Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 06:59:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926899.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_SRR926899 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926899_1.fastq.gz SRR926899_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 06:59:08 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926899.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	36,891,740
Mapped reads	34,693,324 / 94.04%
Unmapped reads	2,198,416 / 5.96%
Mapped paired reads	34,693,324 / 94.04%
Mapped reads, first in pair	17,404,390 / 47.18%
Mapped reads, second in pair	17,288,934 / 46.86%
Mapped reads, both in pair	34,160,462 / 92.6%
Mapped reads, singletons	532,862 / 1.44%
Secondary alignments	0
Supplementary alignments	1,090,091 / 2.95%
Read min/max/mean length	30 / 101 / 102.22
Duplicated reads (estimated)	3,357,143 / 9.1%
Duplication rate	7.65%
Clipped reads	13,721,623 / 37.19%

2.2. ACGT Content

Number/percentage of A's	908,094,778 / 28.43%
Number/percentage of C's	638,257,041 / 19.98%
Number/percentage of T's	916,559,712 / 28.7%
Number/percentage of G's	730,684,922 / 22.88%
Number/percentage of N's	207,988 / 0.01%

GC Percentage	42.86%

2.3. Coverage

Mean	1.0325
Standard Deviation	4.0693

2.4. Mapping Quality

Mean Mapping Quality	52.57

2.5. Insert size

Mean	297,846.41
Standard Deviation	5,384,169.19
P25/Median/P75	128 / 163 / 217

2.6. Mismatches and indels

General error rate	0.92%
Mismatches	28,592,948
Insertions	524,971
Mapped reads with at least one insertion	1.49%
Deletions	1,662,746
Mapped reads with at least one deletion	4.67%
Homopolymer indels	52.36%

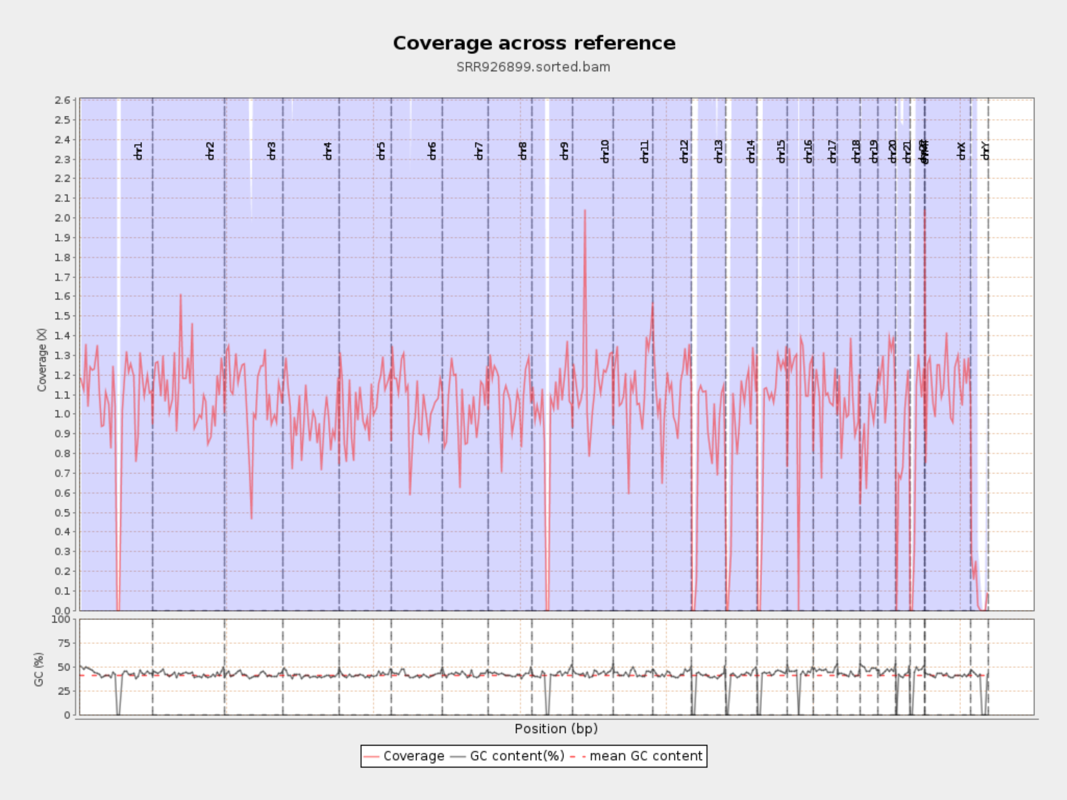
2.7. Chromosome stats

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

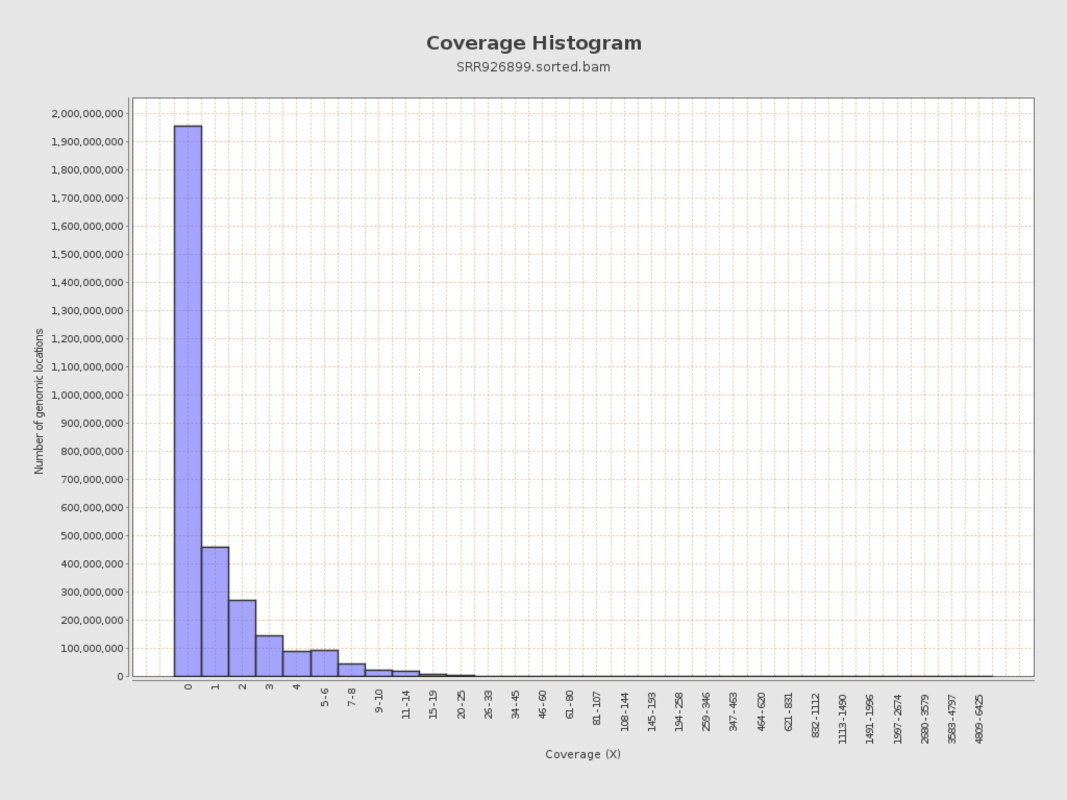
		bases	coverage	deviation
chr1	249250621	263756099	1.0582	3.2861
chr2	243199373	274913191	1.1304	6.4792
chr3	198022430	218175667	1.1018	2.2754
chr4	191154276	186284287	0.9745	2.3437
chr5	180915260	189887143	1.0496	2.1137
chr6	171115067	182138493	1.0644	2.537
chr7	159138663	163078538	1.0248	2.4974
chr8	146364022	160913245	1.0994	2.3804
chr9	141213431	136974716	0.97	3.56
chr10	135534747	162015025	1.1954	12.5442
chr11	135006516	153286984	1.1354	2.5949
chr12	133851895	147911494	1.105	2.5084
chr13	115169878	95391654	0.8283	1.9711
chr14	107349540	95056021	0.8855	2.0636
chr15	102531392	97602305	0.9519	2.1818
chr16	90354753	101557098	1.124	4.954
chr17	81195210	88477607	1.0897	2.5416
chr18	78077248	82164861	1.0524	3.4377
chr19	59128983	54769348	0.9263	2.4322
chr20	63025520	77048506	1.2225	2.4798
chr21	48129895	38691355	0.8039	2.6428
chr22	51304566	41159432	0.8023	2.074
chrMT	16571	33826	2.0413	2.437
chrX	155270560	179375461	1.1552	2.3825

chrY	59373566	5561342	0.0937	2.4963

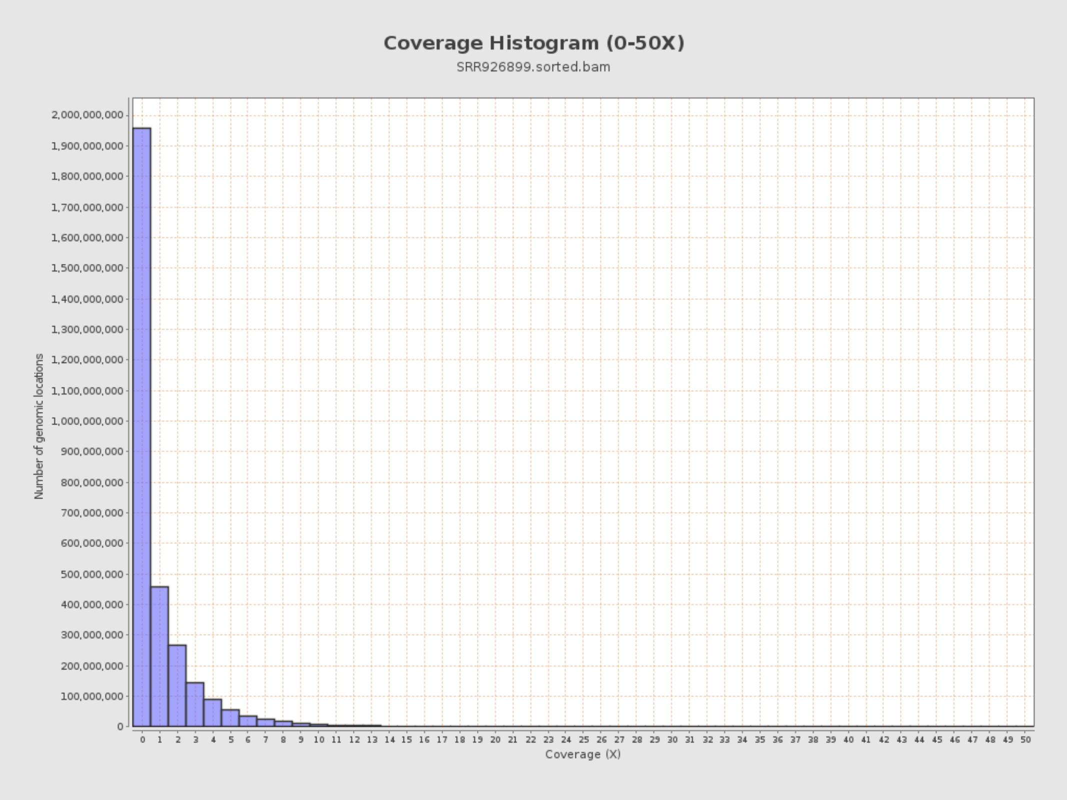
3. Results : Coverage across reference



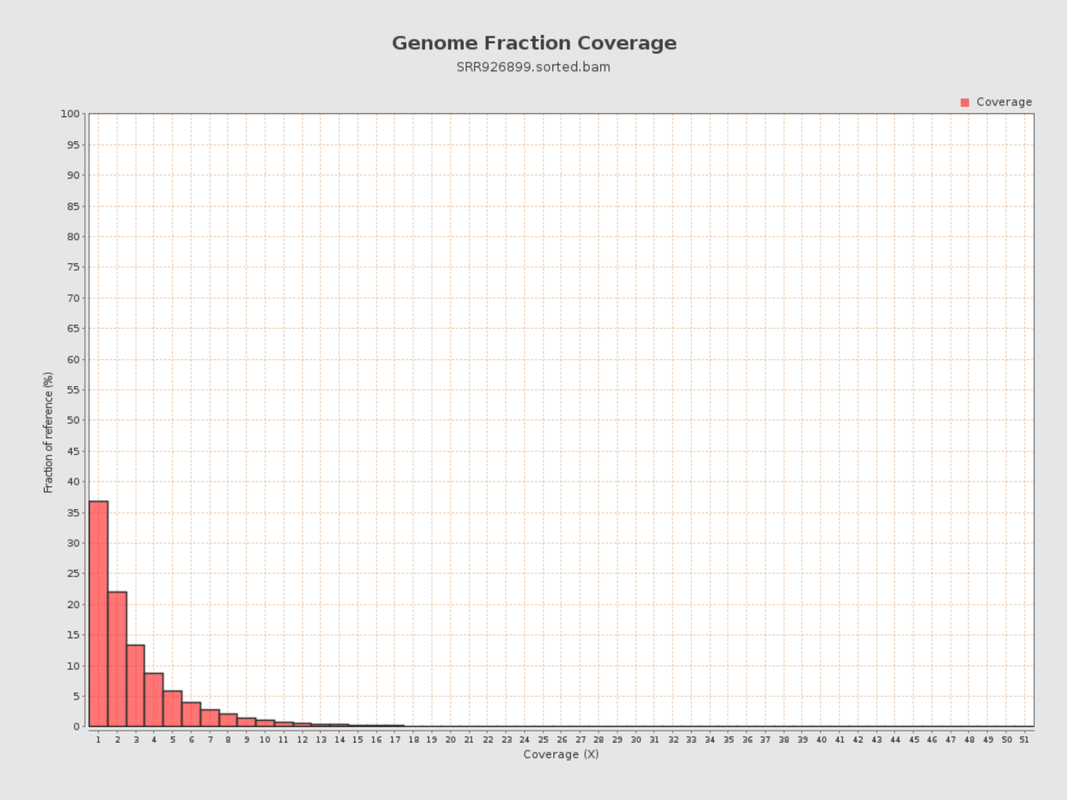
4. Results : Coverage Histogram



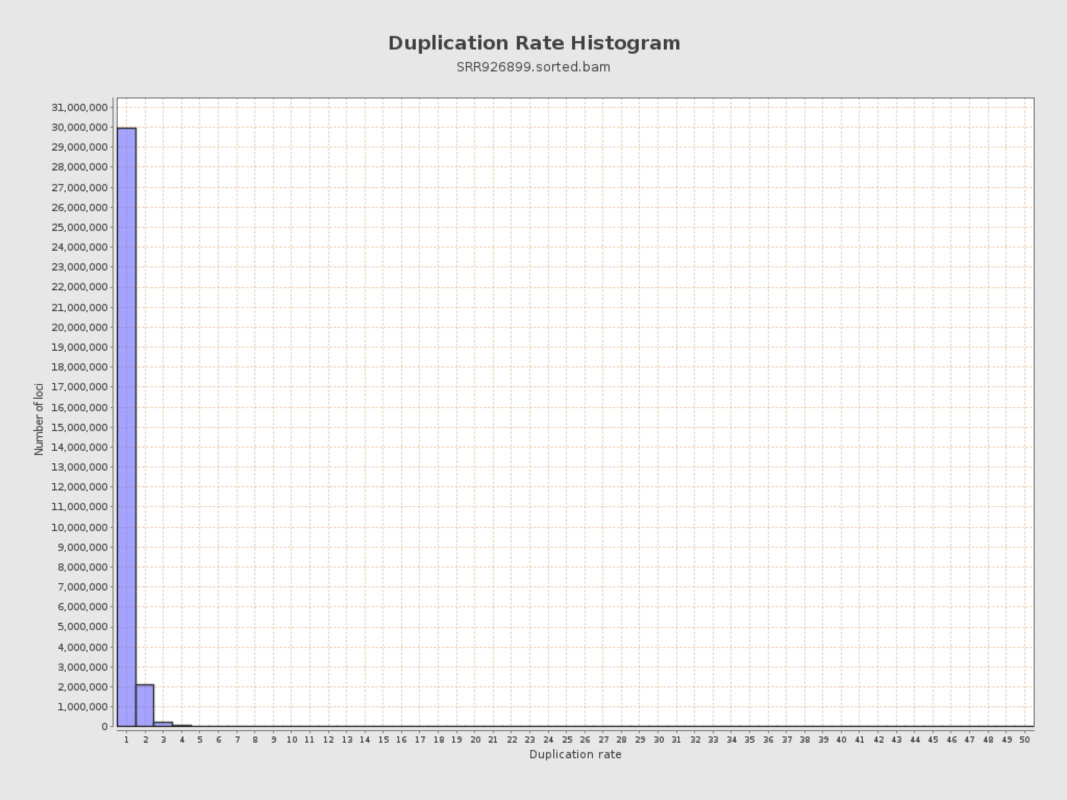
5. Results : Coverage Histogram (0-50X)



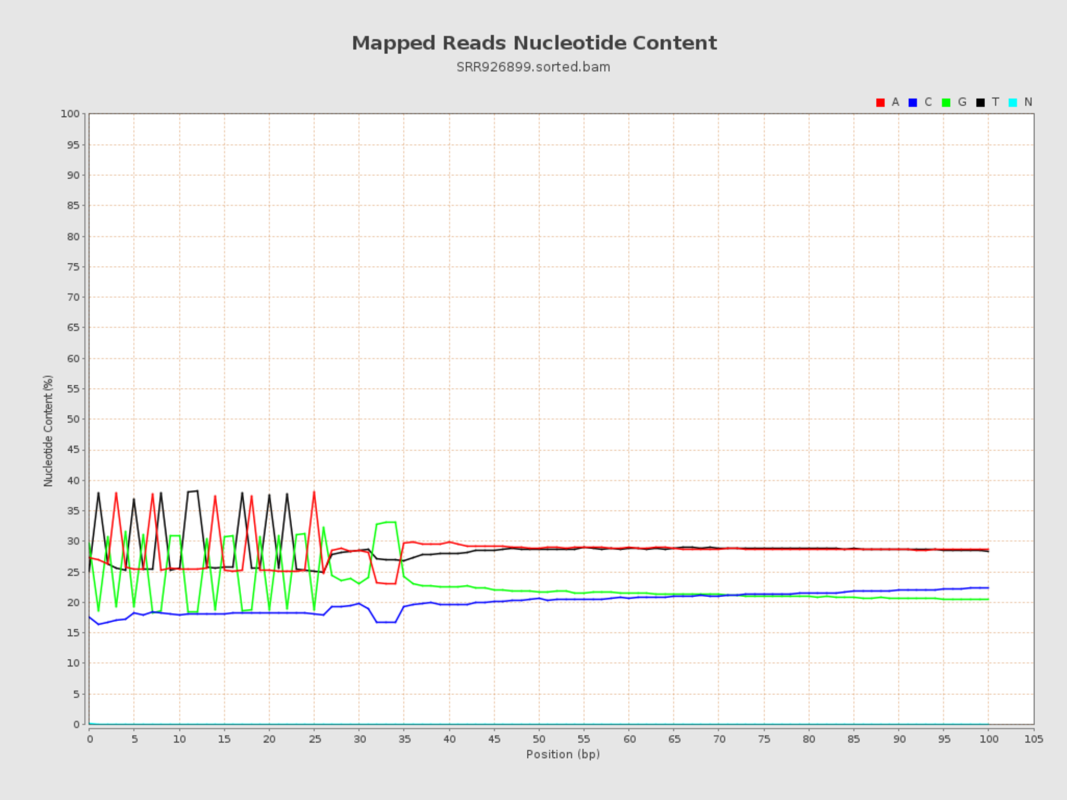
6. Results : Genome Fraction Coverage



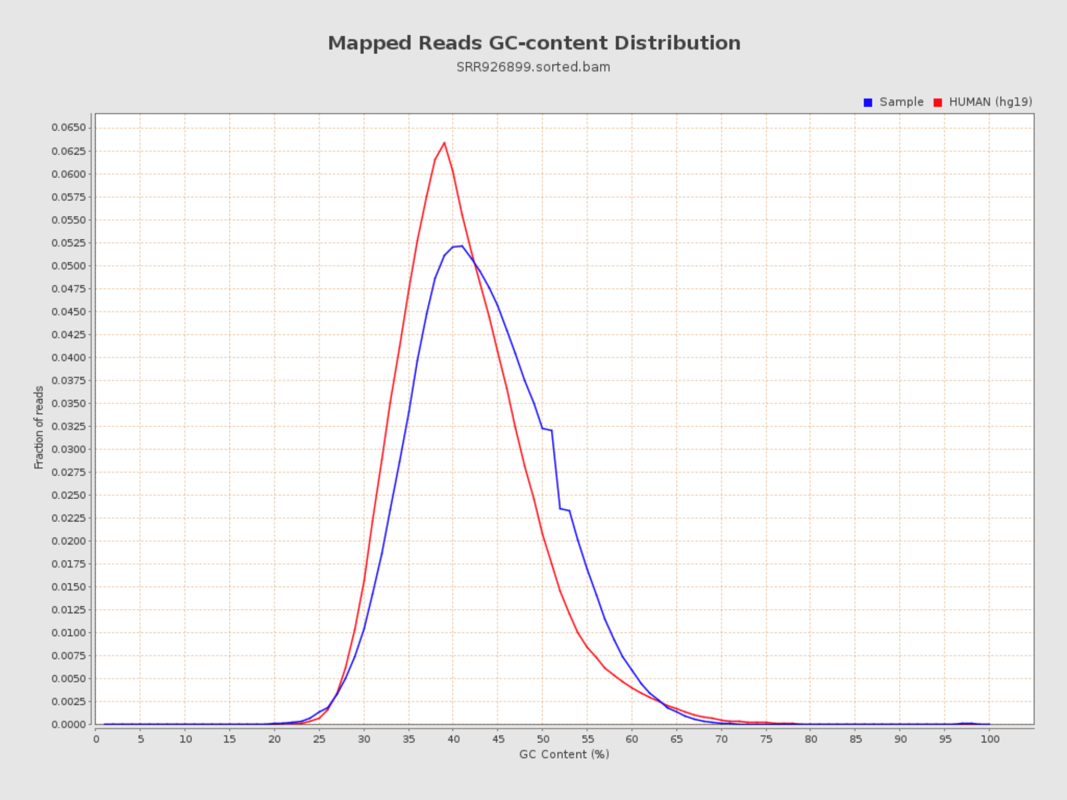
7. Results : Duplication Rate Histogram



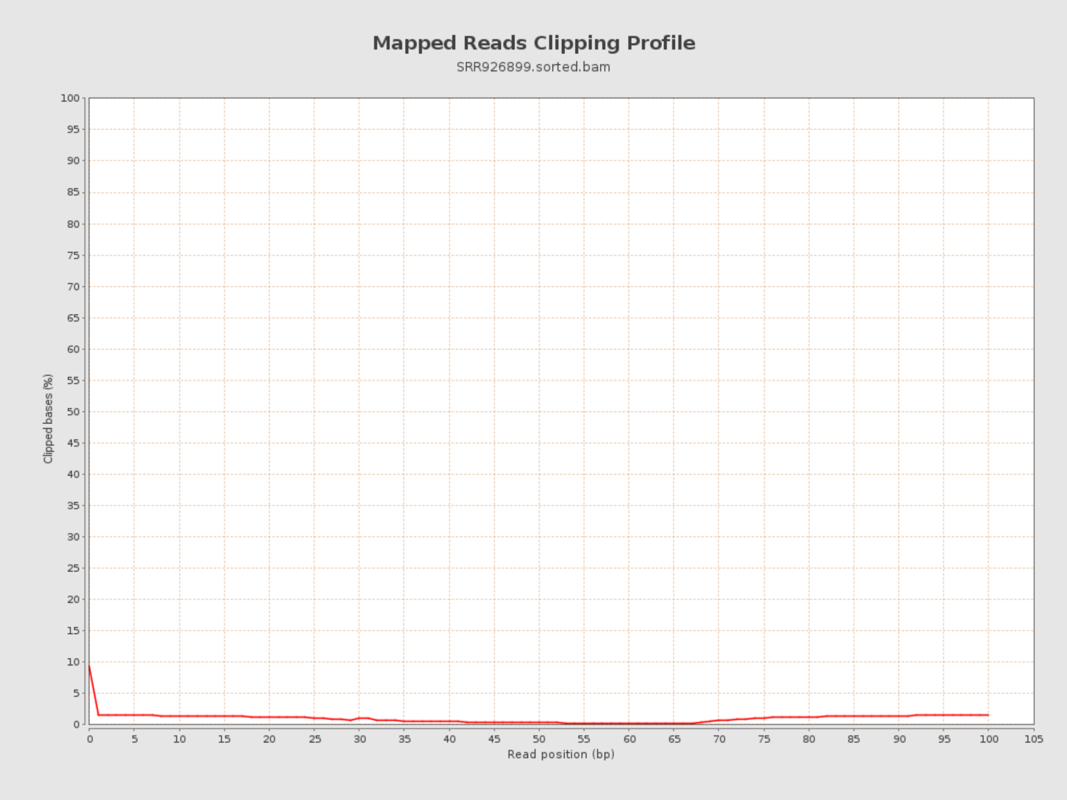
8. Results : Mapped Reads Nucleotide Content



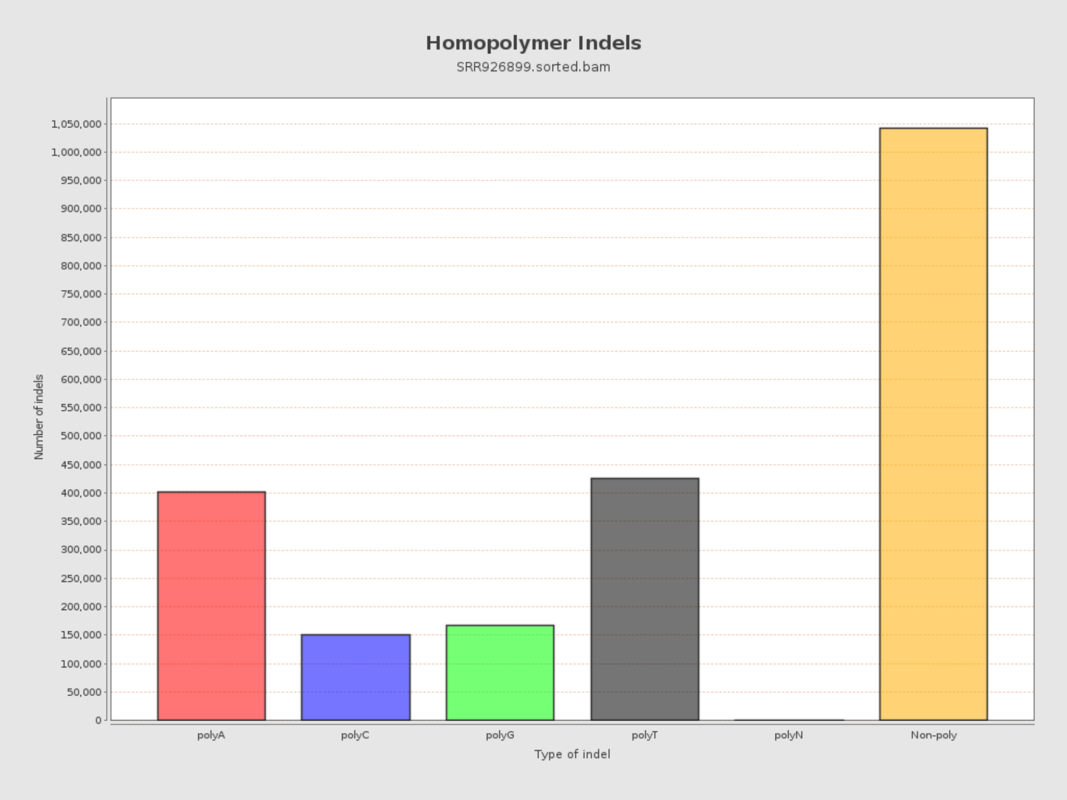
9. Results : Mapped Reads GC-content Distribution



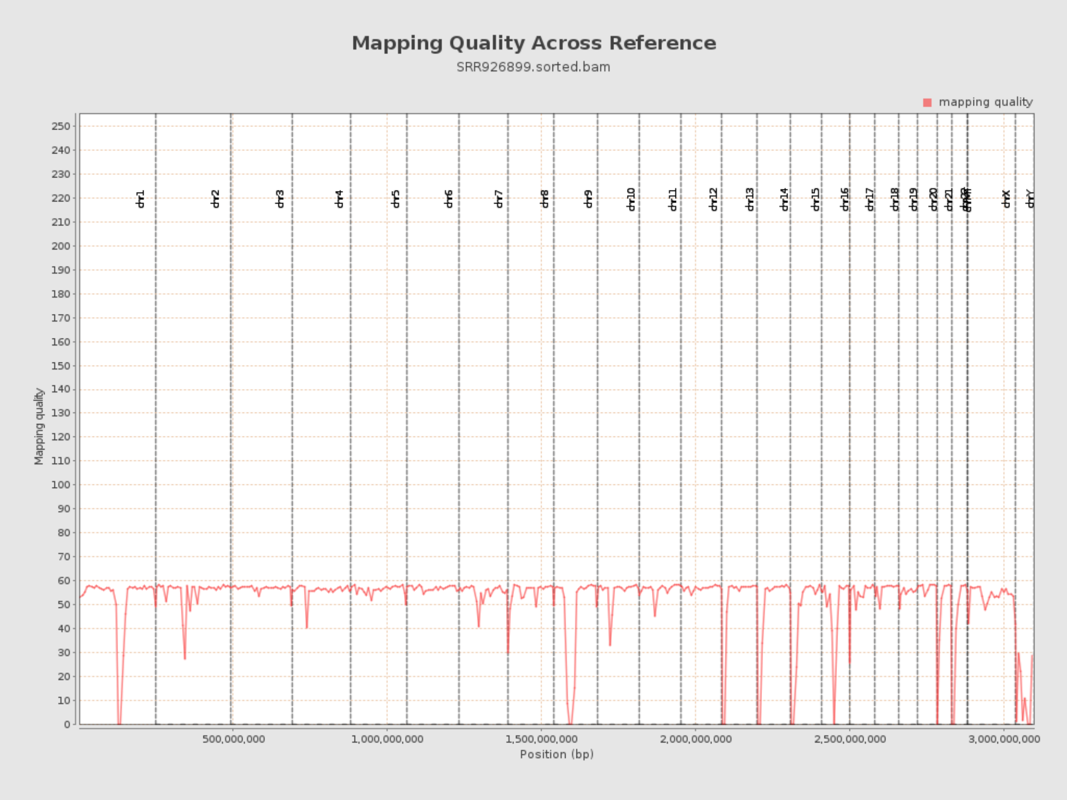
10. Results : Mapped Reads Clipping Profile



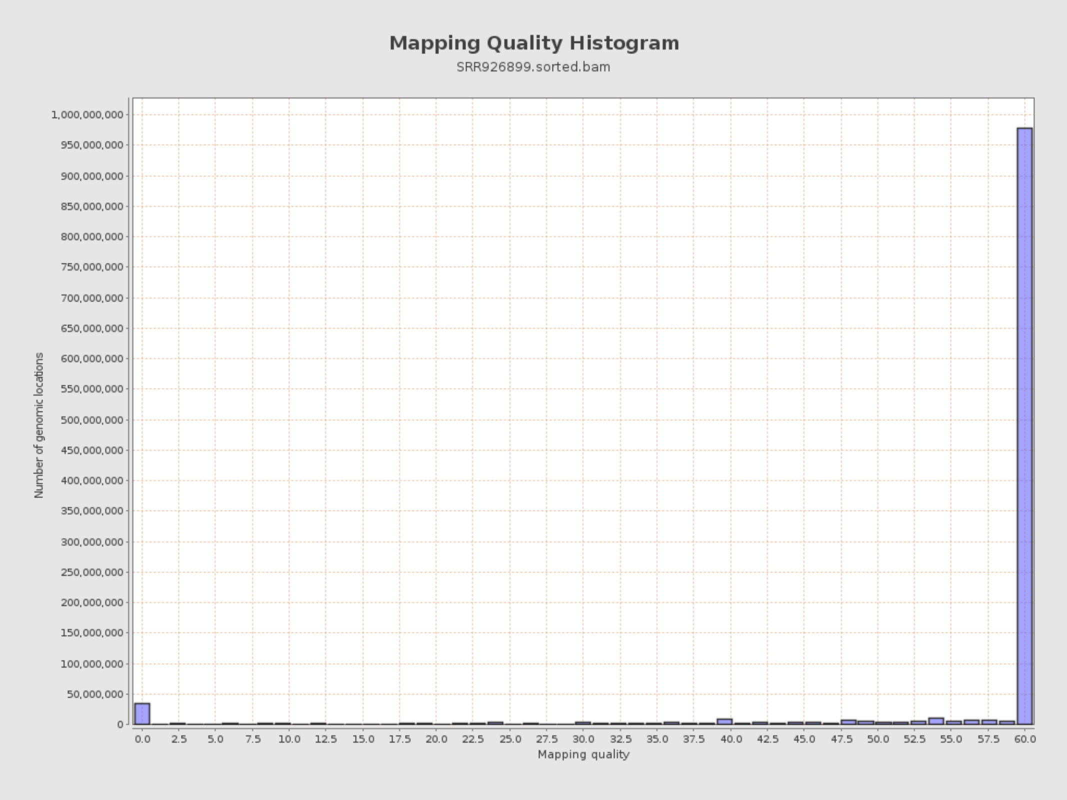
11. Results : Homopolymer Indels



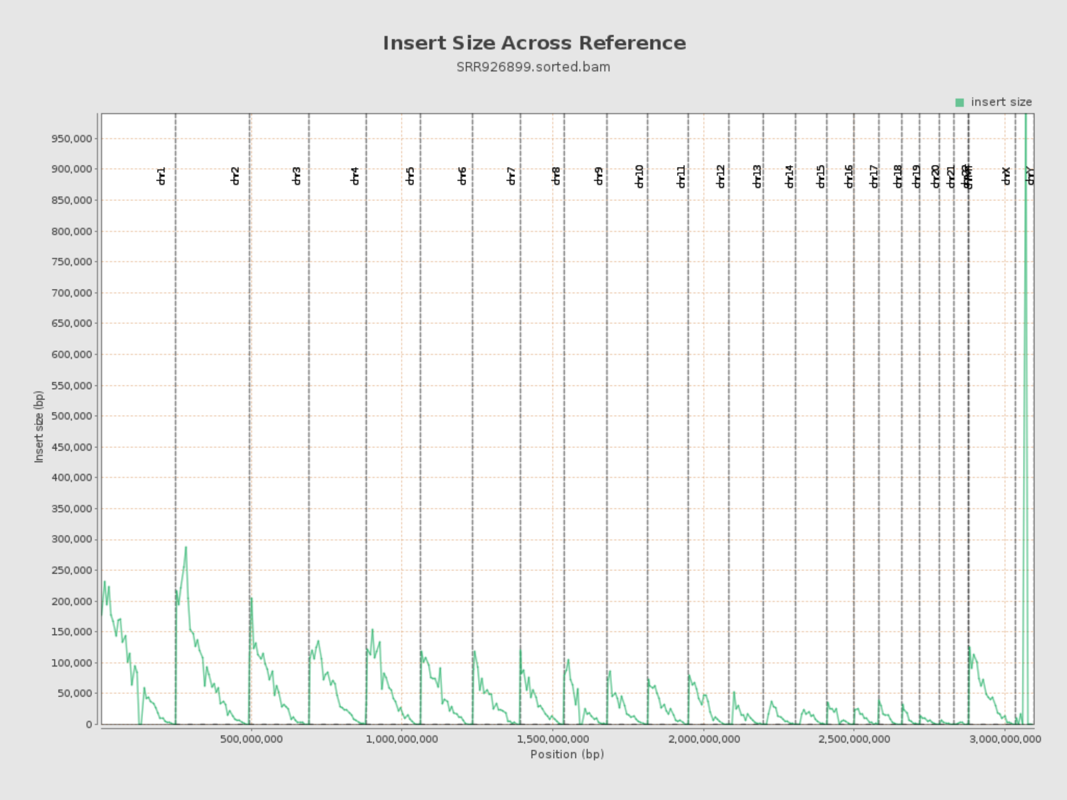
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram