Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 02:35:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926953.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_SRR926953 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926953_1.fastq.gz SRR926953_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 02:35:45 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926953.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,966,454
Mapped reads	13,659,167 / 97.8%
Unmapped reads	307,287 / 2.2%
Mapped paired reads	13,659,167 / 97.8%
Mapped reads, first in pair	6,820,462 / 48.83%
Mapped reads, second in pair	6,838,705 / 48.97%
Mapped reads, both in pair	13,470,346 / 96.45%
Mapped reads, singletons	188,821 / 1.35%
Secondary alignments	0
Supplementary alignments	292,595 / 2.09%
Read min/max/mean length	30 / 101 / 101.87
Duplicated reads (estimated)	759,728 / 5.44%
Duplication rate	4.57%
Clipped reads	4,937,182 / 35.35%

2.2. ACGT Content

Number/percentage of A's	364,049,572 / 28.51%
Number/percentage of C's	257,852,407 / 20.2%
Number/percentage of T's	366,816,934 / 28.73%
Number/percentage of G's	288,008,729 / 22.56%
Number/percentage of N's	53,377 / 0%

GC Percentage	42.75%

2.3. Coverage

Mean	0.4127
Standard Deviation	1.6813

2.4. Mapping Quality

Mean Mapping Quality	53.29

2.5. Insert size

Mean	182,298.79
Standard Deviation	4,200,473.24
P25/Median/P75	144 / 188 / 254

2.6. Mismatches and indels

General error rate	0.97%
Mismatches	12,012,357
Insertions	210,095
Mapped reads with at least one insertion	1.51%
Deletions	642,487
Mapped reads with at least one deletion	4.58%
Homopolymer indels	52.35%

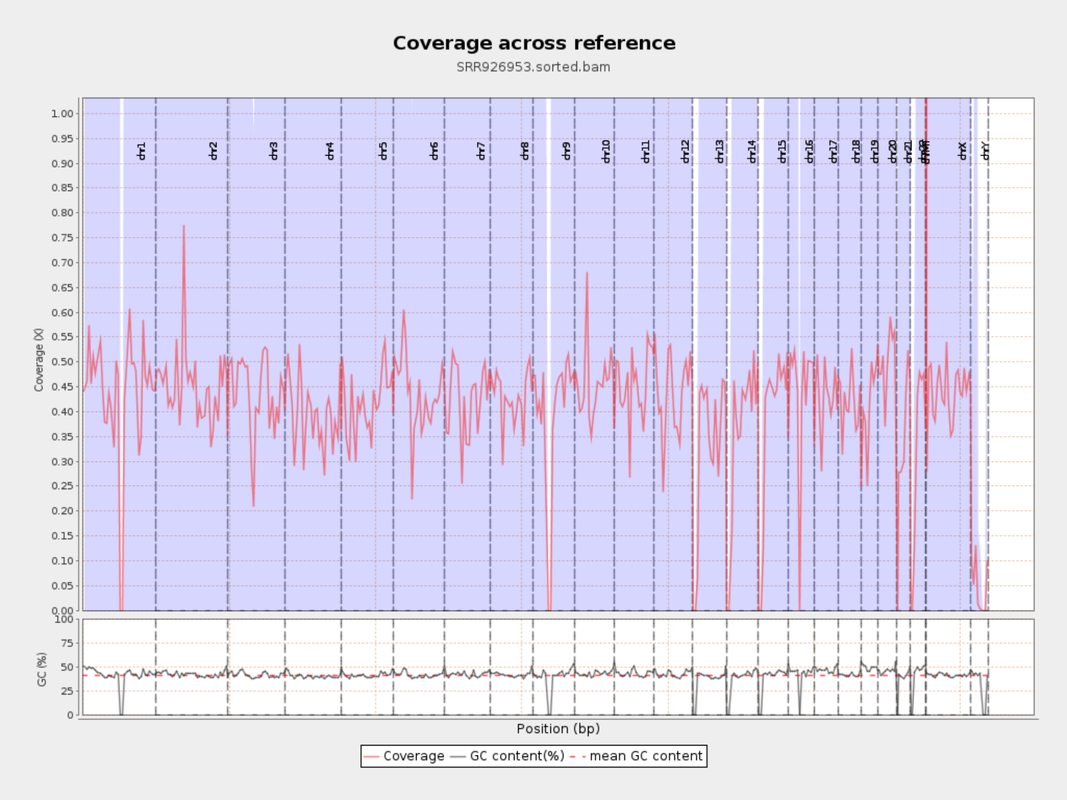
2.7. Chromosome stats

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

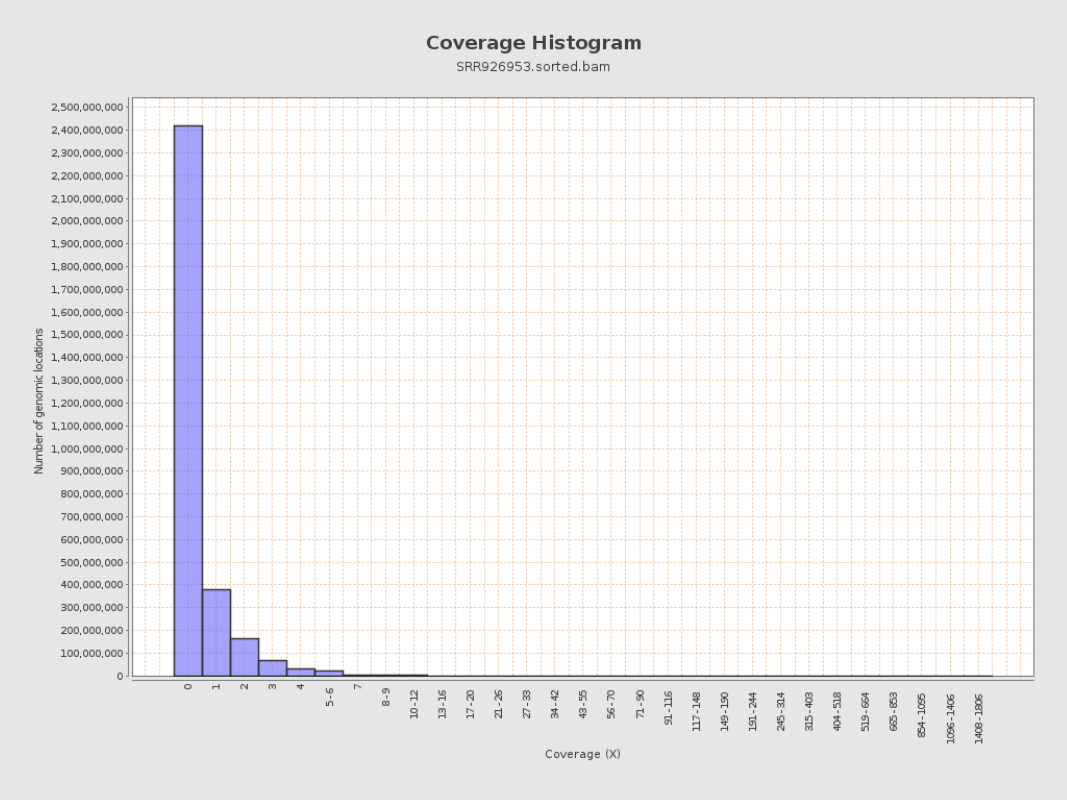
		bases	coverage	deviation
chr1	249250621	108398722	0.4349	2.2031
chr2	243199373	110238741	0.4533	2.8021
chr3	198022430	86166030	0.4351	1.0603
chr4	191154276	75850637	0.3968	1.8188
chr5	180915260	75770465	0.4188	1.0259
chr6	171115067	74500781	0.4354	1.1209
chr7	159138663	67243346	0.4225	1.1791
chr8	146364022	62683957	0.4283	1.107
chr9	141213431	54834705	0.3883	1.7091
chr10	135534747	61620087	0.4546	3.343
chr11	135006516	61014883	0.4519	1.4001
chr12	133851895	58800629	0.4393	1.1132
chr13	115169878	37740511	0.3277	0.896
chr14	107349540	38043691	0.3544	0.9597
chr15	102531392	37903646	0.3697	0.996
chr16	90354753	39286135	0.4348	1.344
chr17	81195210	35083917	0.4321	1.1917
chr18	78077248	32649143	0.4182	1.8758
chr19	59128983	24342762	0.4117	1.5523
chr20	63025520	31534152	0.5003	1.3246
chr21	48129895	16349859	0.3397	1.518
chr22	51304566	16031205	0.3125	0.927
chrMT	16571	621013	37.4759	29.4265
chrX	155270560	68163950	0.439	1.1259

chrY	59373566	2838053	0.0478	1.3742

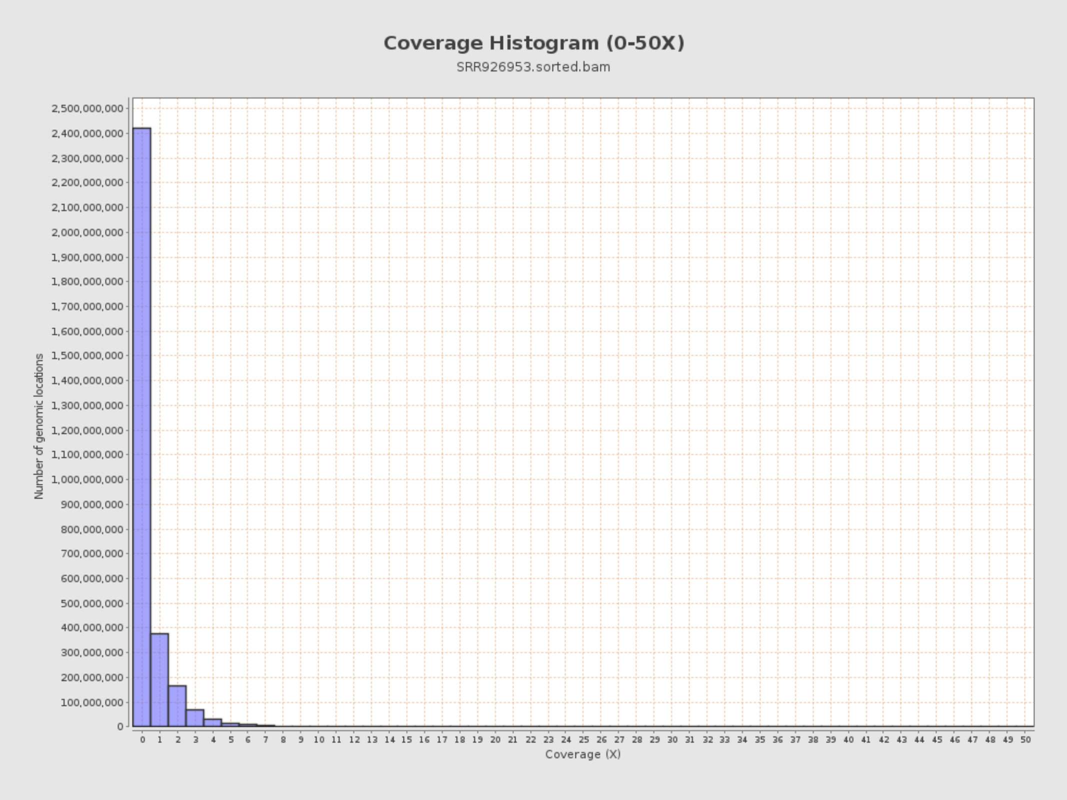
3. Results : Coverage across reference



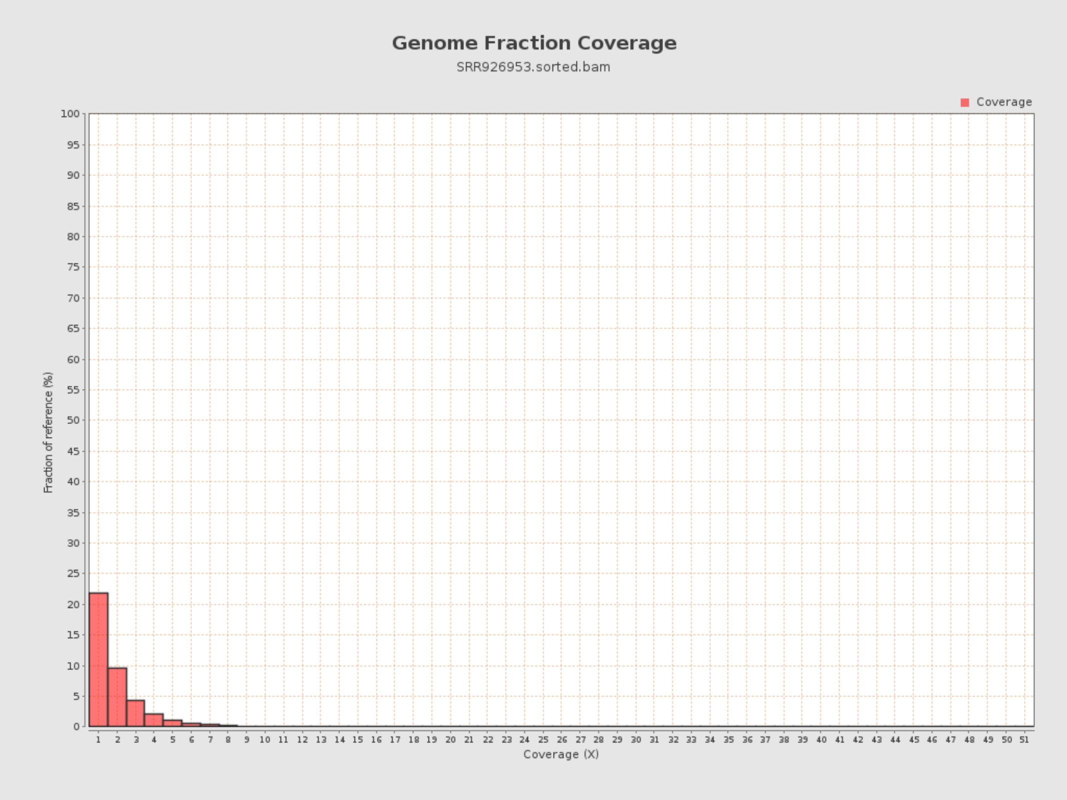
4. Results : Coverage Histogram



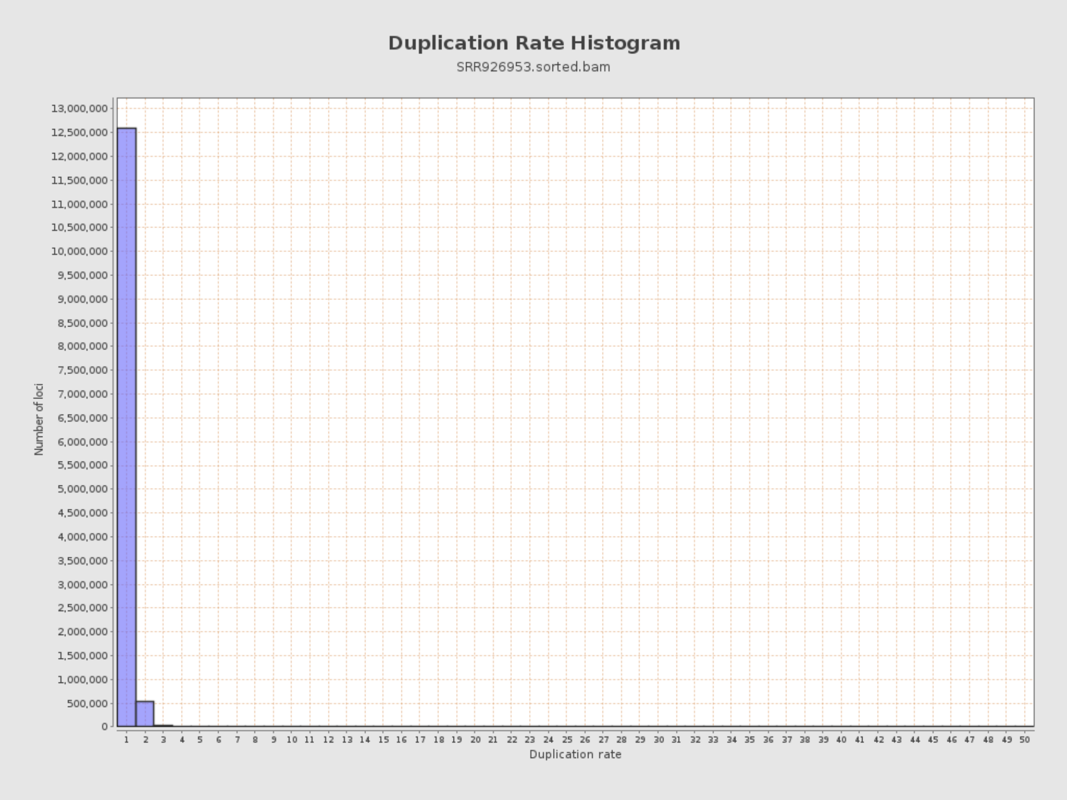
5. Results : Coverage Histogram (0-50X)



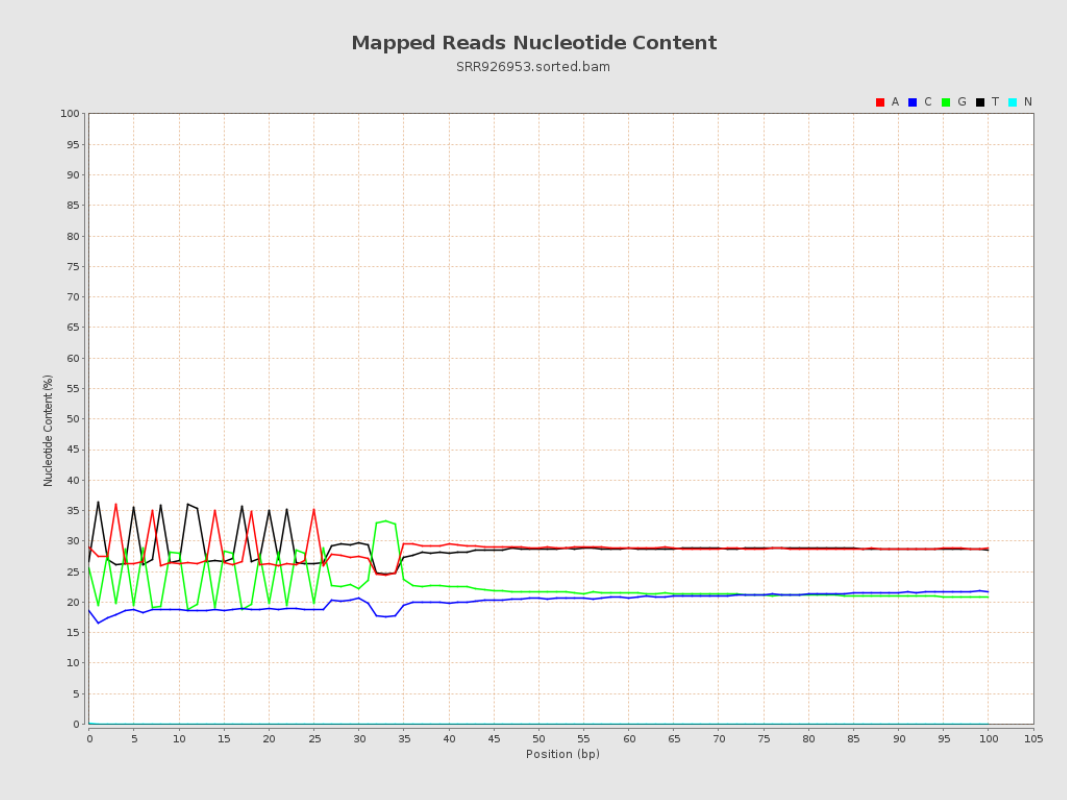
6. Results : Genome Fraction Coverage



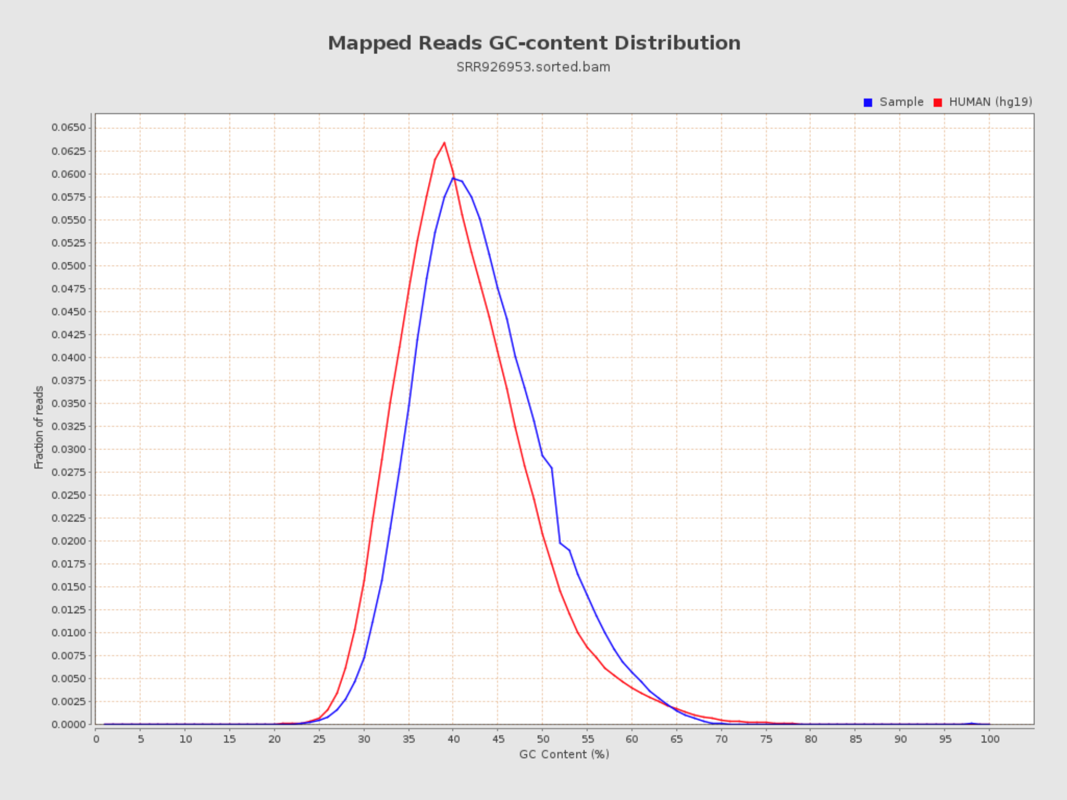
7. Results : Duplication Rate Histogram



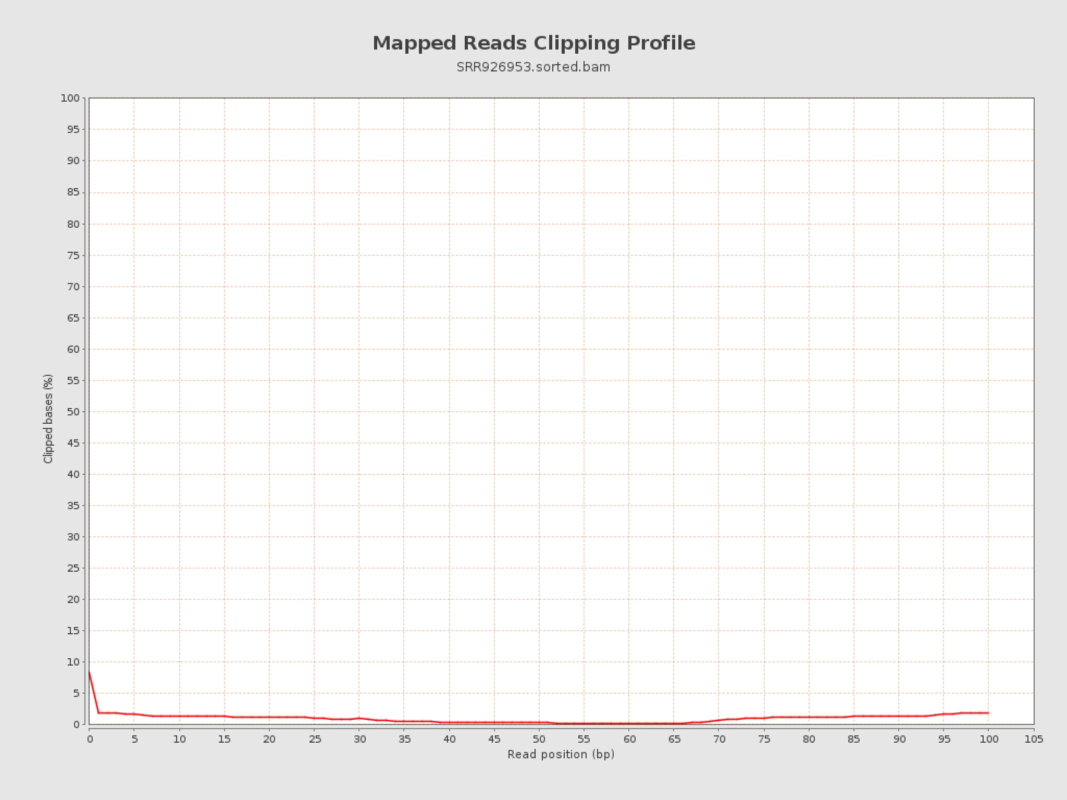
8. Results : Mapped Reads Nucleotide Content



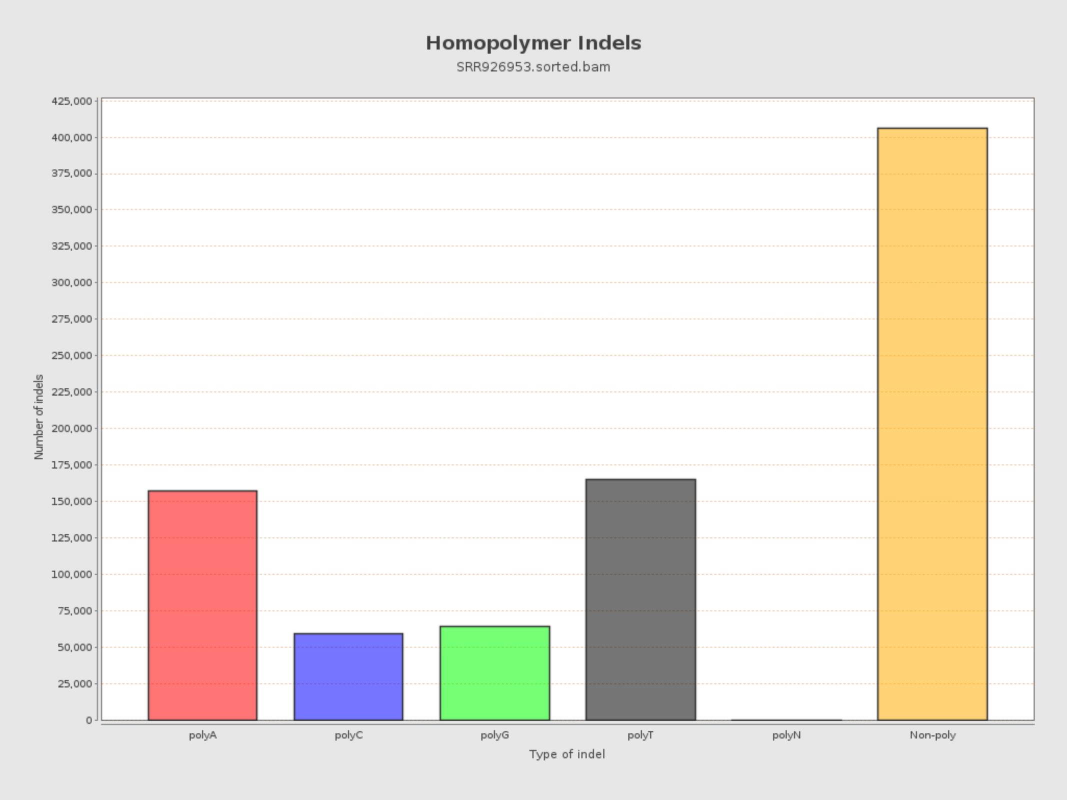
9. Results : Mapped Reads GC-content Distribution



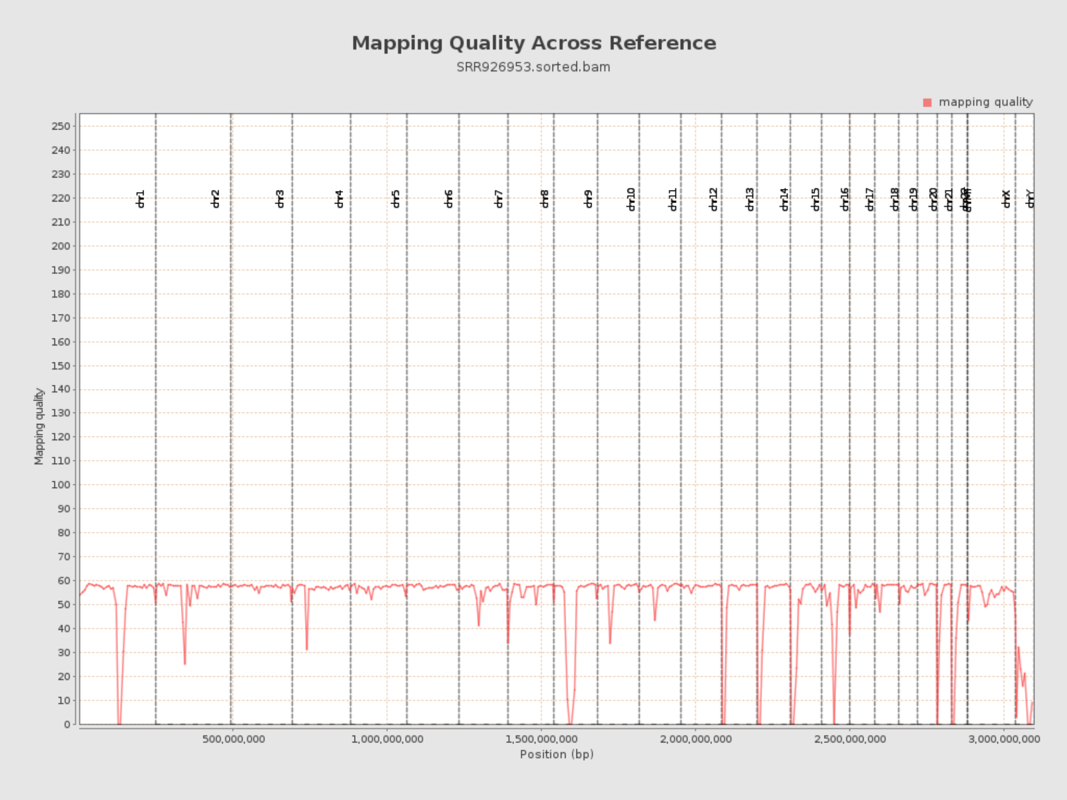
10. Results : Mapped Reads Clipping Profile



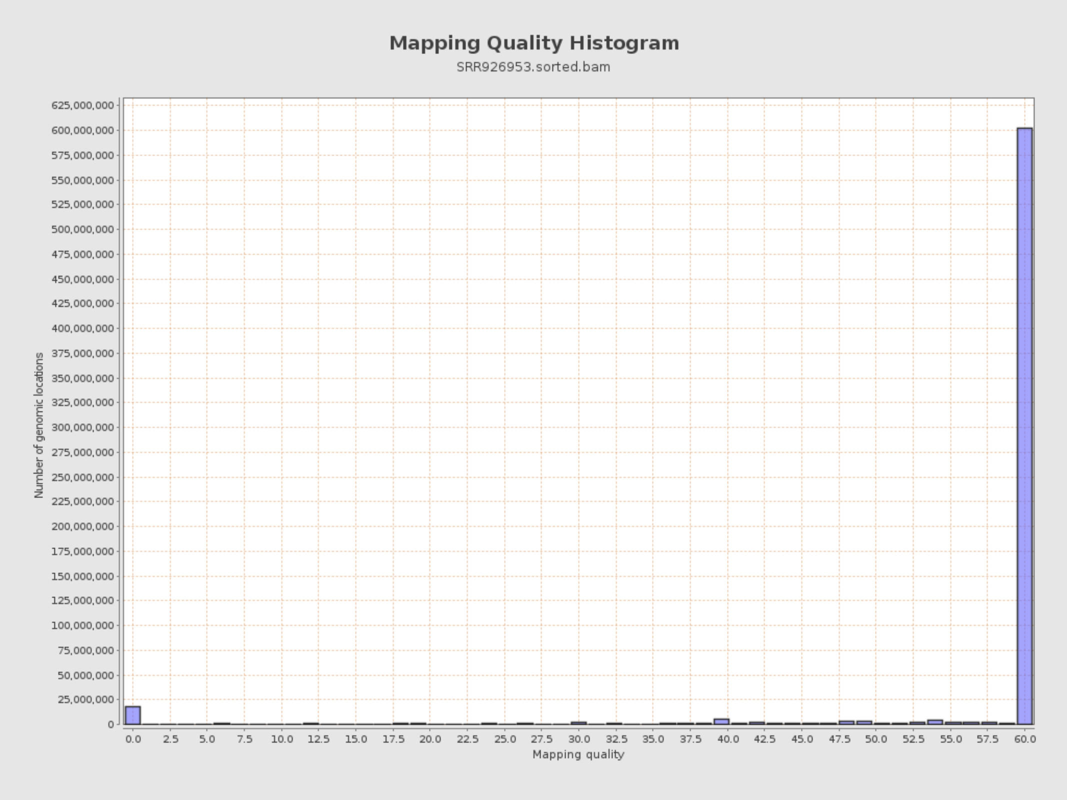
11. Results : Homopolymer Indels



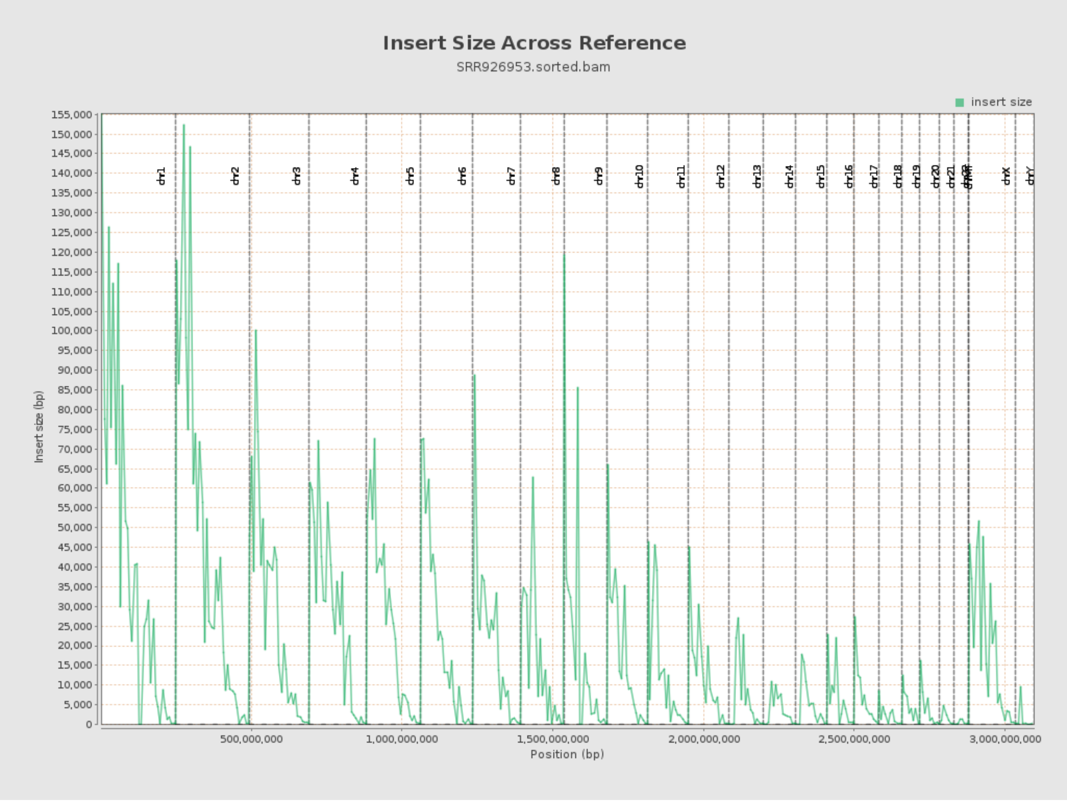
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram