Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 02:59:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926955.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_SRR926955 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926955_1.fastq.gz SRR926955_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 02:59:10 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926955.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,747,364
Mapped reads	10,348,892 / 96.29%
Unmapped reads	398,472 / 3.71%
Mapped paired reads	10,348,892 / 96.29%
Mapped reads, first in pair	5,184,387 / 48.24%
Mapped reads, second in pair	5,164,505 / 48.05%
Mapped reads, both in pair	10,168,216 / 94.61%
Mapped reads, singletons	180,676 / 1.68%
Secondary alignments	0
Supplementary alignments	323,463 / 3.01%
Read min/max/mean length	30 / 101 / 102.25
Duplicated reads (estimated)	674,493 / 6.28%
Duplication rate	5.44%
Clipped reads	4,414,684 / 41.08%

2.2. ACGT Content

Number/percentage of A's	266,946,758 / 28.34%
Number/percentage of C's	185,960,636 / 19.74%
Number/percentage of T's	269,667,627 / 28.63%
Number/percentage of G's	219,326,852 / 23.28%
Number/percentage of N's	49,211 / 0.01%

GC Percentage	43.03%

2.3. Coverage

Mean	0.3045
Standard Deviation	1.1926

2.4. Mapping Quality

Mean Mapping Quality	52.71

2.5. Insert size

Mean	311,015.01
Standard Deviation	5,373,996.24
P25/Median/P75	143 / 188 / 256

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	9,435,655
Insertions	161,905
Mapped reads with at least one insertion	1.54%
Deletions	493,195
Mapped reads with at least one deletion	4.64%
Homopolymer indels	52.38%

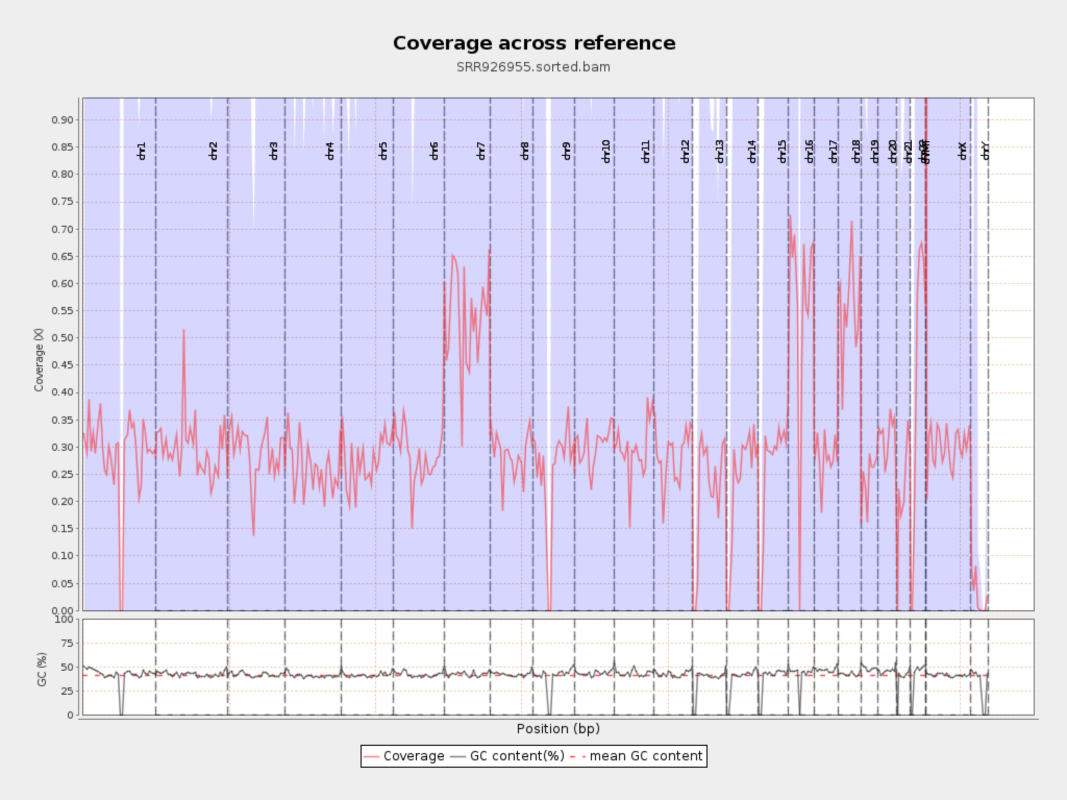
2.7. Chromosome stats

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

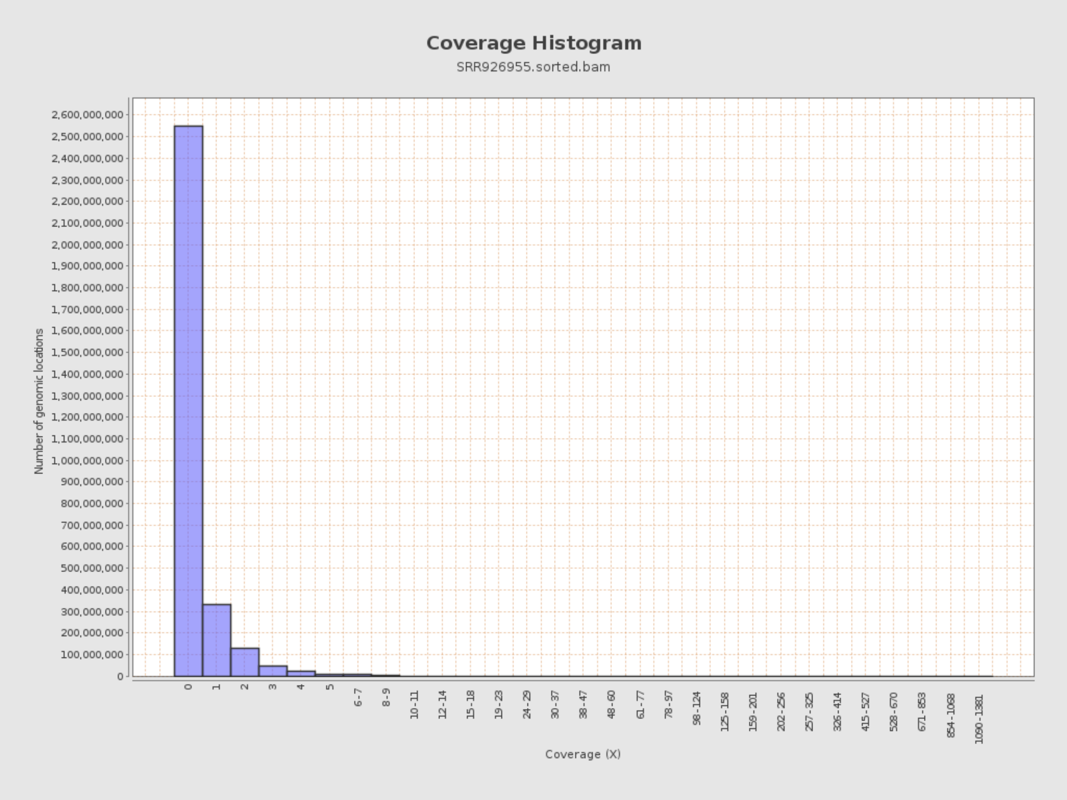
		bases	coverage	deviation
chr1	249250621	71020246	0.2849	1.324
chr2	243199373	72877014	0.2997	1.9148
chr3	198022430	57351539	0.2896	0.7799
chr4	191154276	50466744	0.264	1.1234
chr5	180915260	50208500	0.2775	0.7608
chr6	171115067	48418041	0.283	0.8118
chr7	159138663	85453047	0.537	1.2742
chr8	146364022	41775450	0.2854	0.8582
chr9	141213431	35864258	0.254	1.248
chr10	135534747	40976803	0.3023	1.5708
chr11	135006516	40002745	0.2963	1.0102
chr12	133851895	38236462	0.2857	1.3138
chr13	115169878	25403573	0.2206	0.6779
chr14	107349540	25553977	0.238	0.7202
chr15	102531392	25628656	0.25	0.7476
chr16	90354753	49878827	0.552	1.3242
chr17	81195210	22782536	0.2806	0.8147
chr18	78077248	43285184	0.5544	1.6693
chr19	59128983	14587755	0.2467	0.9584
chr20	63025520	20262136	0.3215	0.8695
chr21	48129895	10937878	0.2273	1.1884
chr22	51304566	22214364	0.433	1.1258
chrMT	16571	1248859	75.3641	81.3461
chrX	155270560	46673090	0.3006	0.8234

chrY	59373566	1567923	0.0264	0.8095

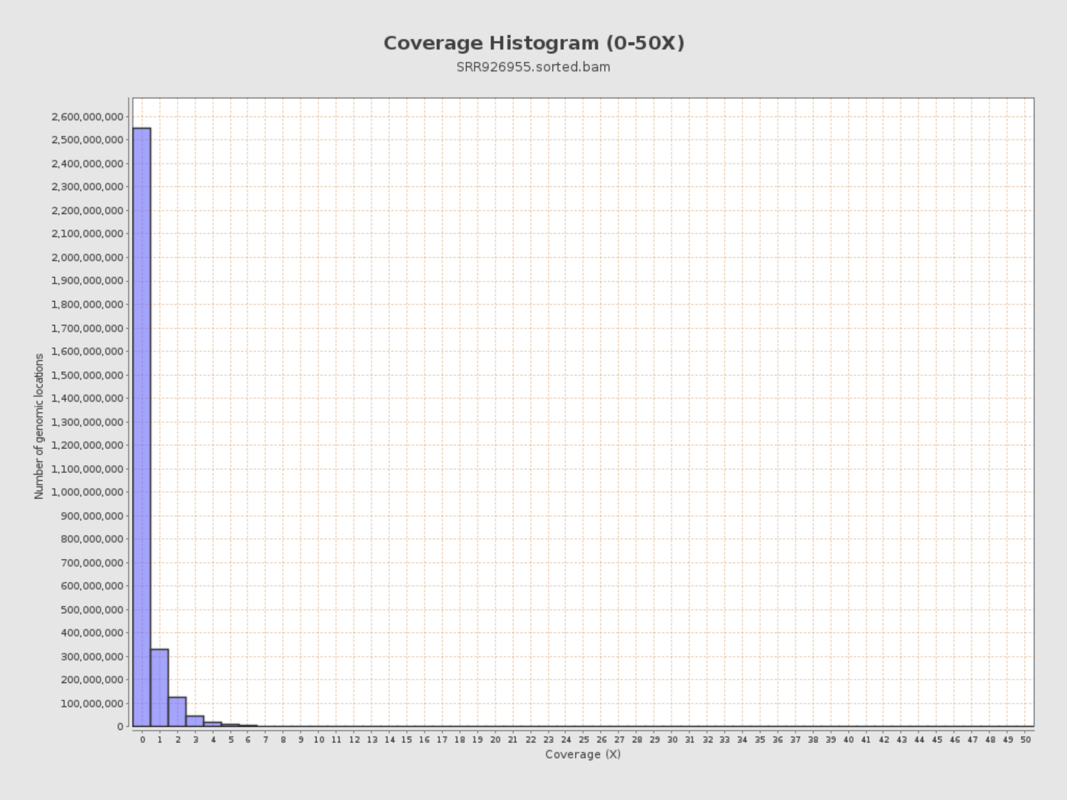
3. Results : Coverage across reference



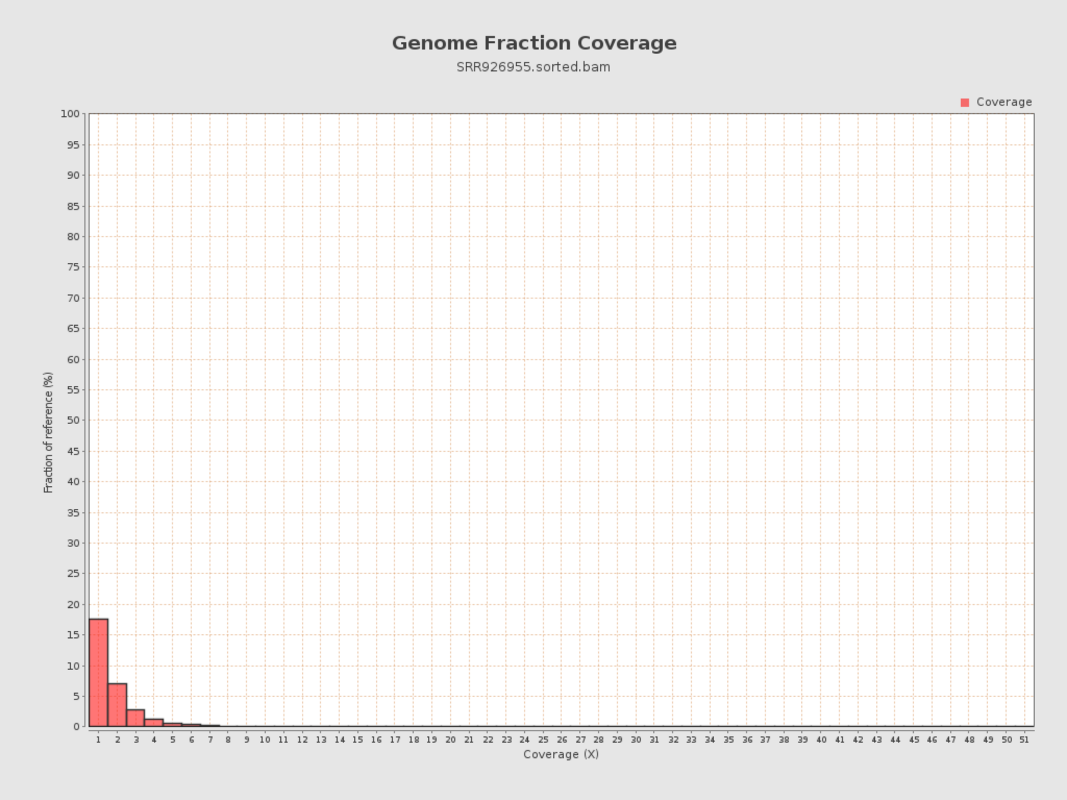
4. Results : Coverage Histogram



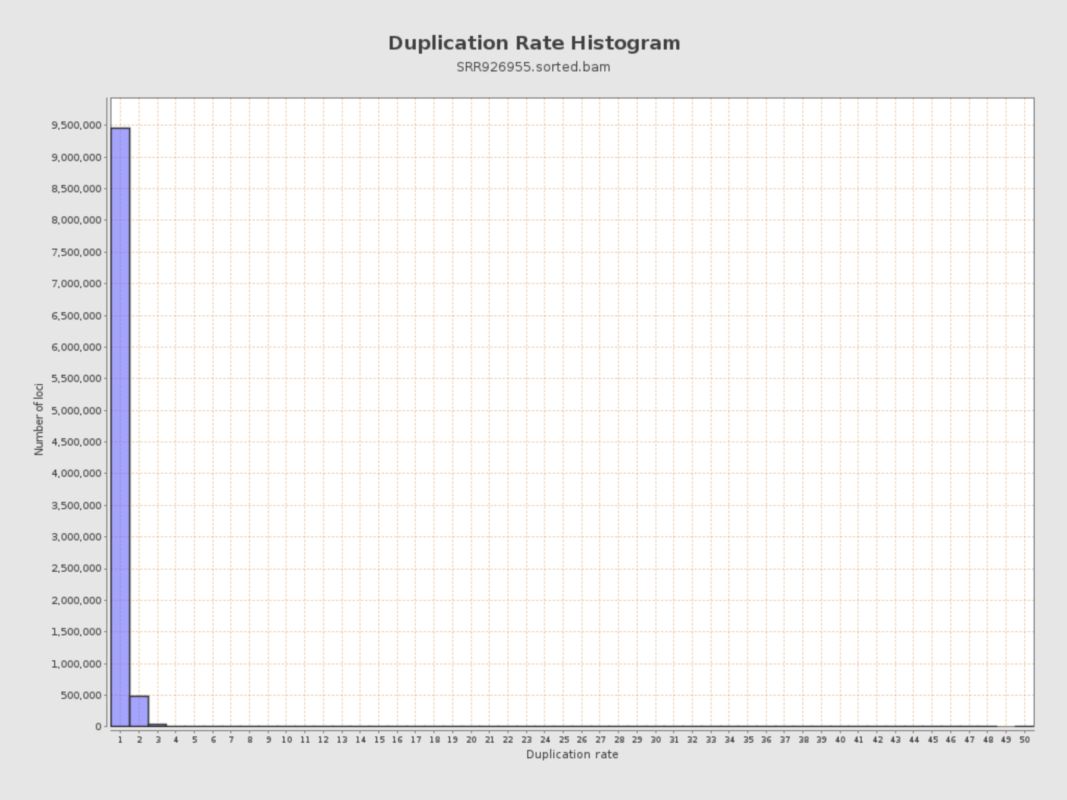
5. Results : Coverage Histogram (0-50X)



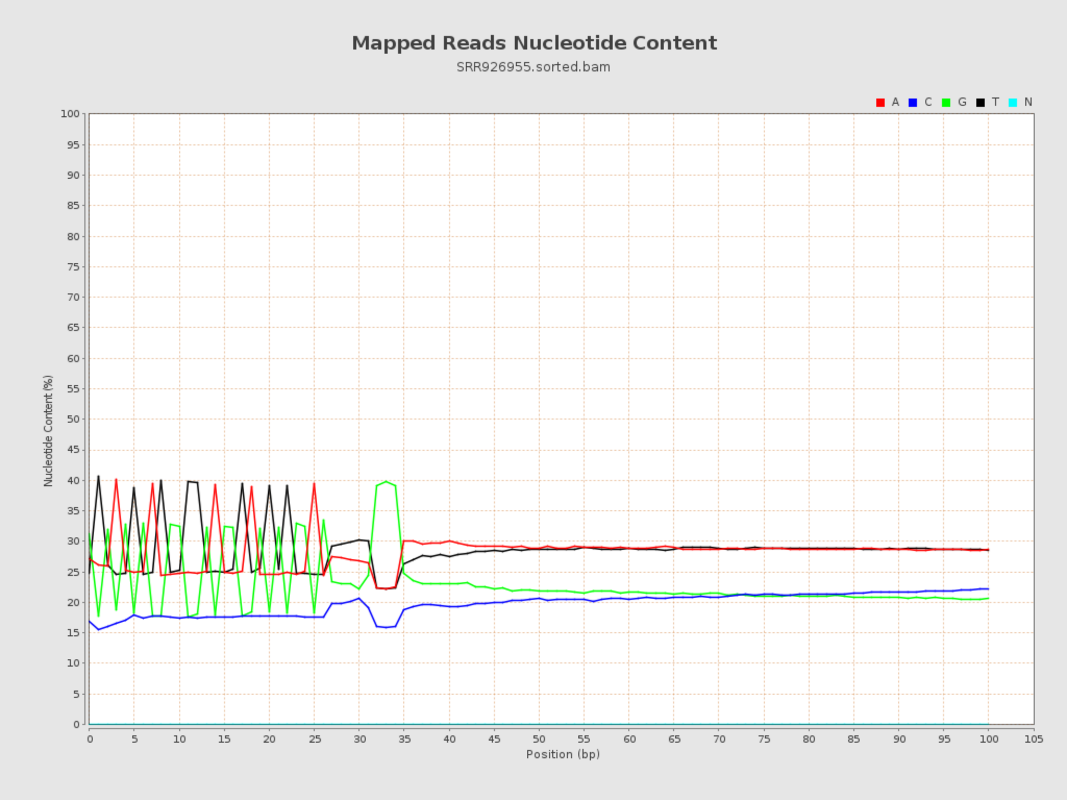
6. Results : Genome Fraction Coverage



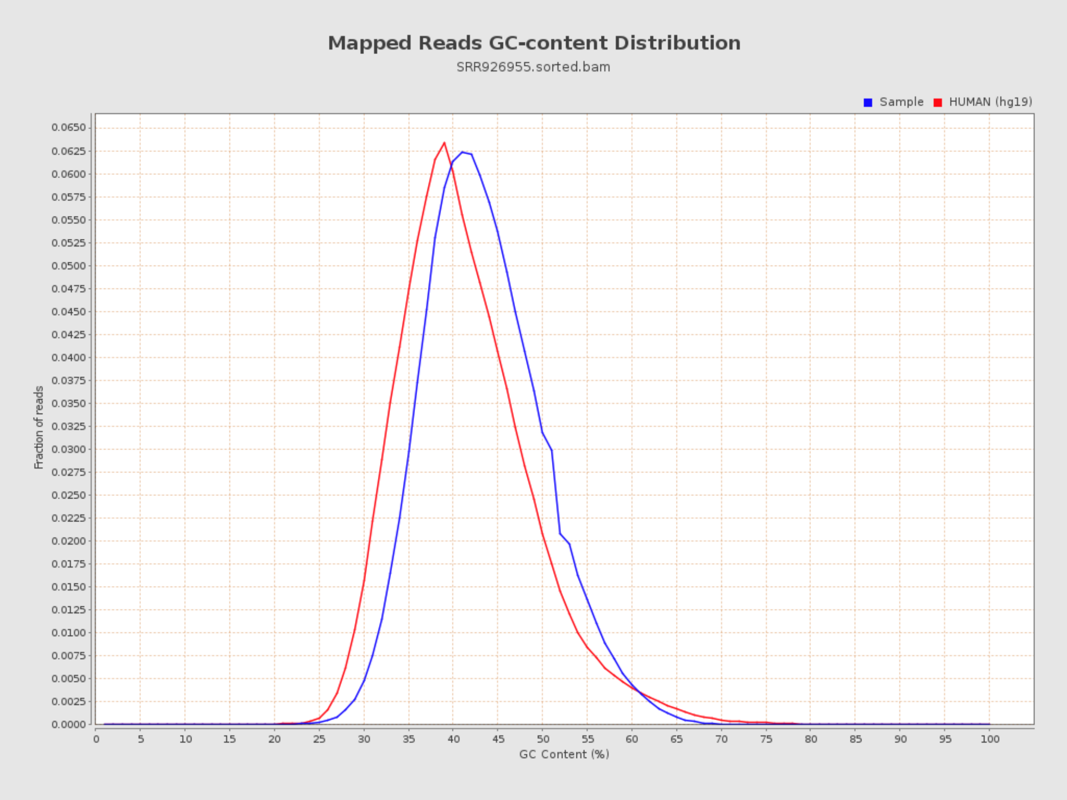
7. Results : Duplication Rate Histogram



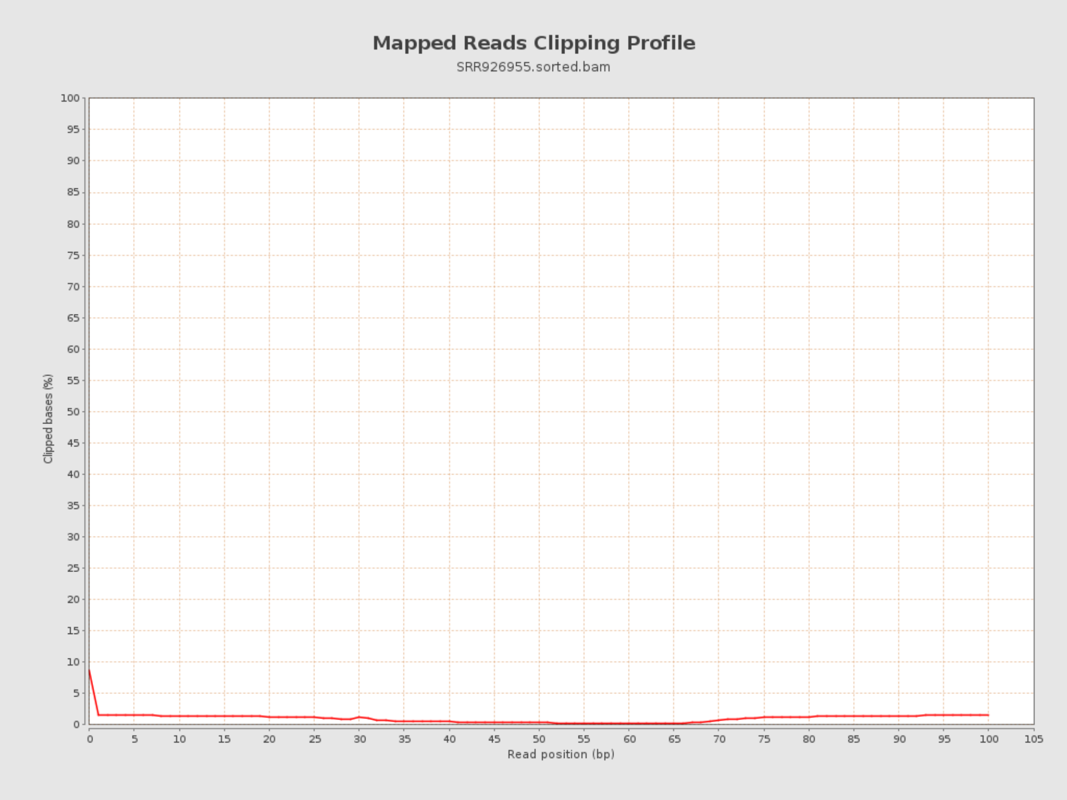
8. Results : Mapped Reads Nucleotide Content



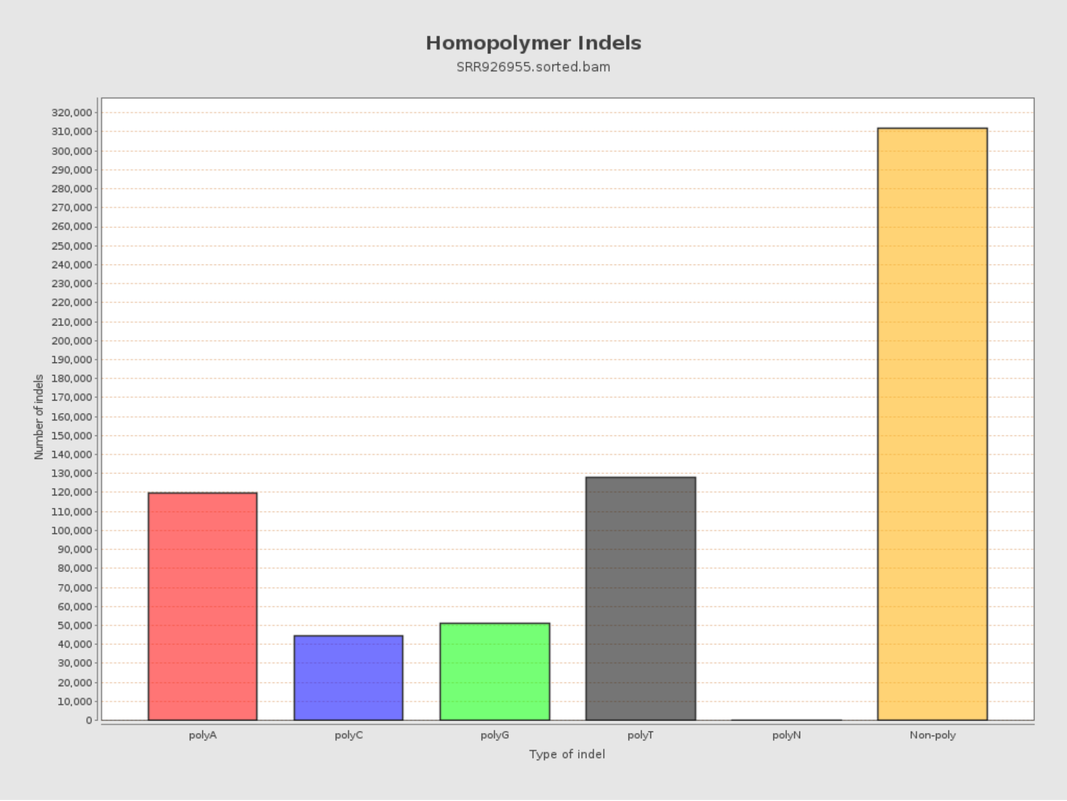
9. Results : Mapped Reads GC-content Distribution



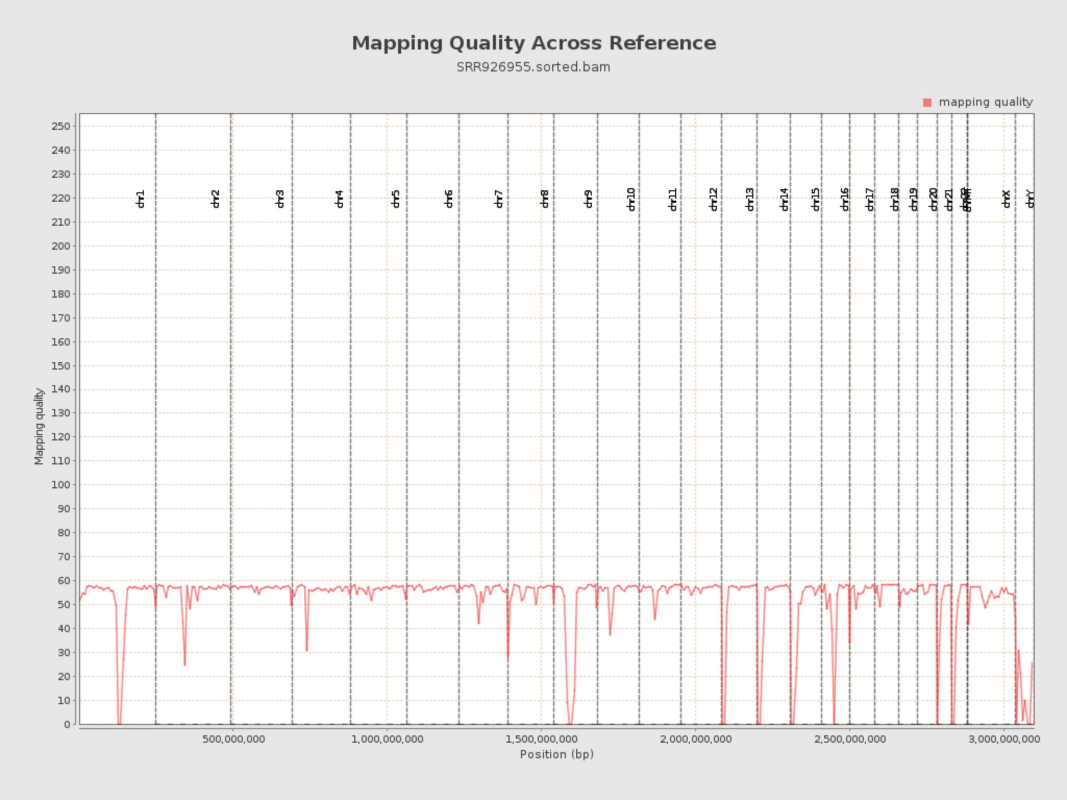
10. Results : Mapped Reads Clipping Profile



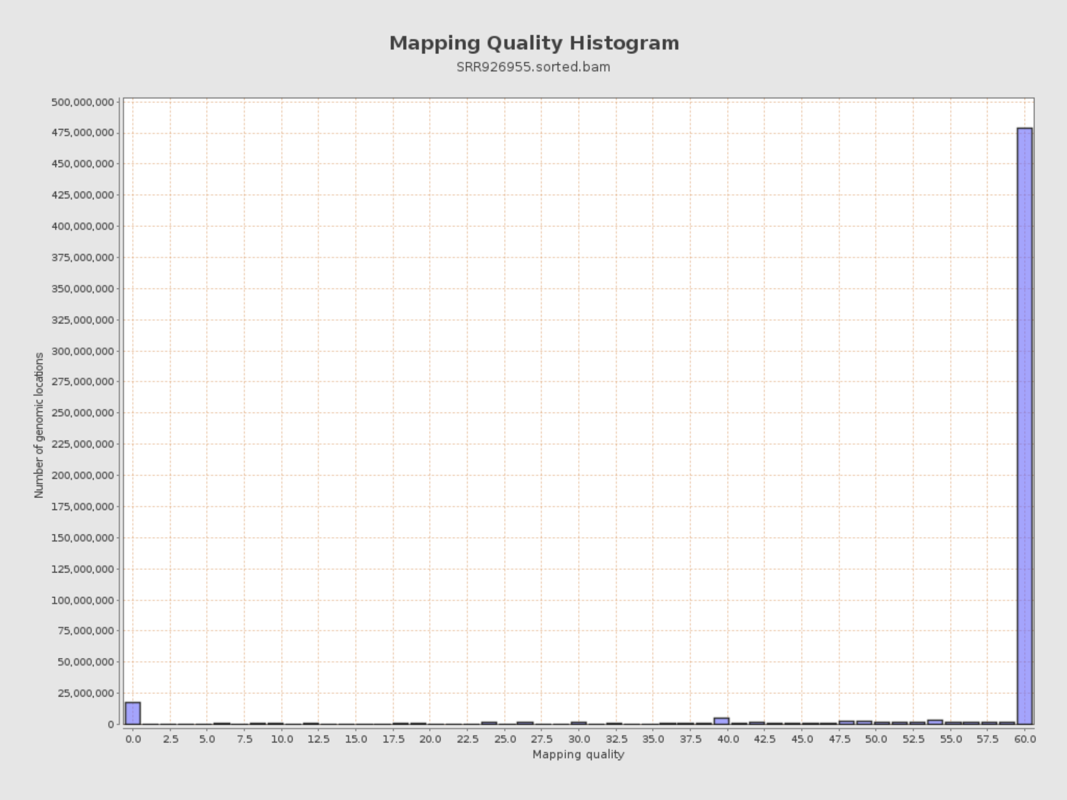
11. Results : Homopolymer Indels



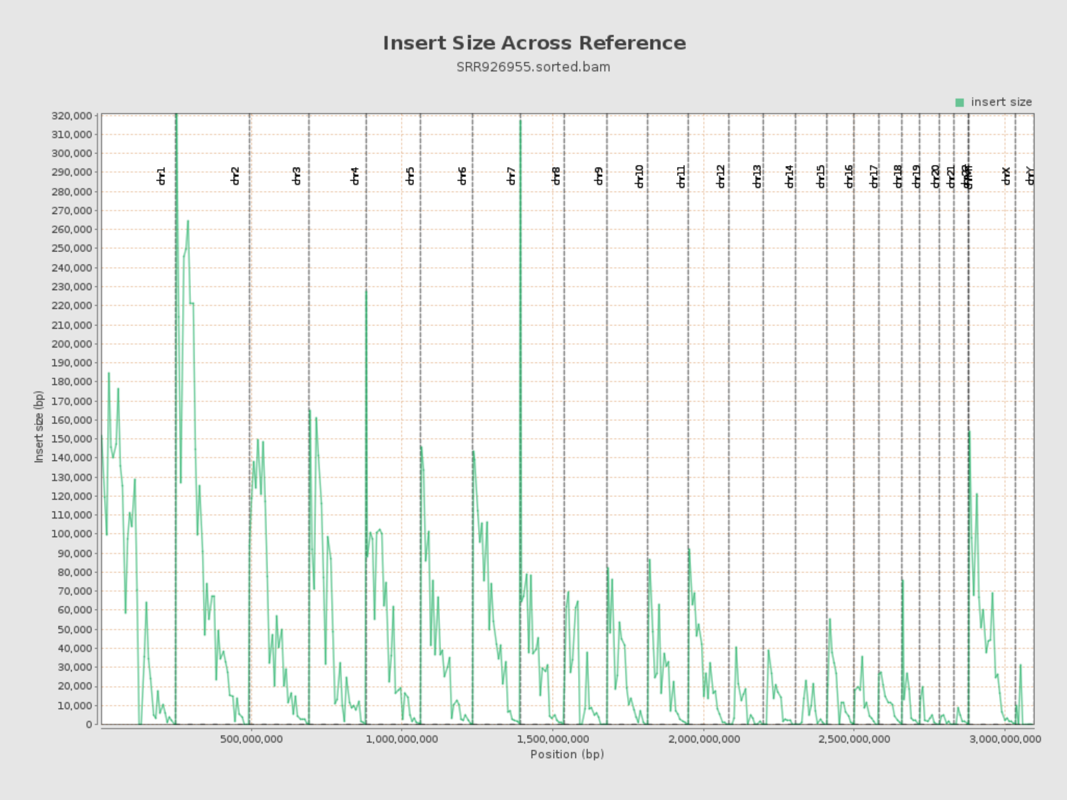
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram