Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 13:36:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927033.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_SRR927033 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927033_1.fastq.gz SRR927033_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 13:36:50 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927033.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	34,415,054
Mapped reads	33,955,297 / 98.66%
Unmapped reads	459,757 / 1.34%
Mapped paired reads	33,955,297 / 98.66%
Mapped reads, first in pair	17,055,392 / 49.56%
Mapped reads, second in pair	16,899,905 / 49.11%
Mapped reads, both in pair	33,696,040 / 97.91%
Mapped reads, singletons	259,257 / 0.75%
Secondary alignments	0
Supplementary alignments	151,181 / 0.44%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	2,226,239 / 6.47%
Duplication rate	5.24%
Clipped reads	6,744,964 / 19.6%

2.2. ACGT Content

Number/percentage of A's	940,013,092 / 28.92%
Number/percentage of C's	651,709,316 / 20.05%
Number/percentage of T's	947,096,513 / 29.14%
Number/percentage of G's	711,347,336 / 21.88%
Number/percentage of N's	550,370 / 0.02%

GC Percentage	41.93%

2.3. Coverage

Mean	1.0508
Standard Deviation	3.8184

2.4. Mapping Quality

Mean Mapping Quality	53.91

2.5. Insert size

Mean	47,199.52
Standard Deviation	2,107,376.14
P25/Median/P75	155 / 196 / 261

2.6. Mismatches and indels

General error rate	1.09%
Mismatches	34,444,721
Insertions	505,407
Mapped reads with at least one insertion	1.46%
Deletions	1,724,499
Mapped reads with at least one deletion	4.95%
Homopolymer indels	53.41%

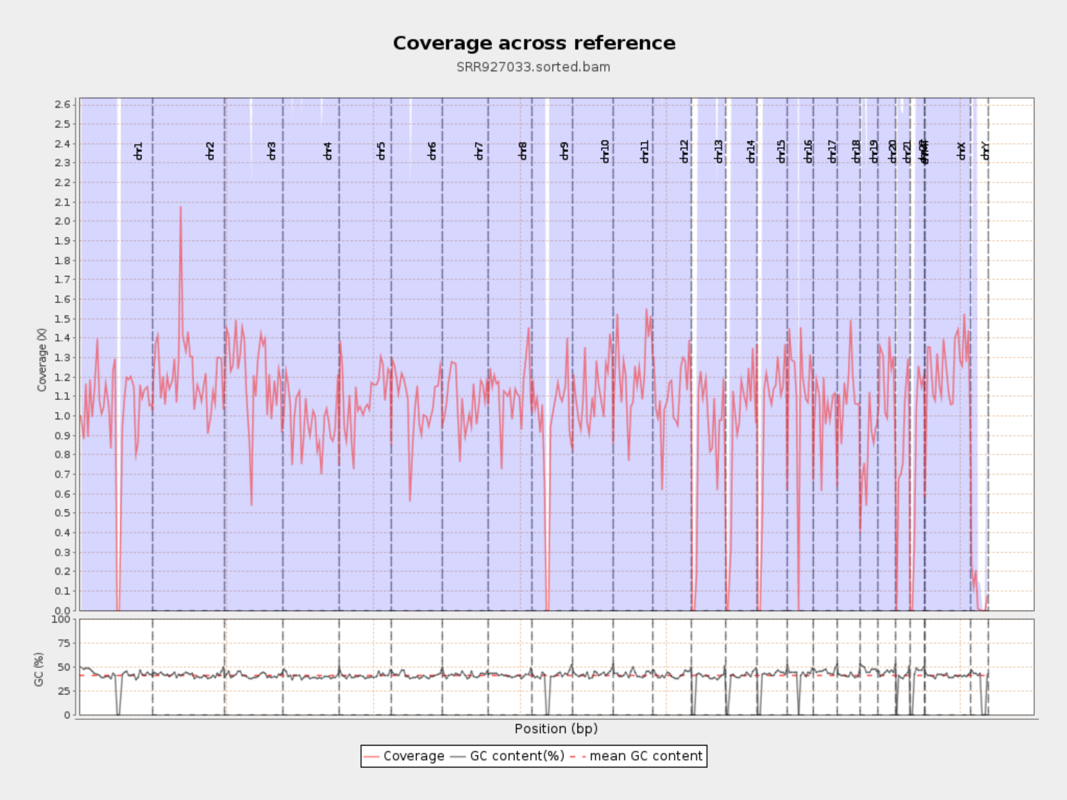
2.7. Chromosome stats

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

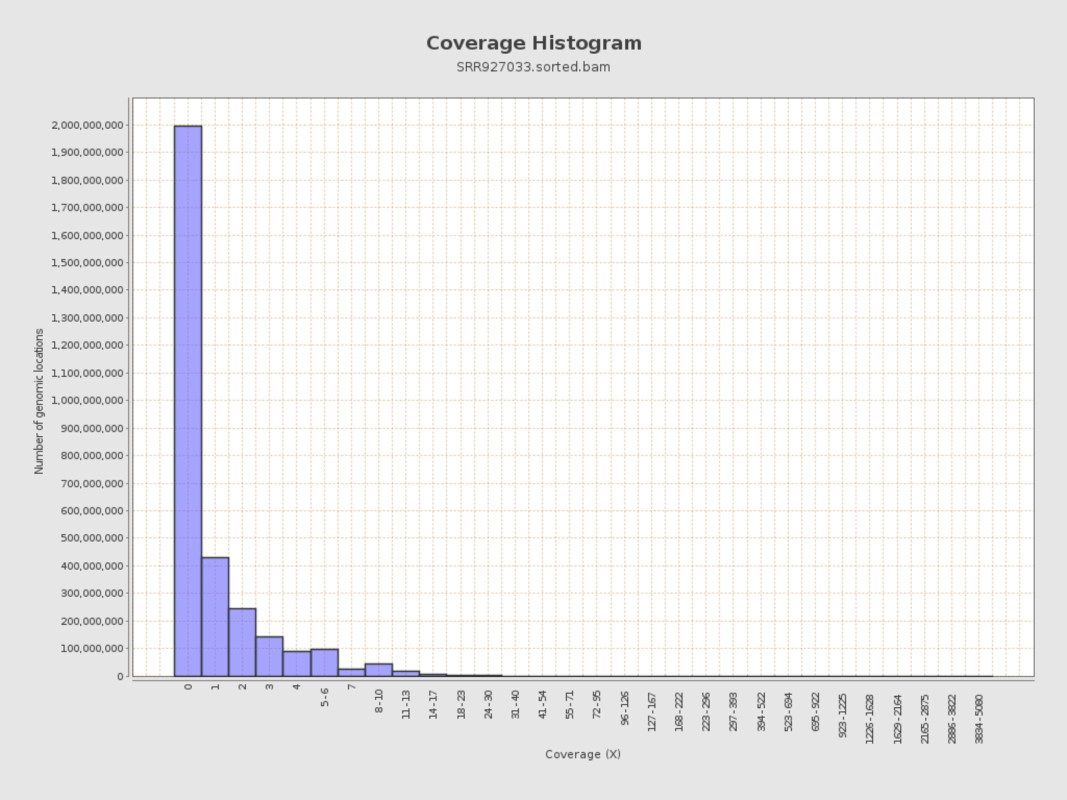
		bases	coverage	deviation
chr1	249250621	252605312	1.0135	5.8637
chr2	243199373	298453281	1.2272	6.6564
chr3	198022430	240334184	1.2137	2.3479
chr4	191154276	186121635	0.9737	2.8316
chr5	180915260	198523358	1.0973	2.2055
chr6	171115067	183386733	1.0717	2.2013
chr7	159138663	170412470	1.0708	2.7954
chr8	146364022	165044541	1.1276	2.5468
chr9	141213431	131266835	0.9296	4.5743
chr10	135534747	153084859	1.1295	5.2107
chr11	135006516	163862353	1.2137	4.2124
chr12	133851895	147834624	1.1045	2.2538
chr13	115169878	97099305	0.8431	1.9247
chr14	107349540	96507501	0.899	2.0648
chr15	102531392	97954130	0.9554	2.1647
chr16	90354753	99673122	1.1031	4.9644
chr17	81195210	81898428	1.0087	3.3953
chr18	78077248	88211511	1.1298	4.7551
chr19	59128983	48258387	0.8162	3.3696
chr20	63025520	75200858	1.1932	2.5712
chr21	48129895	40060823	0.8323	2.6214
chr22	51304566	40714639	0.7936	2.0797
chrMT	16571	9621	0.5806	1.3633
chrX	155270560	192159927	1.2376	2.8582

chrY	59373566	4428597	0.0746	2.0466

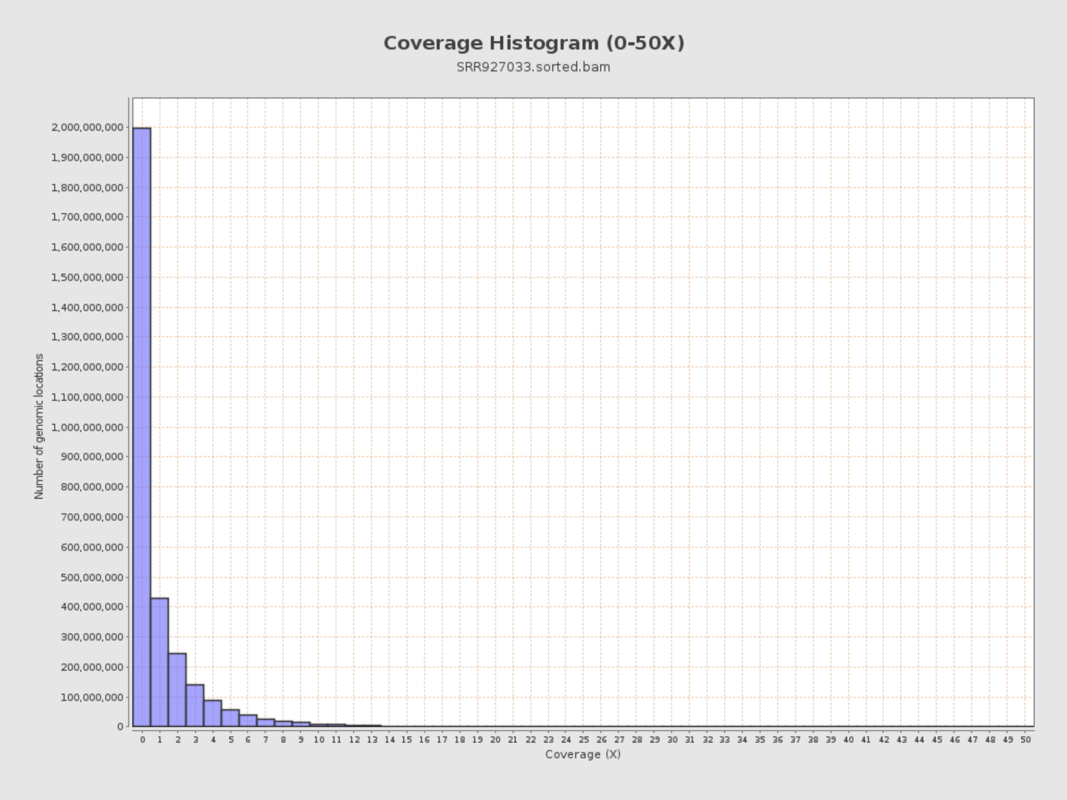
3. Results : Coverage across reference



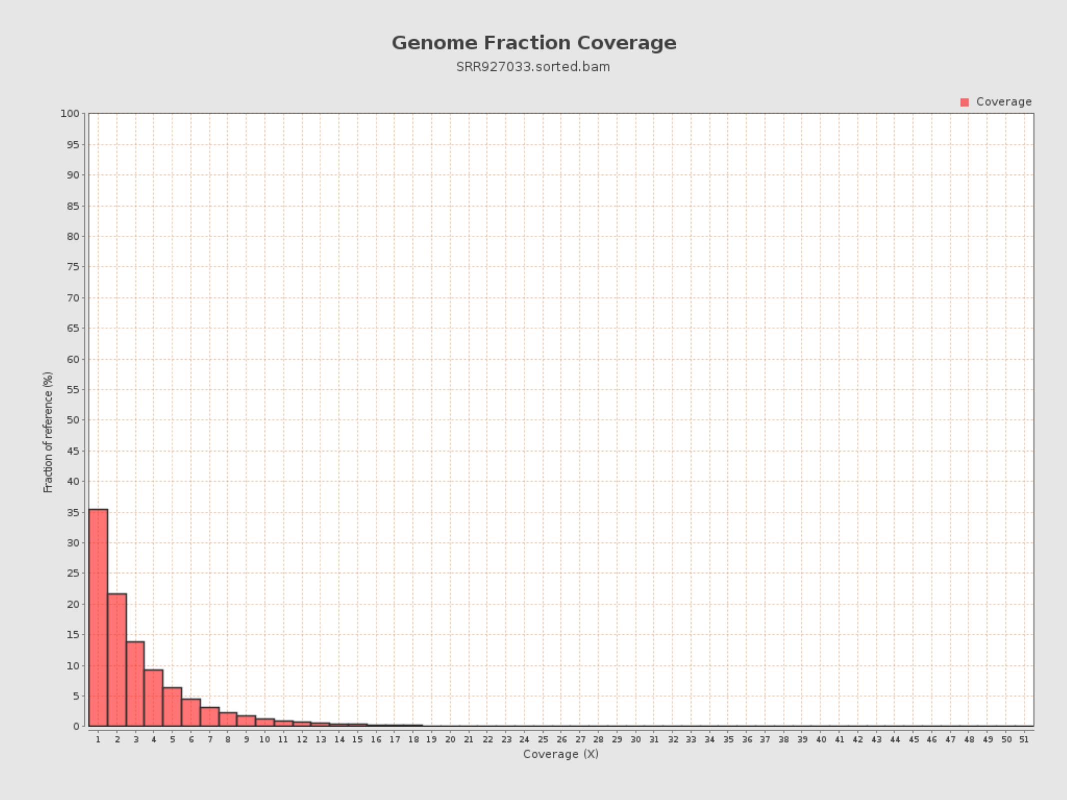
4. Results : Coverage Histogram



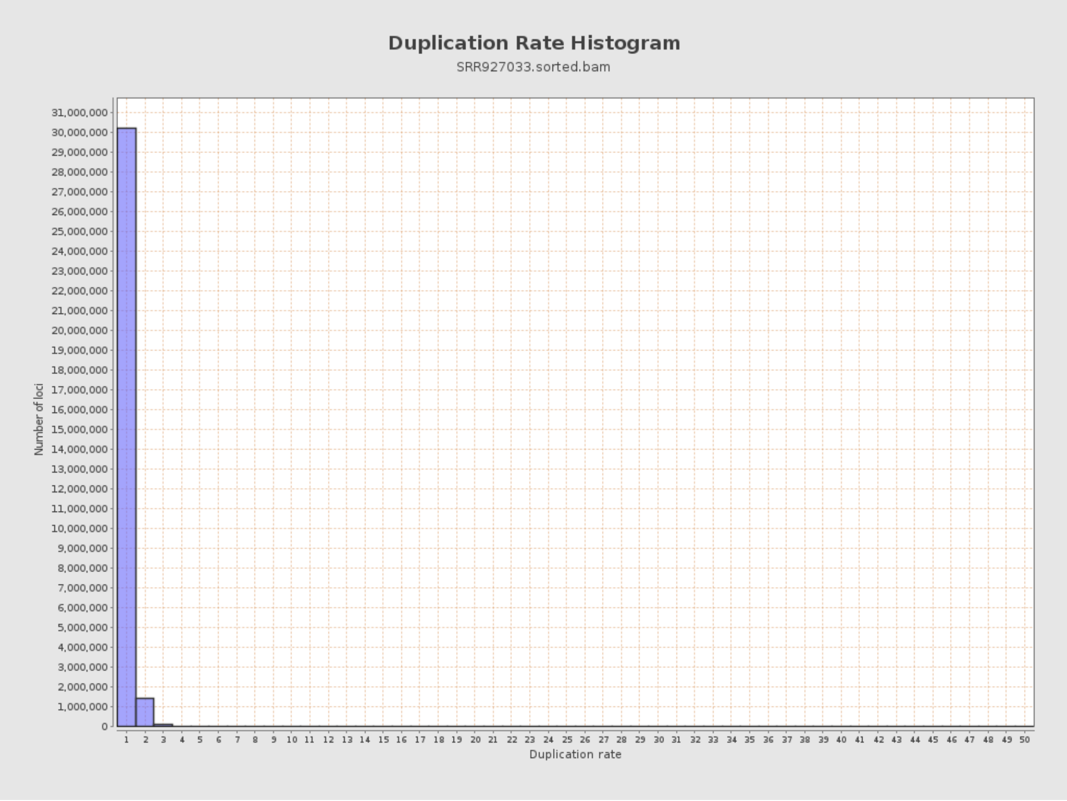
5. Results : Coverage Histogram (0-50X)



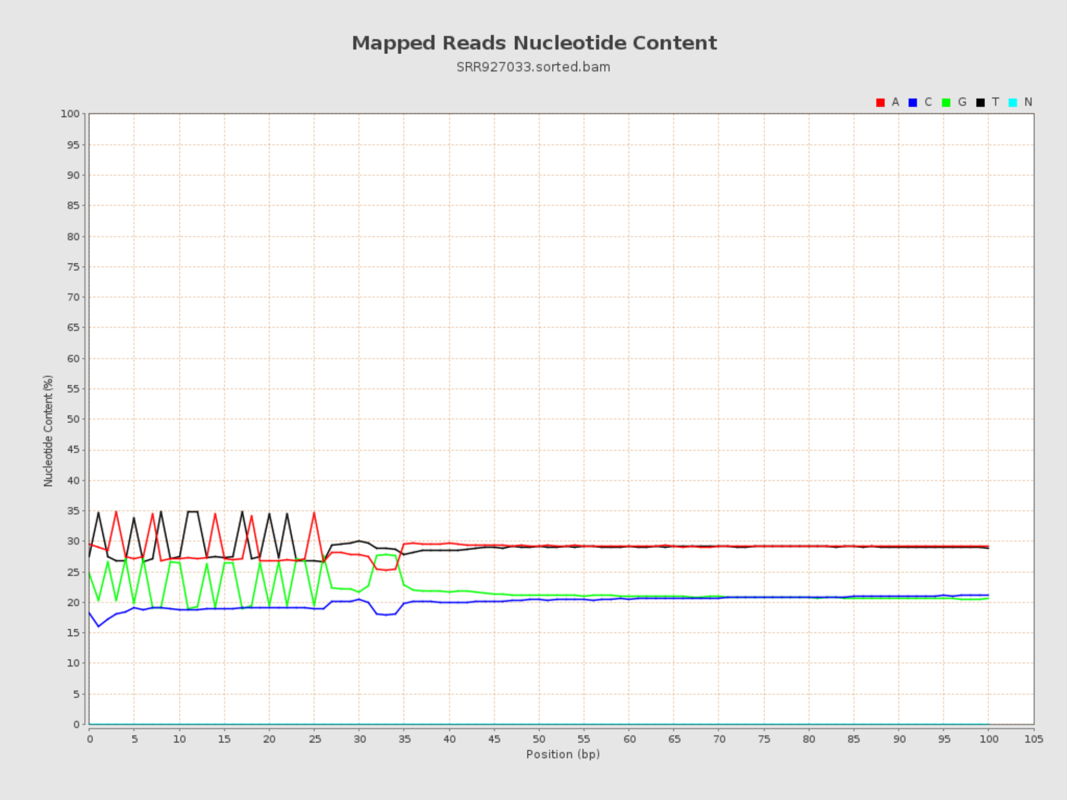
6. Results : Genome Fraction Coverage



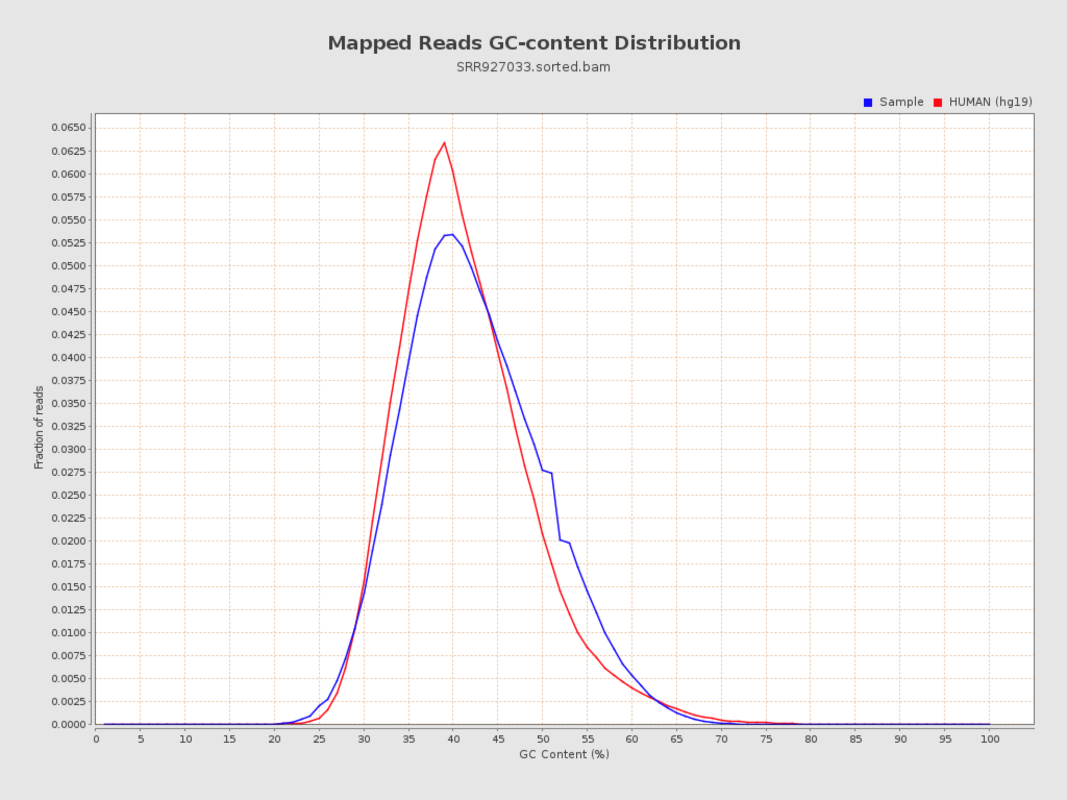
7. Results : Duplication Rate Histogram



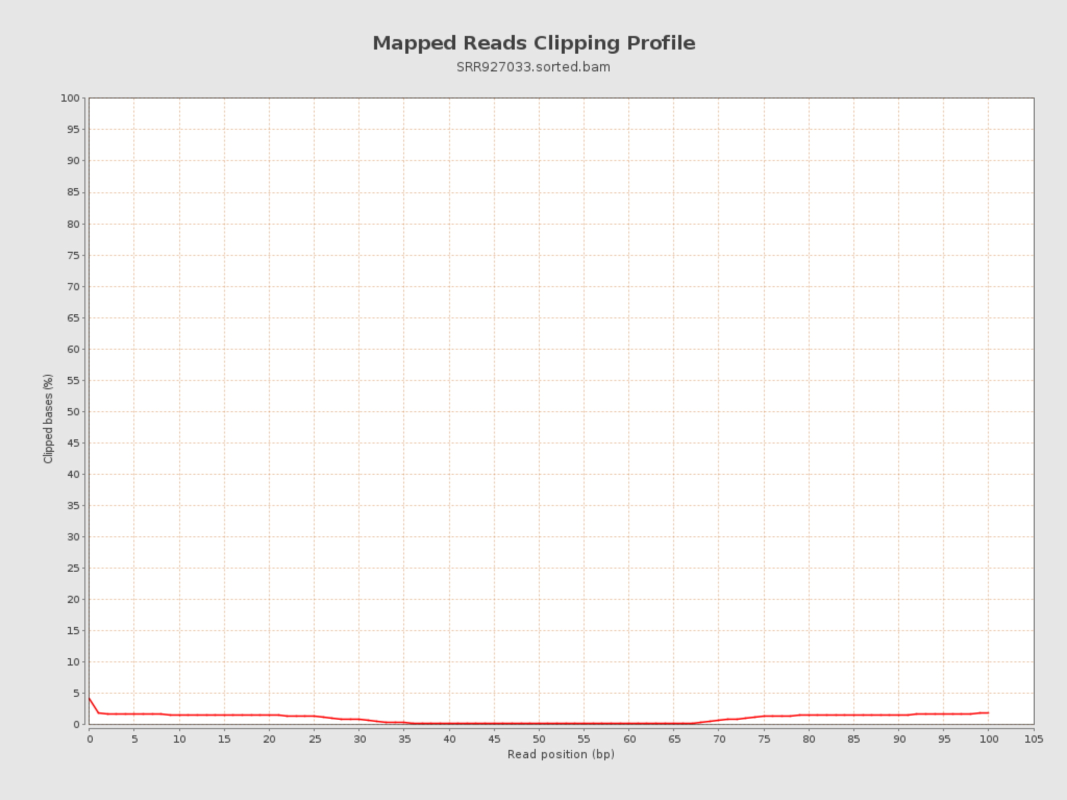
8. Results : Mapped Reads Nucleotide Content



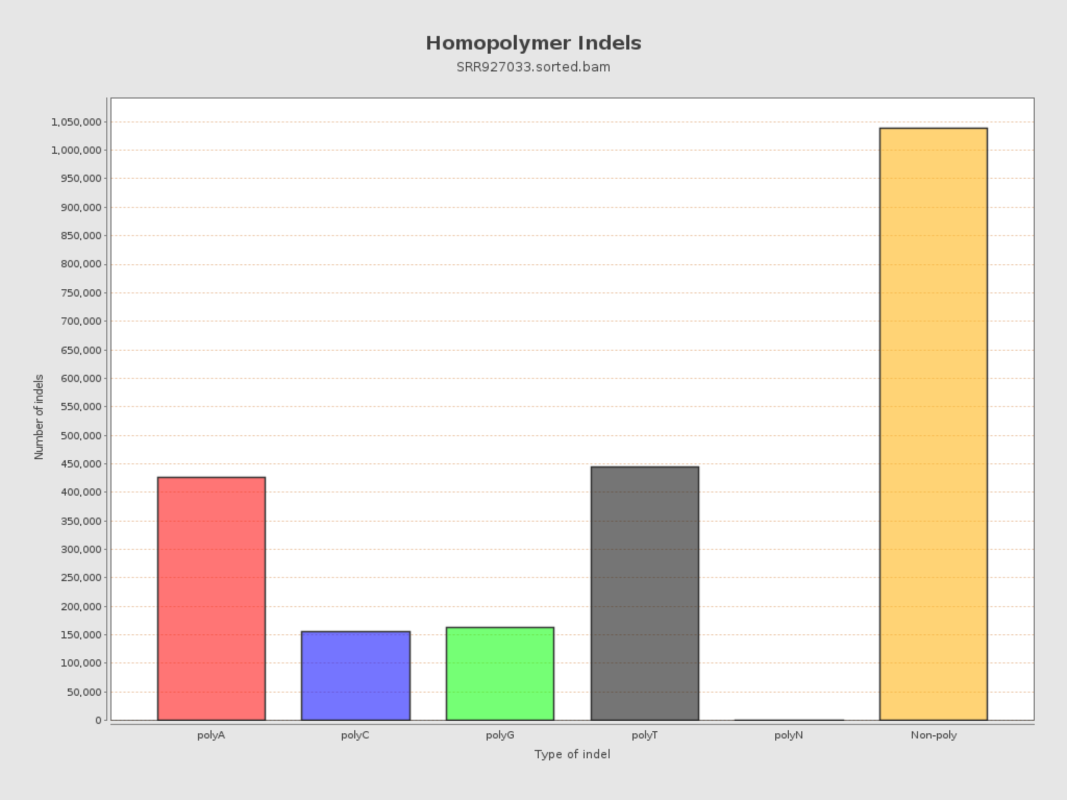
9. Results : Mapped Reads GC-content Distribution



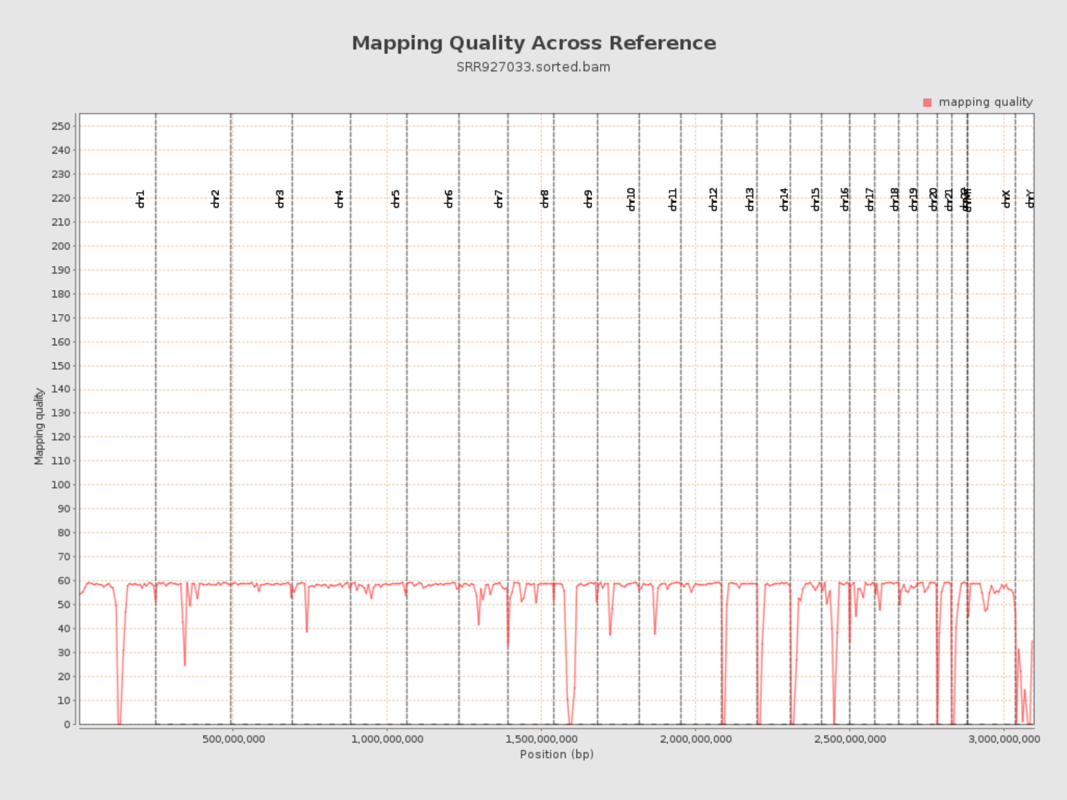
10. Results : Mapped Reads Clipping Profile



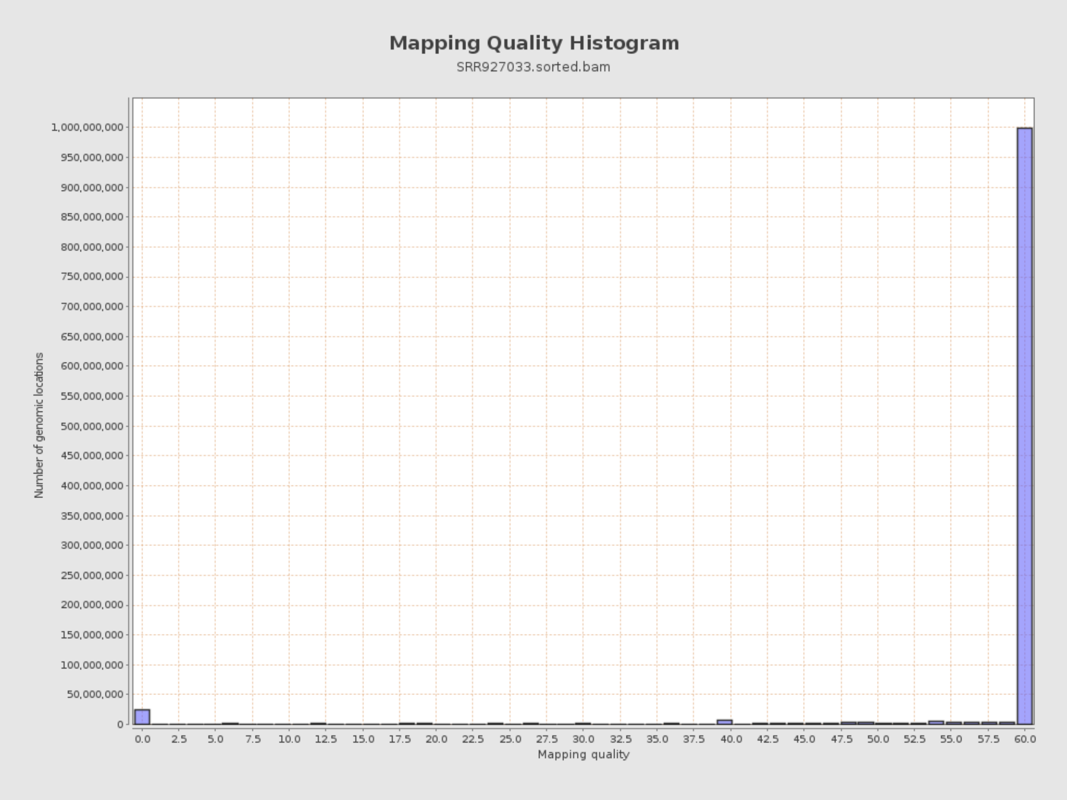
11. Results : Homopolymer Indels



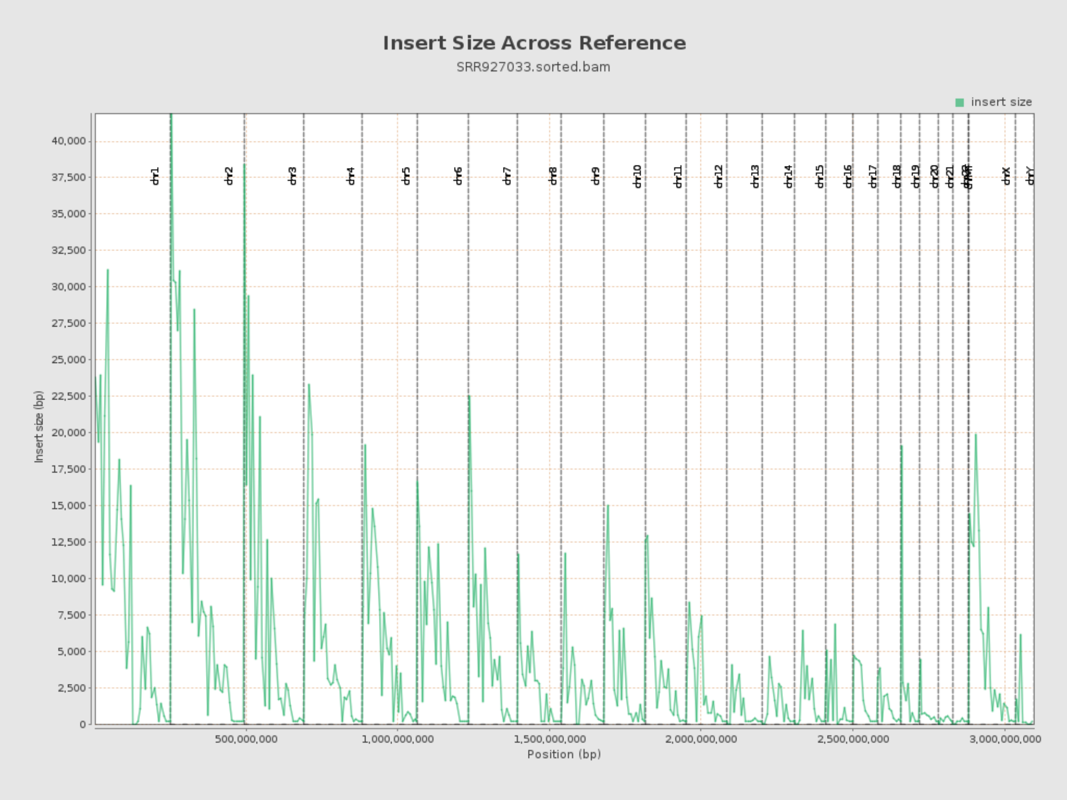
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram