Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/03 15:54:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365343.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_SRR5365343 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365343_1.fastq.gz SRR5365343_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Nov 03 15:54:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365343.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	510,014,896
Mapped reads	488,468,428 / 95.78%
Unmapped reads	21,546,468 / 4.22%
Mapped paired reads	488,468,428 / 95.78%
Mapped reads, first in pair	244,823,078 / 48%
Mapped reads, second in pair	243,645,350 / 47.77%
Mapped reads, both in pair	485,304,404 / 95.15%
Mapped reads, singletons	3,164,024 / 0.62%
Secondary alignments	0
Supplementary alignments	2,359,533 / 0.46%
Read min/max/mean length	30 / 125 / 125.19
Duplicated reads (estimated)	347,755,175 / 68.19%
Duplication rate	41.64%
Clipped reads	349,057,853 / 68.44%

2.2. ACGT Content

Number/percentage of A's	14,818,148,222 / 29.81%
Number/percentage of C's	9,798,112,213 / 19.71%
Number/percentage of T's	14,339,437,317 / 28.84%
Number/percentage of G's	10,734,184,411 / 21.59%
Number/percentage of N's	22,414,945 / 0.05%

GC Percentage	41.3%

2.3. Coverage

Mean	16.0641
Standard Deviation	185.2744

2.4. Mapping Quality

Mean Mapping Quality	53.45

2.5. Insert size

Mean	62,611.07
Standard Deviation	2,427,186.3
P25/Median/P75	122 / 189 / 294

2.6. Mismatches and indels

General error rate	0.69%
Mismatches	314,501,734
Insertions	15,261,129
Mapped reads with at least one insertion	3.05%
Deletions	8,116,418
Mapped reads with at least one deletion	1.62%
Homopolymer indels	49.4%

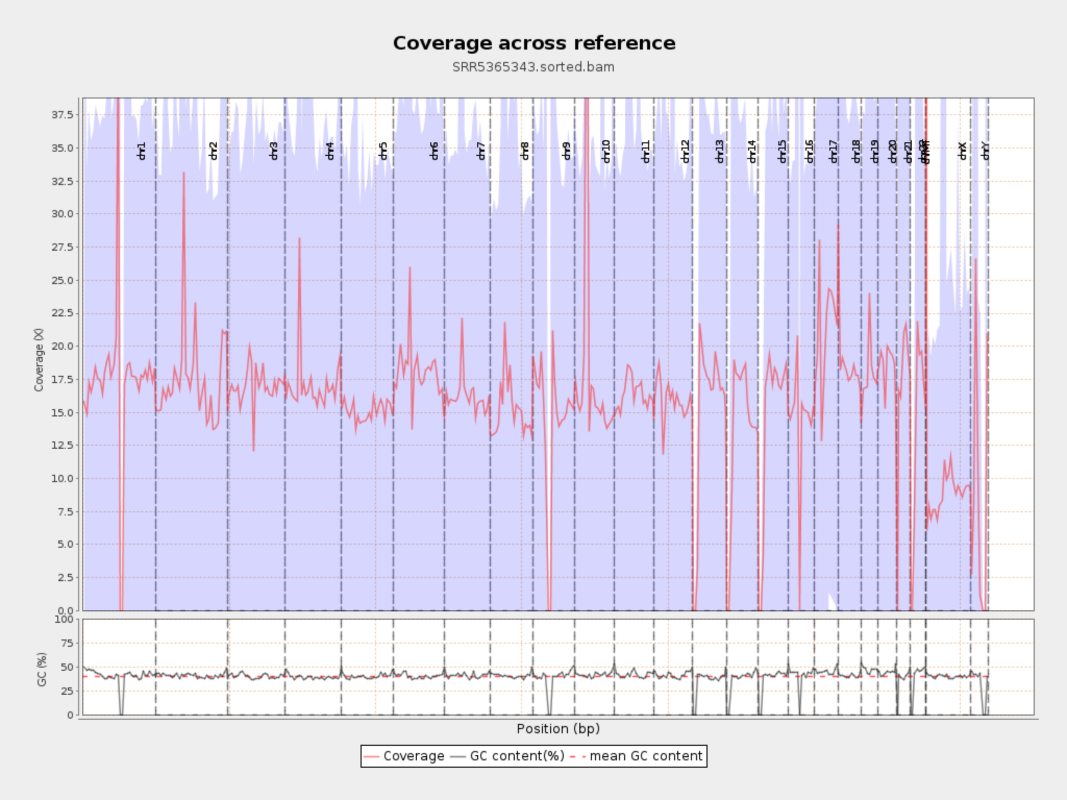
2.7. Chromosome stats

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

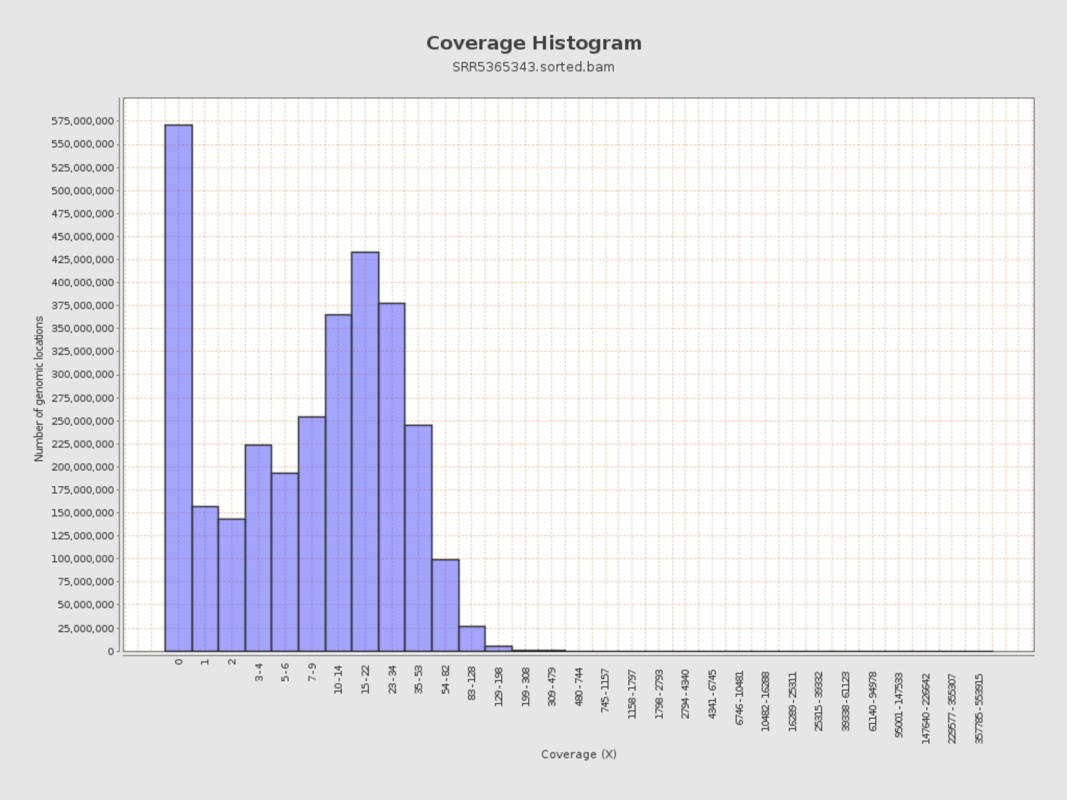
		bases	coverage	deviation
chr1	249250621	4343273141	17.4253	512.3539
chr2	243199373	4266776514	17.5444	107.3944
chr3	198022430	3360176145	16.9687	31.0745
chr4	191154276	3273098093	17.1228	94.5636
chr5	180915260	2728754522	15.0831	20.6423
chr6	171115067	3111659218	18.1846	74.7262
chr7	159138663	2587389931	16.2587	130.1289
chr8	146364022	2224954648	15.2015	67.2383
chr9	141213431	2032975045	14.3965	138.4457
chr10	135534747	2440575607	18.007	326.0477
chr11	135006516	2214013794	16.3993	109.4421
chr12	133851895	2137921511	15.9723	37.5269
chr13	115169878	1733125410	15.0484	19.3241
chr14	107349540	1482329718	13.8084	21.5
chr15	102531392	1463331242	14.272	24.6943
chr16	90354753	1289108669	14.2672	50.483
chr17	81195210	1738970377	21.4172	99.8604
chr18	78077248	1451123340	18.5857	180.3708
chr19	59128983	1068105421	18.064	250.0148
chr20	63025520	1172948083	18.6107	31.9344
chr21	48129895	821965412	17.0781	68.4995
chr22	51304566	687995367	13.41	64.2347
chrMT	16571	184629189	11,141.7047	2,132.6991
chrX	155270560	1375793640	8.8606	42.5351

chrY	59373566	538569799	9.0709	203.5605

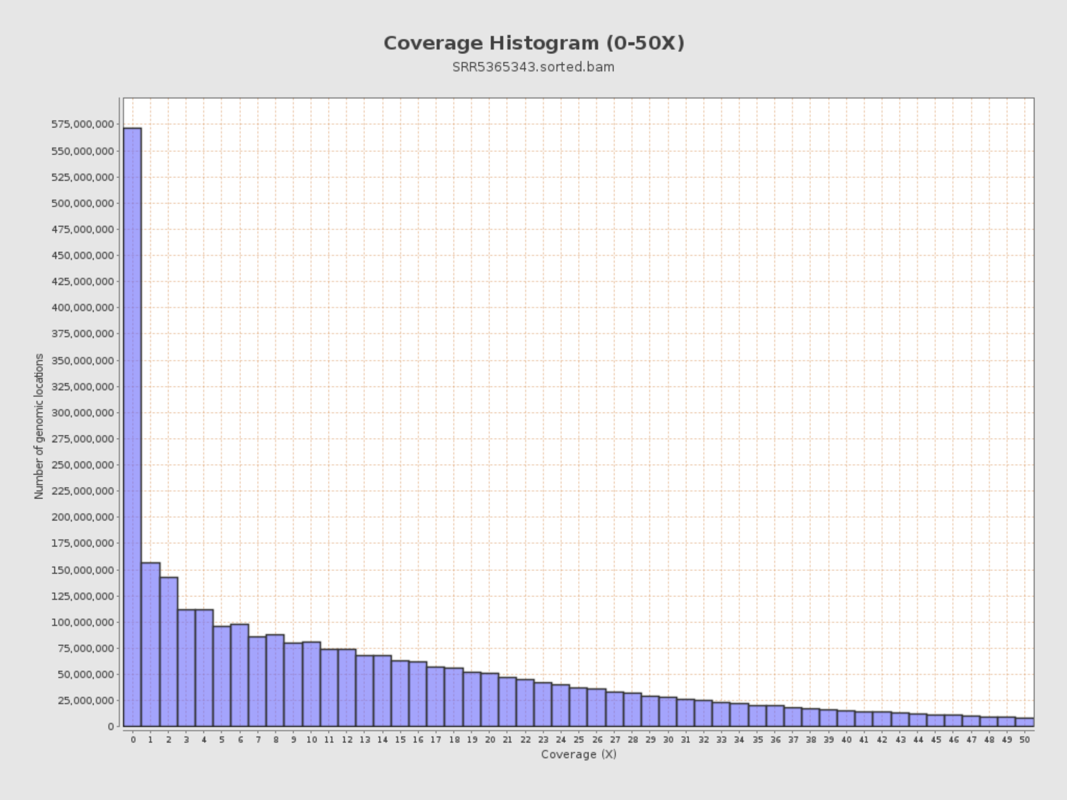
3. Results : Coverage across reference



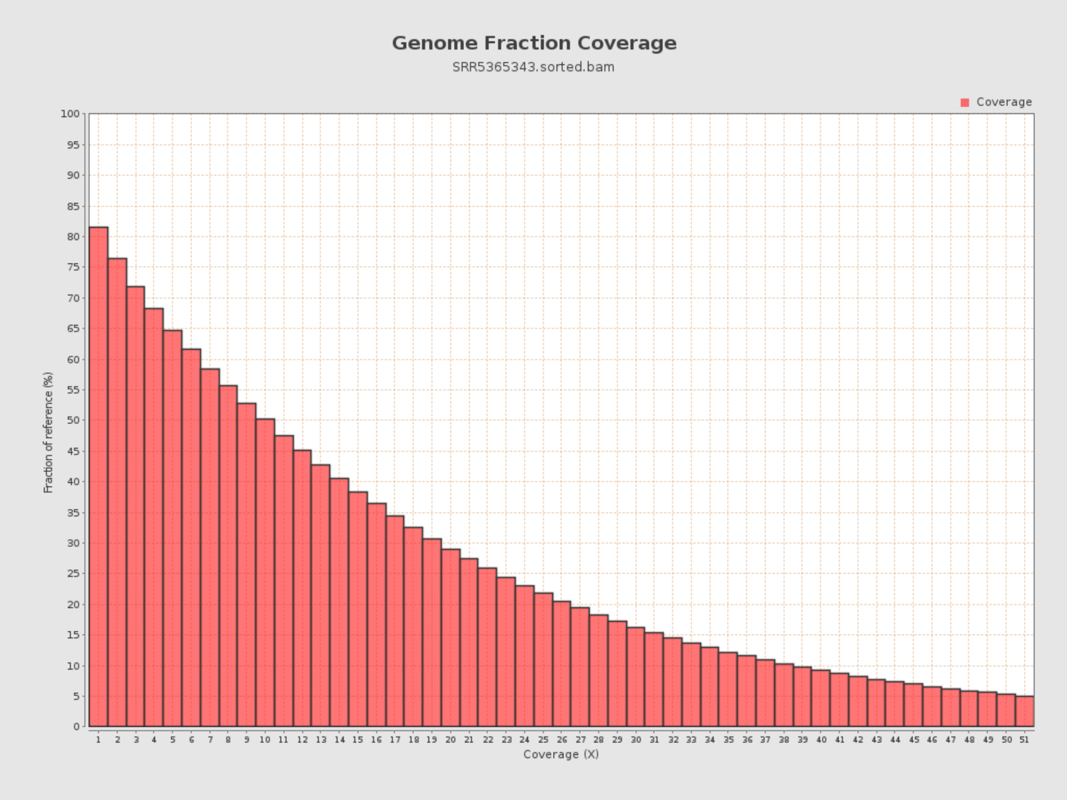
4. Results : Coverage Histogram



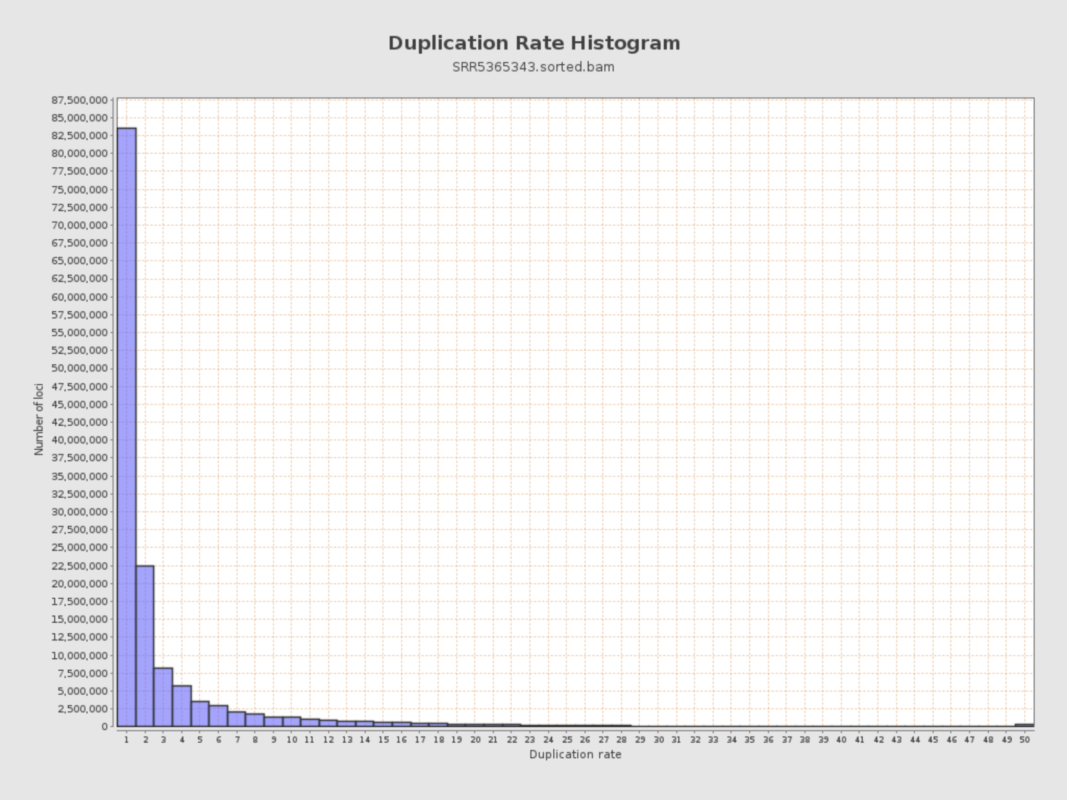
5. Results : Coverage Histogram (0-50X)



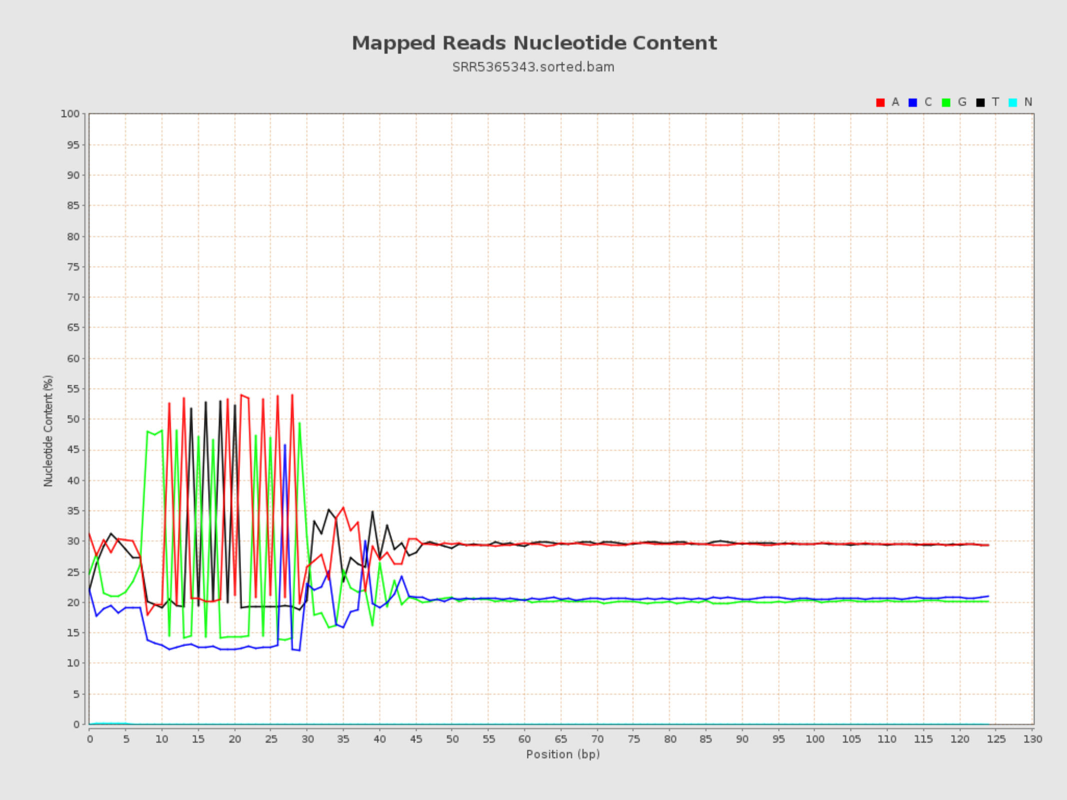
6. Results : Genome Fraction Coverage



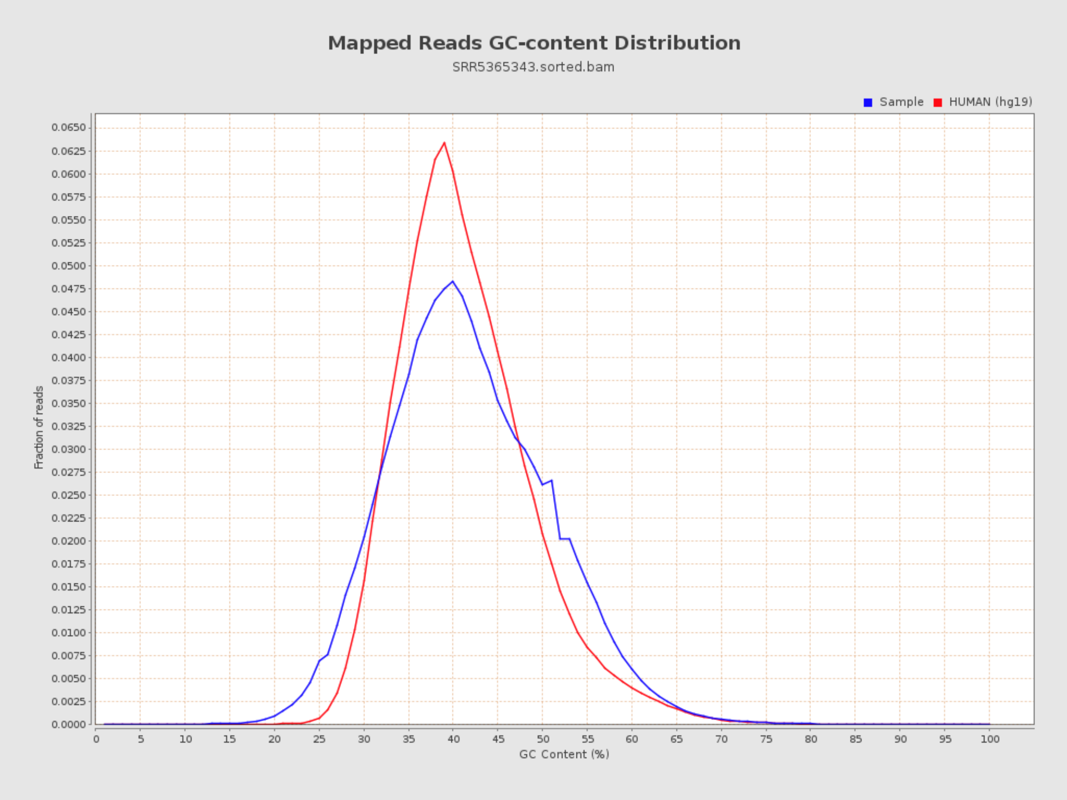
7. Results : Duplication Rate Histogram



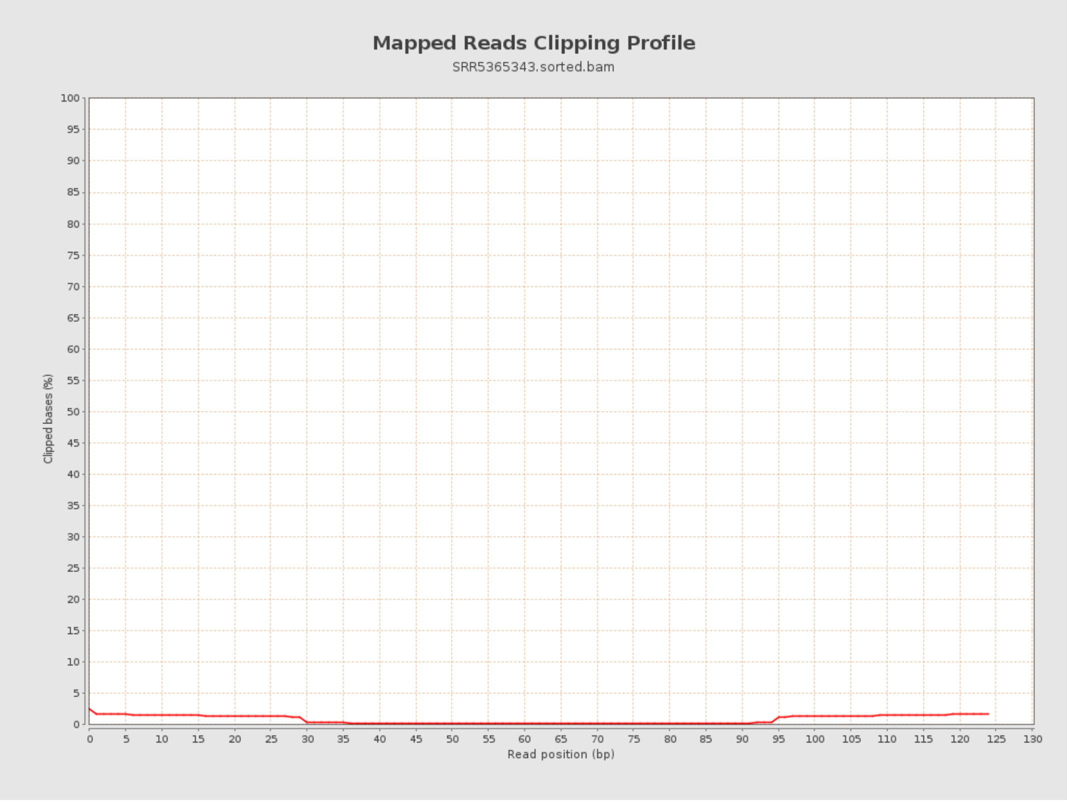
8. Results : Mapped Reads Nucleotide Content



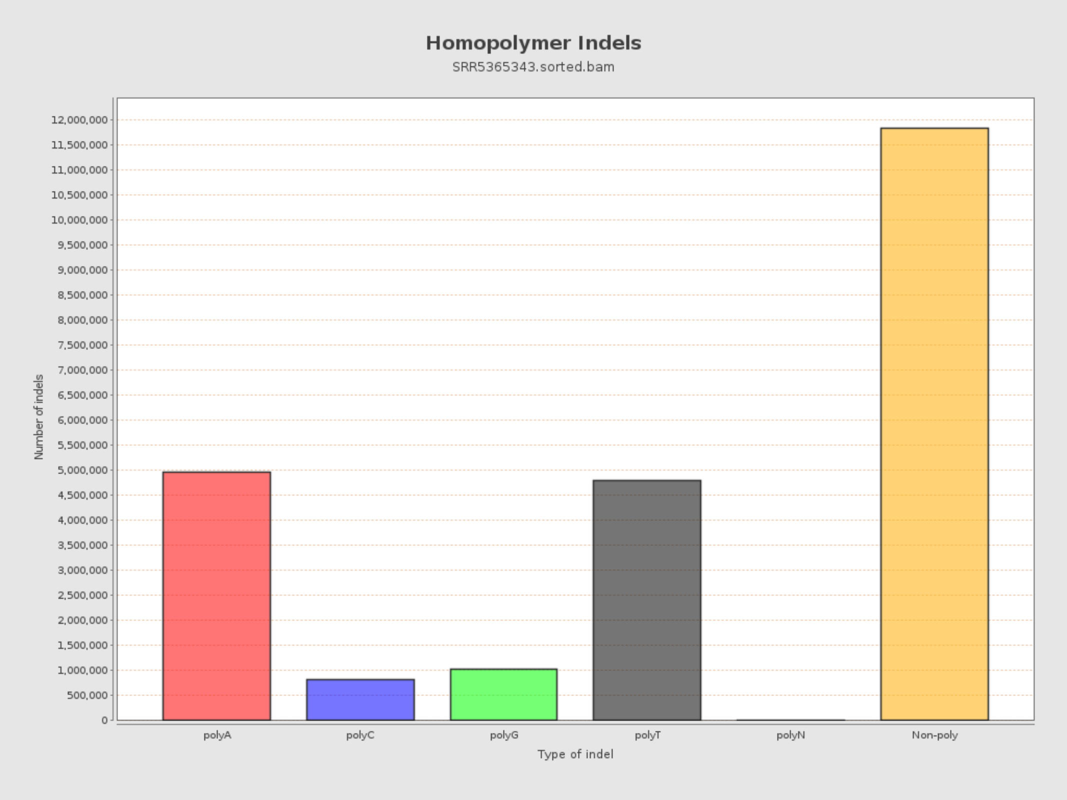
9. Results : Mapped Reads GC-content Distribution



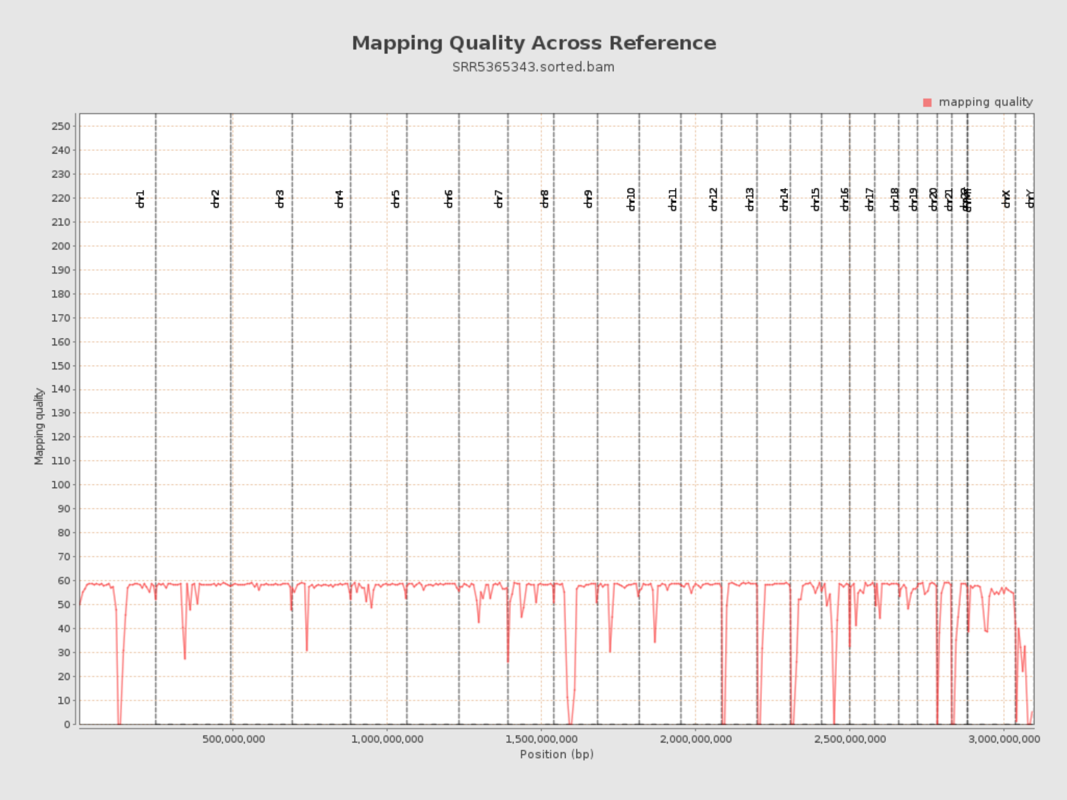
10. Results : Mapped Reads Clipping Profile



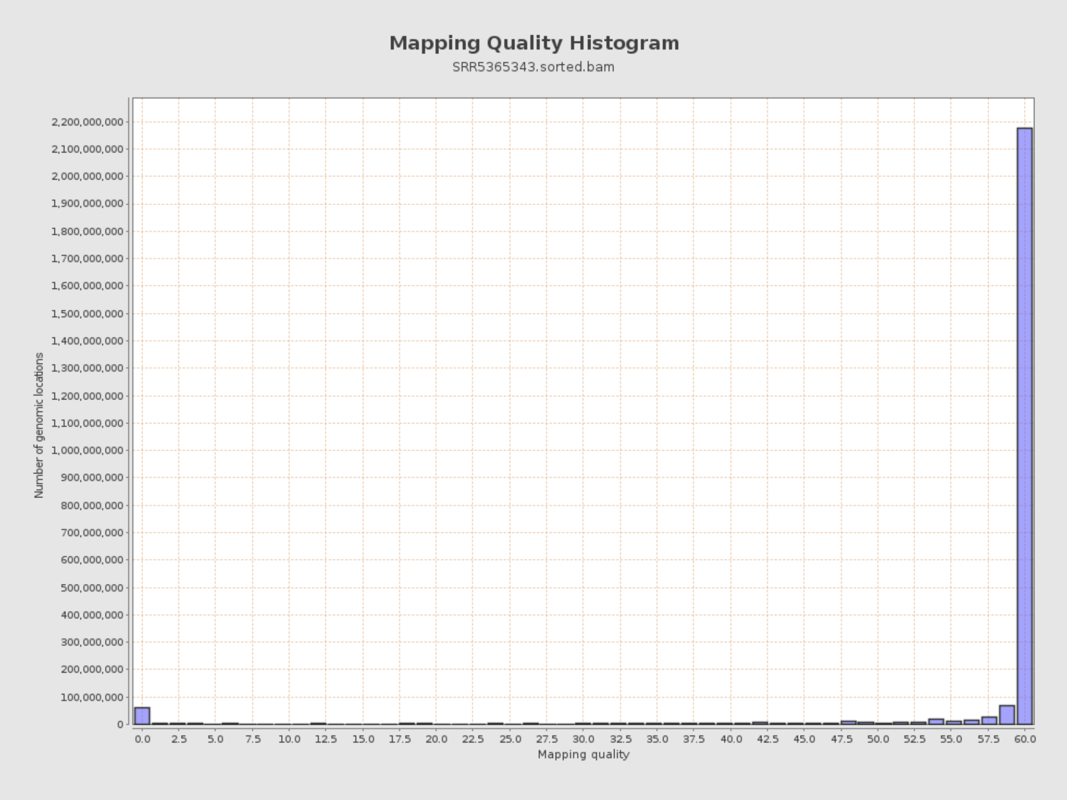
11. Results : Homopolymer Indels



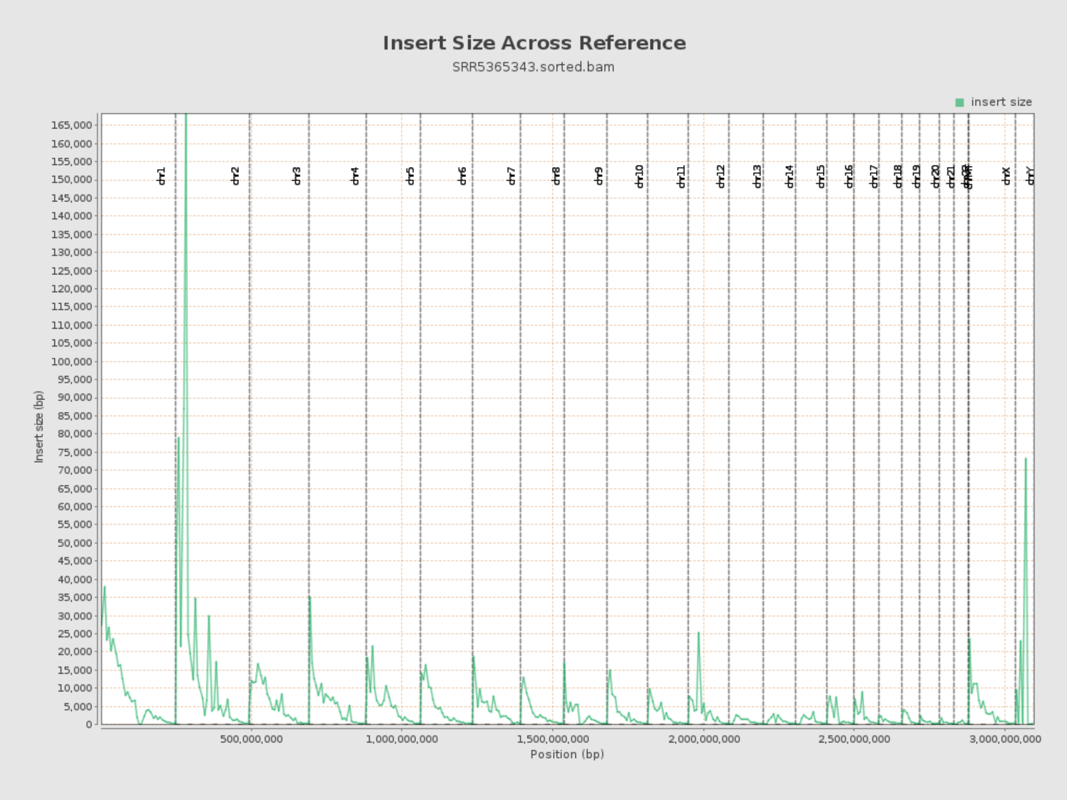
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram