Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 03:34:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926893.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_SRR926893 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926893_1.fastq.gz SRR926893_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 03:34:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926893.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	42,479,856
Mapped reads	39,613,568 / 93.25%
Unmapped reads	2,866,288 / 6.75%
Mapped paired reads	39,613,568 / 93.25%
Mapped reads, first in pair	19,833,854 / 46.69%
Mapped reads, second in pair	19,779,714 / 46.56%
Mapped reads, both in pair	39,153,802 / 92.17%
Mapped reads, singletons	459,766 / 1.08%
Secondary alignments	0
Supplementary alignments	655,328 / 1.54%
Read min/max/mean length	30 / 101 / 101.63
Duplicated reads (estimated)	3,898,918 / 9.18%
Duplication rate	7.96%
Clipped reads	11,820,495 / 27.83%

2.2. ACGT Content

Number/percentage of A's	1,068,963,457 / 28.69%
Number/percentage of C's	753,784,337 / 20.23%
Number/percentage of T's	1,071,742,045 / 28.76%
Number/percentage of G's	831,152,854 / 22.31%
Number/percentage of N's	251,348 / 0.01%

GC Percentage	42.54%

2.3. Coverage

Mean	1.2045
Standard Deviation	5.3838

2.4. Mapping Quality

Mean Mapping Quality	53.15

2.5. Insert size

Mean	122,310.5
Standard Deviation	3,436,494.16
P25/Median/P75	125 / 161 / 217

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	35,417,835
Insertions	599,086
Mapped reads with at least one insertion	1.49%
Deletions	2,047,765
Mapped reads with at least one deletion	5.03%
Homopolymer indels	52.89%

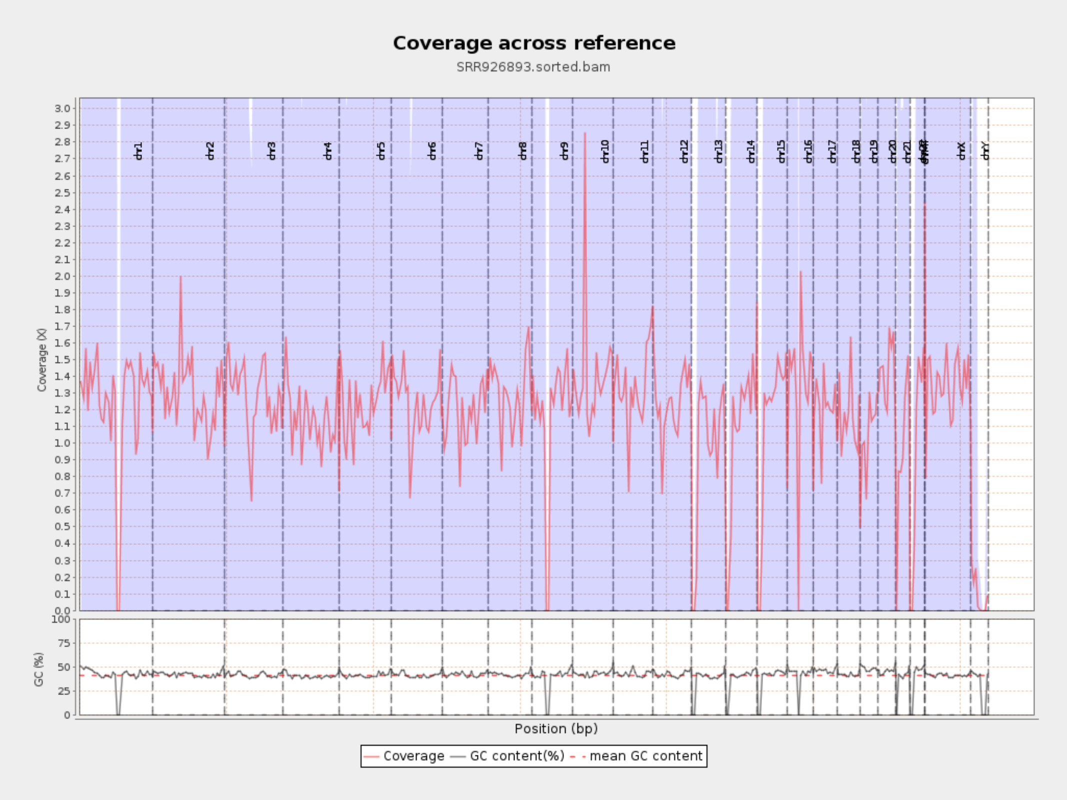
2.7. Chromosome stats

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

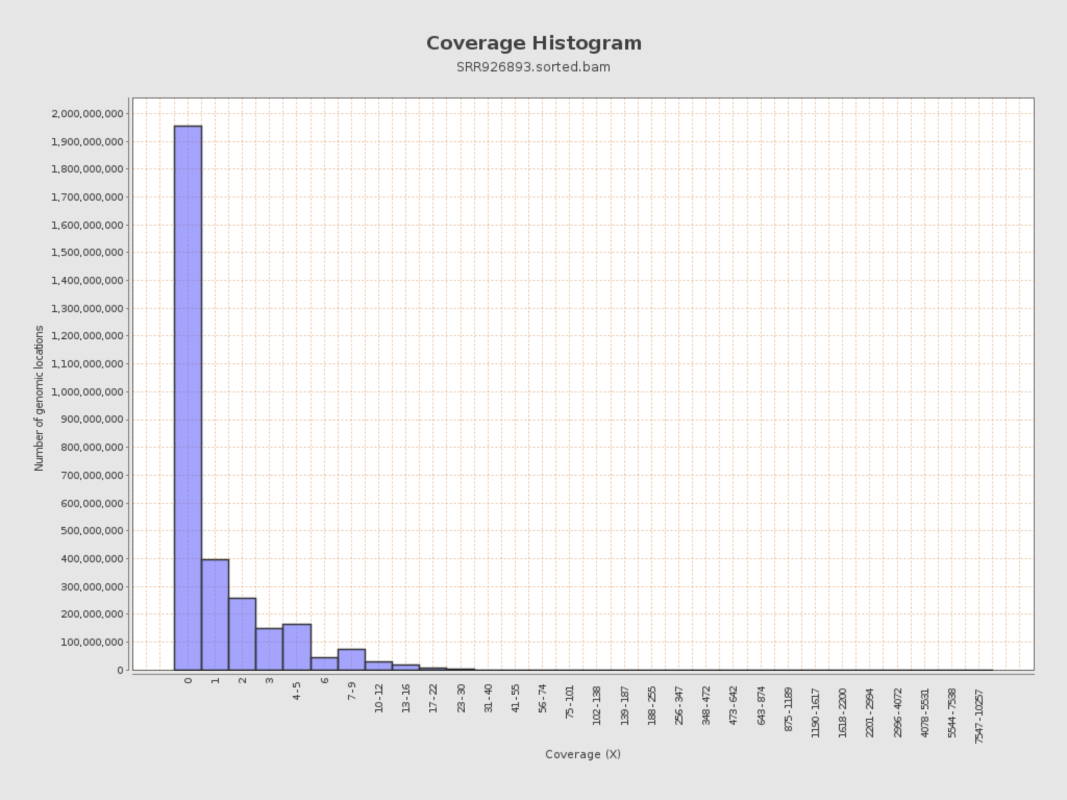
		bases	coverage	deviation
chr1	249250621	308488811	1.2377	4.5785
chr2	243199373	319399125	1.3133	6.0745
chr3	198022430	253828375	1.2818	2.8193
chr4	191154276	221596574	1.1593	2.837
chr5	180915260	225078667	1.2441	2.4958
chr6	171115067	213598014	1.2483	3.127
chr7	159138663	190185917	1.1951	2.7916
chr8	146364022	189554245	1.2951	2.9306
chr9	141213431	162689963	1.1521	4.5346
chr10	135534747	192473340	1.4201	19.0054
chr11	135006516	178962369	1.3256	3.1798
chr12	133851895	166085316	1.2408	2.753
chr13	115169878	110638873	0.9607	2.3044
chr14	107349540	111982823	1.0432	2.4085
chr15	102531392	111869887	1.0911	2.5334
chr16	90354753	119414842	1.3216	7.2828
chr17	81195210	98434259	1.2123	2.9413
chr18	78077248	91892838	1.1769	4.5425
chr19	59128983	61655416	1.0427	3.1162
chr20	63025520	90326242	1.4332	2.9822
chr21	48129895	47662116	0.9903	4.006
chr22	51304566	49181222	0.9586	2.4943
chrMT	16571	40501	2.4441	2.6695
chrX	155270560	208098042	1.3402	2.7603

chrY	59373566	5643316	0.095	2.4672

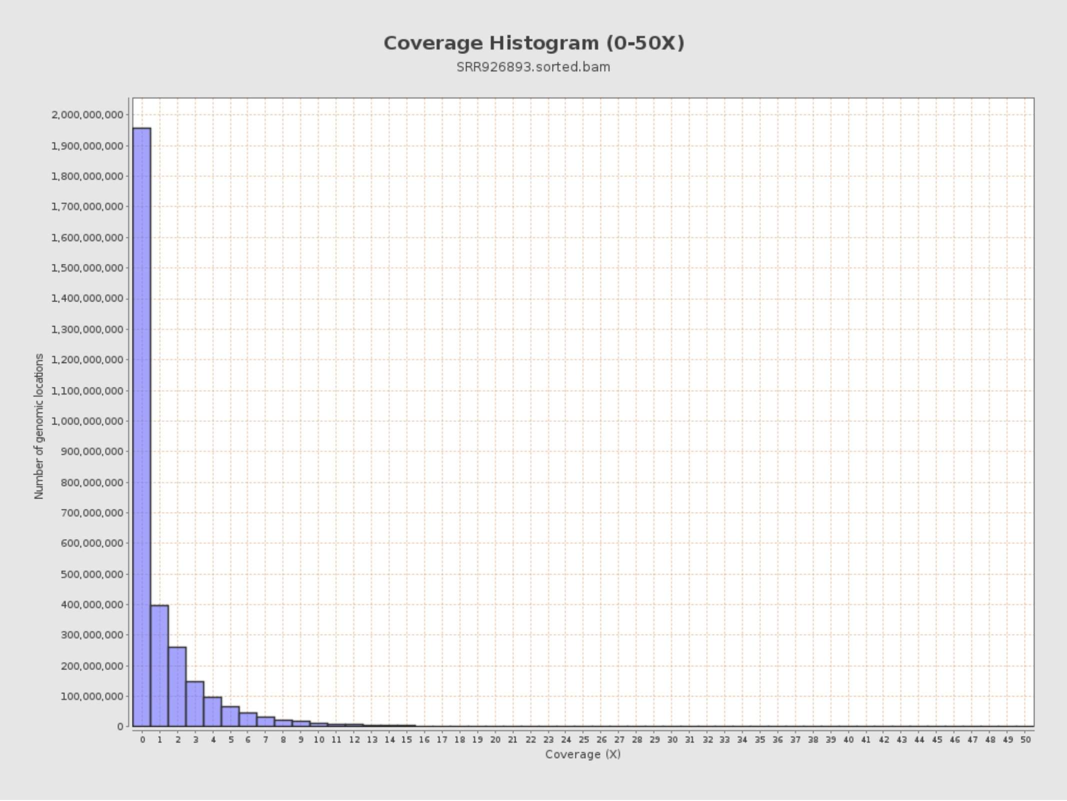
3. Results : Coverage across reference



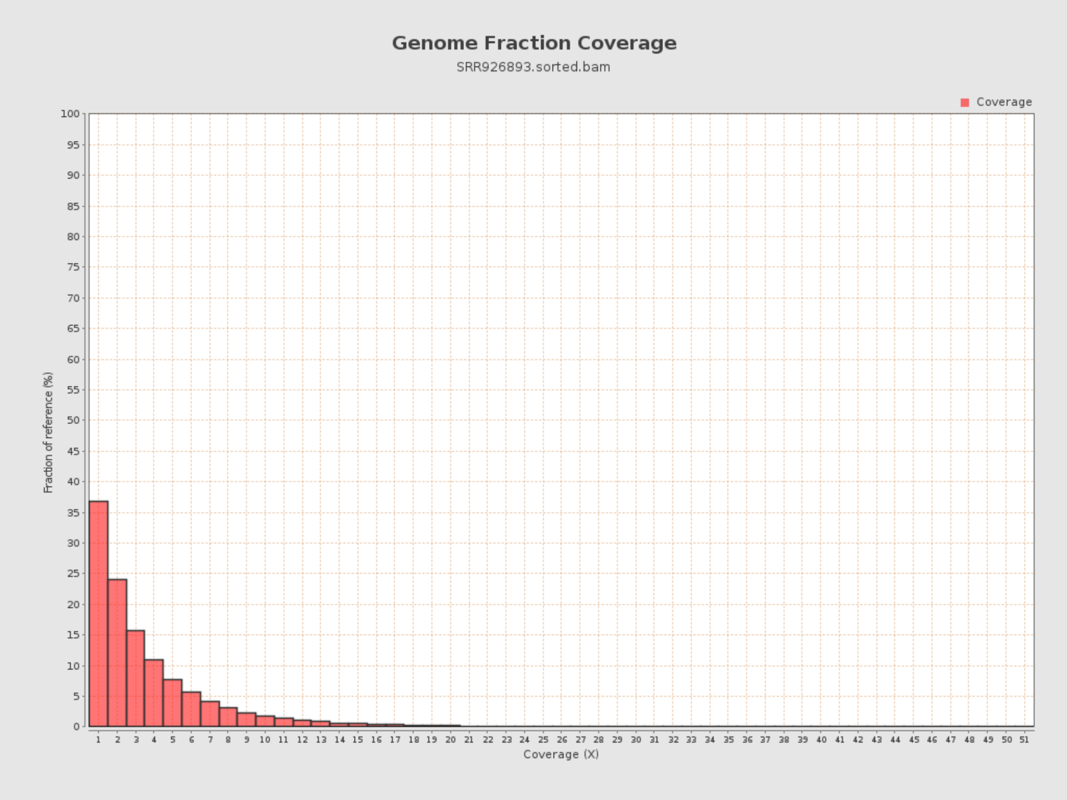
4. Results : Coverage Histogram



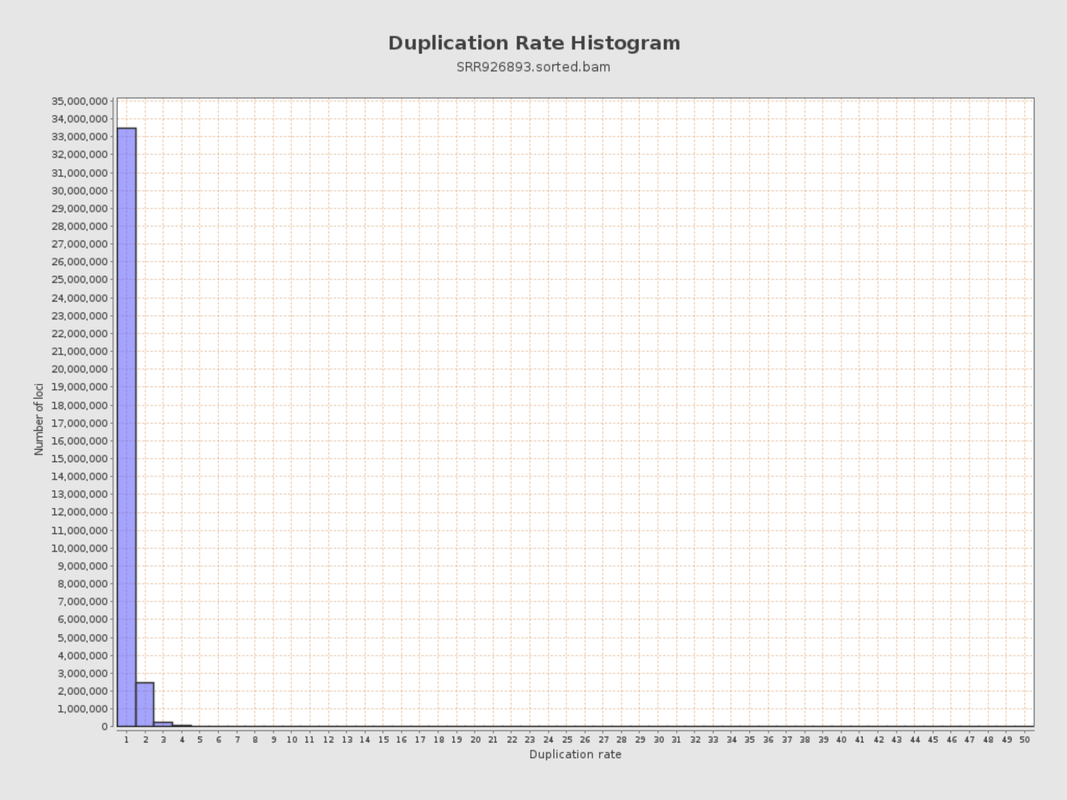
5. Results : Coverage Histogram (0-50X)



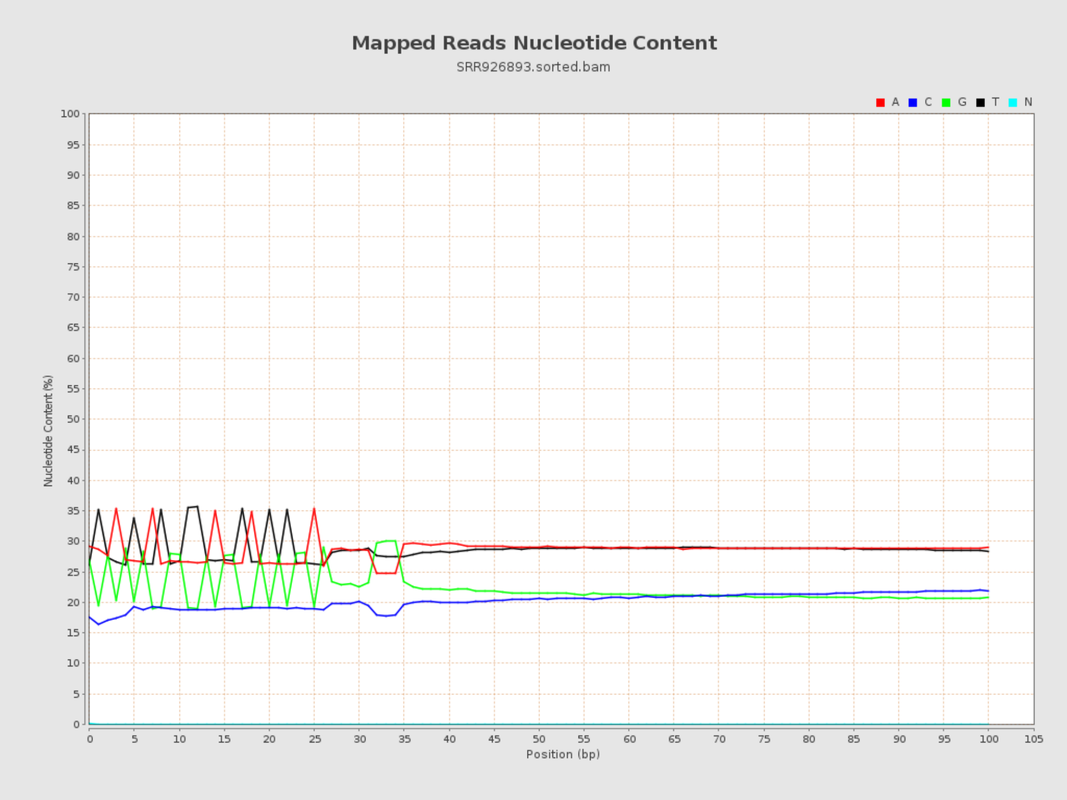
6. Results : Genome Fraction Coverage



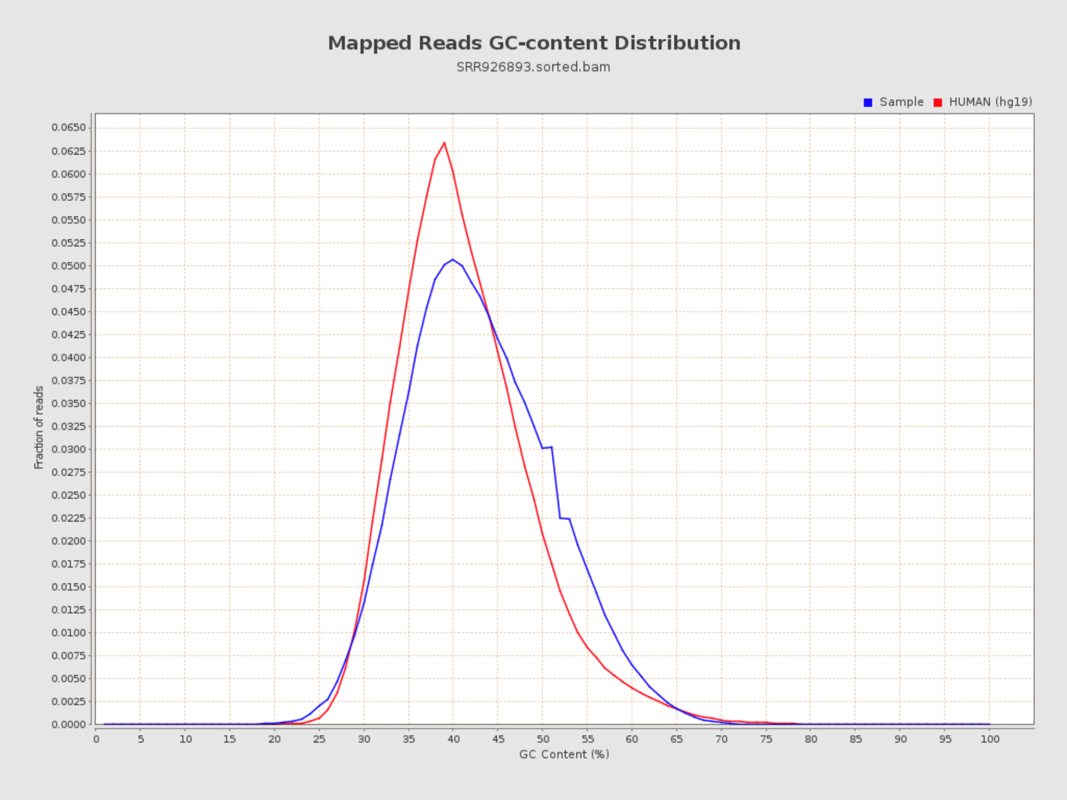
7. Results : Duplication Rate Histogram



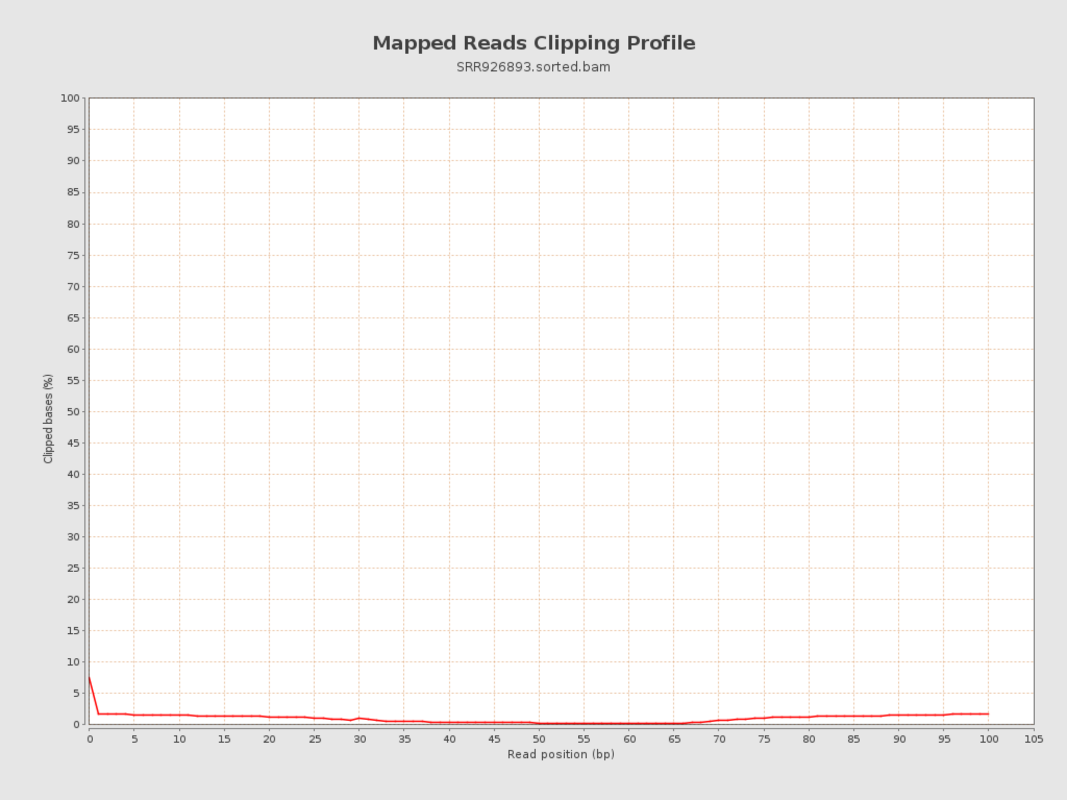
8. Results : Mapped Reads Nucleotide Content



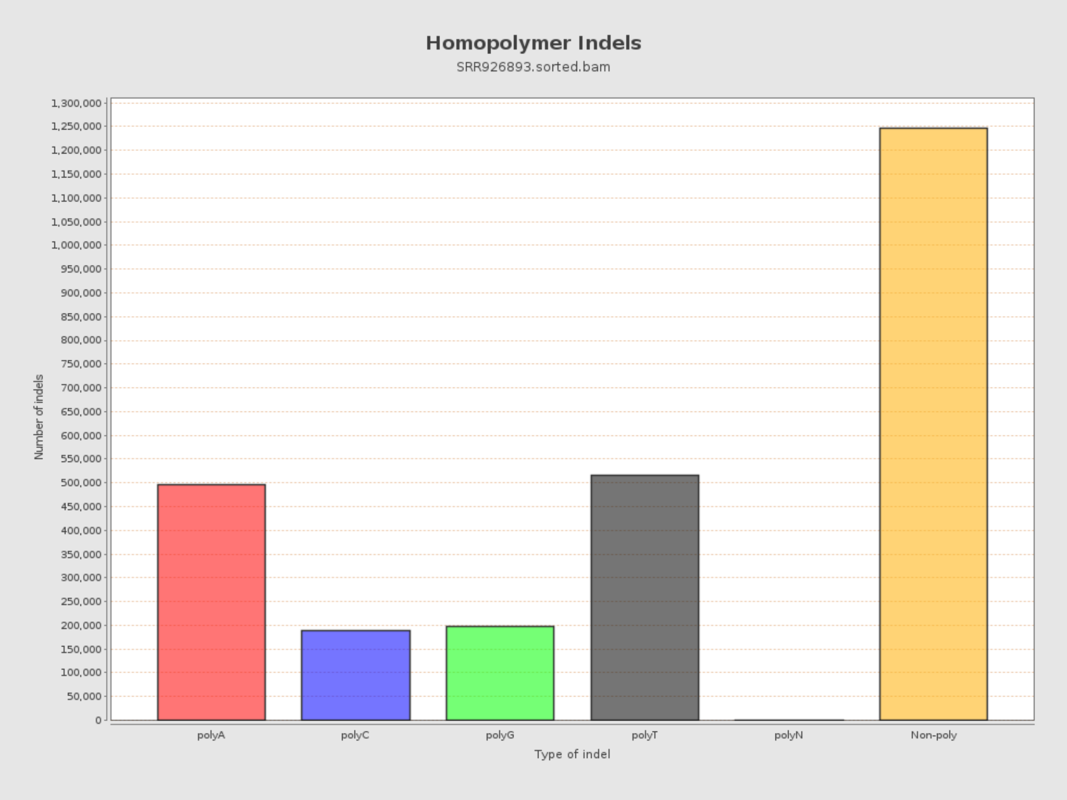
9. Results : Mapped Reads GC-content Distribution



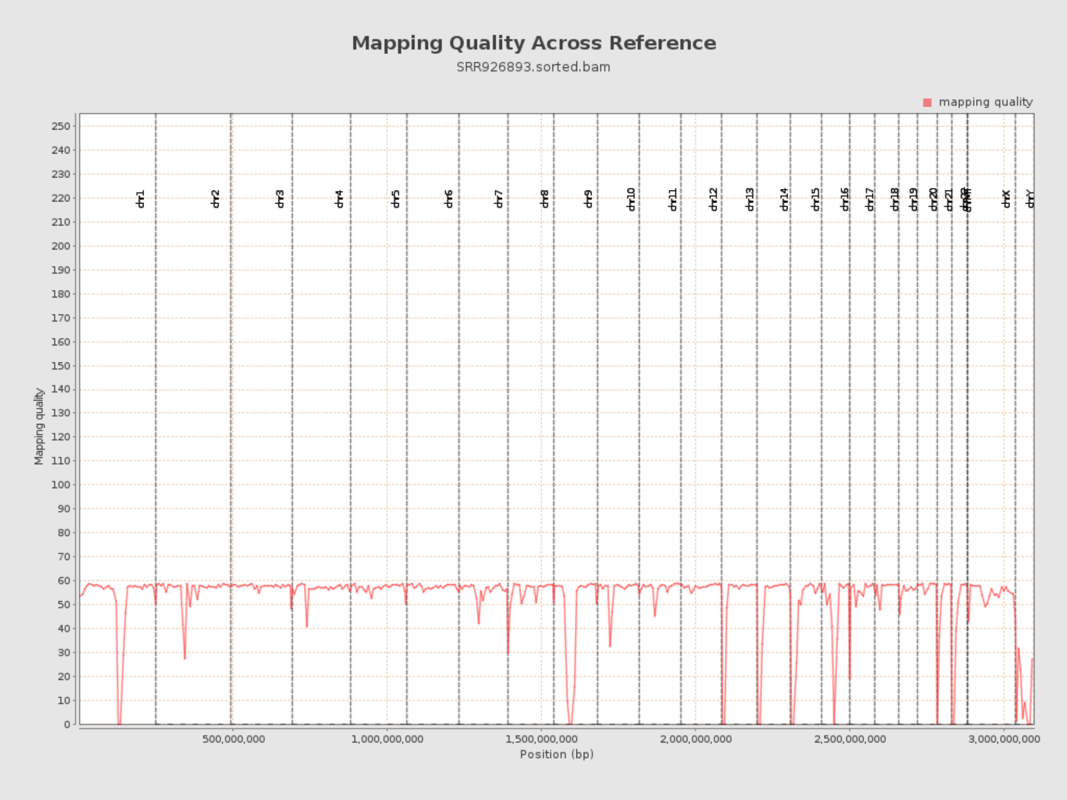
10. Results : Mapped Reads Clipping Profile



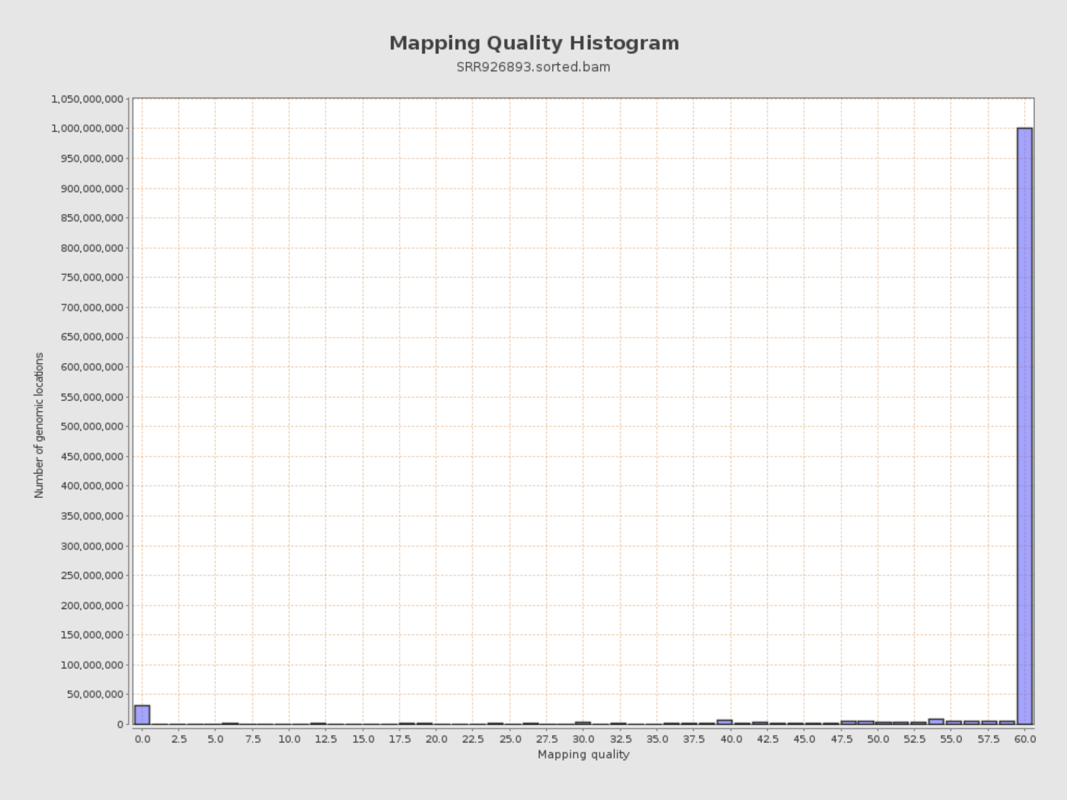
11. Results : Homopolymer Indels



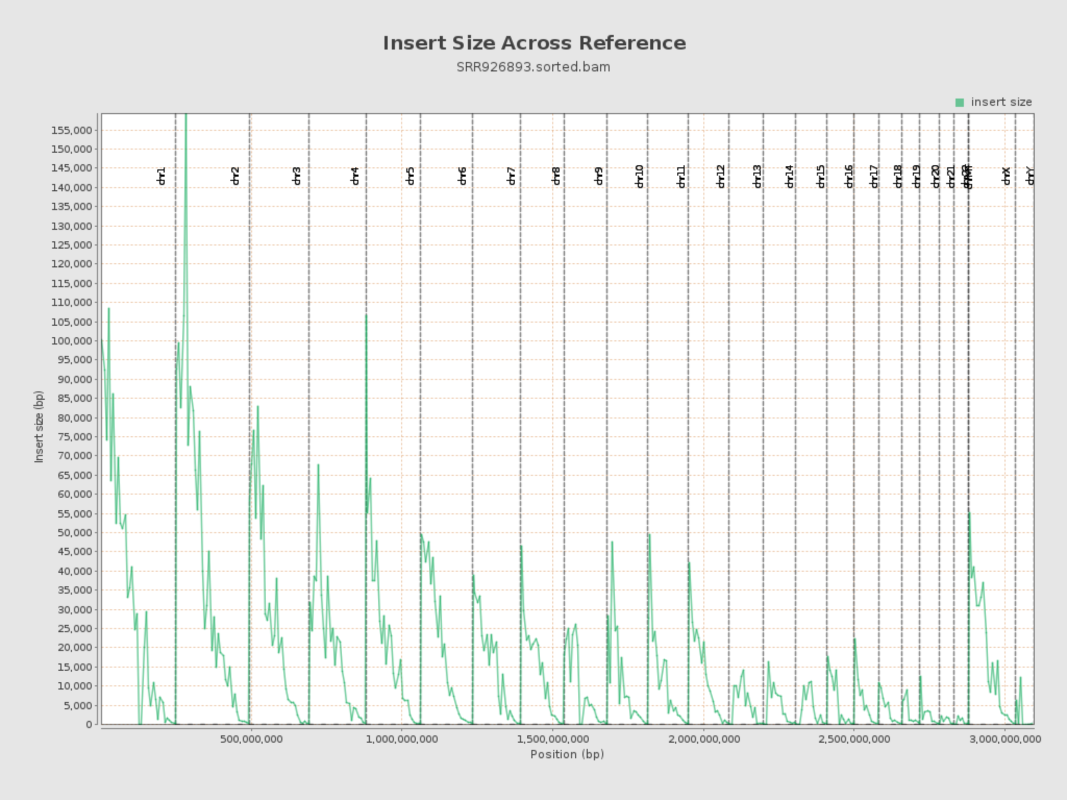
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram