Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 18:31:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926990.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_SRR926990 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926990_1.fastq.gz SRR926990_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 18:31:35 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926990.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,719,630
Mapped reads	29,235,255 / 98.37%
Unmapped reads	484,375 / 1.63%
Mapped paired reads	29,235,255 / 98.37%
Mapped reads, first in pair	14,681,327 / 49.4%
Mapped reads, second in pair	14,553,928 / 48.97%
Mapped reads, both in pair	28,980,352 / 97.51%
Mapped reads, singletons	254,903 / 0.86%
Secondary alignments	0
Supplementary alignments	626,757 / 2.11%
Read min/max/mean length	30 / 101 / 101.87
Duplicated reads (estimated)	2,479,211 / 8.34%
Duplication rate	6.48%
Clipped reads	9,315,267 / 31.34%

2.2. ACGT Content

Number/percentage of A's	771,471,918 / 28.23%
Number/percentage of C's	556,037,368 / 20.34%
Number/percentage of T's	780,331,800 / 28.55%
Number/percentage of G's	625,008,565 / 22.87%
Number/percentage of N's	193,616 / 0.01%

GC Percentage	43.21%

2.3. Coverage

Mean	0.8835
Standard Deviation	3.5645

2.4. Mapping Quality

Mean Mapping Quality	53.21

2.5. Insert size

Mean	206,577.57
Standard Deviation	4,483,611.2
P25/Median/P75	135 / 171 / 227

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	25,994,628
Insertions	468,295
Mapped reads with at least one insertion	1.57%
Deletions	1,458,097
Mapped reads with at least one deletion	4.86%
Homopolymer indels	52.14%

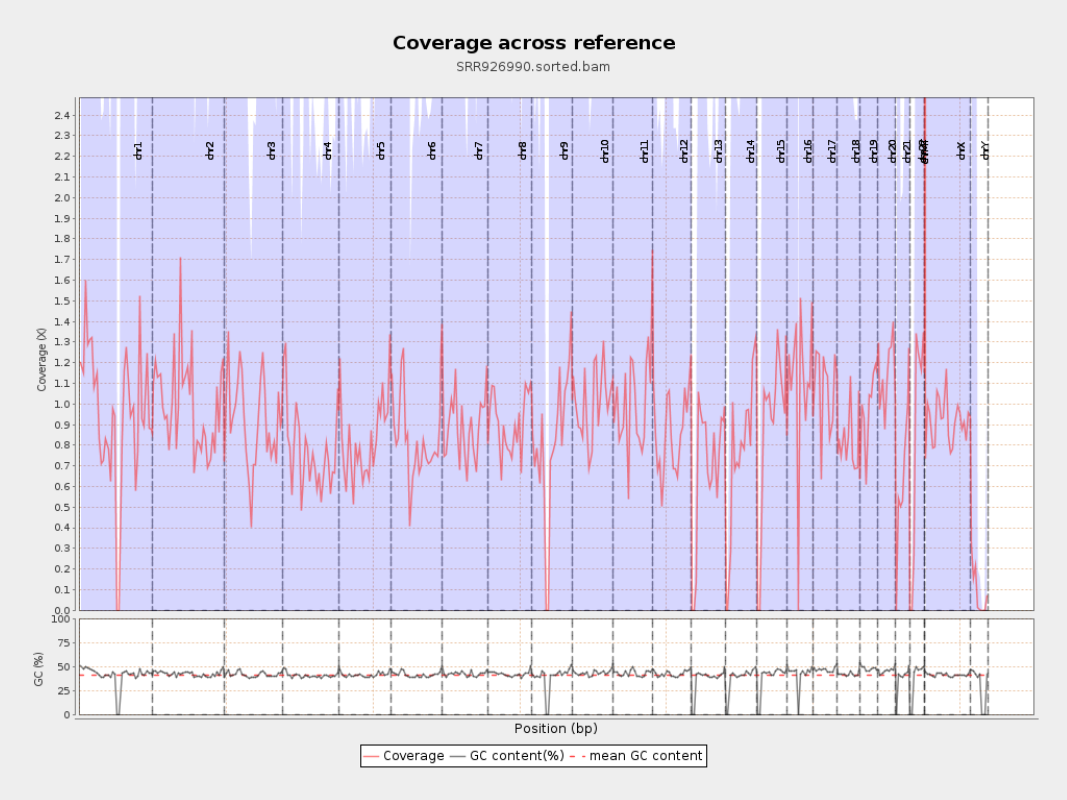
2.7. Chromosome stats

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

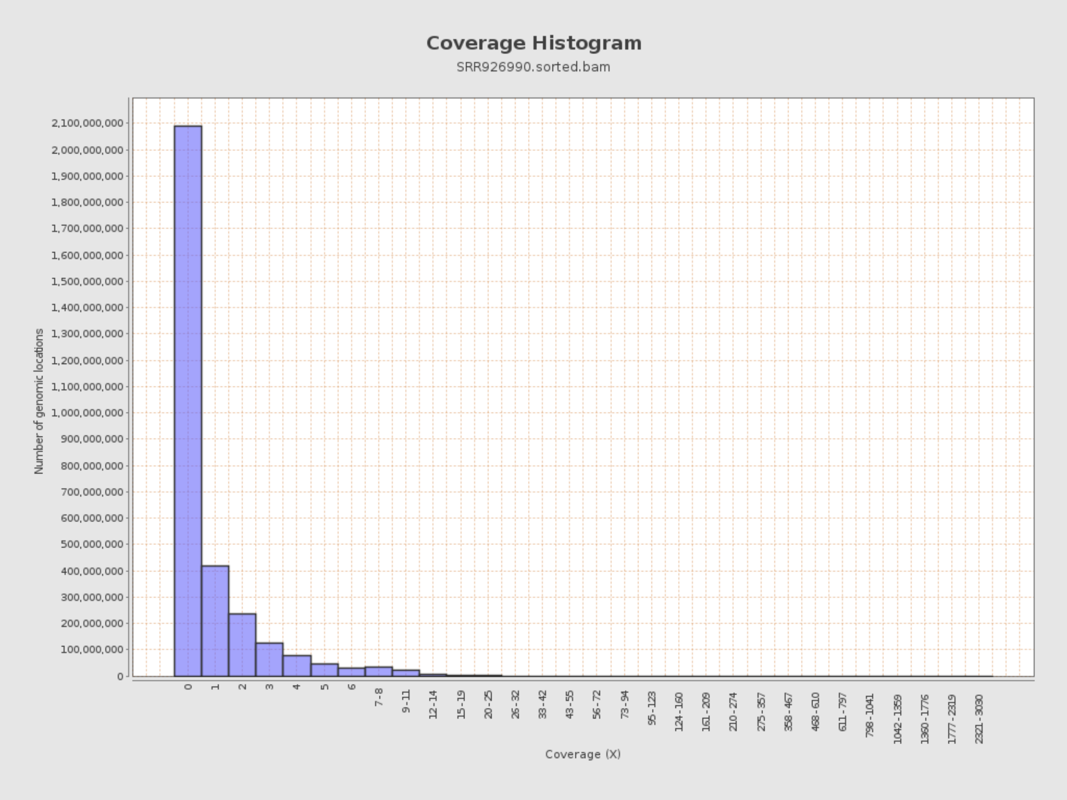
		bases	**coverage**	**deviation**
chr1	249250621	237748303	0.9539	3.7995
chr2	243199373	242568533	0.9974	5.6271
chr3	198022430	181808538	0.9181	1.9344
chr4	191154276	146216136	0.7649	2.7318
chr5	180915260	150366737	0.8311	1.8086
chr6	171115067	140509708	0.8211	2.7258
chr7	159138663	143334535	0.9007	2.7516
chr8	146364022	132110416	0.9026	2.3386
chr9	141213431	114702797	0.8123	4.2931
chr10	135534747	136228841	1.0051	4.2539
chr11	135006516	133460288	0.9885	3.1343
chr12	133851895	114187034	0.8531	2.0343
chr13	115169878	78729916	0.6836	1.6685
chr14	107349540	80627094	0.7511	1.865
chr15	102531392	89481316	0.8727	2.0731
chr16	90354753	99639479	1.1028	5.3394
chr17	81195210	87115044	1.0729	3.356
chr18	78077248	64229988	0.8226	4.4496
chr19	59128983	58192041	0.9842	2.8148
chr20	63025520	72632723	1.1524	2.4424
chr21	48129895	32195903	0.6689	3.4431
chr22	51304566	44001161	0.8576	2.2346
chrMT	16571	7867269	474.7613	361.7858
chrX	155270560	141956882	0.9143	2.1906

chrY	59373566	5250356	0.0884	2.949

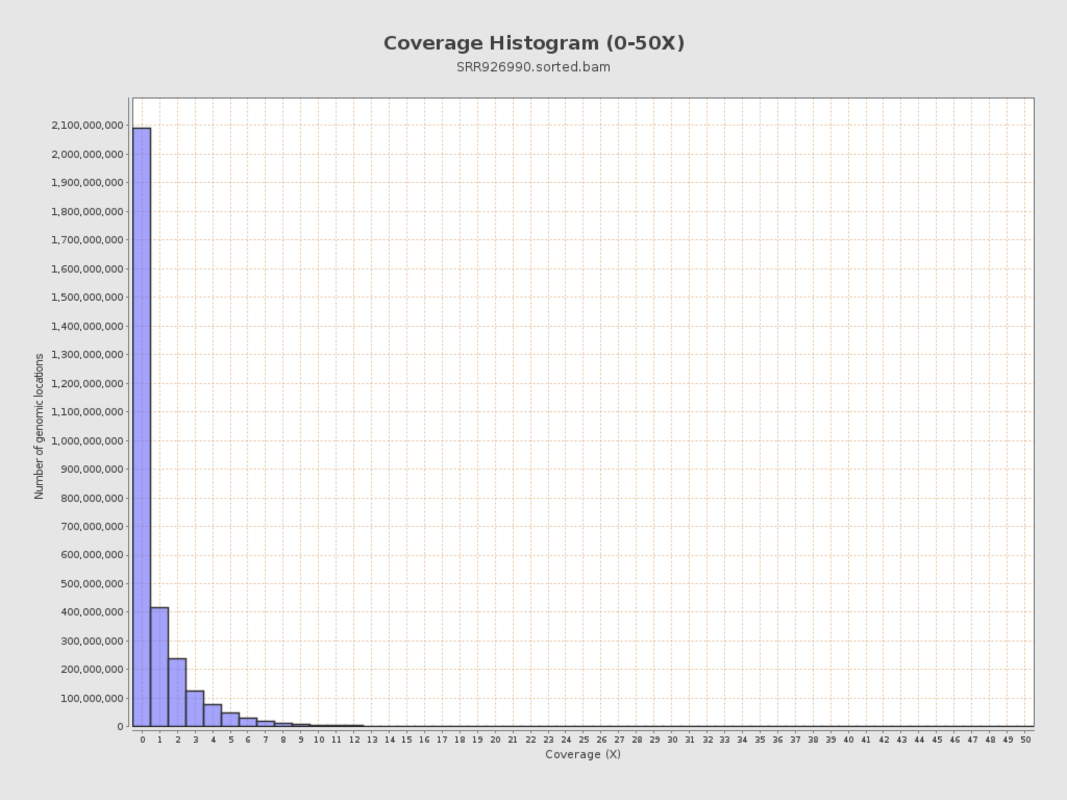
3. Results : Coverage across reference



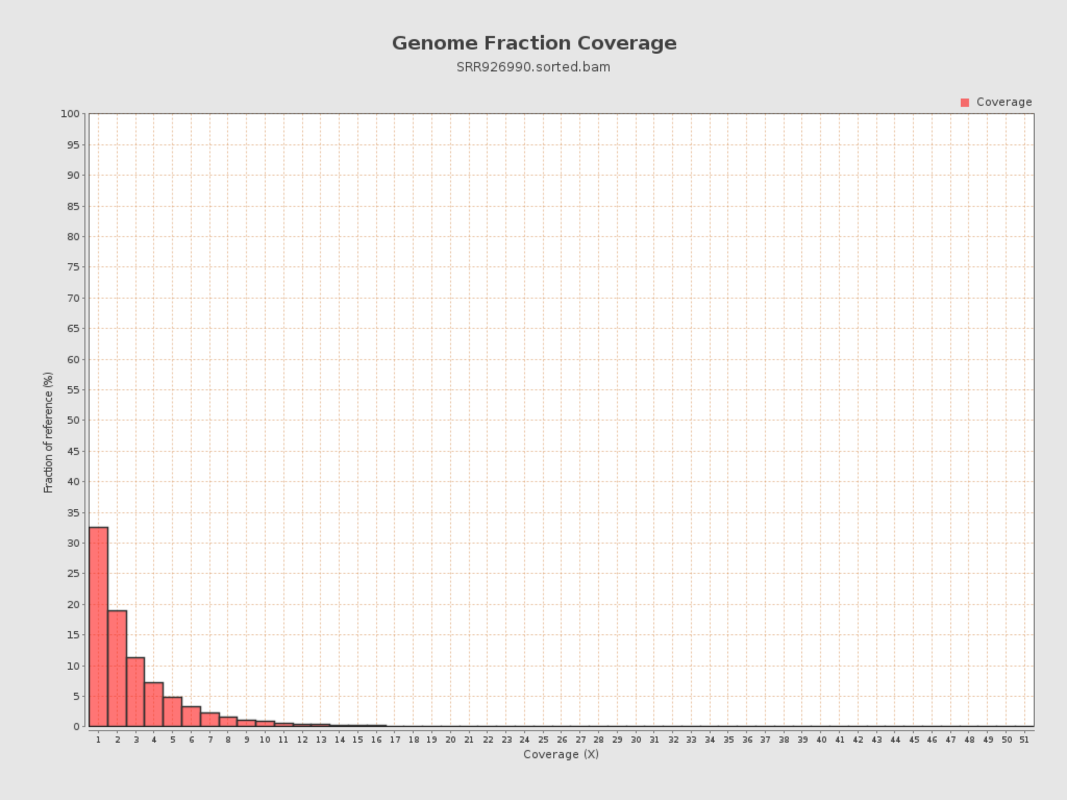
4. Results : Coverage Histogram



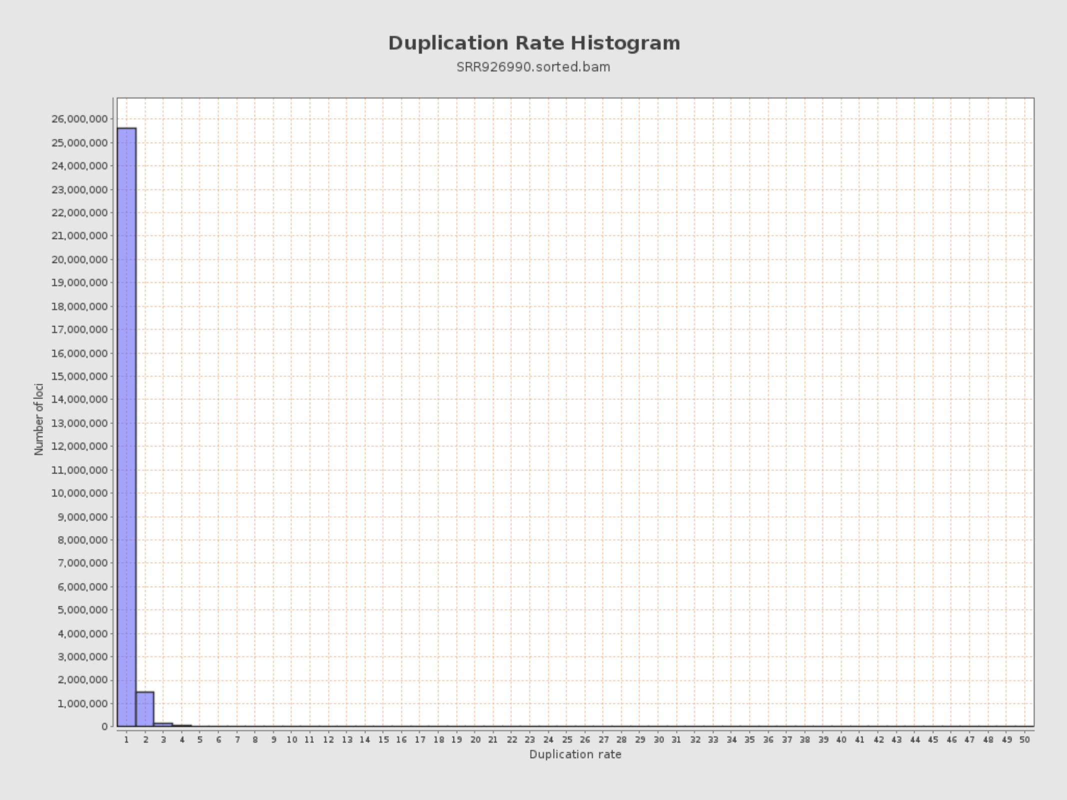
5. Results : Coverage Histogram (0-50X)



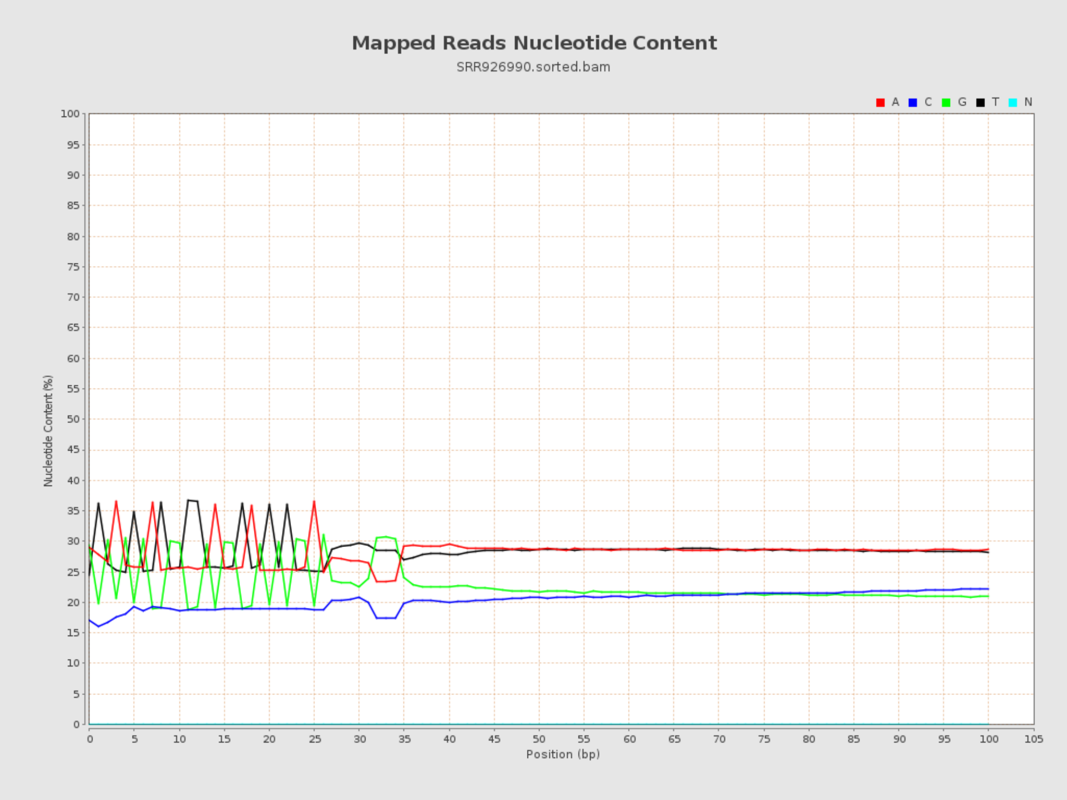
6. Results : Genome Fraction Coverage



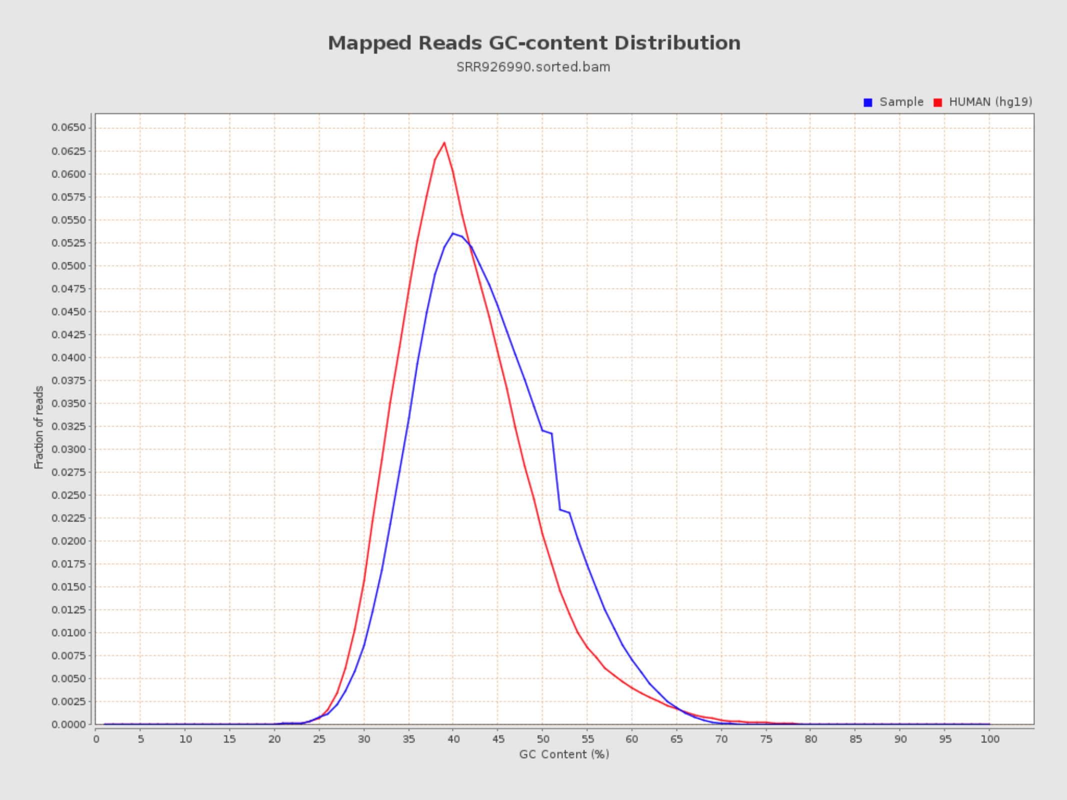
7. Results : Duplication Rate Histogram



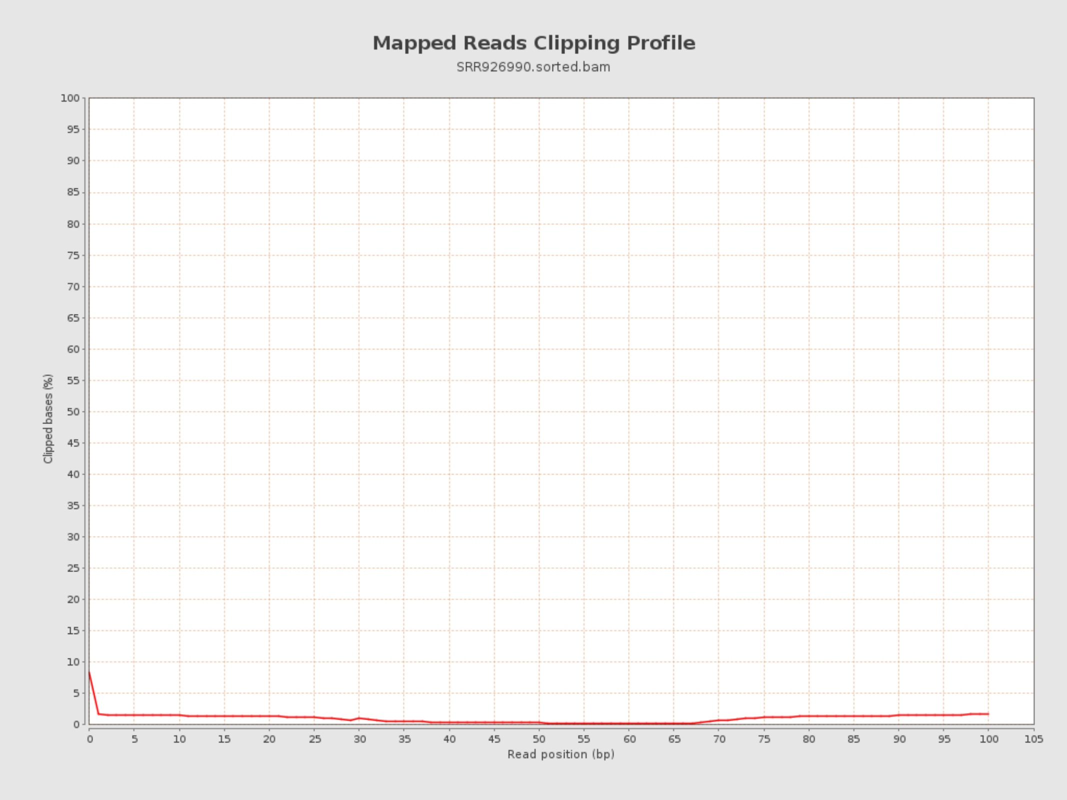
8. Results : Mapped Reads Nucleotide Content



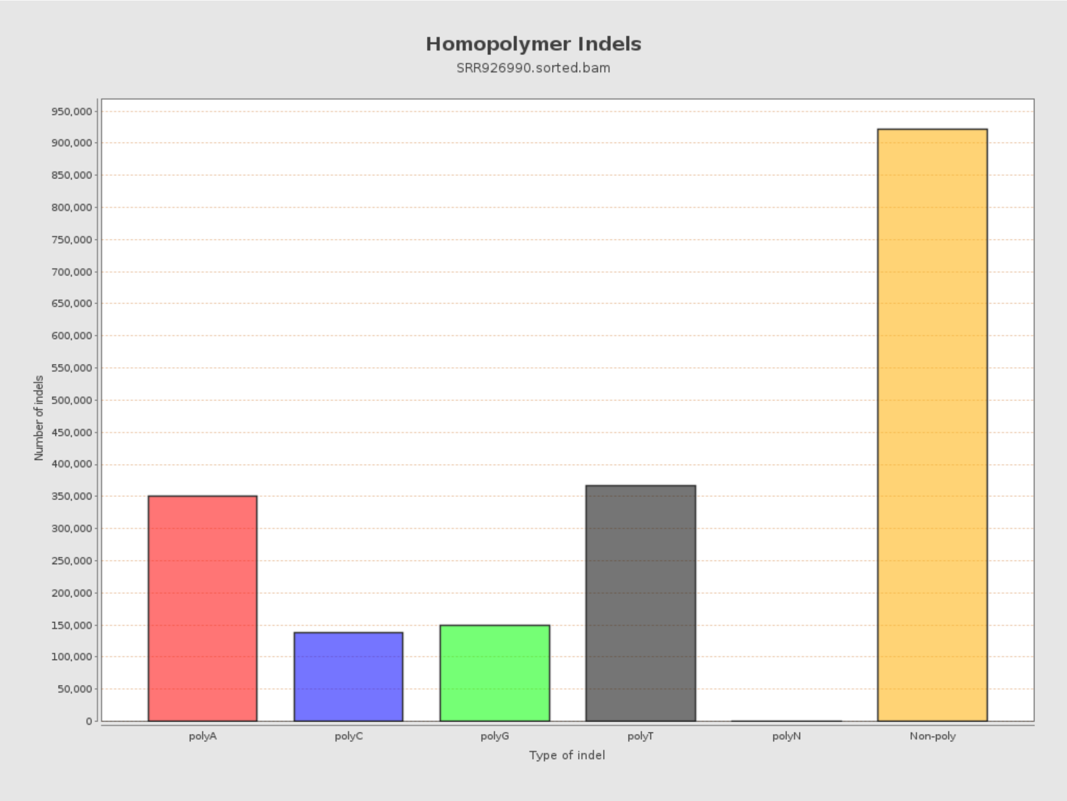
9. Results : Mapped Reads GC-content Distribution



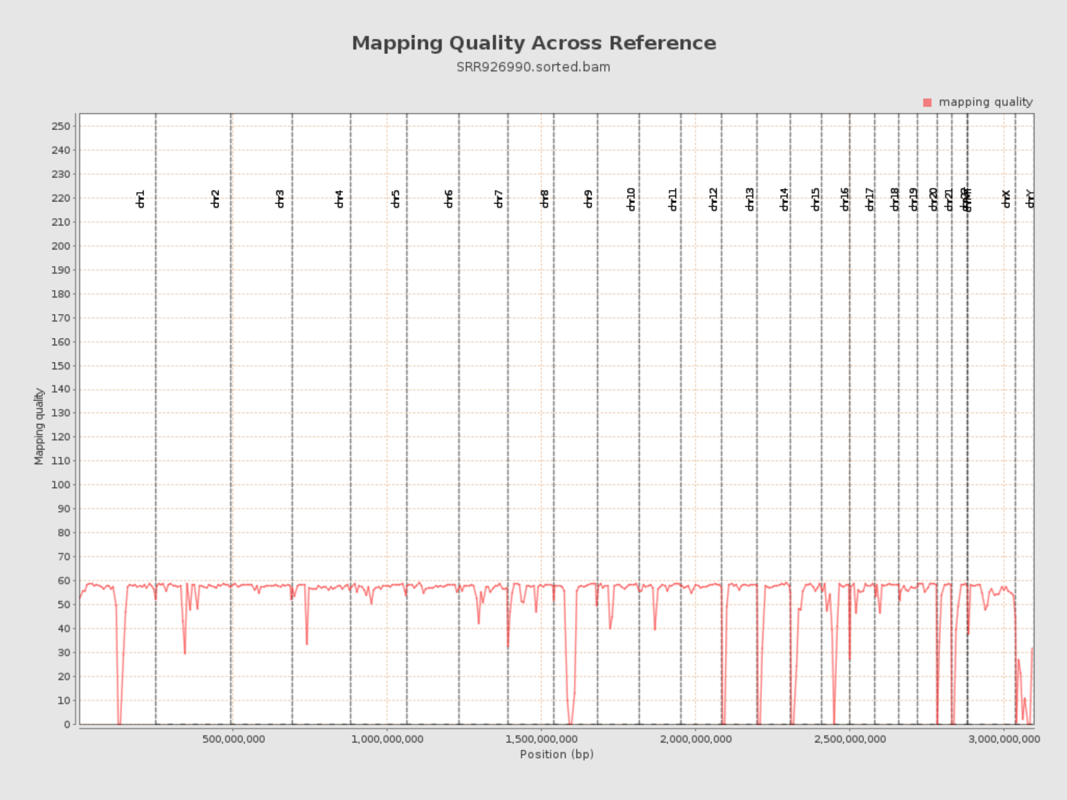
10. Results : Mapped Reads Clipping Profile



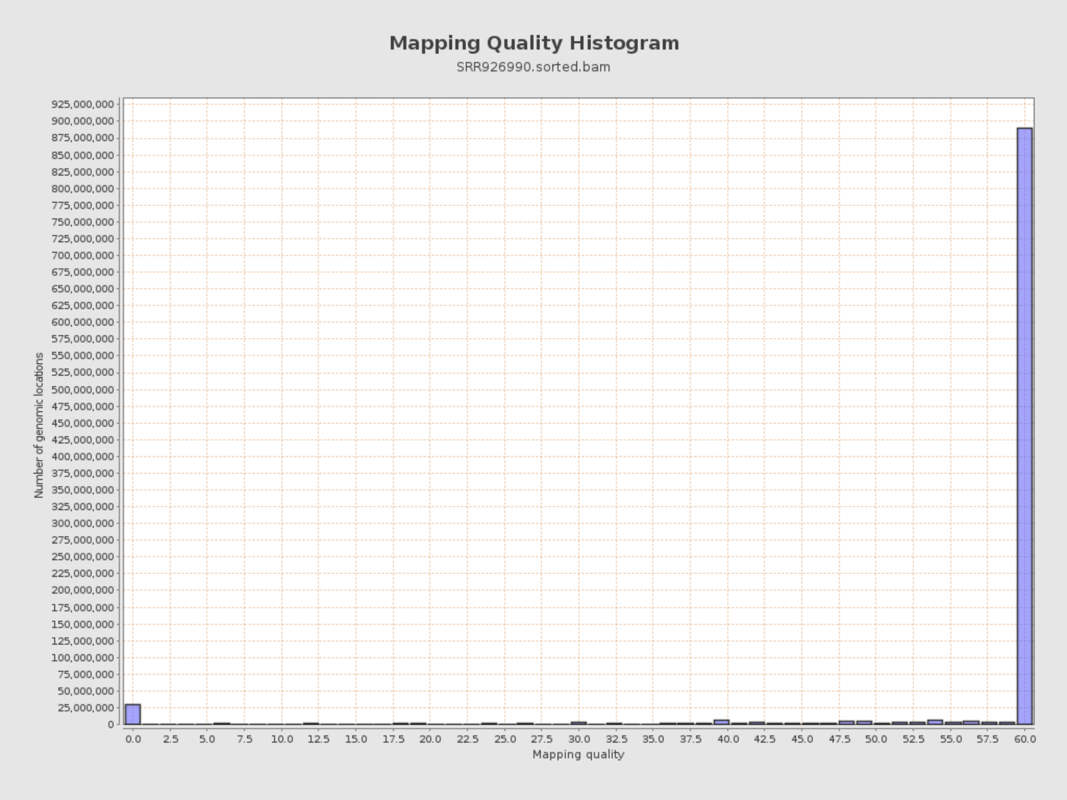
11. Results : Homopolymer Indels



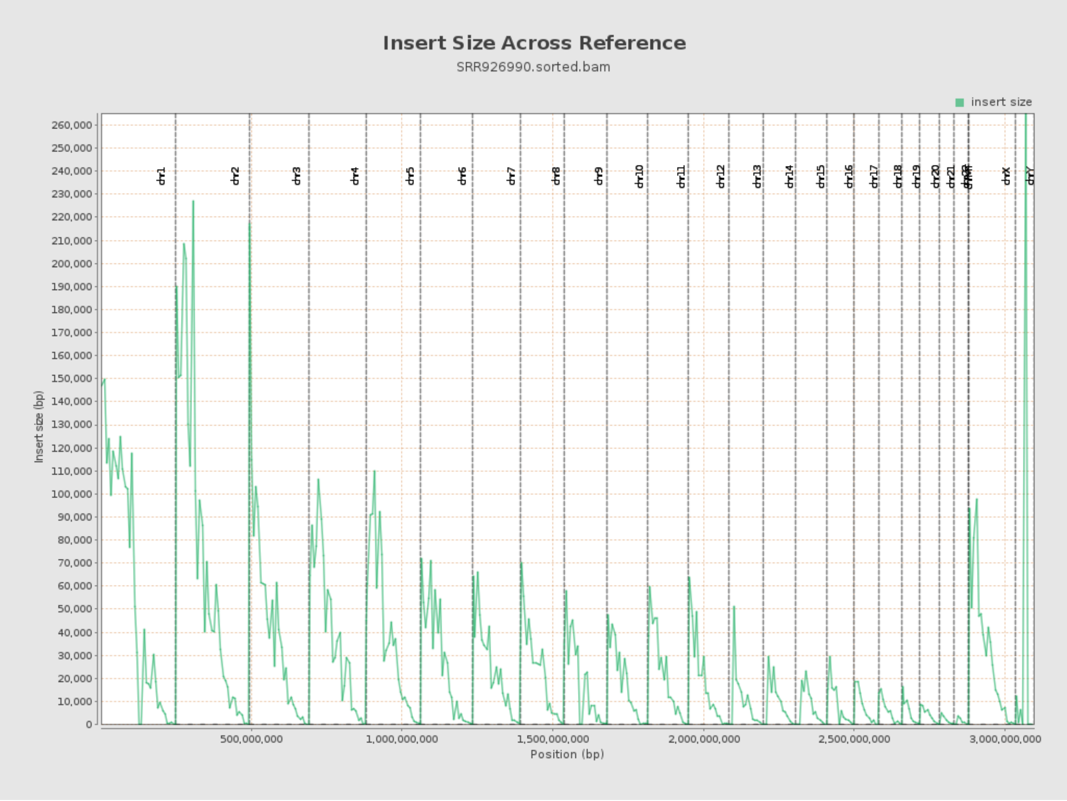
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram