Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 23:47:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926941.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_SRR926941 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926941_1.fastq.gz SRR926941_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 23:47:39 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926941.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,673,208
Mapped reads	7,518,117 / 97.98%
Unmapped reads	155,091 / 2.02%
Mapped paired reads	7,518,117 / 97.98%
Mapped reads, first in pair	3,763,700 / 49.05%
Mapped reads, second in pair	3,754,417 / 48.93%
Mapped reads, both in pair	7,426,974 / 96.79%
Mapped reads, singletons	91,143 / 1.19%
Secondary alignments	0
Supplementary alignments	165,361 / 2.16%
Read min/max/mean length	30 / 101 / 101.89
Duplicated reads (estimated)	331,178 / 4.32%
Duplication rate	3.62%
Clipped reads	2,485,228 / 32.39%

2.2. ACGT Content

Number/percentage of A's	199,761,932 / 28.52%
Number/percentage of C's	139,594,050 / 19.93%
Number/percentage of T's	202,311,946 / 28.88%
Number/percentage of G's	158,636,509 / 22.65%
Number/percentage of N's	148,358 / 0.02%

GC Percentage	42.58%

2.3. Coverage

Mean	0.2264
Standard Deviation	0.9959

2.4. Mapping Quality

Mean Mapping Quality	51.57

2.5. Insert size

Mean	242,888.56
Standard Deviation	4,734,287.46
P25/Median/P75	146 / 189 / 254

2.6. Mismatches and indels

General error rate	0.92%
Mismatches	6,262,914
Insertions	115,345
Mapped reads with at least one insertion	1.51%
Deletions	359,377
Mapped reads with at least one deletion	4.66%
Homopolymer indels	52.66%

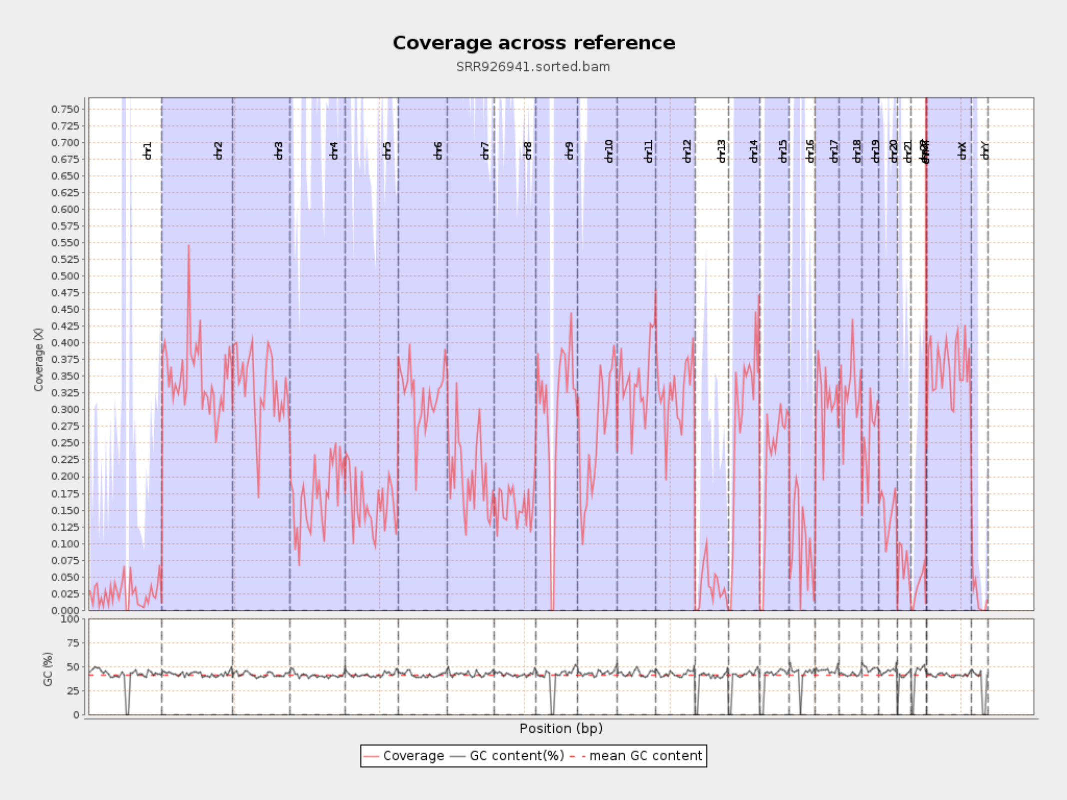
2.7. Chromosome stats

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

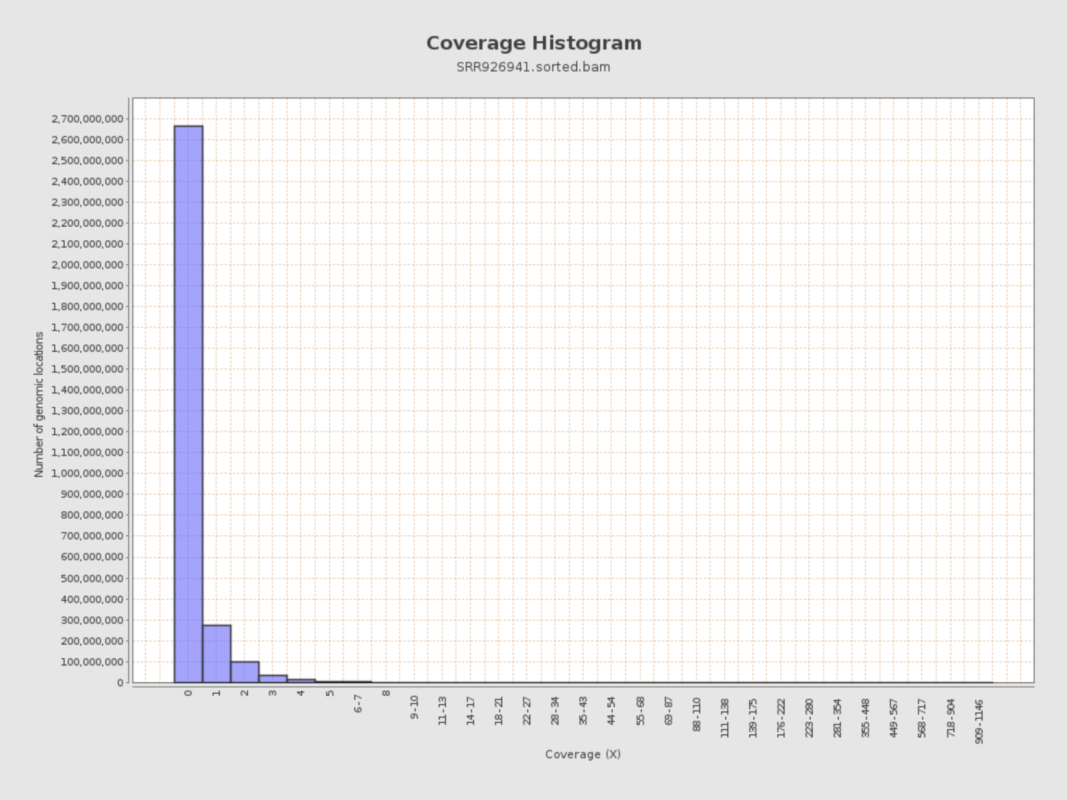
		bases	coverage	deviation
chr1	249250621	6117734	0.0245	0.7817
chr2	243199373	85461987	0.3514	1.9539
chr3	198022430	66223405	0.3344	0.817
chr4	191154276	32690032	0.171	0.8967
chr5	180915260	28530968	0.1577	0.5438
chr6	171115067	55271339	0.323	0.8962
chr7	159138663	32179805	0.2022	0.6705
chr8	146364022	22941180	0.1567	0.5716
chr9	141213431	42321710	0.2997	1.1079
chr10	135534747	35616387	0.2628	0.9694
chr11	135006516	46089803	0.3414	1.5266
chr12	133851895	43484732	0.3249	0.8232
chr13	115169878	3922796	0.0341	0.2474
chr14	107349540	30343591	0.2827	0.7705
chr15	102531392	22672859	0.2211	0.687
chr16	90354753	8811974	0.0975	0.9143
chr17	81195210	25501061	0.3141	1.0318
chr18	78077248	25931510	0.3321	1.0794
chr19	59128983	15367234	0.2599	0.9437
chr20	63025520	9271432	0.1471	0.5547
chr21	48129895	3032065	0.063	0.5526
chr22	51304566	1772542	0.0345	0.2759
chrMT	16571	81804	4.9366	4.8608
chrX	155270560	56157283	0.3617	0.9696

chrY	59373566	1177869	0.0198	0.7896

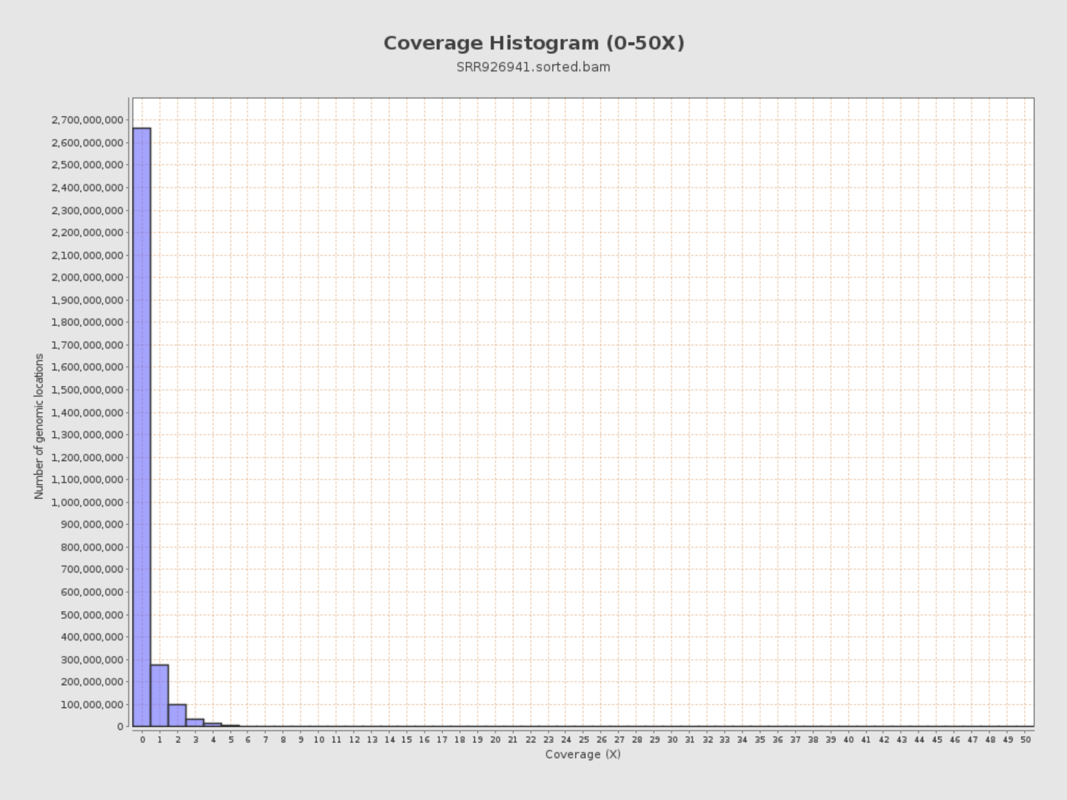
3. Results : Coverage across reference



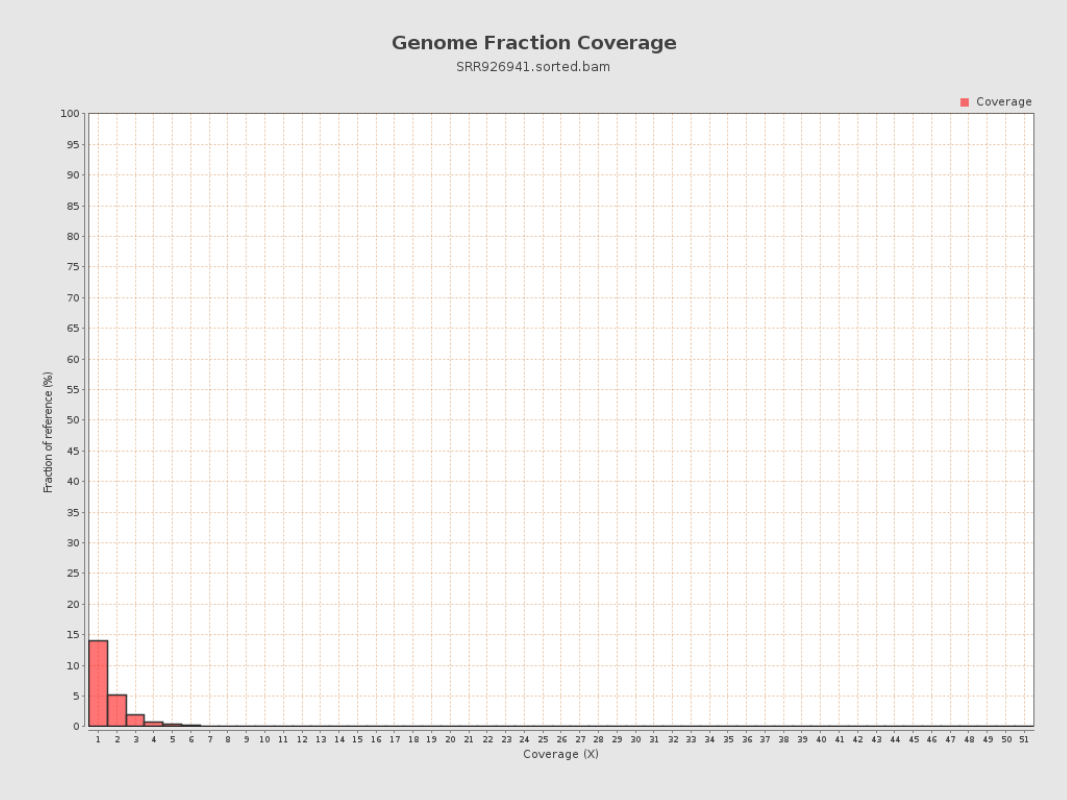
4. Results : Coverage Histogram



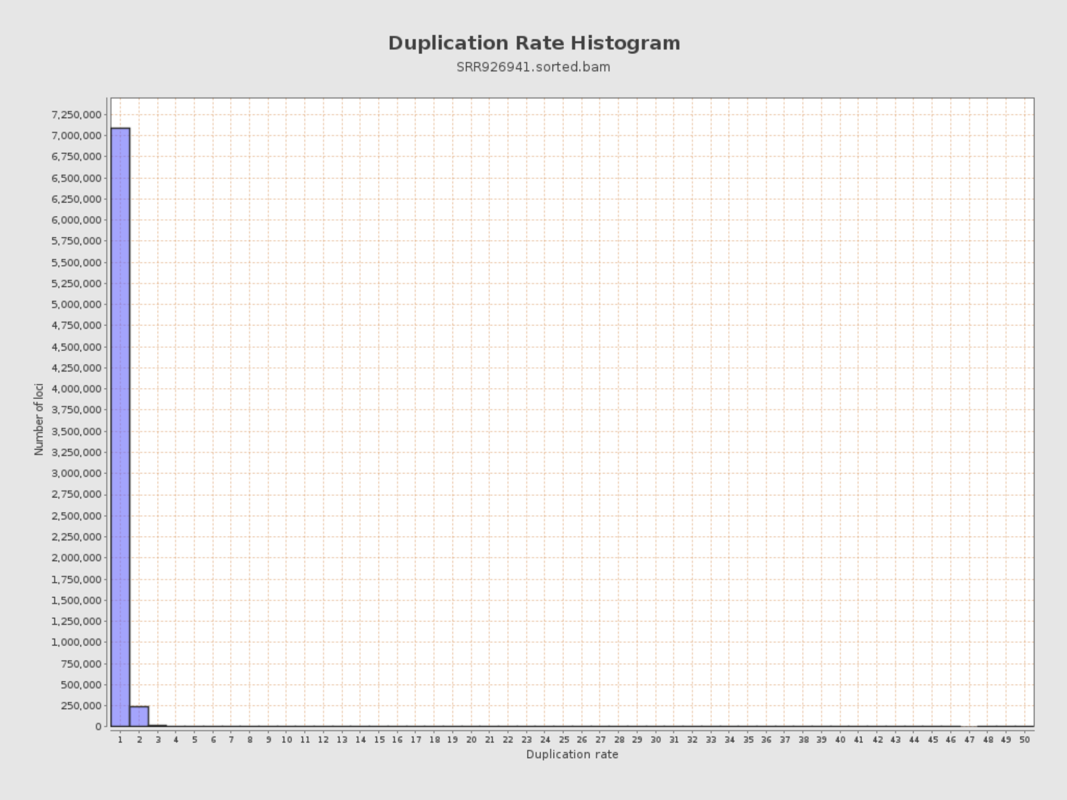
5. Results : Coverage Histogram (0-50X)



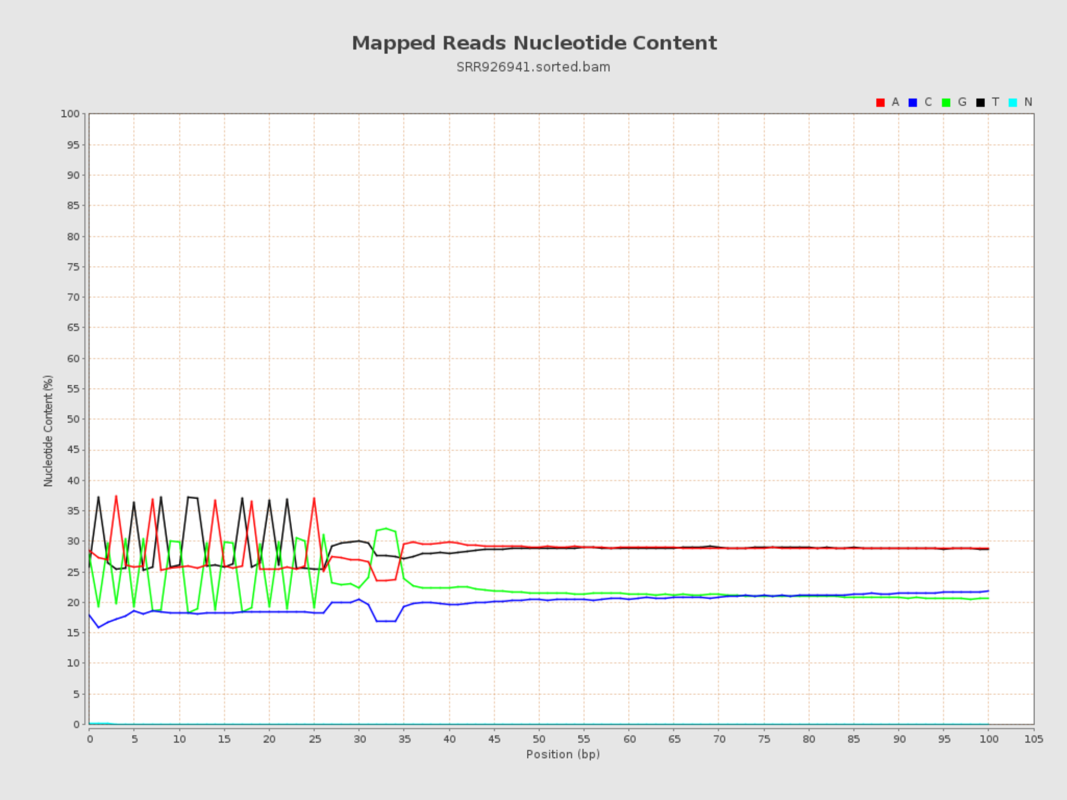
6. Results : Genome Fraction Coverage



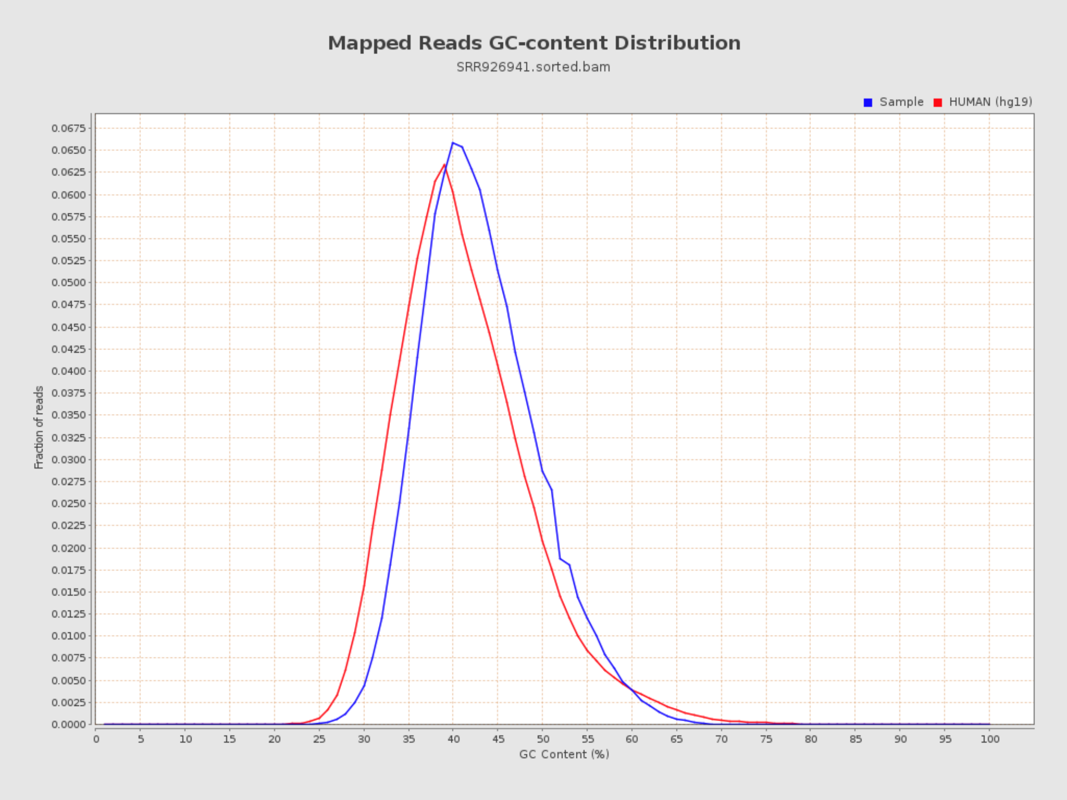
7. Results : Duplication Rate Histogram



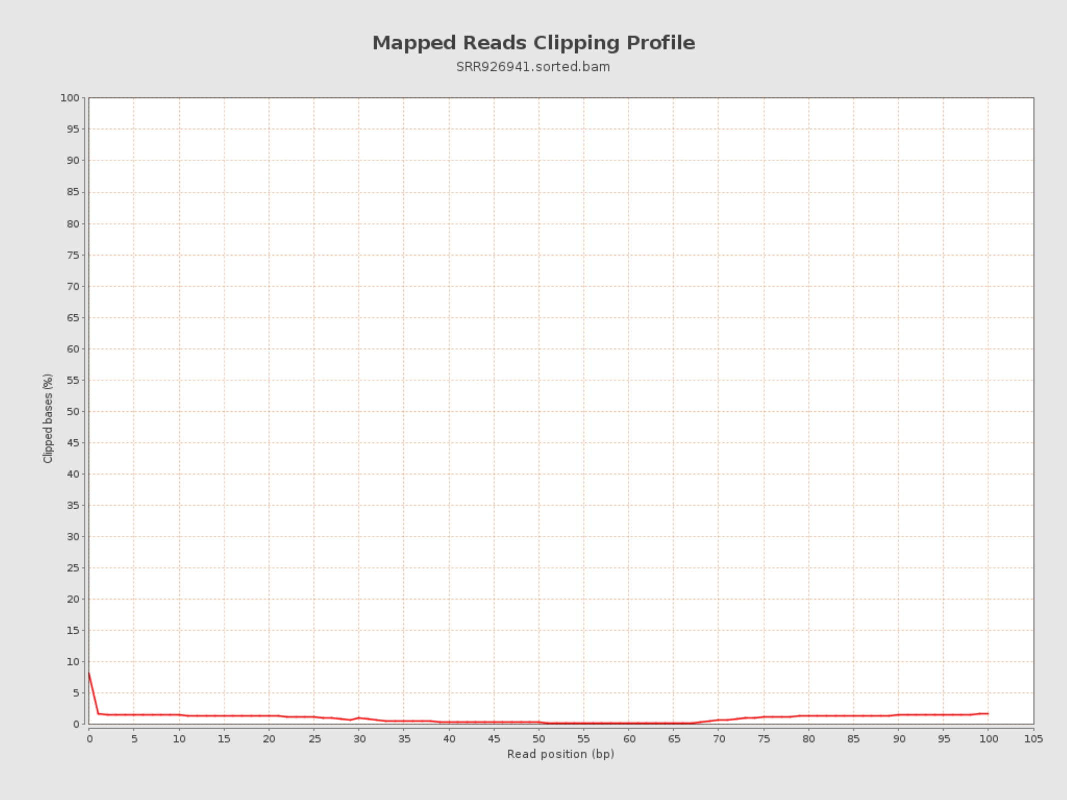
8. Results : Mapped Reads Nucleotide Content



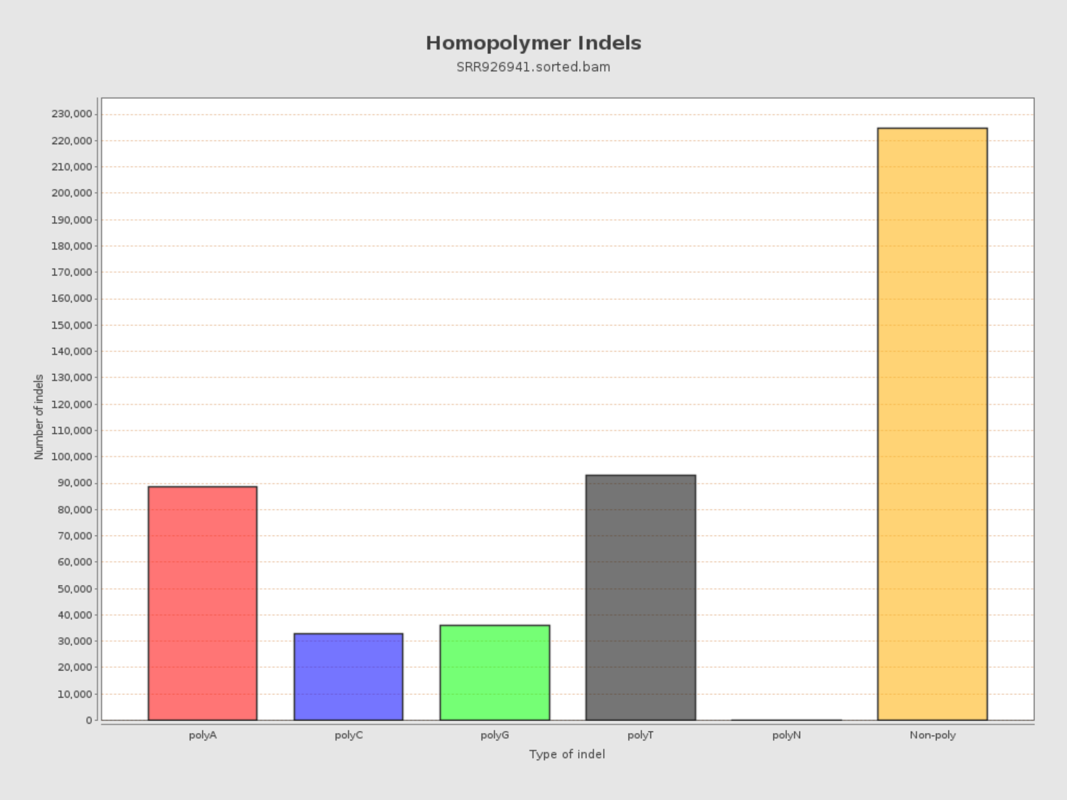
9. Results : Mapped Reads GC-content Distribution



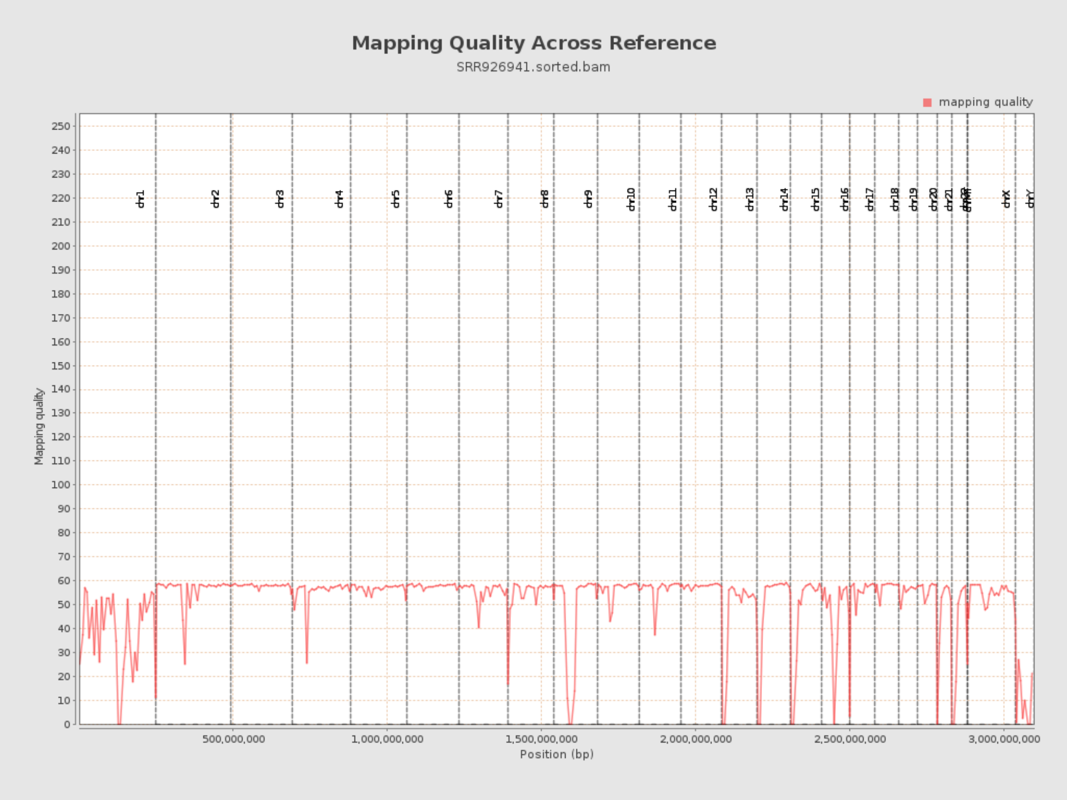
10. Results : Mapped Reads Clipping Profile



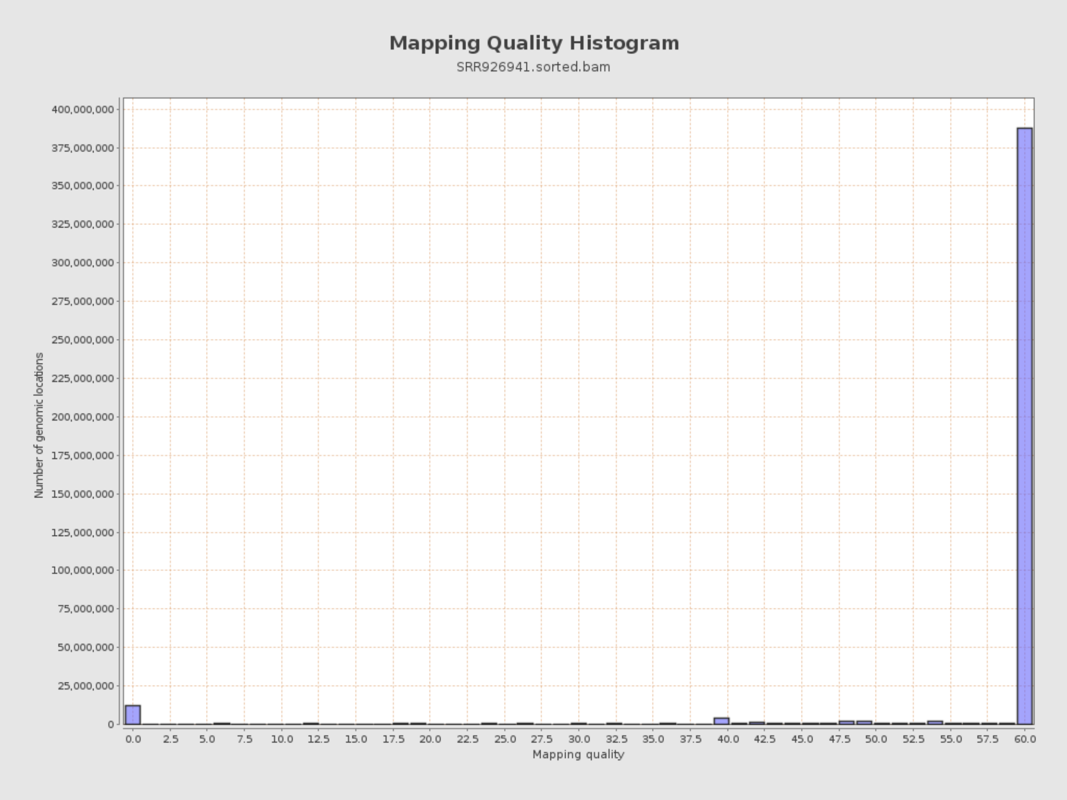
11. Results : Homopolymer Indels



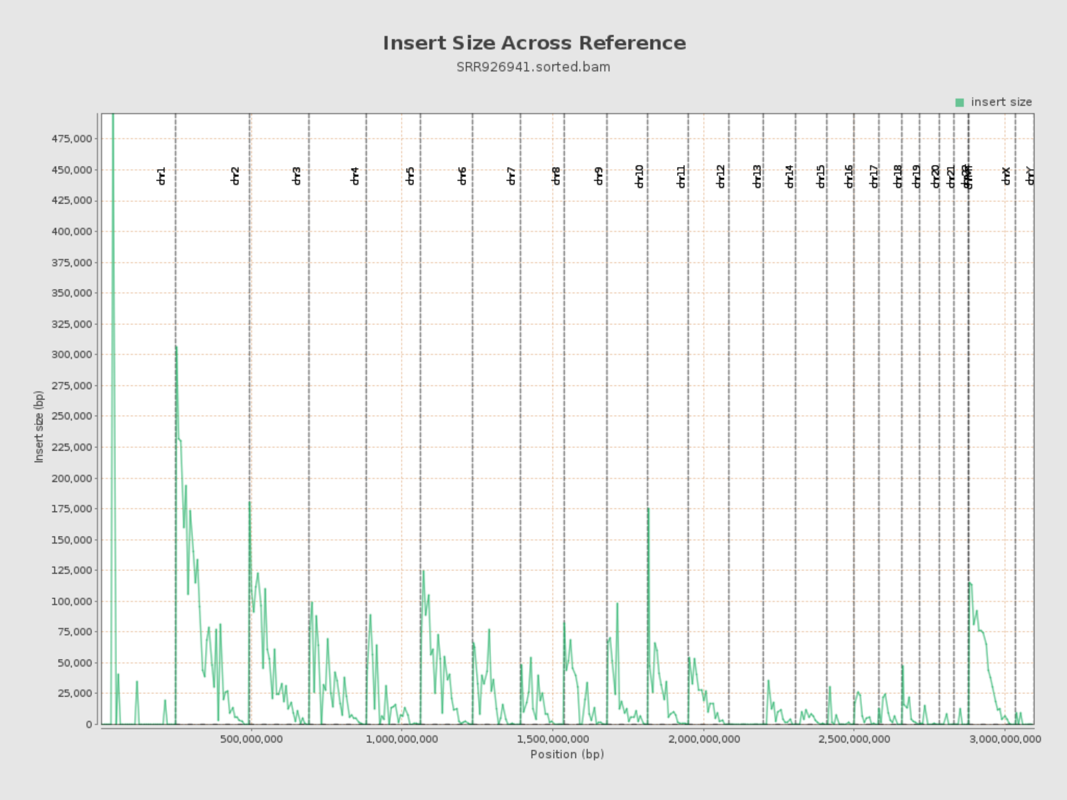
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram