Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 02:24:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926891.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_SRR926891 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926891_1.fastq.gz SRR926891_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 02:24:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926891.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	41,774,588
Mapped reads	39,168,023 / 93.76%
Unmapped reads	2,606,565 / 6.24%
Mapped paired reads	39,168,023 / 93.76%
Mapped reads, first in pair	19,636,785 / 47.01%
Mapped reads, second in pair	19,531,238 / 46.75%
Mapped reads, both in pair	38,753,632 / 92.77%
Mapped reads, singletons	414,391 / 0.99%
Secondary alignments	0
Supplementary alignments	444,152 / 1.06%
Read min/max/mean length	30 / 101 / 101.43
Duplicated reads (estimated)	3,263,726 / 7.81%
Duplication rate	6.64%
Clipped reads	9,665,469 / 23.14%

2.2. ACGT Content

Number/percentage of A's	1,065,083,337 / 28.64%
Number/percentage of C's	755,383,027 / 20.31%
Number/percentage of T's	1,068,976,684 / 28.74%
Number/percentage of G's	829,452,277 / 22.3%
Number/percentage of N's	253,976 / 0.01%

GC Percentage	42.61%

2.3. Coverage

Mean	1.2023
Standard Deviation	5.3798

2.4. Mapping Quality

Mean Mapping Quality	53.4

2.5. Insert size

Mean	98,570.44
Standard Deviation	3,107,590.28
P25/Median/P75	135 / 170 / 224

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	35,347,666
Insertions	584,823
Mapped reads with at least one insertion	1.47%
Deletions	2,019,173
Mapped reads with at least one deletion	5.02%
Homopolymer indels	53.14%

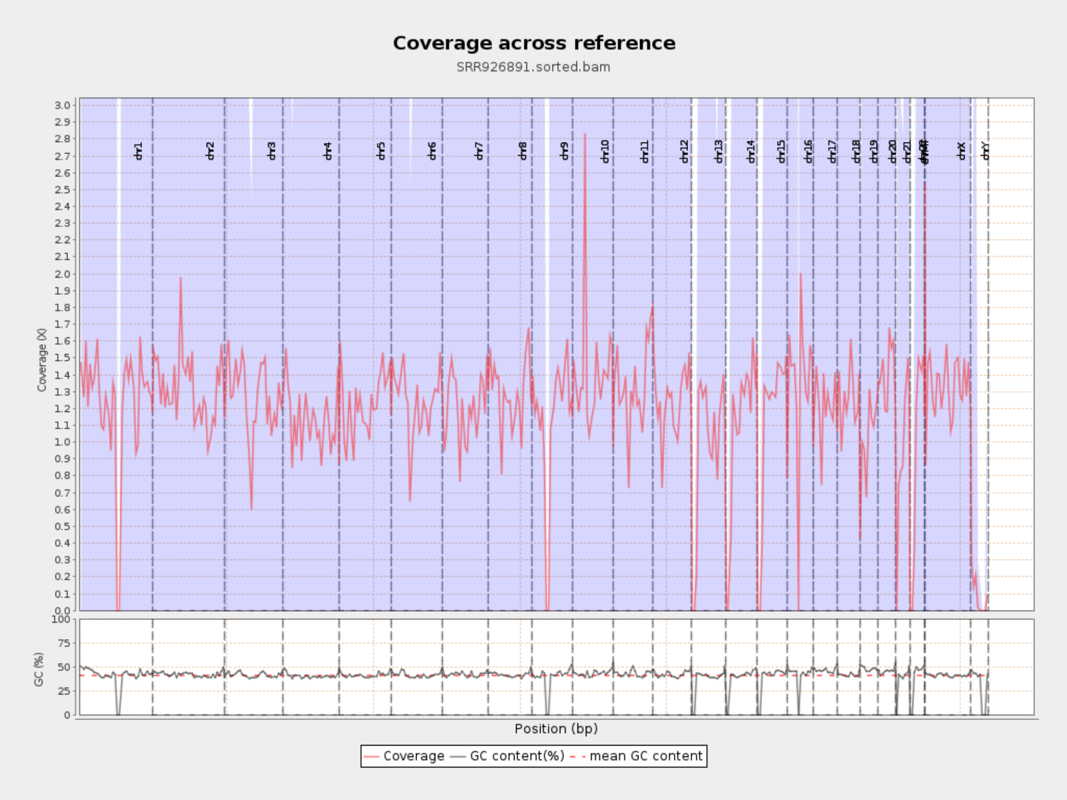
2.7. Chromosome stats

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

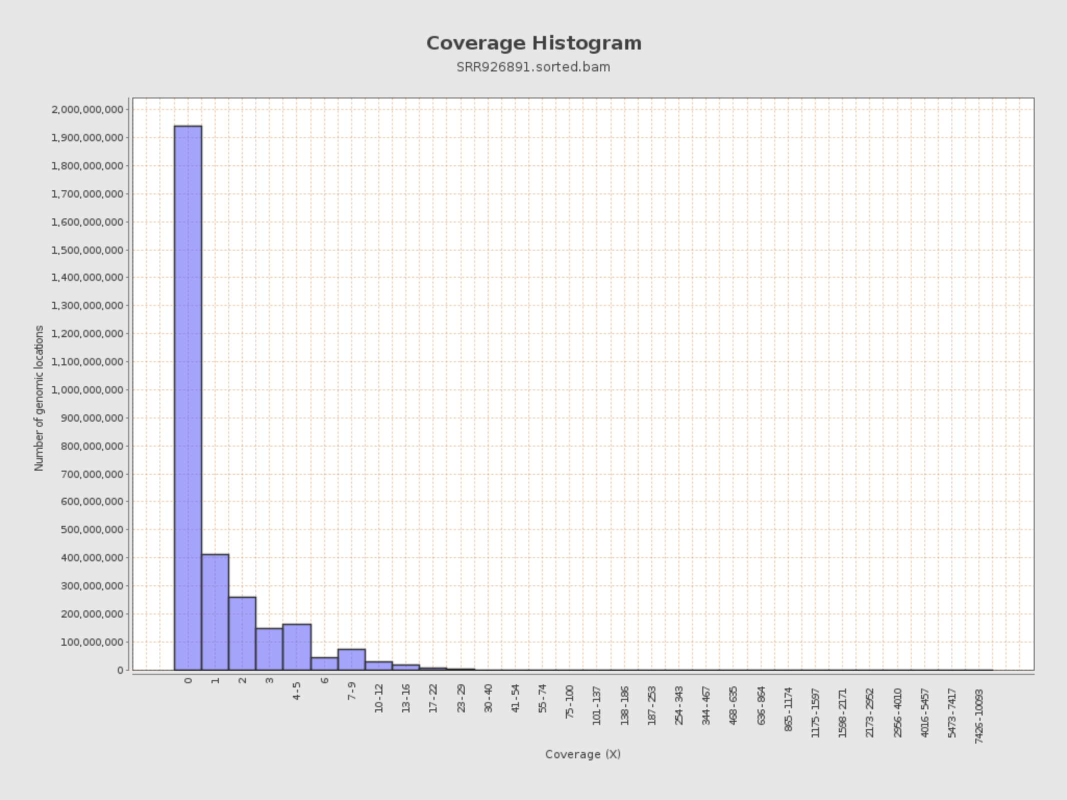
		bases	coverage	deviation
chr1	249250621	306241181	1.2286	4.6923
chr2	243199373	322076765	1.3243	6.3382
chr3	198022430	251601001	1.2706	2.7634
chr4	191154276	217342503	1.137	2.6204
chr5	180915260	223229587	1.2339	2.4712
chr6	171115067	213225812	1.2461	2.5326
chr7	159138663	191393753	1.2027	3.1949
chr8	146364022	188775829	1.2898	2.9292
chr9	141213431	158240262	1.1206	4.5384
chr10	135534747	193475618	1.4275	18.9204
chr11	135006516	178637305	1.3232	3.3309
chr12	133851895	166044682	1.2405	2.8345
chr13	115169878	111806113	0.9708	2.3177
chr14	107349540	113718655	1.0593	2.4202
chr15	102531392	111730744	1.0897	2.5261
chr16	90354753	119920398	1.3272	7.0824
chr17	81195210	98163075	1.209	3.0089
chr18	78077248	100186094	1.2832	4.8244
chr19	59128983	60909592	1.0301	3.1539
chr20	63025520	89348281	1.4177	2.9308
chr21	48129895	46585687	0.9679	3.2526
chr22	51304566	48761496	0.9504	2.428
chrMT	16571	42088	2.5399	2.6522
chrX	155270560	205463965	1.3233	2.7989

chrY	59373566	5060234	0.0852	1.7031

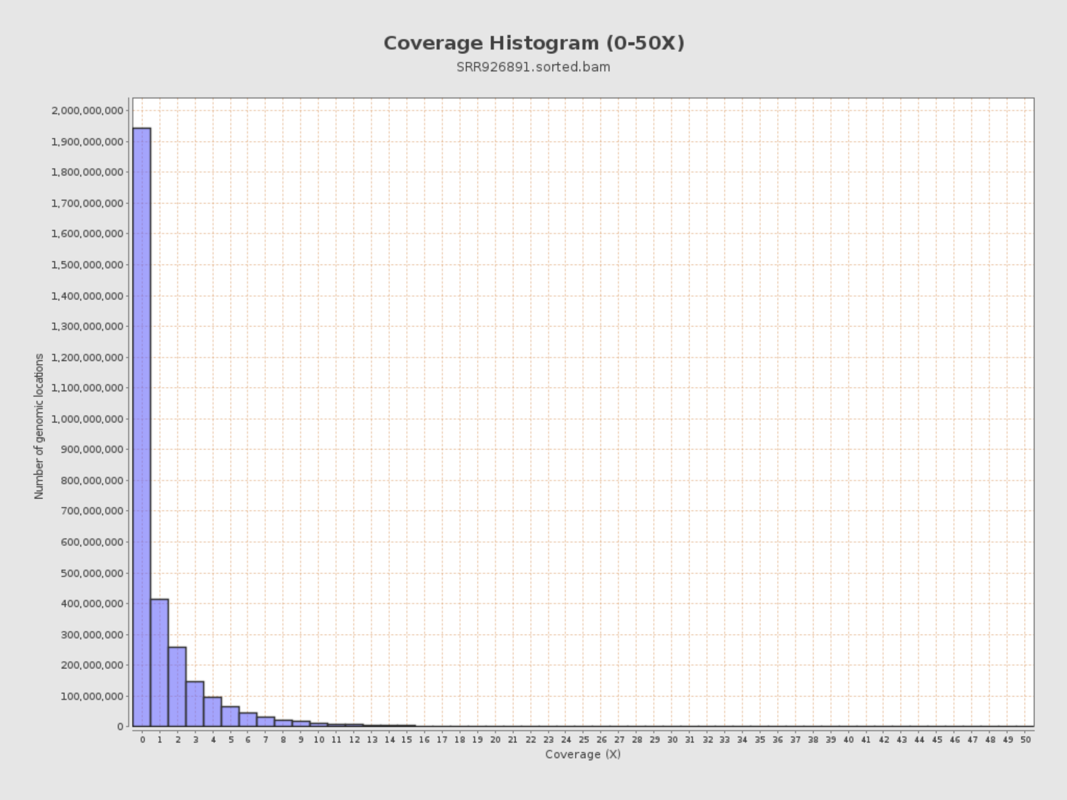
3. Results : Coverage across reference



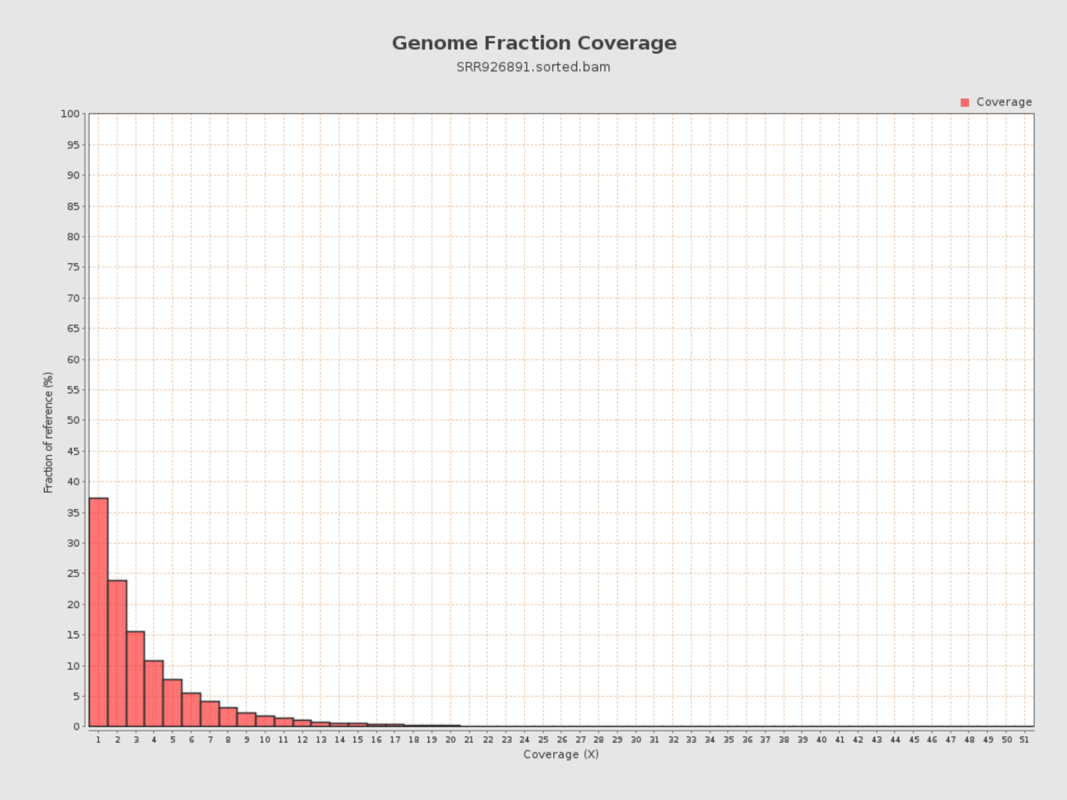
4. Results : Coverage Histogram



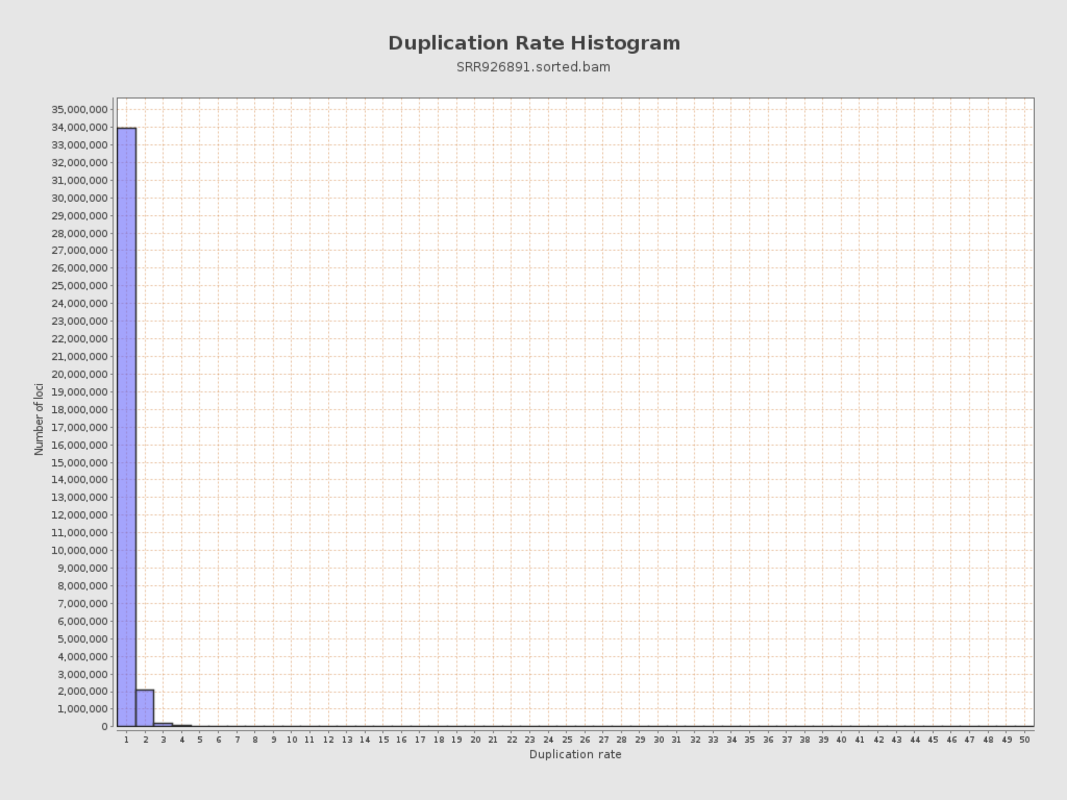
5. Results : Coverage Histogram (0-50X)



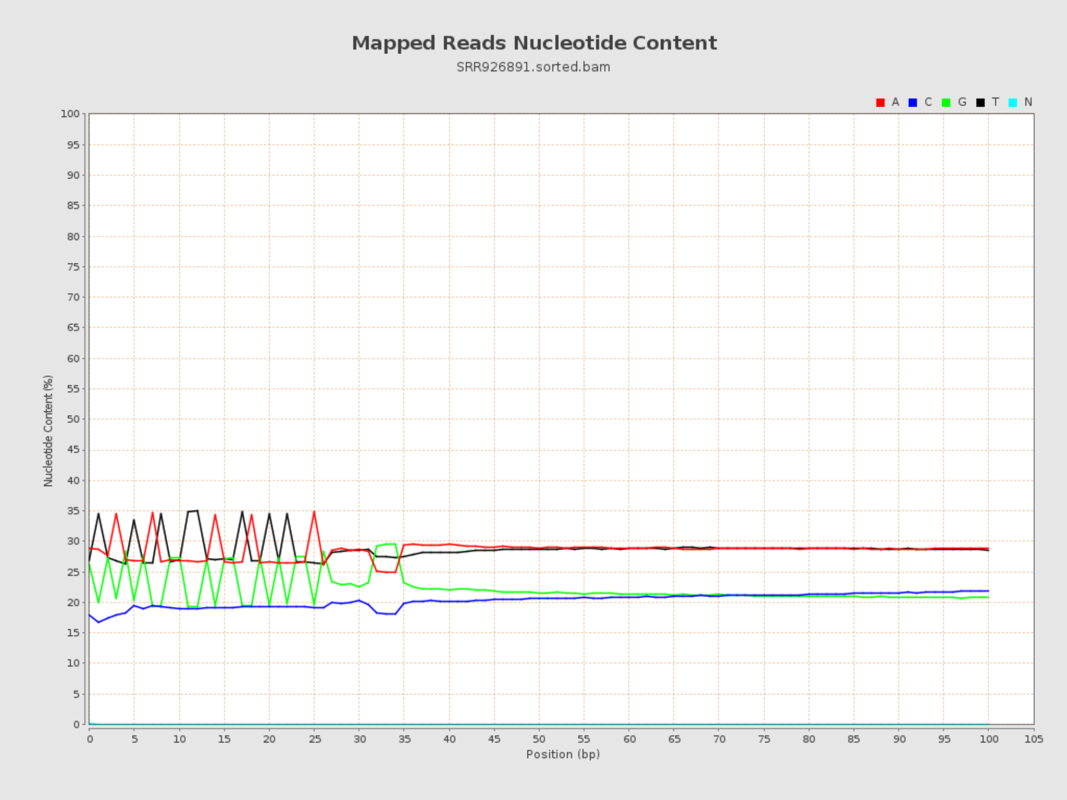
6. Results : Genome Fraction Coverage



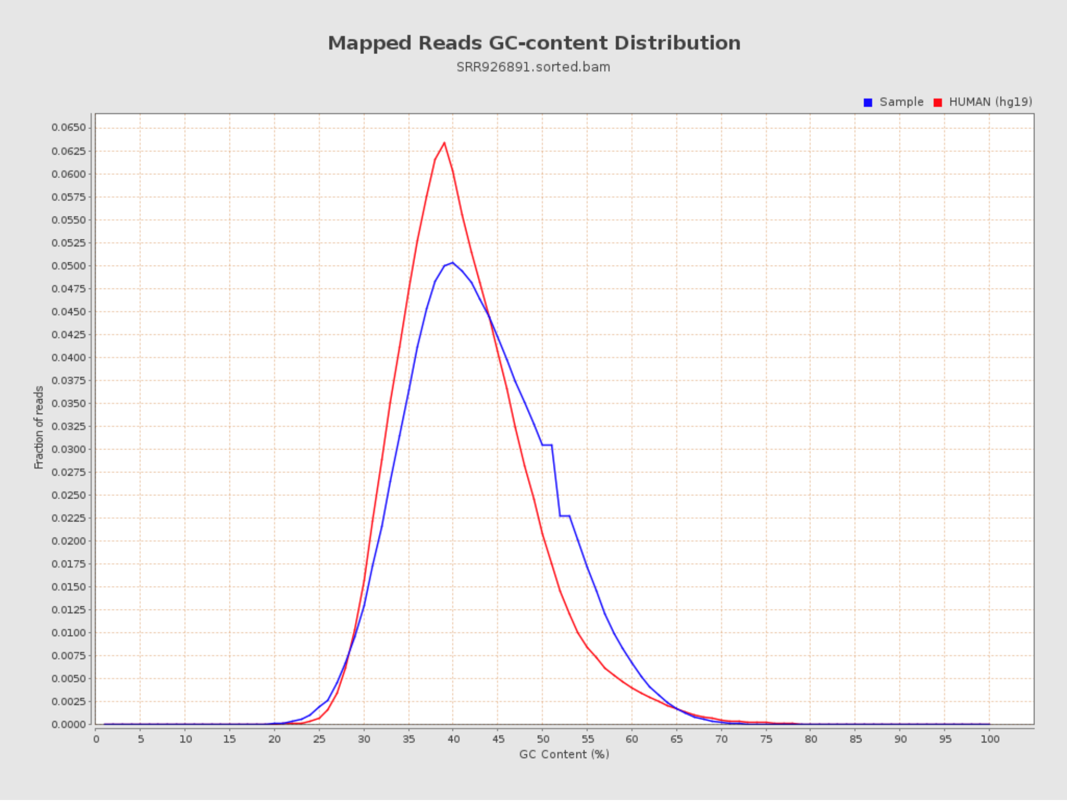
7. Results : Duplication Rate Histogram



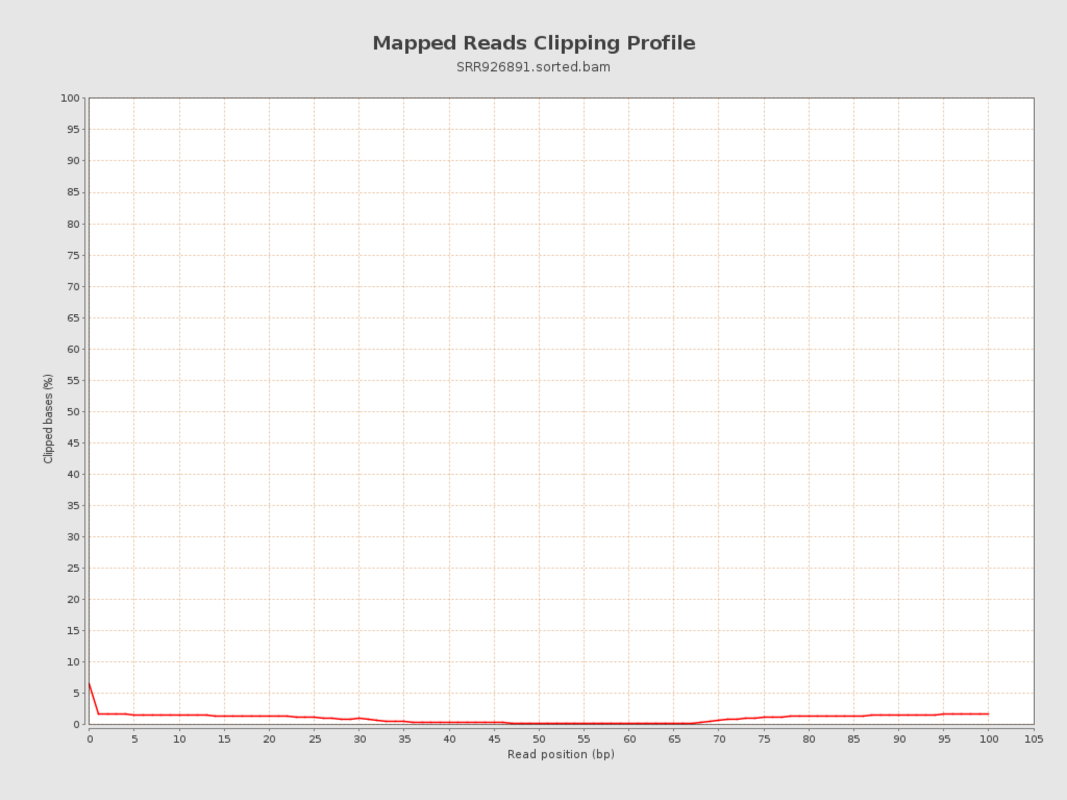
8. Results : Mapped Reads Nucleotide Content



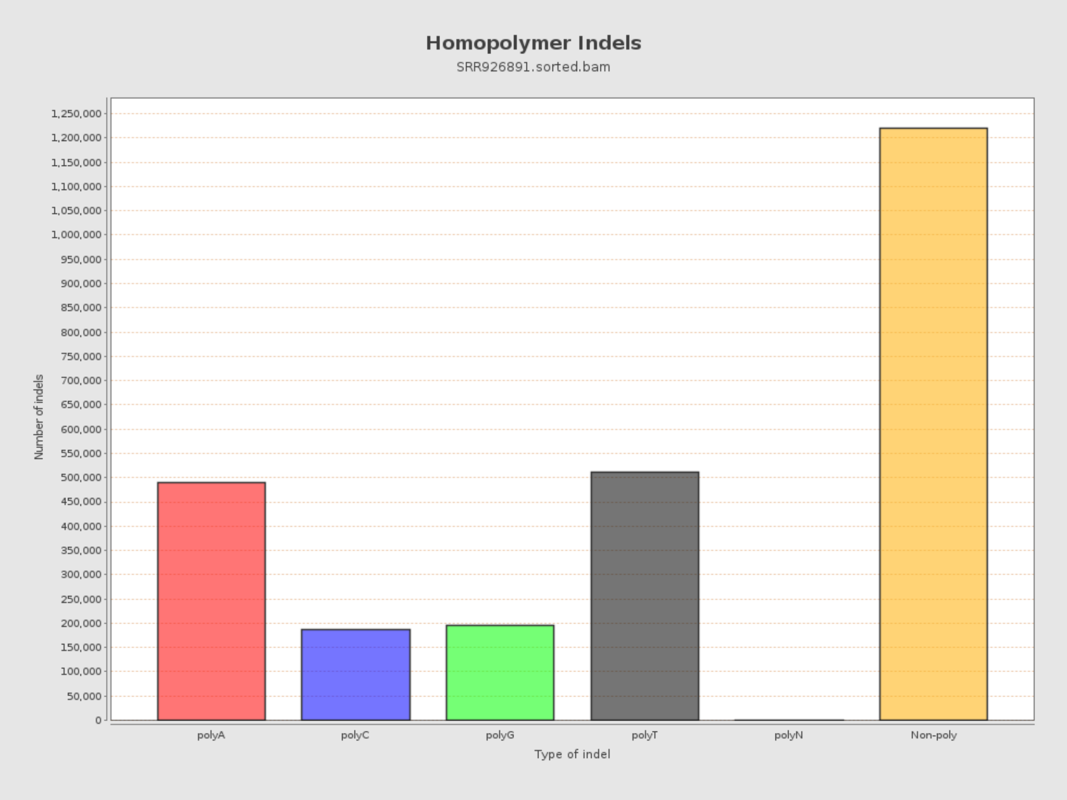
9. Results : Mapped Reads GC-content Distribution



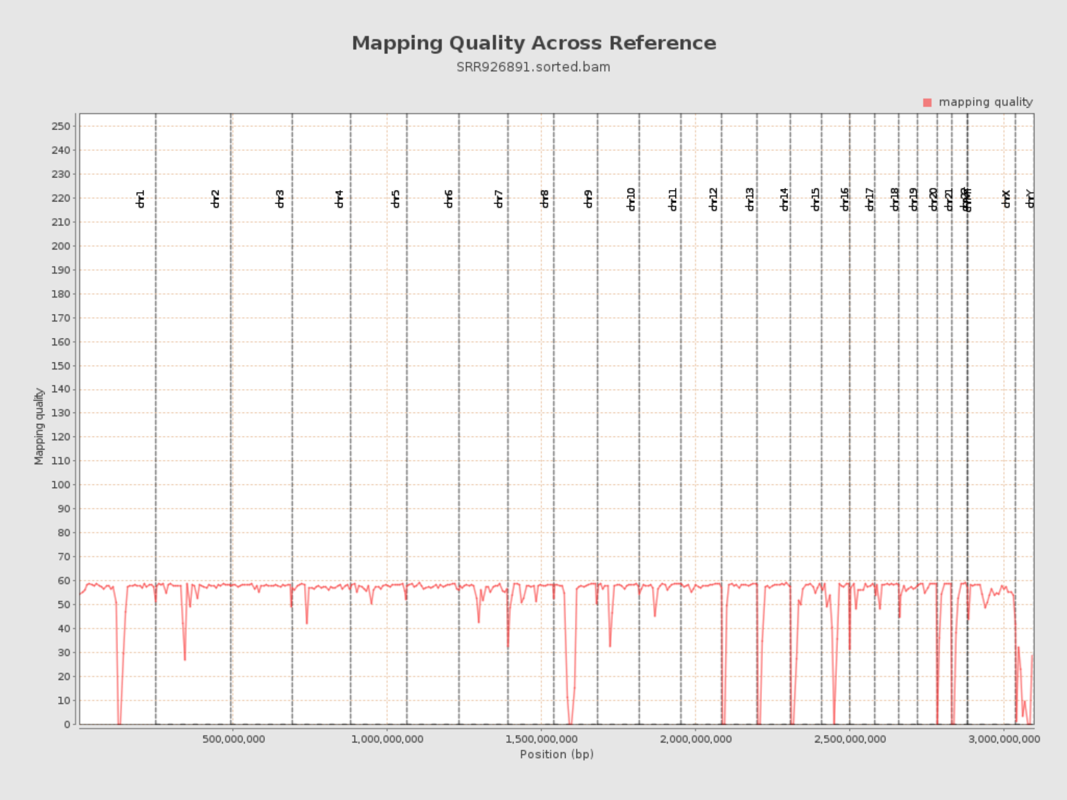
10. Results : Mapped Reads Clipping Profile



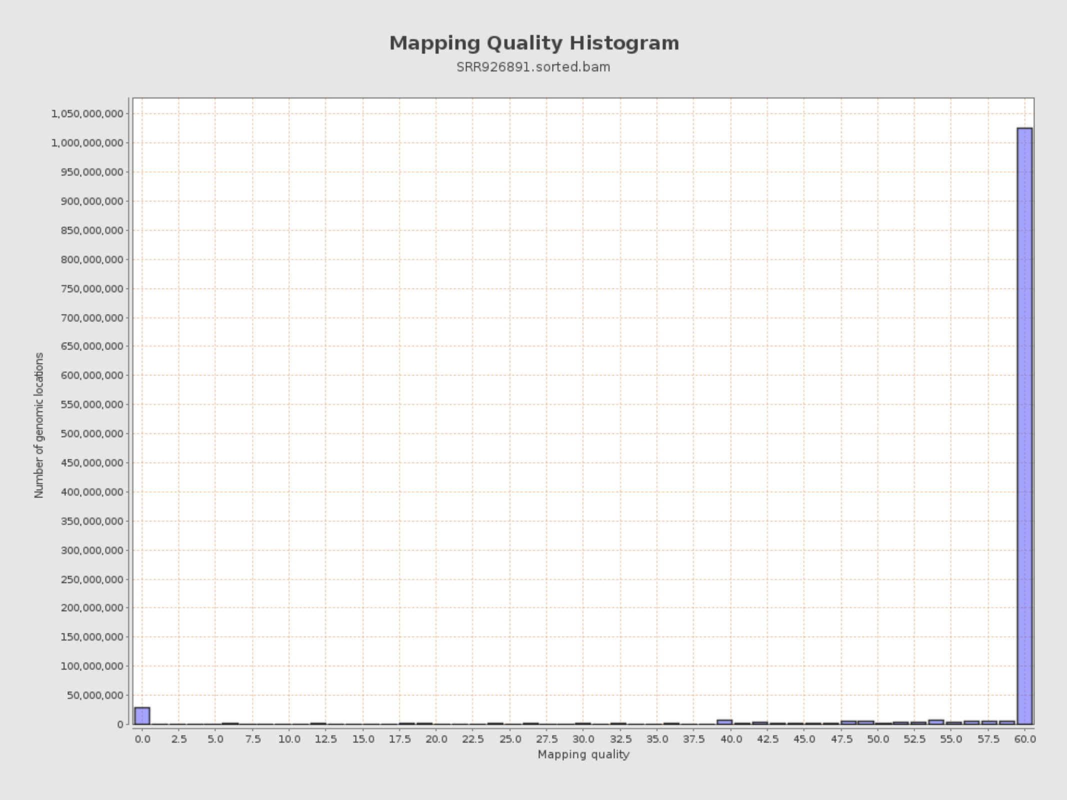
11. Results : Homopolymer Indels



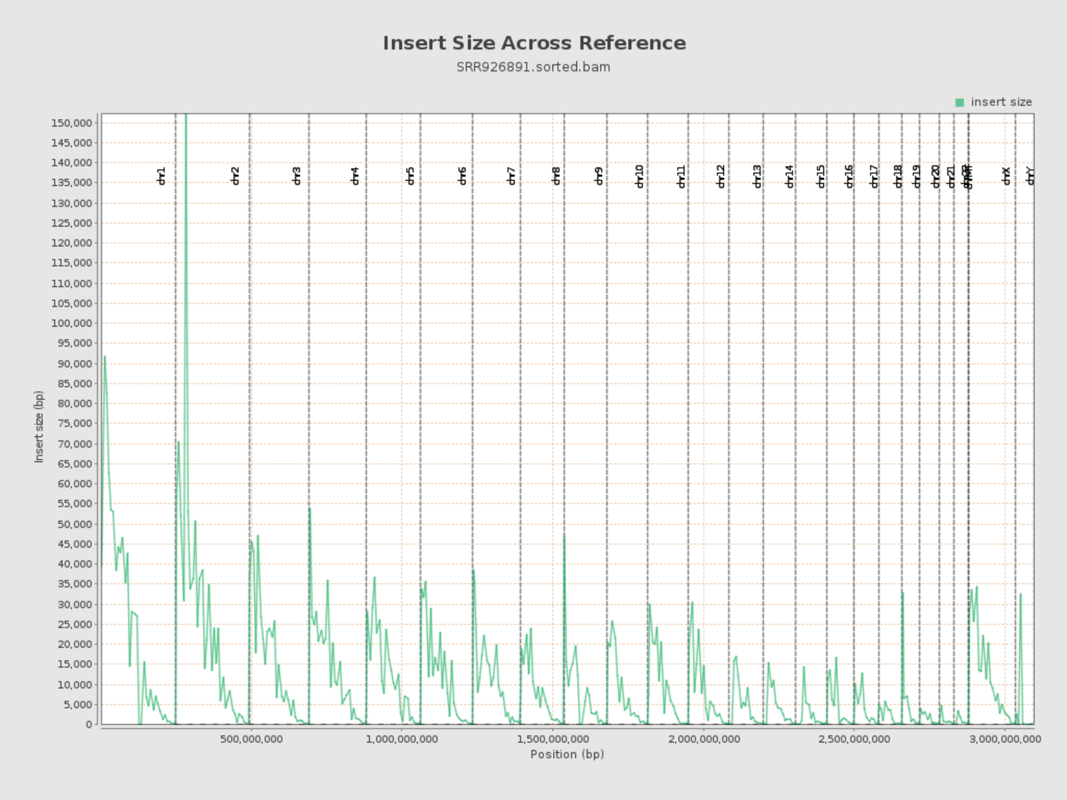
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram