Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 17:24:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926918.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_SRR926918 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926918_1.fastq.gz SRR926918_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 17:24:49 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926918.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,257,728
Mapped reads	25,076,174 / 95.5%
Unmapped reads	1,181,554 / 4.5%
Mapped paired reads	25,076,174 / 95.5%
Mapped reads, first in pair	12,630,702 / 48.1%
Mapped reads, second in pair	12,445,472 / 47.4%
Mapped reads, both in pair	24,577,604 / 93.6%
Mapped reads, singletons	498,570 / 1.9%
Secondary alignments	0
Supplementary alignments	827,917 / 3.15%
Read min/max/mean length	30 / 101 / 102.3
Duplicated reads (estimated)	2,718,647 / 10.35%
Duplication rate	8.48%
Clipped reads	12,669,566 / 48.25%

2.2. ACGT Content

Number/percentage of A's	636,311,538 / 28.56%
Number/percentage of C's	424,986,616 / 19.07%
Number/percentage of T's	648,920,842 / 29.12%
Number/percentage of G's	517,726,558 / 23.24%
Number/percentage of N's	170,482 / 0.01%

GC Percentage	42.31%

2.3. Coverage

Mean	0.7203
Standard Deviation	2.7169

2.4. Mapping Quality

Mean Mapping Quality	52.44

2.5. Insert size

Mean	401,970.12
Standard Deviation	6,222,694.31
P25/Median/P75	135 / 182 / 251

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	23,509,477
Insertions	383,070
Mapped reads with at least one insertion	1.5%
Deletions	1,227,231
Mapped reads with at least one deletion	4.77%
Homopolymer indels	51.97%

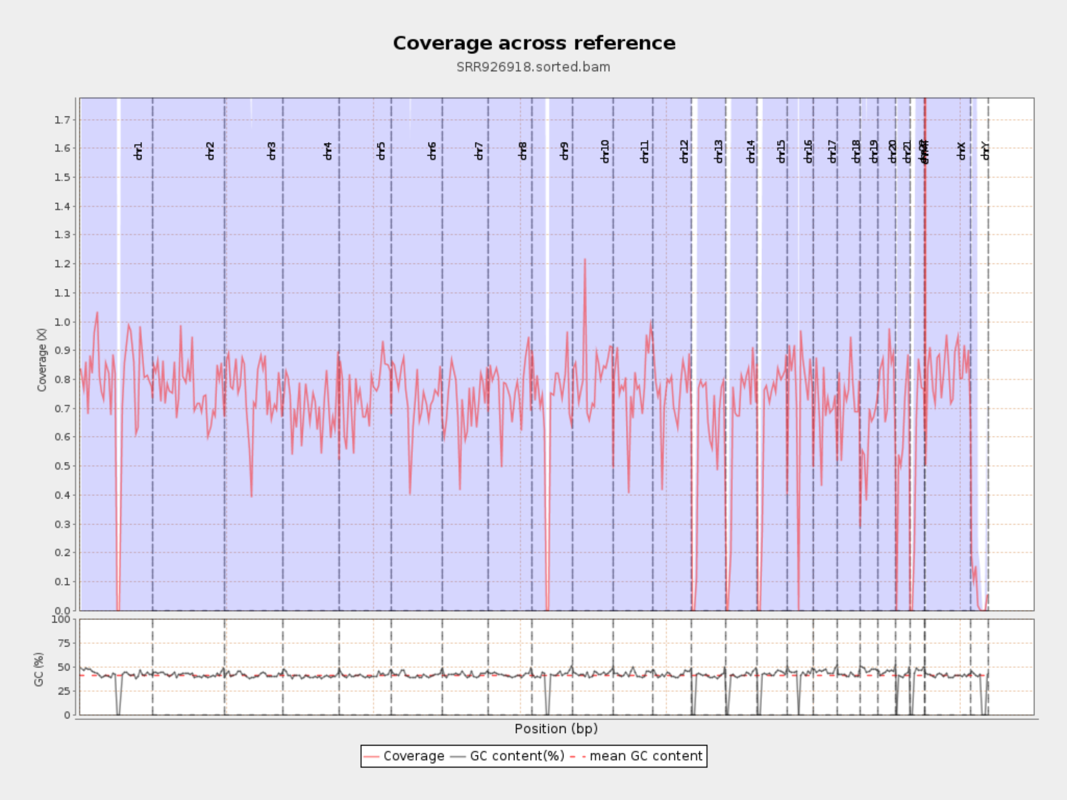
2.7. Chromosome stats

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

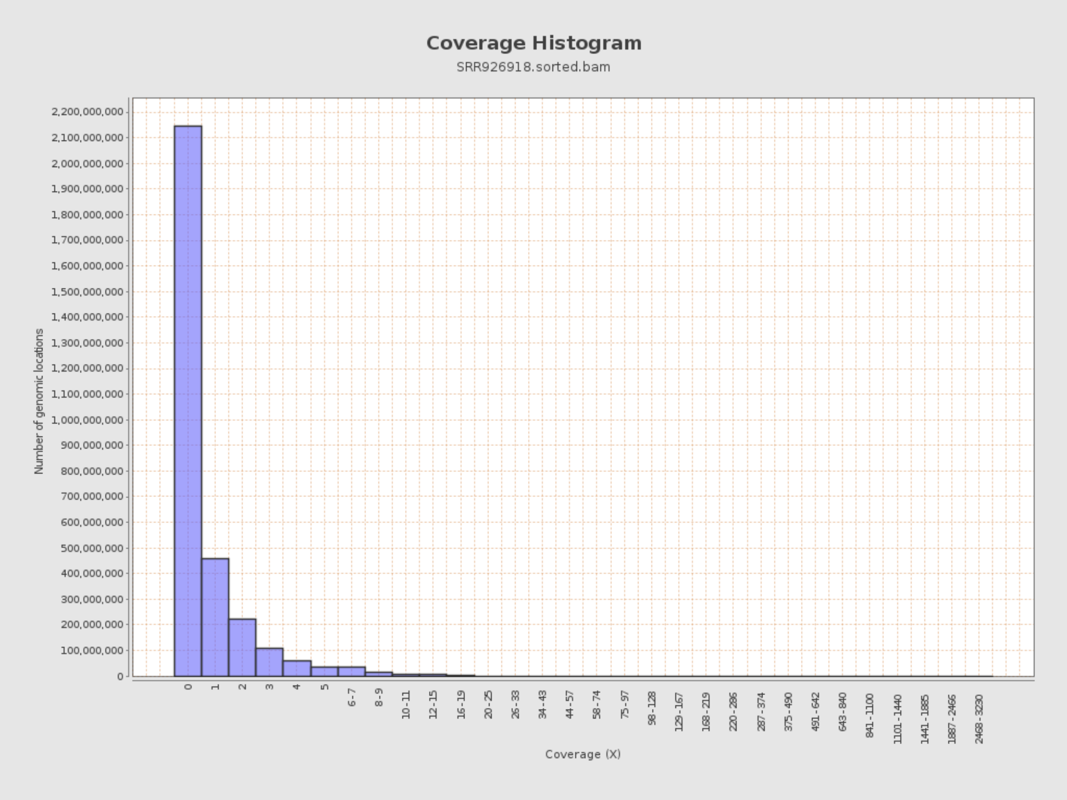
		bases	coverage	deviation
chr1	249250621	193410826	0.776	2.2736
chr2	243199373	188019959	0.7731	3.2044
chr3	198022430	150348922	0.7593	1.692
chr4	191154276	134586948	0.7041	1.7471
chr5	180915260	135763940	0.7504	1.6333
chr6	171115067	127083441	0.7427	1.6309
chr7	159138663	113240100	0.7116	1.8398
chr8	146364022	112414786	0.768	1.7932
chr9	141213431	96545471	0.6837	2.5849
chr10	135534747	111945965	0.826	6.4809
chr11	135006516	104875730	0.7768	2.0586
chr12	133851895	101045592	0.7549	1.7924
chr13	115169878	67268880	0.5841	1.4535
chr14	107349540	67391211	0.6278	1.553
chr15	102531392	65473270	0.6386	1.6202
chr16	90354753	66983763	0.7413	3.2299
chr17	81195210	56138976	0.6914	1.6698
chr18	78077248	58625014	0.7509	2.4714
chr19	59128983	34888902	0.59	1.6465
chr20	63025520	50812191	0.8062	1.8063
chr21	48129895	28195083	0.5858	2.0158
chr22	51304566	26682500	0.5201	1.4814
chrMT	16571	7147354	431.317	300.7388
chrX	155270560	127470995	0.821	1.7888

chrY	59373566	3552799	0.0598	1.5111

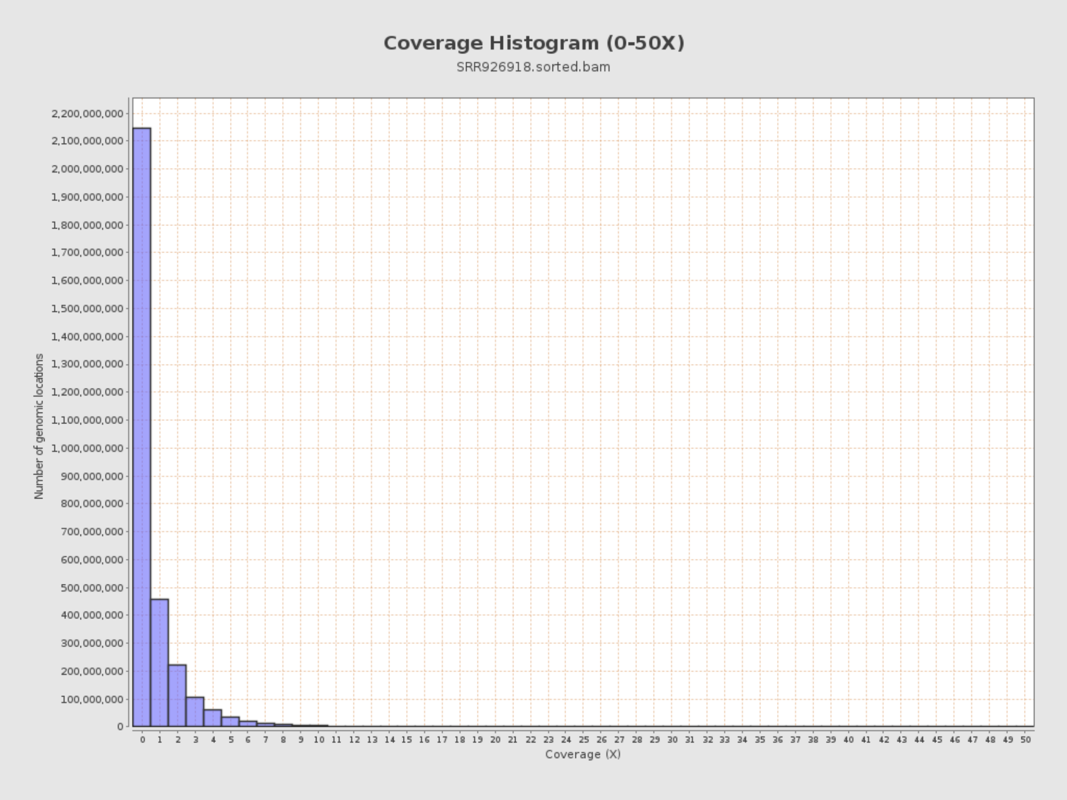
3. Results : Coverage across reference



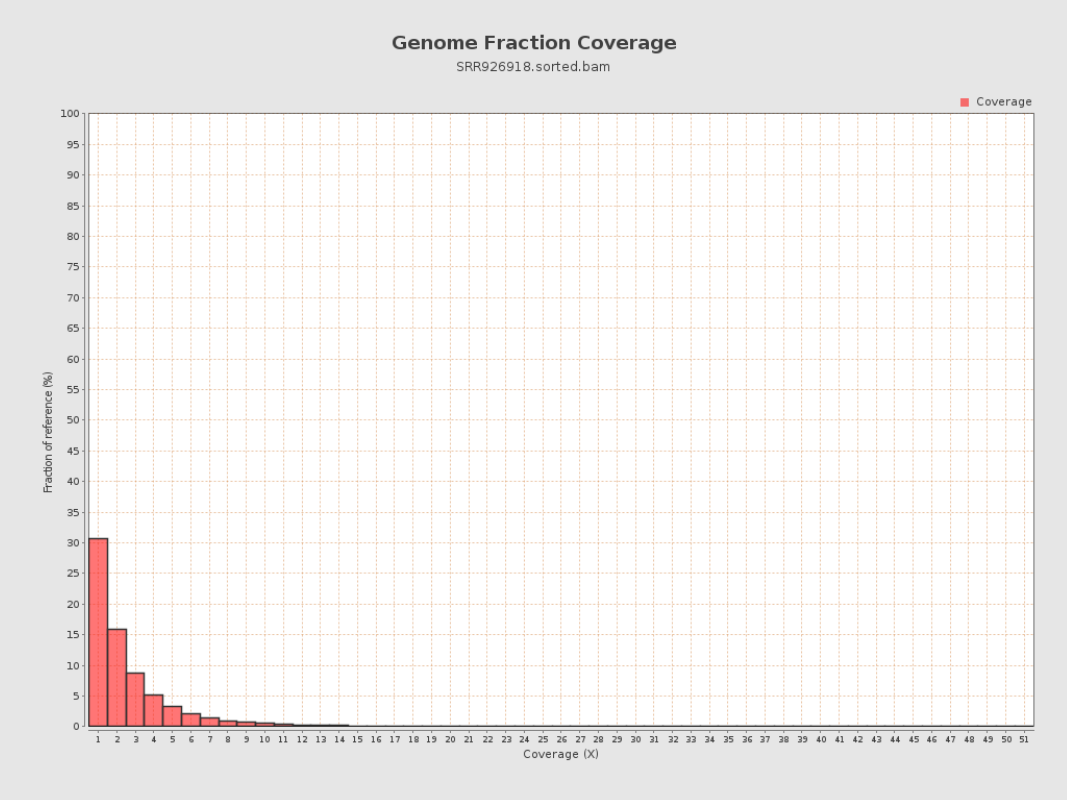
4. Results : Coverage Histogram



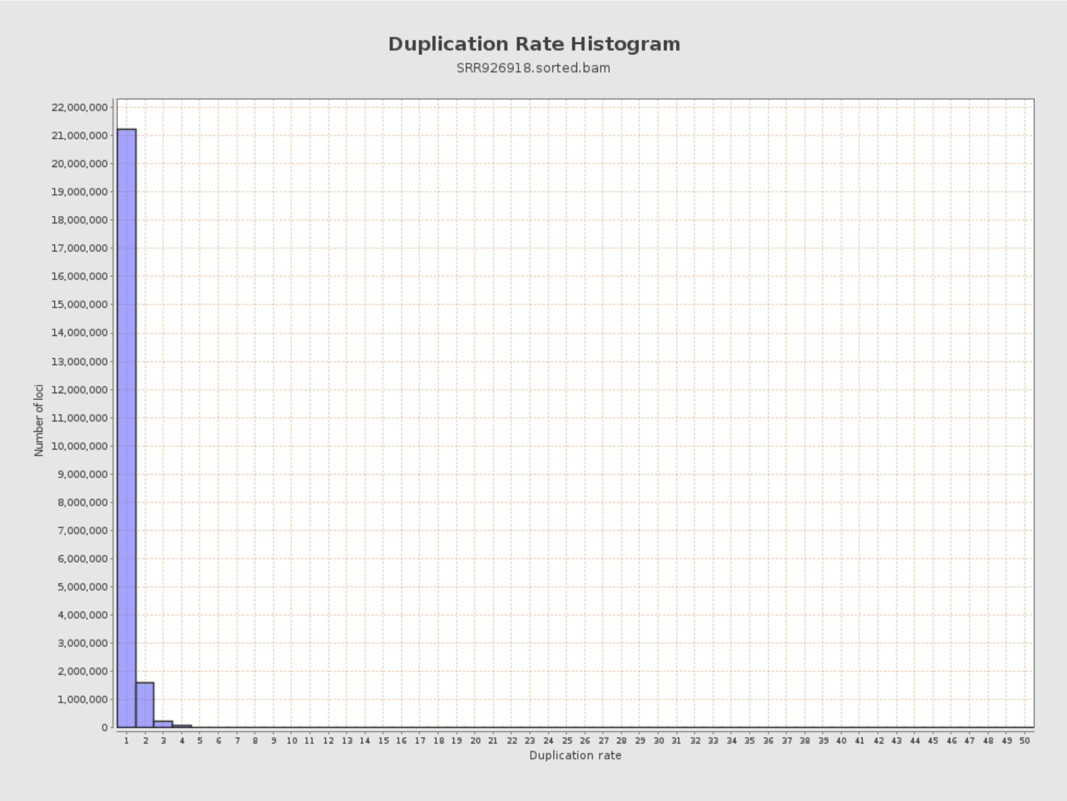
5. Results : Coverage Histogram (0-50X)



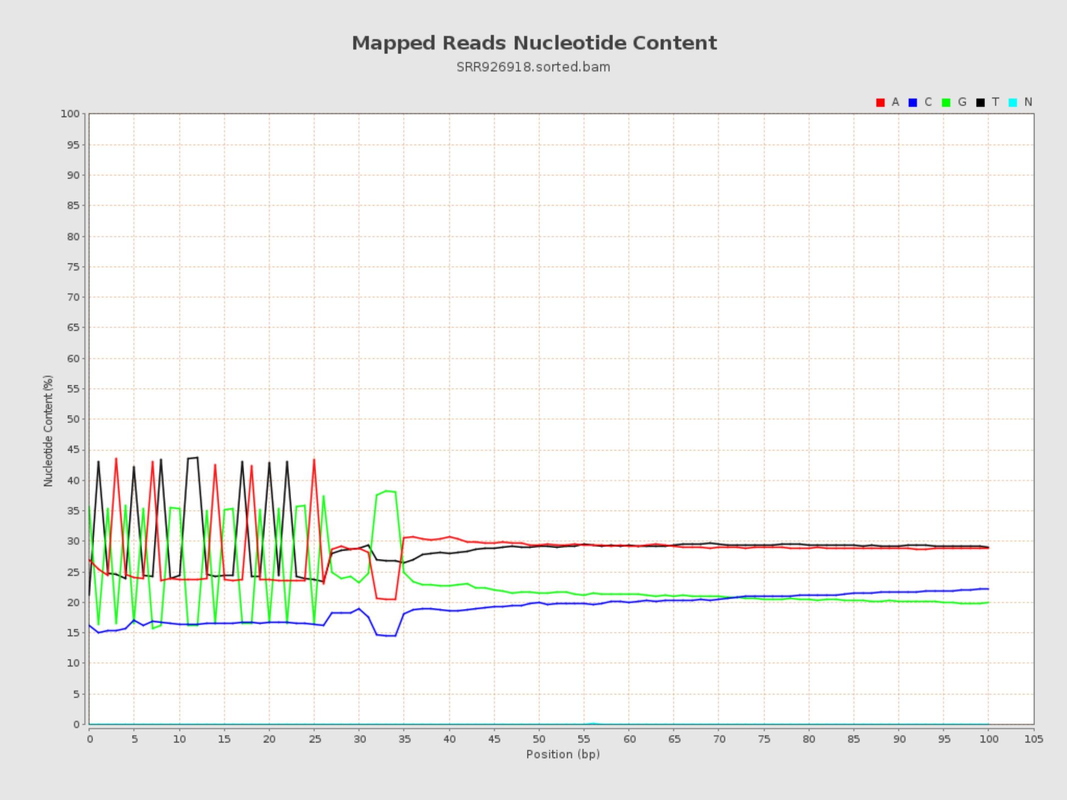
6. Results : Genome Fraction Coverage



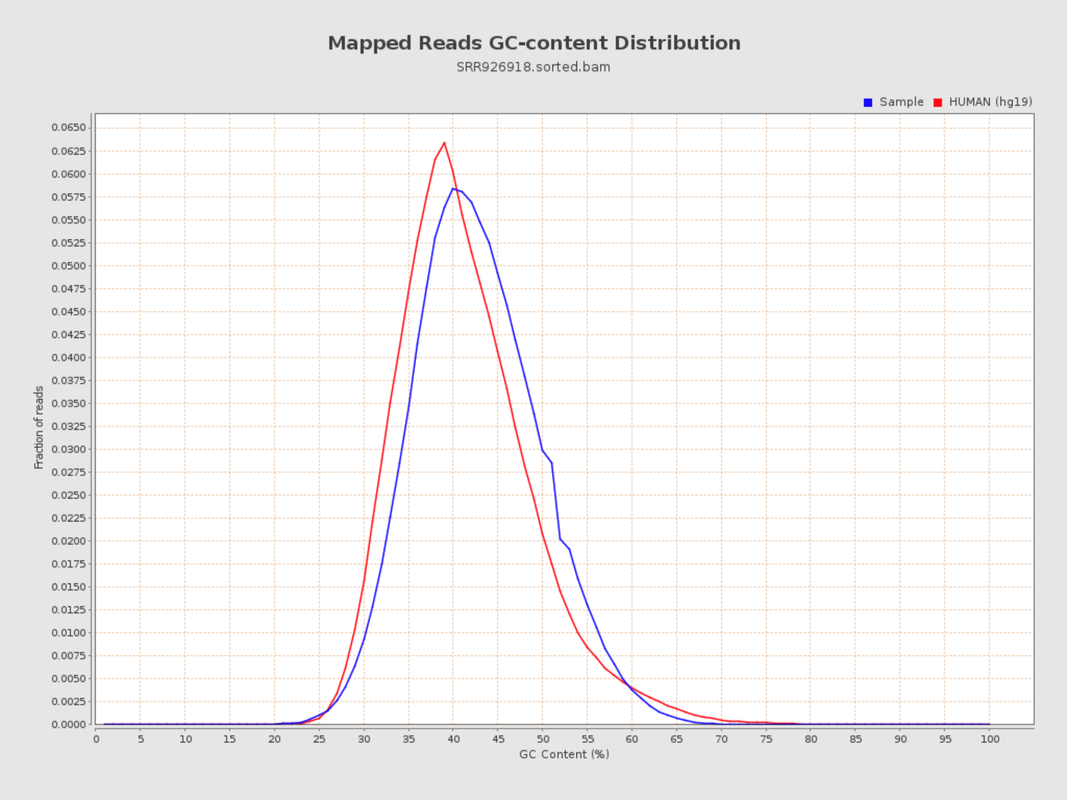
7. Results : Duplication Rate Histogram



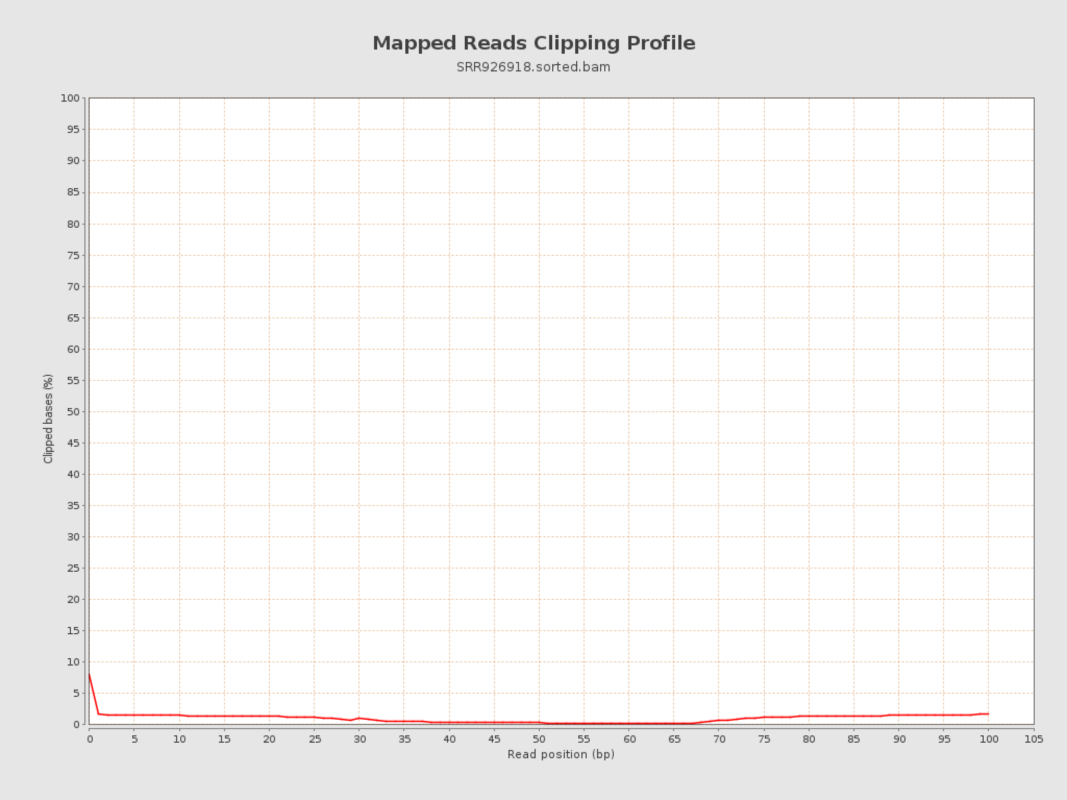
8. Results : Mapped Reads Nucleotide Content



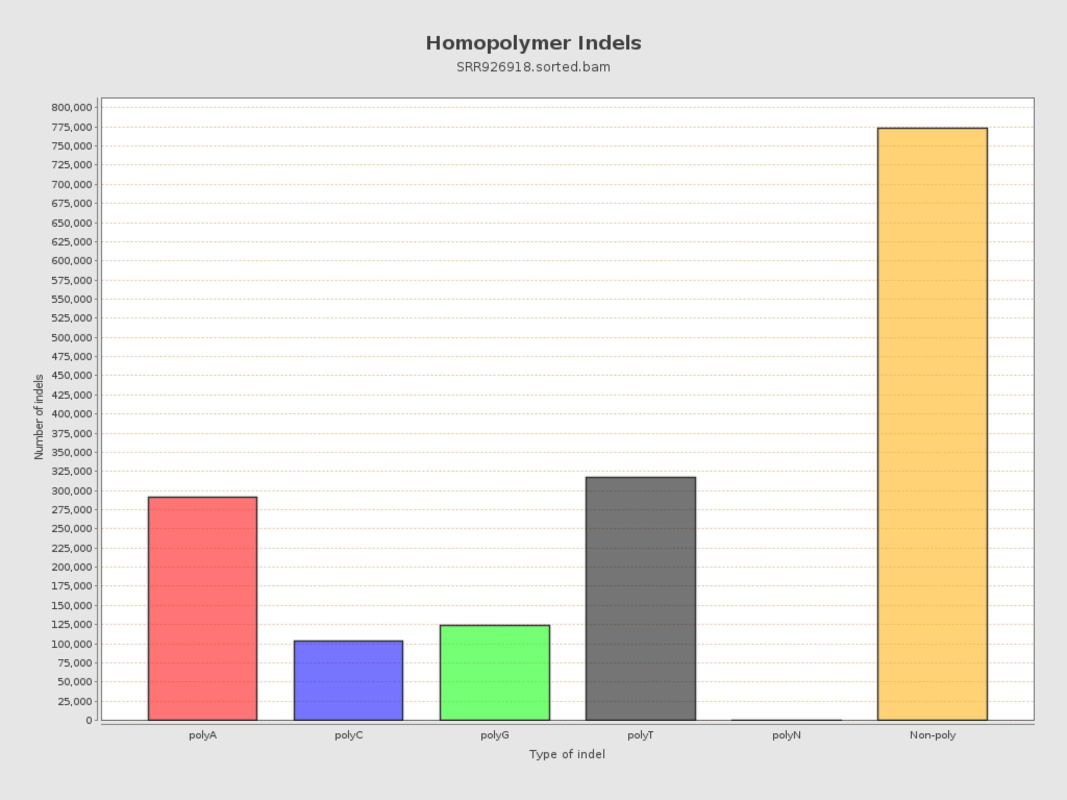
9. Results : Mapped Reads GC-content Distribution



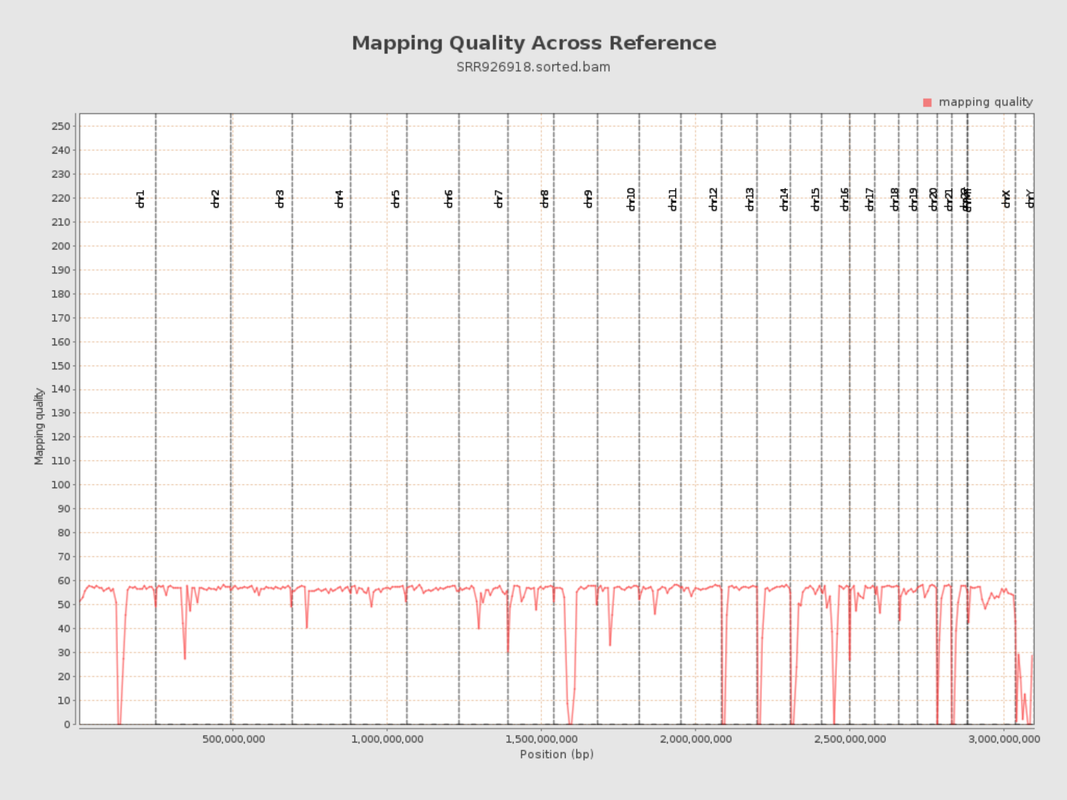
10. Results : Mapped Reads Clipping Profile



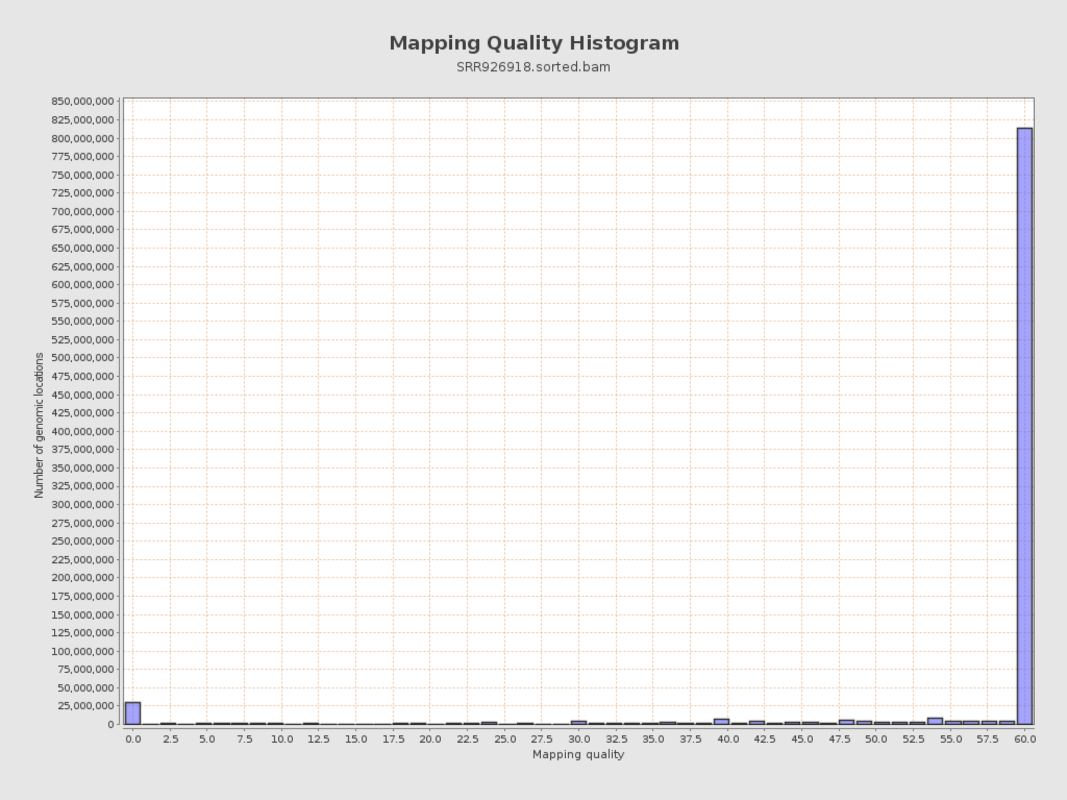
11. Results : Homopolymer Indels



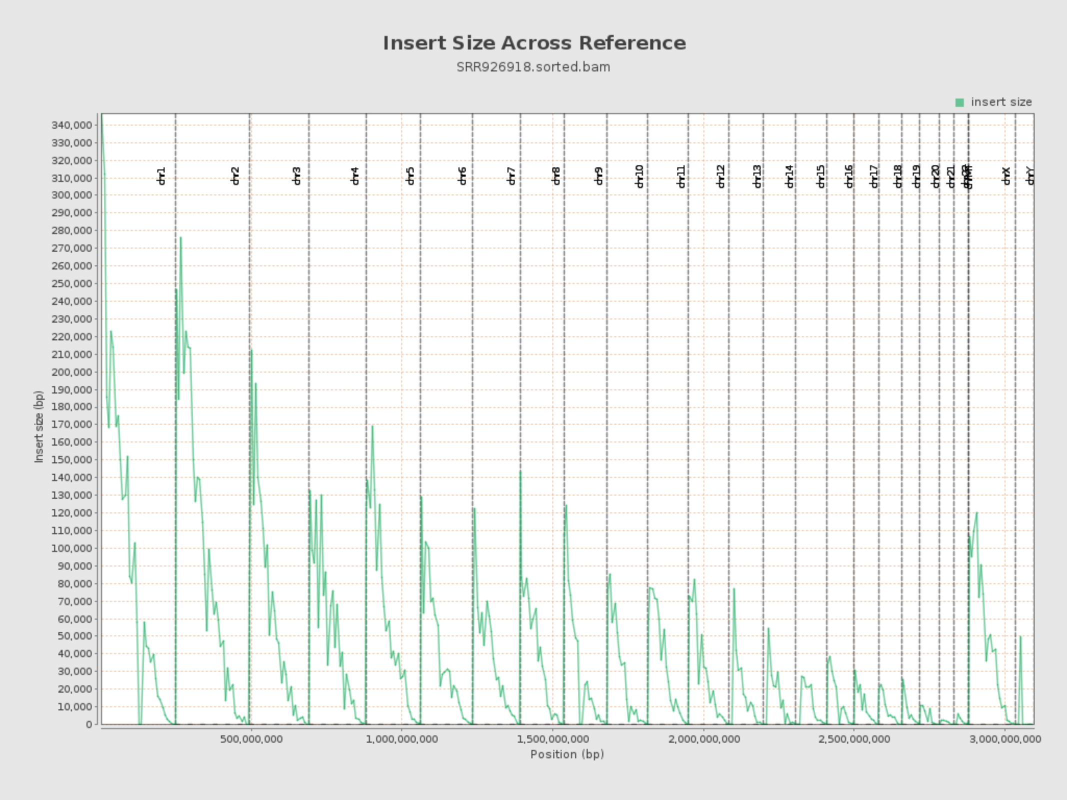
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram