Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 23:56:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927052.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_SRR927052 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927052_1.fastq.gz SRR927052_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 23:56:15 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927052.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,420,902
Mapped reads	29,867,334 / 98.18%
Unmapped reads	553,568 / 1.82%
Mapped paired reads	29,867,334 / 98.18%
Mapped reads, first in pair	14,977,018 / 49.23%
Mapped reads, second in pair	14,890,316 / 48.95%
Mapped reads, both in pair	29,558,156 / 97.16%
Mapped reads, singletons	309,178 / 1.02%
Secondary alignments	0
Supplementary alignments	531,667 / 1.75%
Read min/max/mean length	30 / 101 / 101.72
Duplicated reads (estimated)	2,150,040 / 7.07%
Duplication rate	5.75%
Clipped reads	7,354,317 / 24.18%

2.2. ACGT Content

Number/percentage of A's	813,362,863 / 28.57%
Number/percentage of C's	578,330,449 / 20.32%
Number/percentage of T's	820,978,429 / 28.84%
Number/percentage of G's	633,660,027 / 22.26%
Number/percentage of N's	255,418 / 0.01%

GC Percentage	42.58%

2.3. Coverage

Mean	0.9202
Standard Deviation	3.4247

2.4. Mapping Quality

Mean Mapping Quality	53.38

2.5. Insert size

Mean	167,999.8
Standard Deviation	3,989,551.95
P25/Median/P75	146 / 187 / 250

2.6. Mismatches and indels

General error rate	0.97%
Mismatches	26,769,597
Insertions	470,735
Mapped reads with at least one insertion	1.55%
Deletions	1,521,612
Mapped reads with at least one deletion	4.96%
Homopolymer indels	52.74%

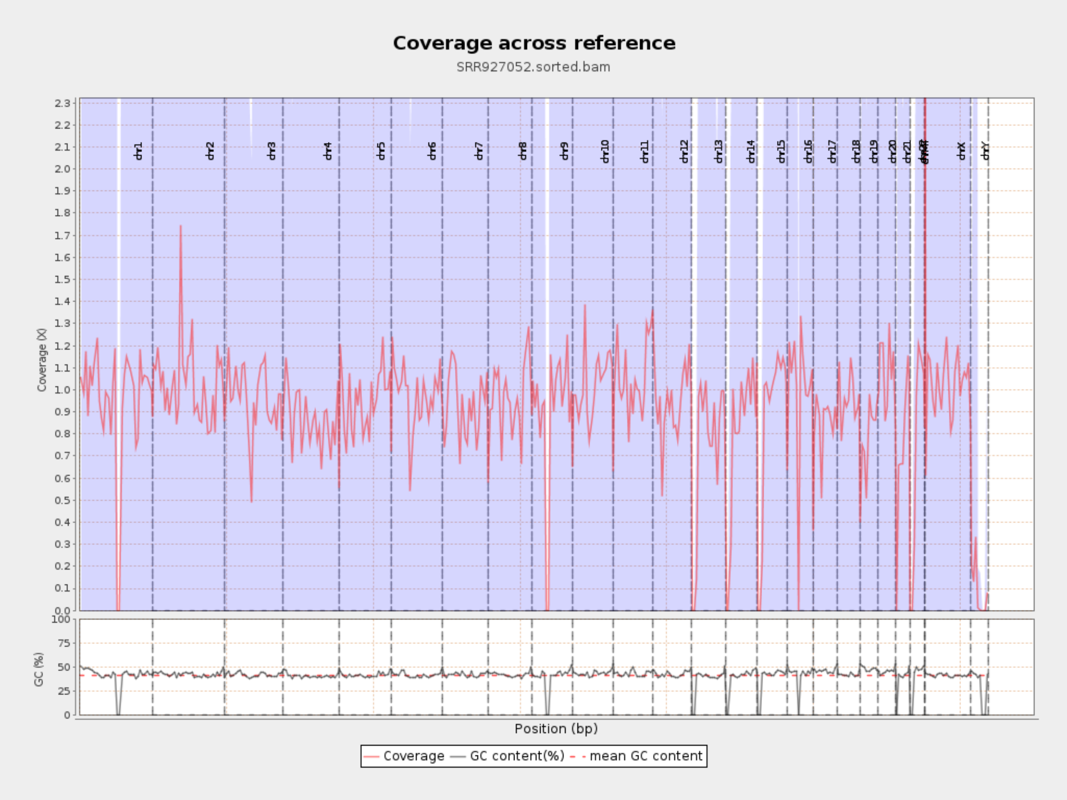
2.7. Chromosome stats

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

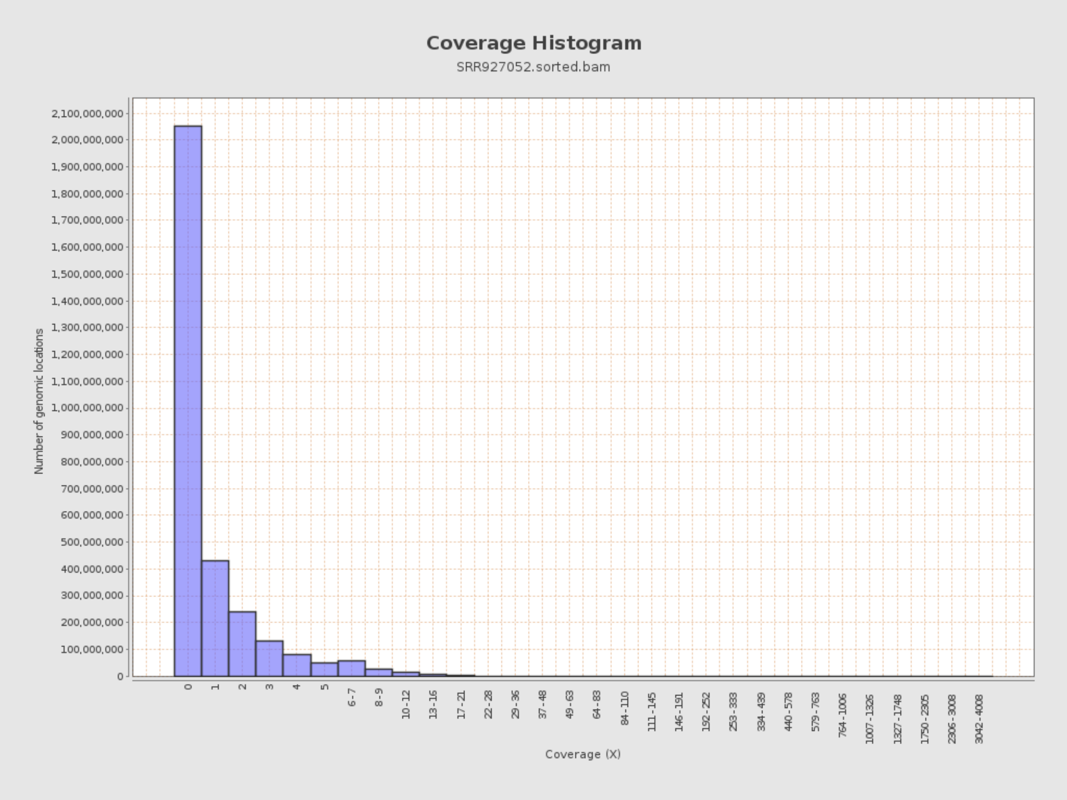
		bases	coverage	deviation
chr1	249250621	236847363	0.9502	4.7735
chr2	243199373	251389068	1.0337	5.504
chr3	198022430	190230883	0.9607	1.9714
chr4	191154276	165245990	0.8645	2.9747
chr5	180915260	172387830	0.9529	1.9495
chr6	171115067	167105333	0.9766	2.0144
chr7	159138663	148190522	0.9312	2.6974
chr8	146364022	142088292	0.9708	2.3836
chr9	141213431	125854559	0.8912	4.5192
chr10	135534747	139677154	1.0306	5.0635
chr11	135006516	140813396	1.043	3.8744
chr12	133851895	126471563	0.9449	2.3063
chr13	115169878	84956830	0.7377	1.7647
chr14	107349540	83884679	0.7814	1.8393
chr15	102531392	87000328	0.8485	1.9616
chr16	90354753	89010658	0.9851	4.3632
chr17	81195210	69160844	0.8518	2.5128
chr18	78077248	76035187	0.9738	4.6752
chr19	59128983	46116011	0.7799	2.9491
chr20	63025520	68070437	1.08	2.3224
chr21	48129895	36530671	0.759	2.8196
chr22	51304566	37899958	0.7387	1.9109
chrMT	16571	154932	9.3496	7.9395
chrX	155270560	158280202	1.0194	2.3462

chrY	59373566	5357207	0.0902	3.9577

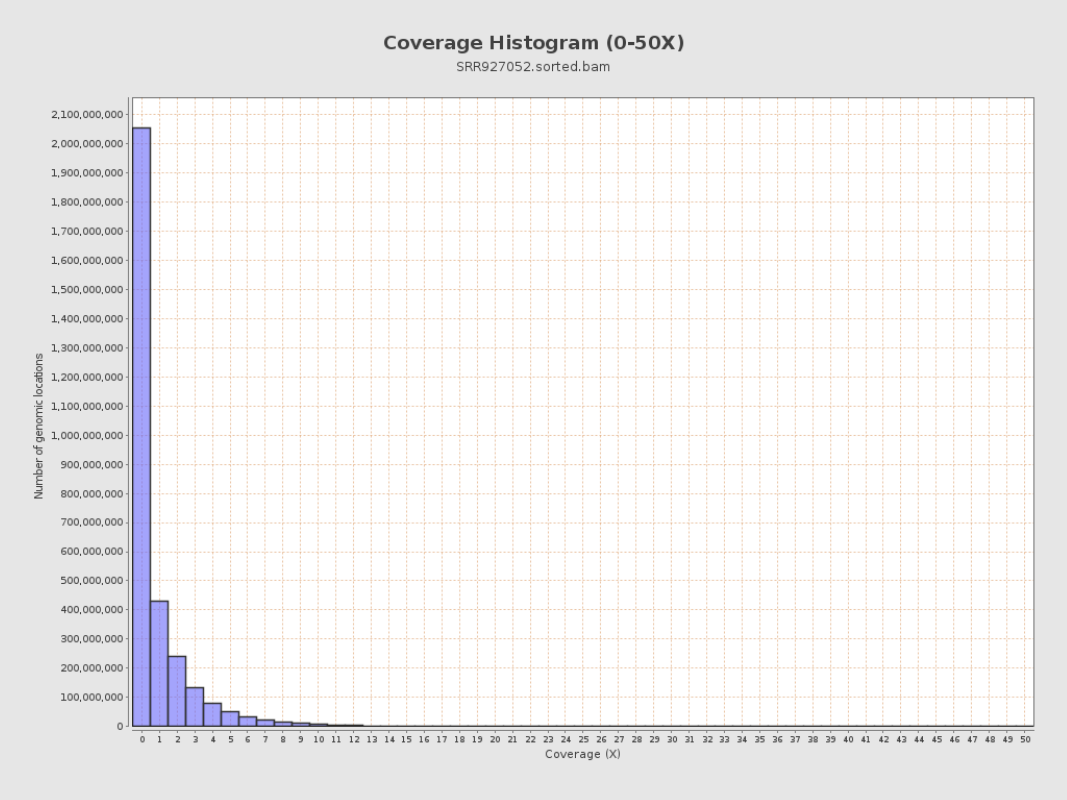
3. Results : Coverage across reference



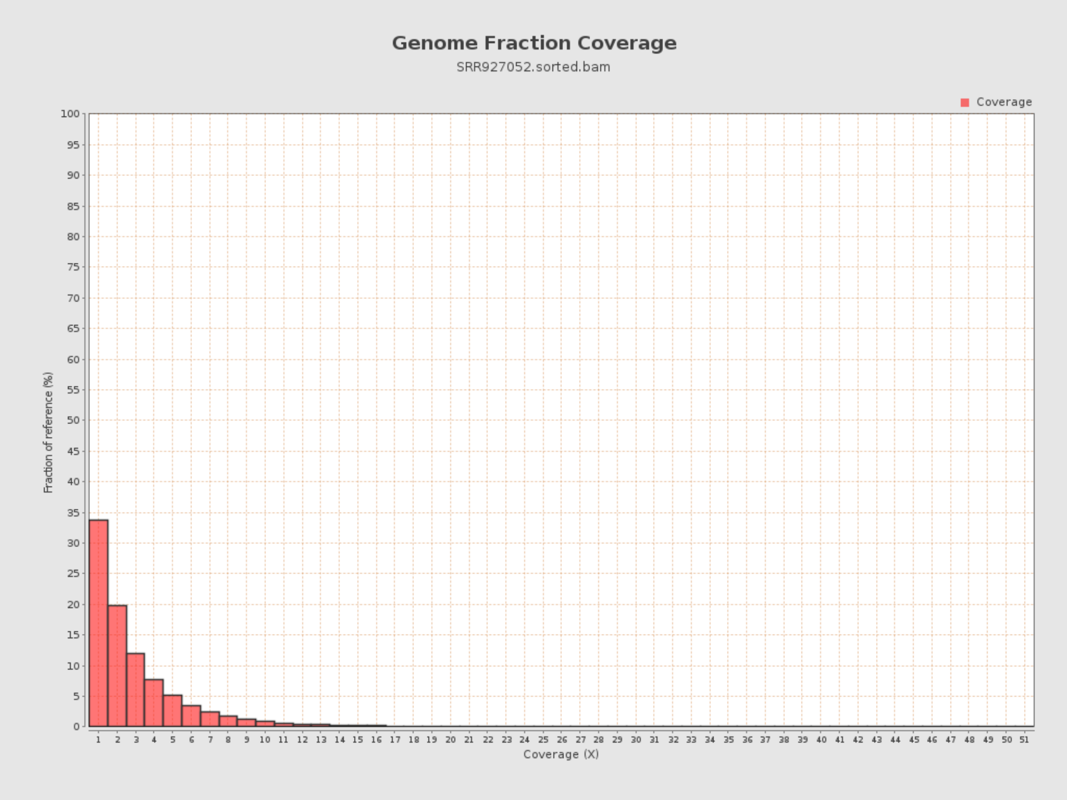
4. Results : Coverage Histogram



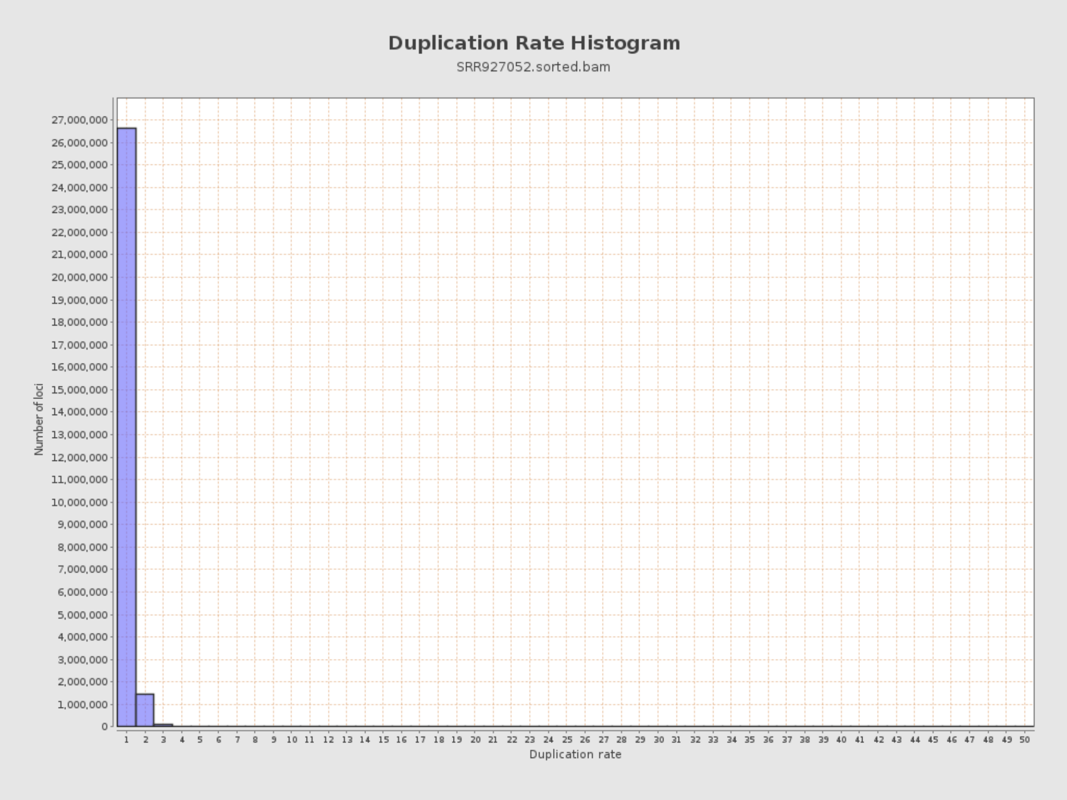
5. Results : Coverage Histogram (0-50X)



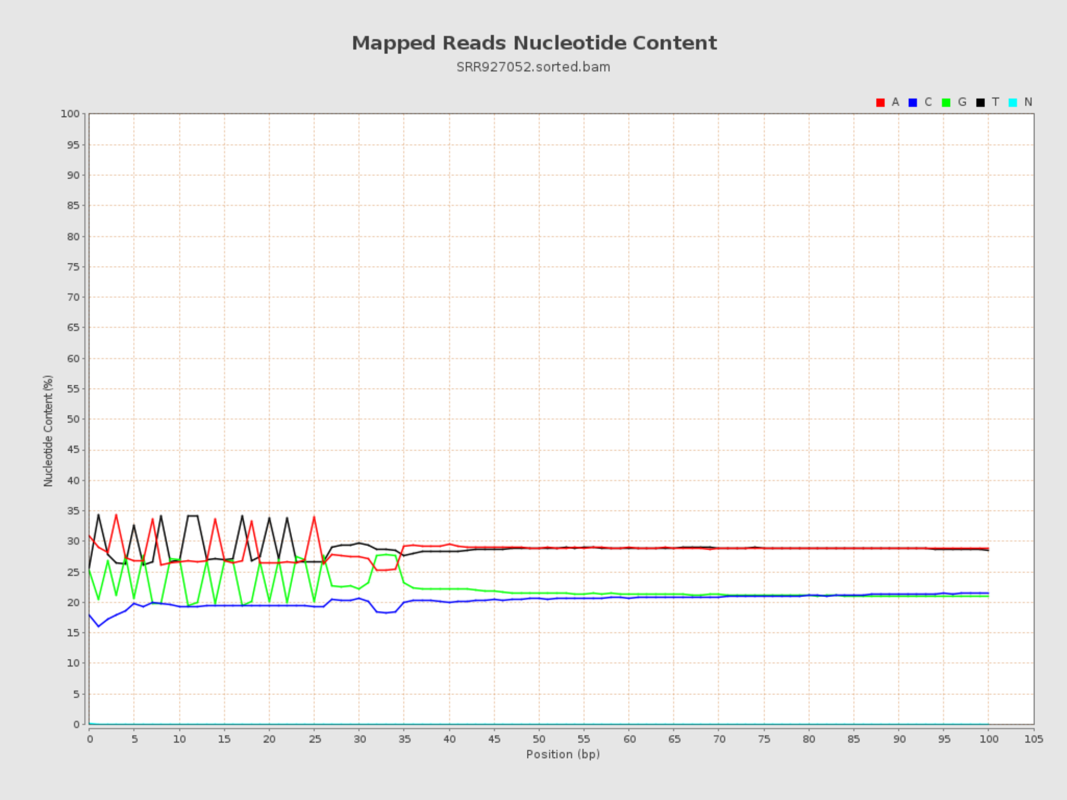
6. Results : Genome Fraction Coverage



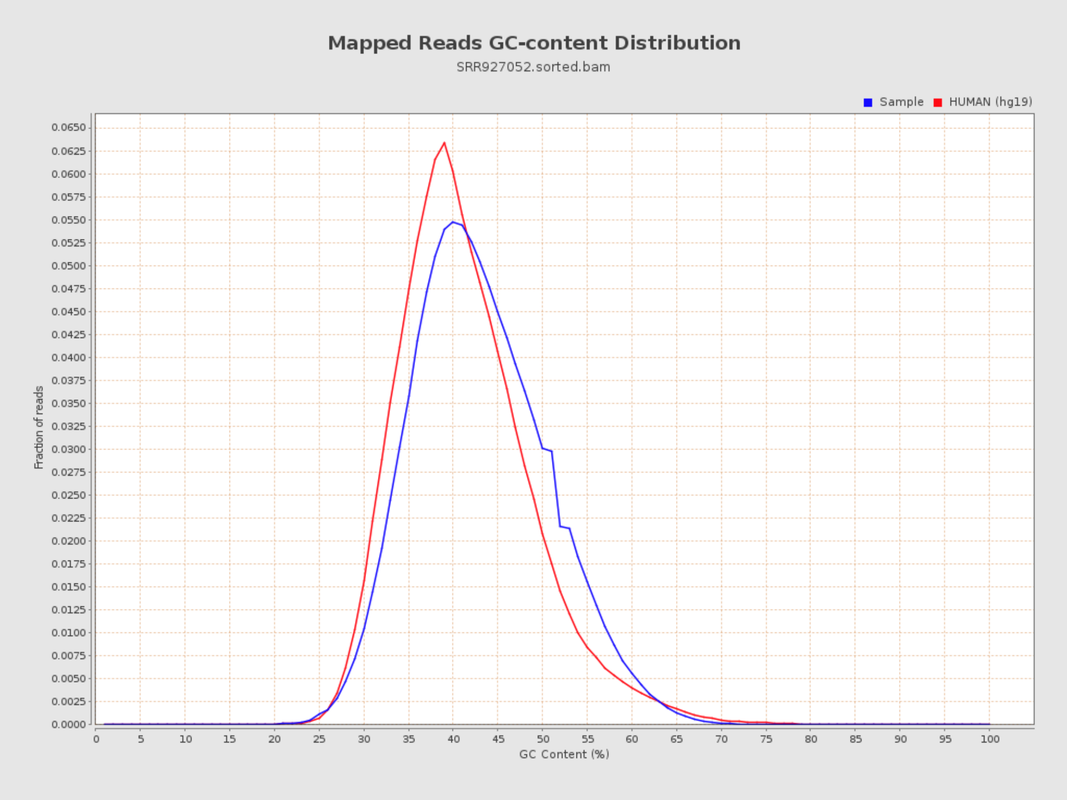
7. Results : Duplication Rate Histogram



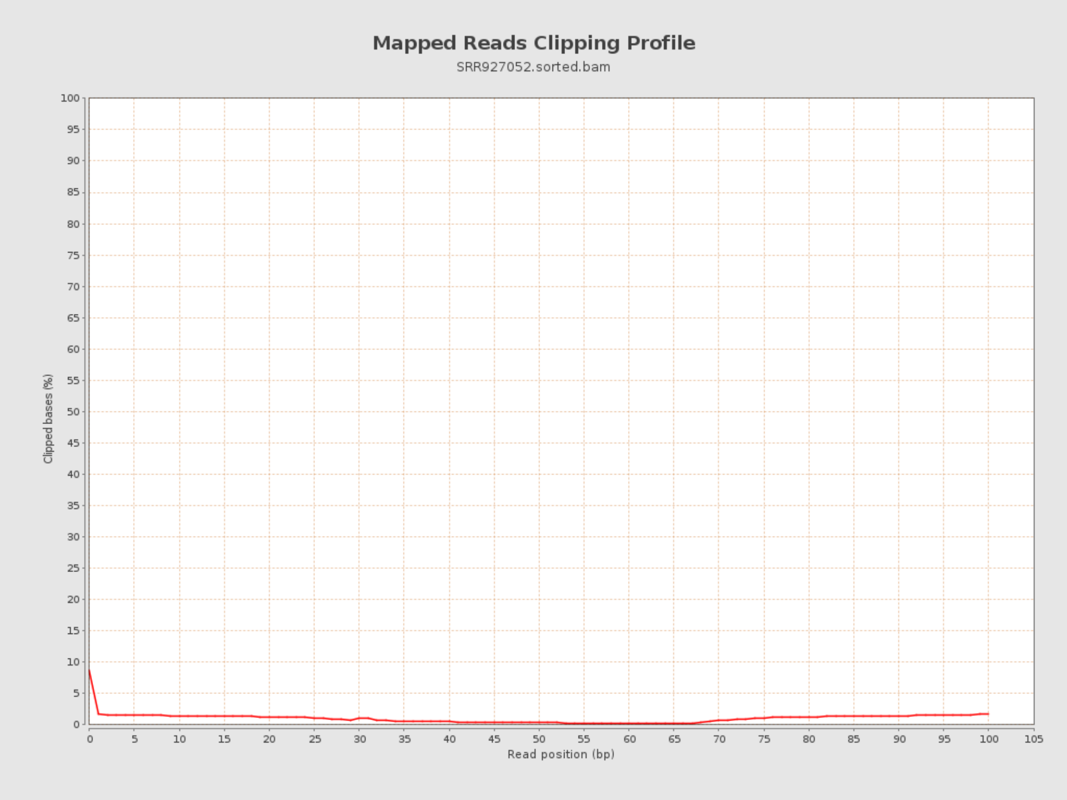
8. Results : Mapped Reads Nucleotide Content



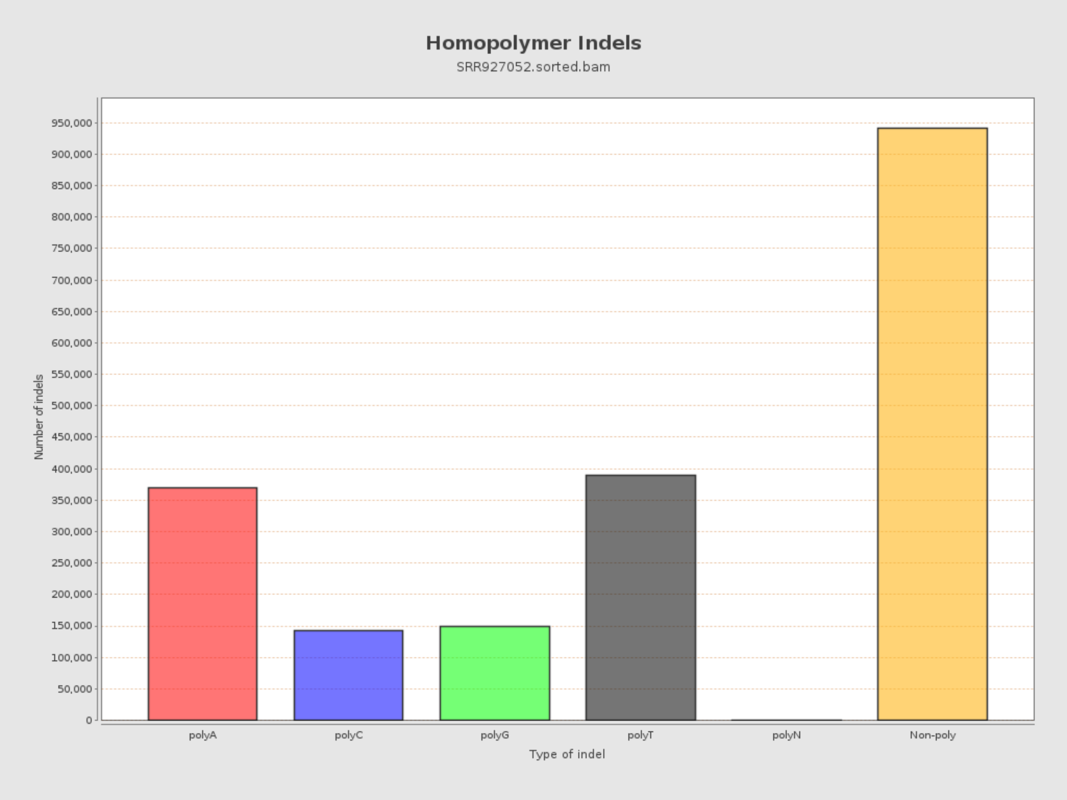
9. Results : Mapped Reads GC-content Distribution



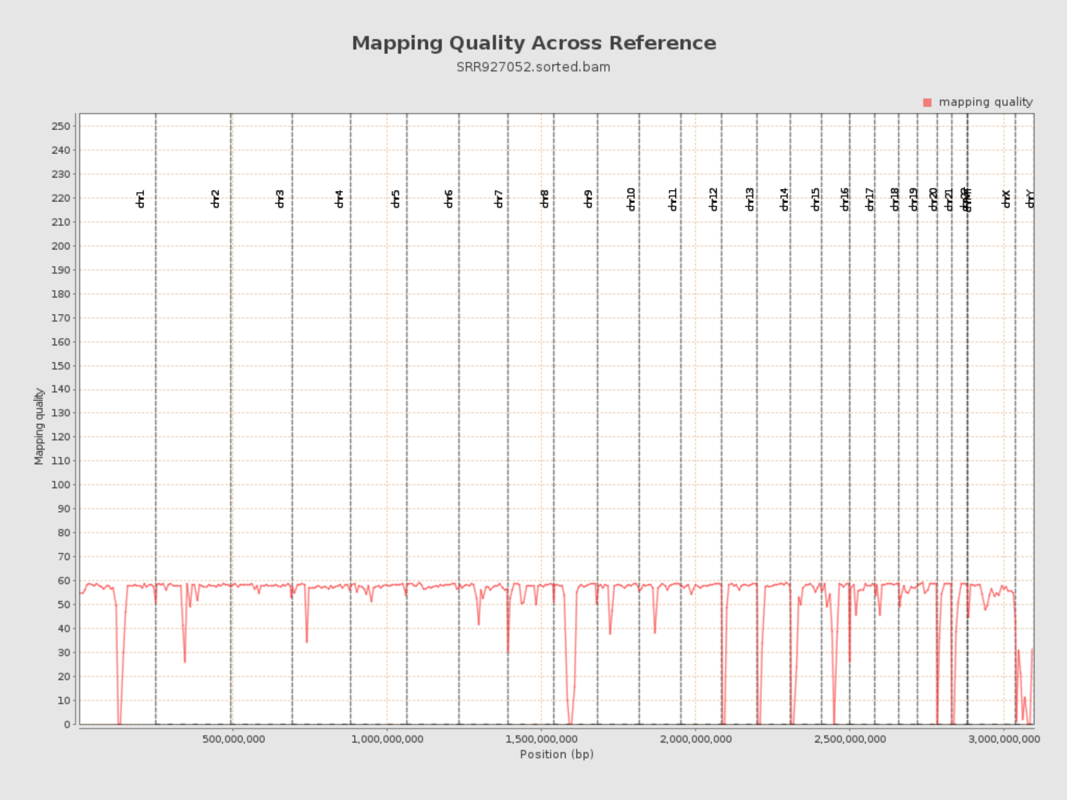
10. Results : Mapped Reads Clipping Profile



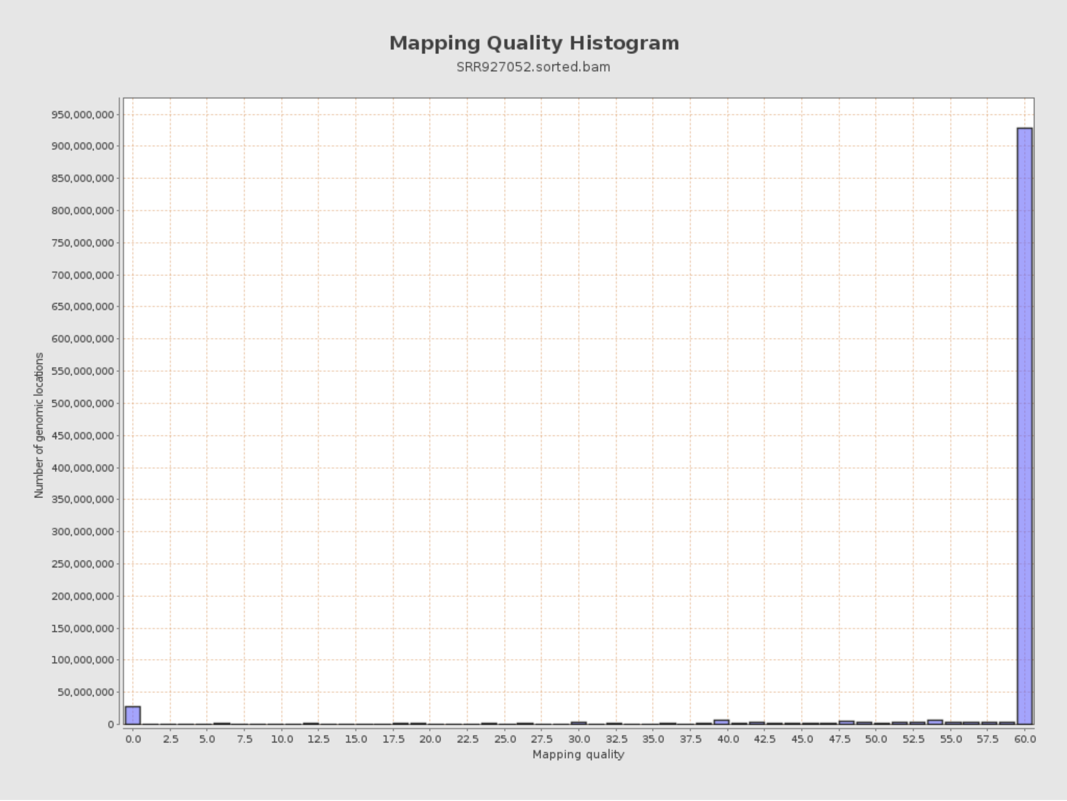
11. Results : Homopolymer Indels



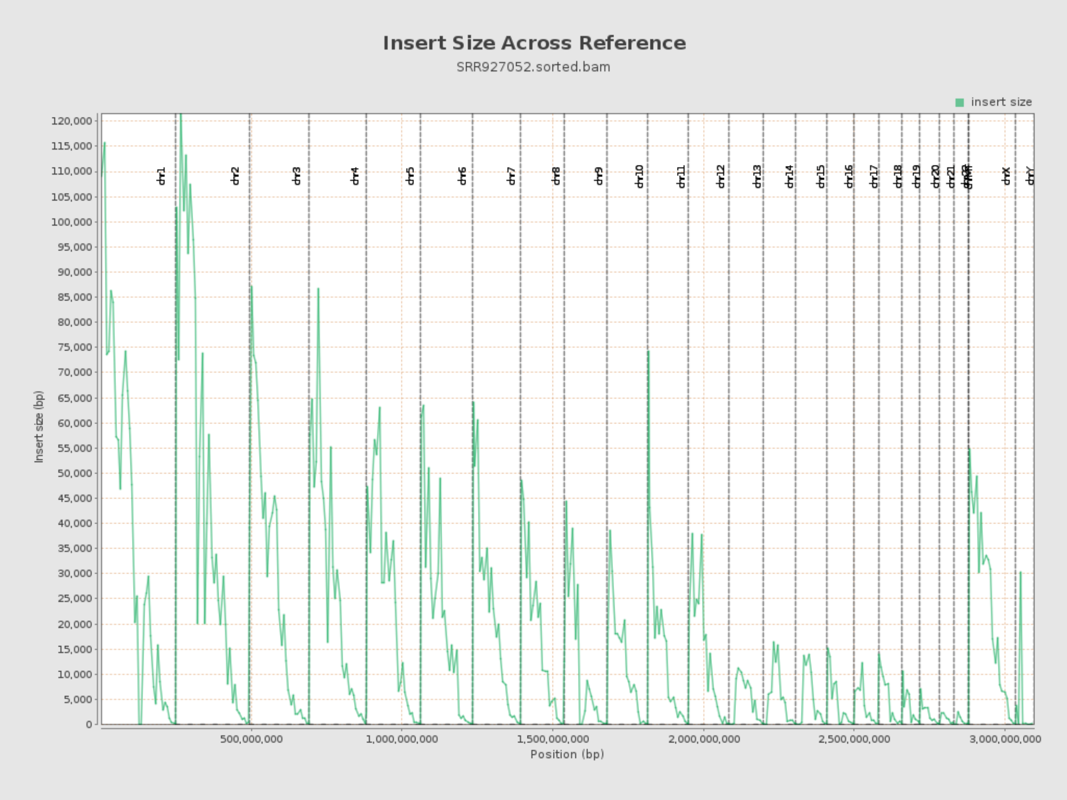
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram