Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 05:16:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926896.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_SRR926896 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926896_1.fastq.gz SRR926896_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 05:16:10 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926896.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,069,352
Mapped reads	27,902,346 / 95.99%
Unmapped reads	1,167,006 / 4.01%
Mapped paired reads	27,902,346 / 95.99%
Mapped reads, first in pair	14,030,551 / 48.27%
Mapped reads, second in pair	13,871,795 / 47.72%
Mapped reads, both in pair	27,420,688 / 94.33%
Mapped reads, singletons	481,658 / 1.66%
Secondary alignments	0
Supplementary alignments	877,519 / 3.02%
Read min/max/mean length	30 / 101 / 102.25
Duplicated reads (estimated)	3,461,804 / 11.91%
Duplication rate	9.7%
Clipped reads	14,567,196 / 50.11%

2.2. ACGT Content

Number/percentage of A's	692,558,605 / 28.13%
Number/percentage of C's	478,464,281 / 19.43%
Number/percentage of T's	707,357,653 / 28.73%
Number/percentage of G's	583,509,907 / 23.7%
Number/percentage of N's	187,368 / 0.01%

GC Percentage	43.13%

2.3. Coverage

Mean	0.796
Standard Deviation	2.6606

2.4. Mapping Quality

Mean Mapping Quality	52.47

2.5. Insert size

Mean	363,344.96
Standard Deviation	5,939,426.67
P25/Median/P75	130 / 174 / 239

2.6. Mismatches and indels

General error rate	1.1%
Mismatches	26,265,348
Insertions	434,476
Mapped reads with at least one insertion	1.53%
Deletions	1,379,300
Mapped reads with at least one deletion	4.81%
Homopolymer indels	51.67%

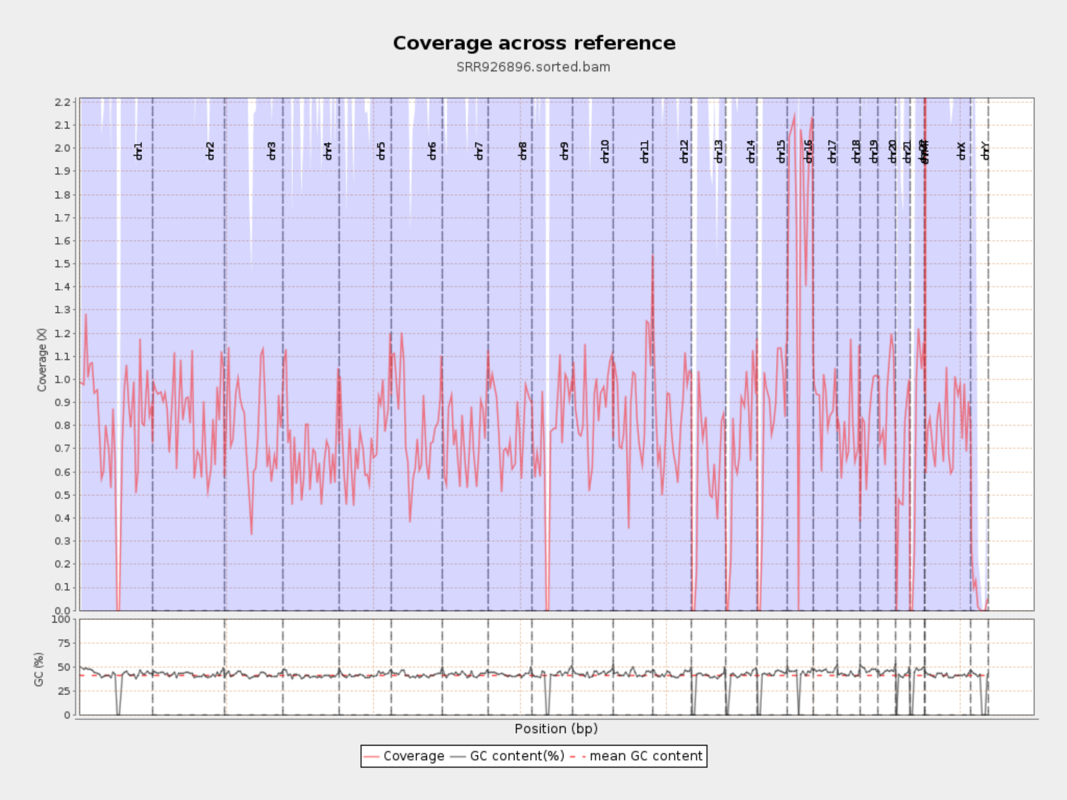
2.7. Chromosome stats

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

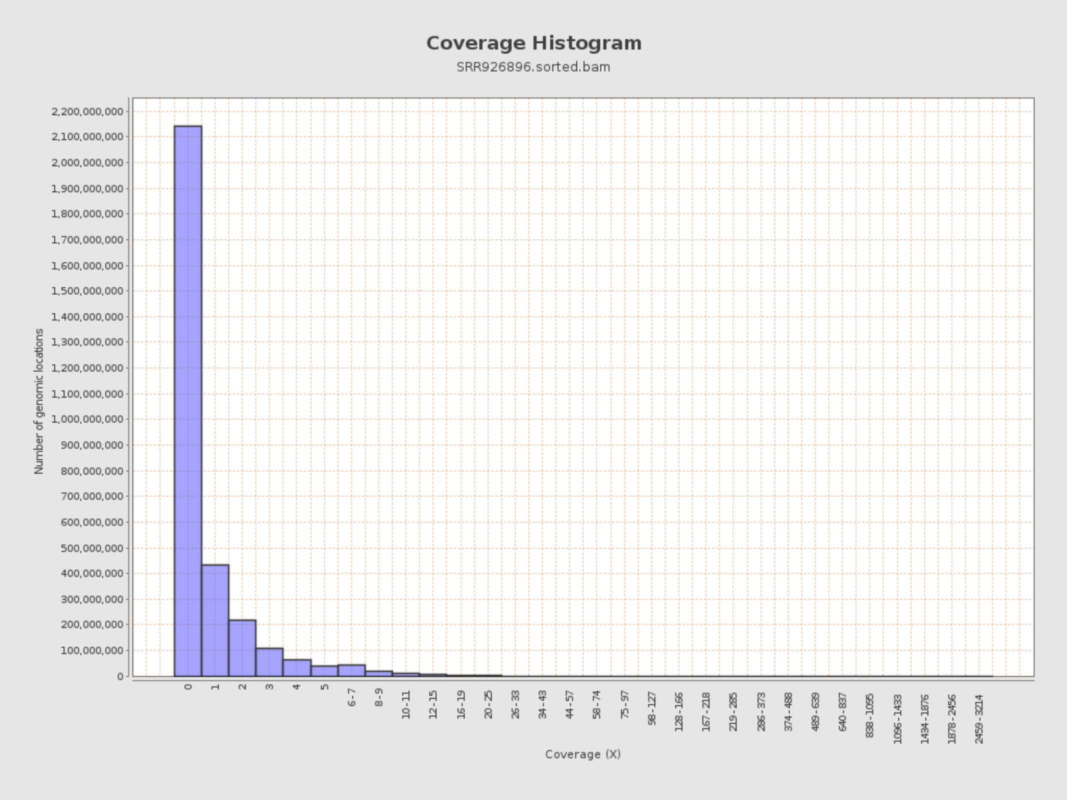
		bases	coverage	deviation
chr1	249250621	201619056	0.8089	2.3344
chr2	243199373	204730502	0.8418	3.1033
chr3	198022430	153978483	0.7776	1.8418
chr4	191154276	131346525	0.6871	1.8343
chr5	180915260	133400289	0.7374	1.7438
chr6	171115067	135383406	0.7912	1.8457
chr7	159138663	117606921	0.739	1.9627
chr8	146364022	116152048	0.7936	1.9529
chr9	141213431	104291646	0.7385	2.6397
chr10	135534747	120684739	0.8904	6.2847
chr11	135006516	118853738	0.8804	2.2982
chr12	133851895	109665989	0.8193	2.0449
chr13	115169878	67798876	0.5887	1.5736
chr14	107349540	73696212	0.6865	1.7636
chr15	102531392	79371929	0.7741	1.9867
chr16	90354753	156713622	1.7344	5.875
chr17	81195210	72320658	0.8907	2.1003
chr18	78077248	61710961	0.7904	2.298
chr19	59128983	49694324	0.8404	2.198
chr20	63025520	58466003	0.9277	2.1625
chr21	48129895	29587572	0.6147	2.146
chr22	51304566	38090126	0.7424	2.0394
chrMT	16571	1832962	110.6126	77.3265
chrX	155270560	123422989	0.7949	1.8582

chrY	59373566	3696510	0.0623	1.2514

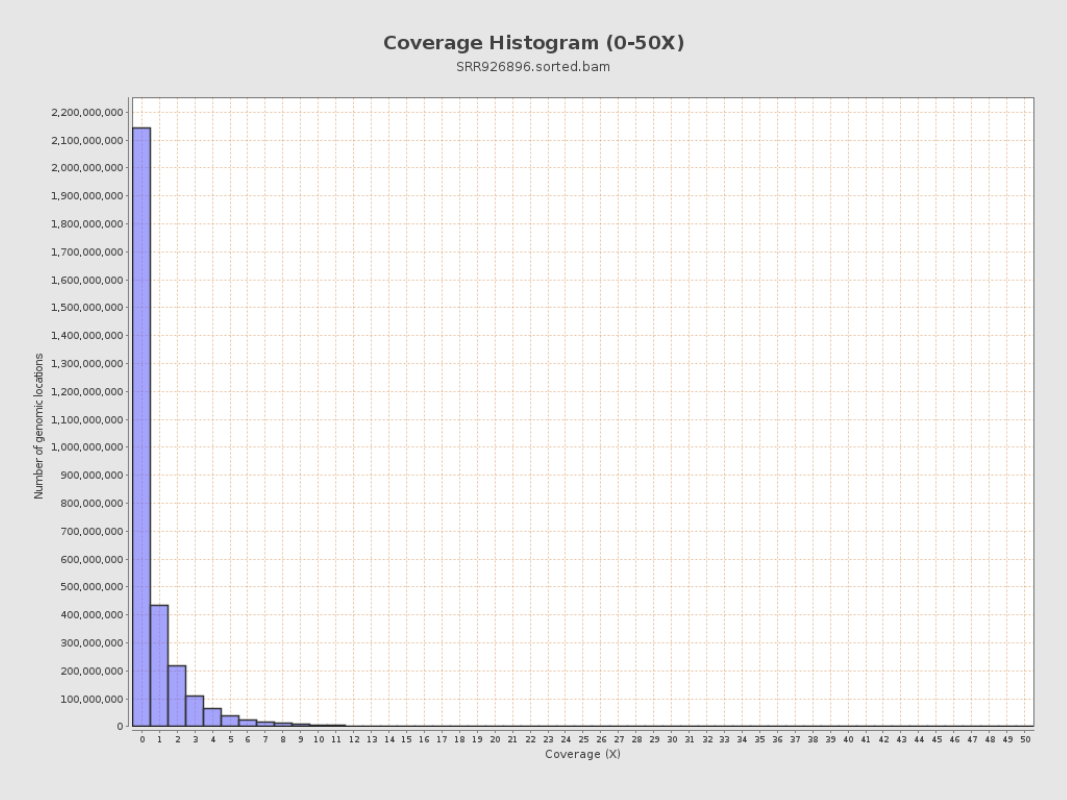
3. Results : Coverage across reference



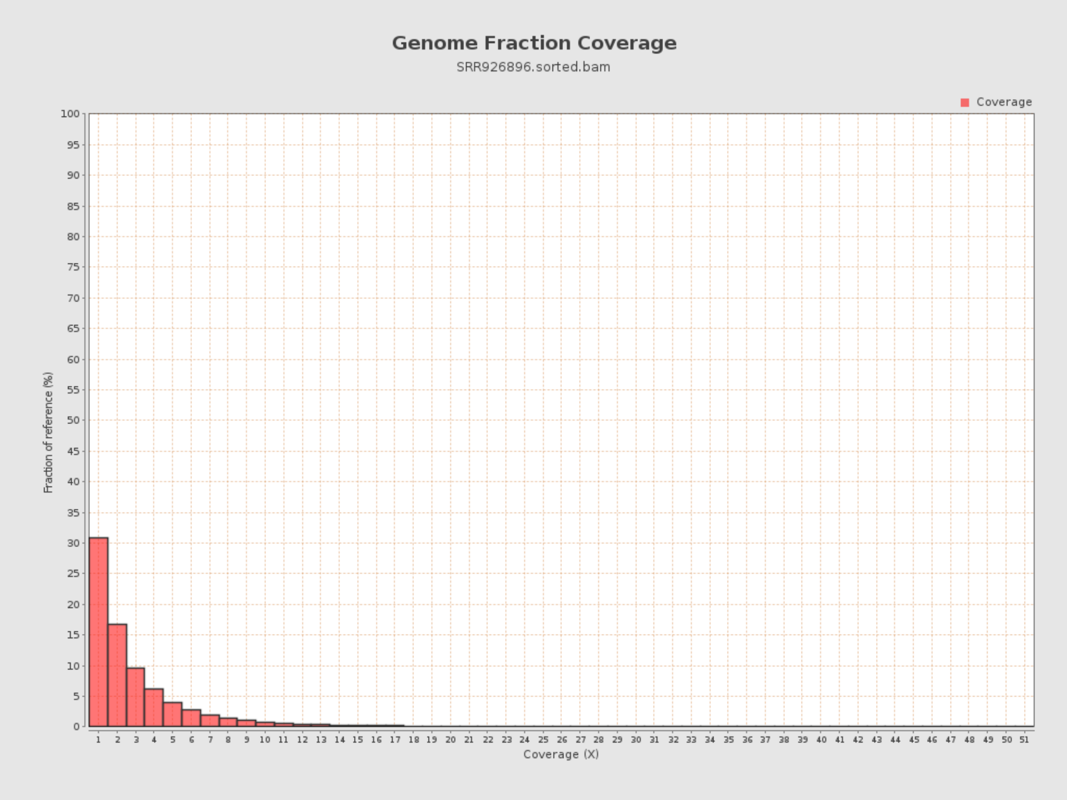
4. Results : Coverage Histogram



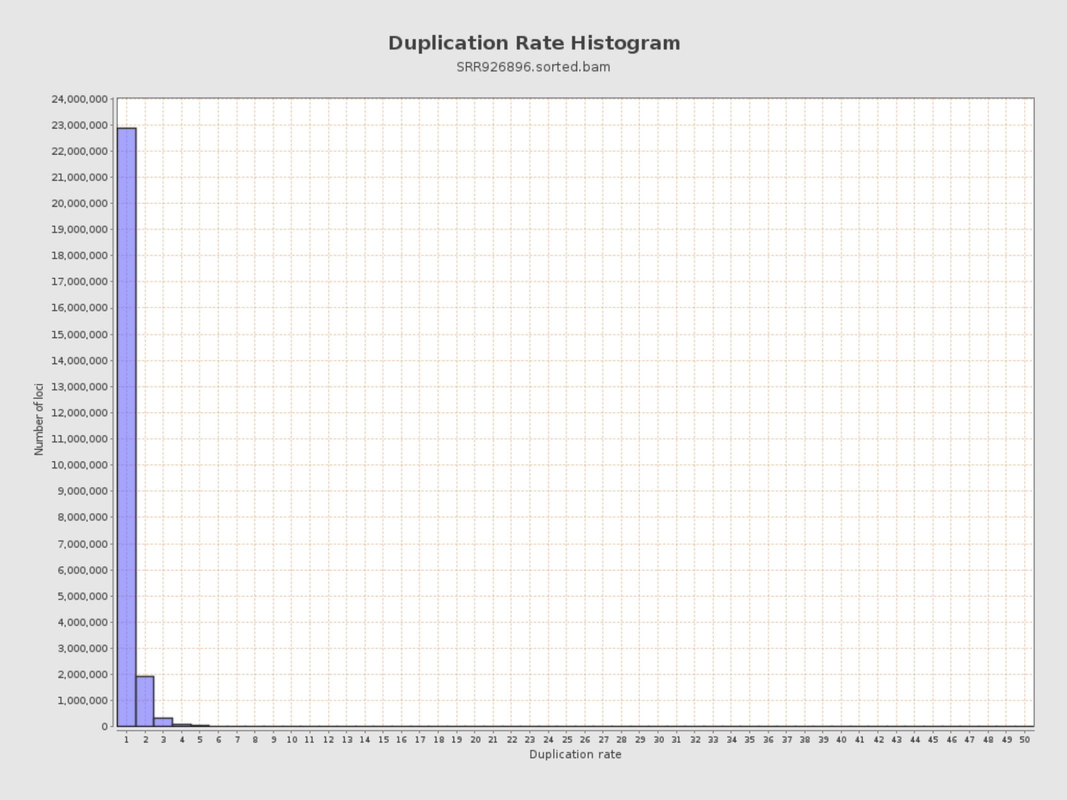
5. Results : Coverage Histogram (0-50X)



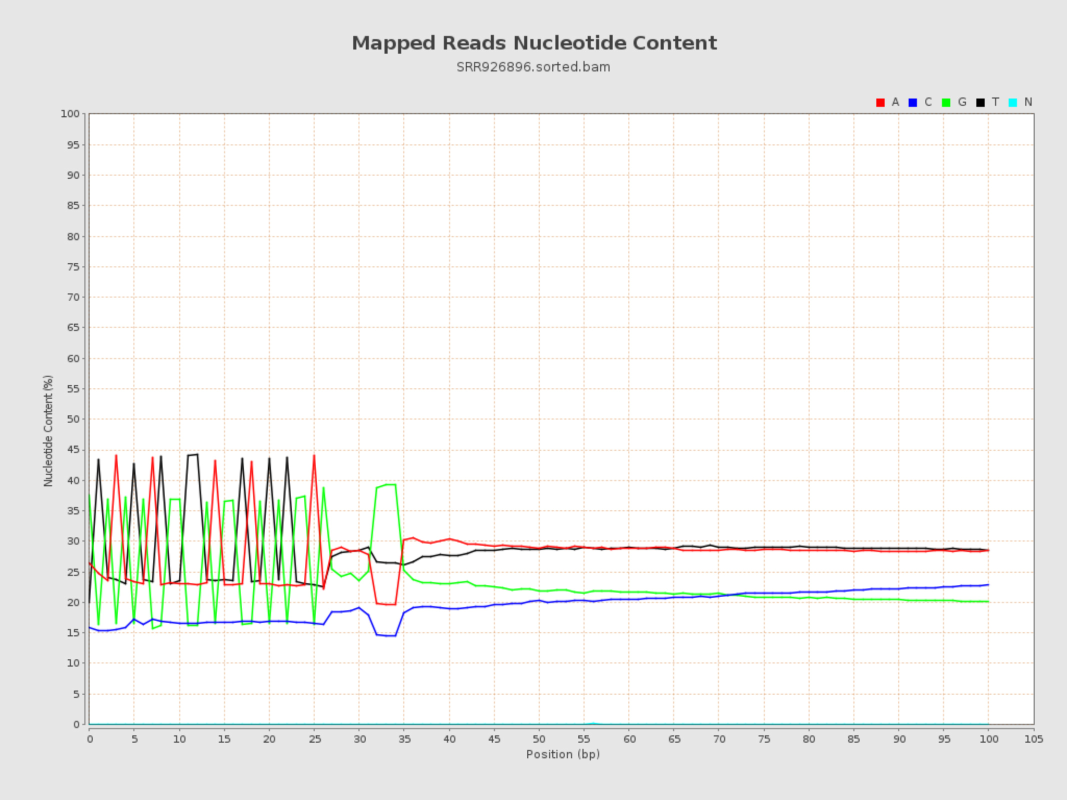
6. Results : Genome Fraction Coverage



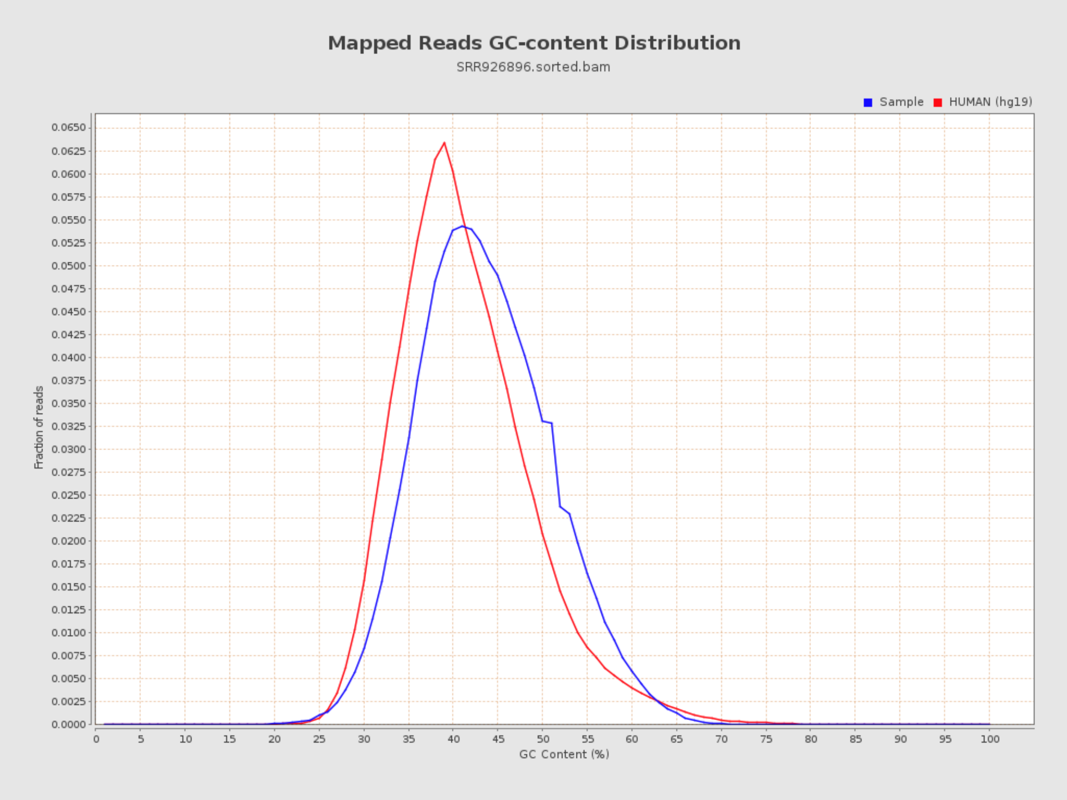
7. Results : Duplication Rate Histogram



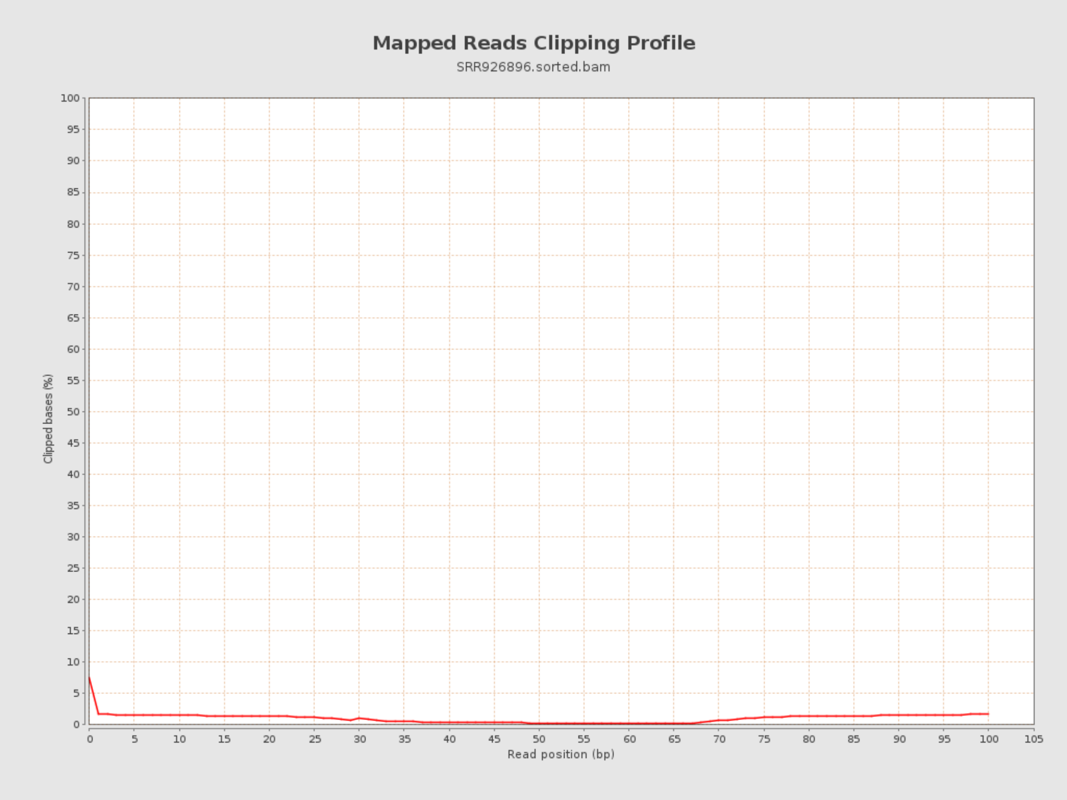
8. Results : Mapped Reads Nucleotide Content



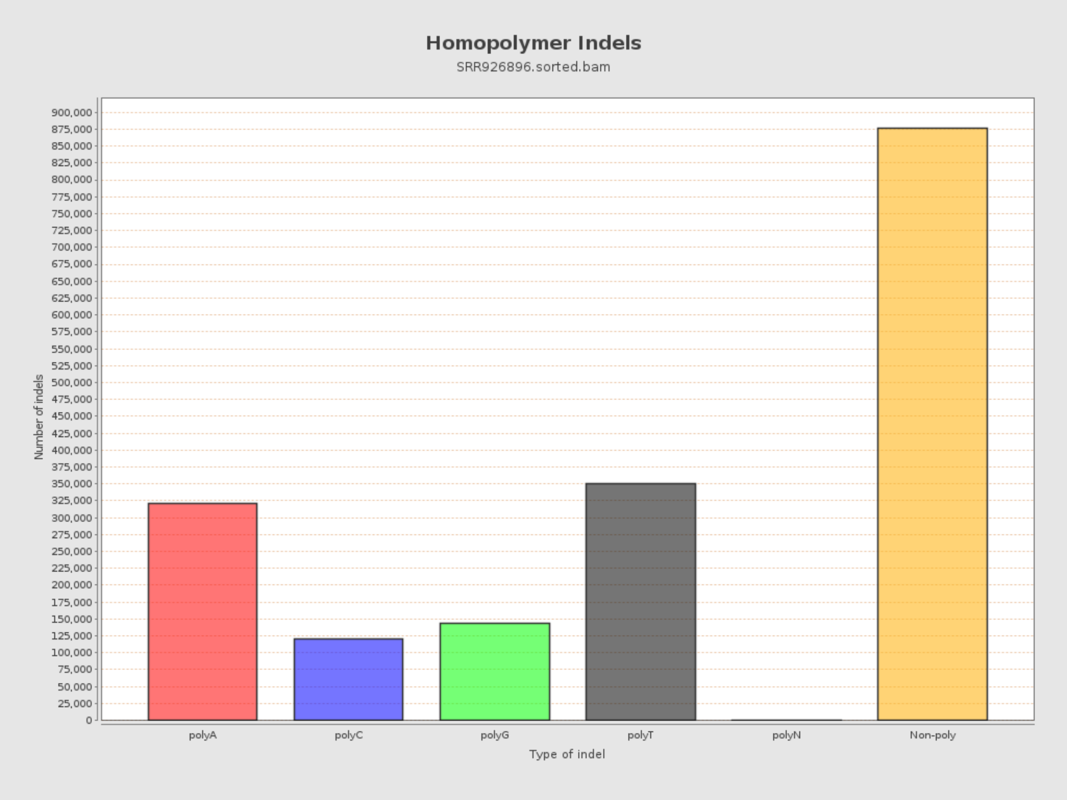
9. Results : Mapped Reads GC-content Distribution



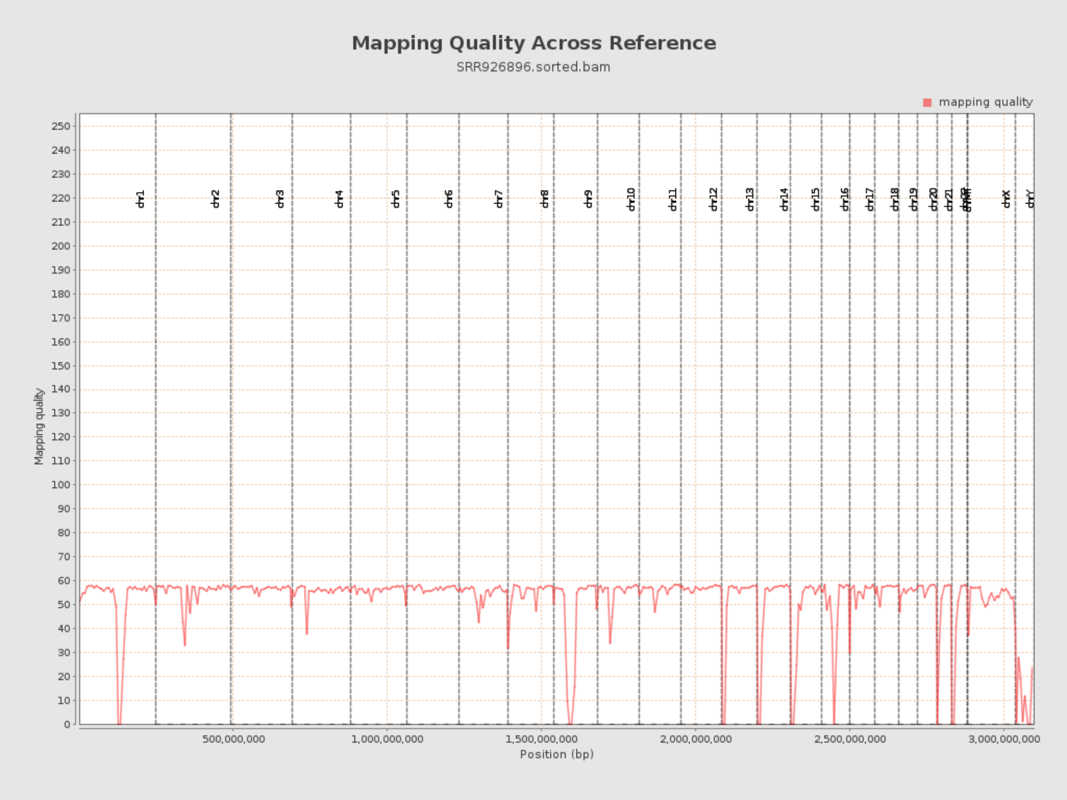
10. Results : Mapped Reads Clipping Profile



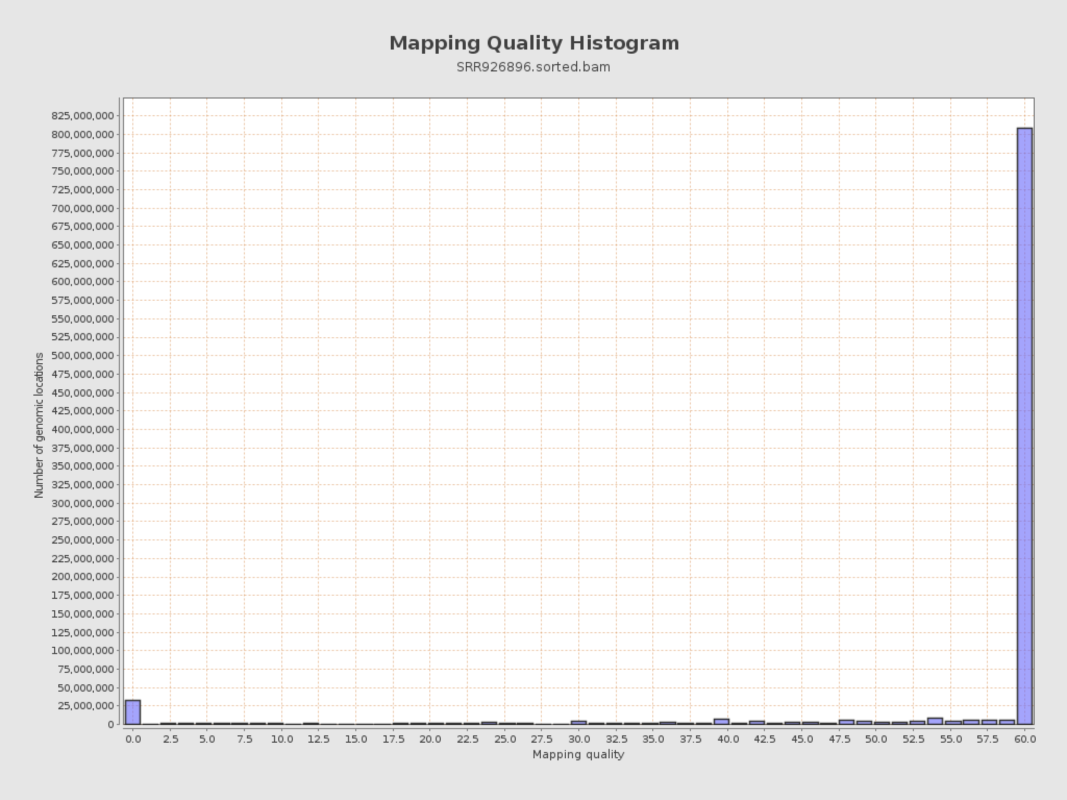
11. Results : Homopolymer Indels



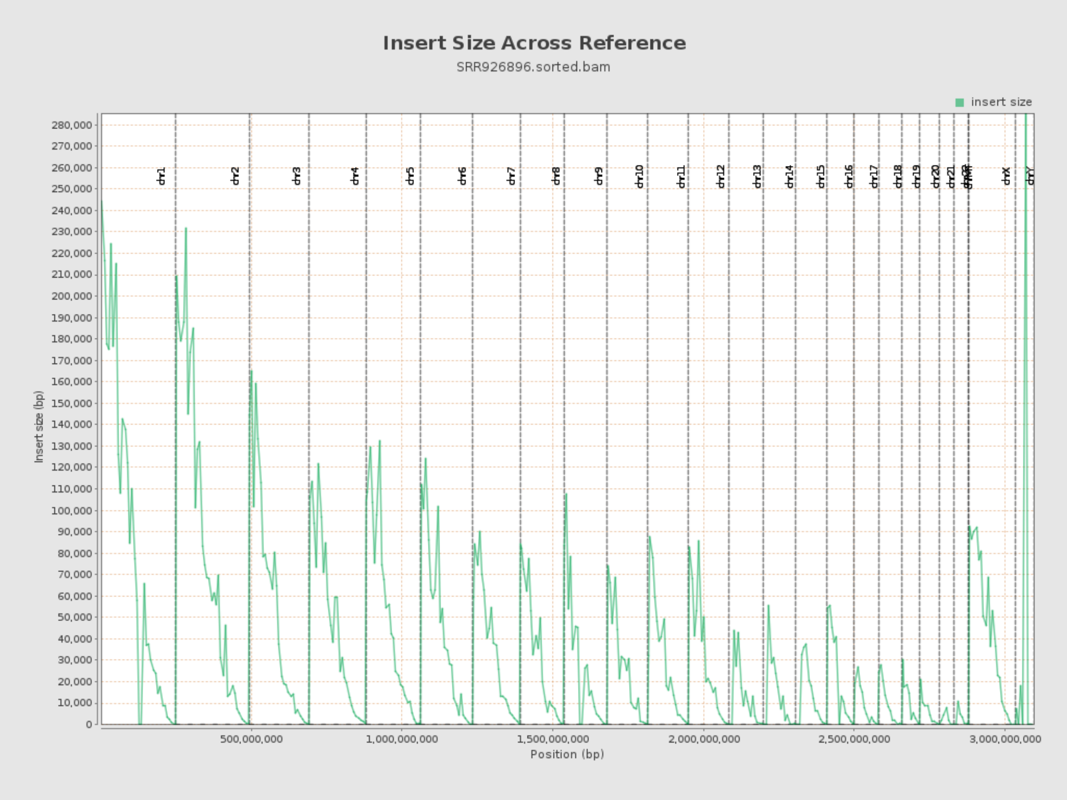
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram