Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/25 08:30:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927069.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_SRR927069 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927069_1.fastq.gz SRR927069_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 25 08:30:48 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927069.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,200,026
Mapped reads	17,895,373 / 98.33%
Unmapped reads	304,653 / 1.67%
Mapped paired reads	17,895,373 / 98.33%
Mapped reads, first in pair	8,988,094 / 49.39%
Mapped reads, second in pair	8,907,279 / 48.94%
Mapped reads, both in pair	17,725,428 / 97.39%
Mapped reads, singletons	169,945 / 0.93%
Secondary alignments	0
Supplementary alignments	119,314 / 0.66%
Read min/max/mean length	30 / 101 / 101.27
Duplicated reads (estimated)	895,872 / 4.92%
Duplication rate	3.97%
Clipped reads	4,027,031 / 22.13%

2.2. ACGT Content

Number/percentage of A's	496,467,847 / 29.14%
Number/percentage of C's	336,591,914 / 19.75%
Number/percentage of T's	501,407,983 / 29.43%
Number/percentage of G's	369,211,326 / 21.67%
Number/percentage of N's	279,134 / 0.02%

GC Percentage	41.42%

2.3. Coverage

Mean	0.5508
Standard Deviation	2.1974

2.4. Mapping Quality

Mean Mapping Quality	53.63

2.5. Insert size

Mean	73,513.32
Standard Deviation	2,669,086.35
P25/Median/P75	148 / 192 / 258

2.6. Mismatches and indels

General error rate	1.11%
Mismatches	18,404,199
Insertions	276,986
Mapped reads with at least one insertion	1.52%
Deletions	923,221
Mapped reads with at least one deletion	5.02%
Homopolymer indels	53.16%

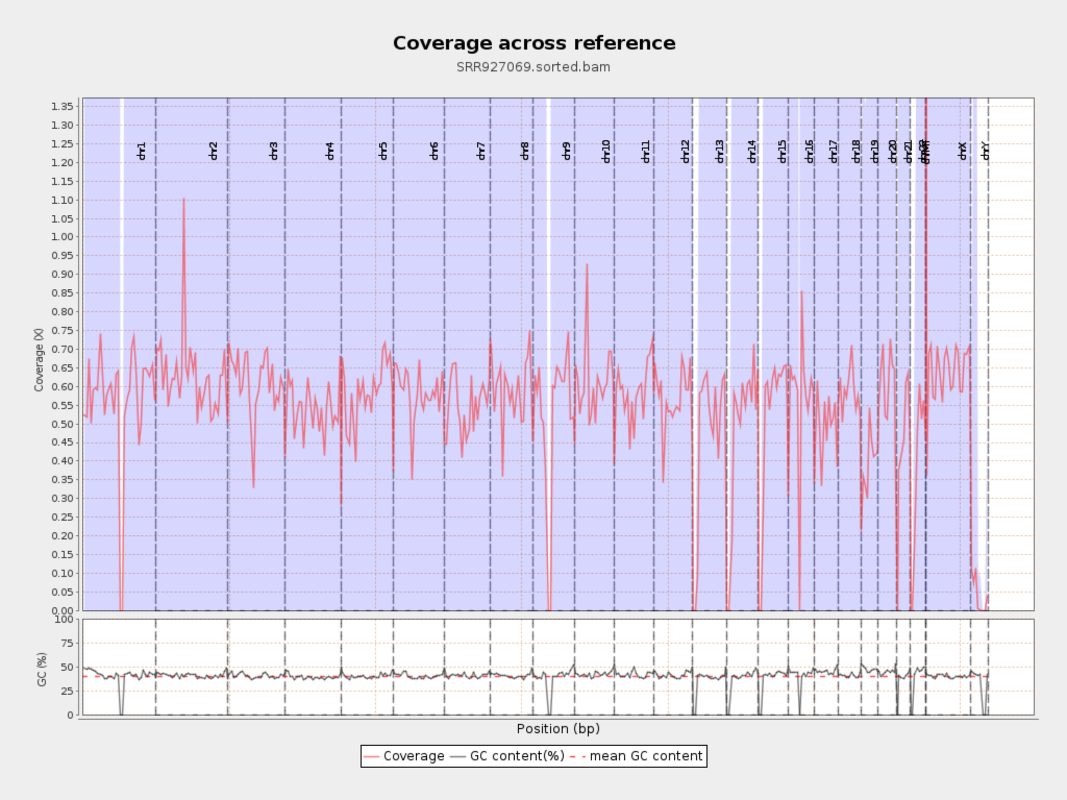
2.7. Chromosome stats

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

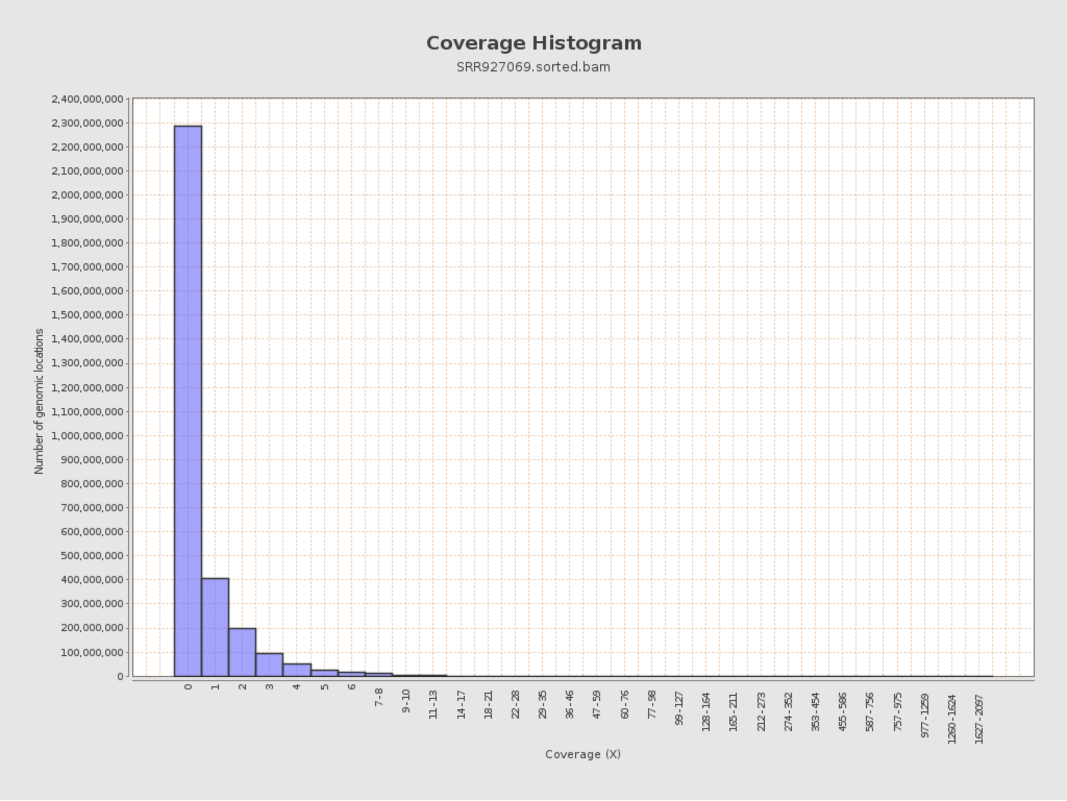
		bases	coverage	deviation
chr1	249250621	140091182	0.562	2.493
chr2	243199373	153344235	0.6305	3.7397
chr3	198022430	120255538	0.6073	1.3057
chr4	191154276	103570515	0.5418	1.6292
chr5	180915260	105401028	0.5826	1.2611
chr6	171115067	100053081	0.5847	1.2771
chr7	159138663	86939153	0.5463	1.629
chr8	146364022	86616591	0.5918	1.5224
chr9	141213431	73973158	0.5238	3.1714
chr10	135534747	82857744	0.6113	4.2293
chr11	135006516	78910742	0.5845	2.2216
chr12	133851895	76452682	0.5712	1.2678
chr13	115169878	53672443	0.466	1.1281
chr14	107349540	51241649	0.4773	1.1985
chr15	102531392	51523591	0.5025	1.227
chr16	90354753	50464384	0.5585	2.9289
chr17	81195210	40534640	0.4992	1.5283
chr18	78077248	45834414	0.587	3.1708
chr19	59128983	23430193	0.3963	1.5626
chr20	63025520	38598189	0.6124	1.4075
chr21	48129895	21472924	0.4461	1.4644
chr22	51304566	18872227	0.3678	1.0798
chrMT	16571	56110	3.386	3.9941
chrX	155270560	98680675	0.6355	1.5327

chrY	59373566	2394826	0.0403	1.0866

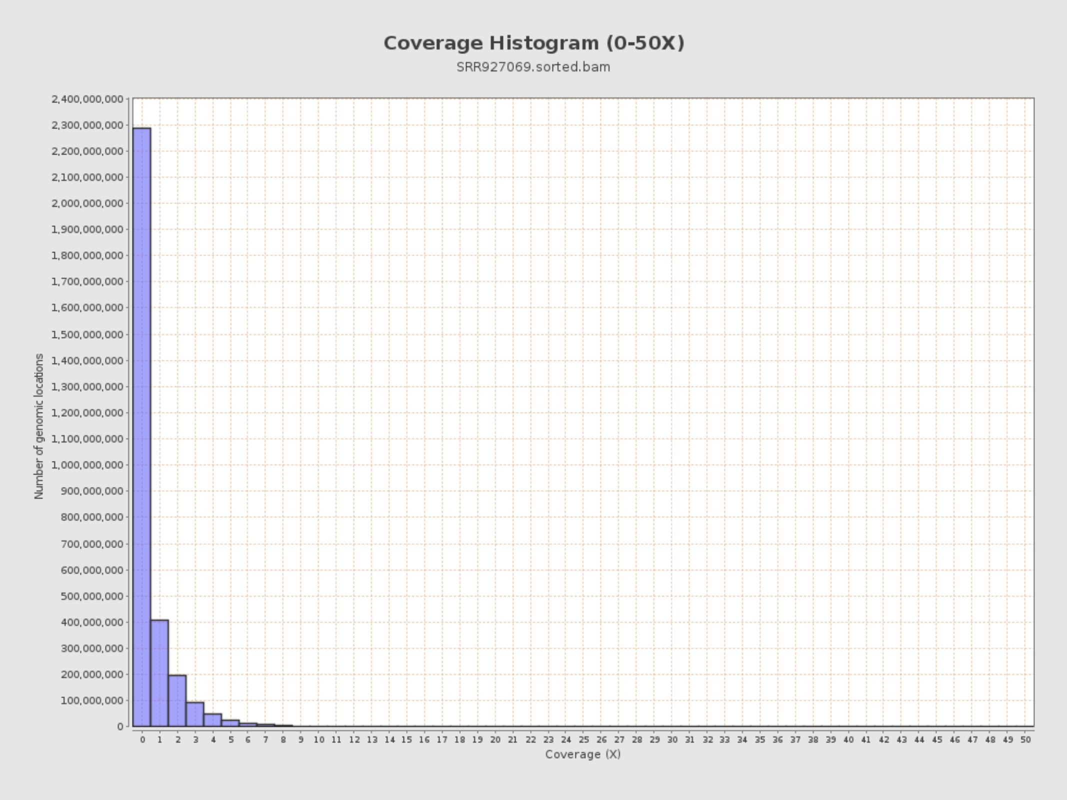
3. Results : Coverage across reference



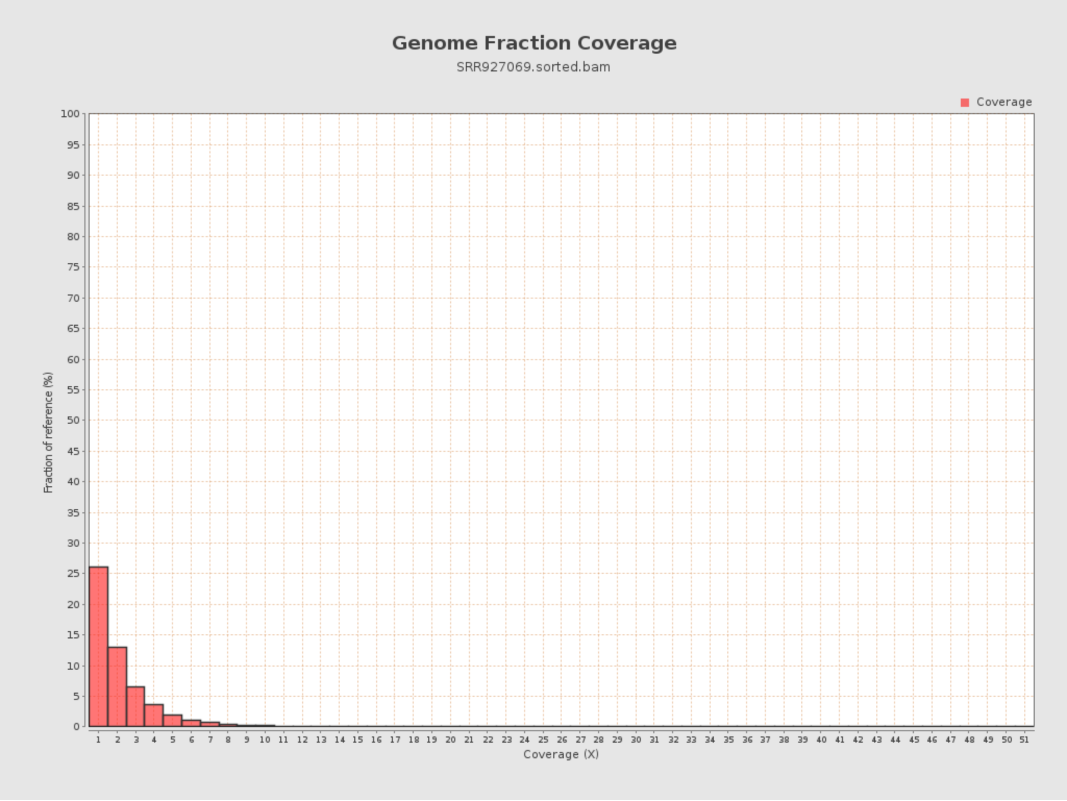
4. Results : Coverage Histogram



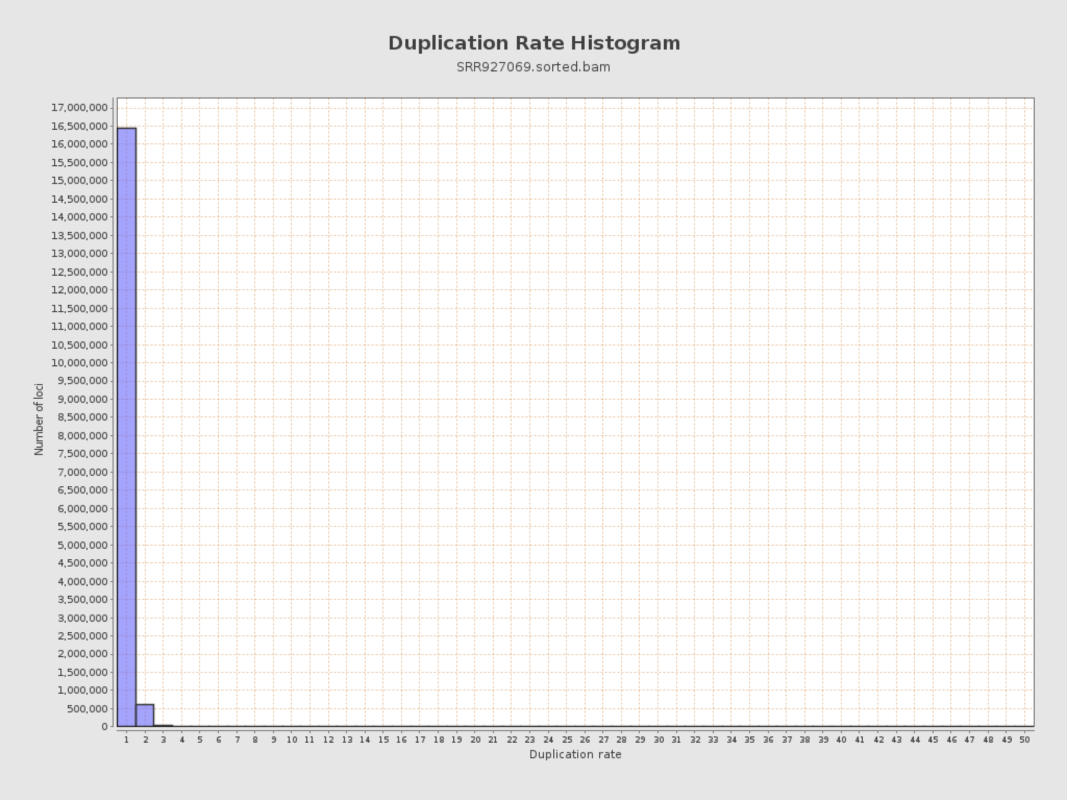
5. Results : Coverage Histogram (0-50X)



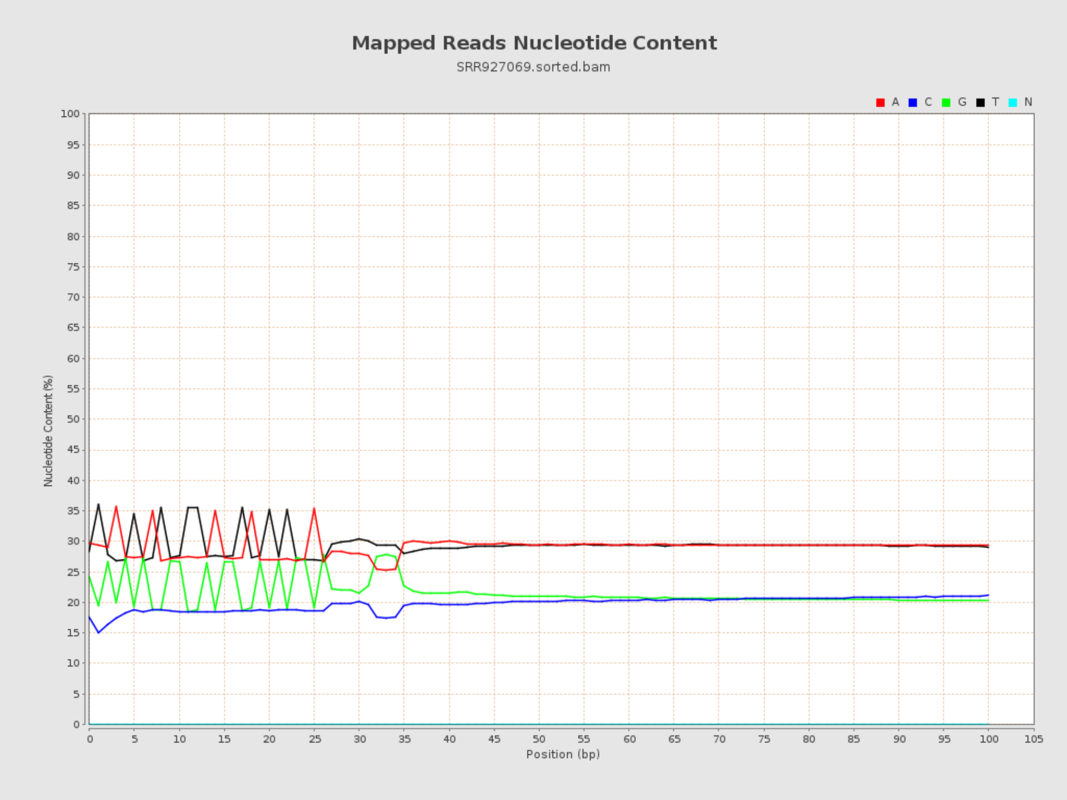
6. Results : Genome Fraction Coverage



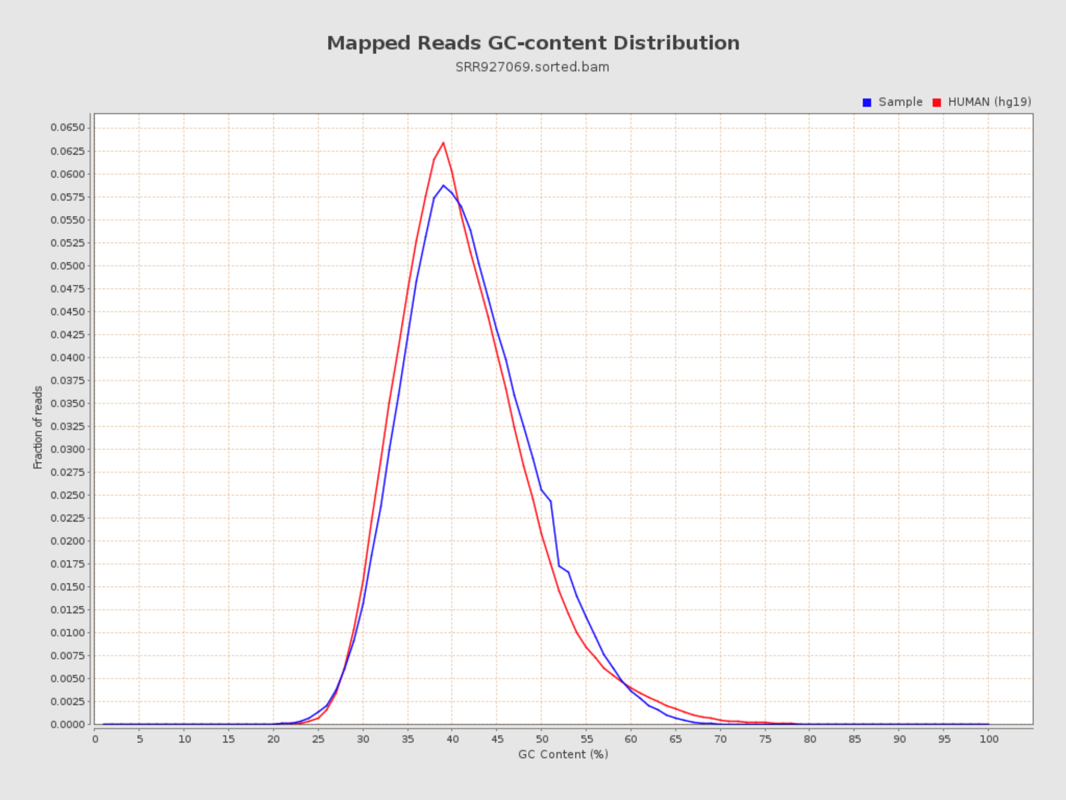
7. Results : Duplication Rate Histogram



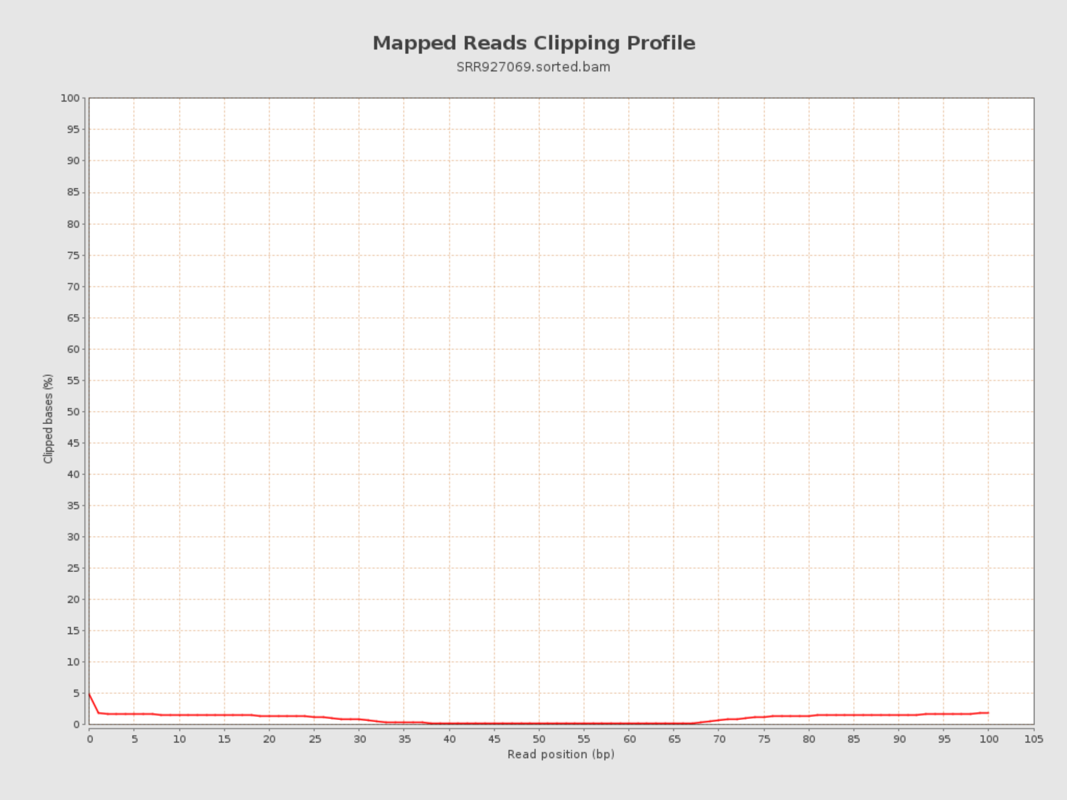
8. Results : Mapped Reads Nucleotide Content



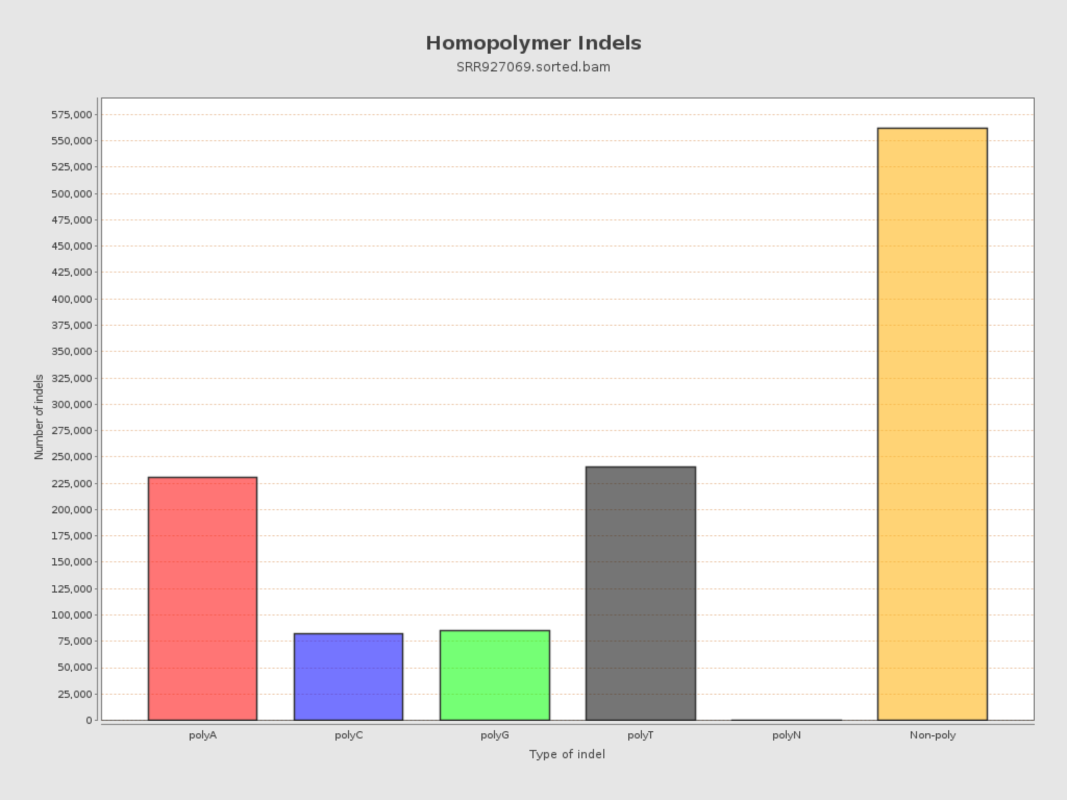
9. Results : Mapped Reads GC-content Distribution



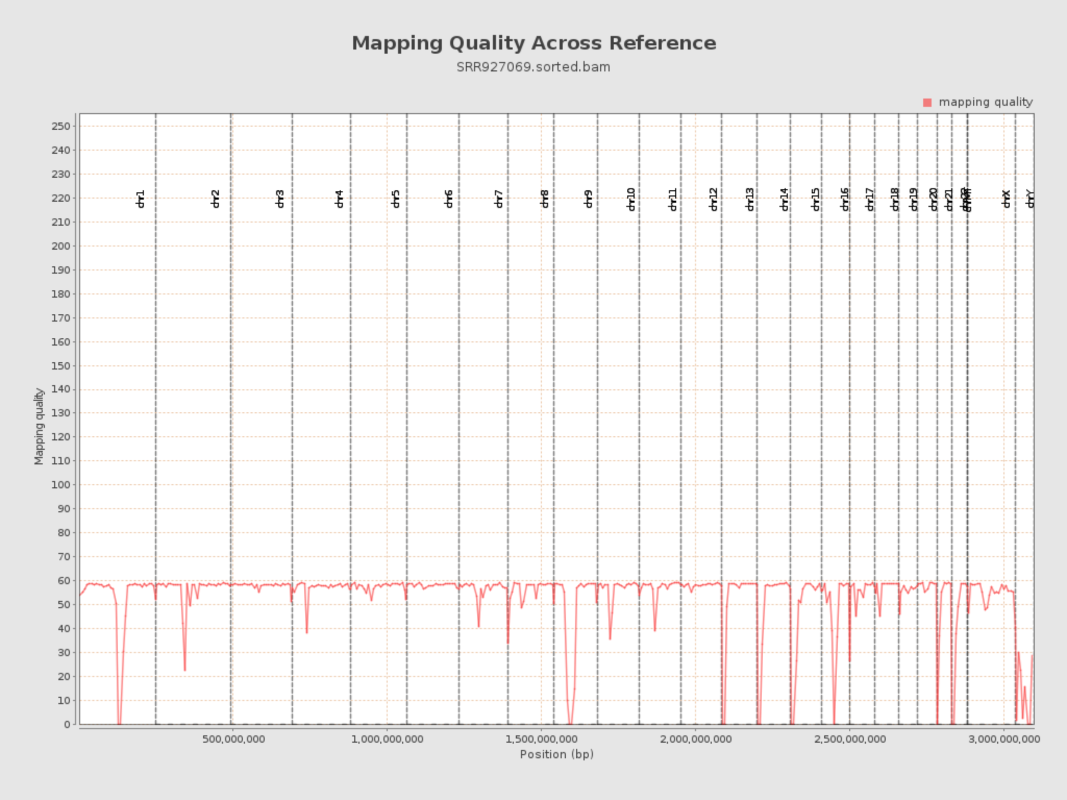
10. Results : Mapped Reads Clipping Profile



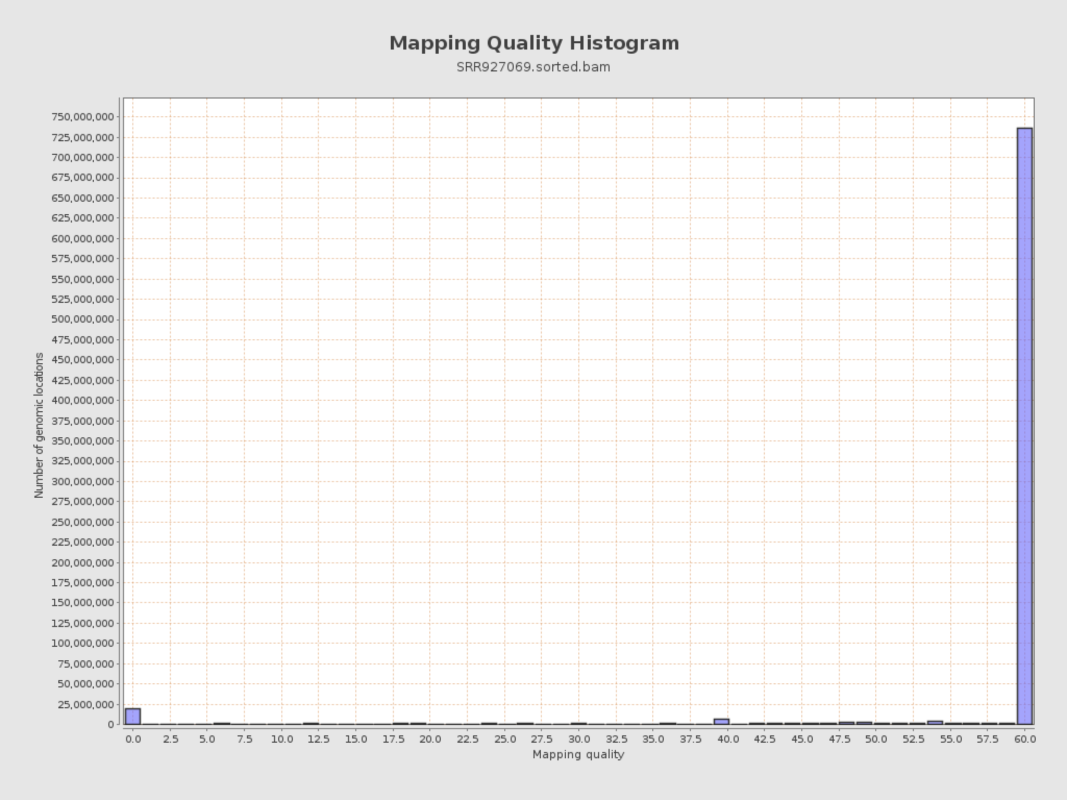
11. Results : Homopolymer Indels



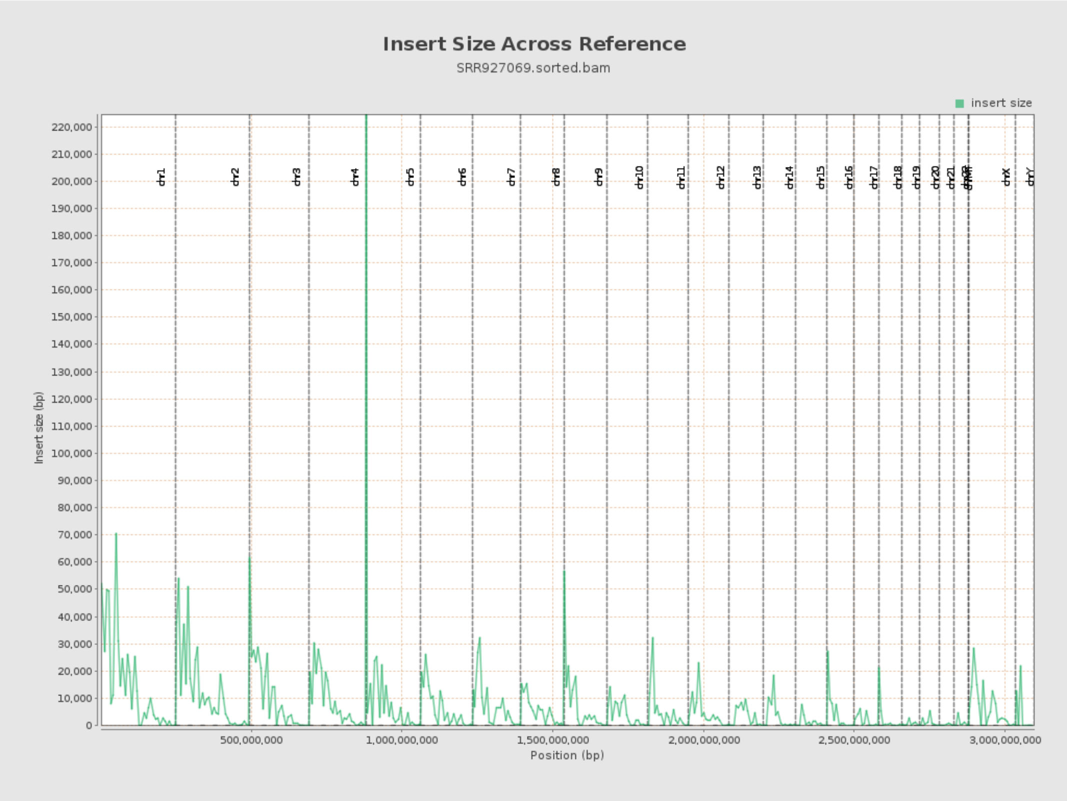
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram