Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 20:09:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926925.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_SRR926925 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926925_1.fastq.gz SRR926925_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 20:09:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926925.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,845,990
Mapped reads	11,565,116 / 97.63%
Unmapped reads	280,874 / 2.37%
Mapped paired reads	11,565,116 / 97.63%
Mapped reads, first in pair	5,803,525 / 48.99%
Mapped reads, second in pair	5,761,591 / 48.64%
Mapped reads, both in pair	11,433,550 / 96.52%
Mapped reads, singletons	131,566 / 1.11%
Secondary alignments	0
Supplementary alignments	110,241 / 0.93%
Read min/max/mean length	30 / 101 / 101.38
Duplicated reads (estimated)	620,011 / 5.23%
Duplication rate	4.22%
Clipped reads	3,765,800 / 31.79%

2.2. ACGT Content

Number/percentage of A's	306,120,115 / 28.67%
Number/percentage of C's	207,463,763 / 19.43%
Number/percentage of T's	311,231,930 / 29.15%
Number/percentage of G's	242,650,806 / 22.73%
Number/percentage of N's	213,587 / 0.02%

GC Percentage	42.16%

2.3. Coverage

Mean	0.3452
Standard Deviation	1.5225

2.4. Mapping Quality

Mean Mapping Quality	53.43

2.5. Insert size

Mean	95,858.57
Standard Deviation	3,029,613.85
P25/Median/P75	155 / 202 / 272

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	10,236,374
Insertions	176,569
Mapped reads with at least one insertion	1.5%
Deletions	587,410
Mapped reads with at least one deletion	4.94%
Homopolymer indels	52.89%

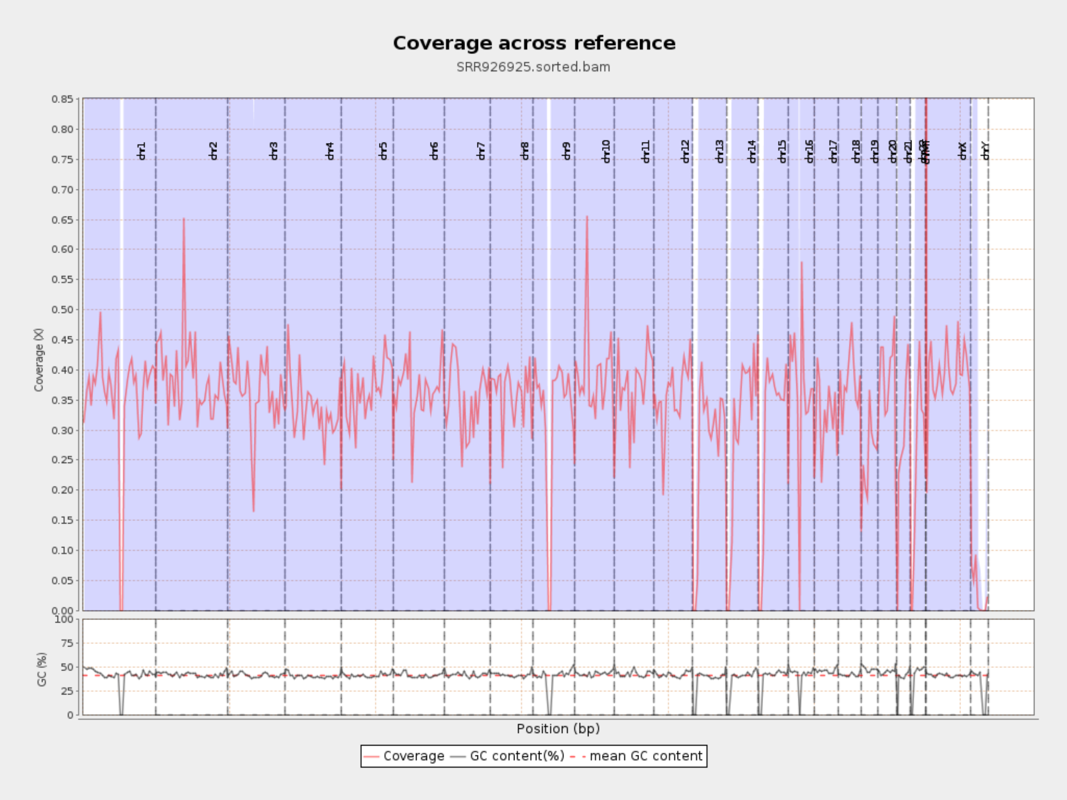
2.7. Chromosome stats

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

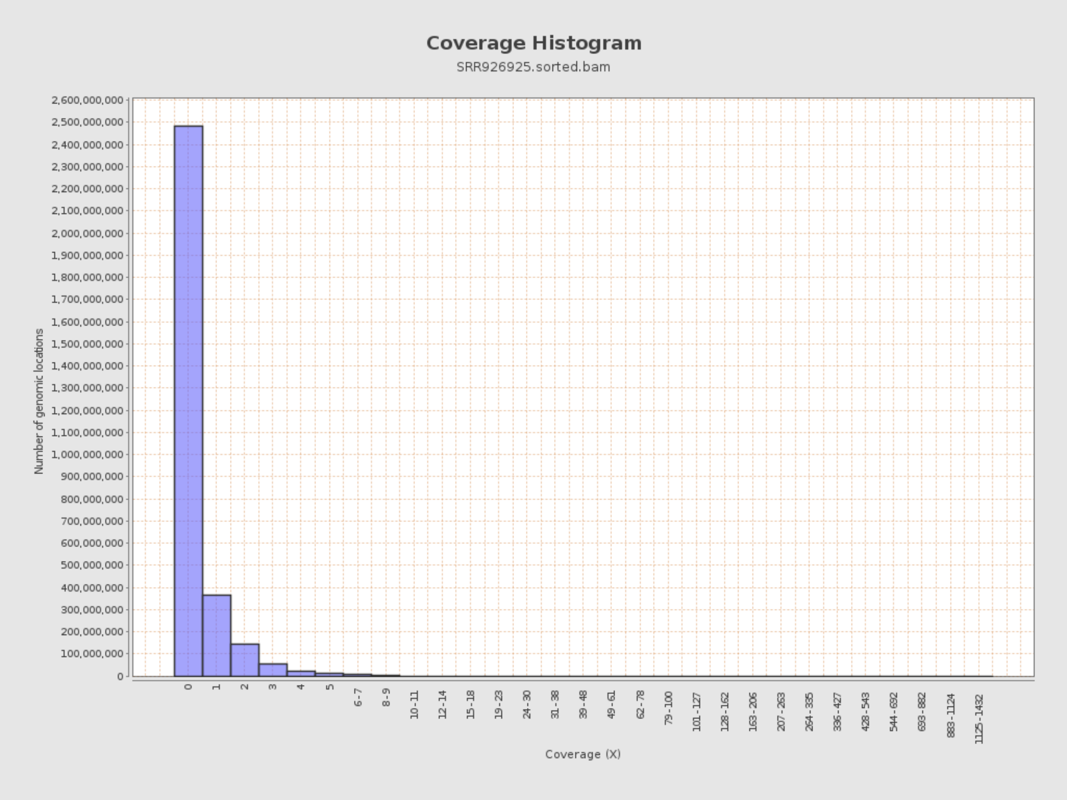
		bases	coverage	deviation
chr1	249250621	88601583	0.3555	1.6312
chr2	243199373	94518831	0.3886	2.3206
chr3	198022430	71780754	0.3625	0.8926
chr4	191154276	64724698	0.3386	1.3981
chr5	180915260	66613723	0.3682	0.8959
chr6	171115067	63197268	0.3693	1.8356
chr7	159138663	56173334	0.353	1.0512
chr8	146364022	52711508	0.3601	1.0015
chr9	141213431	46196124	0.3271	1.7231
chr10	135534747	53318920	0.3934	3.3012
chr11	135006516	50232375	0.3721	1.1321
chr12	133851895	48163965	0.3598	0.9025
chr13	115169878	31621272	0.2746	0.7679
chr14	107349540	32135637	0.2994	0.8271
chr15	102531392	30932837	0.3017	0.828
chr16	90354753	32370143	0.3583	2.0736
chr17	81195210	26432722	0.3255	1.0838
chr18	78077248	29468721	0.3774	1.8521
chr19	59128983	15237523	0.2577	1.163
chr20	63025520	24825403	0.3939	0.9904
chr21	48129895	14017622	0.2912	1.1664
chr22	51304566	12554219	0.2447	0.7686
chrMT	16571	282692	17.0594	13.8627
chrX	155270560	60679164	0.3908	0.9925

chrY	59373566	1722779	0.029	1.1398

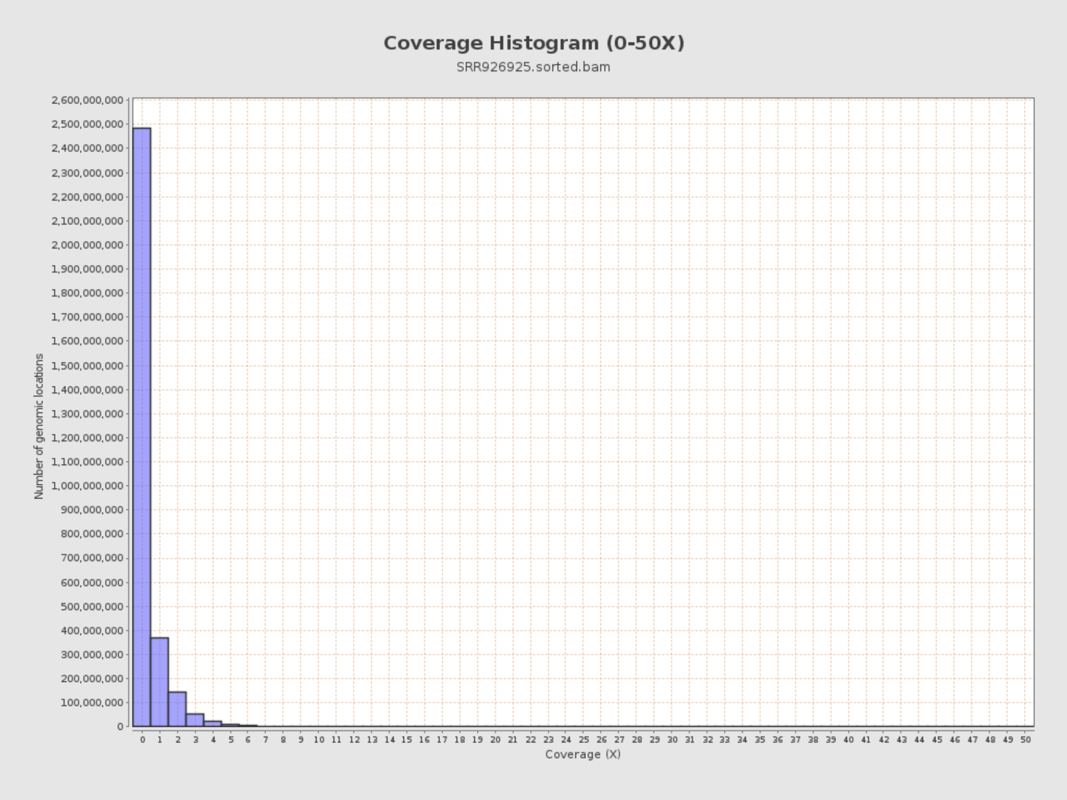
3. Results : Coverage across reference



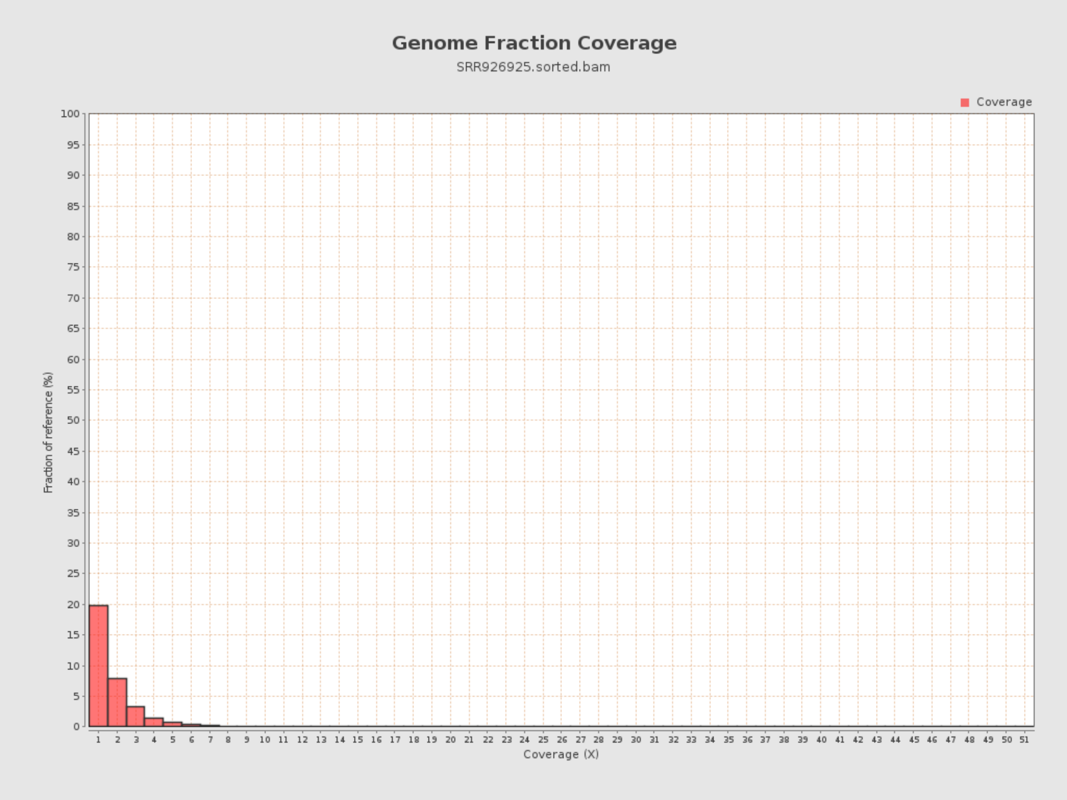
4. Results : Coverage Histogram



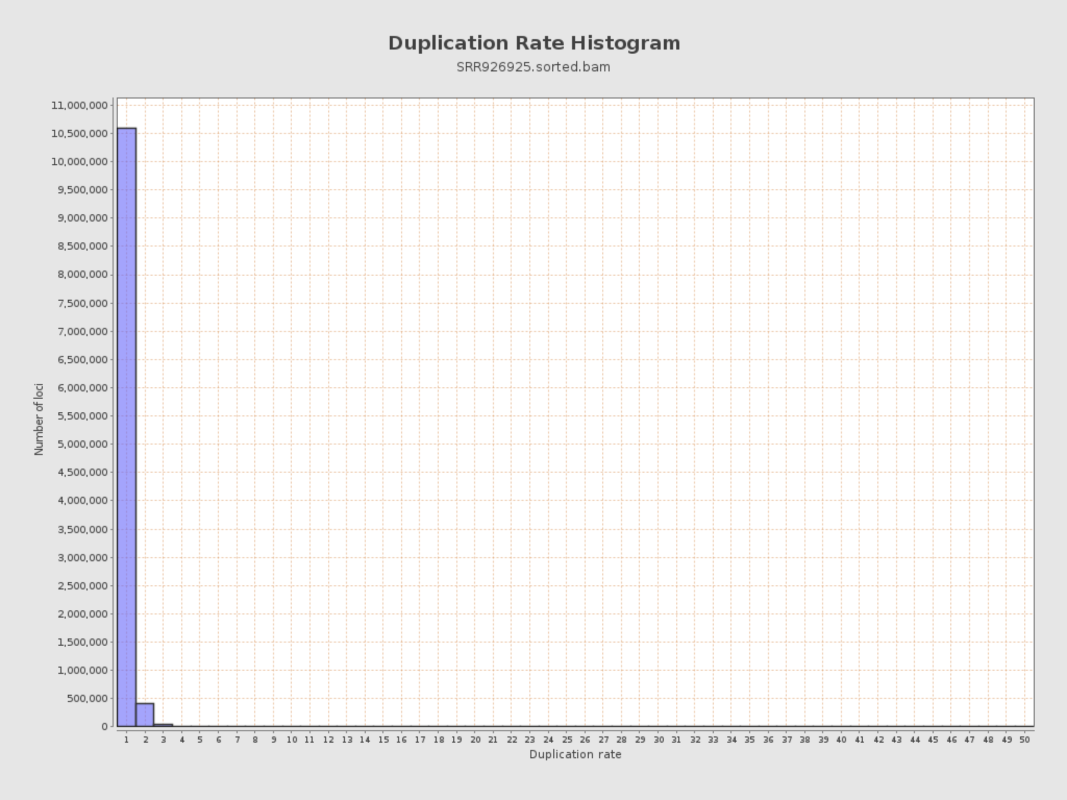
5. Results : Coverage Histogram (0-50X)



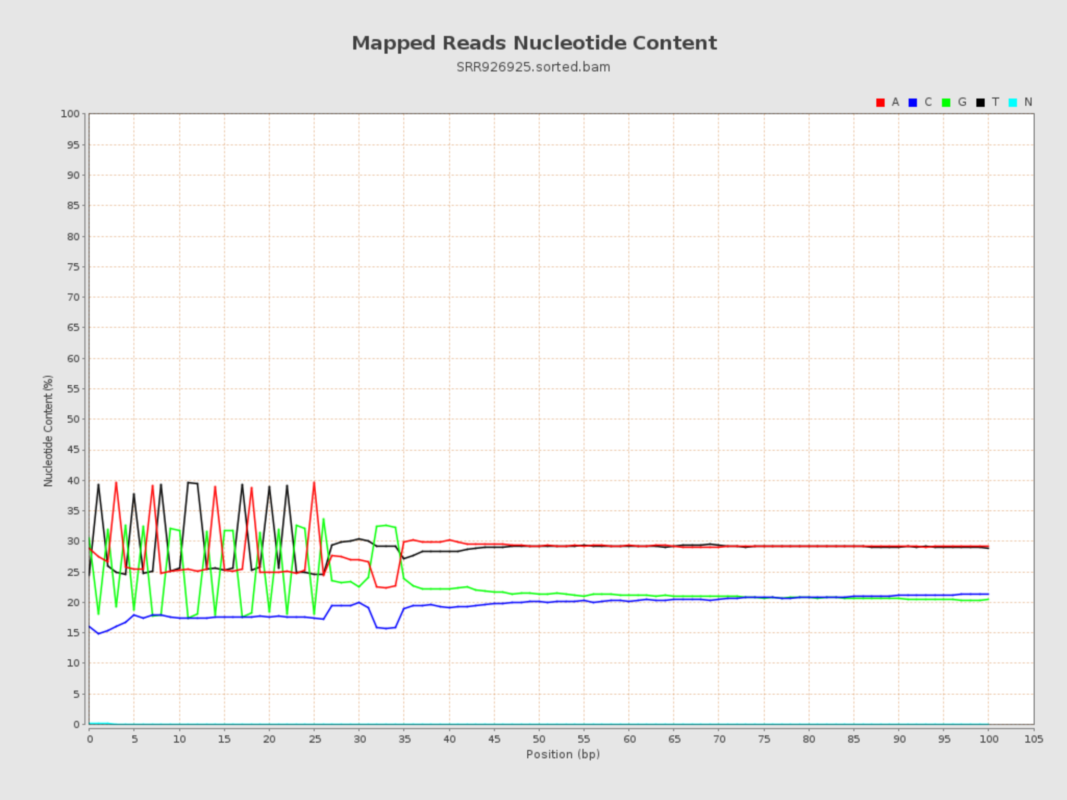
6. Results : Genome Fraction Coverage



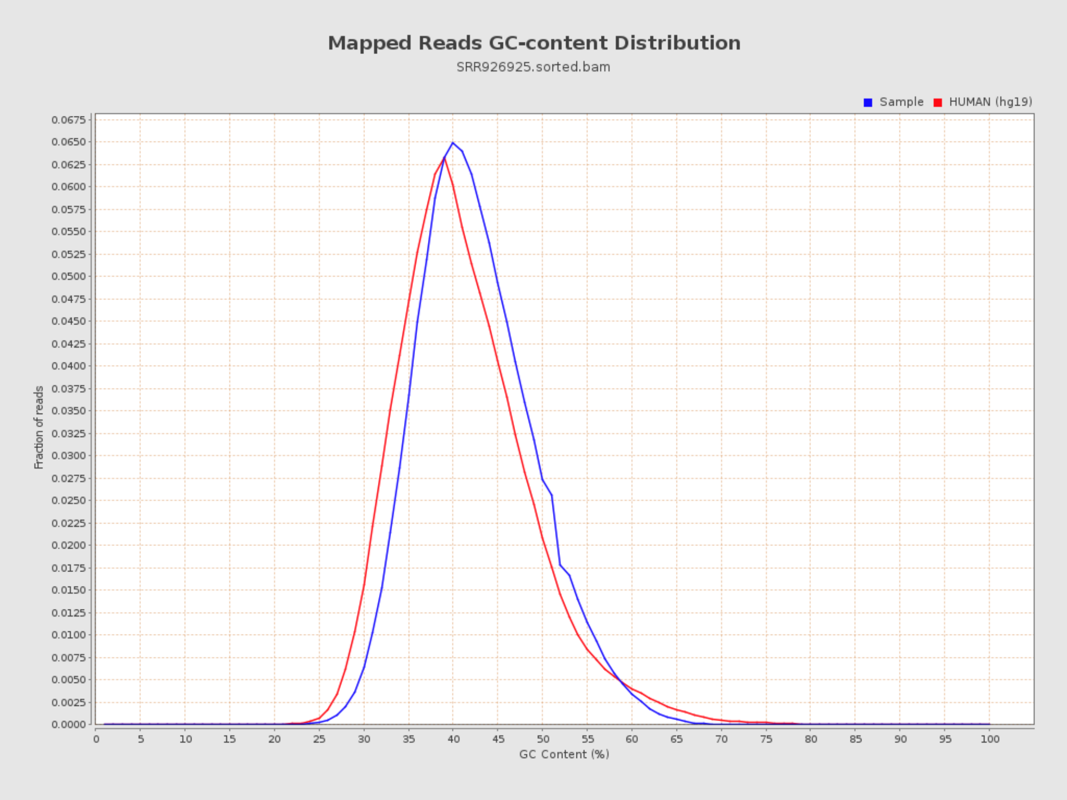
7. Results : Duplication Rate Histogram



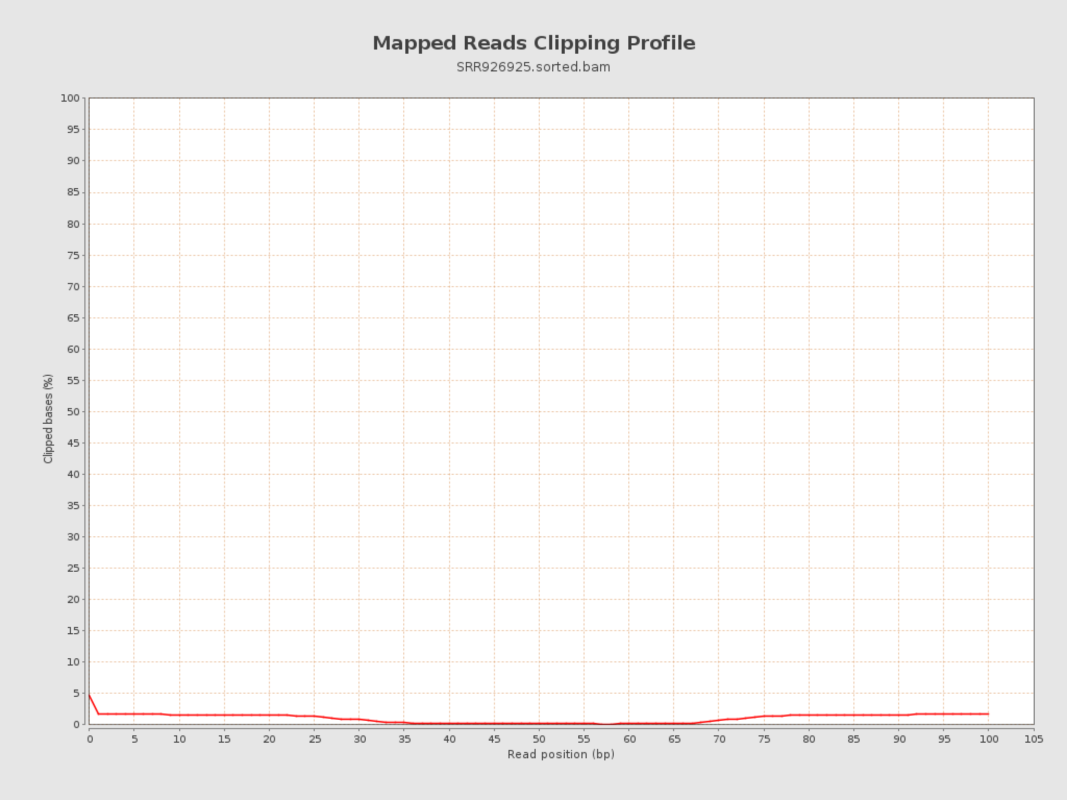
8. Results : Mapped Reads Nucleotide Content



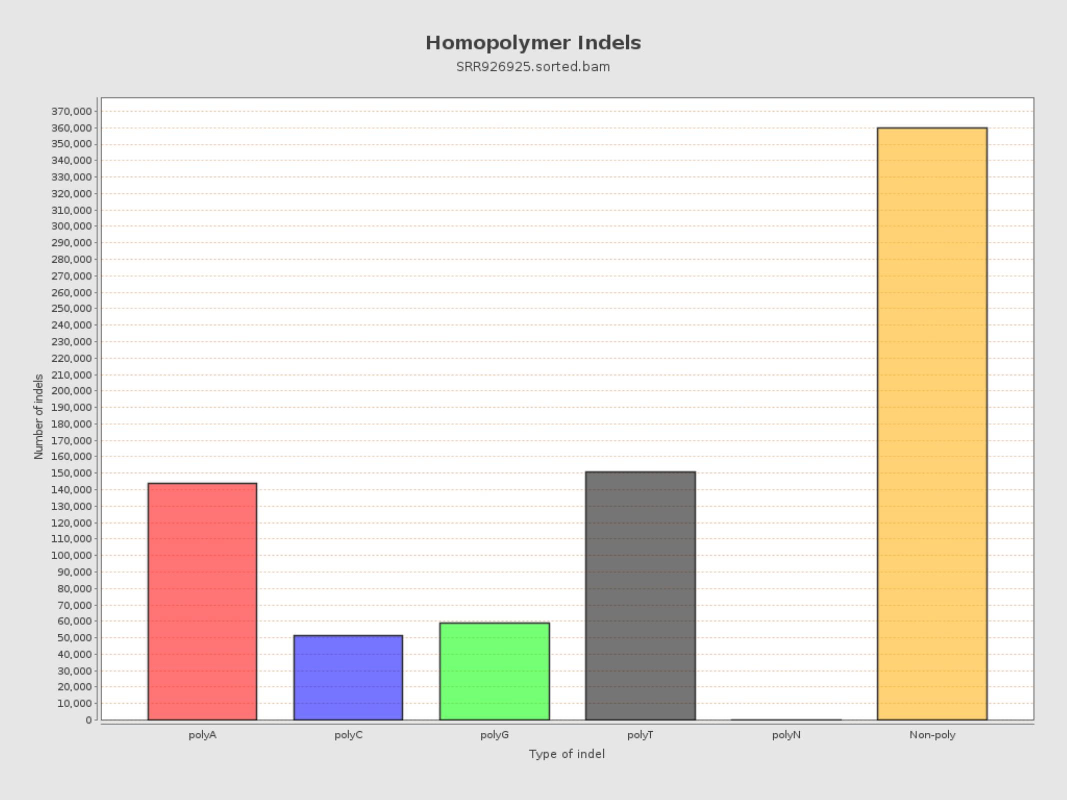
9. Results : Mapped Reads GC-content Distribution



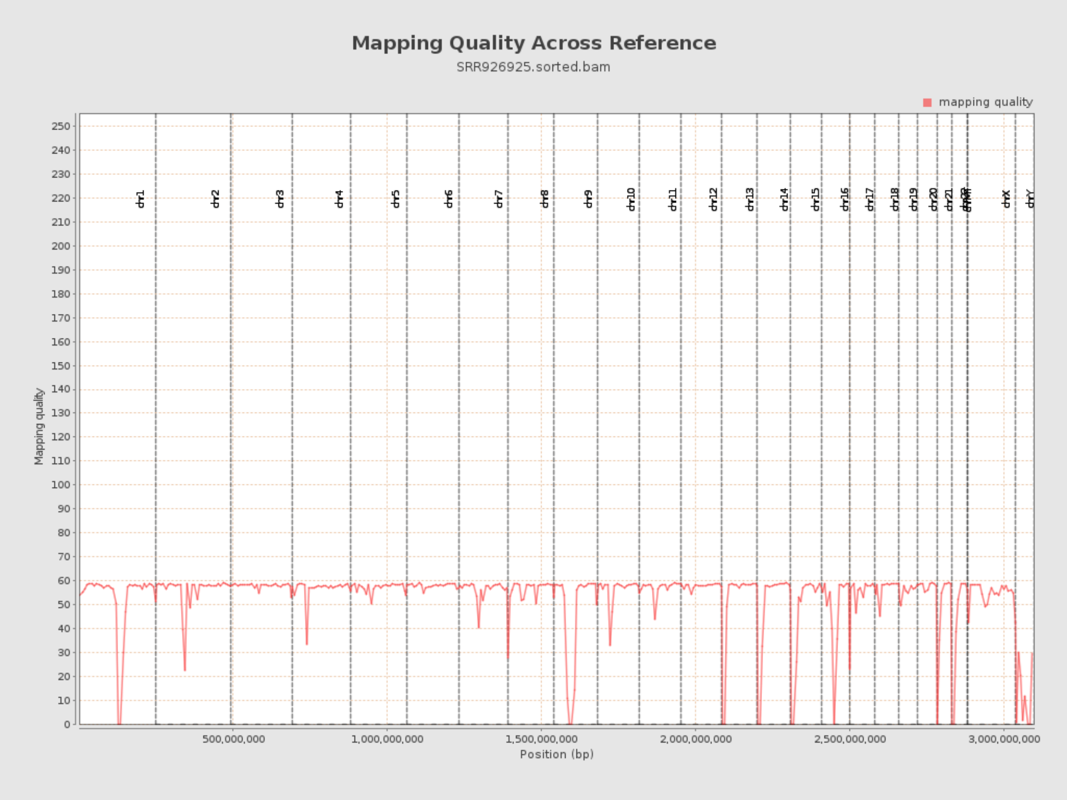
10. Results : Mapped Reads Clipping Profile



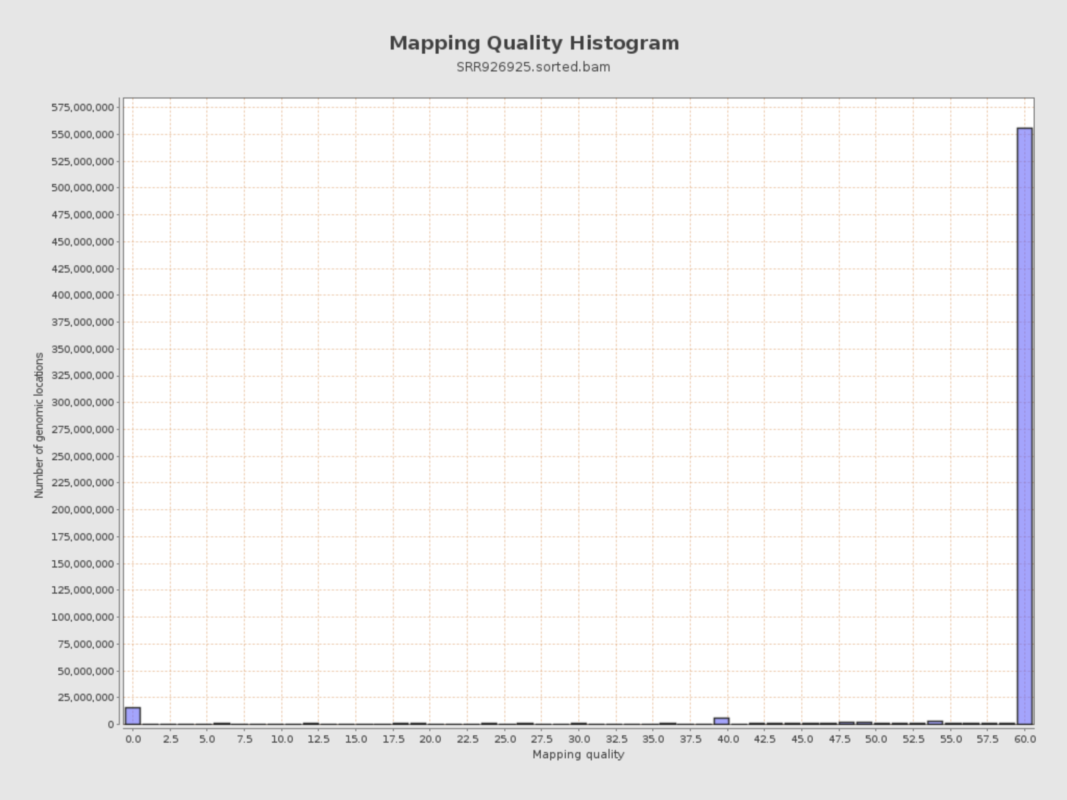
11. Results : Homopolymer Indels



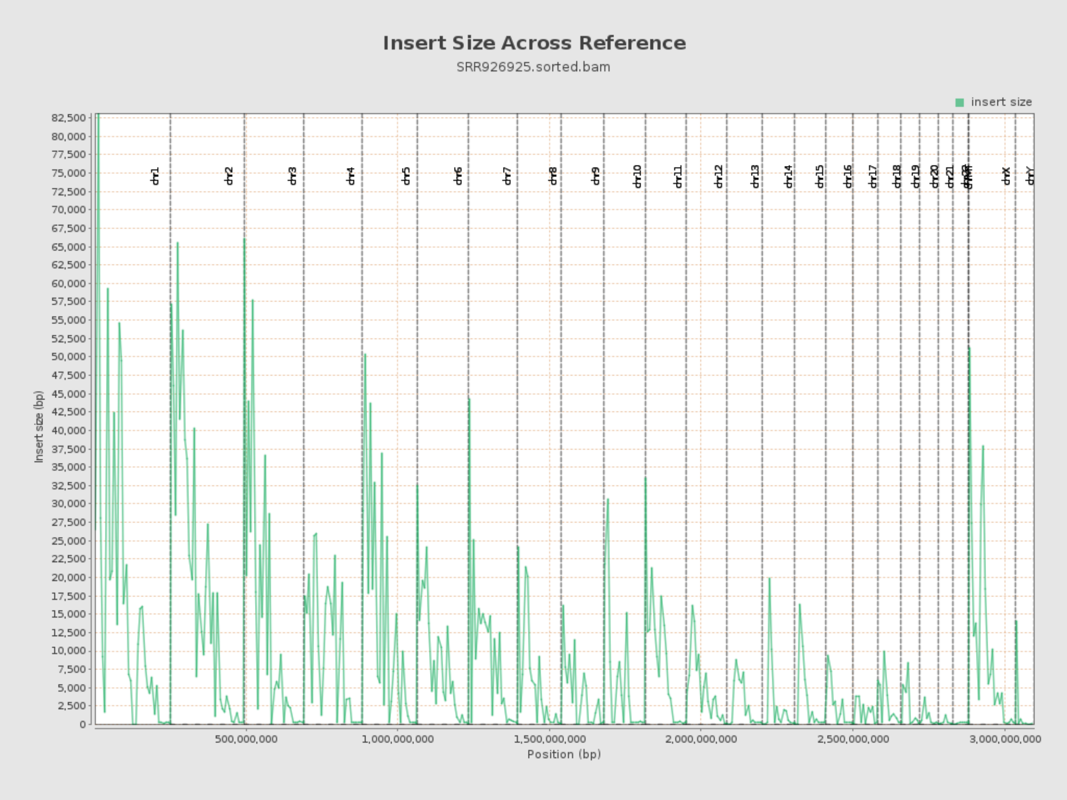
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram