Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 16:20:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926916.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_SRR926916 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926916_1.fastq.gz SRR926916_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 16:20:15 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926916.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	33,525,776
Mapped reads	29,986,594 / 89.44%
Unmapped reads	3,539,182 / 10.56%
Mapped paired reads	29,986,594 / 89.44%
Mapped reads, first in pair	15,051,651 / 44.9%
Mapped reads, second in pair	14,934,943 / 44.55%
Mapped reads, both in pair	29,572,200 / 88.21%
Mapped reads, singletons	414,394 / 1.24%
Secondary alignments	0
Supplementary alignments	441,698 / 1.32%
Read min/max/mean length	30 / 101 / 101.54
Duplicated reads (estimated)	2,420,349 / 7.22%
Duplication rate	6.46%
Clipped reads	10,549,522 / 31.47%

2.2. ACGT Content

Number/percentage of A's	775,331,210 / 28.09%
Number/percentage of C's	554,893,470 / 20.11%
Number/percentage of T's	784,076,448 / 28.41%
Number/percentage of G's	645,378,637 / 23.38%
Number/percentage of N's	249,010 / 0.01%

GC Percentage	43.49%

2.3. Coverage

Mean	0.8922
Standard Deviation	3.0052

2.4. Mapping Quality

Mean Mapping Quality	52.97

2.5. Insert size

Mean	166,286.41
Standard Deviation	4,044,763.45
P25/Median/P75	143 / 184 / 247

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	27,993,661
Insertions	439,722
Mapped reads with at least one insertion	1.44%
Deletions	1,427,444
Mapped reads with at least one deletion	4.64%
Homopolymer indels	52.39%

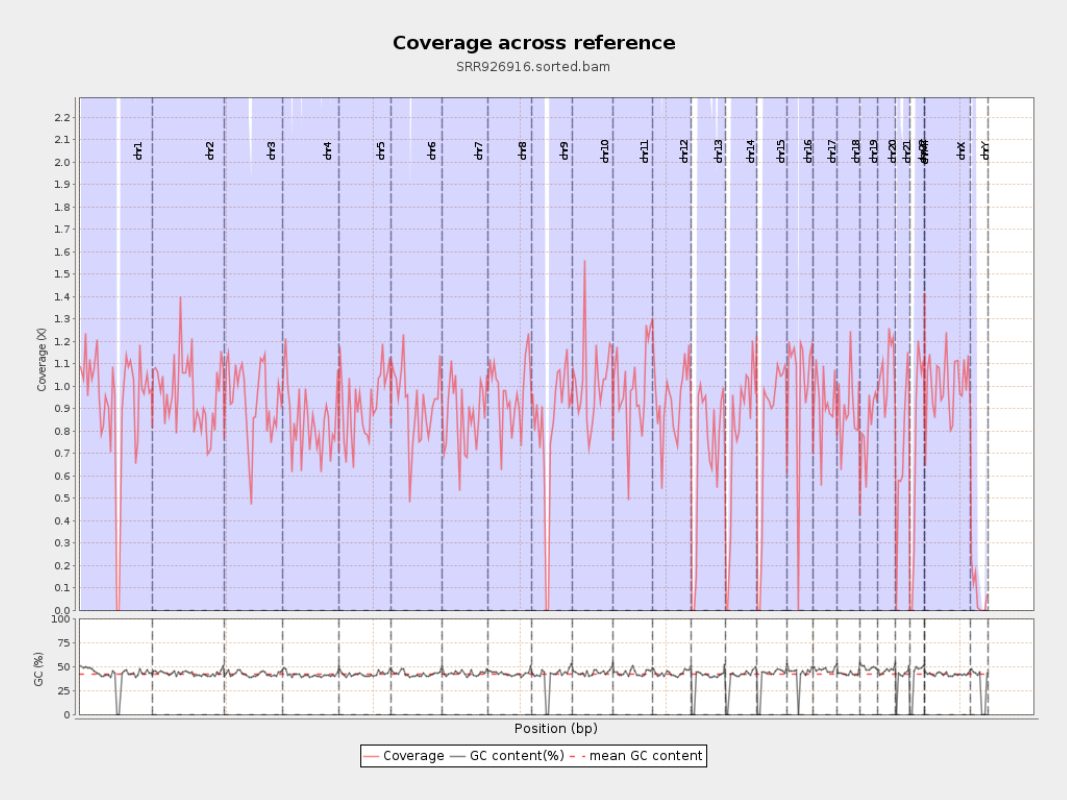
2.7. Chromosome stats

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

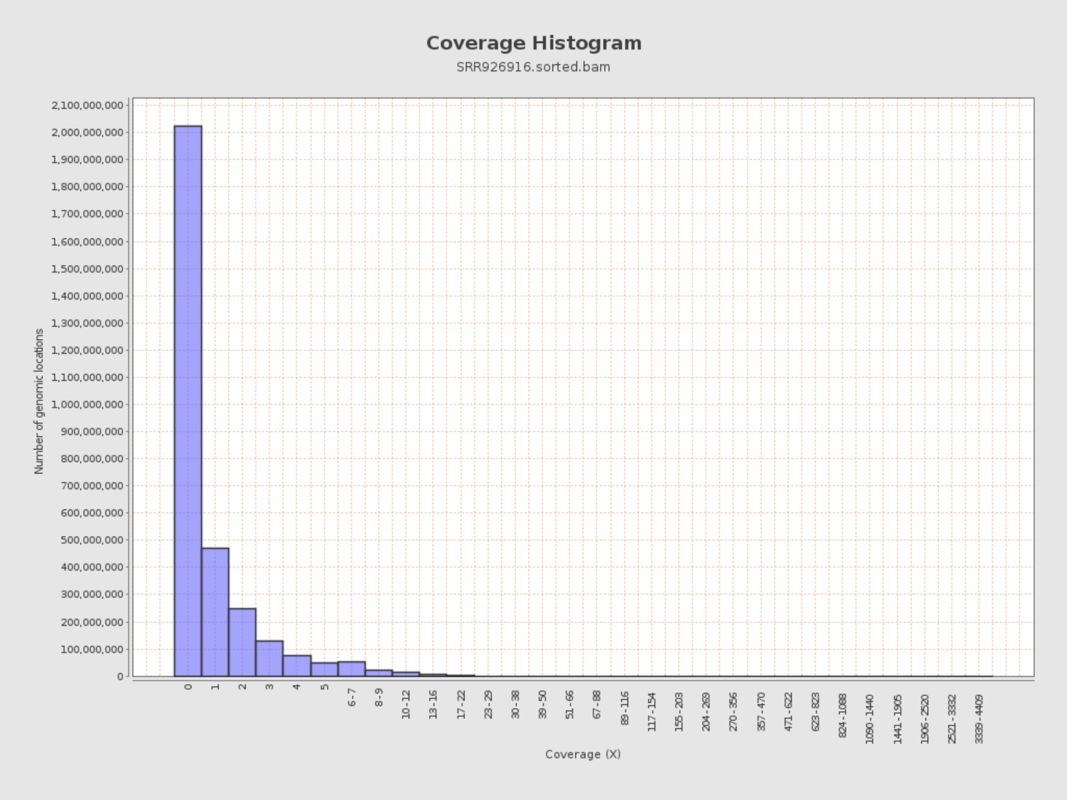
		bases	coverage	deviation
chr1	249250621	231789205	0.9299	2.7491
chr2	243199373	236675066	0.9732	4.0996
chr3	198022430	185836402	0.9385	1.9174
chr4	191154276	161083548	0.8427	2.075
chr5	180915260	166973187	0.9229	1.8695
chr6	171115067	157808783	0.9222	2.1553
chr7	159138663	138062075	0.8676	1.9967
chr8	146364022	141654309	0.9678	2.0626
chr9	141213431	115647585	0.819	2.7995
chr10	135534747	138450325	1.0215	8.5257
chr11	135006516	133483385	0.9887	2.2861
chr12	133851895	125300271	0.9361	1.9645
chr13	115169878	80793545	0.7015	1.6135
chr14	107349540	83857114	0.7812	1.7648
chr15	102531392	82592547	0.8055	1.857
chr16	90354753	89893887	0.9949	4.2553
chr17	81195210	74561458	0.9183	2.1386
chr18	78077248	71155054	0.9113	2.9259
chr19	59128983	48198491	0.8151	2.1349
chr20	63025520	67418453	1.0697	2.1481
chr21	48129895	34256593	0.7118	2.6367
chr22	51304566	37102125	0.7232	1.852
chrMT	16571	23516	1.4191	1.8253
chrX	155270560	155231028	0.9997	2.0312

chrY	59373566	4130442	0.0696	1.4976

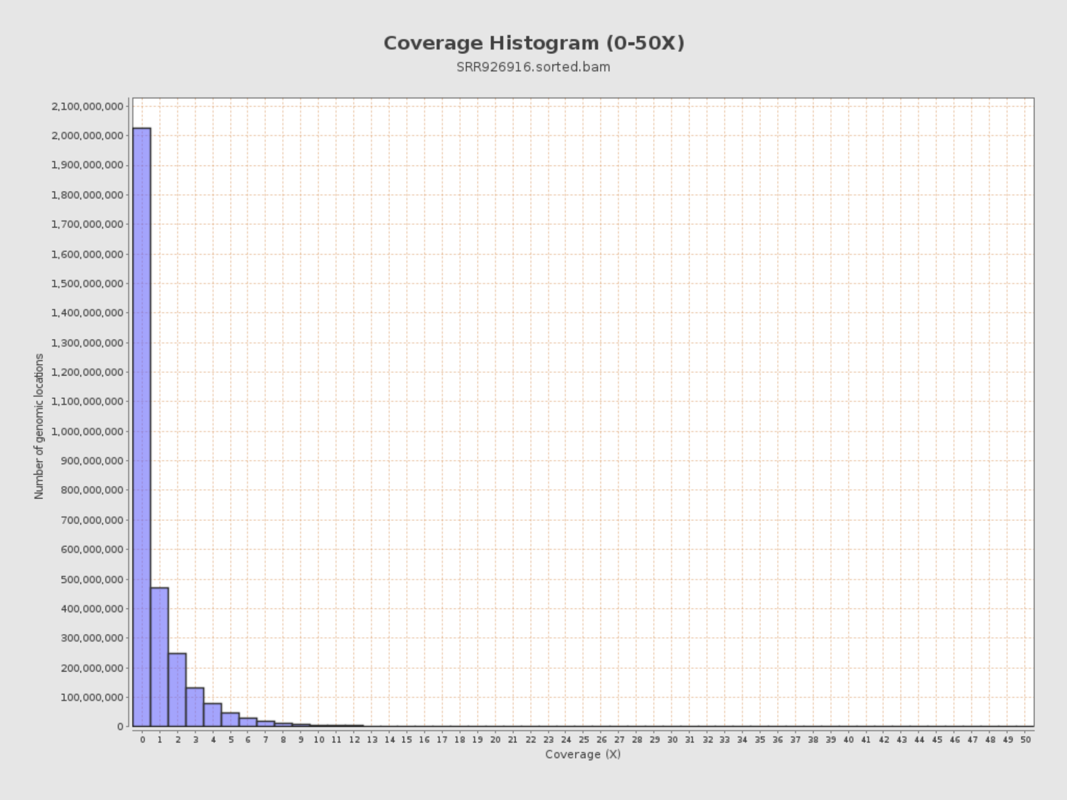
3. Results : Coverage across reference



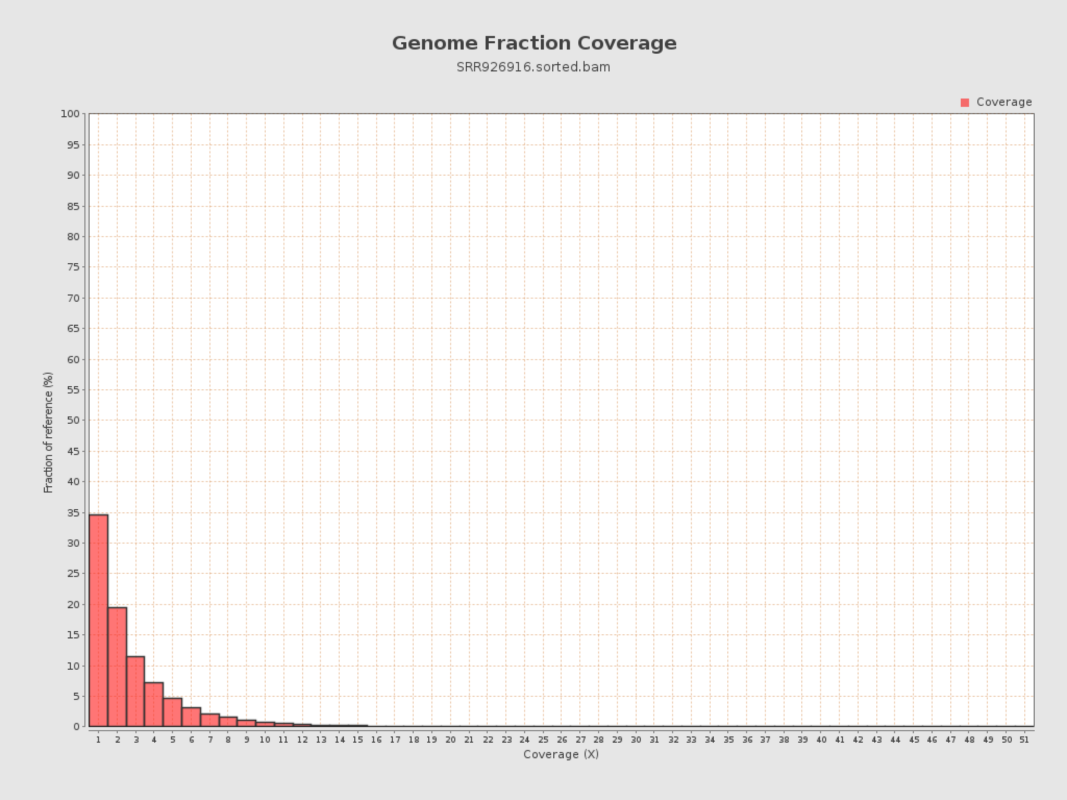
4. Results : Coverage Histogram



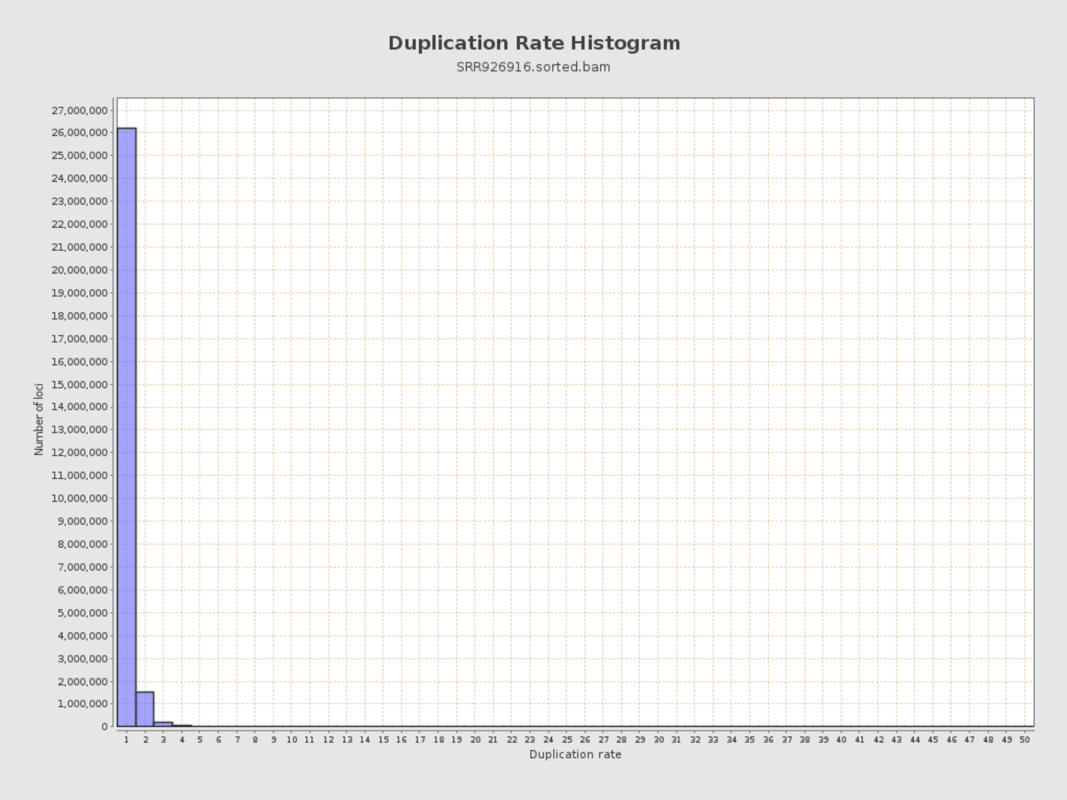
5. Results : Coverage Histogram (0-50X)



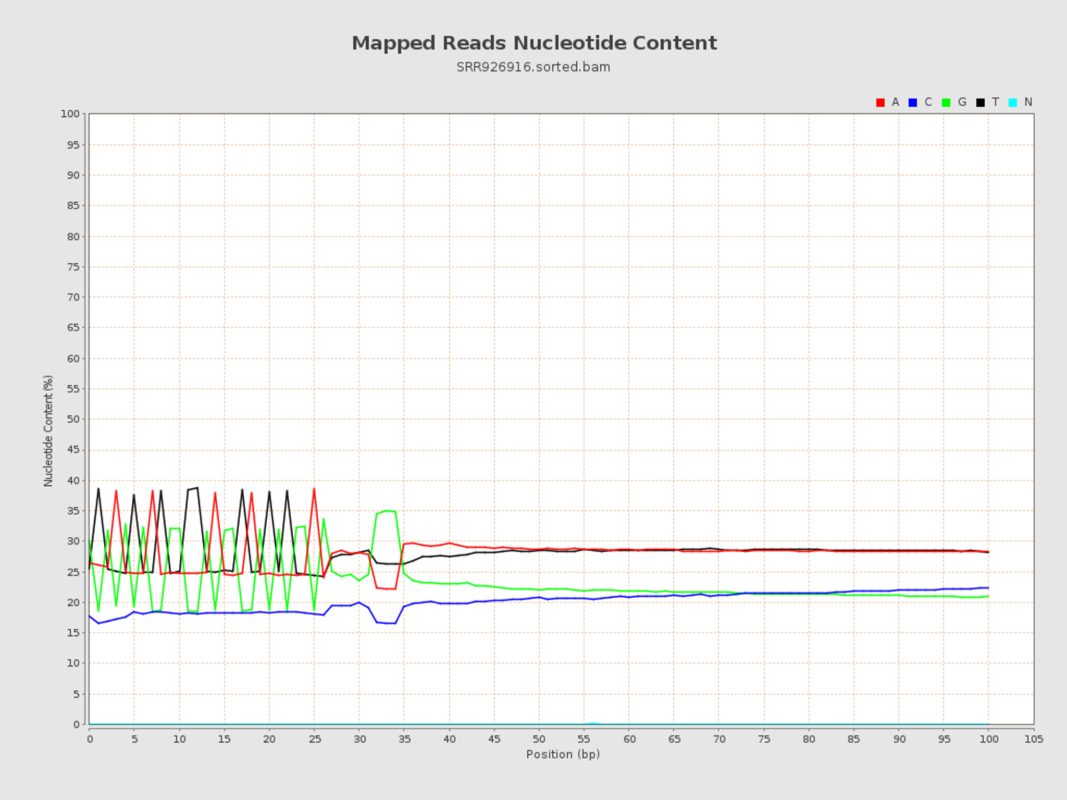
6. Results : Genome Fraction Coverage



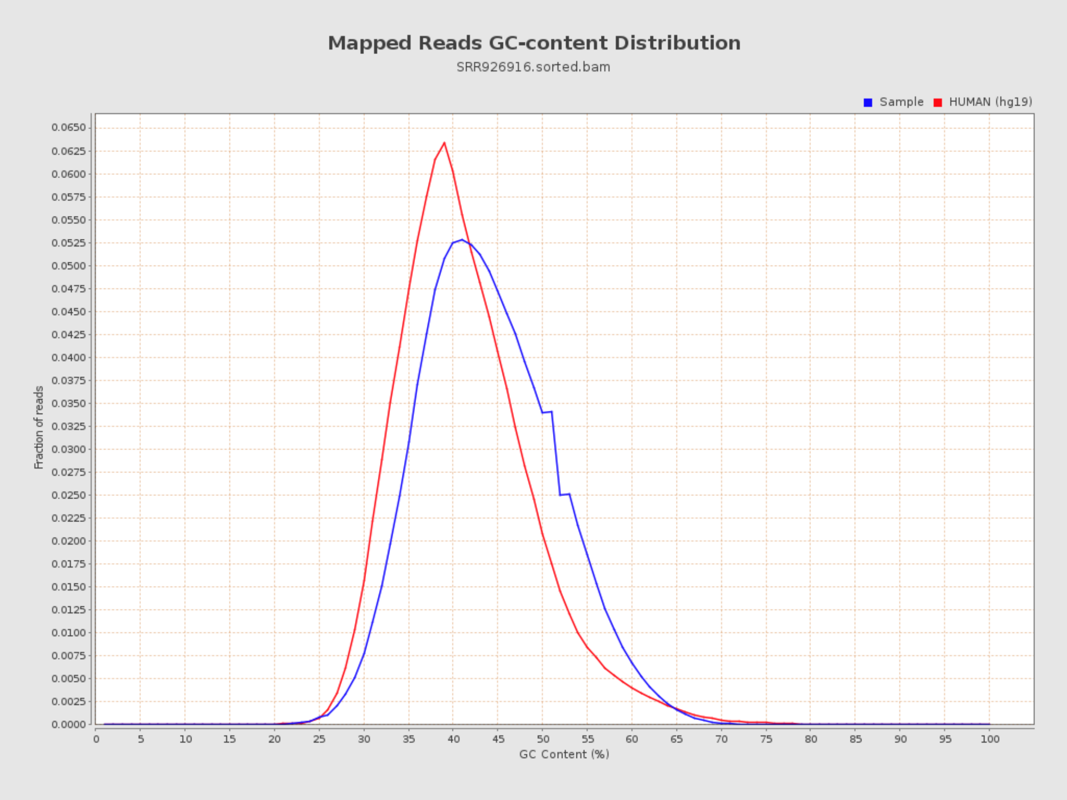
7. Results : Duplication Rate Histogram



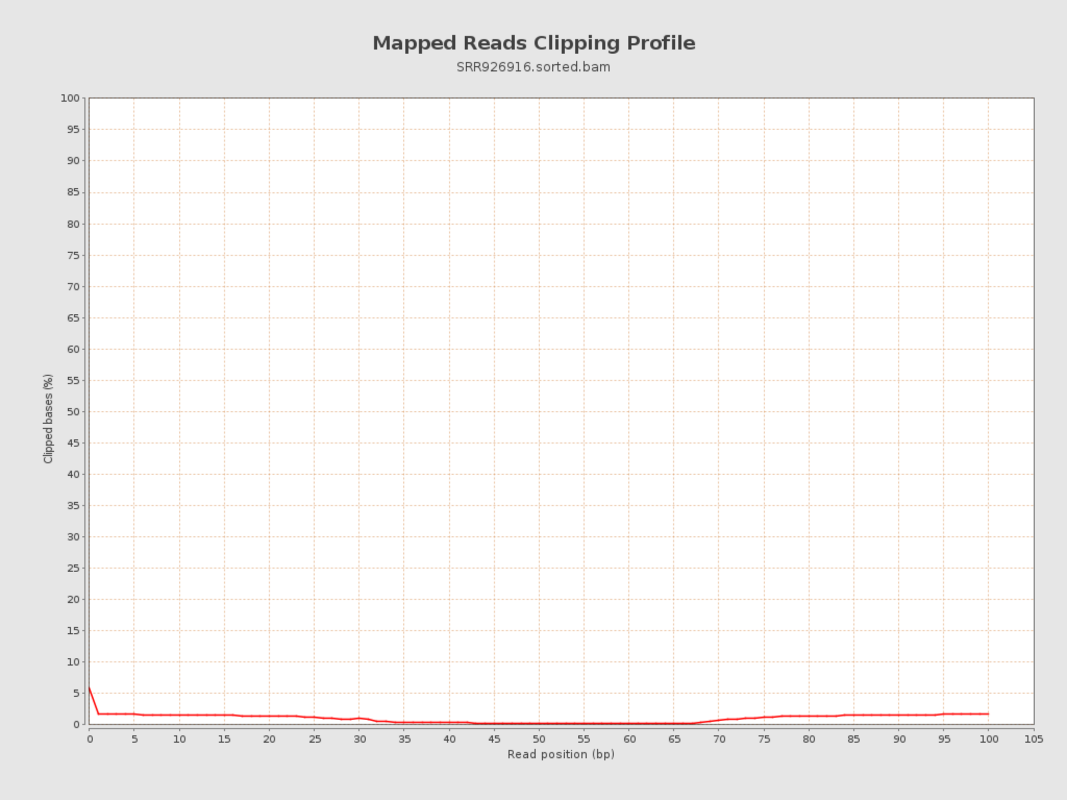
8. Results : Mapped Reads Nucleotide Content



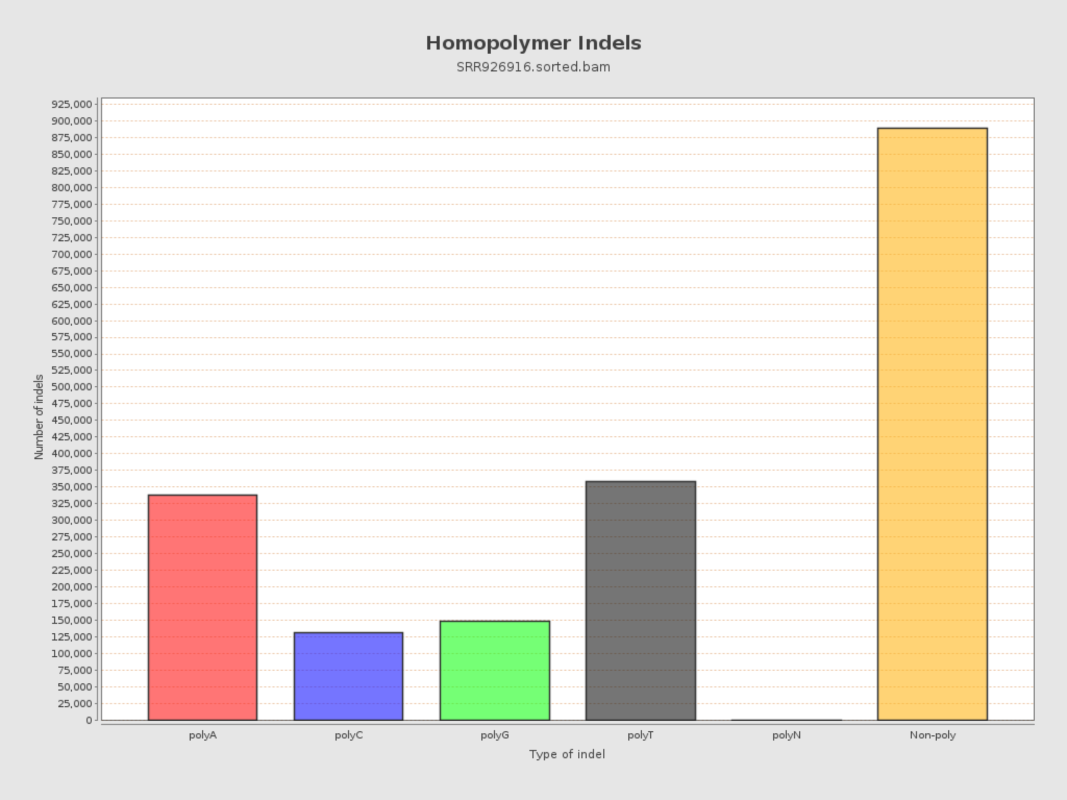
9. Results : Mapped Reads GC-content Distribution



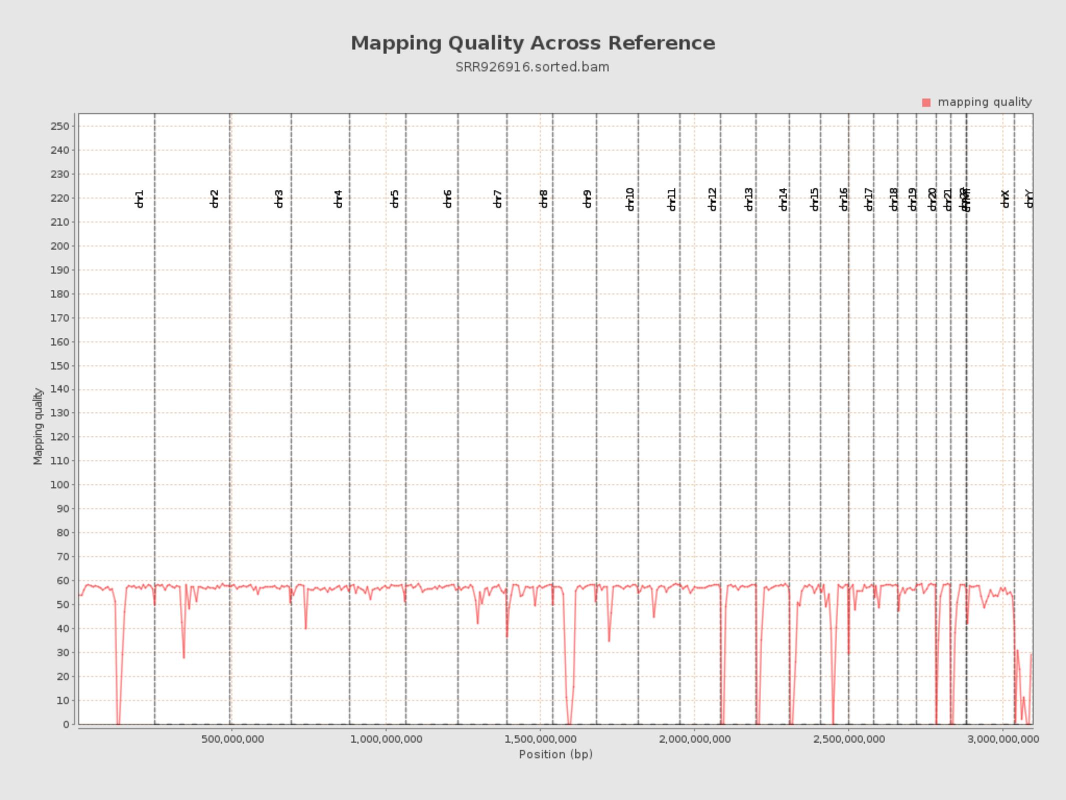
10. Results : Mapped Reads Clipping Profile



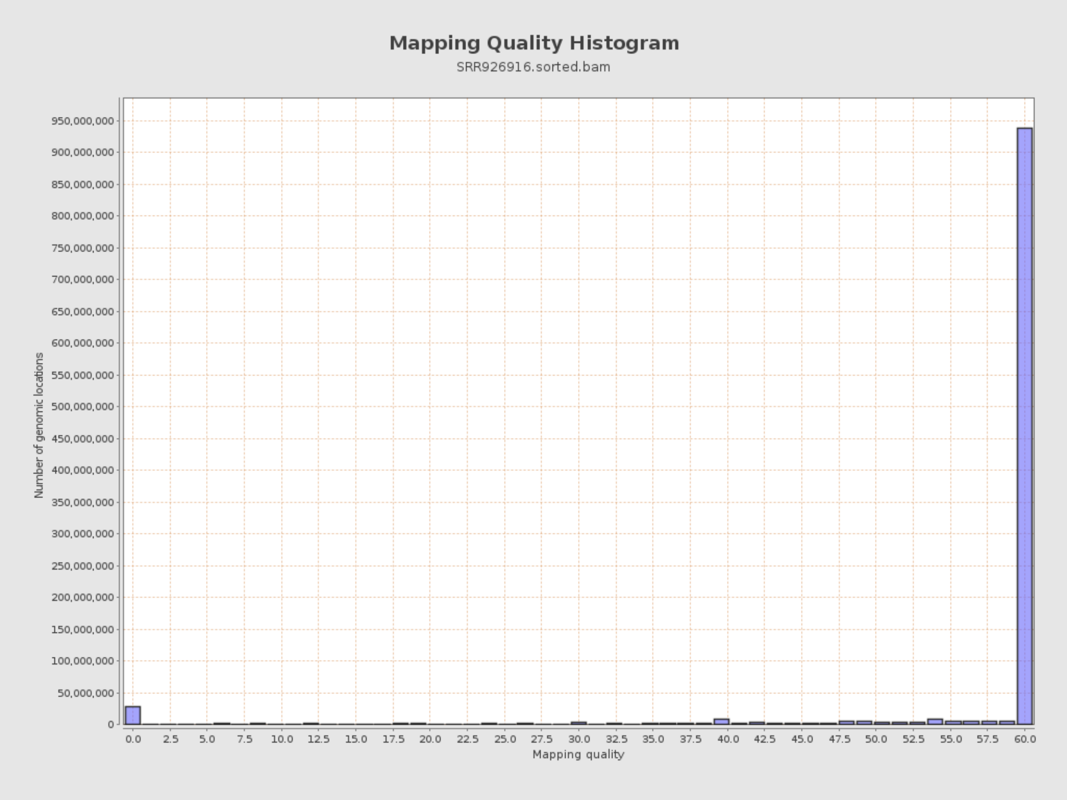
11. Results : Homopolymer Indels



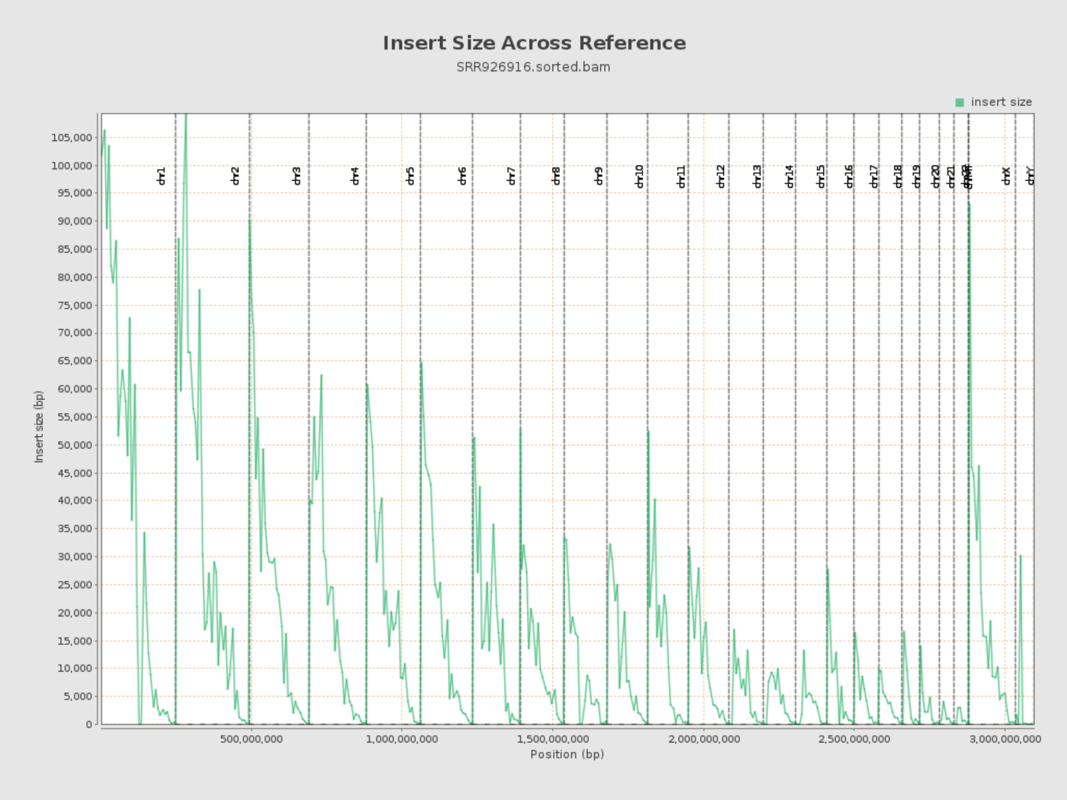
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram