Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/25 03:29:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927059.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_SRR927059 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927059_1.fastq.gz SRR927059_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 25 03:29:16 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927059.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,109,306
Mapped reads	27,541,804 / 97.98%
Unmapped reads	567,502 / 2.02%
Mapped paired reads	27,541,804 / 97.98%
Mapped reads, first in pair	13,825,200 / 49.18%
Mapped reads, second in pair	13,716,604 / 48.8%
Mapped reads, both in pair	27,227,258 / 96.86%
Mapped reads, singletons	314,546 / 1.12%
Secondary alignments	0
Supplementary alignments	666,698 / 2.37%
Read min/max/mean length	30 / 101 / 101.98
Duplicated reads (estimated)	1,913,194 / 6.81%
Duplication rate	5.64%
Clipped reads	8,505,423 / 30.26%

2.2. ACGT Content

Number/percentage of A's	733,833,137 / 28.34%
Number/percentage of C's	525,472,632 / 20.29%
Number/percentage of T's	740,437,515 / 28.59%
Number/percentage of G's	589,525,346 / 22.77%
Number/percentage of N's	179,940 / 0.01%

GC Percentage	43.06%

2.3. Coverage

Mean	0.8371
Standard Deviation	2.6595

2.4. Mapping Quality

Mean Mapping Quality	53.04

2.5. Insert size

Mean	255,271.28
Standard Deviation	4,997,723.11
P25/Median/P75	148 / 190 / 254

2.6. Mismatches and indels

General error rate	0.97%
Mismatches	24,229,155
Insertions	446,307
Mapped reads with at least one insertion	1.59%
Deletions	1,331,268
Mapped reads with at least one deletion	4.71%
Homopolymer indels	52.22%

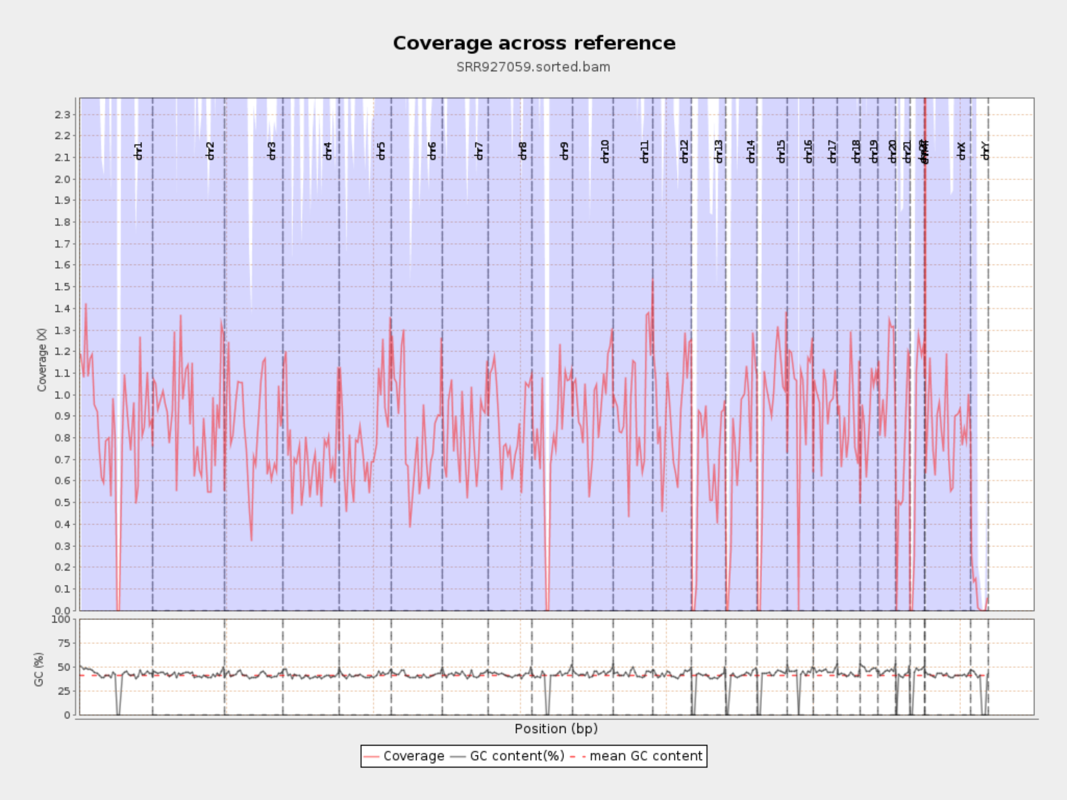
2.7. Chromosome stats

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

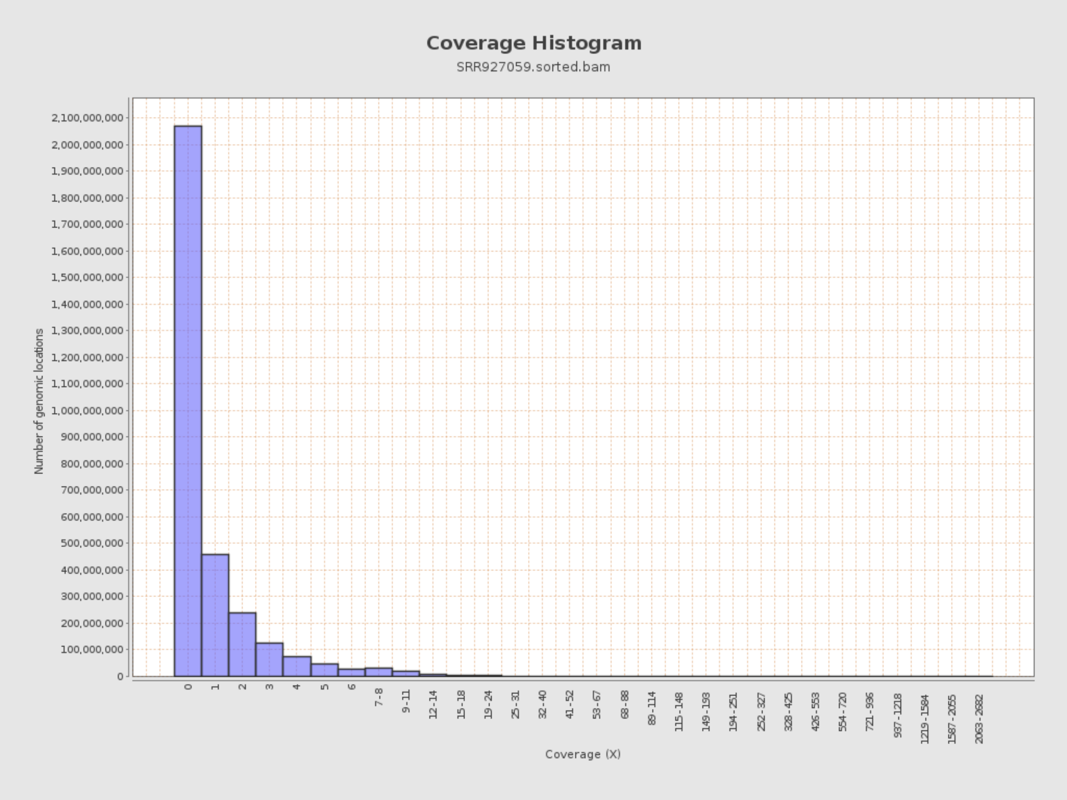
		bases	coverage	deviation
chr1	249250621	211033442	0.8467	2.8606
chr2	243199373	222836047	0.9163	4.5195
chr3	198022430	166328049	0.8399	1.7515
chr4	191154276	137339127	0.7185	2.091
chr5	180915260	147721528	0.8165	1.7248
chr6	171115067	141135940	0.8248	1.7635
chr7	159138663	131210157	0.8245	2.0721
chr8	146364022	125989855	0.8608	1.9578
chr9	141213431	112036504	0.7934	2.7125
chr10	135534747	129511494	0.9556	4.3006
chr11	135006516	127489272	0.9443	2.4947
chr12	133851895	122055364	0.9119	2.0422
chr13	115169878	72420553	0.6288	1.5327
chr14	107349540	82156112	0.7653	1.7498
chr15	102531392	90458318	0.8822	1.9465
chr16	90354753	89579228	0.9914	4.1504
chr17	81195210	79419086	0.9781	2.2098
chr18	78077248	69239945	0.8868	2.8497
chr19	59128983	54554463	0.9226	2.3047
chr20	63025520	67925709	1.0777	2.1727
chr21	48129895	32878543	0.6831	2.1753
chr22	51304566	41337756	0.8057	2.024
chrMT	16571	2780454	167.7904	117.9067
chrX	155270560	129923991	0.8368	1.8399

chrY	59373566	4054551	0.0683	2.1945

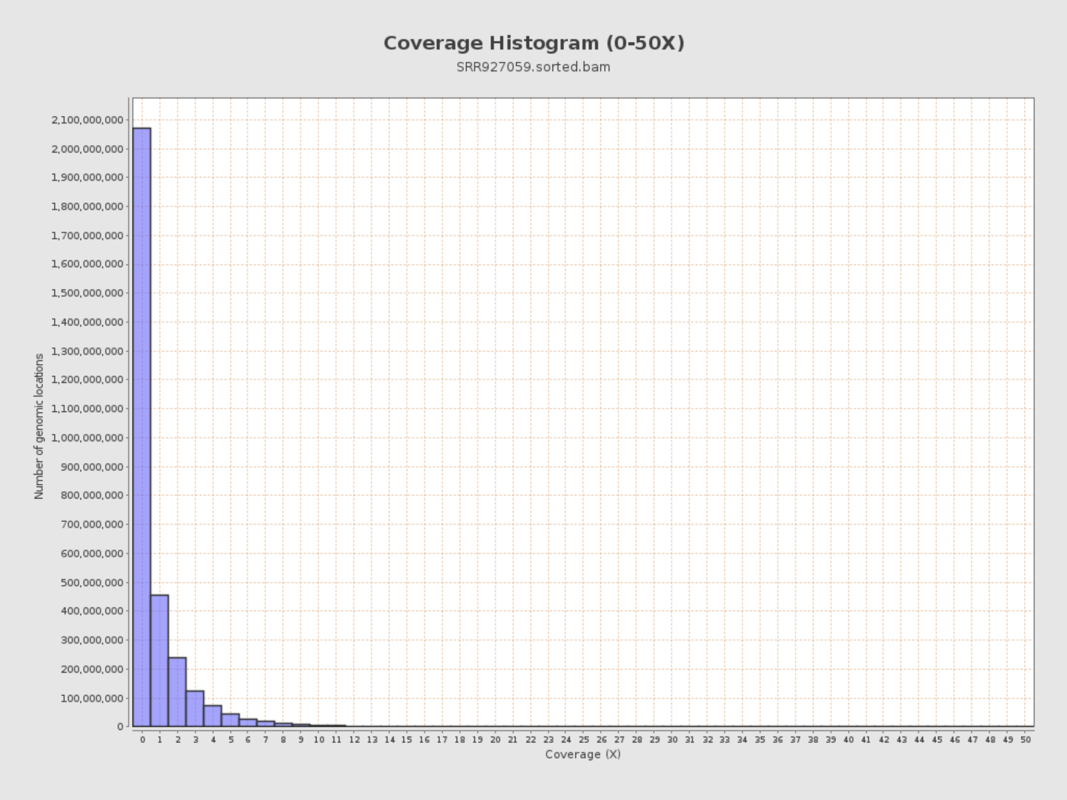
3. Results : Coverage across reference



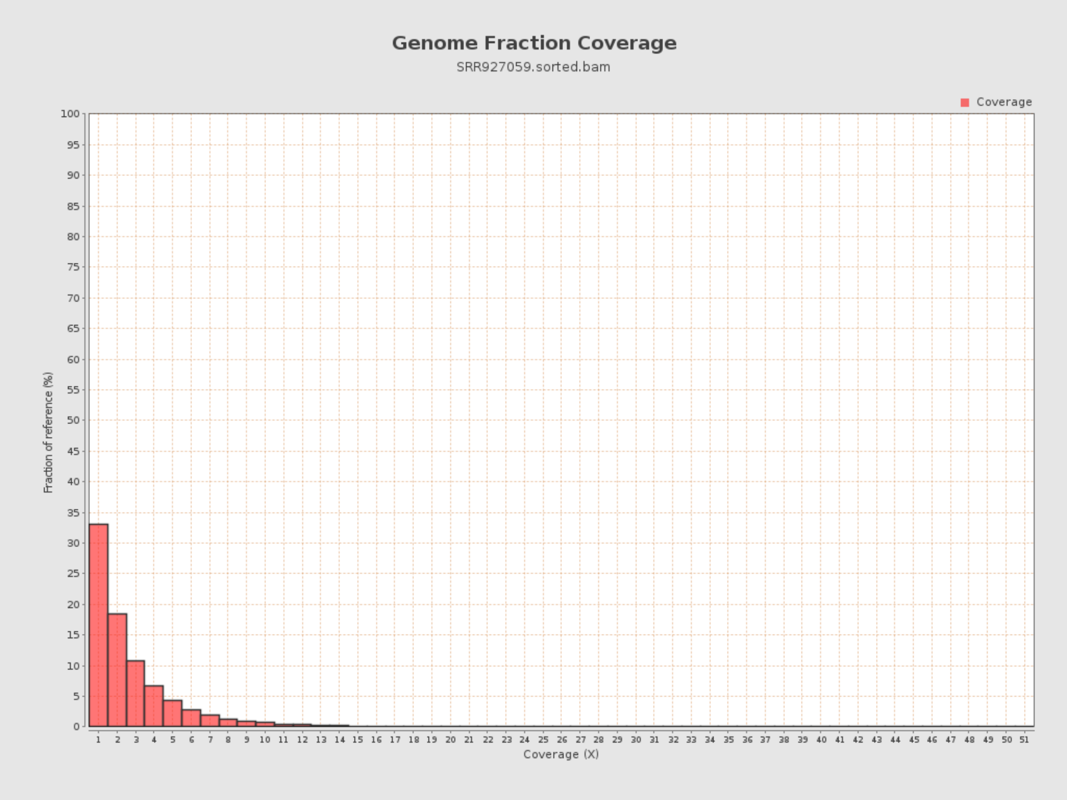
4. Results : Coverage Histogram



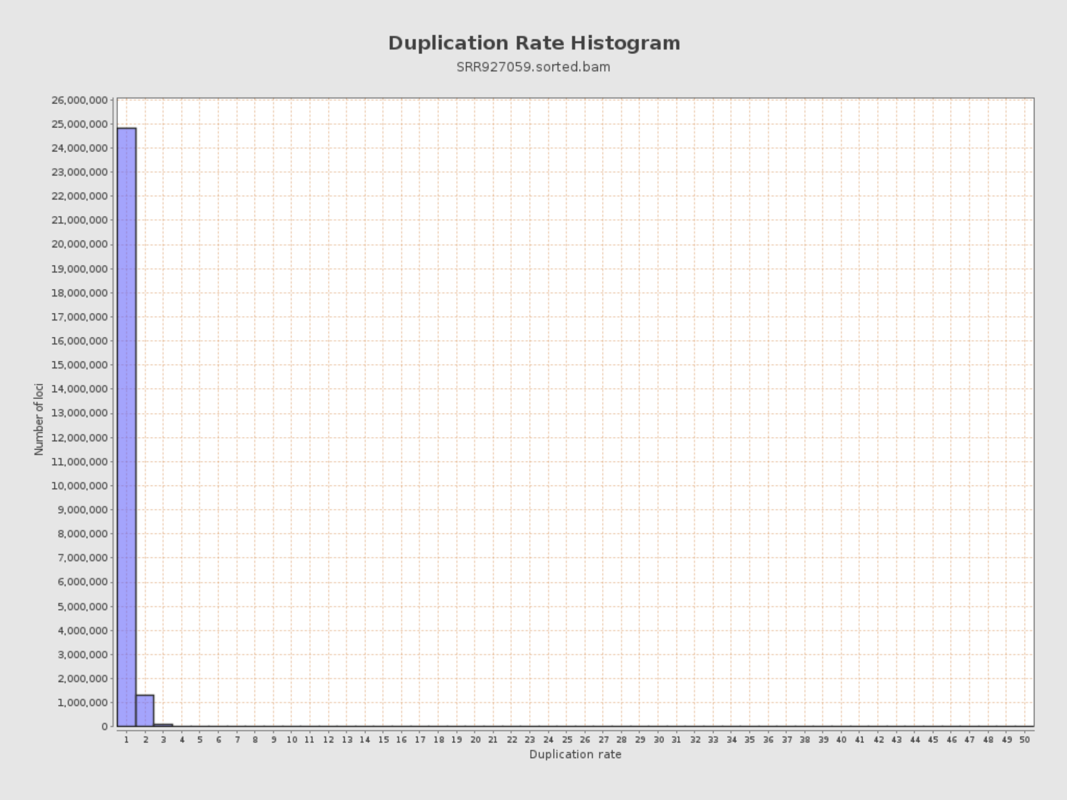
5. Results : Coverage Histogram (0-50X)



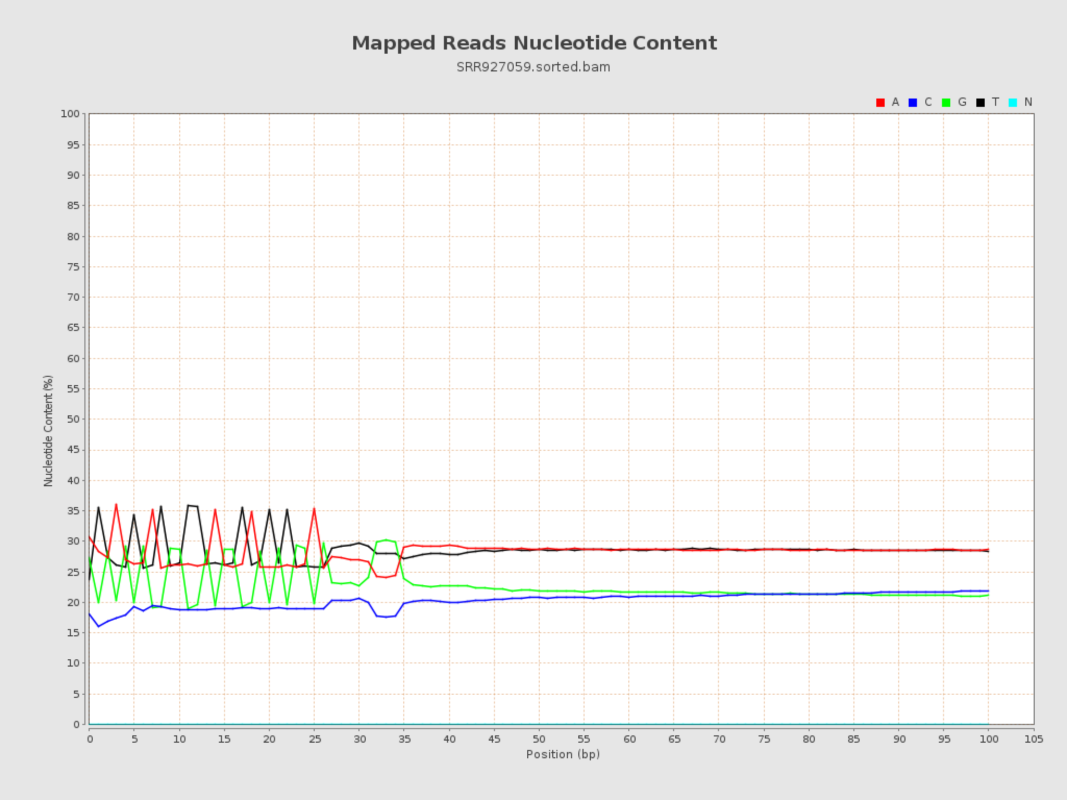
6. Results : Genome Fraction Coverage



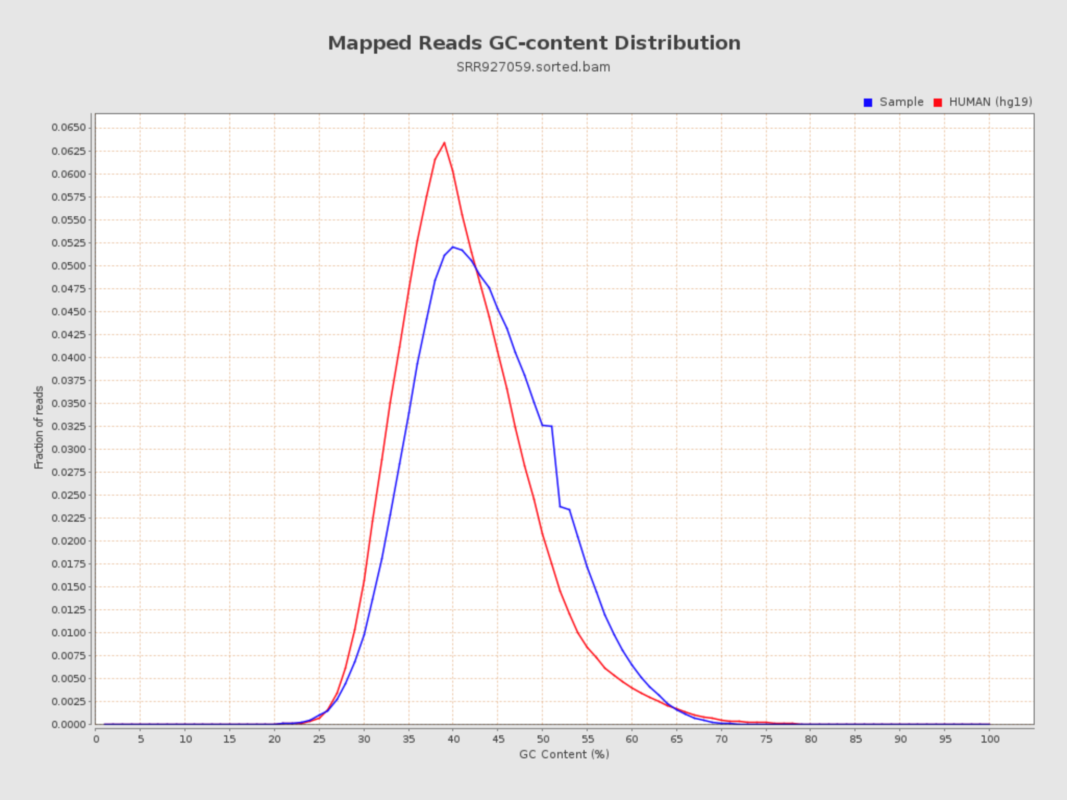
7. Results : Duplication Rate Histogram



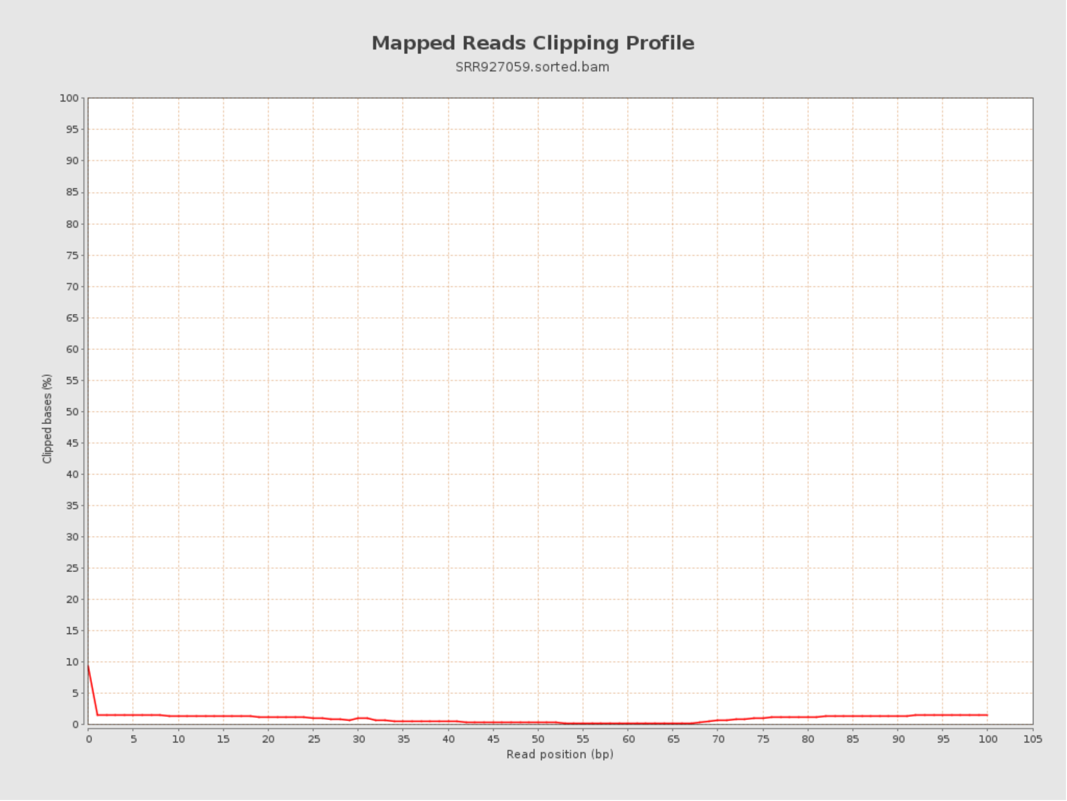
8. Results : Mapped Reads Nucleotide Content



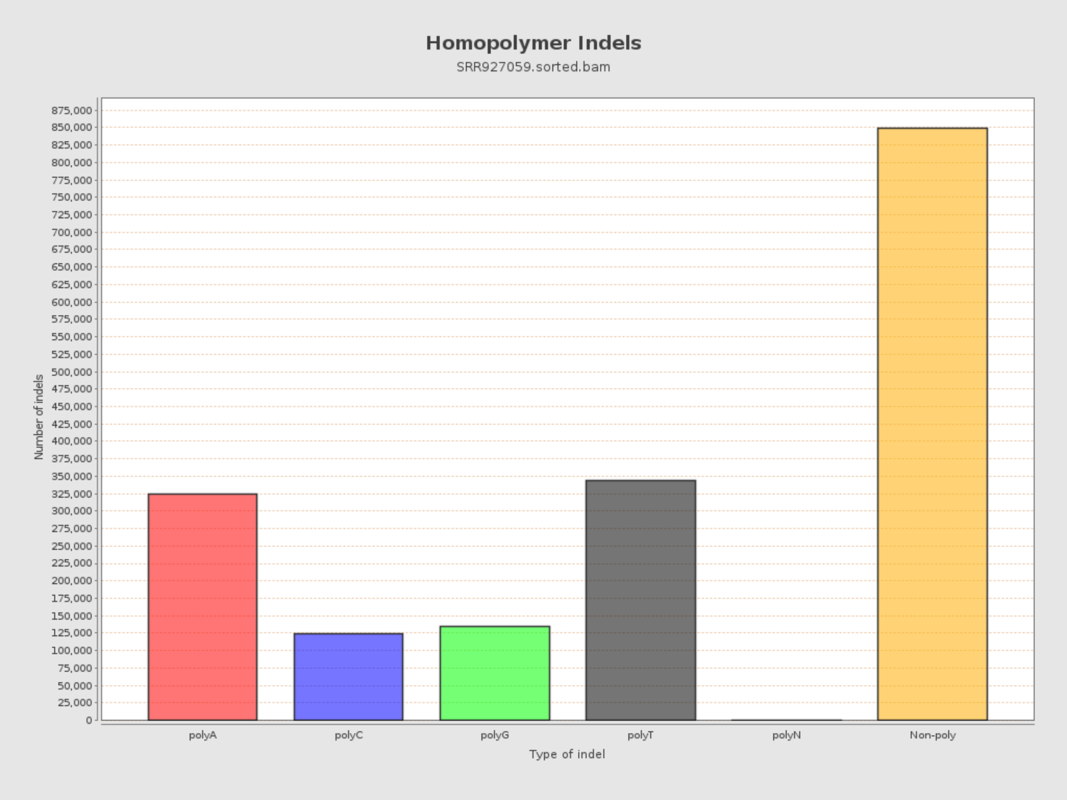
9. Results : Mapped Reads GC-content Distribution



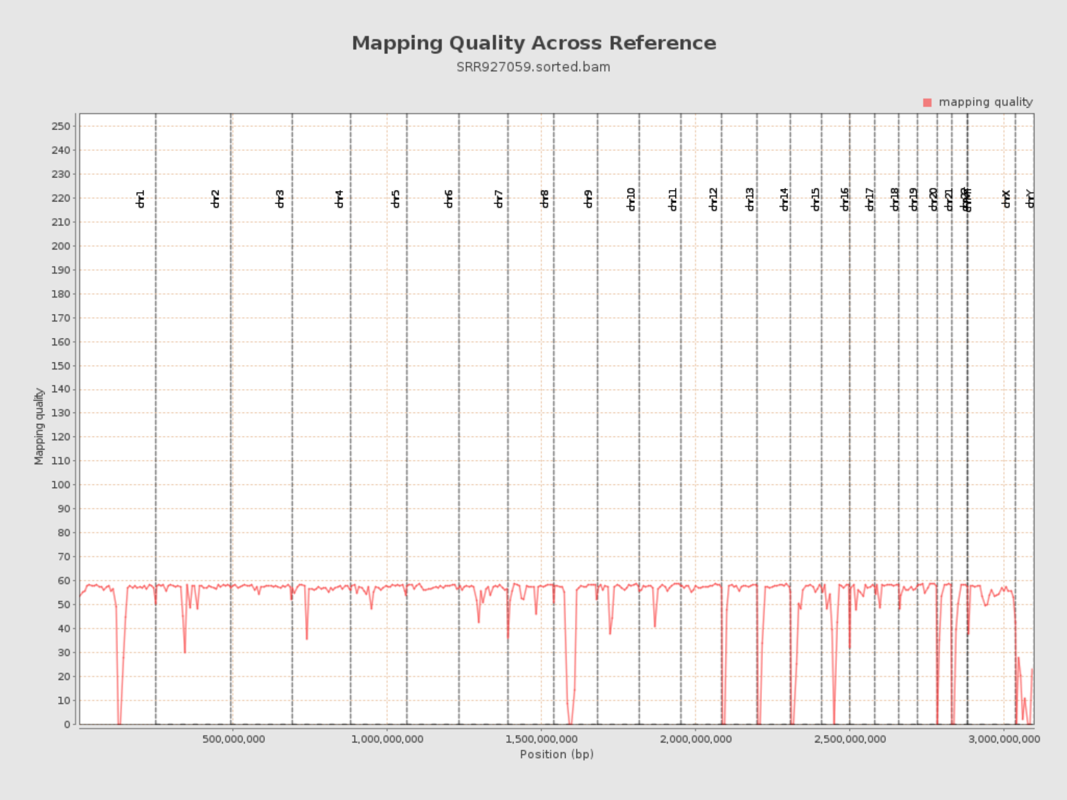
10. Results : Mapped Reads Clipping Profile



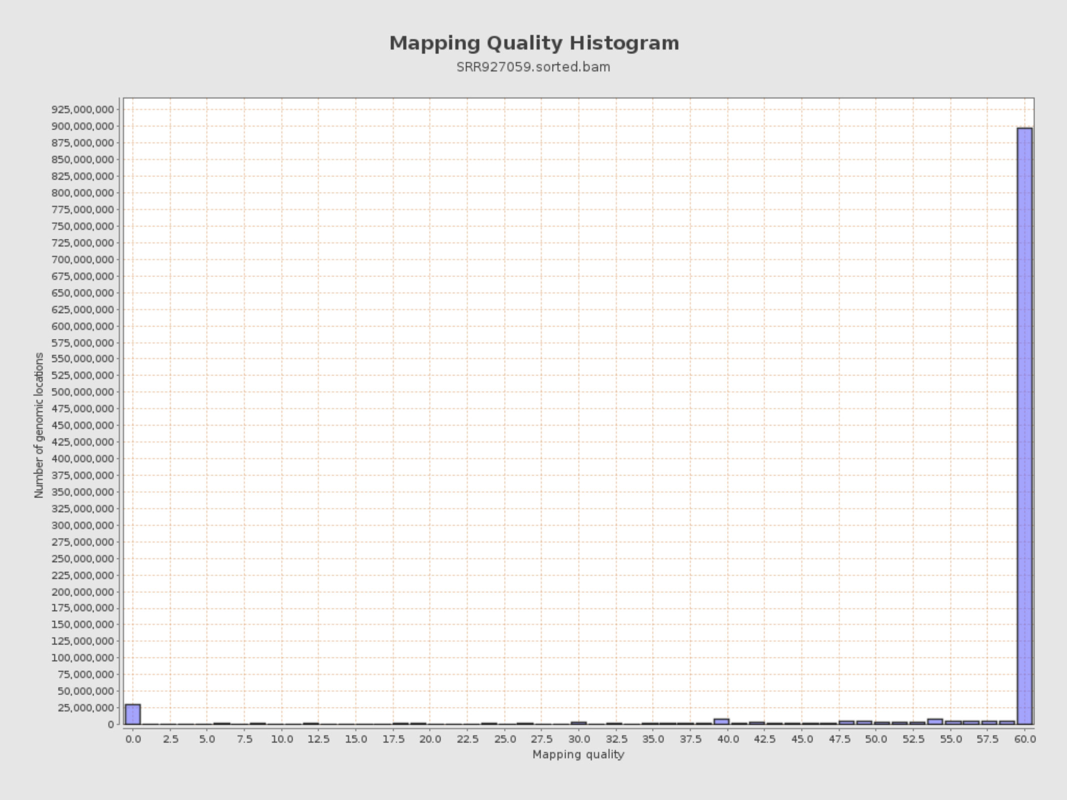
11. Results : Homopolymer Indels



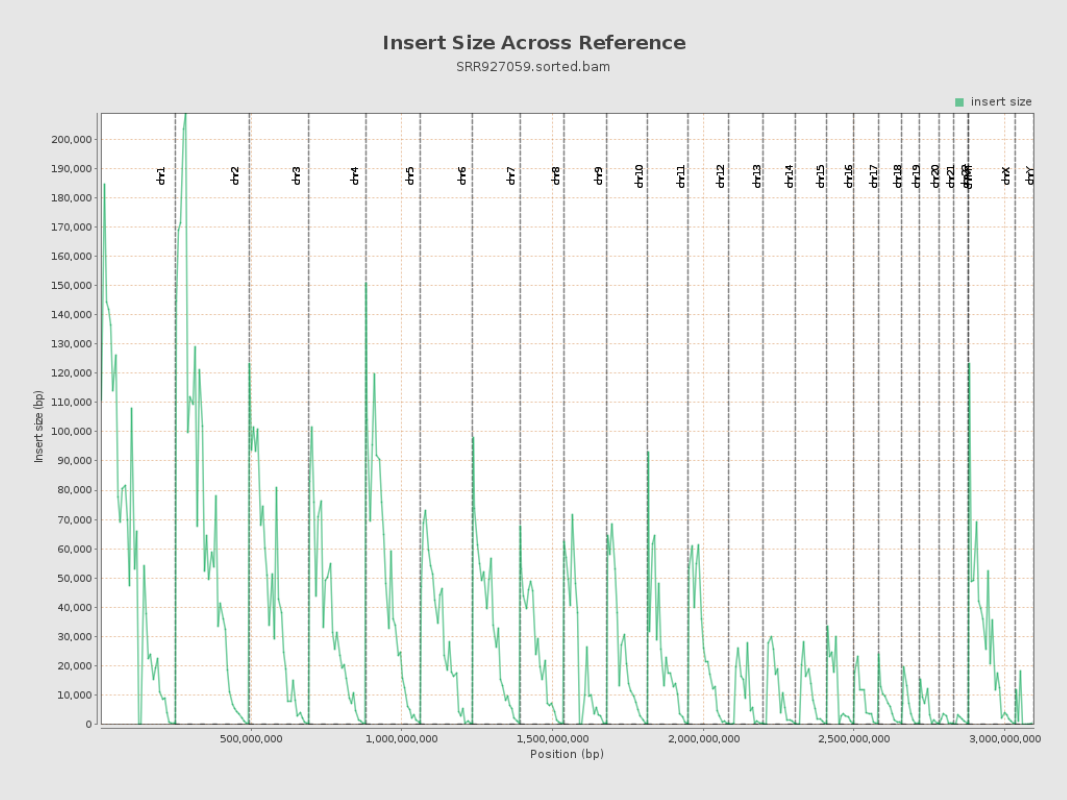
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram