Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 00:10:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926887.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_SRR926887 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926887_1.fastq.gz SRR926887_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 00:10:29 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926887.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	35,763,590
Mapped reads	31,457,295 / 87.96%
Unmapped reads	4,306,295 / 12.04%
Mapped paired reads	31,457,295 / 87.96%
Mapped reads, first in pair	15,769,232 / 44.09%
Mapped reads, second in pair	15,688,063 / 43.87%
Mapped reads, both in pair	31,182,644 / 87.19%
Mapped reads, singletons	274,651 / 0.77%
Secondary alignments	0
Supplementary alignments	232,248 / 0.65%
Read min/max/mean length	30 / 101 / 101.26
Duplicated reads (estimated)	2,372,555 / 6.63%
Duplication rate	6.03%
Clipped reads	7,764,972 / 21.71%

2.2. ACGT Content

Number/percentage of A's	844,841,537 / 28.39%
Number/percentage of C's	607,930,059 / 20.43%
Number/percentage of T's	848,992,322 / 28.53%
Number/percentage of G's	674,220,762 / 22.65%
Number/percentage of N's	206,431 / 0.01%

GC Percentage	43.08%

2.3. Coverage

Mean	0.9621
Standard Deviation	3.5834

2.4. Mapping Quality

Mean Mapping Quality	53.55

2.5. Insert size

Mean	61,824.92
Standard Deviation	2,461,294.75
P25/Median/P75	137 / 173 / 226

2.6. Mismatches and indels

General error rate	0.95%
Mismatches	27,355,050
Insertions	464,336
Mapped reads with at least one insertion	1.45%
Deletions	1,605,903
Mapped reads with at least one deletion	4.97%
Homopolymer indels	53.14%

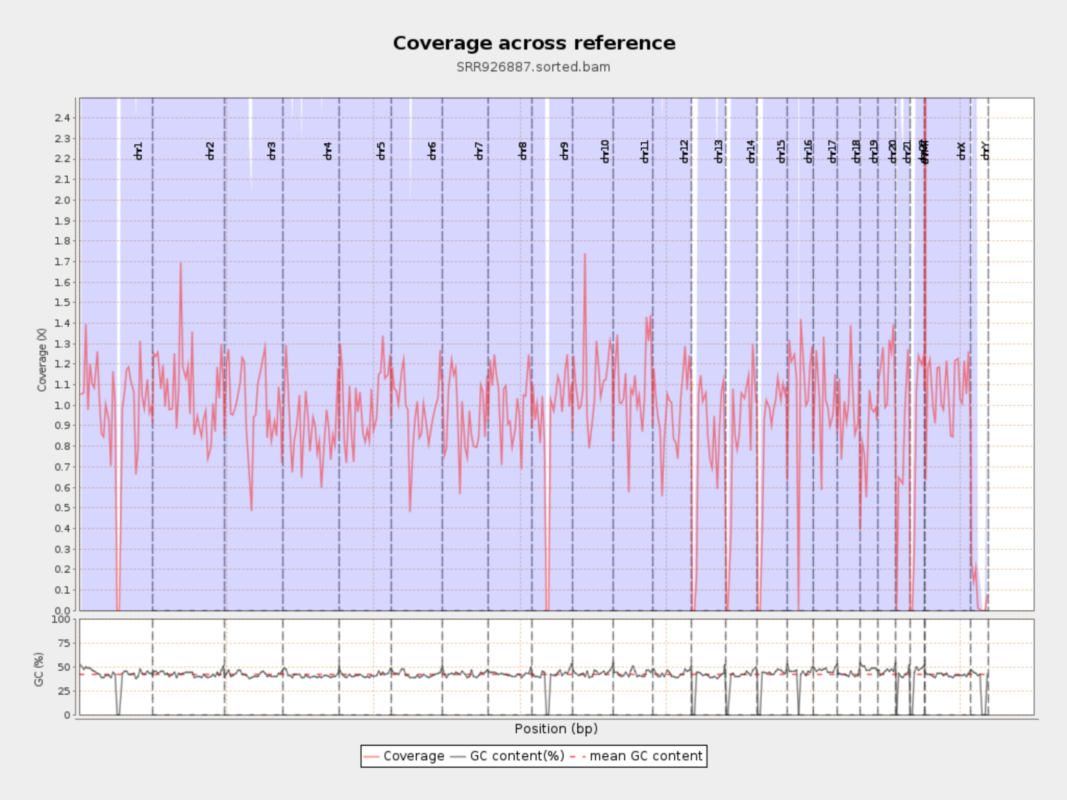
2.7. Chromosome stats

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

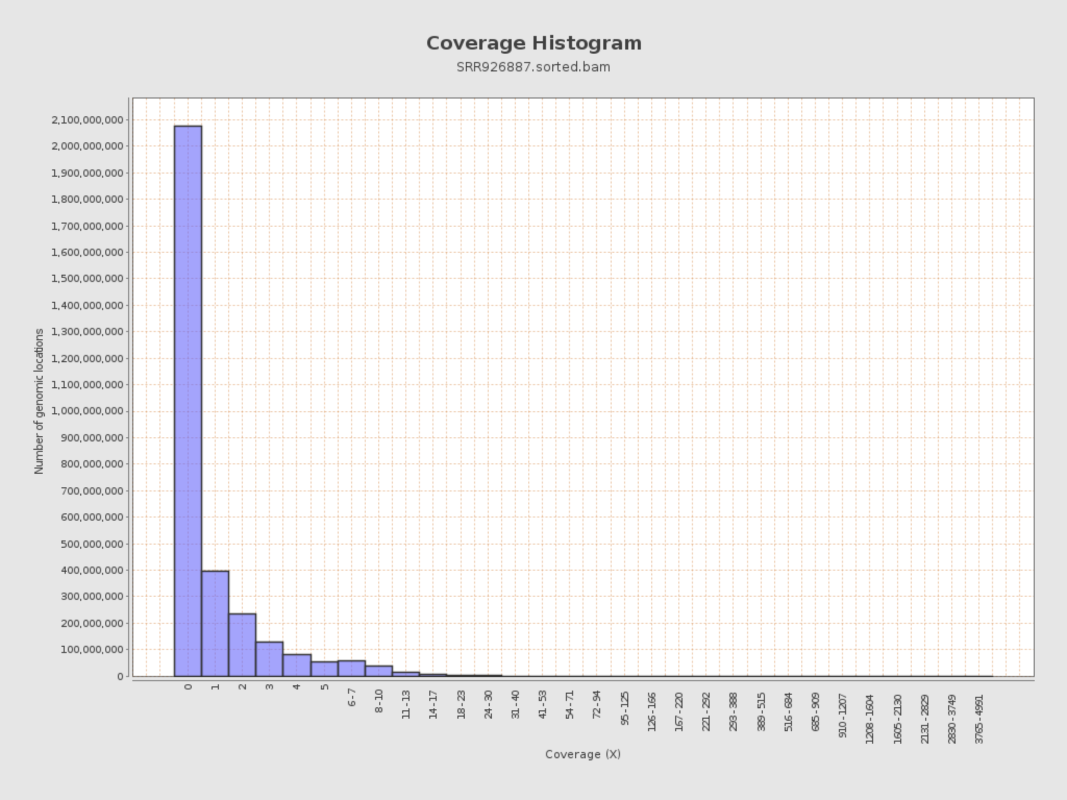
		bases	coverage	deviation
chr1	249250621	242621943	0.9734	3.3616
chr2	243199373	260573808	1.0714	5.4231
chr3	198022430	198515424	1.0025	2.1747
chr4	191154276	170585611	0.8924	2.3813
chr5	180915260	182774924	1.0103	2.1267
chr6	171115067	167102256	0.9765	2.1052
chr7	159138663	149340870	0.9384	2.3074
chr8	146364022	148655495	1.0157	2.433
chr9	141213431	129623624	0.9179	3.6632
chr10	135534747	153150029	1.13	9.6458
chr11	135006516	147297904	1.091	2.6839
chr12	133851895	131875656	0.9852	2.309
chr13	115169878	89217568	0.7747	1.9349
chr14	107349540	89068175	0.8297	2.0204
chr15	102531392	84788604	0.827	2.0809
chr16	90354753	97019512	1.0738	5.257
chr17	81195210	82290911	1.0135	2.5856
chr18	78077248	79335269	1.0161	3.8429
chr19	59128983	50726003	0.8579	2.5044
chr20	63025520	74650454	1.1844	2.5353
chr21	48129895	37471871	0.7786	3.536
chr22	51304566	41200770	0.8031	2.138
chrMT	16571	384487	23.2024	15.8697
chrX	155270560	165579718	1.0664	2.3129

chrY	59373566	4598832	0.0775	2.0249

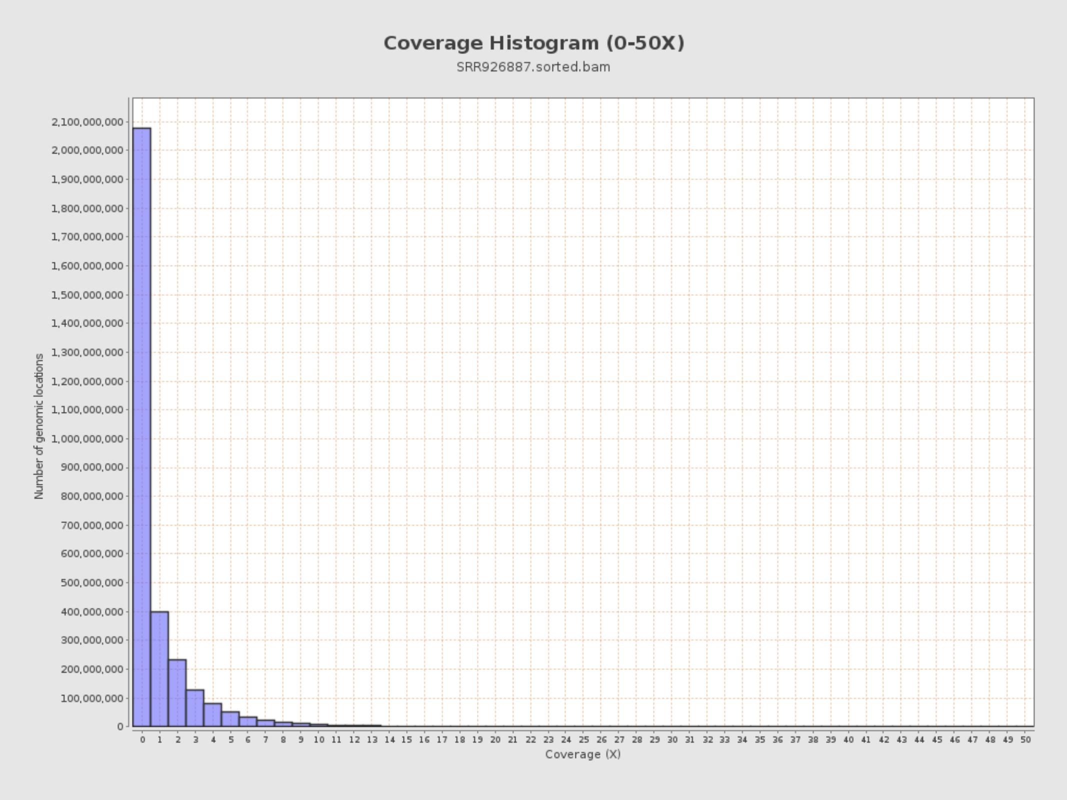
3. Results : Coverage across reference



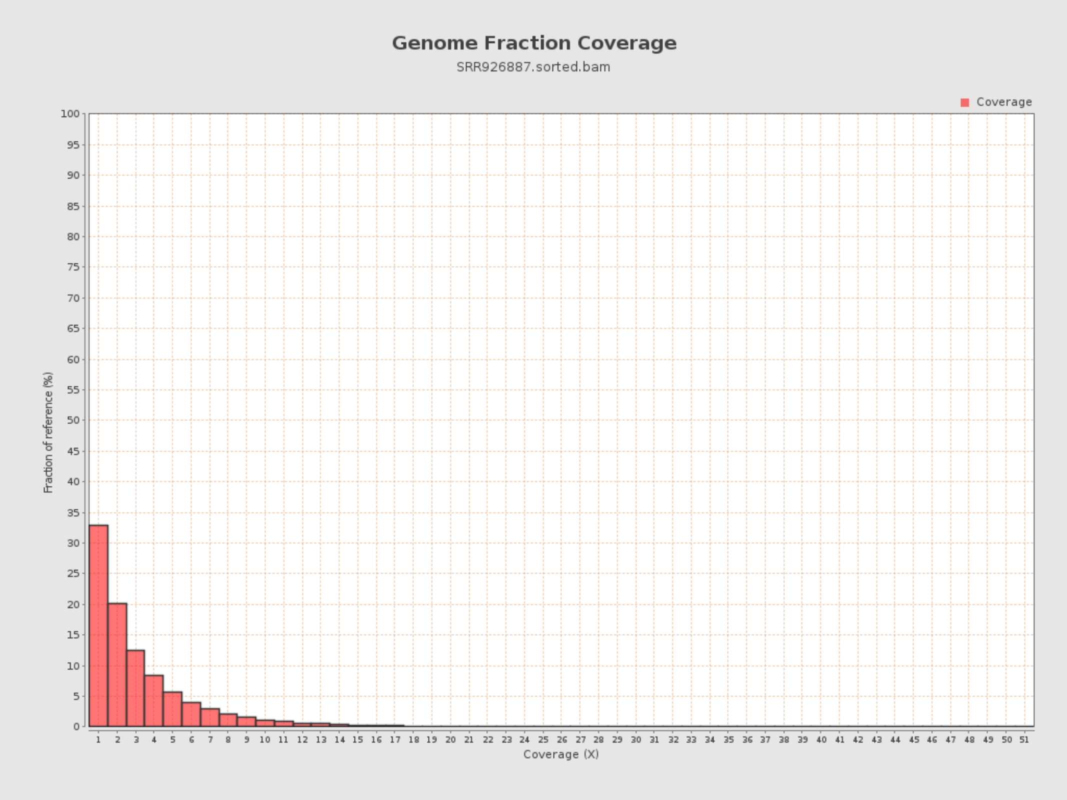
4. Results : Coverage Histogram



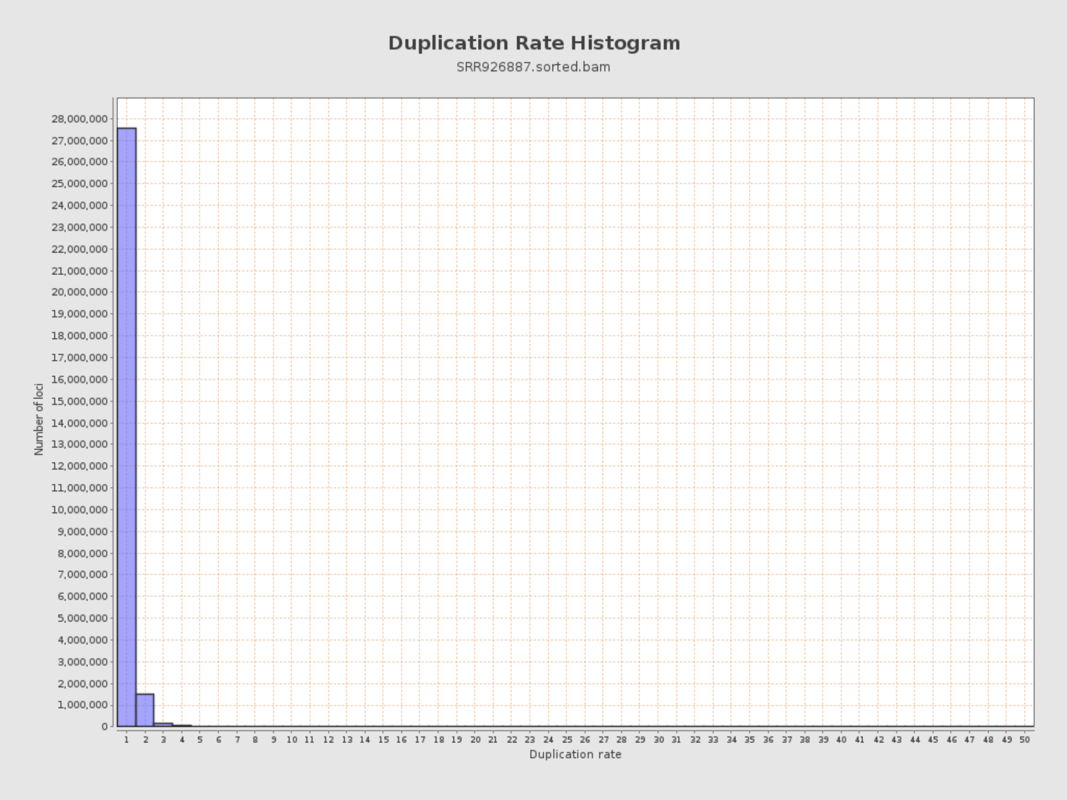
5. Results : Coverage Histogram (0-50X)



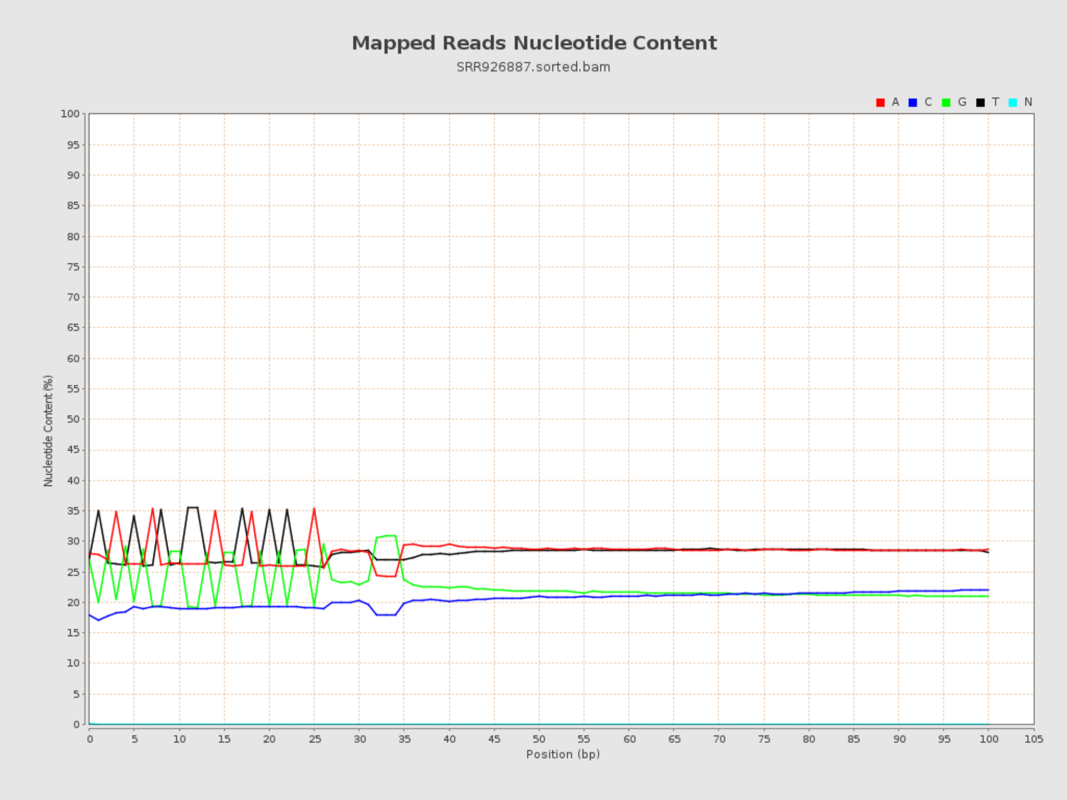
6. Results : Genome Fraction Coverage



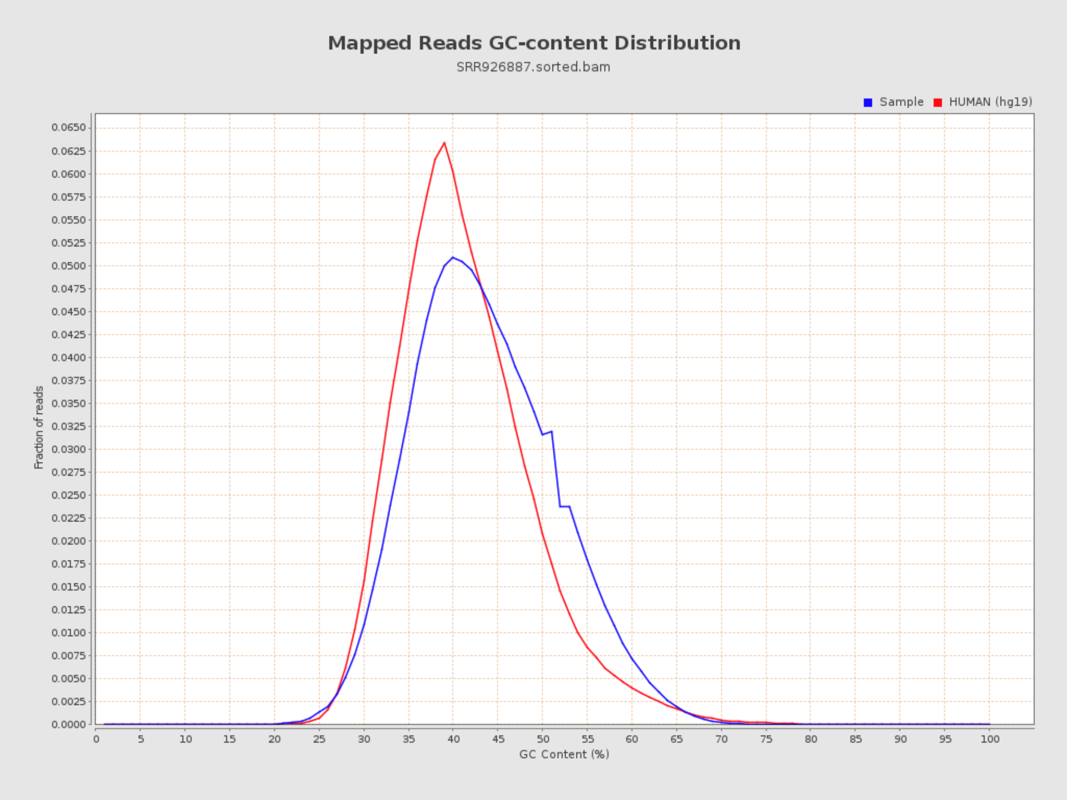
7. Results : Duplication Rate Histogram



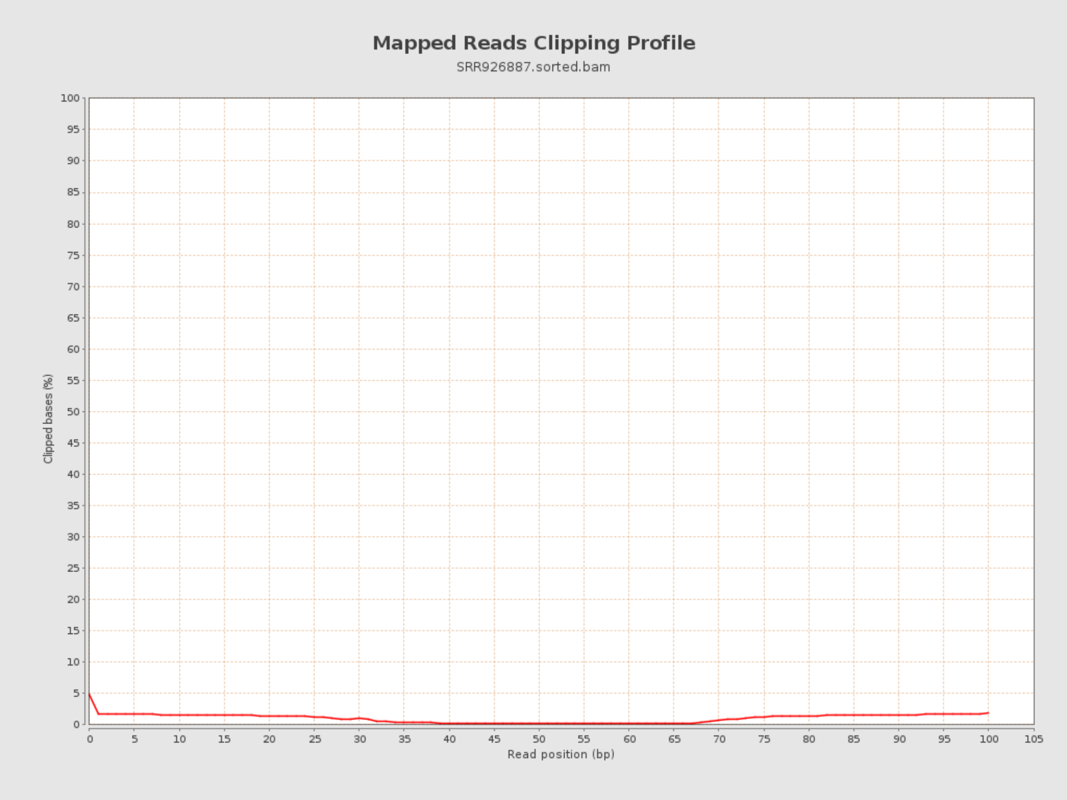
8. Results : Mapped Reads Nucleotide Content



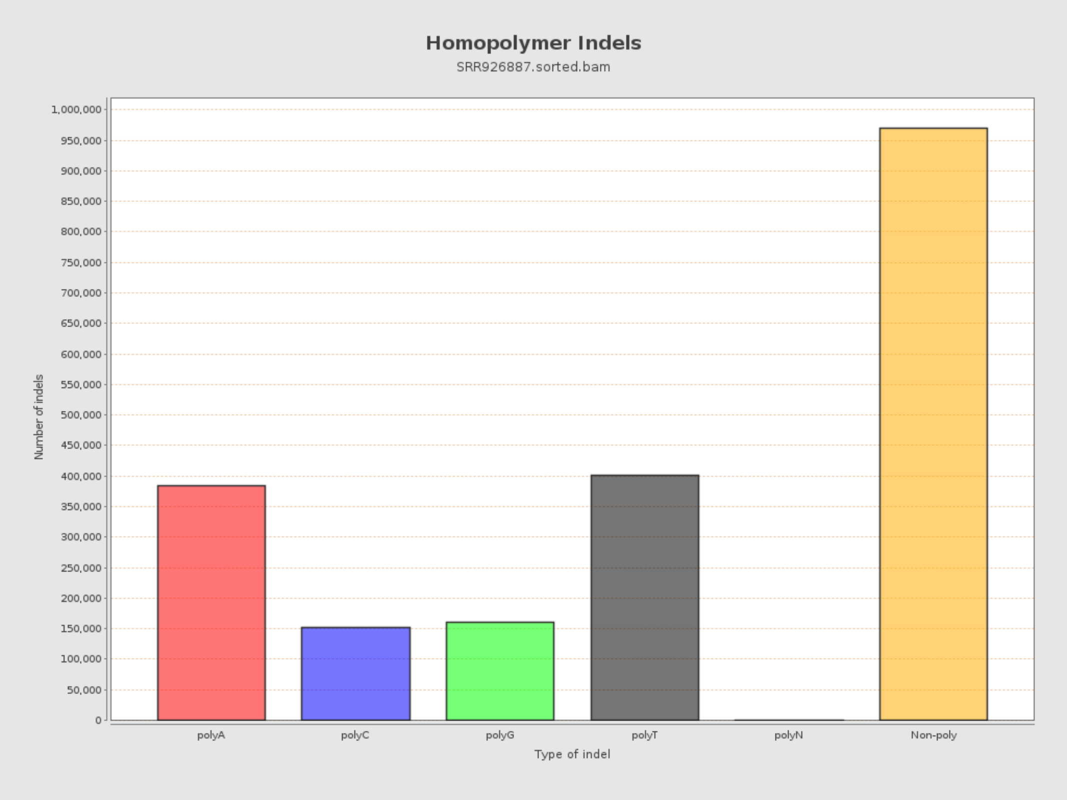
9. Results : Mapped Reads GC-content Distribution



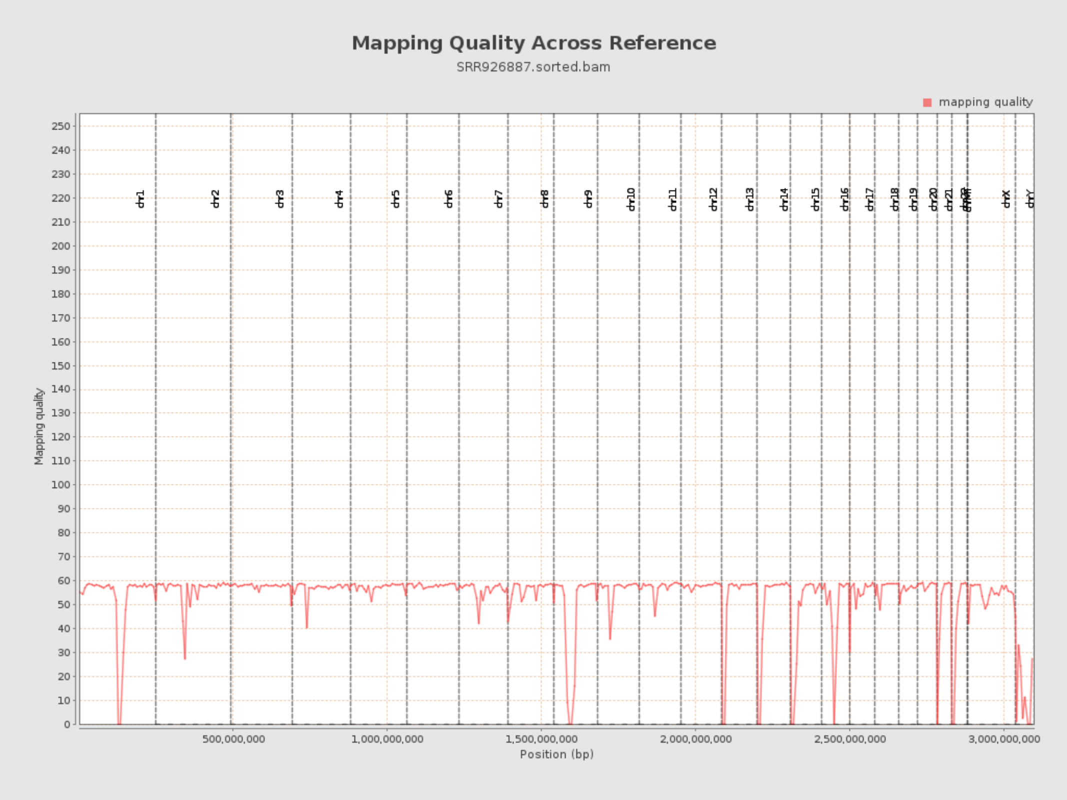
10. Results : Mapped Reads Clipping Profile



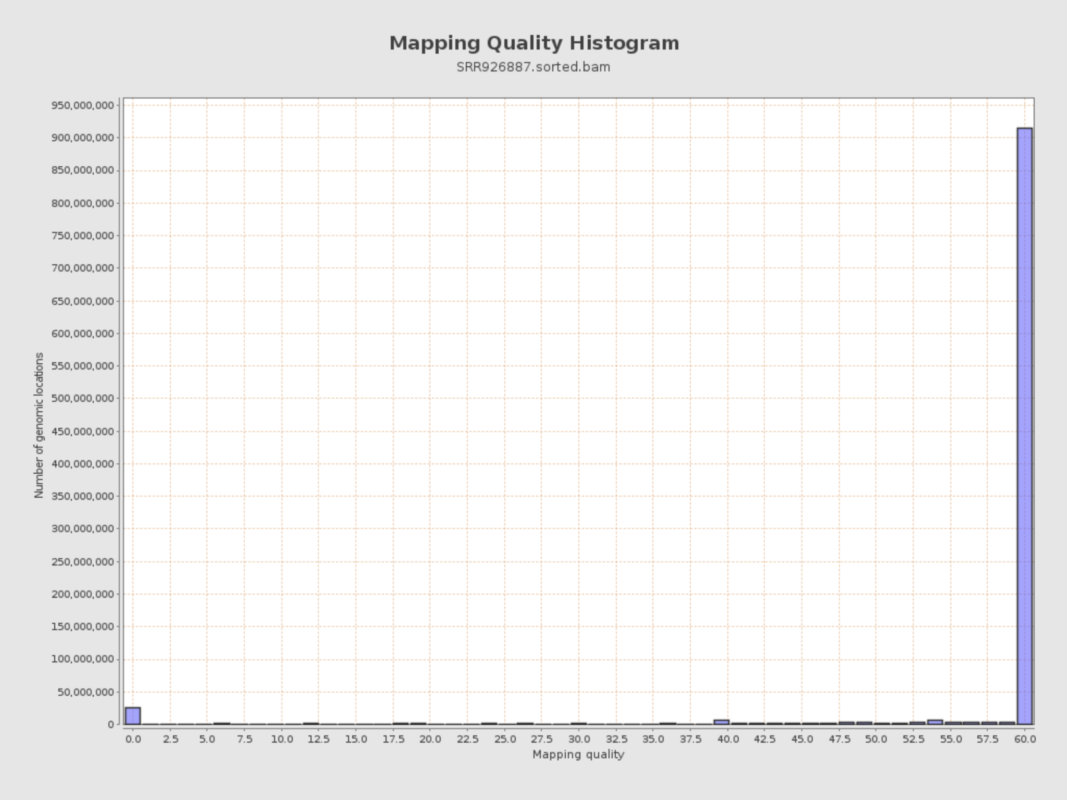
11. Results : Homopolymer Indels



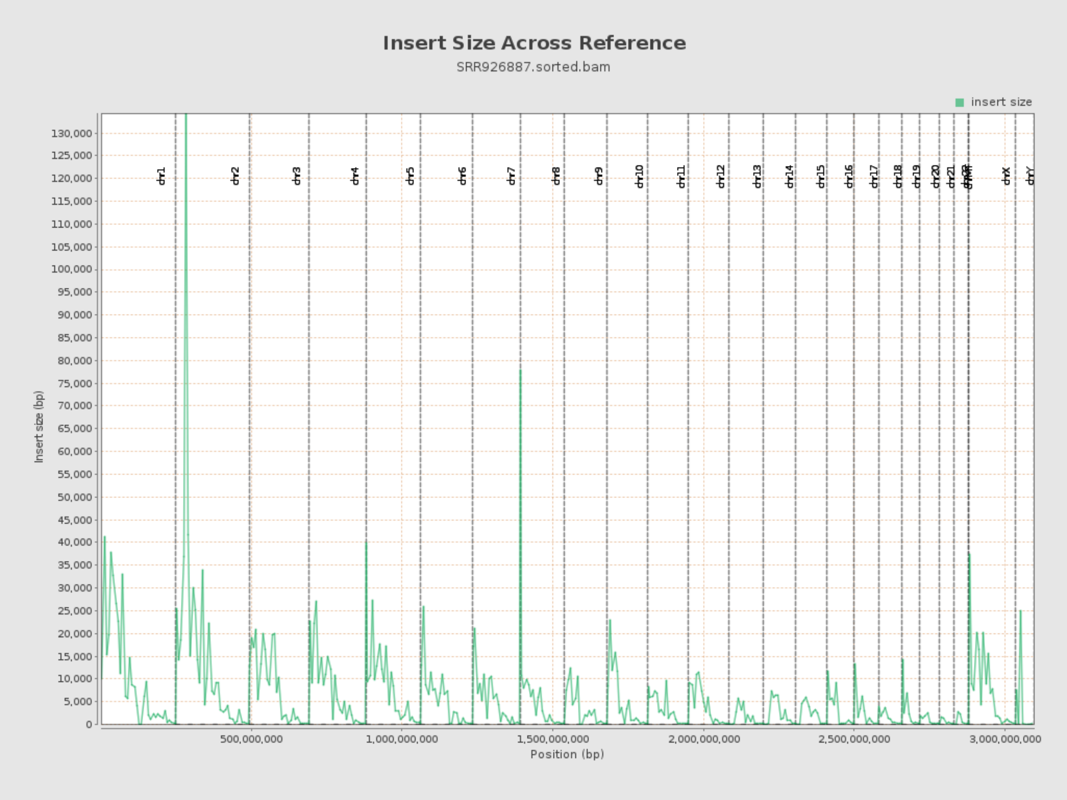
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram