Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 20:08:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927045.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_SRR927045 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927045_1.fastq.gz SRR927045_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 20:08:47 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927045.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,059,932
Mapped reads	18,411,488 / 96.6%
Unmapped reads	648,444 / 3.4%
Mapped paired reads	18,411,488 / 96.6%
Mapped reads, first in pair	9,239,522 / 48.48%
Mapped reads, second in pair	9,171,966 / 48.12%
Mapped reads, both in pair	18,036,976 / 94.63%
Mapped reads, singletons	374,512 / 1.96%
Secondary alignments	0
Supplementary alignments	760,728 / 3.99%
Read min/max/mean length	30 / 101 / 102.66
Duplicated reads (estimated)	1,533,731 / 8.05%
Duplication rate	6.72%
Clipped reads	10,069,487 / 52.83%

2.2. ACGT Content

Number/percentage of A's	471,080,071 / 28.67%
Number/percentage of C's	315,802,736 / 19.22%
Number/percentage of T's	486,045,399 / 29.58%
Number/percentage of G's	370,088,045 / 22.52%
Number/percentage of N's	191,411 / 0.01%

GC Percentage	41.74%

2.3. Coverage

Mean	0.5312
Standard Deviation	2.1145

2.4. Mapping Quality

Mean Mapping Quality	52.32

2.5. Insert size

Mean	383,212.34
Standard Deviation	6,045,617.7
P25/Median/P75	129 / 171 / 232

2.6. Mismatches and indels

General error rate	1.1%
Mismatches	17,623,236
Insertions	279,460
Mapped reads with at least one insertion	1.49%
Deletions	812,288
Mapped reads with at least one deletion	4.3%
Homopolymer indels	51.21%

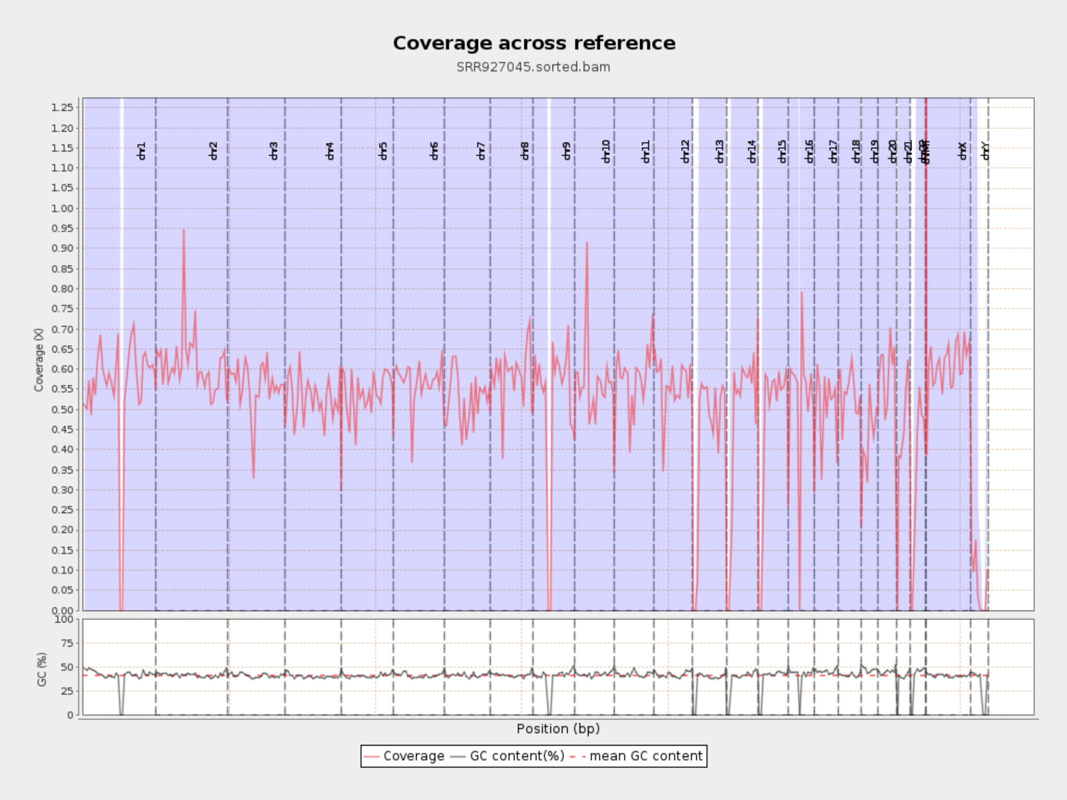
2.7. Chromosome stats

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

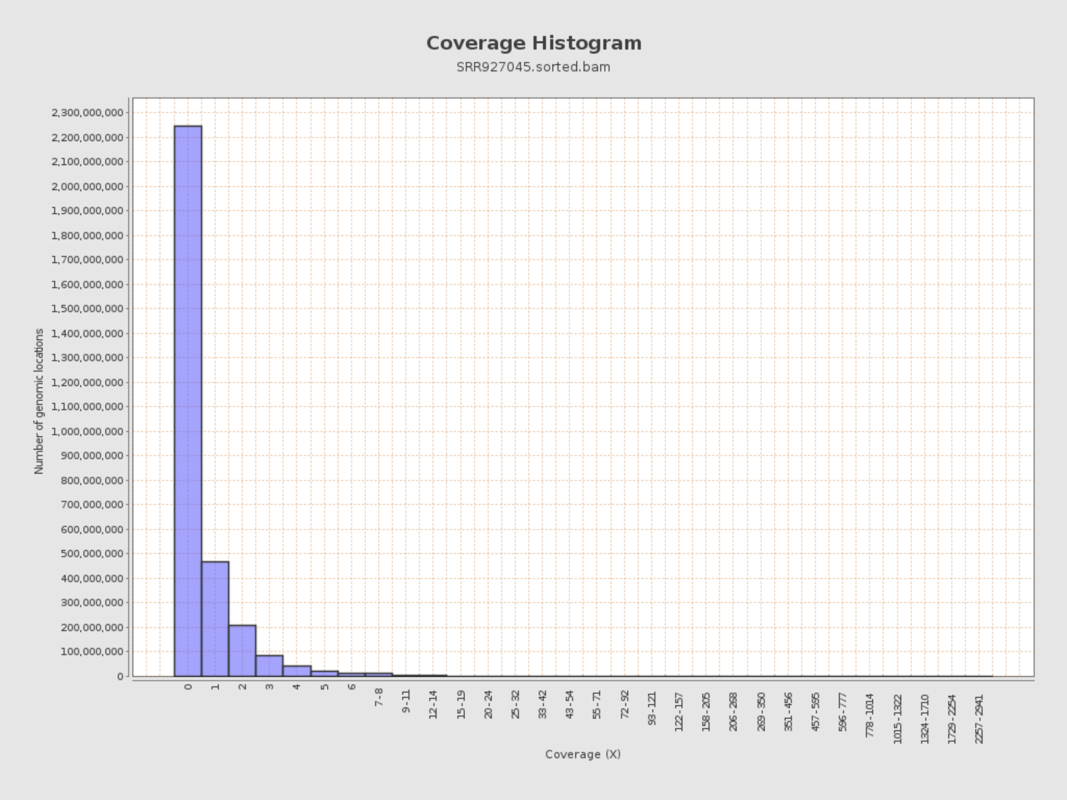
		bases	coverage	deviation
chr1	249250621	138174437	0.5544	3.1027
chr2	243199373	149524814	0.6148	3.2397
chr3	198022430	110367083	0.5573	1.2049
chr4	191154276	101488436	0.5309	1.8098
chr5	180915260	97779343	0.5405	1.1569
chr6	171115067	97483592	0.5697	1.2531
chr7	159138663	83379547	0.5239	1.7106
chr8	146364022	86382414	0.5902	1.4399
chr9	141213431	73433381	0.52	2.6392
chr10	135534747	76703666	0.5659	3.9886
chr11	135006516	77643649	0.5751	2.0175
chr12	133851895	75460153	0.5638	1.2109
chr13	115169878	49145149	0.4267	1.0237
chr14	107349540	50715076	0.4724	1.1729
chr15	102531392	47298358	0.4613	1.1196
chr16	90354753	46877045	0.5188	2.966
chr17	81195210	41682331	0.5134	1.5618
chr18	78077248	42119265	0.5395	2.5165
chr19	59128983	25488184	0.4311	1.7754
chr20	63025520	37077534	0.5883	1.3135
chr21	48129895	20624820	0.4285	1.5188
chr22	51304566	17290883	0.337	0.9976
chrMT	16571	78428	4.7328	2.3597
chrX	155270560	94238582	0.6069	1.3965

chrY	59373566	3955573	0.0666	1.5543

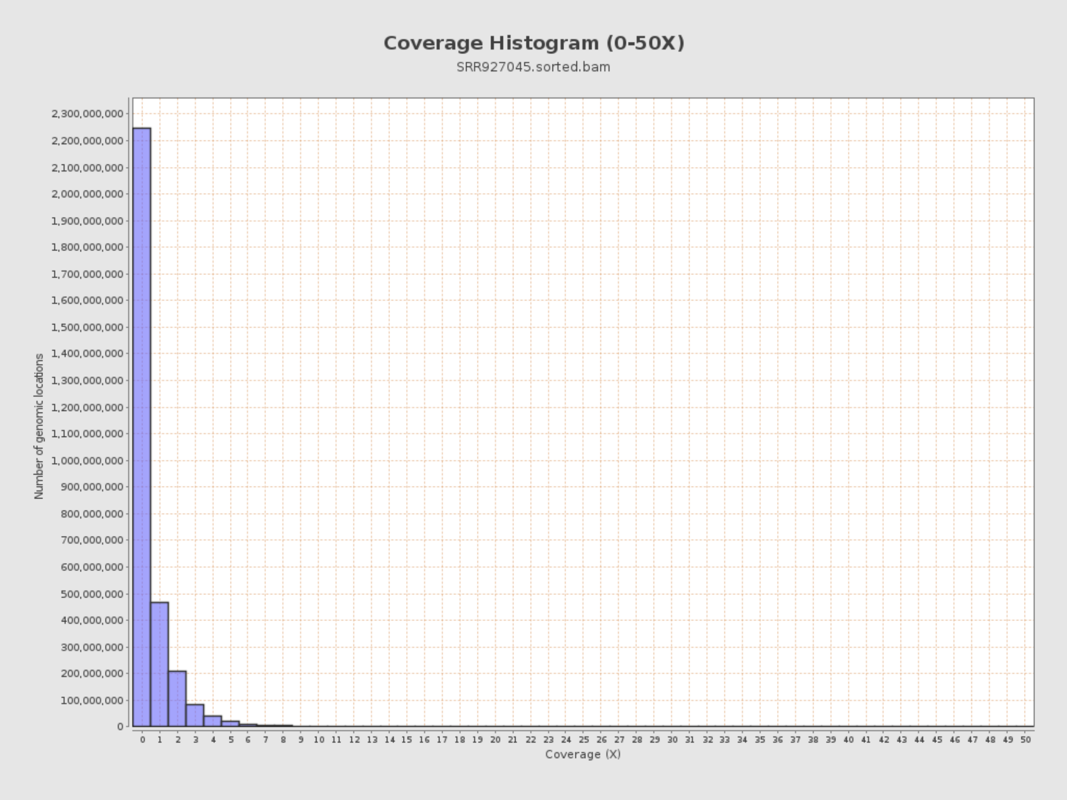
3. Results : Coverage across reference



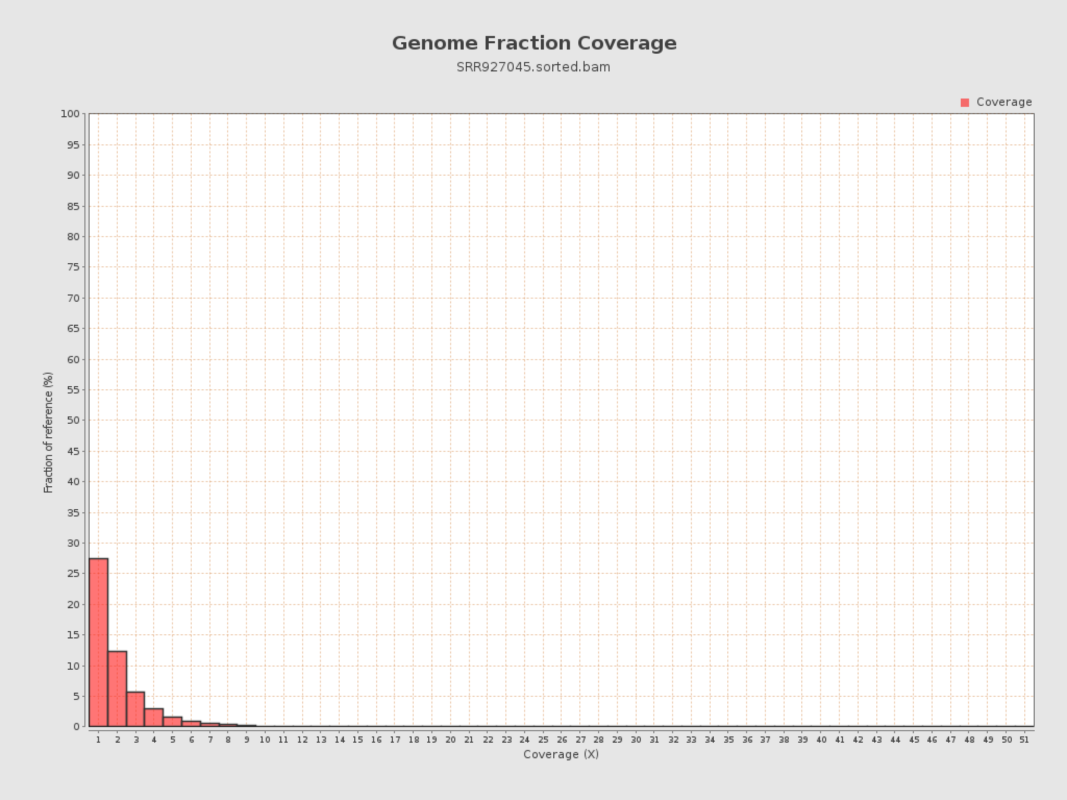
4. Results : Coverage Histogram



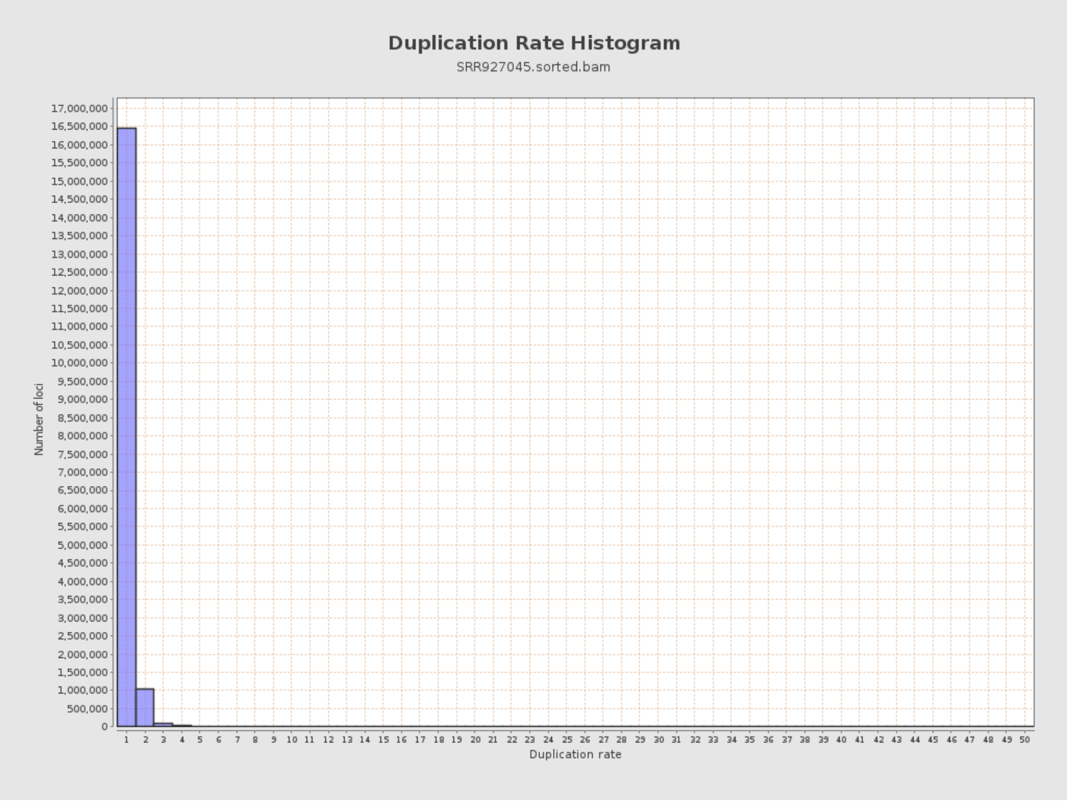
5. Results : Coverage Histogram (0-50X)



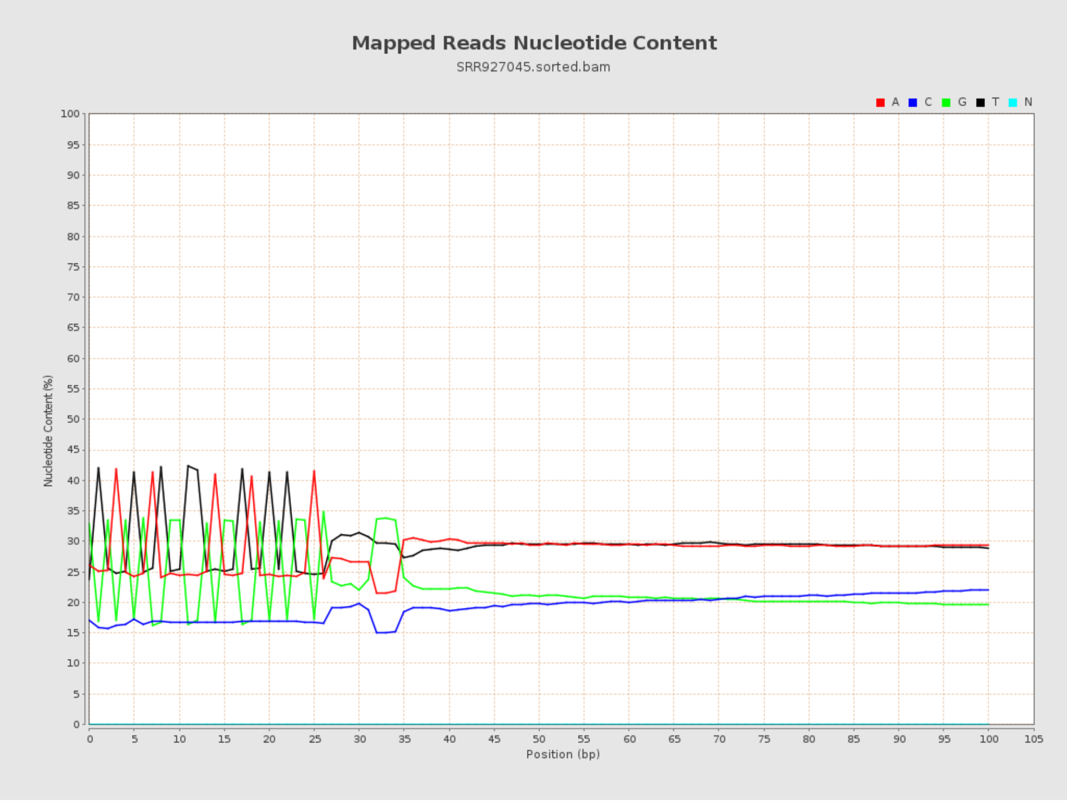
6. Results : Genome Fraction Coverage



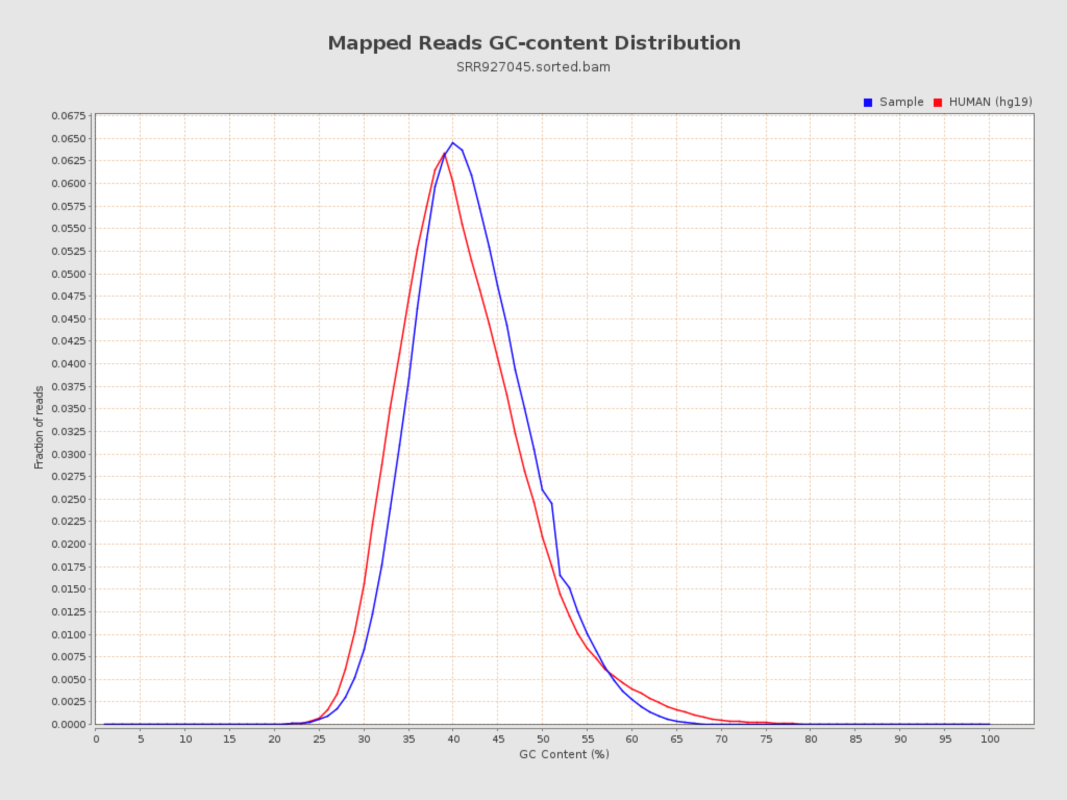
7. Results : Duplication Rate Histogram



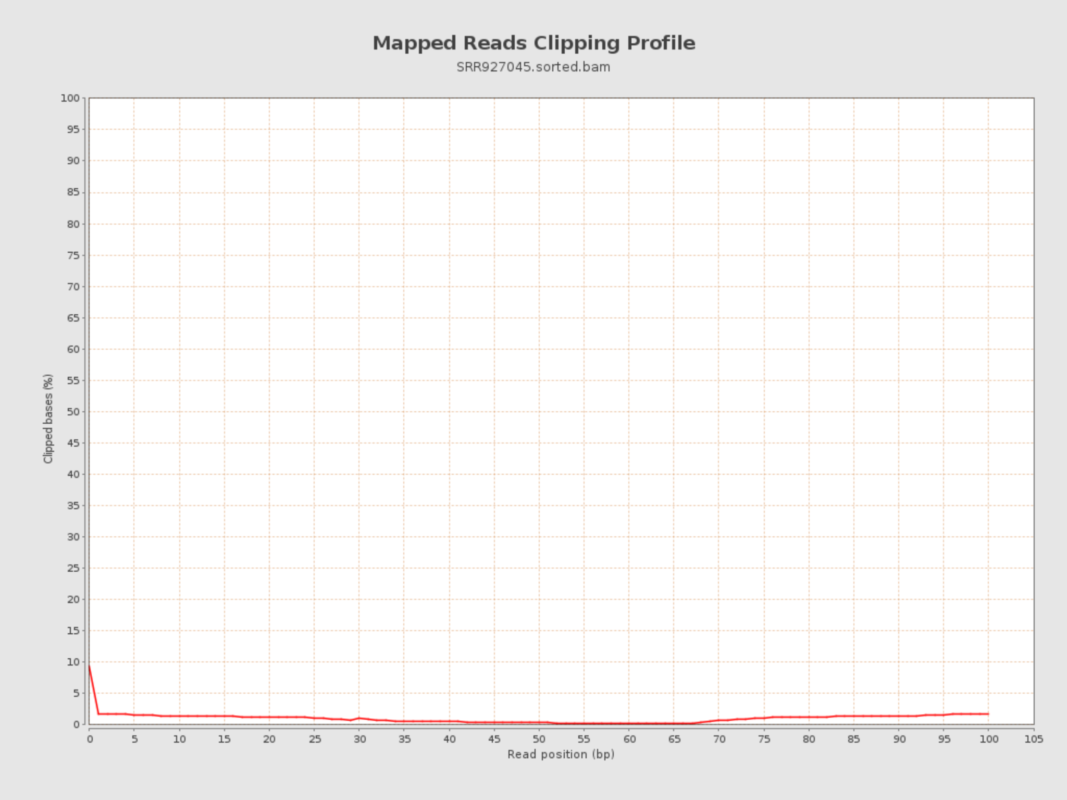
8. Results : Mapped Reads Nucleotide Content



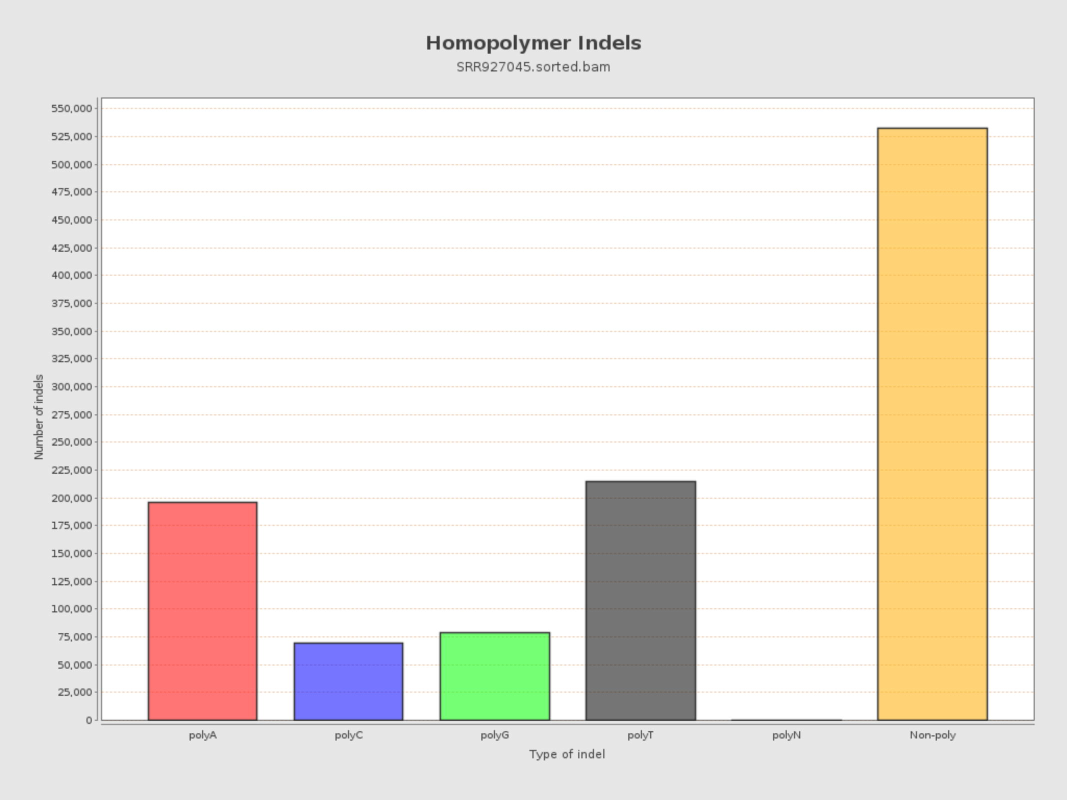
9. Results : Mapped Reads GC-content Distribution



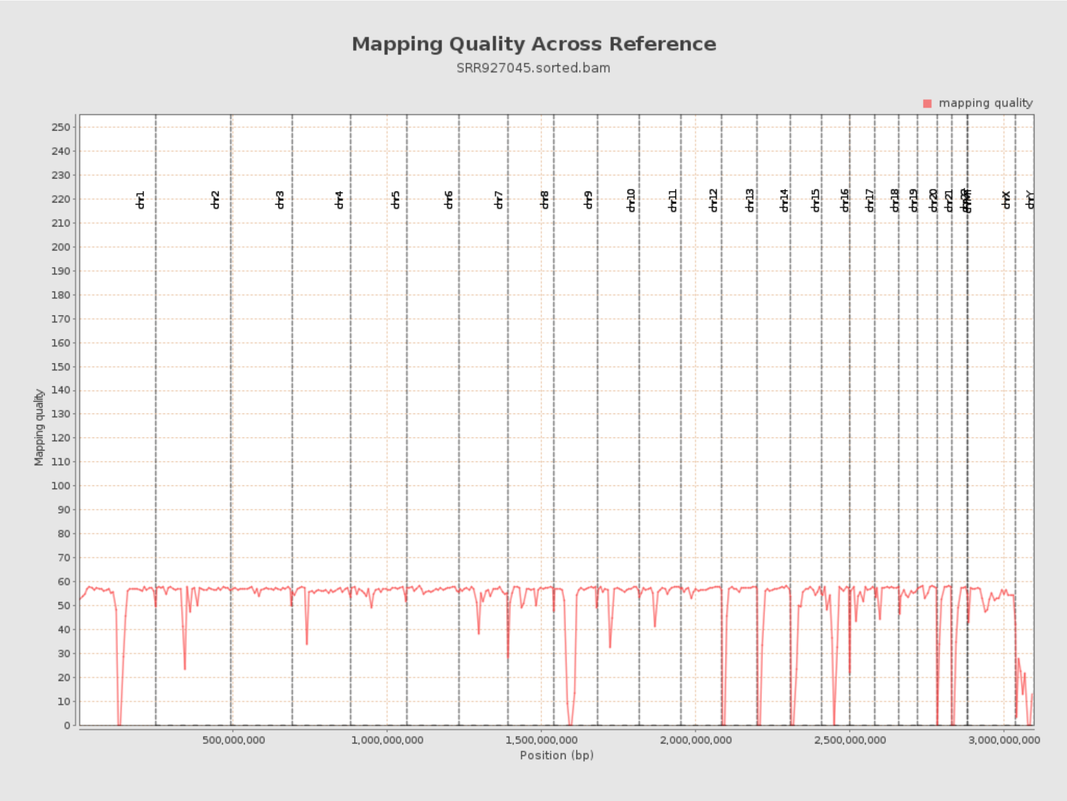
10. Results : Mapped Reads Clipping Profile



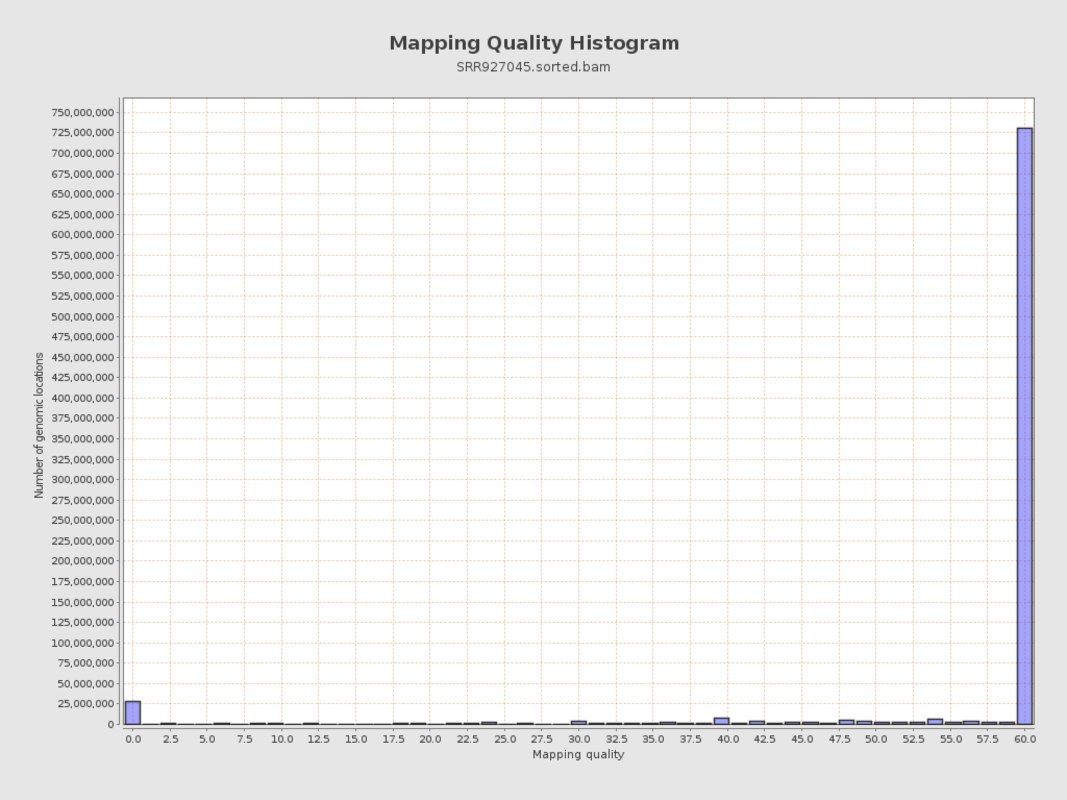
11. Results : Homopolymer Indels



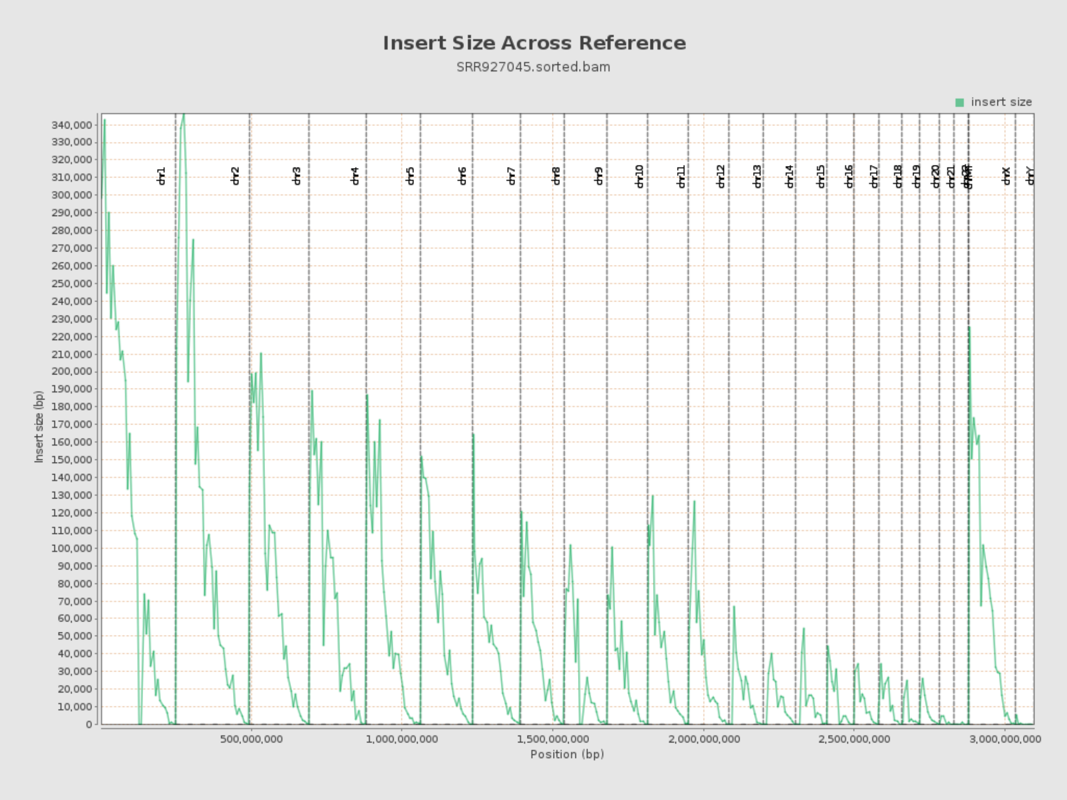
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram