Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 06:24:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926965.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_SRR926965 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926965_1.fastq.gz SRR926965_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 06:24:29 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926965.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,902,012
Mapped reads	19,299,636 / 96.97%
Unmapped reads	602,376 / 3.03%
Mapped paired reads	19,299,636 / 96.97%
Mapped reads, first in pair	9,702,324 / 48.75%
Mapped reads, second in pair	9,597,312 / 48.22%
Mapped reads, both in pair	18,975,400 / 95.34%
Mapped reads, singletons	324,236 / 1.63%
Secondary alignments	0
Supplementary alignments	666,323 / 3.35%
Read min/max/mean length	30 / 101 / 102.38
Duplicated reads (estimated)	2,070,874 / 10.41%
Duplication rate	8.8%
Clipped reads	10,125,908 / 50.88%

2.2. ACGT Content

Number/percentage of A's	484,420,022 / 28.42%
Number/percentage of C's	326,508,061 / 19.15%
Number/percentage of T's	502,966,907 / 29.51%
Number/percentage of G's	390,565,930 / 22.91%
Number/percentage of N's	125,050 / 0.01%

GC Percentage	42.07%

2.3. Coverage

Mean	0.5511
Standard Deviation	2.1368

2.4. Mapping Quality

Mean Mapping Quality	52.42

2.5. Insert size

Mean	348,089.9
Standard Deviation	5,766,455.17
P25/Median/P75	123 / 163 / 220

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	17,067,890
Insertions	303,481
Mapped reads with at least one insertion	1.54%
Deletions	922,526
Mapped reads with at least one deletion	4.66%
Homopolymer indels	51.51%

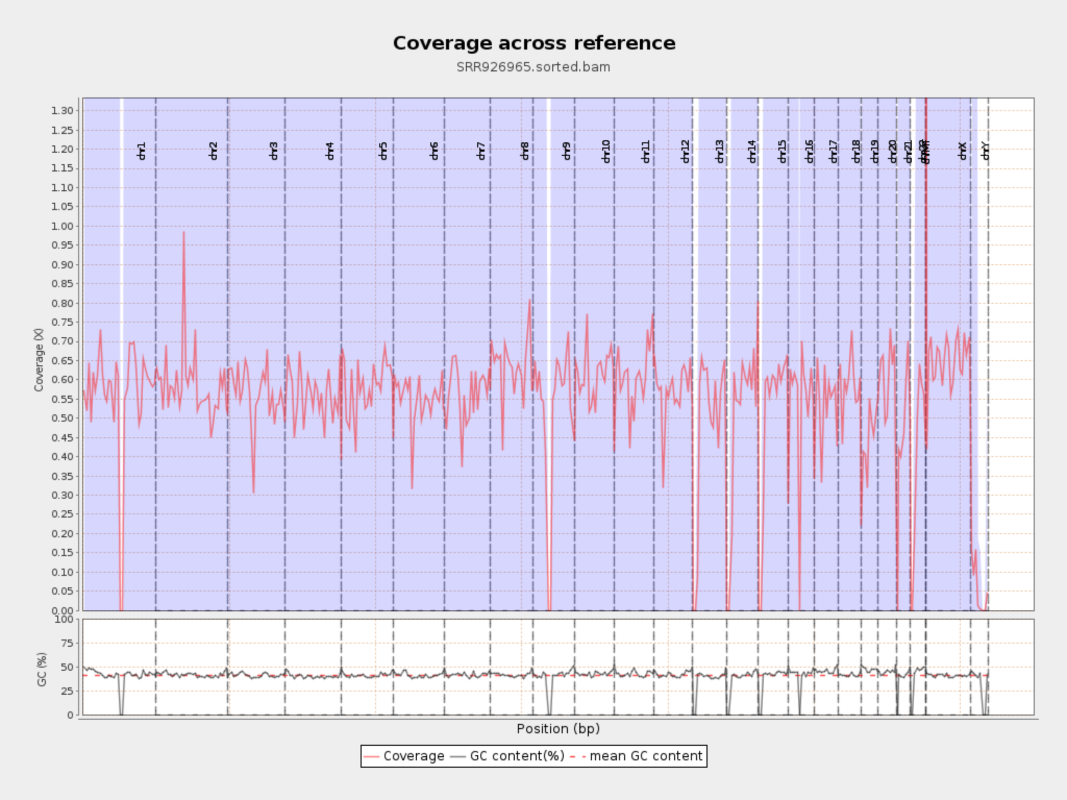
2.7. Chromosome stats

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

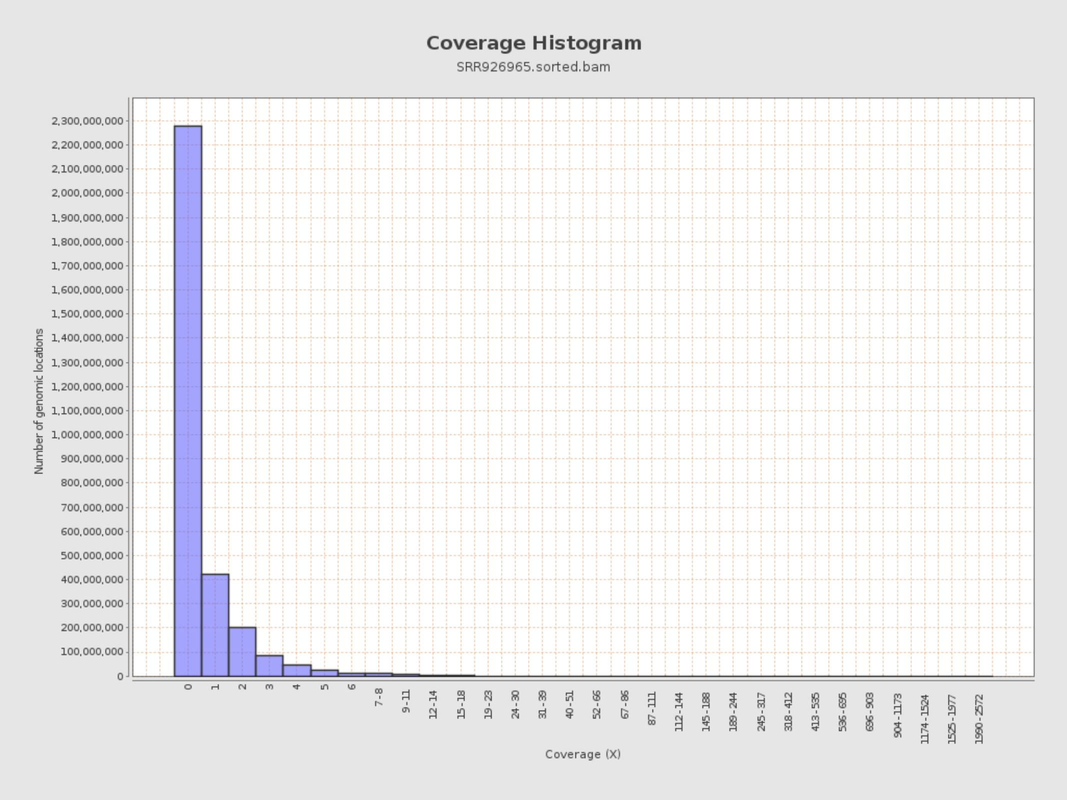
		bases	coverage	deviation
chr1	249250621	139840541	0.561	2.2339
chr2	243199373	142823895	0.5873	3.9601
chr3	198022430	111223660	0.5617	1.2909
chr4	191154276	107894203	0.5644	1.8249
chr5	180915260	105396693	0.5826	1.3165
chr6	171115067	94281972	0.551	1.4507
chr7	159138663	89683215	0.5636	1.9192
chr8	146364022	93357329	0.6378	1.6264
chr9	141213431	73059318	0.5174	2.5958
chr10	135534747	83146557	0.6135	2.9322
chr11	135006516	81769545	0.6057	2.671
chr12	133851895	76714008	0.5731	1.5981
chr13	115169878	54673225	0.4747	1.2425
chr14	107349540	52620082	0.4902	1.3124
chr15	102531392	50715606	0.4946	1.3273
chr16	90354753	47851825	0.5296	2.6235
chr17	81195210	43901872	0.5407	1.5611
chr18	78077248	45900166	0.5879	2.7156
chr19	59128983	26301971	0.4448	1.5101
chr20	63025520	38518635	0.6112	1.4614
chr21	48129895	22376946	0.4649	1.7643
chr22	51304566	20015422	0.3901	1.1862
chrMT	16571	93075	5.6167	5.1143
chrX	155270560	100575056	0.6477	1.6266

chrY	59373566	3218620	0.0542	1.7255

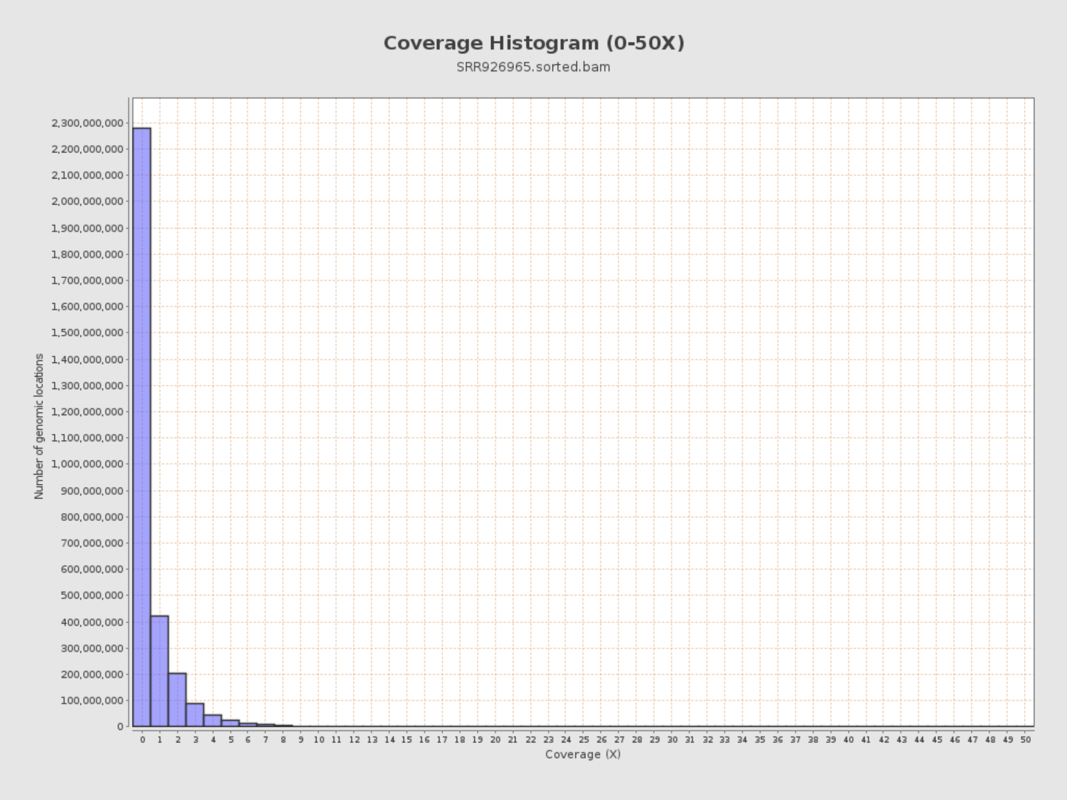
3. Results : Coverage across reference



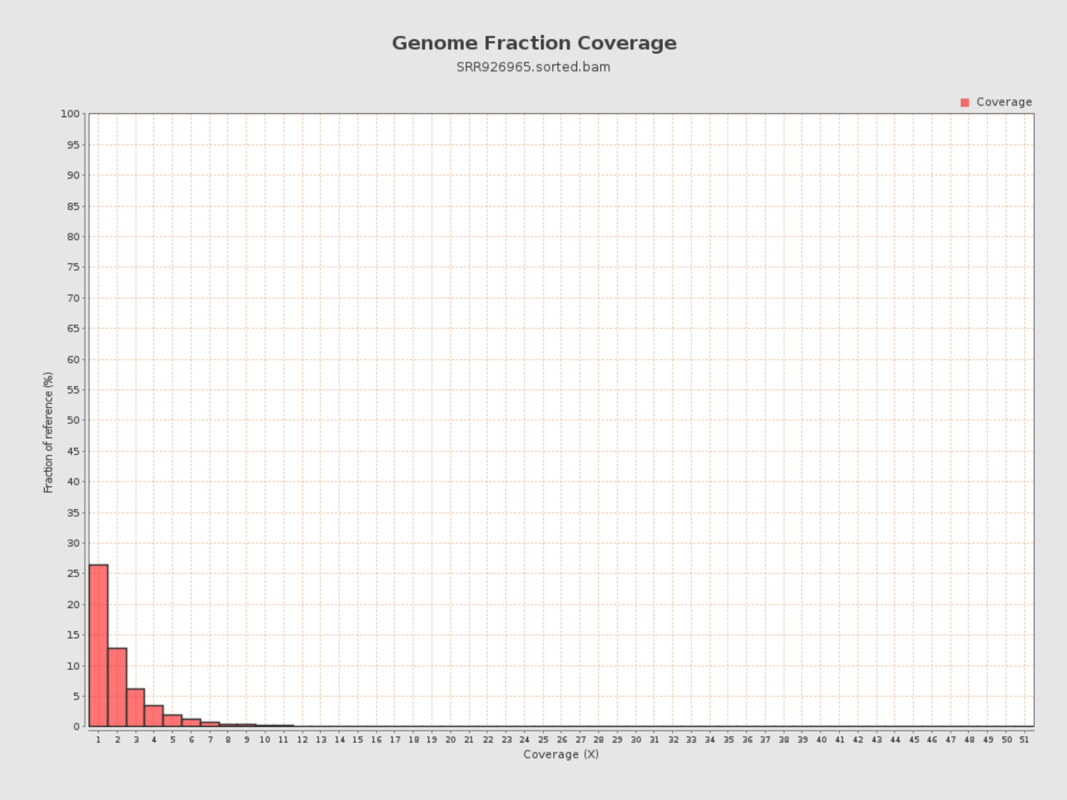
4. Results : Coverage Histogram



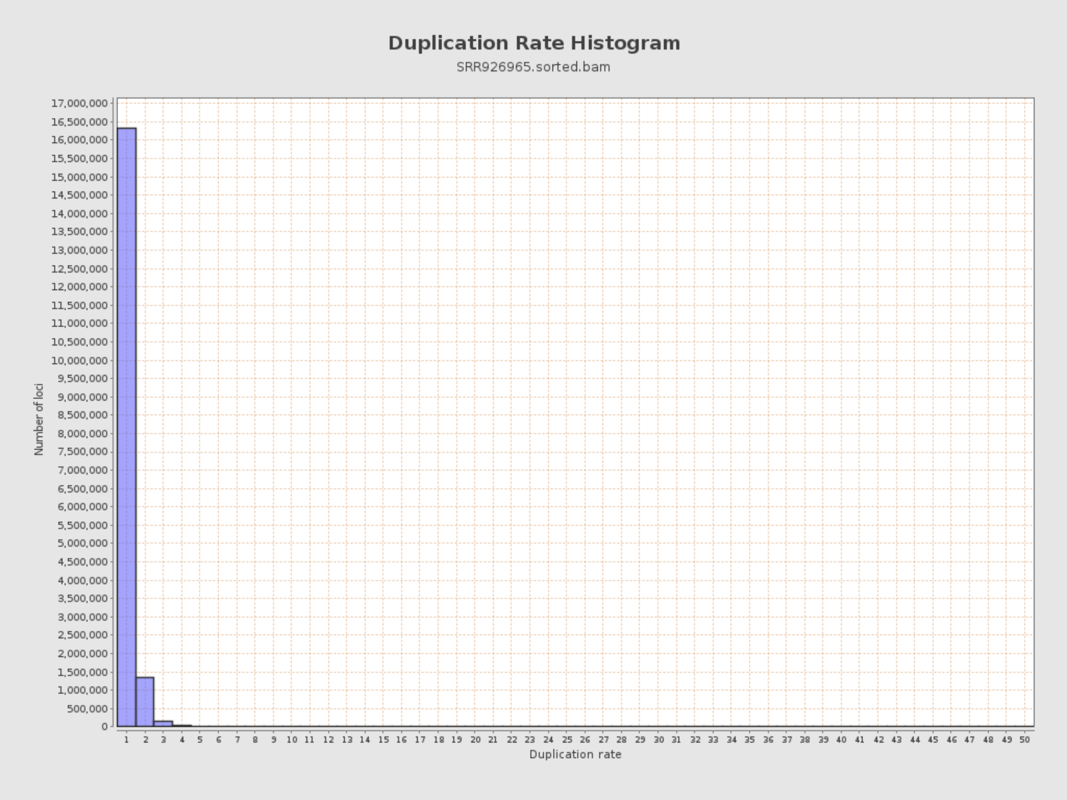
5. Results : Coverage Histogram (0-50X)



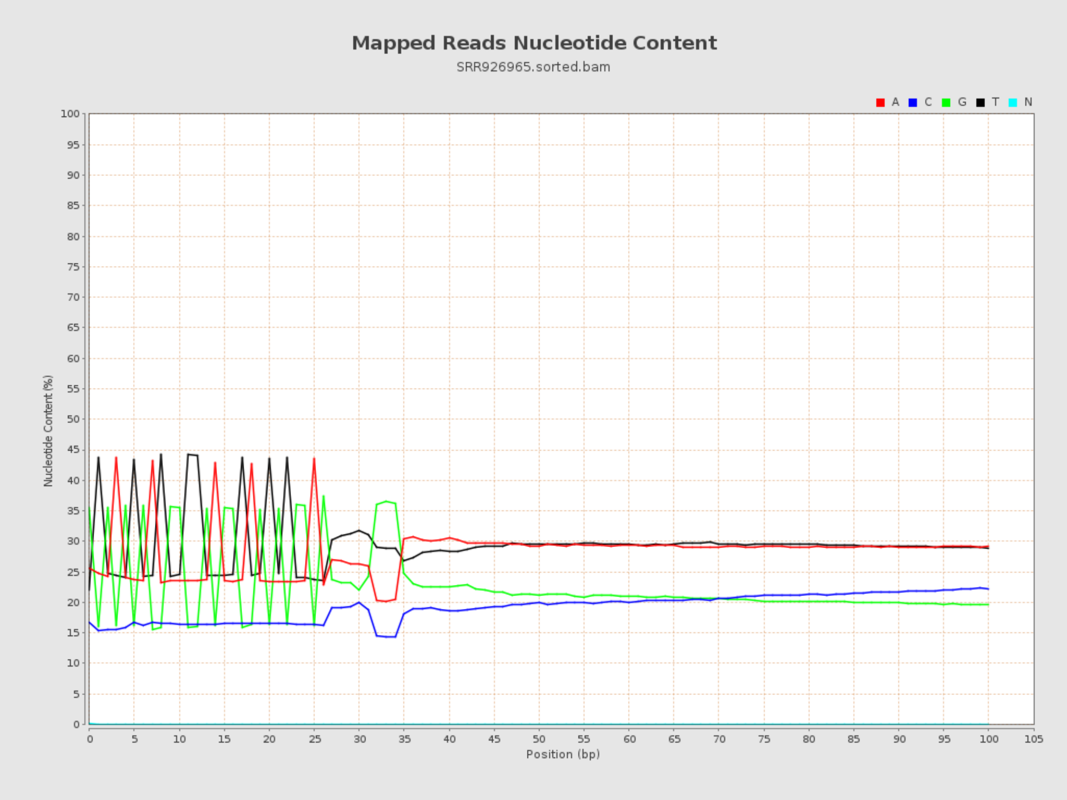
6. Results : Genome Fraction Coverage



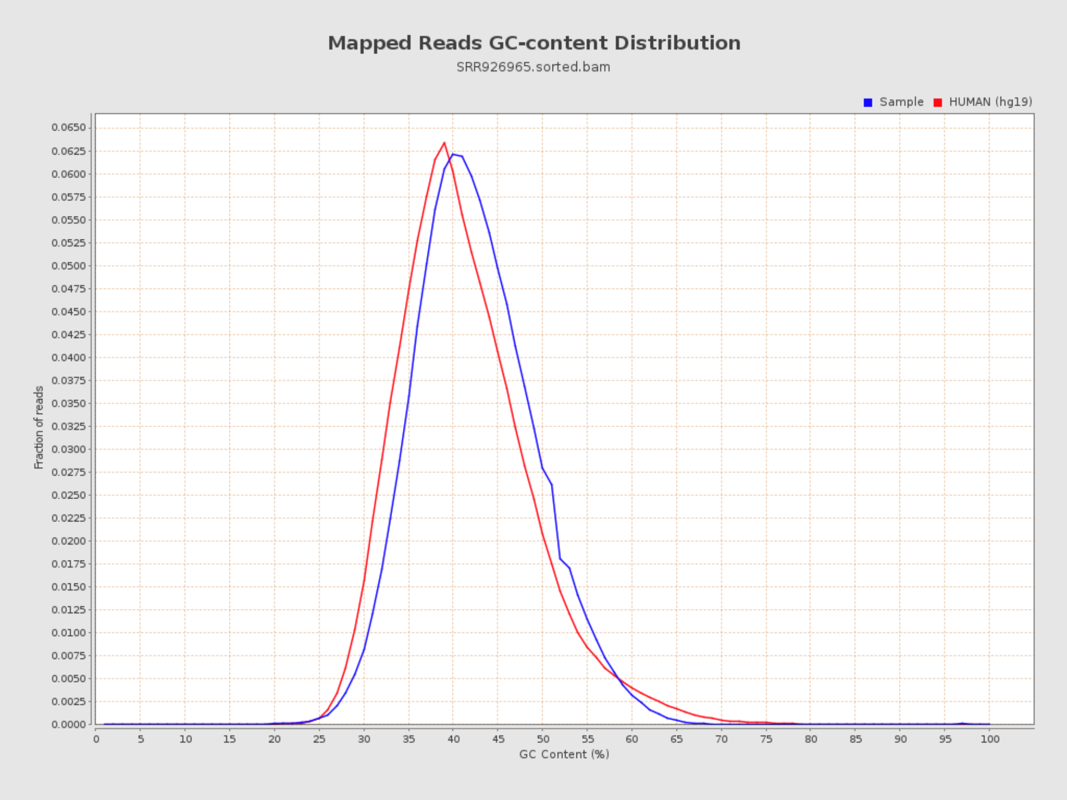
7. Results : Duplication Rate Histogram



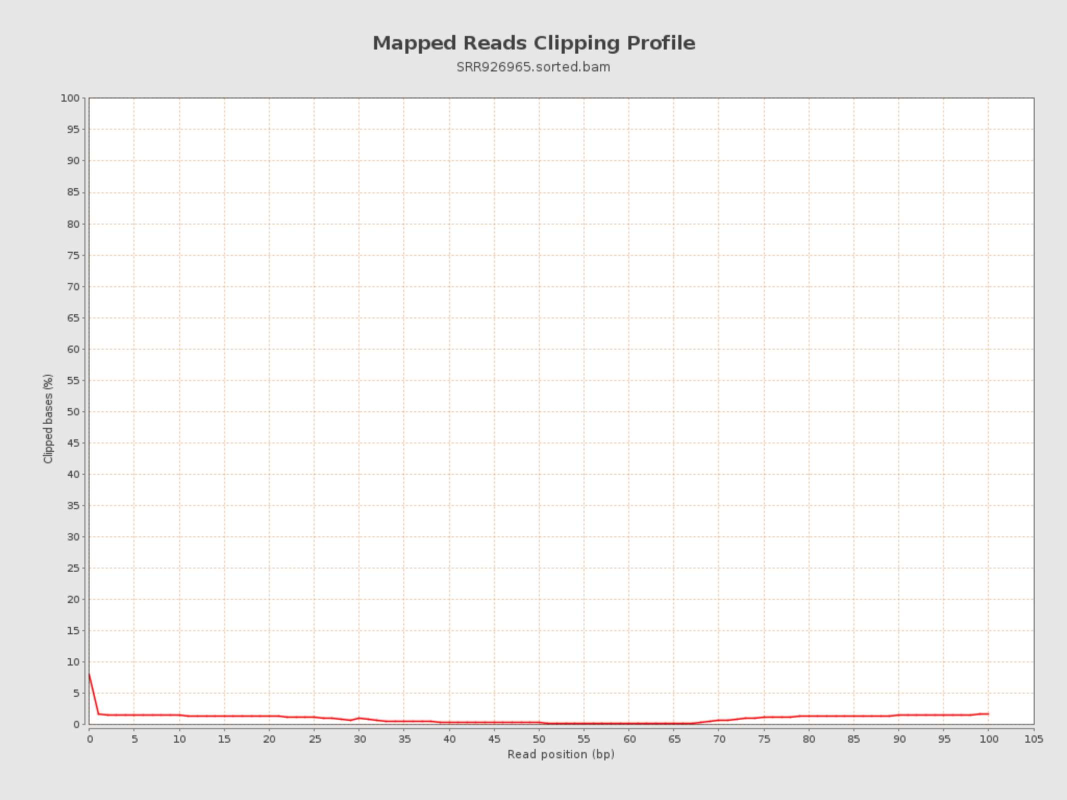
8. Results : Mapped Reads Nucleotide Content



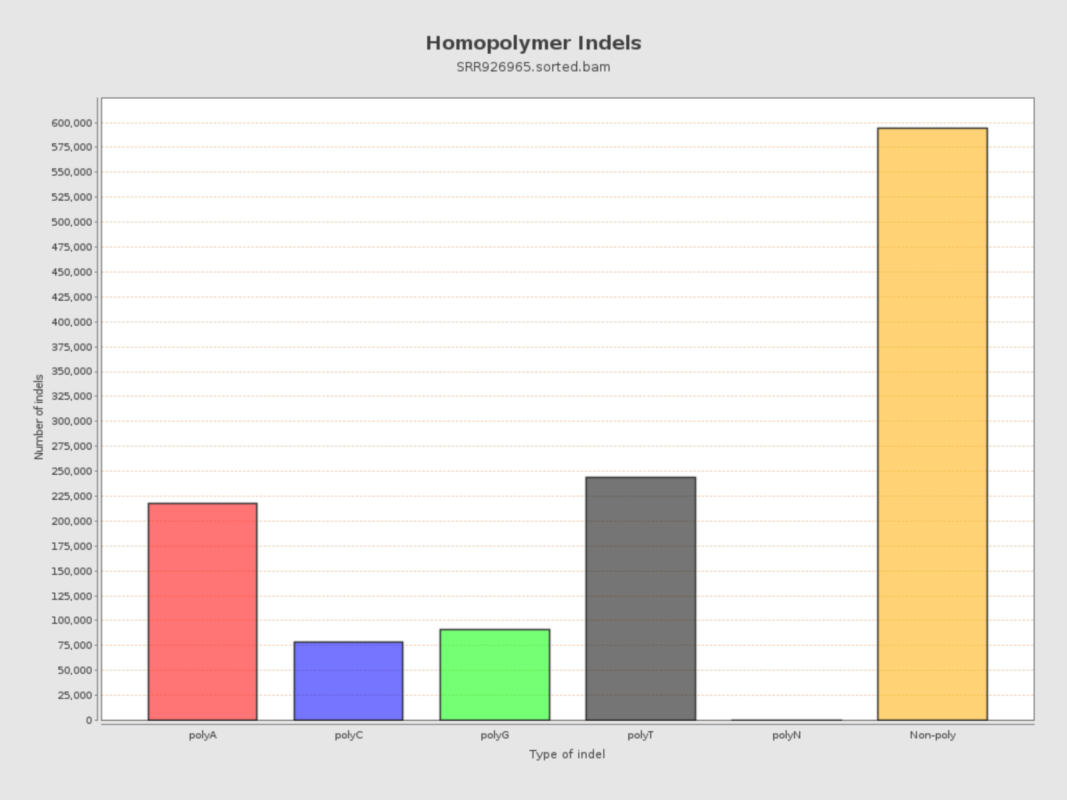
9. Results : Mapped Reads GC-content Distribution



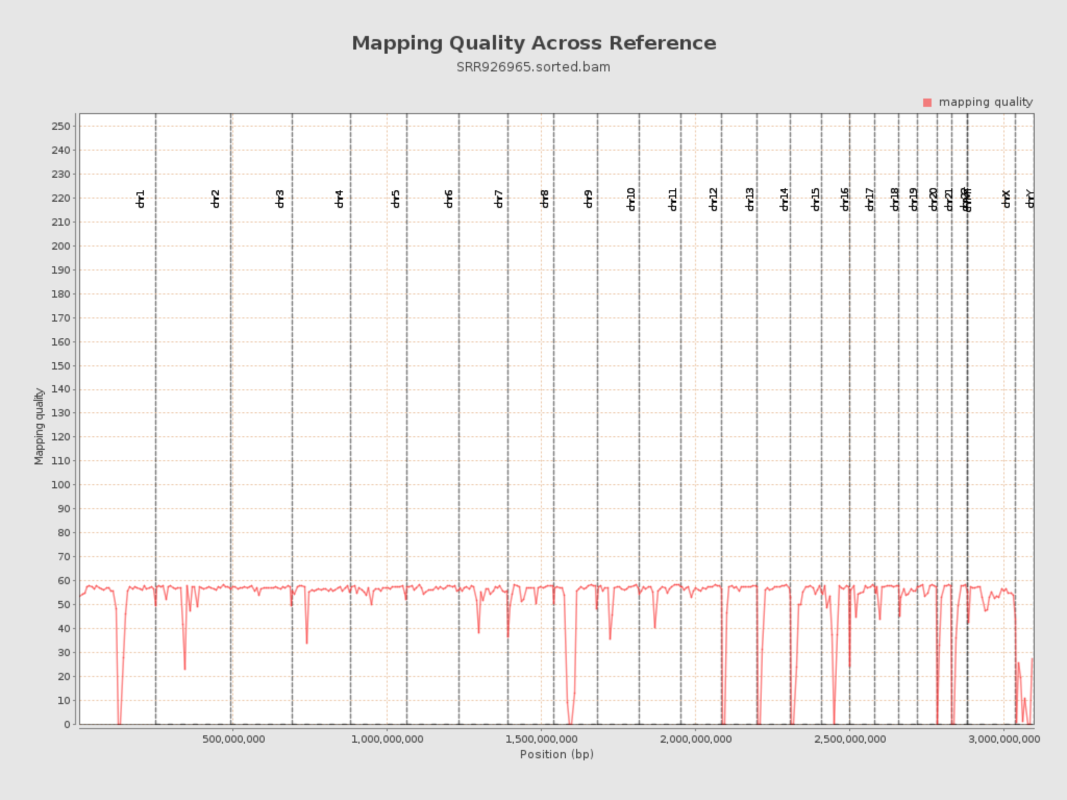
10. Results : Mapped Reads Clipping Profile



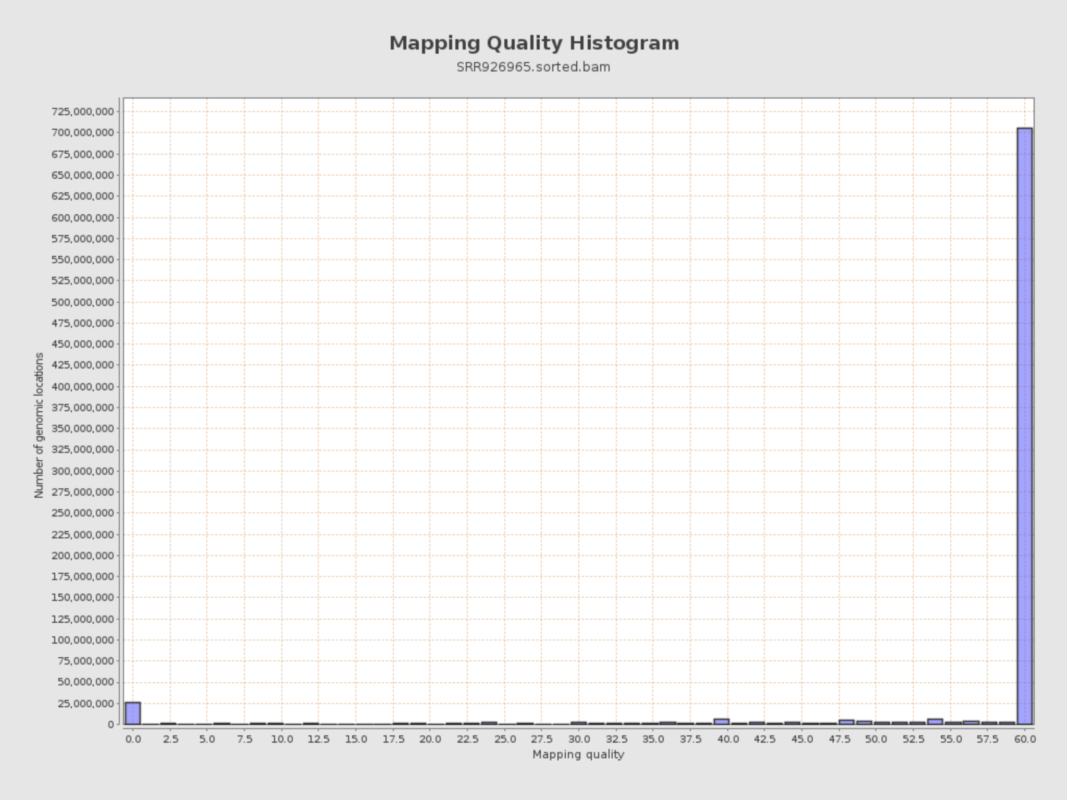
11. Results : Homopolymer Indels



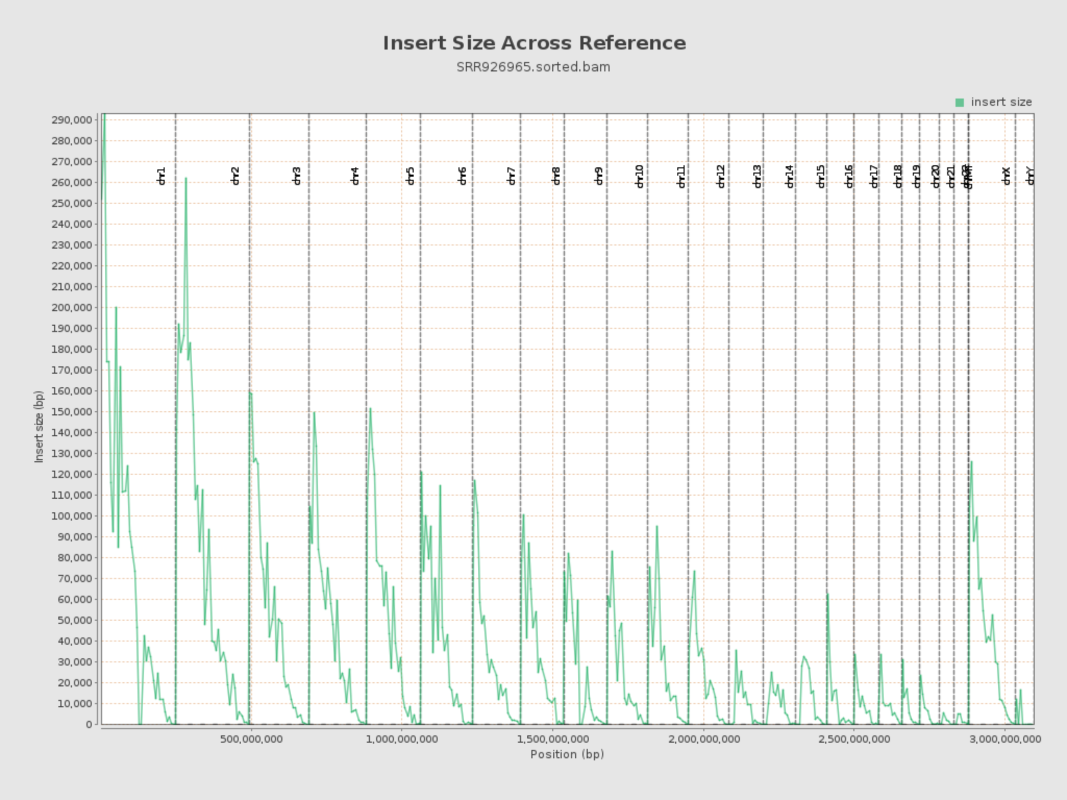
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram