Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 05:46:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926897.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_SRR926897 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926897_1.fastq.gz SRR926897_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 05:46:23 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926897.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,515,742
Mapped reads	21,255,882 / 90.39%
Unmapped reads	2,259,860 / 9.61%
Mapped paired reads	21,255,882 / 90.39%
Mapped reads, first in pair	10,688,967 / 45.45%
Mapped reads, second in pair	10,566,915 / 44.94%
Mapped reads, both in pair	20,859,846 / 88.71%
Mapped reads, singletons	396,036 / 1.68%
Secondary alignments	0
Supplementary alignments	556,387 / 2.37%
Read min/max/mean length	30 / 101 / 101.98
Duplicated reads (estimated)	1,817,578 / 7.73%
Duplication rate	6.95%
Clipped reads	9,794,573 / 41.65%

2.2. ACGT Content

Number/percentage of A's	538,701,280 / 28.22%
Number/percentage of C's	373,284,456 / 19.56%
Number/percentage of T's	547,469,556 / 28.68%
Number/percentage of G's	449,158,821 / 23.53%
Number/percentage of N's	154,702 / 0.01%

GC Percentage	43.09%

2.3. Coverage

Mean	0.6171
Standard Deviation	2.0821

2.4. Mapping Quality

Mean Mapping Quality	52.39

2.5. Insert size

Mean	303,765.04
Standard Deviation	5,423,955.96
P25/Median/P75	136 / 181 / 248

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	19,792,910
Insertions	324,395
Mapped reads with at least one insertion	1.5%
Deletions	1,017,063
Mapped reads with at least one deletion	4.66%
Homopolymer indels	51.77%

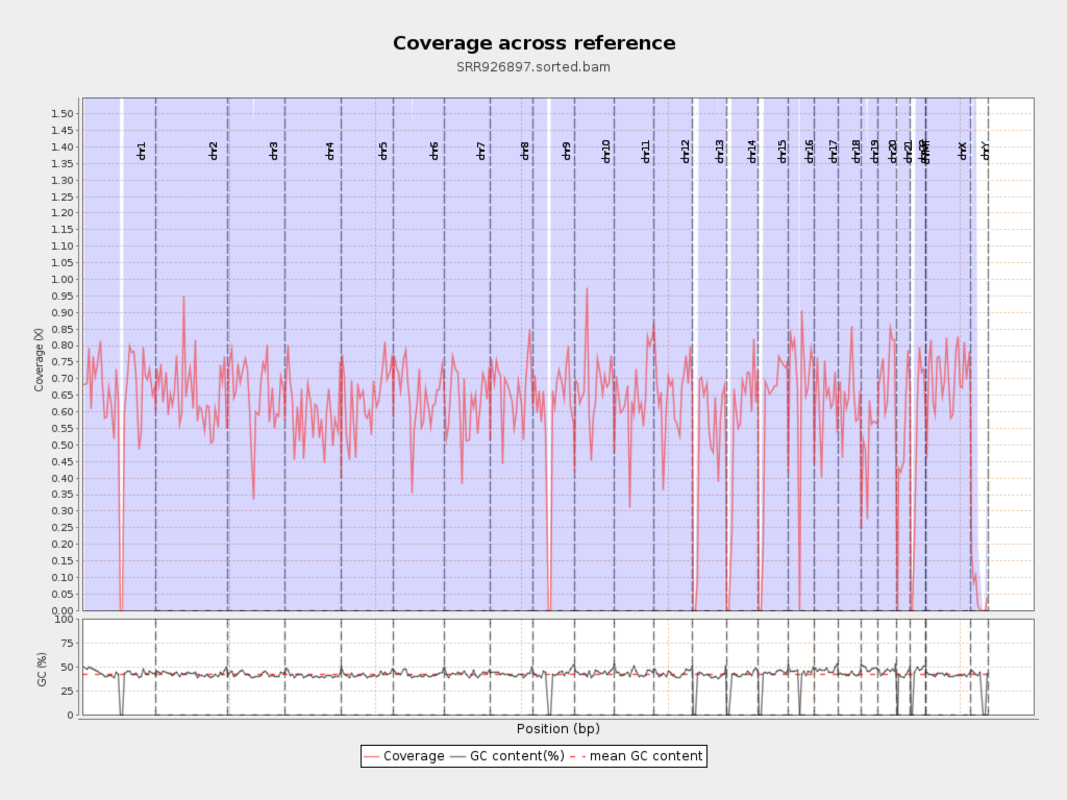
2.7. Chromosome stats

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

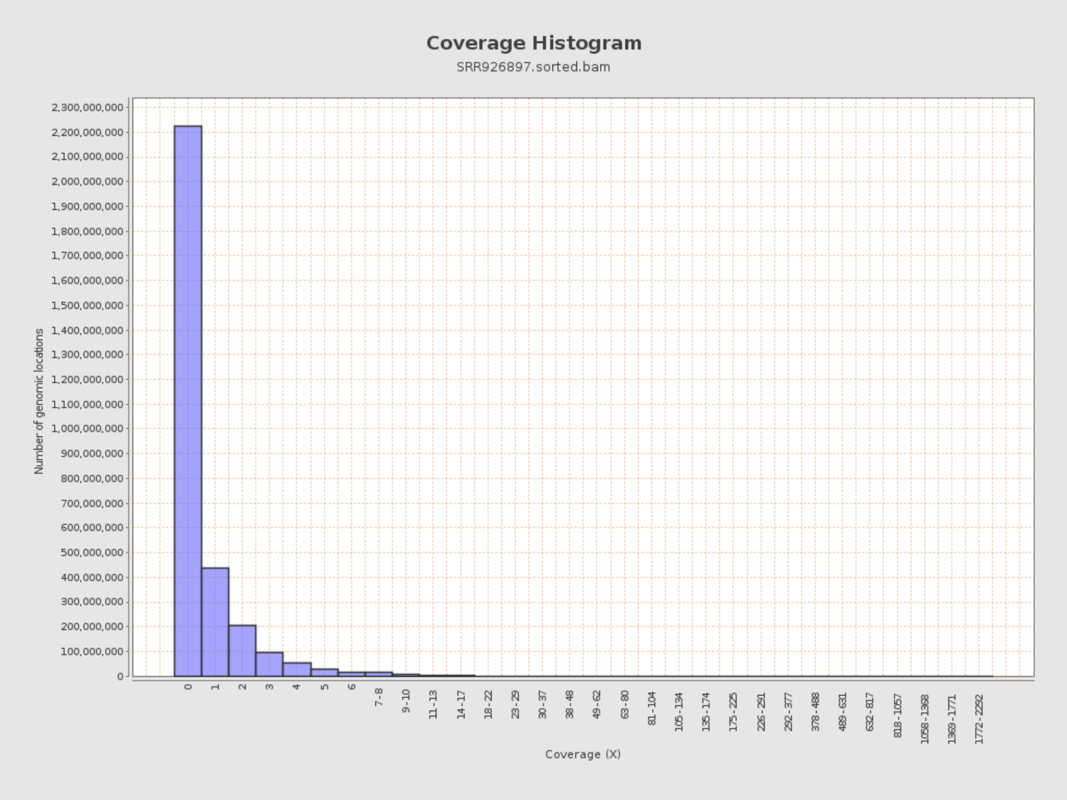
		bases	coverage	deviation
chr1	249250621	159582979	0.6403	1.8619
chr2	243199373	159132853	0.6543	2.8473
chr3	198022430	129355338	0.6532	1.4585
chr4	191154276	114152657	0.5972	1.5141
chr5	180915260	116461358	0.6437	1.4282
chr6	171115067	110984942	0.6486	1.4399
chr7	159138663	99553712	0.6256	1.6363
chr8	146364022	97815318	0.6683	1.5926
chr9	141213431	82276736	0.5826	2.4823
chr10	135534747	91685389	0.6765	5.0569
chr11	135006516	87064722	0.6449	1.7457
chr12	133851895	87734756	0.6555	1.547
chr13	115169878	57482558	0.4991	1.2582
chr14	107349540	58440493	0.5444	1.3555
chr15	102531392	58182418	0.5675	1.4465
chr16	90354753	61406229	0.6796	3.1454
chr17	81195210	51580338	0.6353	1.5536
chr18	78077248	49986577	0.6402	2.398
chr19	59128983	29872707	0.5052	1.4312
chr20	63025520	45772712	0.7263	1.6352
chr21	48129895	24511962	0.5093	1.7618
chr22	51304566	25002171	0.4873	1.353
chrMT	16571	10722	0.647	0.974
chrX	155270560	109412823	0.7047	1.5747

chrY	59373566	2792799	0.047	0.9767

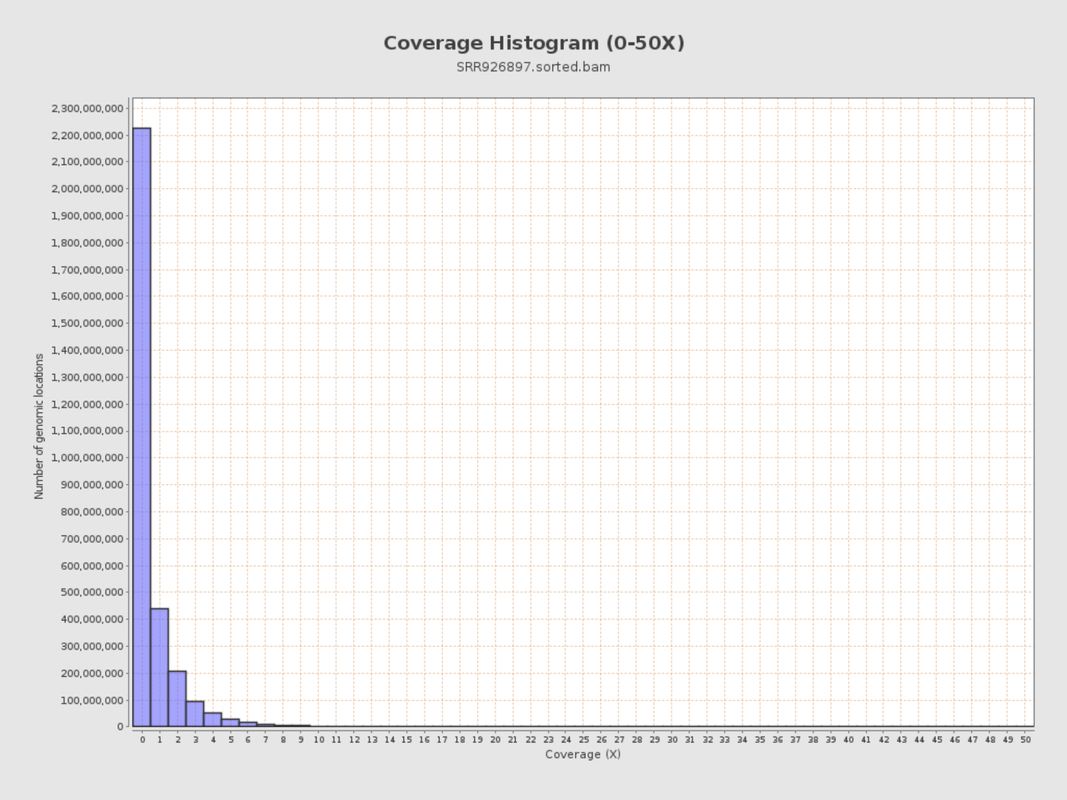
3. Results : Coverage across reference



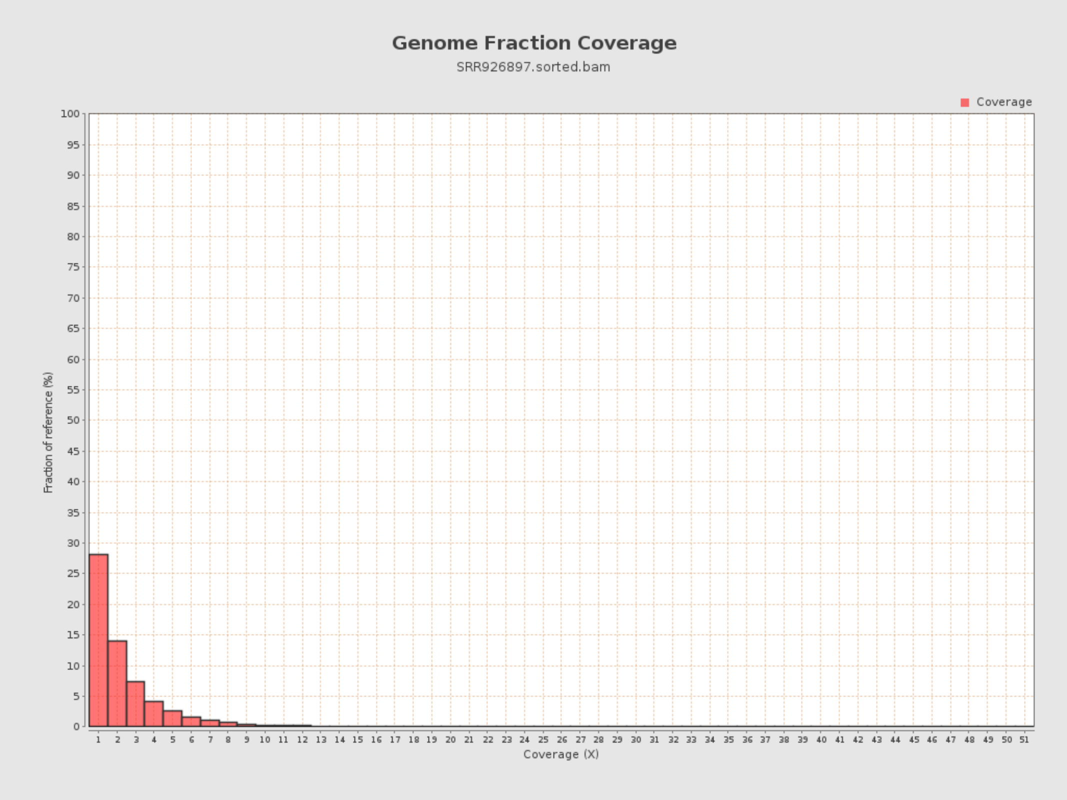
4. Results : Coverage Histogram



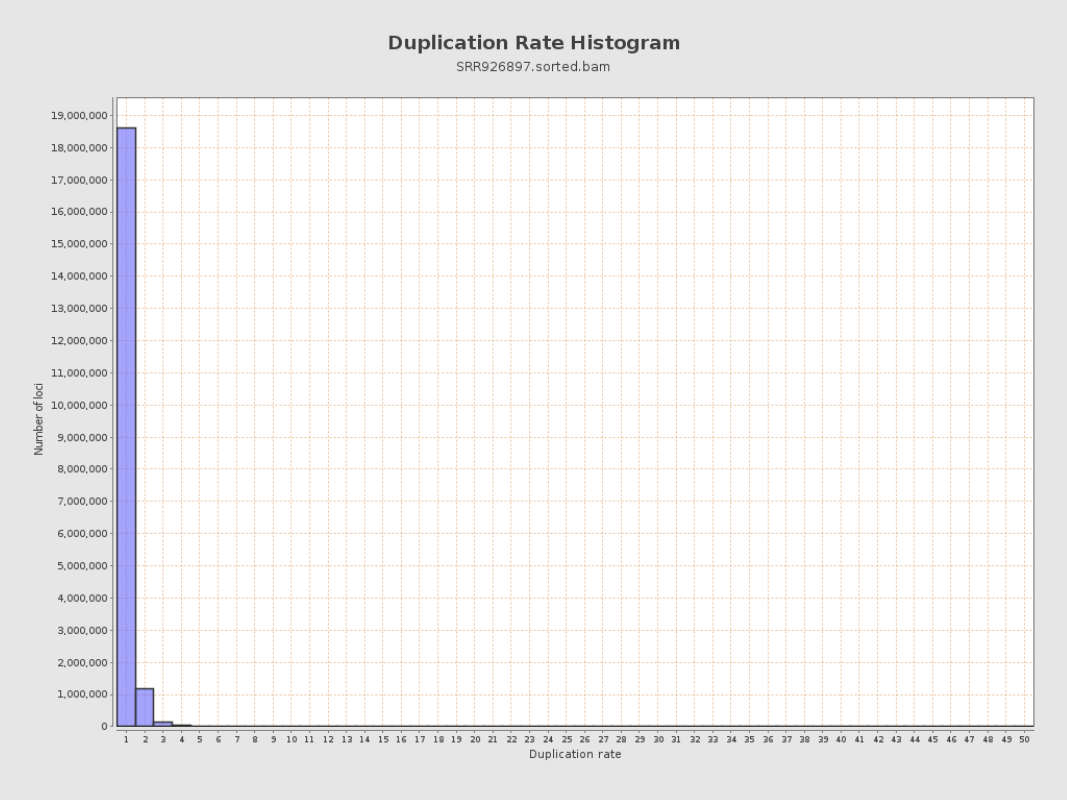
5. Results : Coverage Histogram (0-50X)



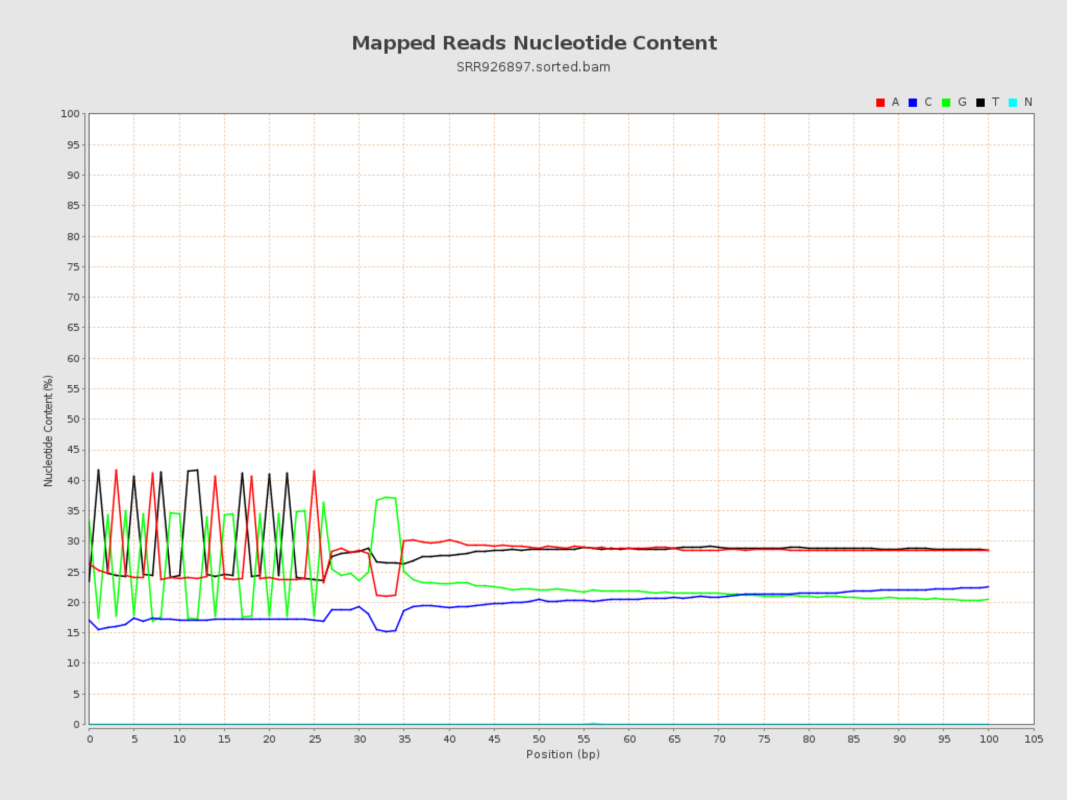
6. Results : Genome Fraction Coverage



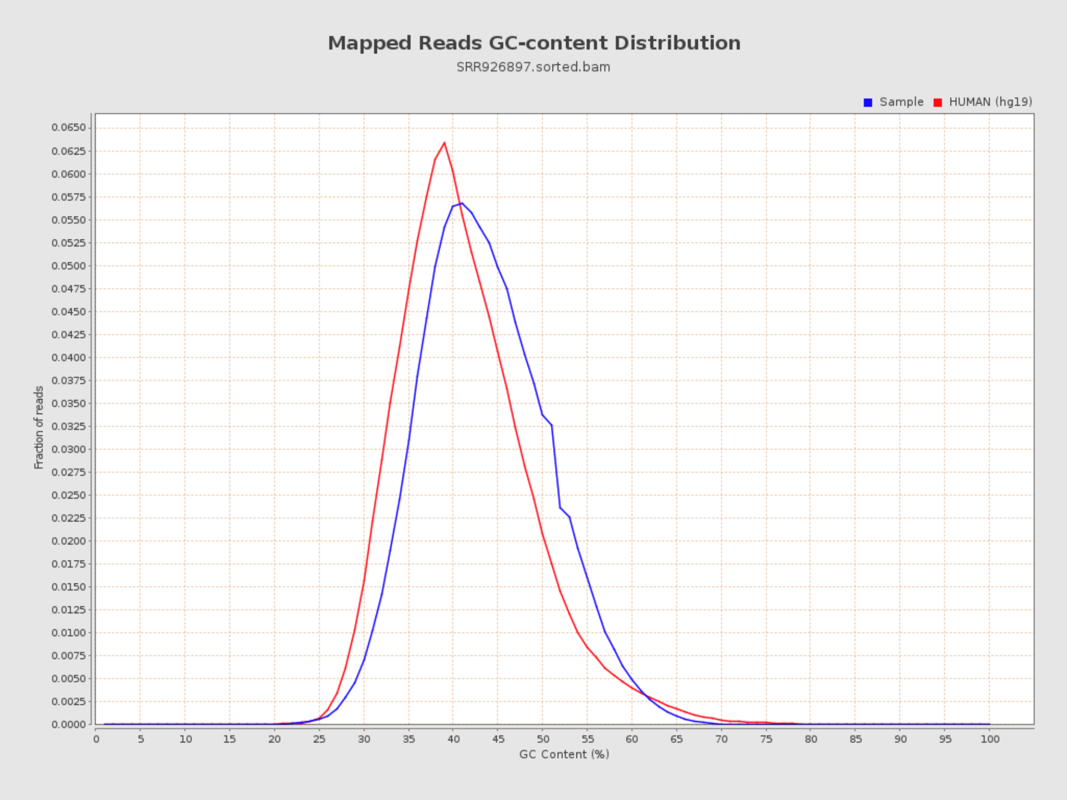
7. Results : Duplication Rate Histogram



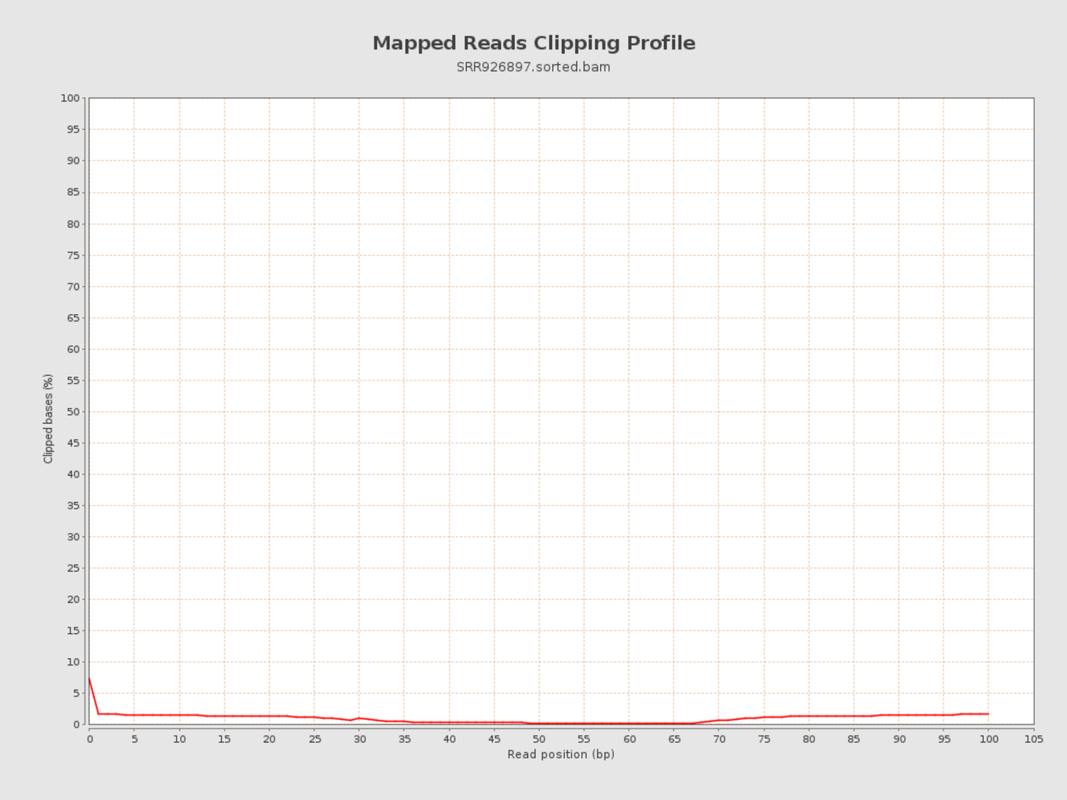
8. Results : Mapped Reads Nucleotide Content



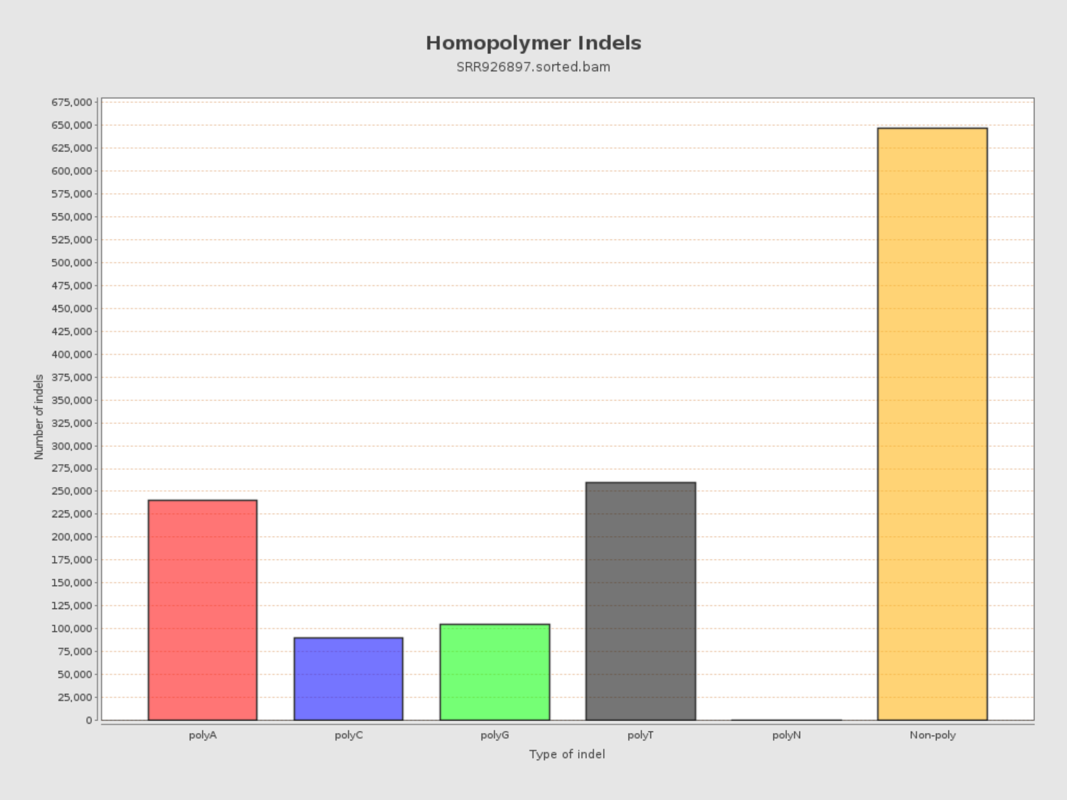
9. Results : Mapped Reads GC-content Distribution



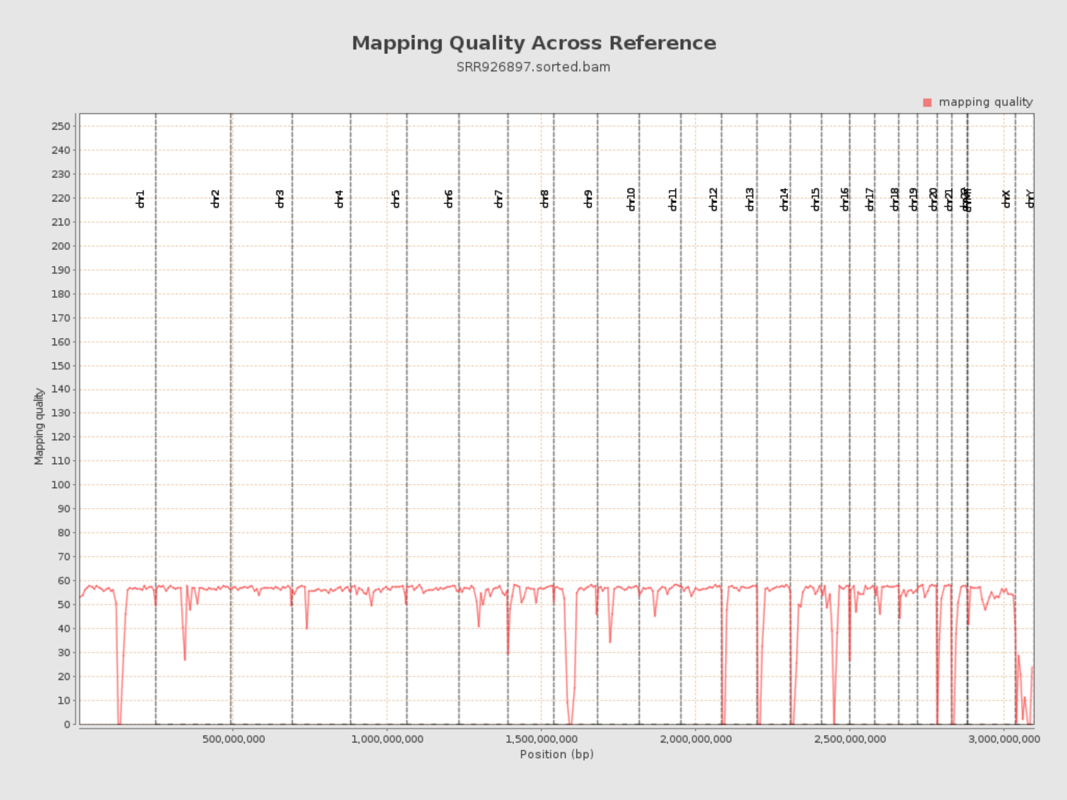
10. Results : Mapped Reads Clipping Profile



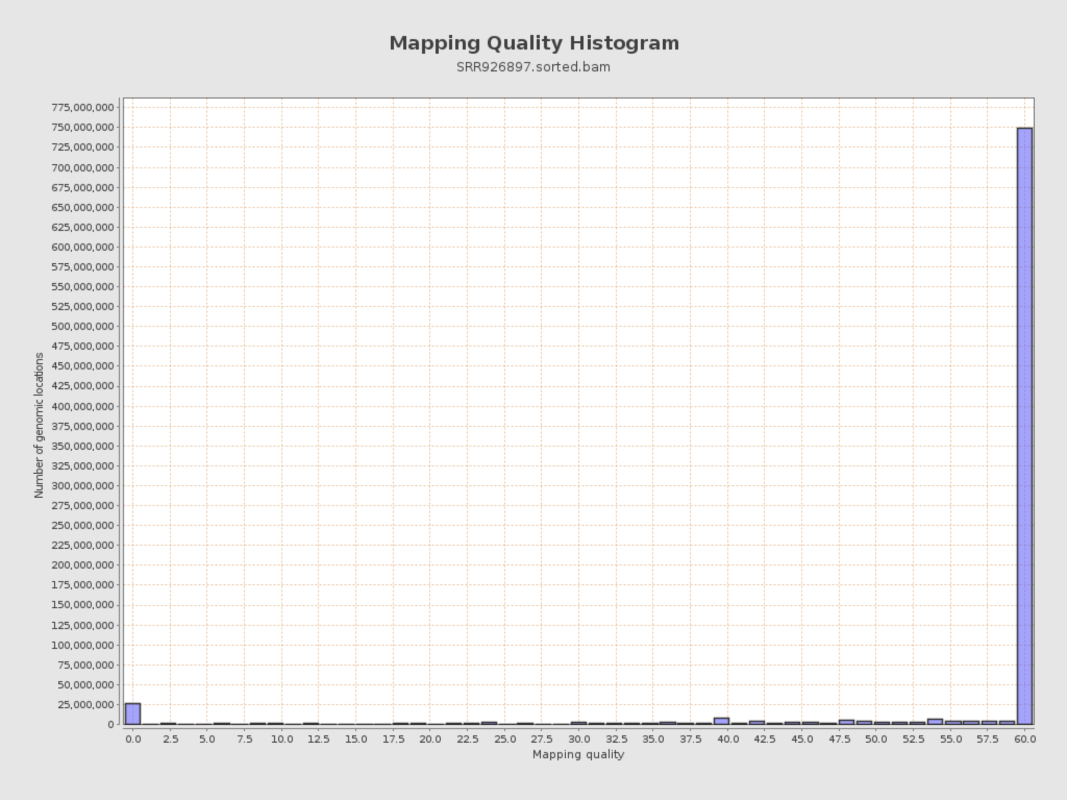
11. Results : Homopolymer Indels



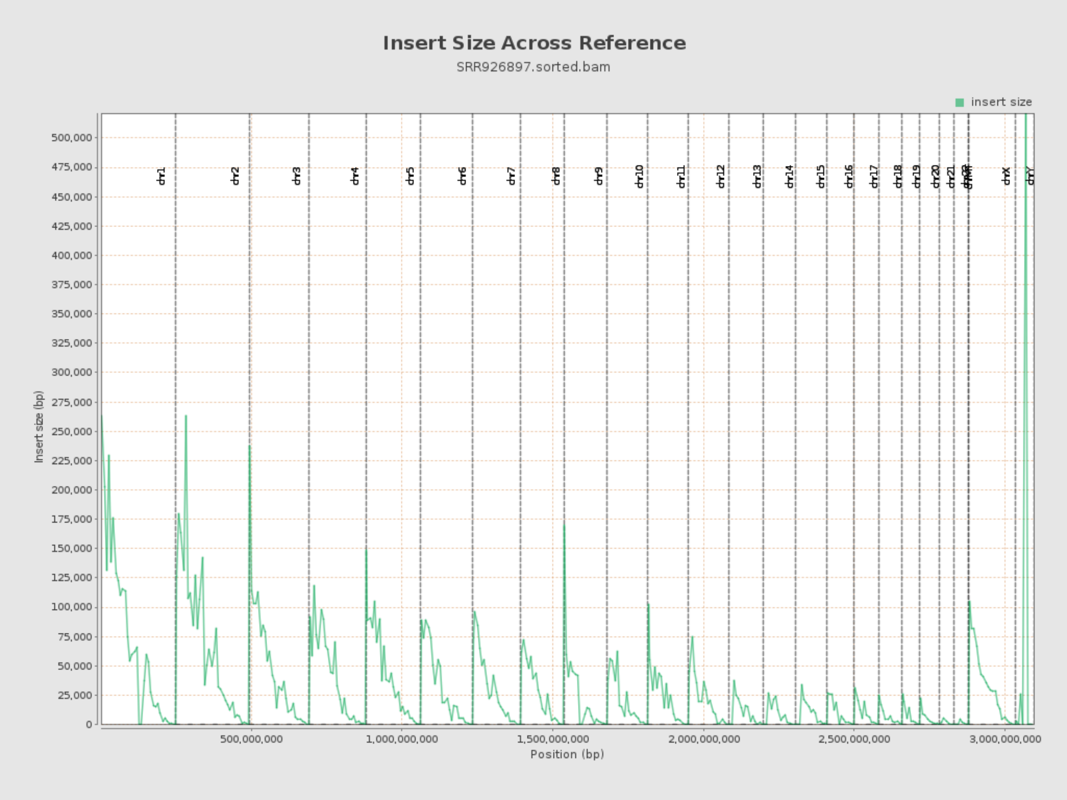
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram