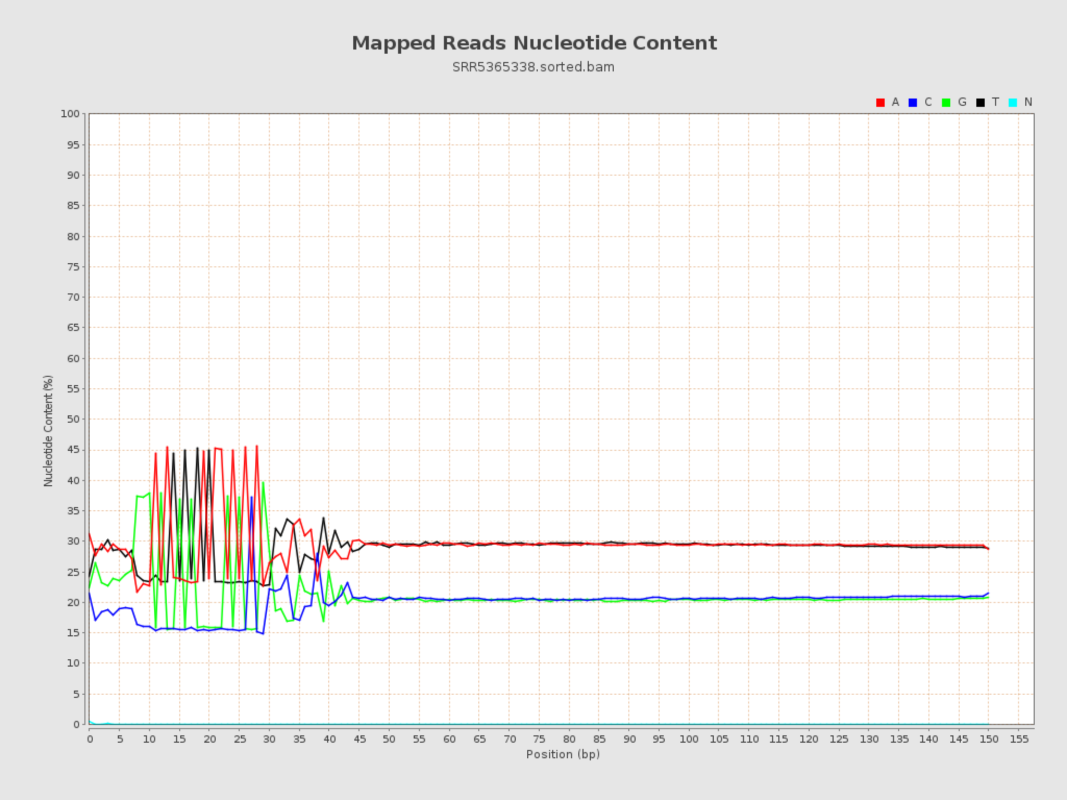
6. Results : Genome Fraction Coverage



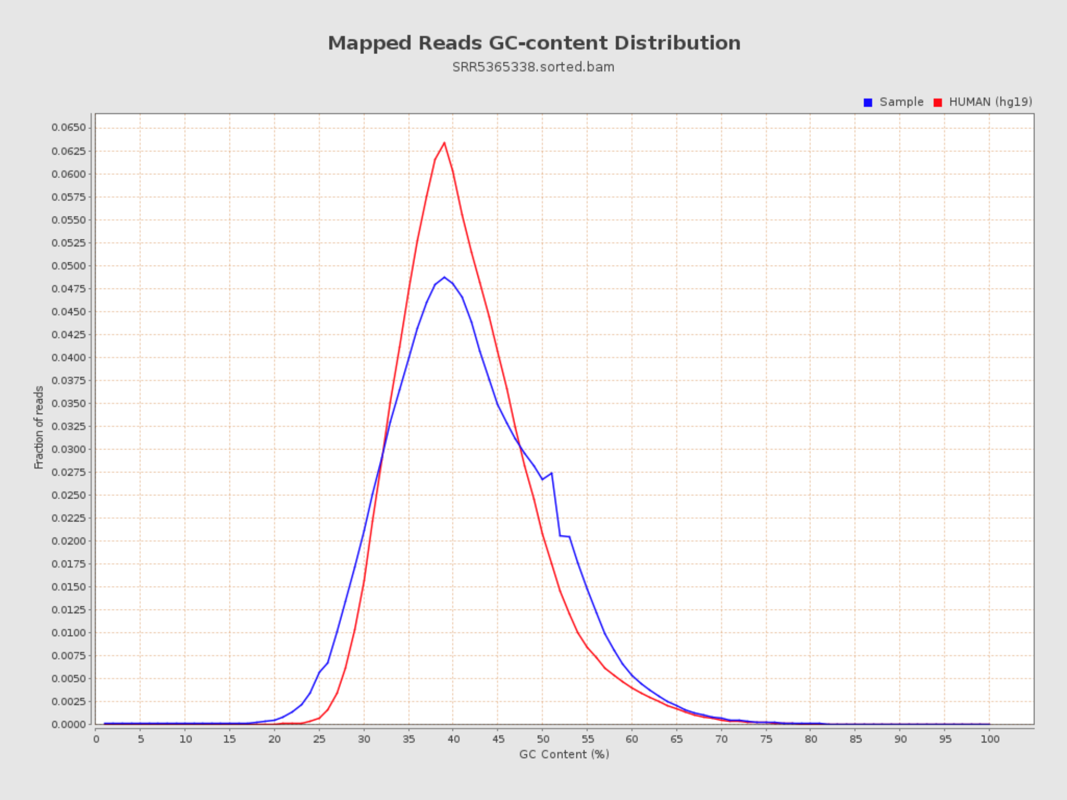
7. Results : Duplication Rate Histogram



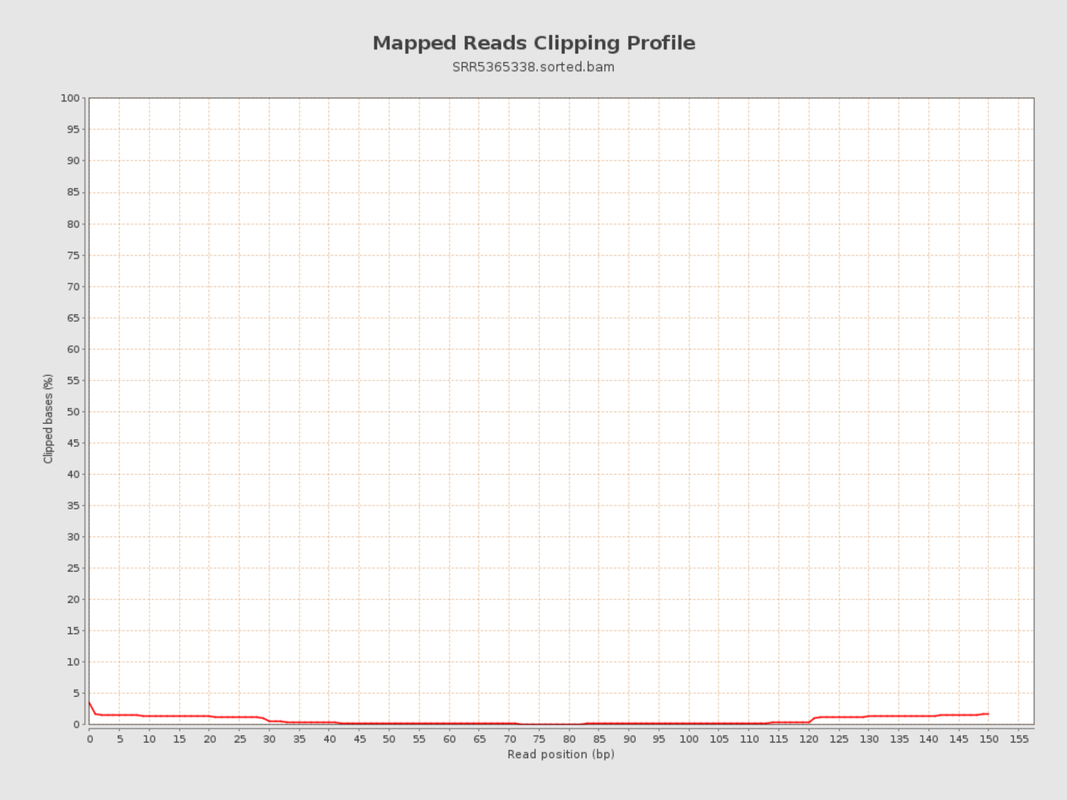
8. Results : Mapped Reads Nucleotide Content



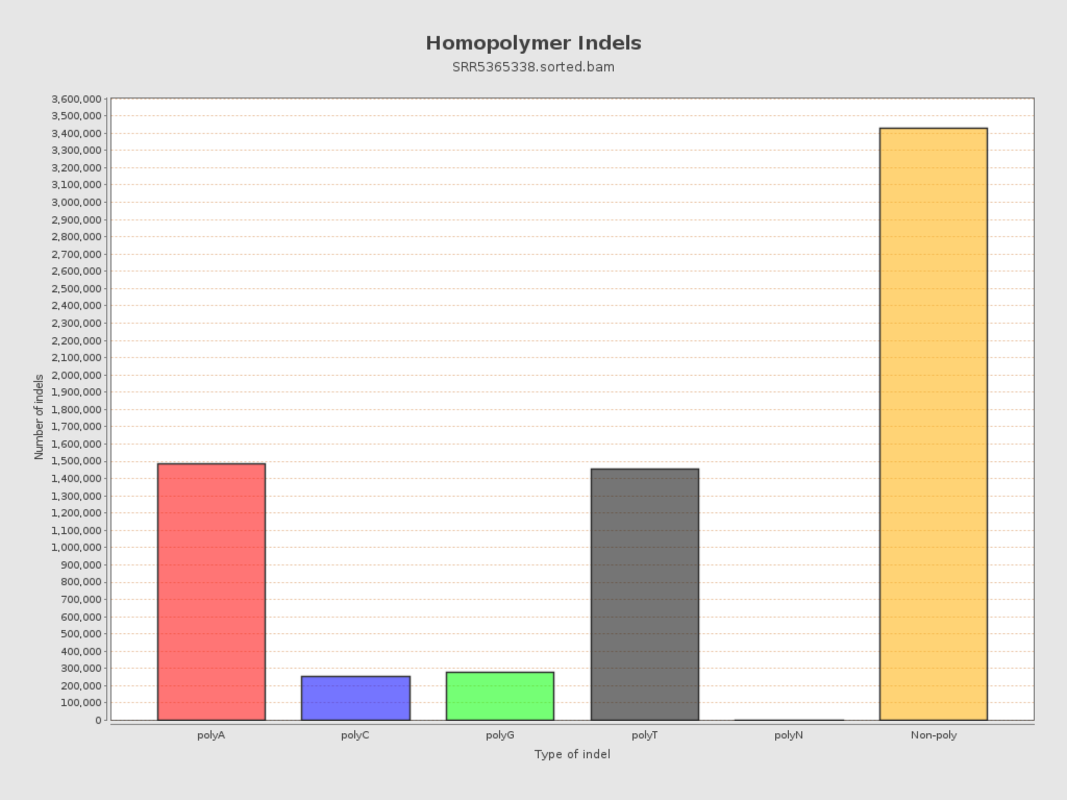
9. Results : Mapped Reads GC-content Distribution



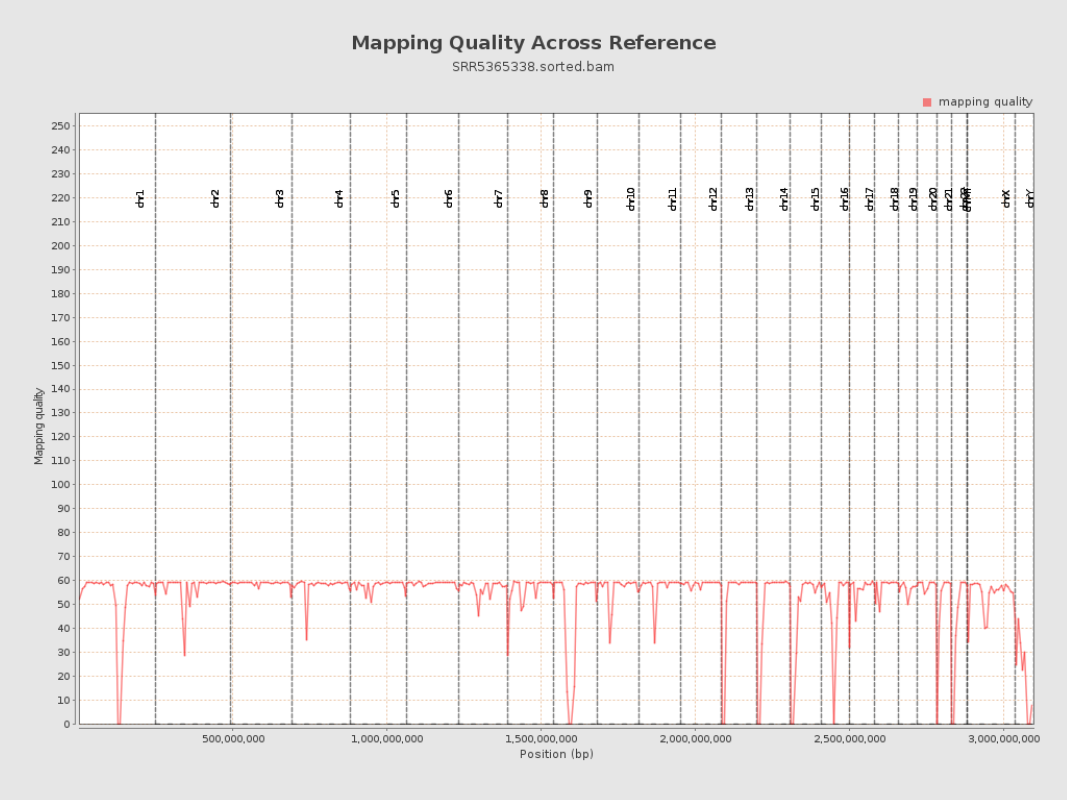
10. Results : Mapped Reads Clipping Profile



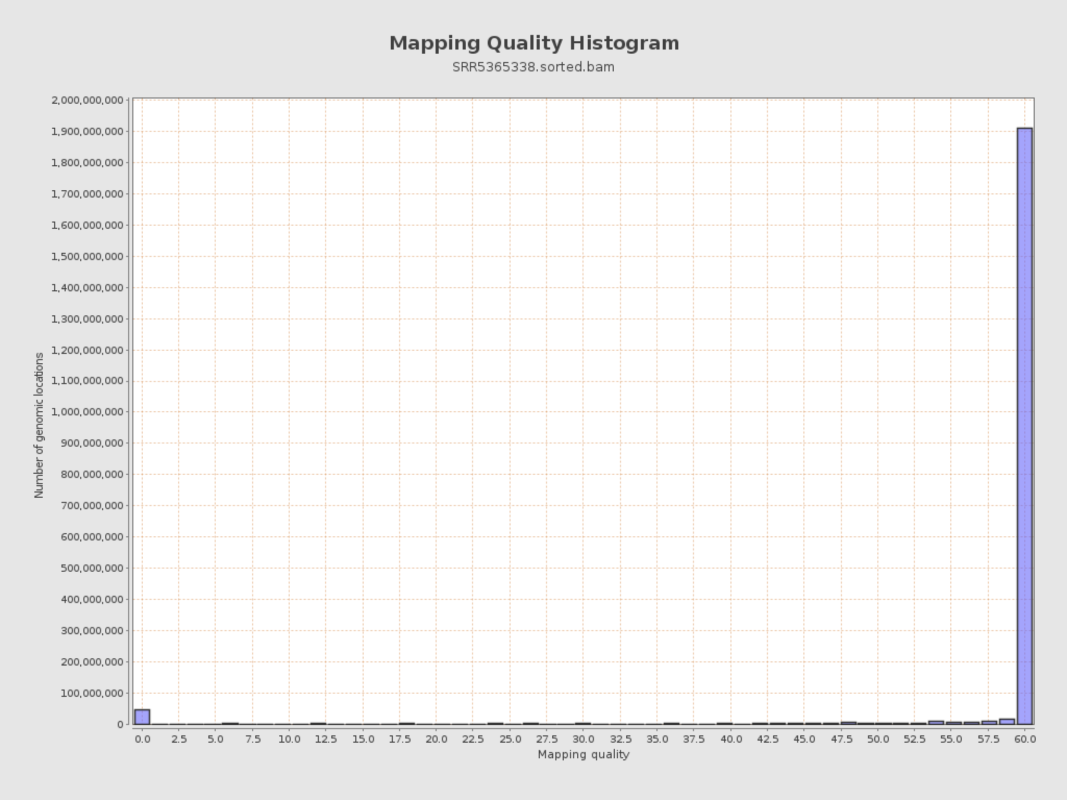
11. Results : Homopolymer Indels



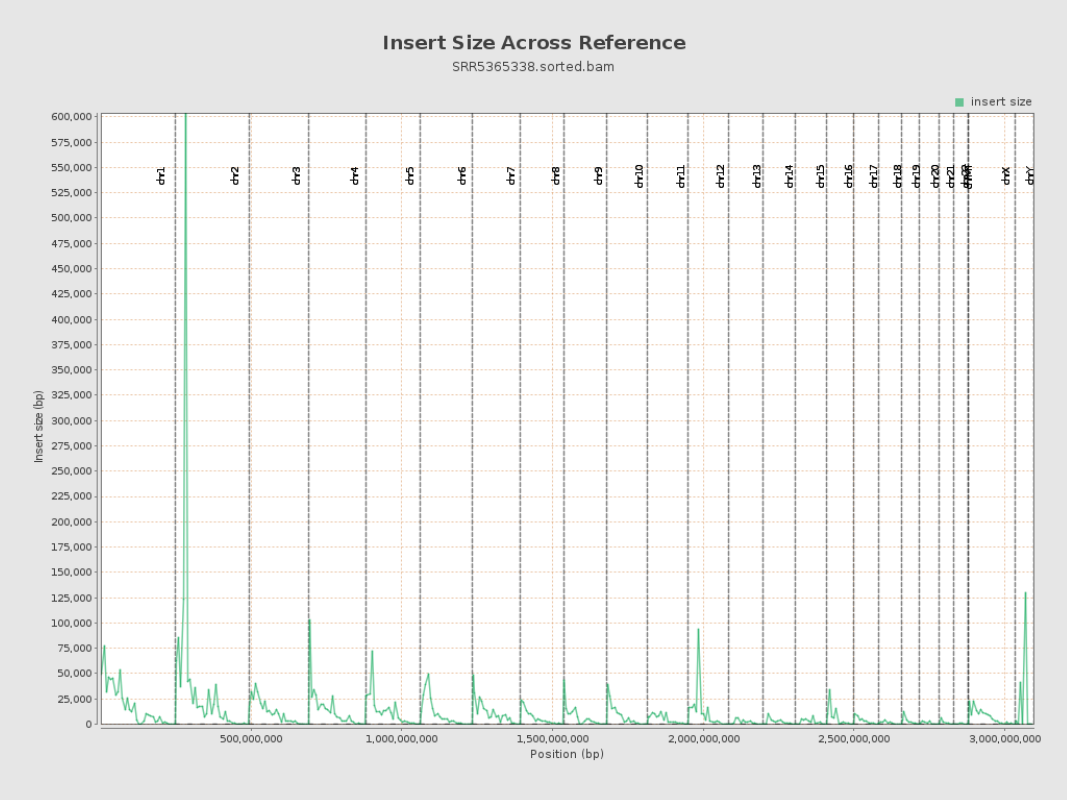
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram