Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 11:51:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926908.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_SRR926908 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926908_1.fastq.gz SRR926908_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 11:51:16 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926908.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,974,058
Mapped reads	25,218,204 / 93.49%
Unmapped reads	1,755,854 / 6.51%
Mapped paired reads	25,218,204 / 93.49%
Mapped reads, first in pair	12,678,178 / 47%
Mapped reads, second in pair	12,540,026 / 46.49%
Mapped reads, both in pair	24,920,456 / 92.39%
Mapped reads, singletons	297,748 / 1.1%
Secondary alignments	0
Supplementary alignments	226,512 / 0.84%
Read min/max/mean length	30 / 101 / 101.34
Duplicated reads (estimated)	1,640,374 / 6.08%
Duplication rate	5.23%
Clipped reads	6,902,726 / 25.59%

2.2. ACGT Content

Number/percentage of A's	674,572,027 / 28.52%
Number/percentage of C's	472,812,916 / 19.99%
Number/percentage of T's	680,166,543 / 28.76%
Number/percentage of G's	537,201,606 / 22.71%
Number/percentage of N's	223,518 / 0.01%

GC Percentage	42.71%

2.3. Coverage

Mean	0.7646
Standard Deviation	2.6402

2.4. Mapping Quality

Mean Mapping Quality	53.52

2.5. Insert size

Mean	100,558.83
Standard Deviation	3,127,457.63
P25/Median/P75	155 / 198 / 262

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	24,548,634
Insertions	383,649
Mapped reads with at least one insertion	1.5%
Deletions	1,304,164
Mapped reads with at least one deletion	5.03%
Homopolymer indels	53.02%

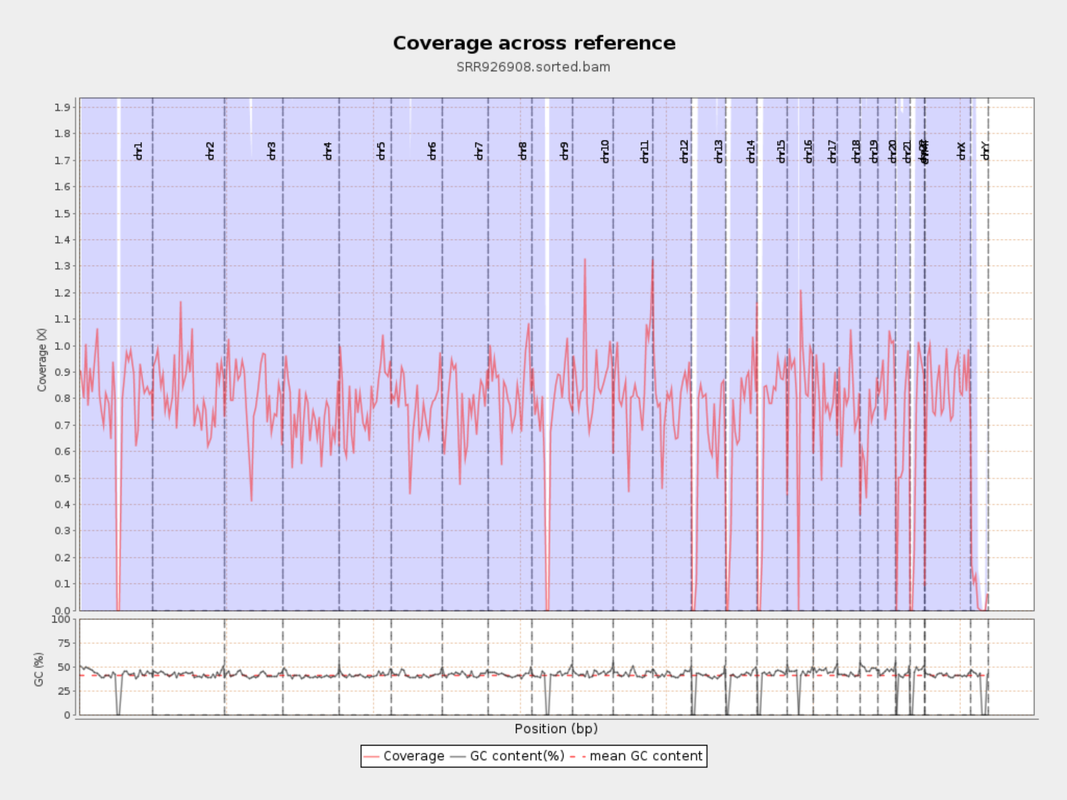
2.7. Chromosome stats

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

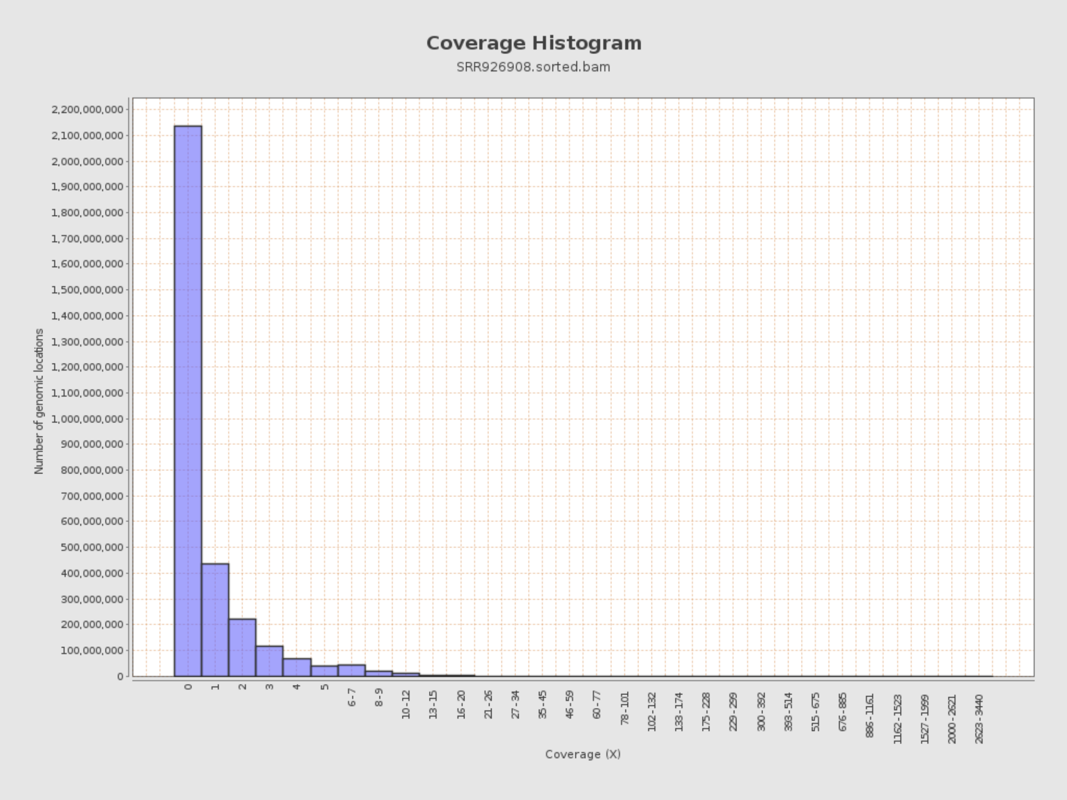
		bases	coverage	deviation
chr1	249250621	197479778	0.7923	2.663
chr2	243199373	203322043	0.836	3.6099
chr3	198022430	160632485	0.8112	1.7203
chr4	191154276	139369661	0.7291	1.8097
chr5	180915260	144001074	0.796	1.6729
chr6	171115067	132185297	0.7725	1.6661
chr7	159138663	121616777	0.7642	1.7578
chr8	146364022	122600453	0.8376	1.9074
chr9	141213431	101535326	0.719	2.5449
chr10	135534747	119620122	0.8826	7.0049
chr11	135006516	113670543	0.842	2.0235
chr12	133851895	104858497	0.7834	1.7385
chr13	115169878	70995410	0.6164	1.4692
chr14	107349540	71631973	0.6673	1.5968
chr15	102531392	70804729	0.6906	1.6614
chr16	90354753	75536803	0.836	4.4369
chr17	81195210	63138369	0.7776	1.9246
chr18	78077248	62919814	0.8059	2.6537
chr19	59128983	39034196	0.6602	1.8729
chr20	63025520	56241295	0.8924	1.9222
chr21	48129895	29940377	0.6221	2.299
chr22	51304566	31279918	0.6097	1.6468
chrMT	16571	1568	0.0946	0.4084
chrX	155270560	131096876	0.8443	1.7883

chrY	59373566	3307581	0.0557	1.2466

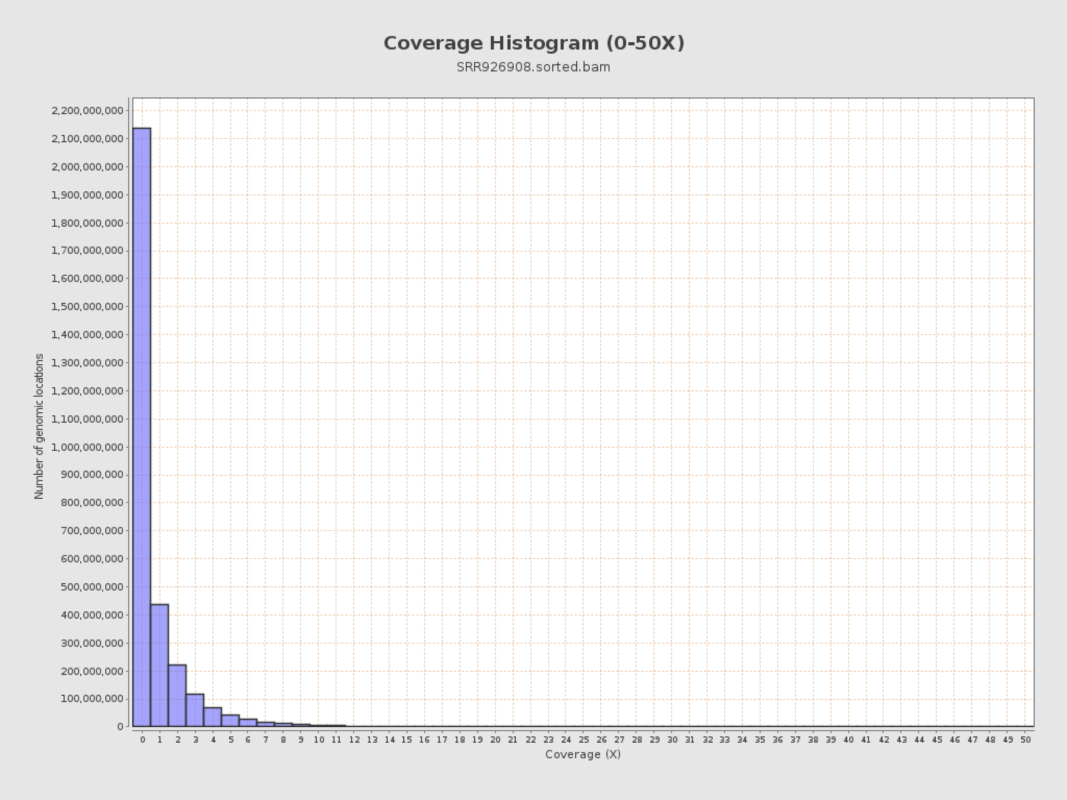
3. Results : Coverage across reference



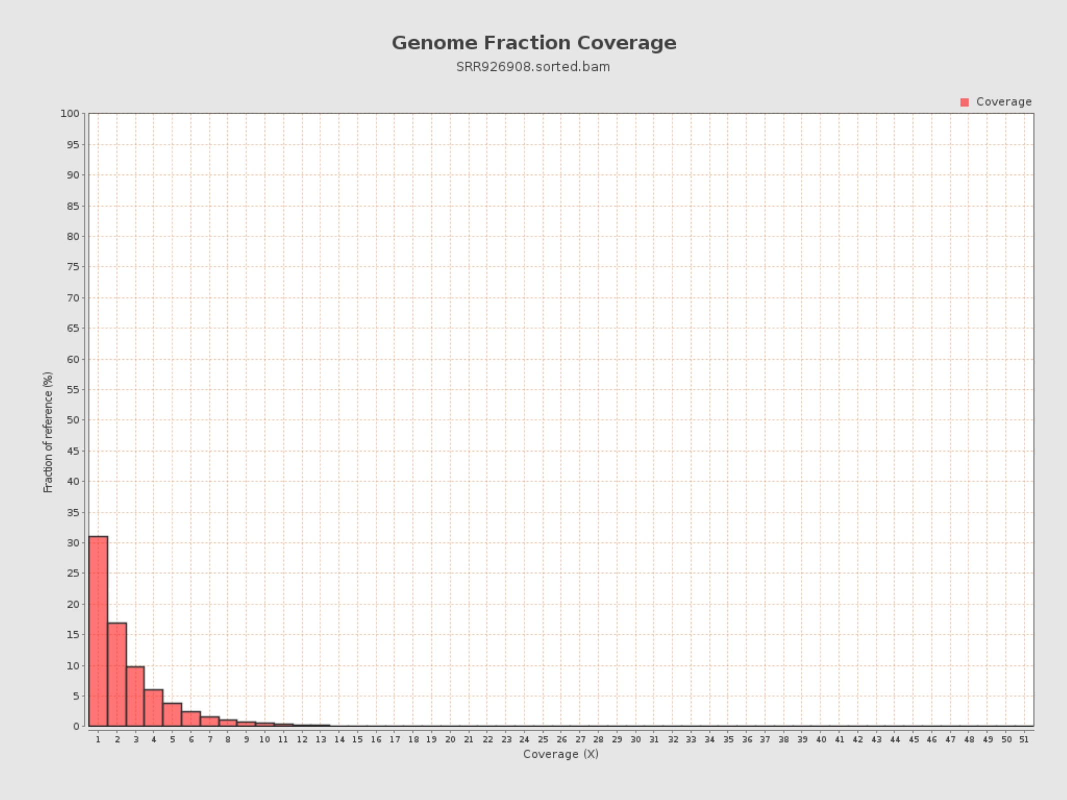
4. Results : Coverage Histogram



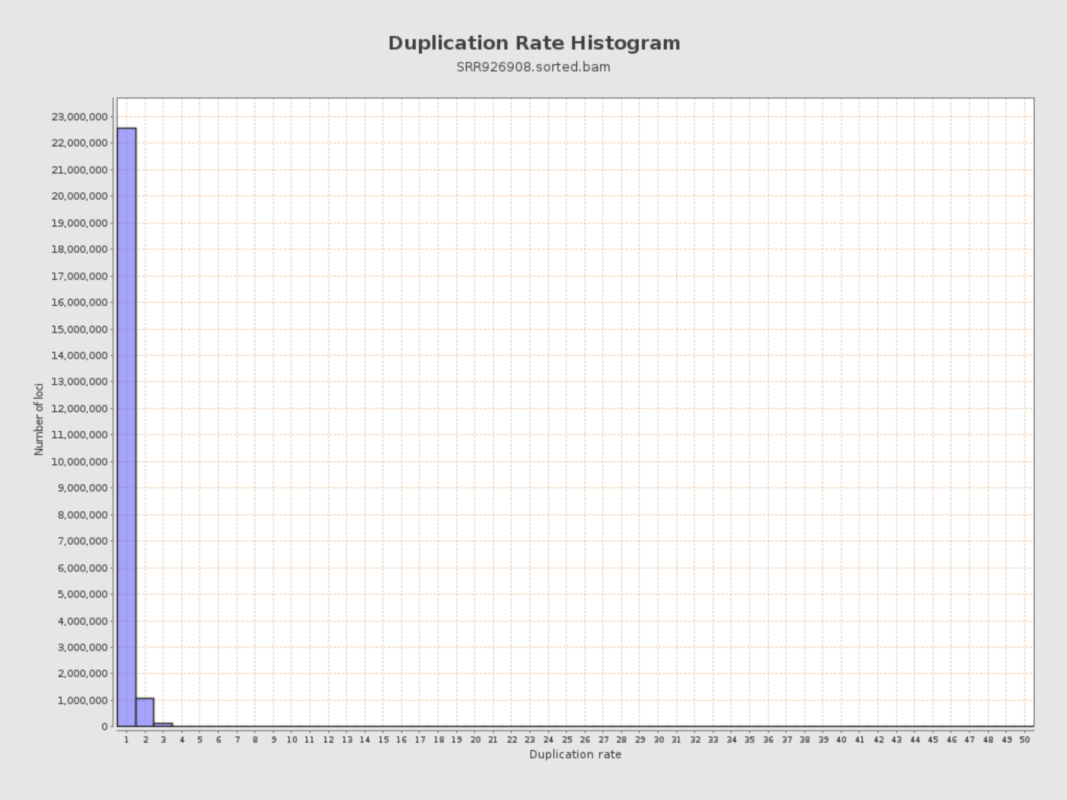
5. Results : Coverage Histogram (0-50X)



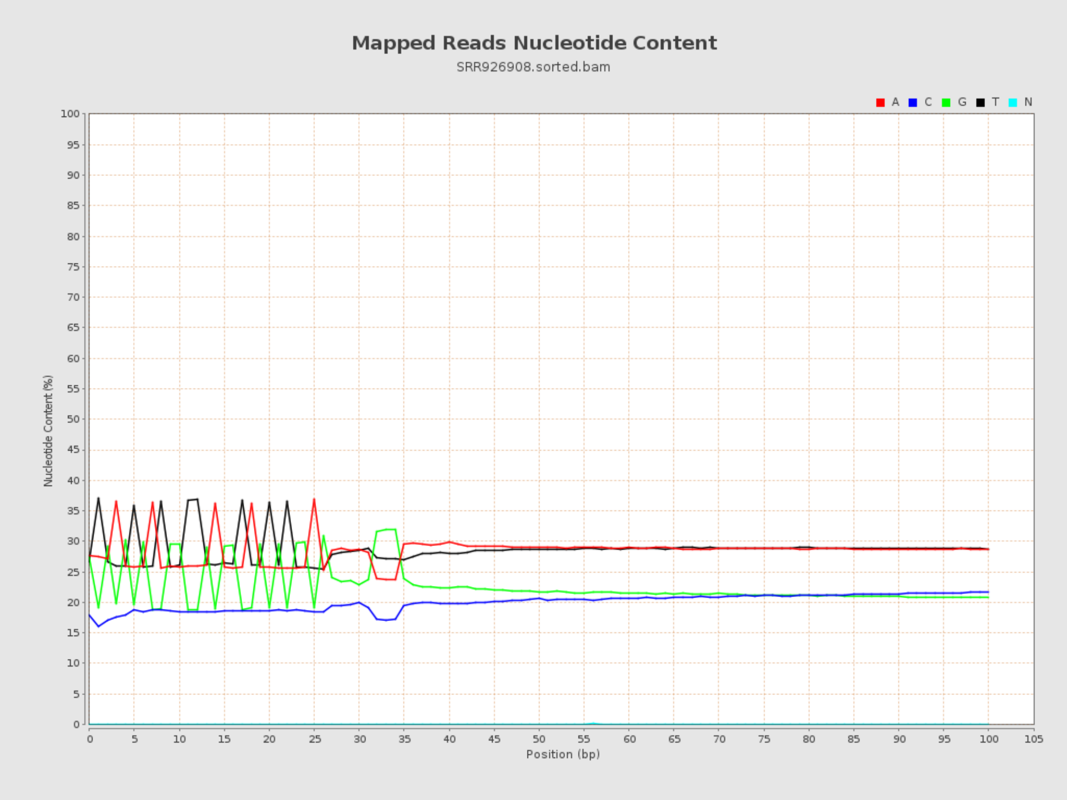
6. Results : Genome Fraction Coverage



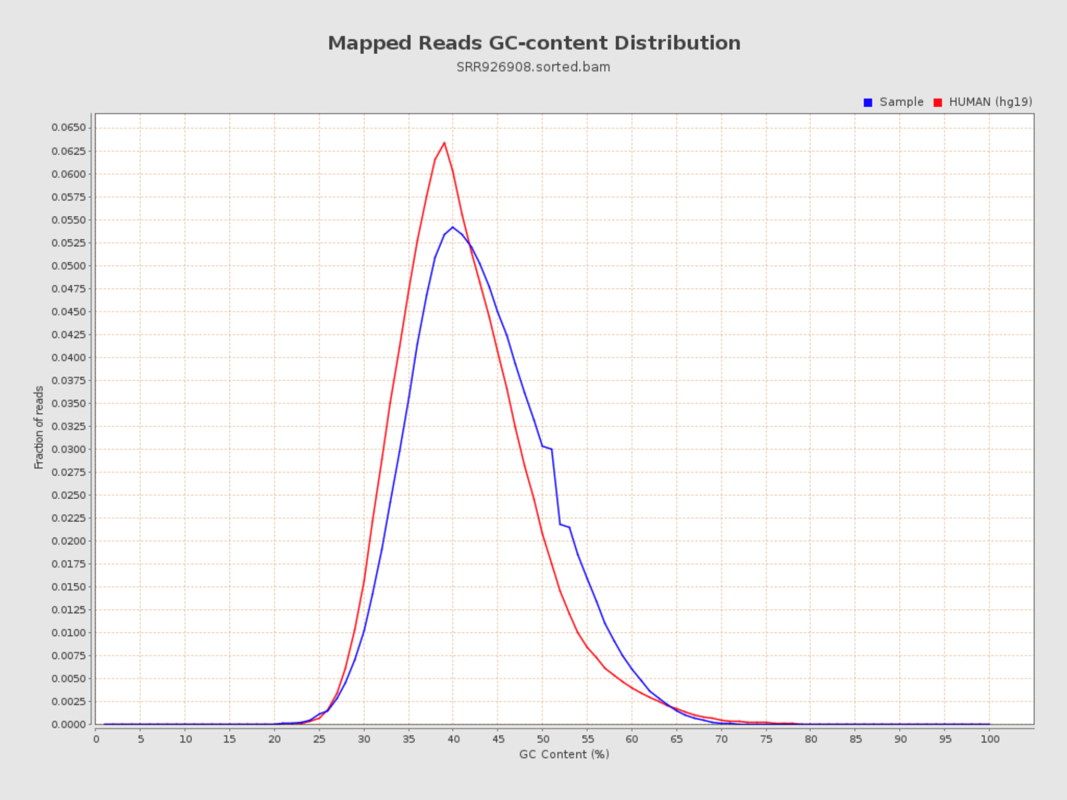
7. Results : Duplication Rate Histogram



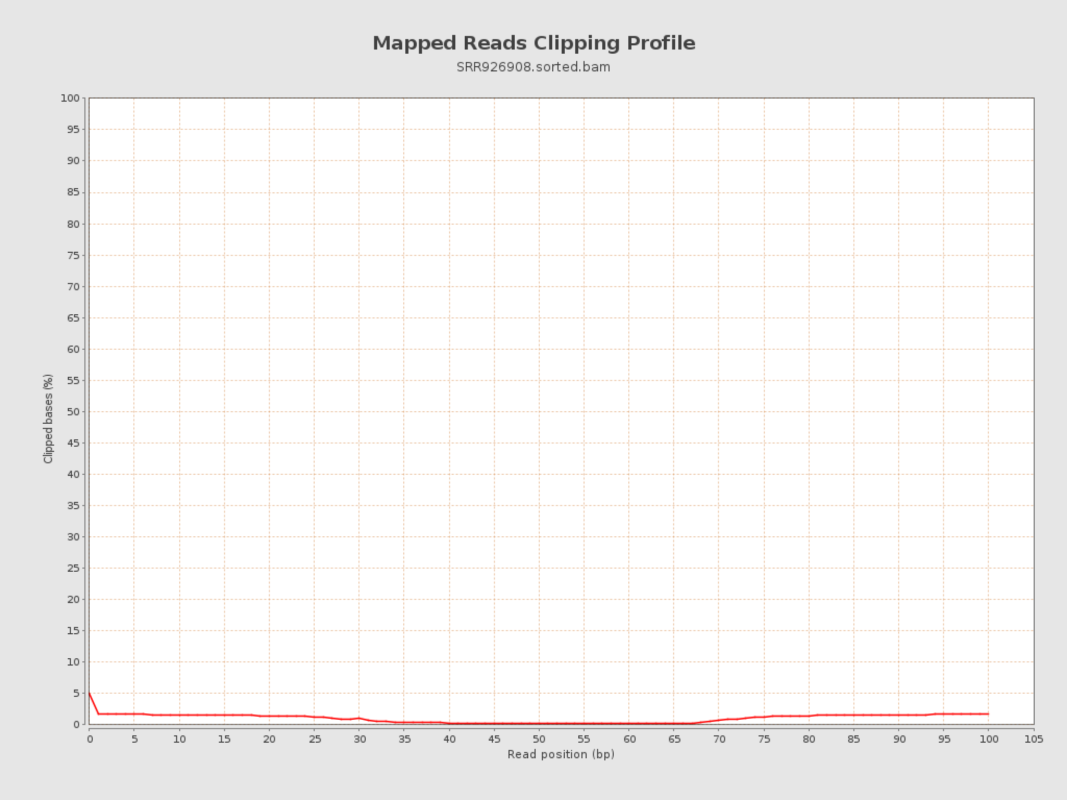
8. Results : Mapped Reads Nucleotide Content



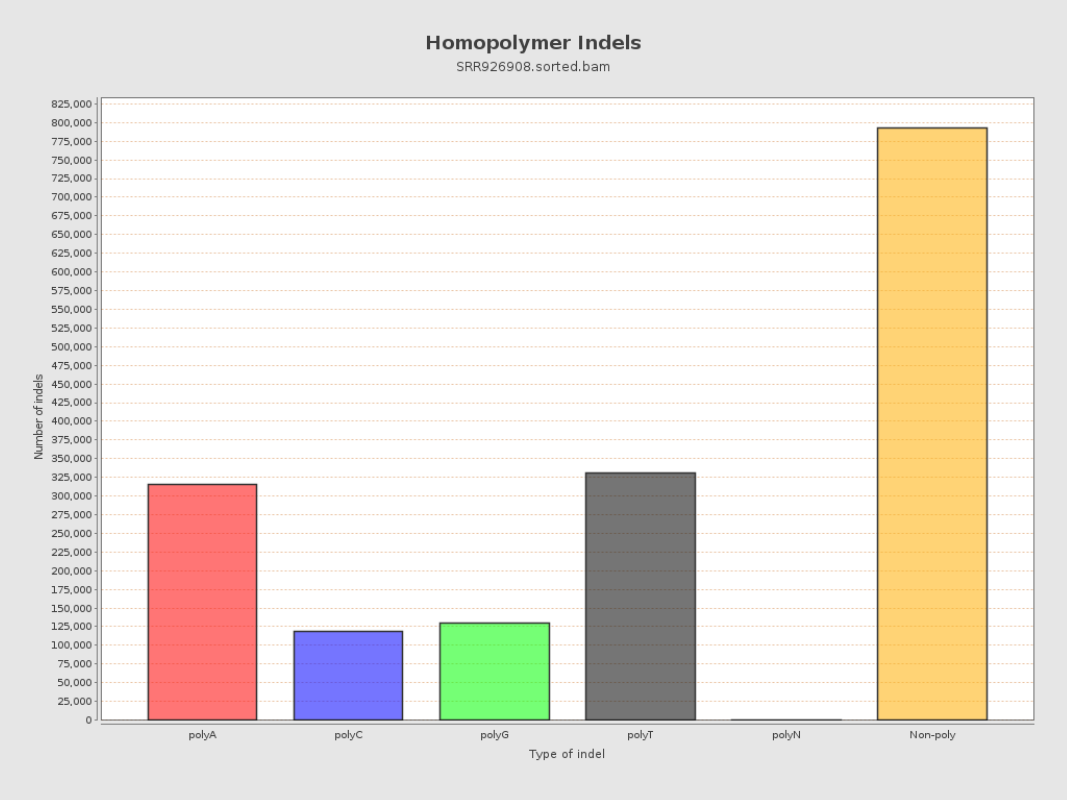
9. Results : Mapped Reads GC-content Distribution



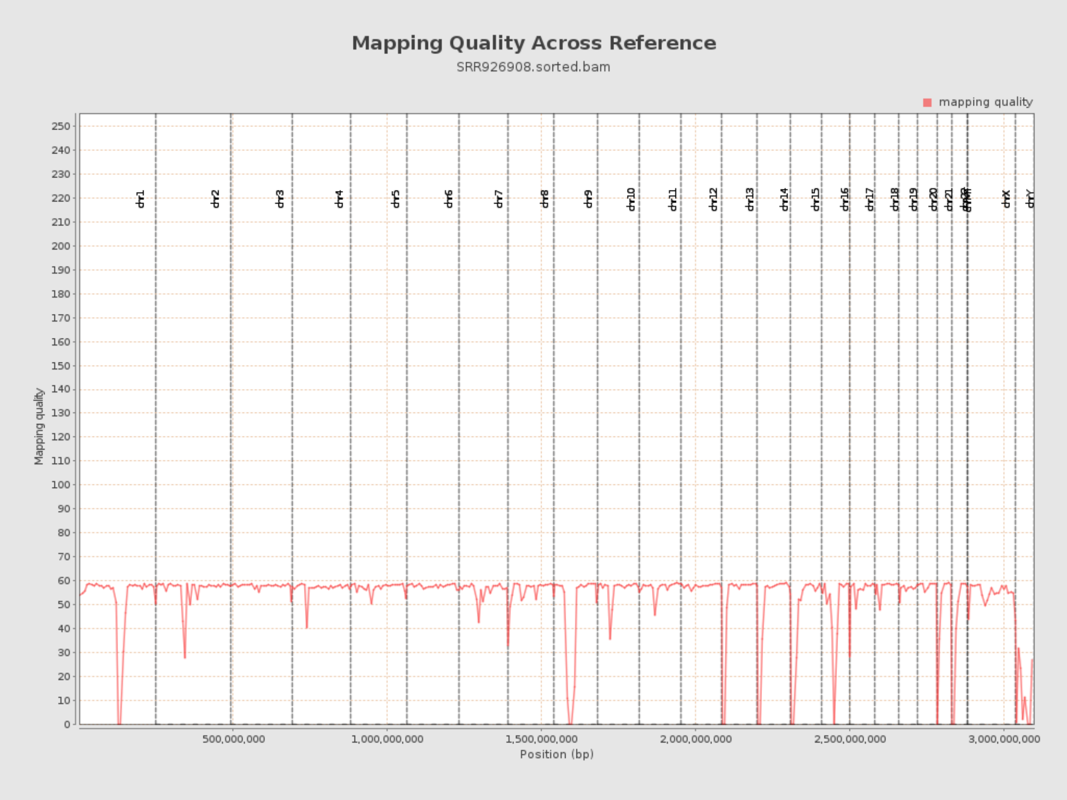
10. Results : Mapped Reads Clipping Profile



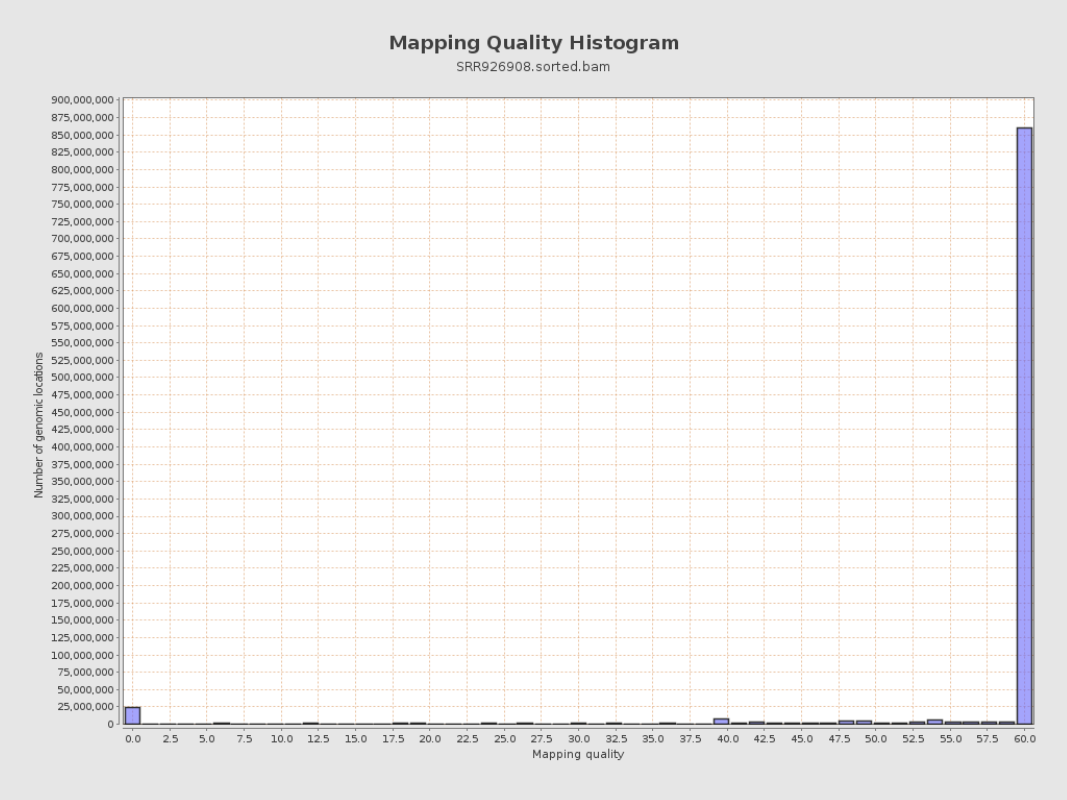
11. Results : Homopolymer Indels



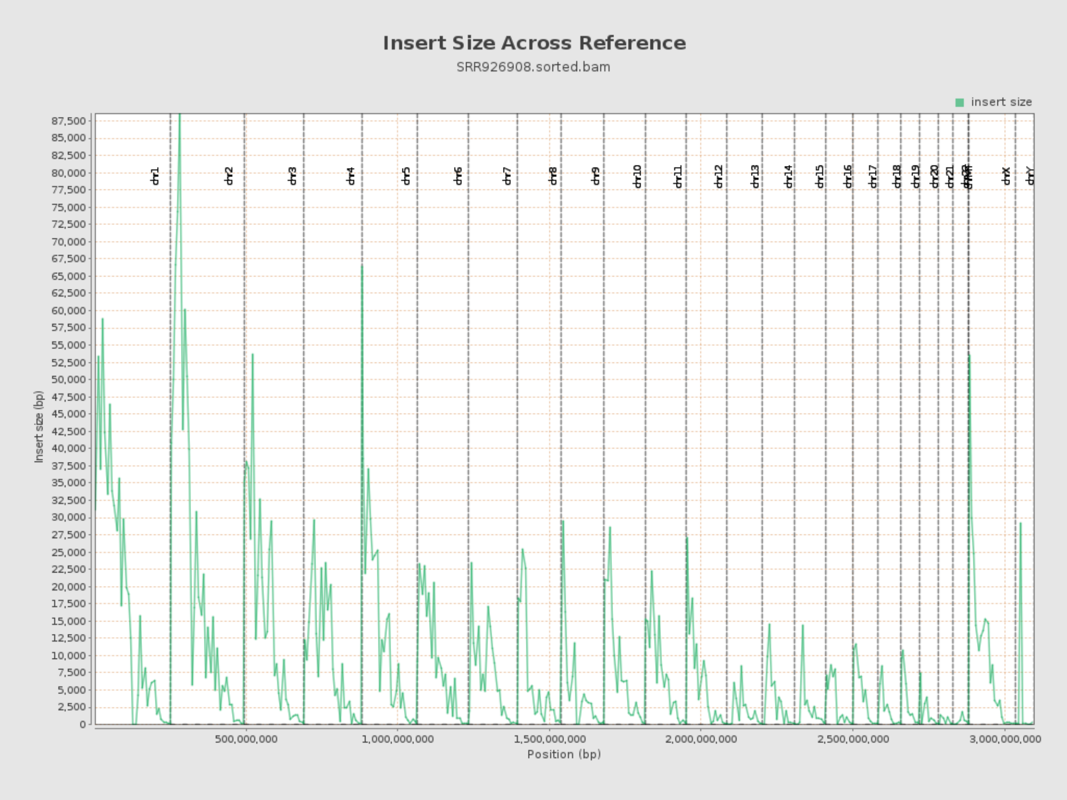
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram