Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 10:51:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926906.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_SRR926906 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926906_1.fastq.gz SRR926906_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 10:51:55 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926906.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,865,384
Mapped reads	28,012,864 / 97.05%
Unmapped reads	852,520 / 2.95%
Mapped paired reads	28,012,864 / 97.05%
Mapped reads, first in pair	14,012,539 / 48.54%
Mapped reads, second in pair	14,000,325 / 48.5%
Mapped reads, both in pair	27,645,202 / 95.77%
Mapped reads, singletons	367,662 / 1.27%
Secondary alignments	0
Supplementary alignments	1,249,539 / 4.33%
Read min/max/mean length	30 / 101 / 102.81
Duplicated reads (estimated)	2,743,252 / 9.5%
Duplication rate	7.62%
Clipped reads	13,181,447 / 45.67%

2.2. ACGT Content

Number/percentage of A's	717,951,620 / 28.21%
Number/percentage of C's	505,777,556 / 19.87%
Number/percentage of T's	724,448,151 / 28.47%
Number/percentage of G's	596,398,762 / 23.44%
Number/percentage of N's	287,510 / 0.01%

GC Percentage	43.31%

2.3. Coverage

Mean	0.8227
Standard Deviation	3.6333

2.4. Mapping Quality

Mean Mapping Quality	52.11

2.5. Insert size

Mean	488,636.86
Standard Deviation	6,883,332.33
P25/Median/P75	131 / 169 / 224

2.6. Mismatches and indels

General error rate	1.01%
Mismatches	24,971,842
Insertions	448,147
Mapped reads with at least one insertion	1.57%
Deletions	1,373,641
Mapped reads with at least one deletion	4.78%
Homopolymer indels	51.48%

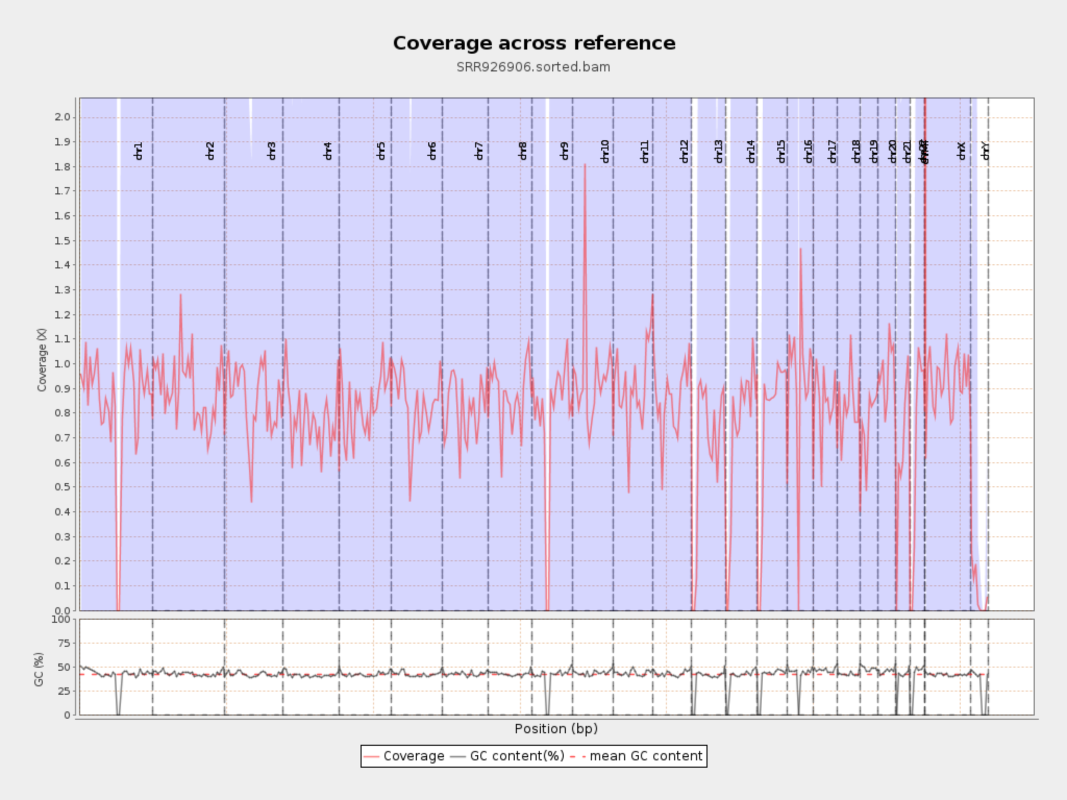
2.7. Chromosome stats

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

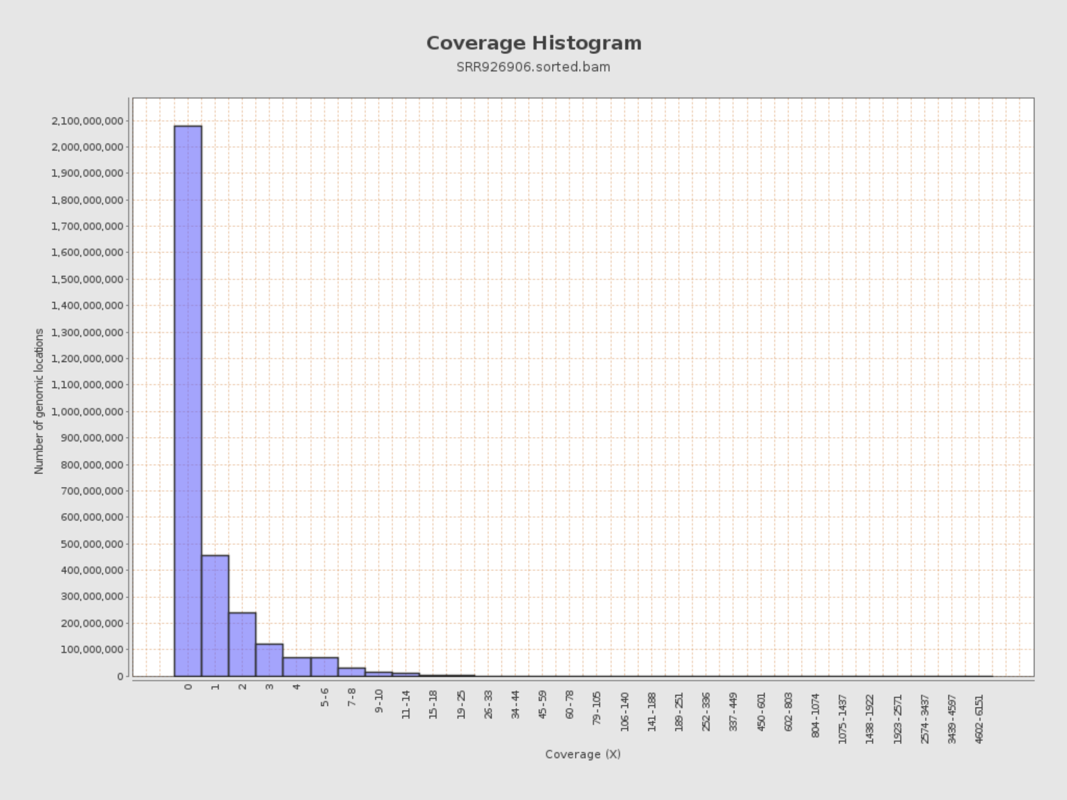
		bases	coverage	deviation
chr1	249250621	210327131	0.8438	2.6369
chr2	243199373	218893172	0.9001	5.4559
chr3	198022430	170405567	0.8605	1.9784
chr4	191154276	148896236	0.7789	2.0344
chr5	180915260	152237708	0.8415	1.7666
chr6	171115067	143599934	0.8392	1.7742
chr7	159138663	130331685	0.819	2.1702
chr8	146364022	128174921	0.8757	1.9754
chr9	141213431	110437275	0.7821	3.3395
chr10	135534747	129787758	0.9576	11.5407
chr11	135006516	121961351	0.9034	2.4416
chr12	133851895	115266052	0.8611	1.9043
chr13	115169878	75160764	0.6526	1.5528
chr14	107349540	76507179	0.7127	1.6888
chr15	102531392	76041918	0.7416	1.7473
chr16	90354753	83511227	0.9243	5.3527
chr17	81195210	68228074	0.8403	2.0087
chr18	78077248	66314452	0.8493	3.2513
chr19	59128983	44552802	0.7535	2.0392
chr20	63025520	60765846	0.9641	2.076
chr21	48129895	32236993	0.6698	2.5622
chr22	51304566	33327804	0.6496	1.7643
chrMT	16571	2311260	139.4762	92.2752
chrX	155270560	143351893	0.9232	1.9513

chrY	59373566	4276266	0.072	2.0598

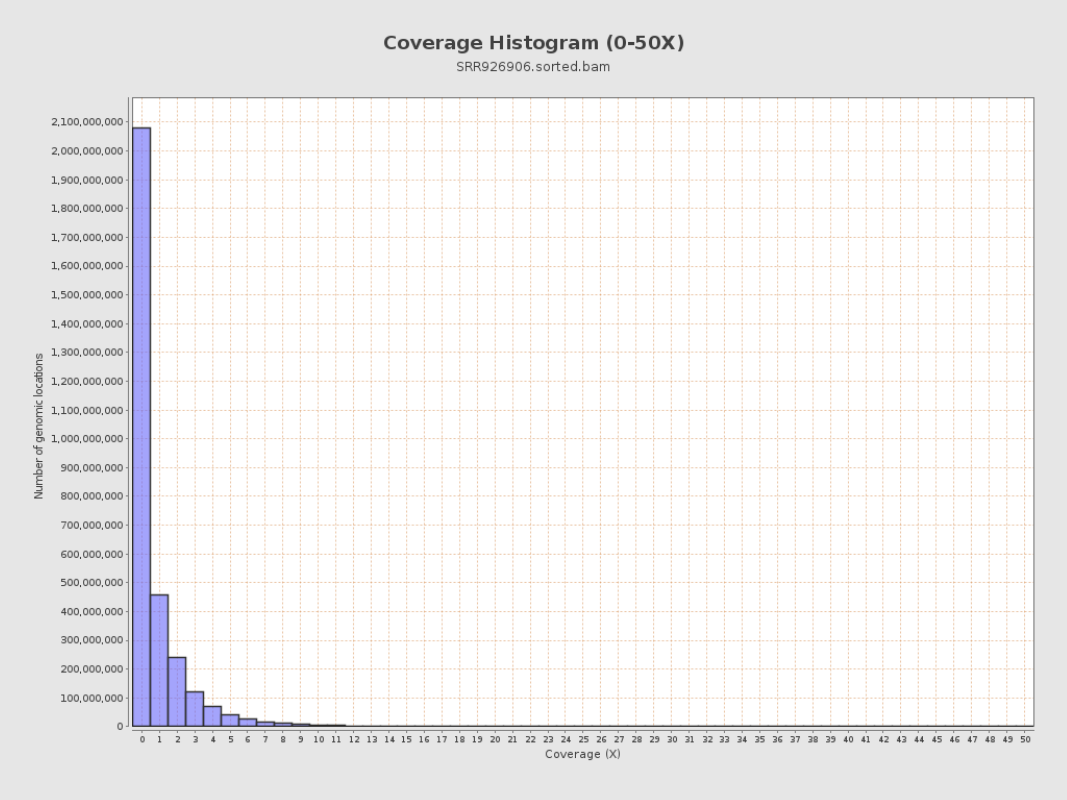
3. Results : Coverage across reference



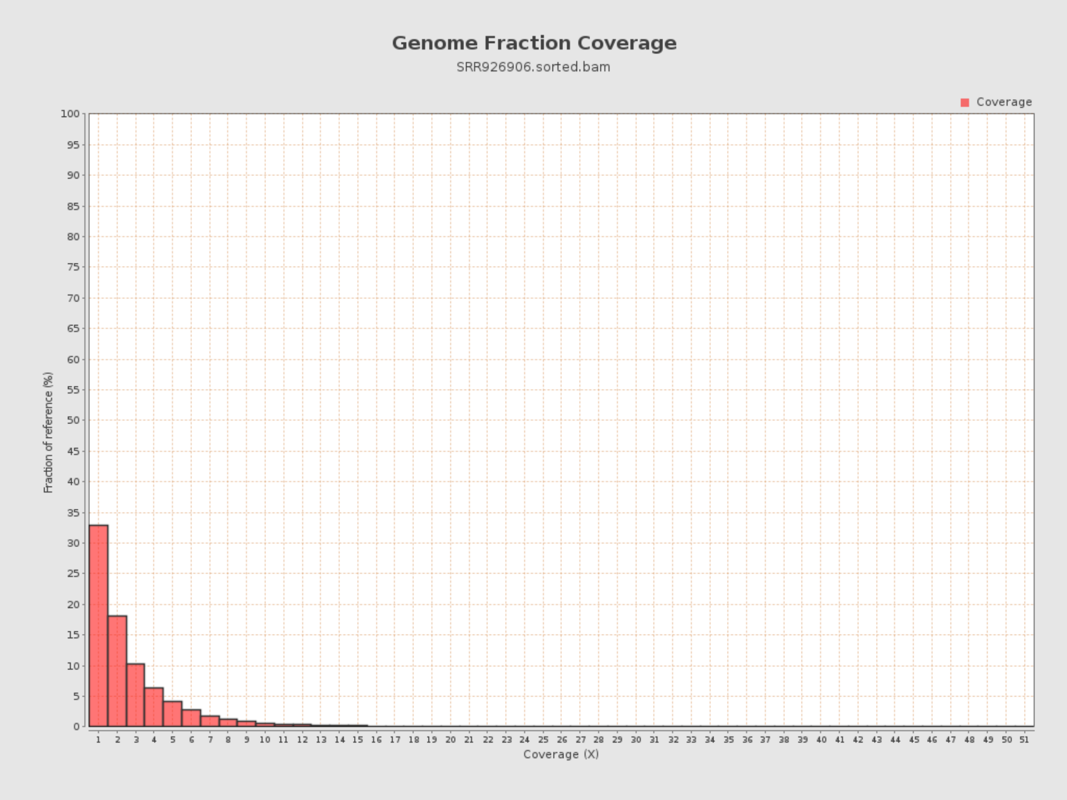
4. Results : Coverage Histogram



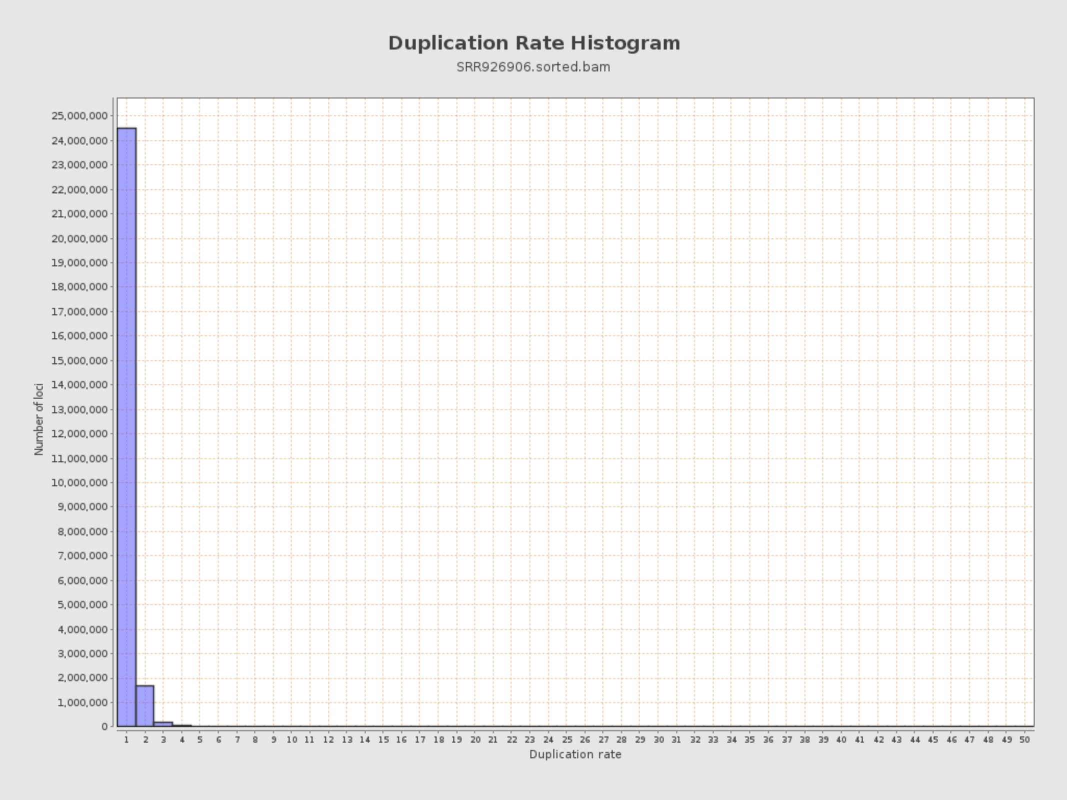
5. Results : Coverage Histogram (0-50X)



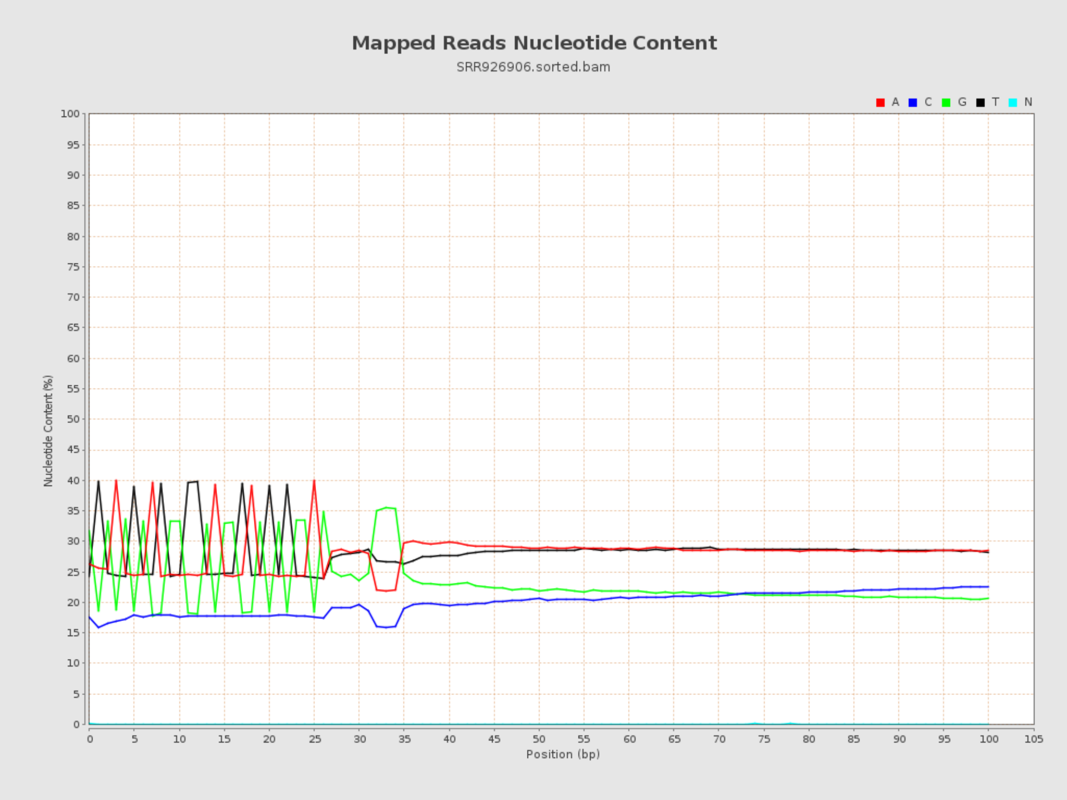
6. Results : Genome Fraction Coverage



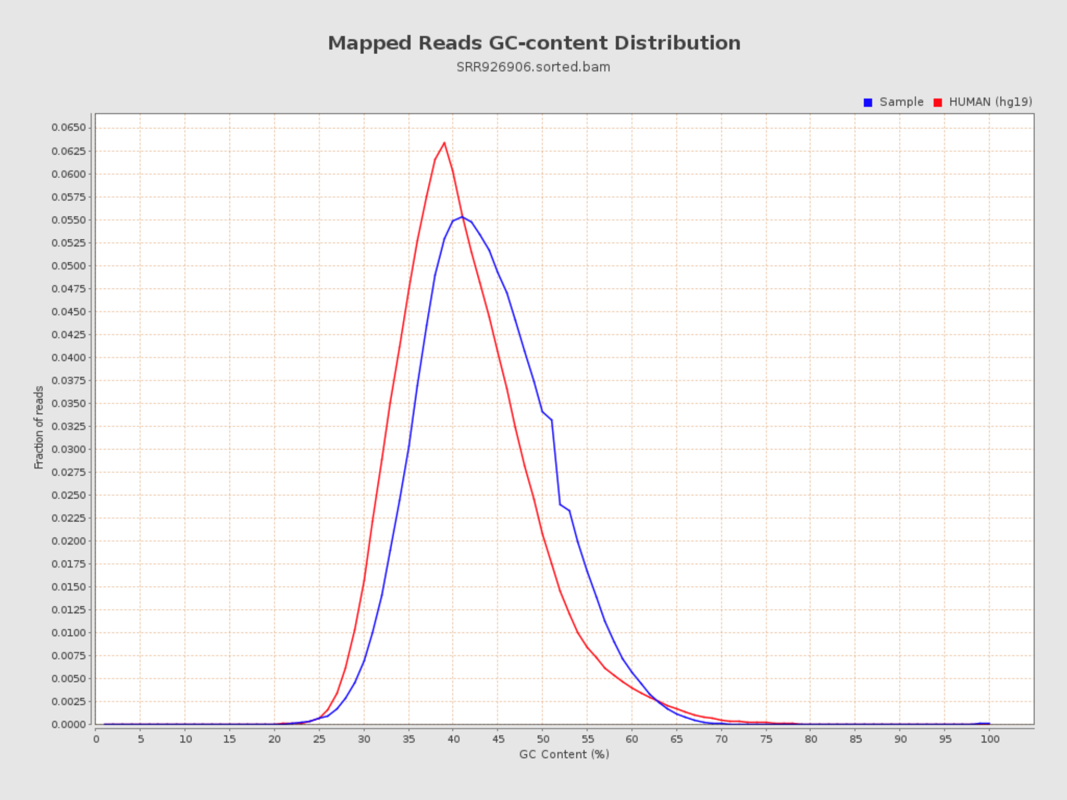
7. Results : Duplication Rate Histogram



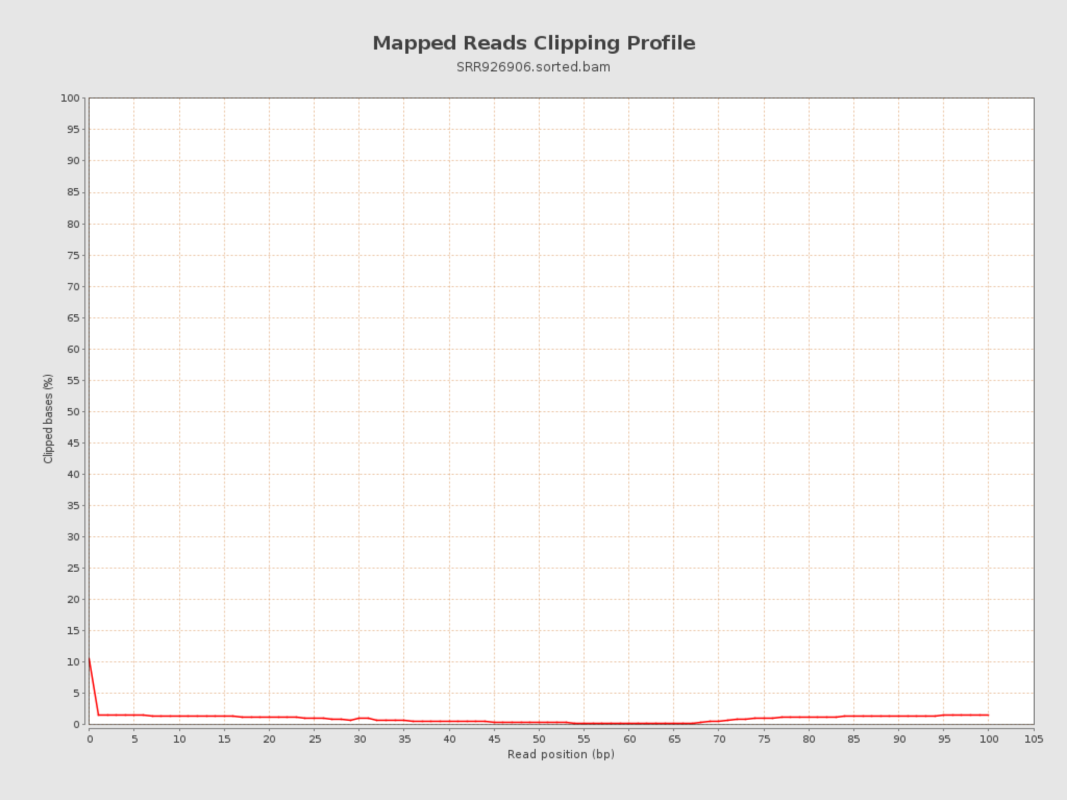
8. Results : Mapped Reads Nucleotide Content



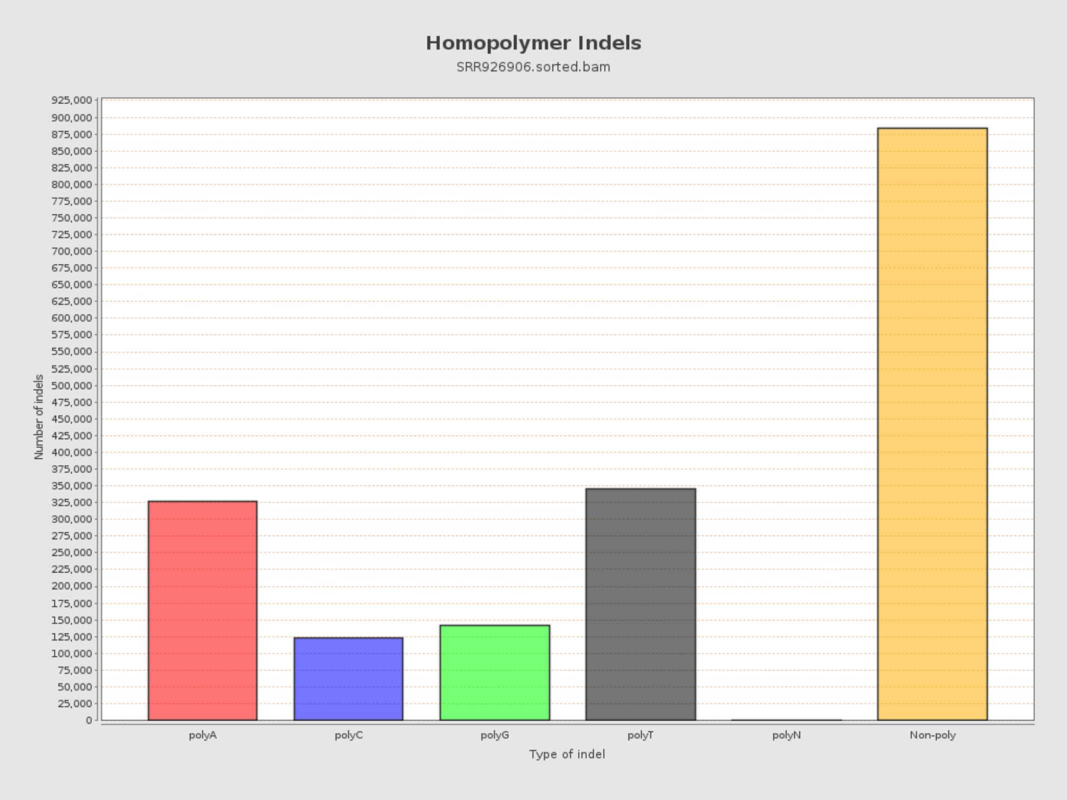
9. Results : Mapped Reads GC-content Distribution



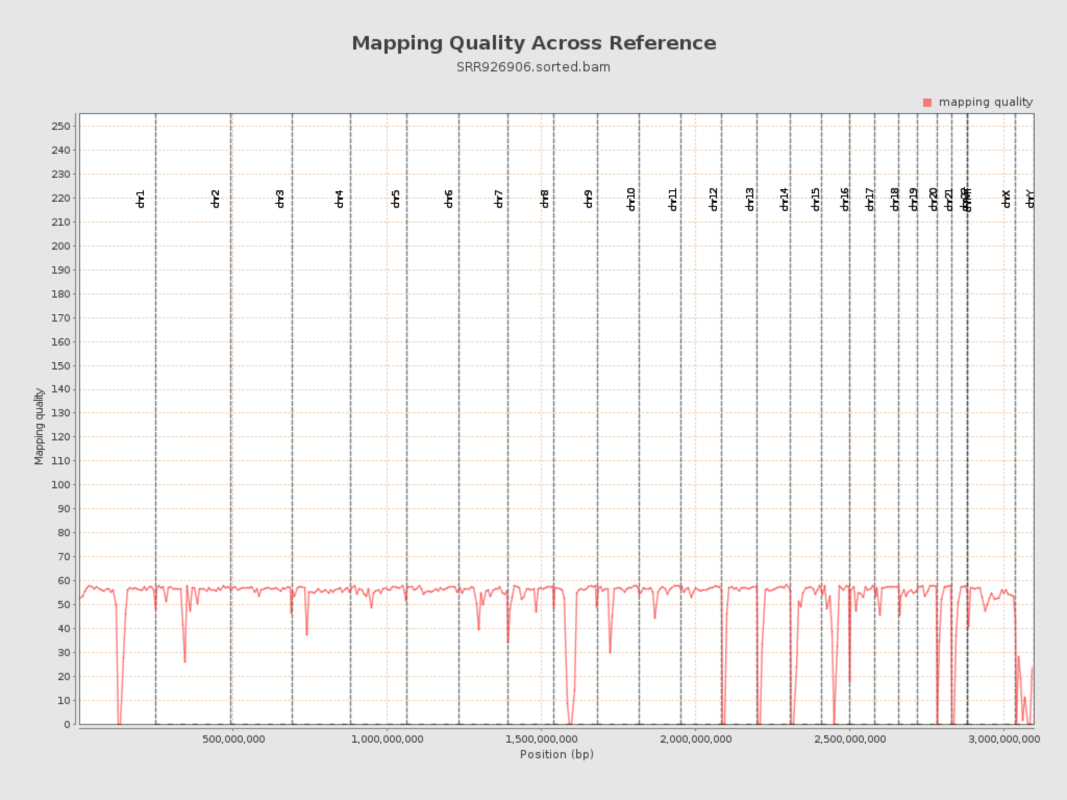
10. Results : Mapped Reads Clipping Profile



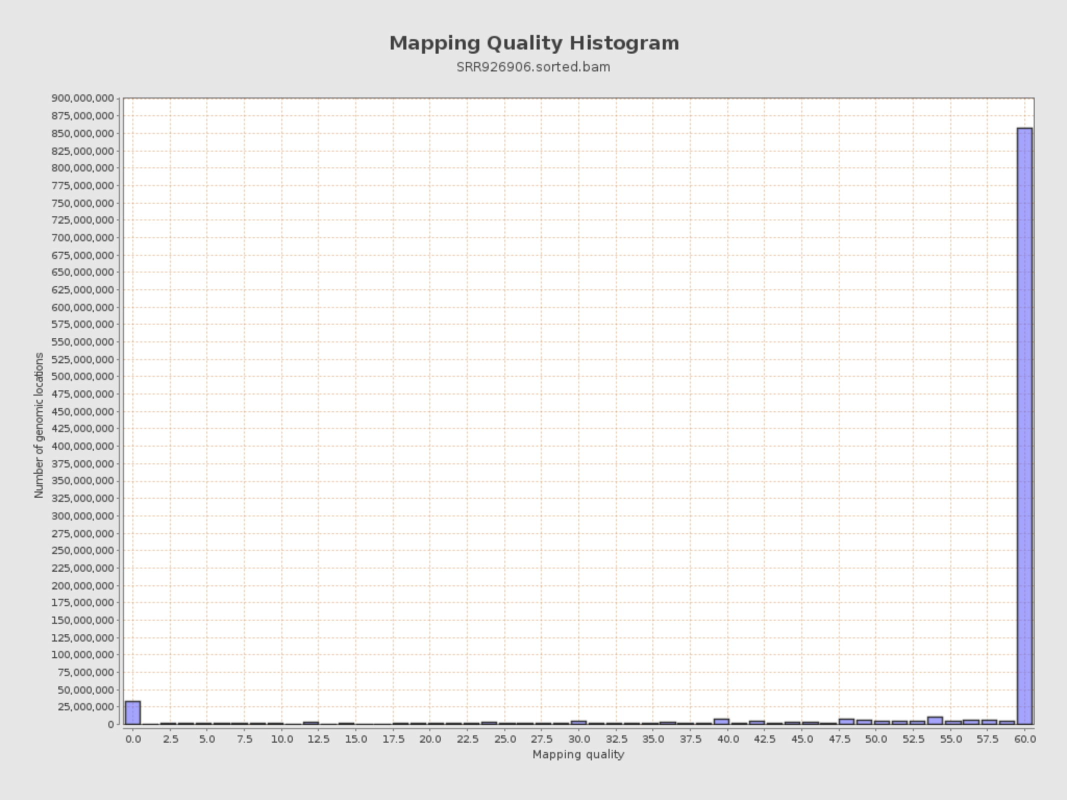
11. Results : Homopolymer Indels



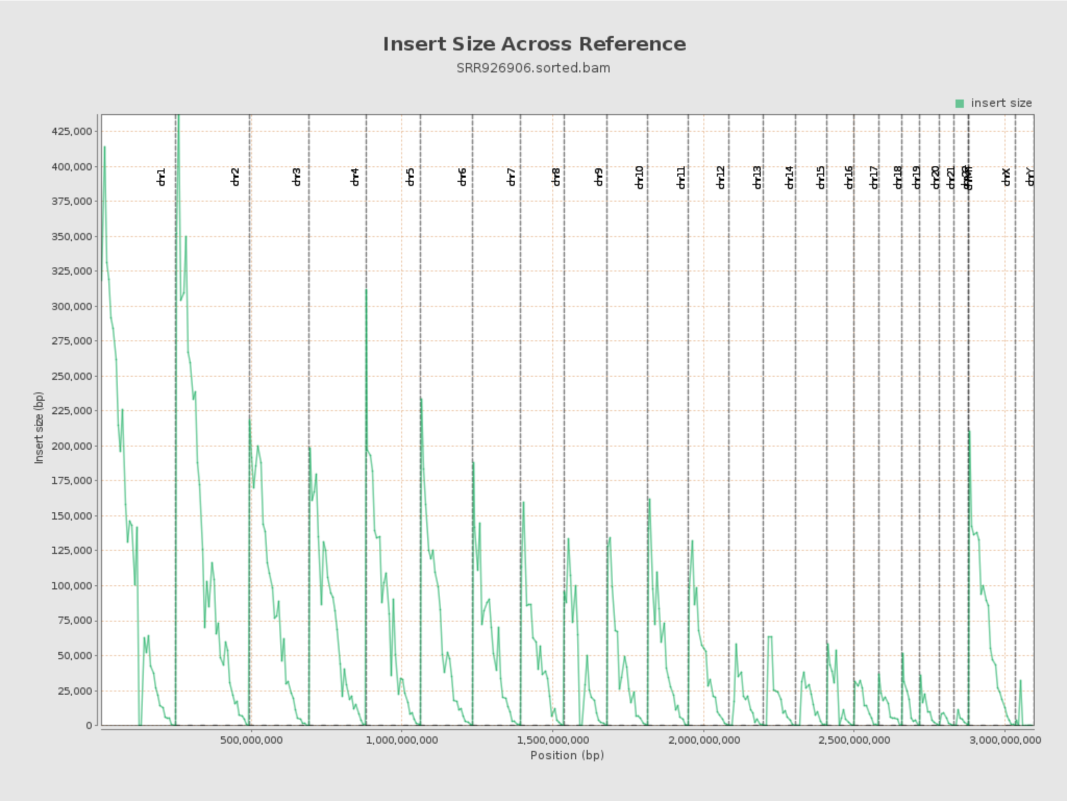
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram