Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 21:44:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926932.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_SRR926932 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926932_1.fastq.gz SRR926932_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 21:44:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926932.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,670,104
Mapped reads	12,256,780 / 96.74%
Unmapped reads	413,324 / 3.26%
Mapped paired reads	12,256,780 / 96.74%
Mapped reads, first in pair	6,154,403 / 48.57%
Mapped reads, second in pair	6,102,377 / 48.16%
Mapped reads, both in pair	12,048,308 / 95.09%
Mapped reads, singletons	208,472 / 1.65%
Secondary alignments	0
Supplementary alignments	328,073 / 2.59%
Read min/max/mean length	30 / 101 / 102.06
Duplicated reads (estimated)	984,407 / 7.77%
Duplication rate	6.81%
Clipped reads	6,368,498 / 50.26%

2.2. ACGT Content

Number/percentage of A's	303,163,788 / 28.15%
Number/percentage of C's	205,044,547 / 19.04%
Number/percentage of T's	315,515,601 / 29.3%
Number/percentage of G's	253,178,175 / 23.51%
Number/percentage of N's	49,782 / 0%

GC Percentage	42.55%

2.3. Coverage

Mean	0.3482
Standard Deviation	1.4435

2.4. Mapping Quality

Mean Mapping Quality	52.68

2.5. Insert size

Mean	280,872.35
Standard Deviation	5,289,779.91
P25/Median/P75	132 / 176 / 239

2.6. Mismatches and indels

General error rate	0.97%
Mismatches	10,114,273
Insertions	186,658
Mapped reads with at least one insertion	1.5%
Deletions	579,207
Mapped reads with at least one deletion	4.6%
Homopolymer indels	52.05%

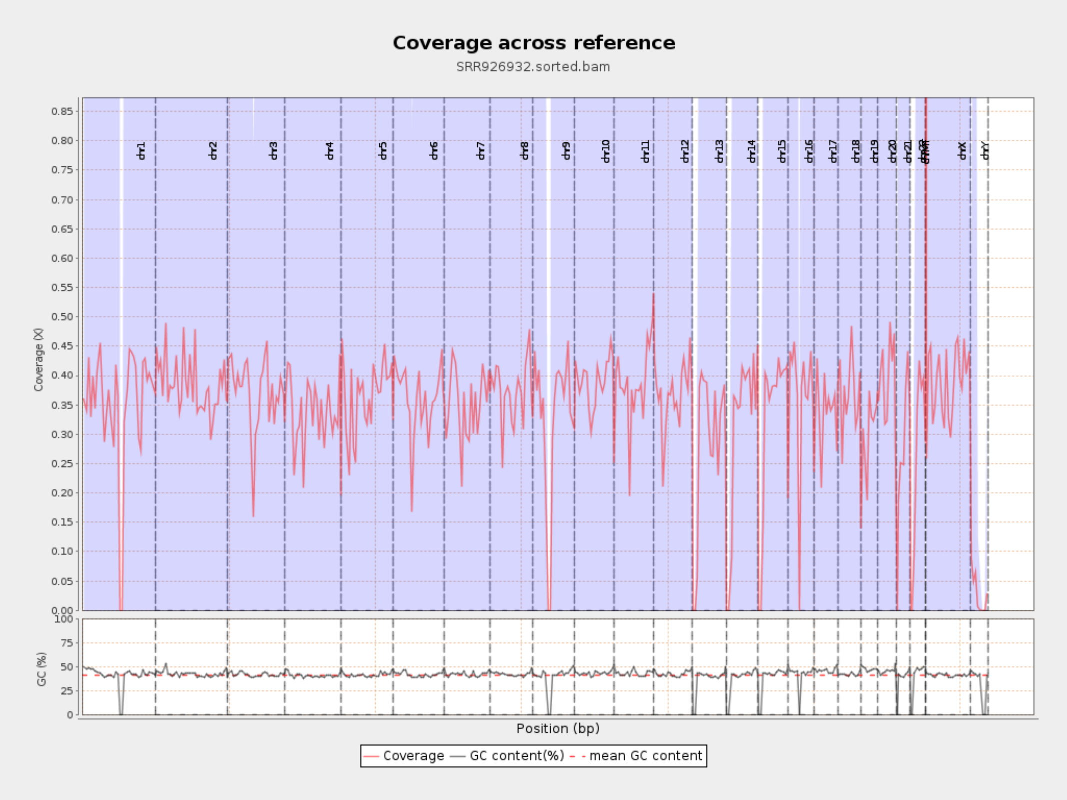
2.7. Chromosome stats

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

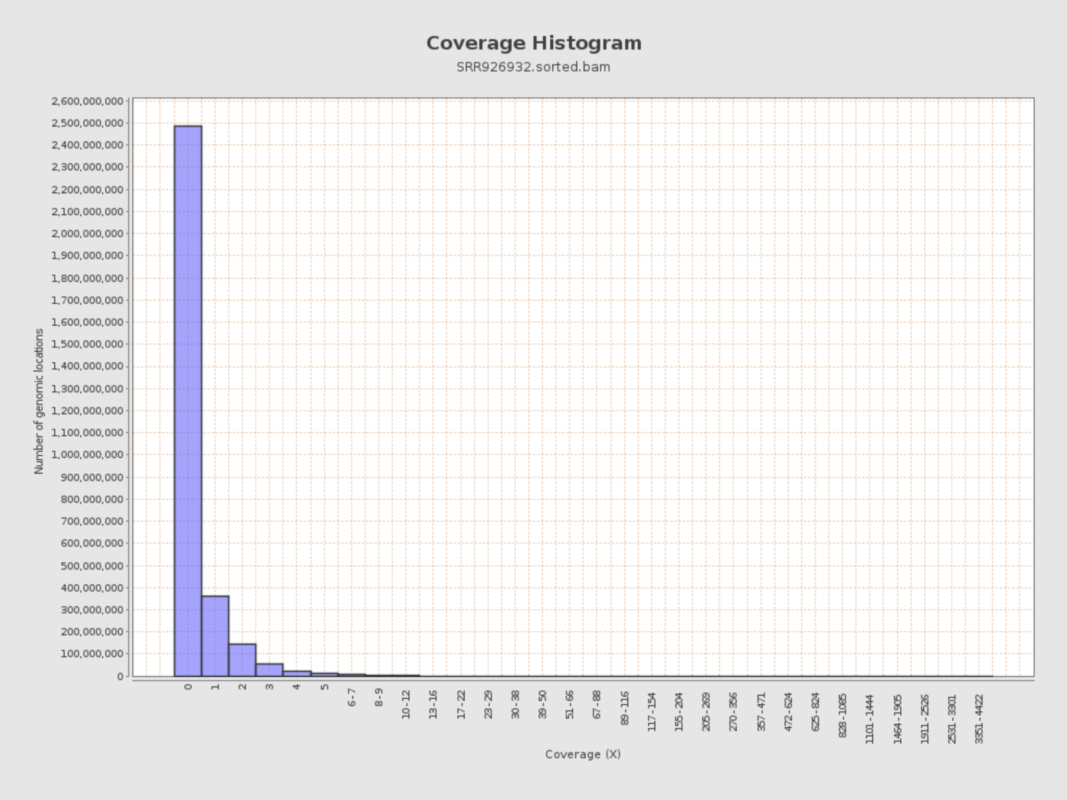
		bases	coverage	deviation
chr1	249250621	87595149	0.3514	1.409
chr2	243199373	93375739	0.3839	3.4708
chr3	198022430	73416026	0.3707	0.9476
chr4	191154276	64812461	0.3391	1.082
chr5	180915260	66373939	0.3669	0.9318
chr6	171115067	61565232	0.3598	0.9995
chr7	159138663	55818321	0.3508	1.0538
chr8	146364022	54758020	0.3741	0.9874
chr9	141213431	46287258	0.3278	1.1562
chr10	135534747	52729621	0.389	1.5304
chr11	135006516	51699341	0.3829	1.0797
chr12	133851895	49476488	0.3696	0.9806
chr13	115169878	32702572	0.284	0.8227
chr14	107349540	33276791	0.31	0.9298
chr15	102531392	32896826	0.3208	0.9056
chr16	90354753	32138384	0.3557	1.3196
chr17	81195210	27717588	0.3414	0.9578
chr18	78077248	28816330	0.3691	1.1993
chr19	59128983	17649005	0.2985	1.0675
chr20	63025520	25273633	0.401	1.0163
chr21	48129895	13313914	0.2766	1.0685
chr22	51304566	13244306	0.2582	0.8373
chrMT	16571	1278697	77.1647	63.8311
chrX	155270560	59967371	0.3862	0.9995

chrY	59373566	1623846	0.0273	0.7408

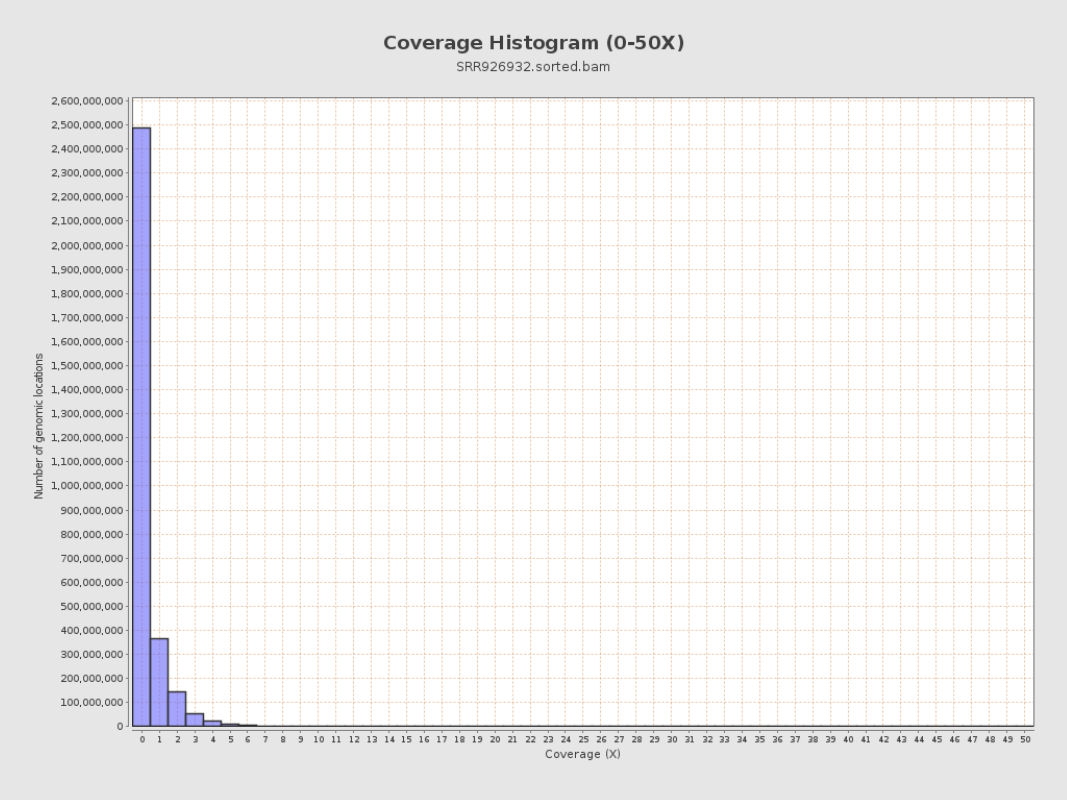
3. Results : Coverage across reference



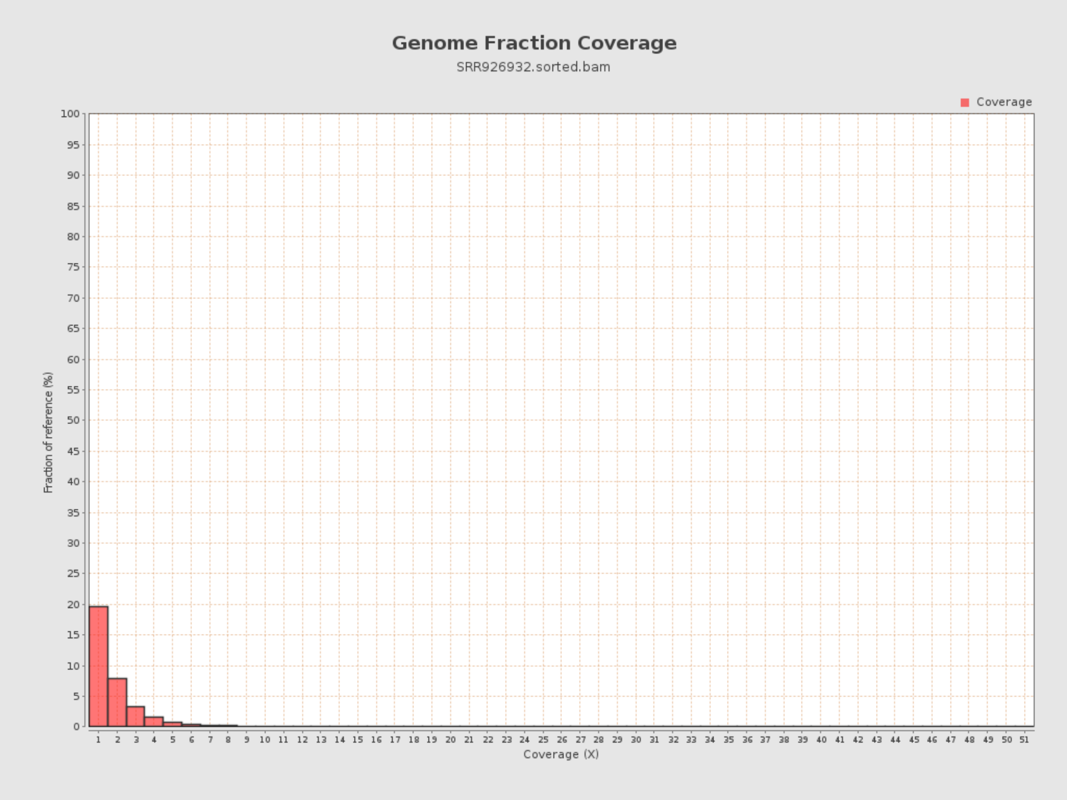
4. Results : Coverage Histogram



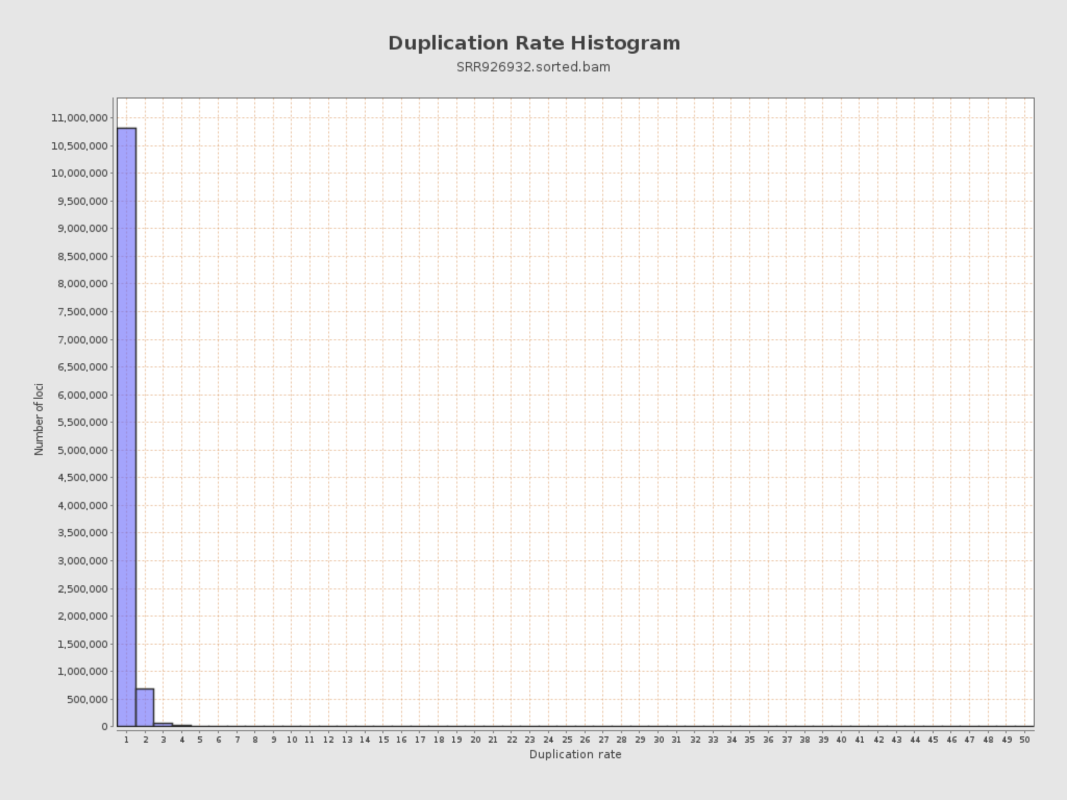
5. Results : Coverage Histogram (0-50X)



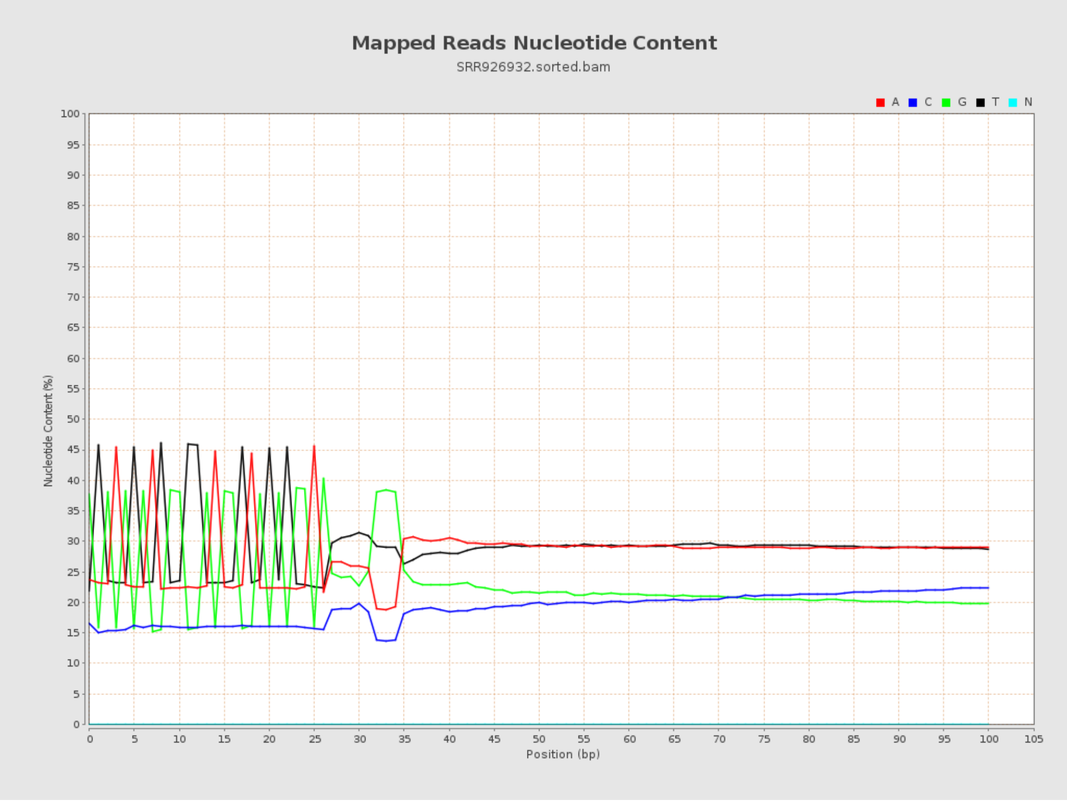
6. Results : Genome Fraction Coverage



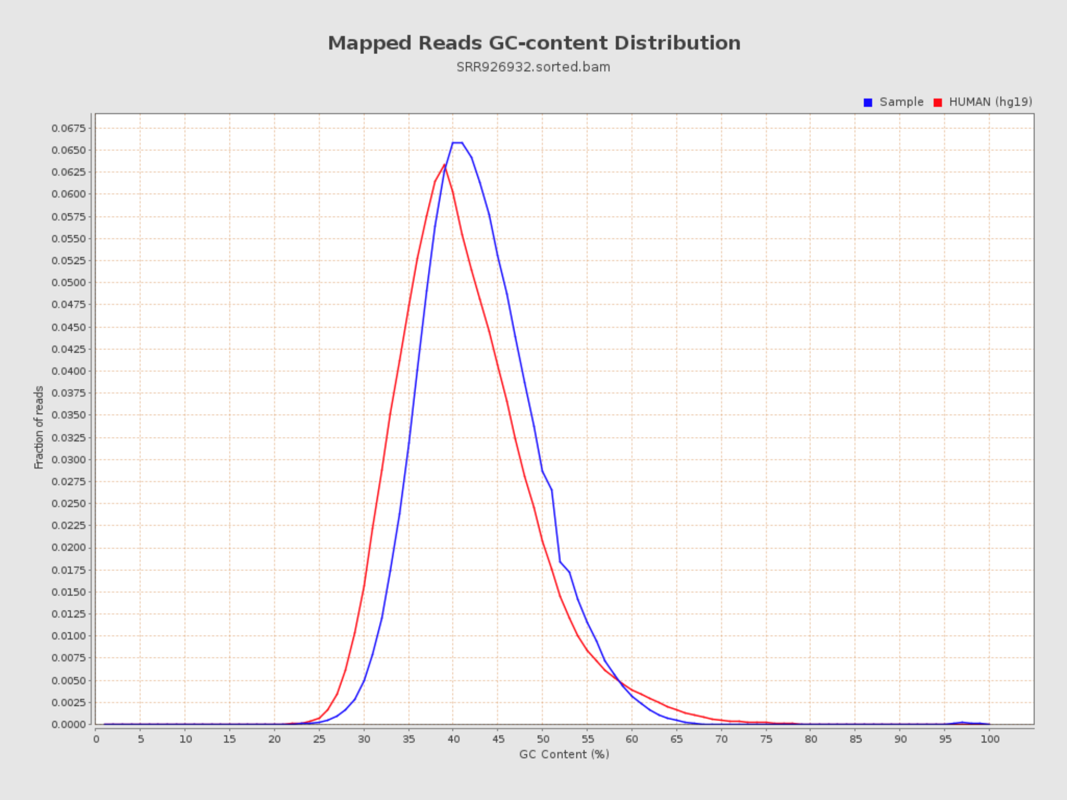
7. Results : Duplication Rate Histogram



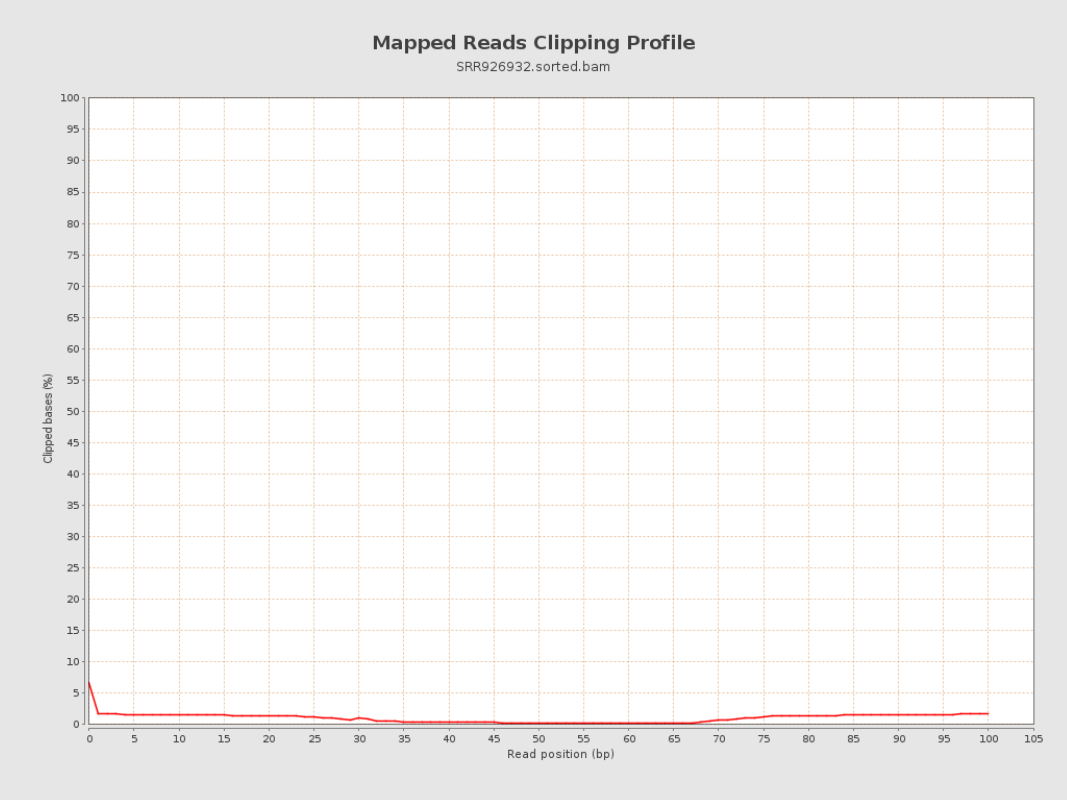
8. Results : Mapped Reads Nucleotide Content



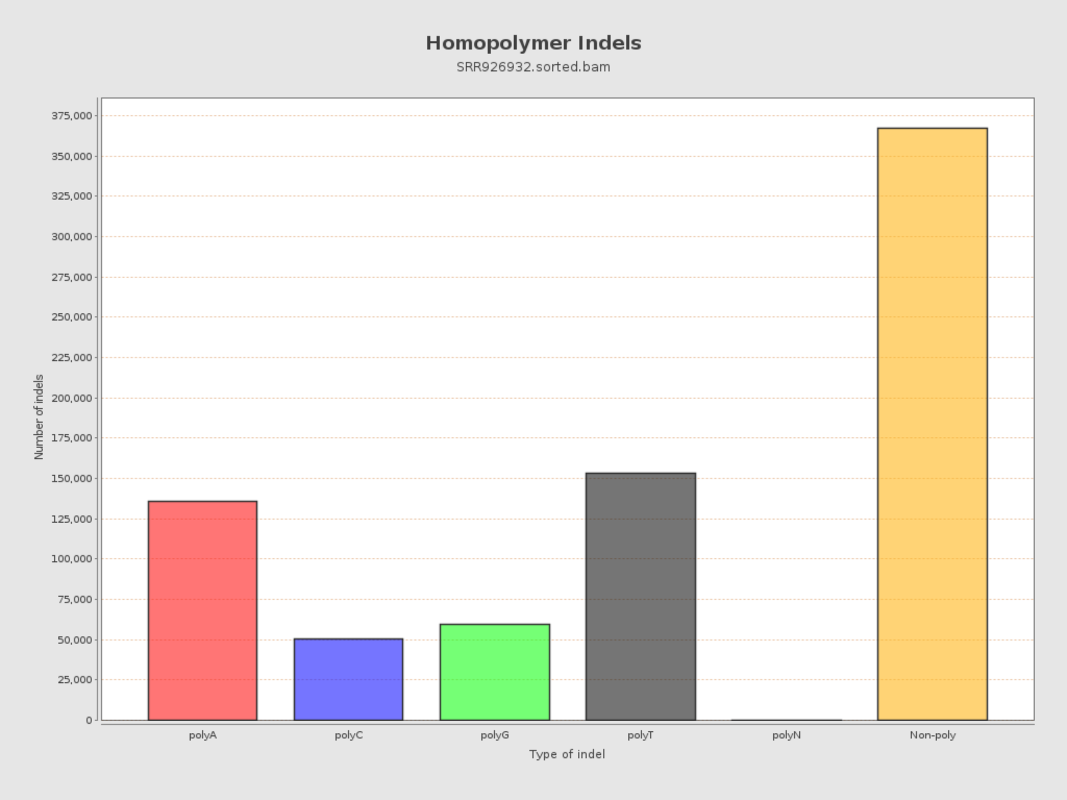
9. Results : Mapped Reads GC-content Distribution



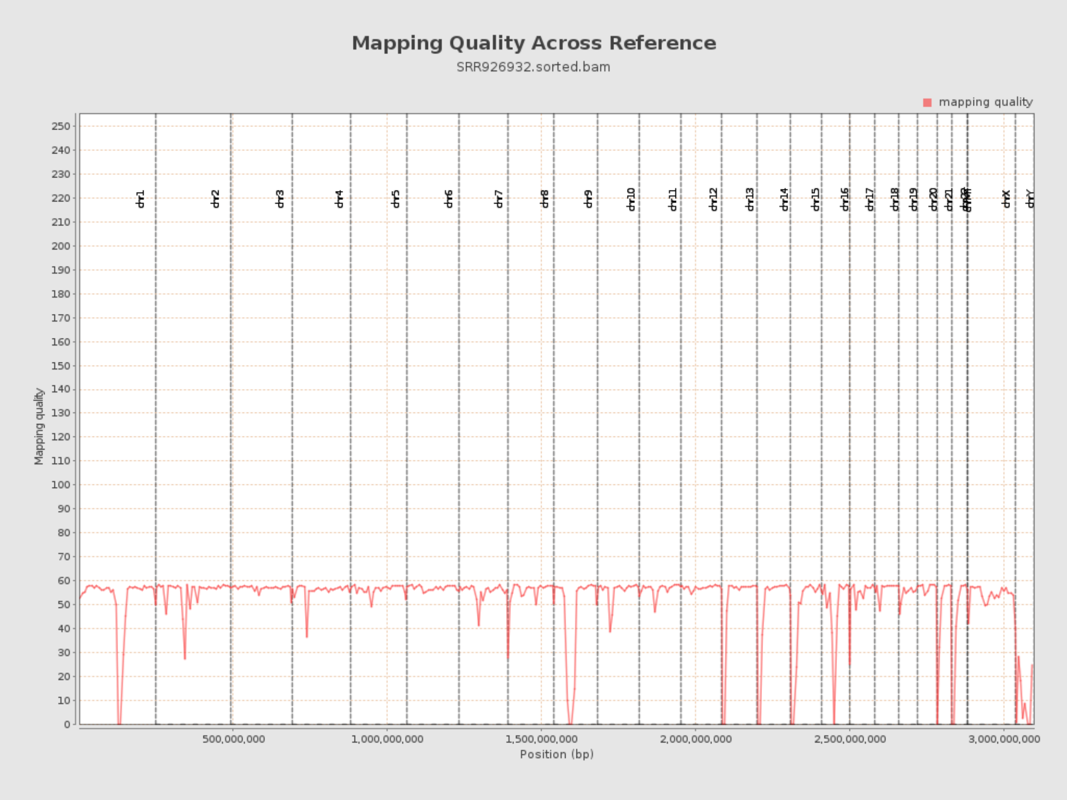
10. Results : Mapped Reads Clipping Profile



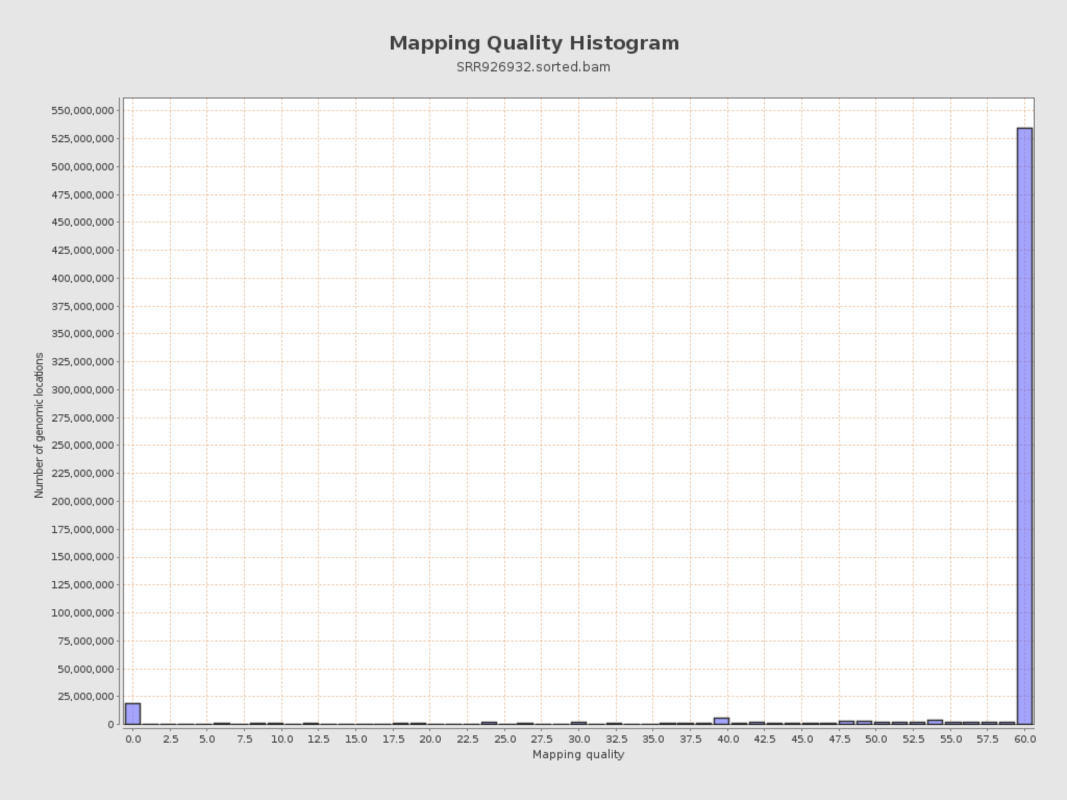
11. Results : Homopolymer Indels



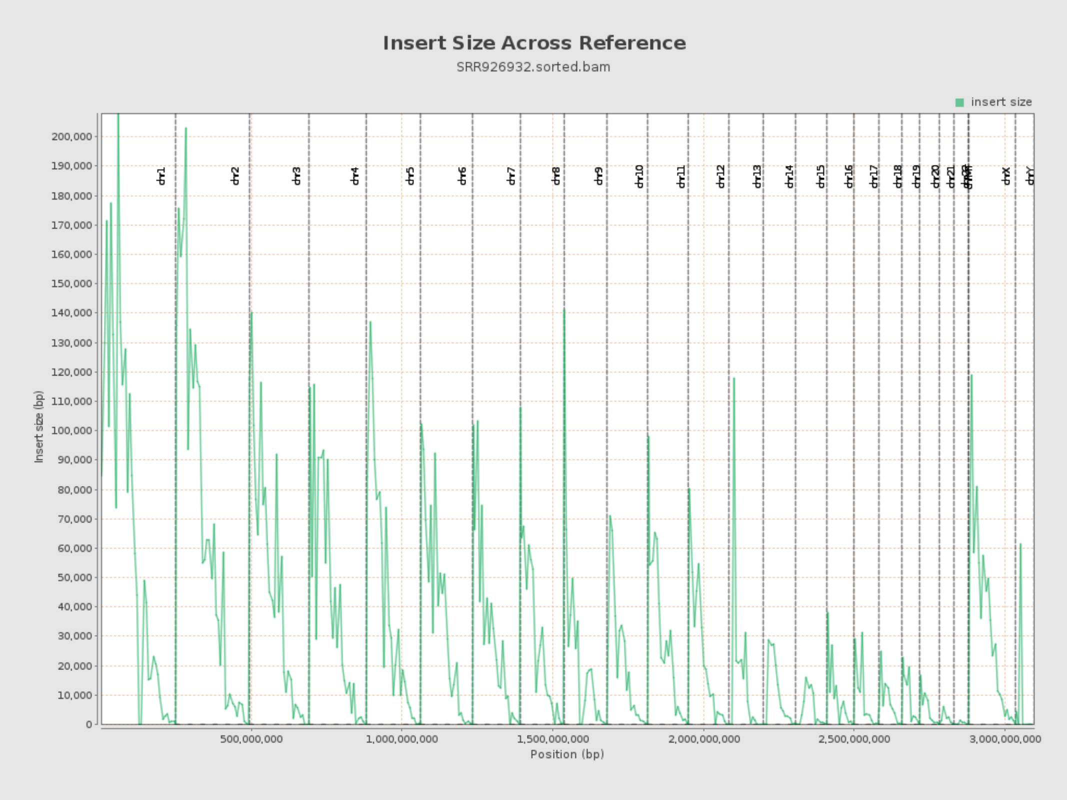
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram