Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 01:35:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927006.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_SRR927006 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927006_1.fastq.gz SRR927006_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 01:35:48 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927006.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	37,455,724
Mapped reads	36,881,485 / 98.47%
Unmapped reads	574,239 / 1.53%
Mapped paired reads	36,881,485 / 98.47%
Mapped reads, first in pair	18,511,251 / 49.42%
Mapped reads, second in pair	18,370,234 / 49.05%
Mapped reads, both in pair	36,517,692 / 97.5%
Mapped reads, singletons	363,793 / 0.97%
Secondary alignments	0
Supplementary alignments	345,263 / 0.92%
Read min/max/mean length	30 / 101 / 101.38
Duplicated reads (estimated)	3,118,190 / 8.33%
Duplication rate	6.53%
Clipped reads	9,261,220 / 24.73%

2.2. ACGT Content

Number/percentage of A's	1,008,025,331 / 28.94%
Number/percentage of C's	684,174,937 / 19.64%
Number/percentage of T's	1,022,328,817 / 29.35%
Number/percentage of G's	768,147,508 / 22.05%
Number/percentage of N's	396,965 / 0.01%

GC Percentage	41.7%

2.3. Coverage

Mean	1.126
Standard Deviation	4.5398

2.4. Mapping Quality

Mean Mapping Quality	53.59

2.5. Insert size

Mean	94,515.85
Standard Deviation	3,015,728.22
P25/Median/P75	157 / 202 / 267

2.6. Mismatches and indels

General error rate	0.93%
Mismatches	31,528,793
Insertions	579,499
Mapped reads with at least one insertion	1.54%
Deletions	1,892,304
Mapped reads with at least one deletion	4.99%
Homopolymer indels	53.19%

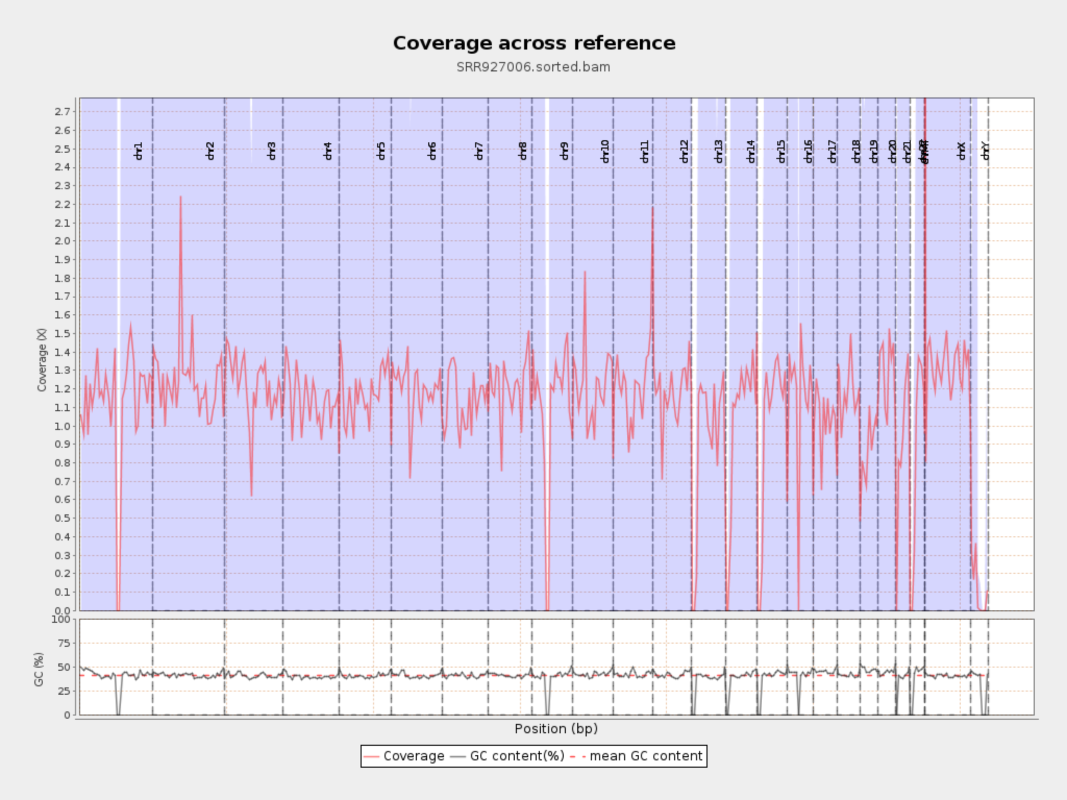
2.7. Chromosome stats

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

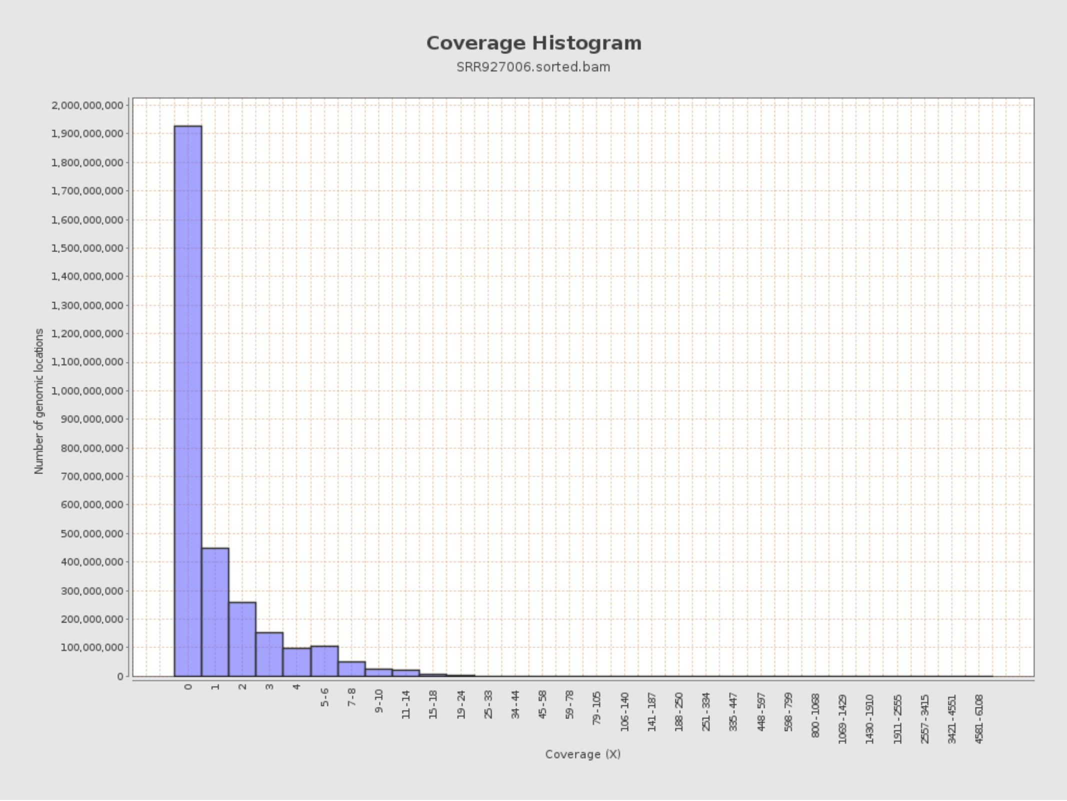
		bases	coverage	deviation
chr1	249250621	281408566	1.129	6.9189
chr2	243199373	304773517	1.2532	7.4859
chr3	198022430	241575895	1.2199	2.3277
chr4	191154276	218592030	1.1435	3.2878
chr5	180915260	212808618	1.1763	2.2657
chr6	171115067	205520657	1.2011	3.8047
chr7	159138663	179992148	1.131	3.429
chr8	146364022	177729429	1.2143	2.7214
chr9	141213431	151376434	1.072	5.6232
chr10	135534747	166405801	1.2278	8.2662
chr11	135006516	163038610	1.2076	4.0941
chr12	133851895	158409827	1.1835	2.3598
chr13	115169878	105191217	0.9134	1.9835
chr14	107349540	107909400	1.0052	2.2364
chr15	102531392	100459670	0.9798	2.156
chr16	90354753	102285044	1.132	5.2364
chr17	81195210	83382159	1.0269	2.9366
chr18	78077248	93616696	1.199	5.8929
chr19	59128983	51615885	0.8729	3.9617
chr20	63025520	81977986	1.3007	2.706
chr21	48129895	44925040	0.9334	3.7649
chr22	51304566	43213836	0.8423	2.1288
chrMT	16571	227587	13.7341	12.7373
chrX	155270560	202682195	1.3053	2.853

chrY	59373566	6645930	0.1119	4.0576

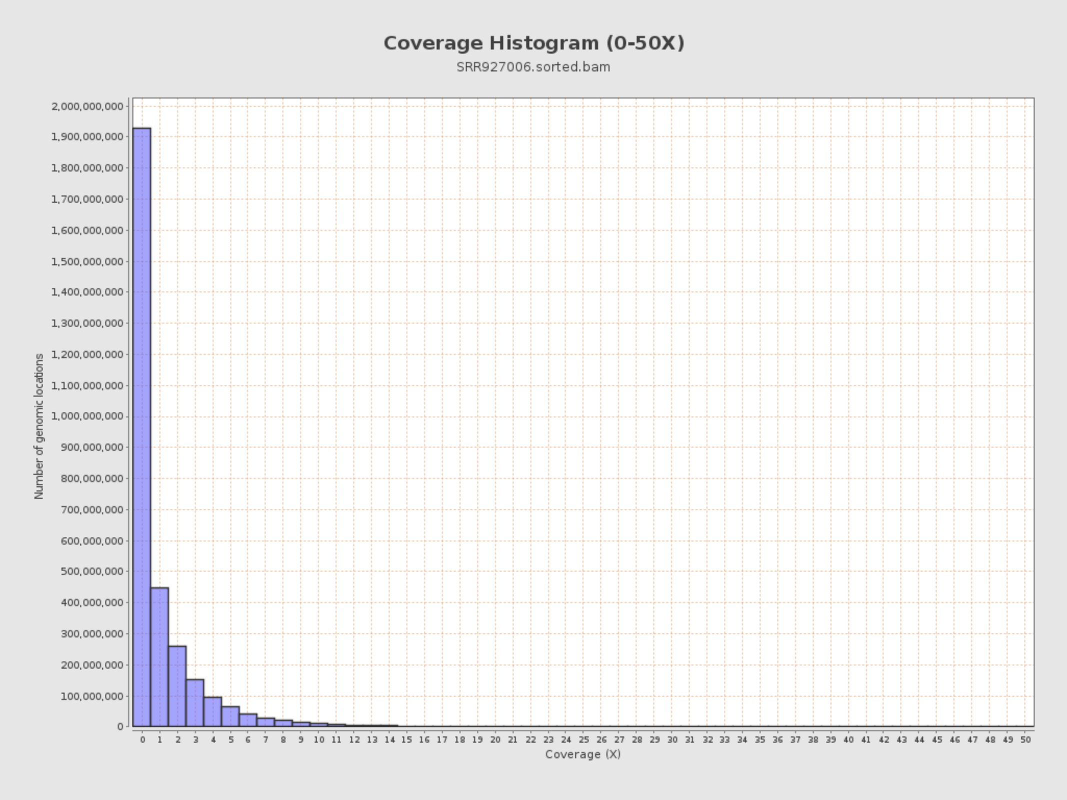
3. Results : Coverage across reference



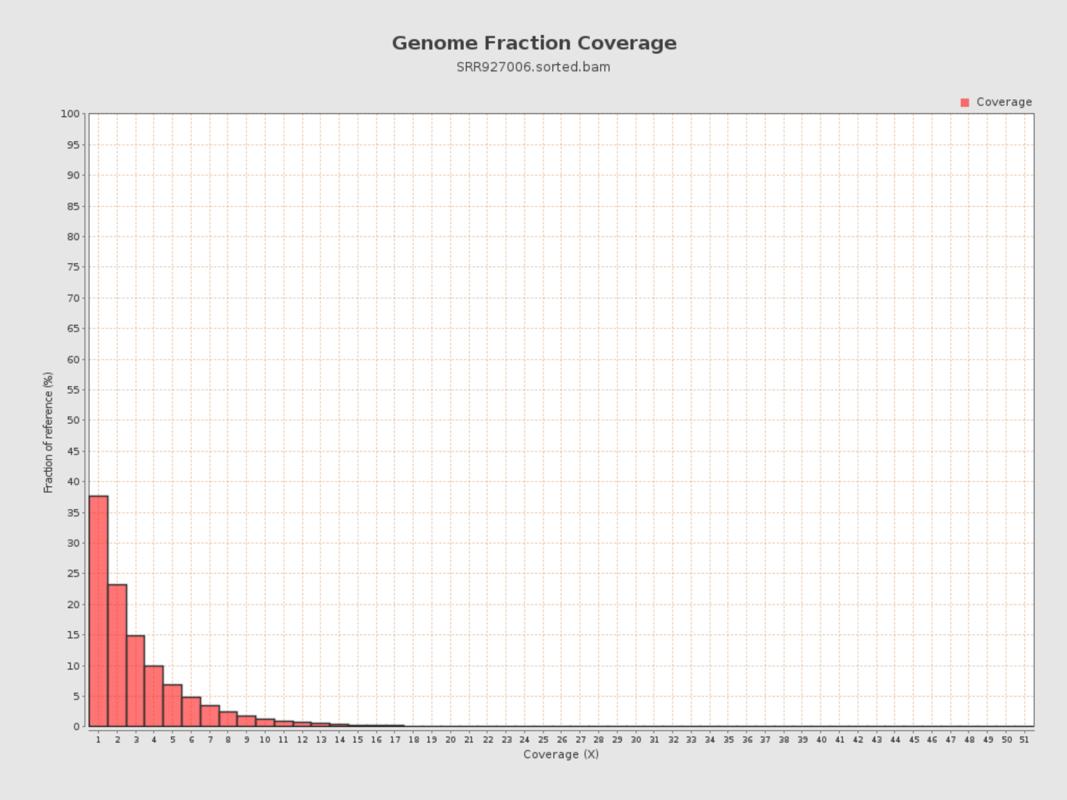
4. Results : Coverage Histogram



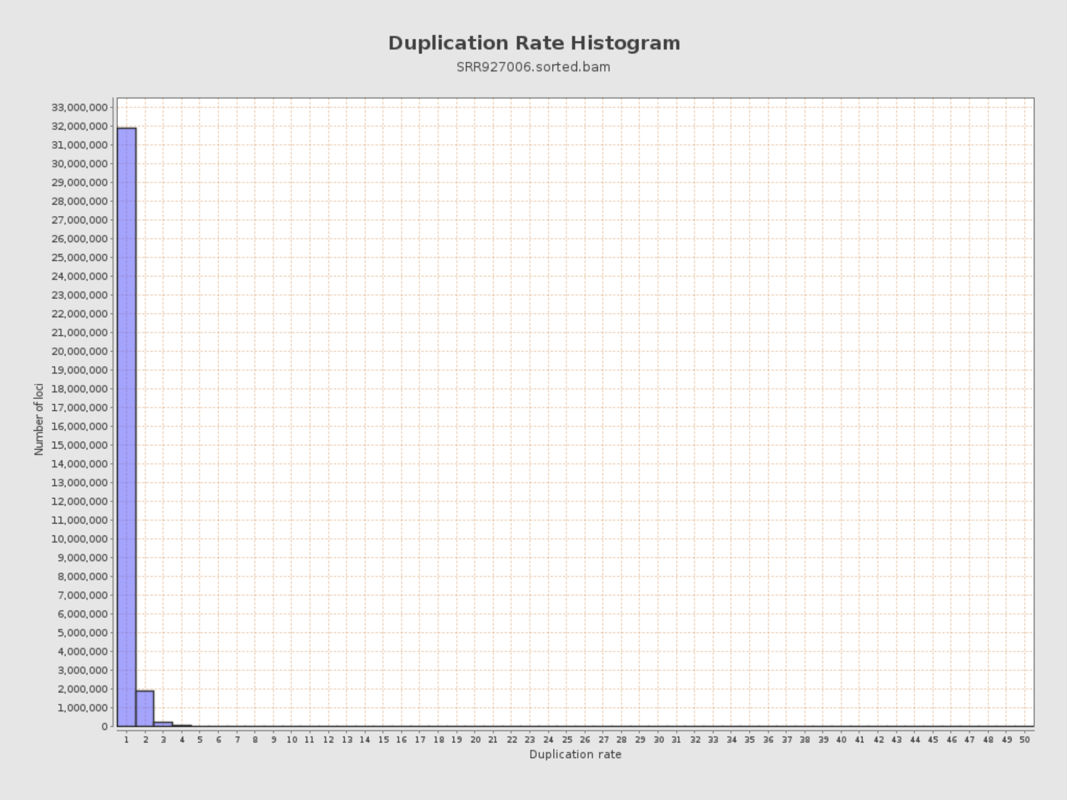
5. Results : Coverage Histogram (0-50X)



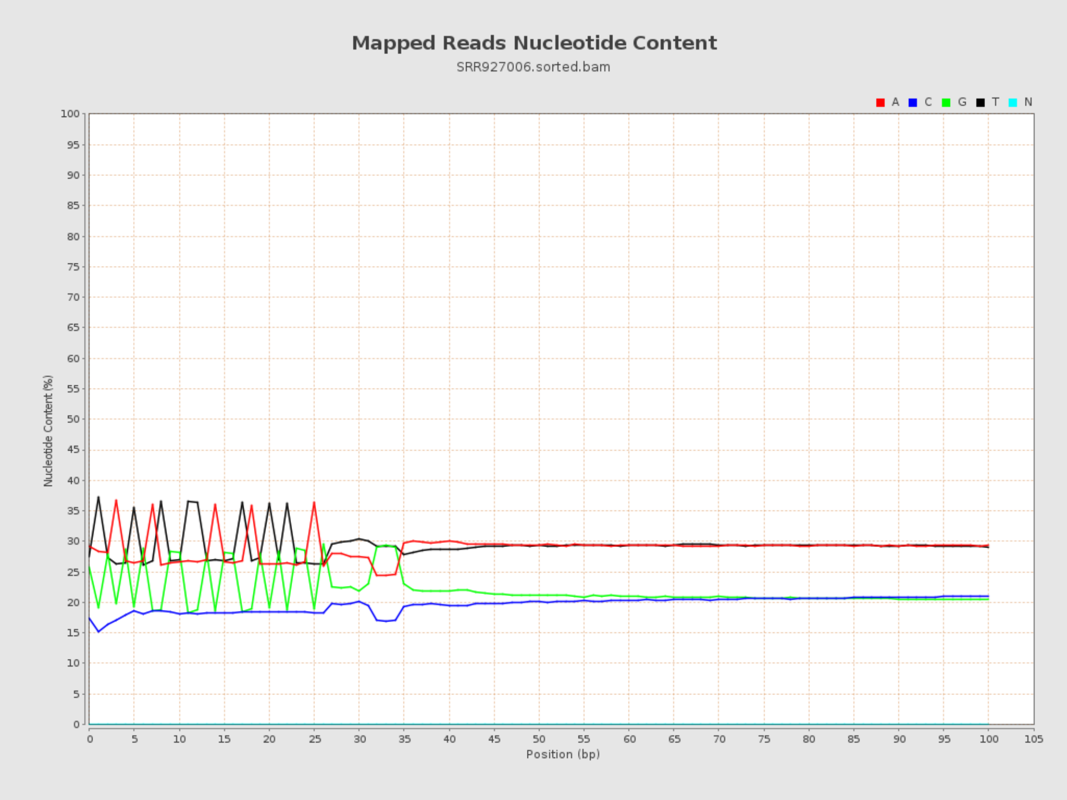
6. Results : Genome Fraction Coverage



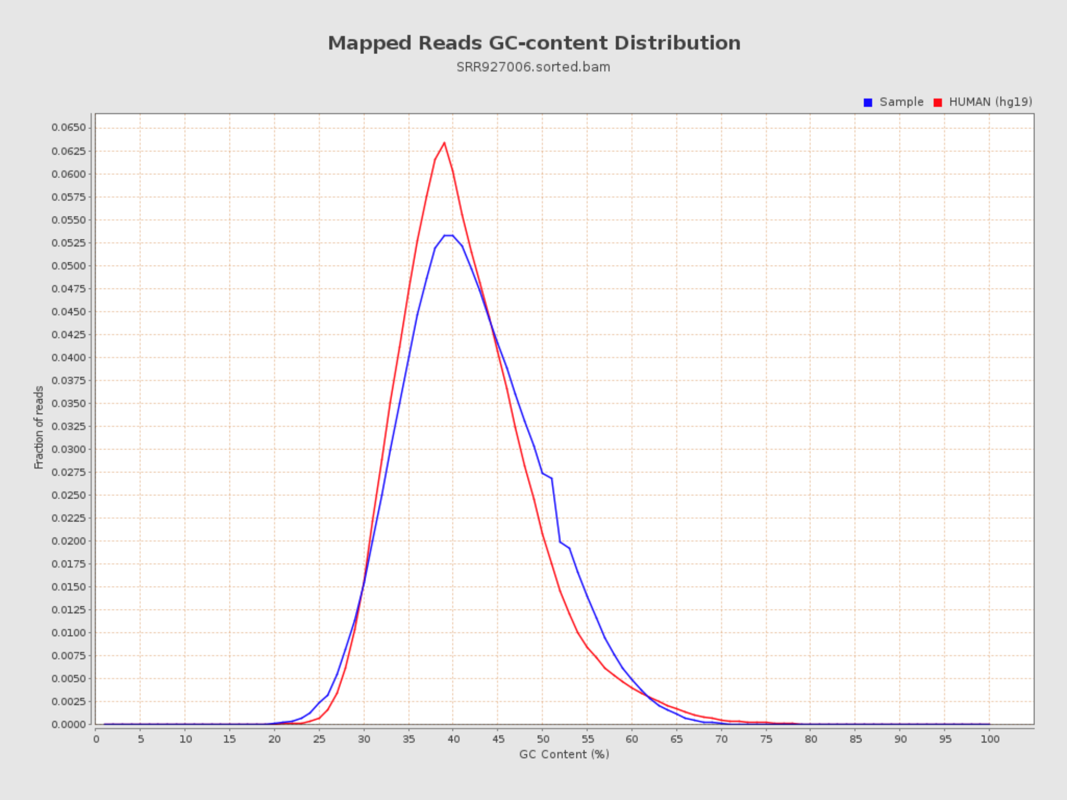
7. Results : Duplication Rate Histogram



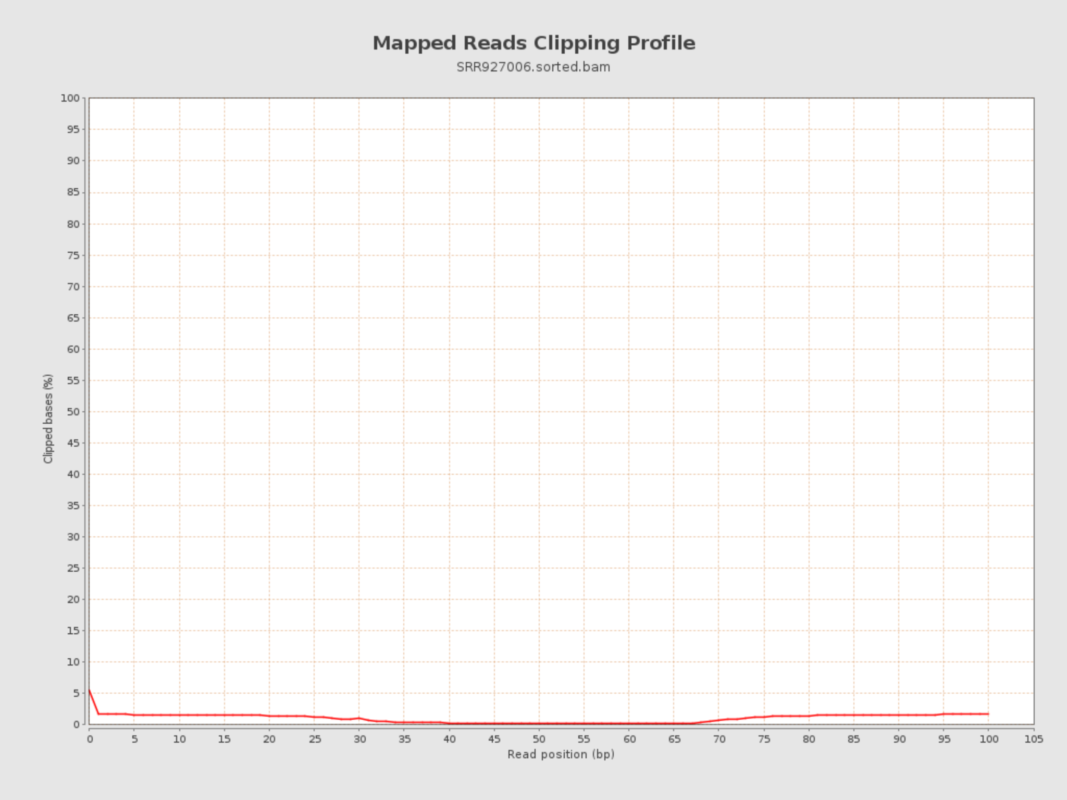
8. Results : Mapped Reads Nucleotide Content



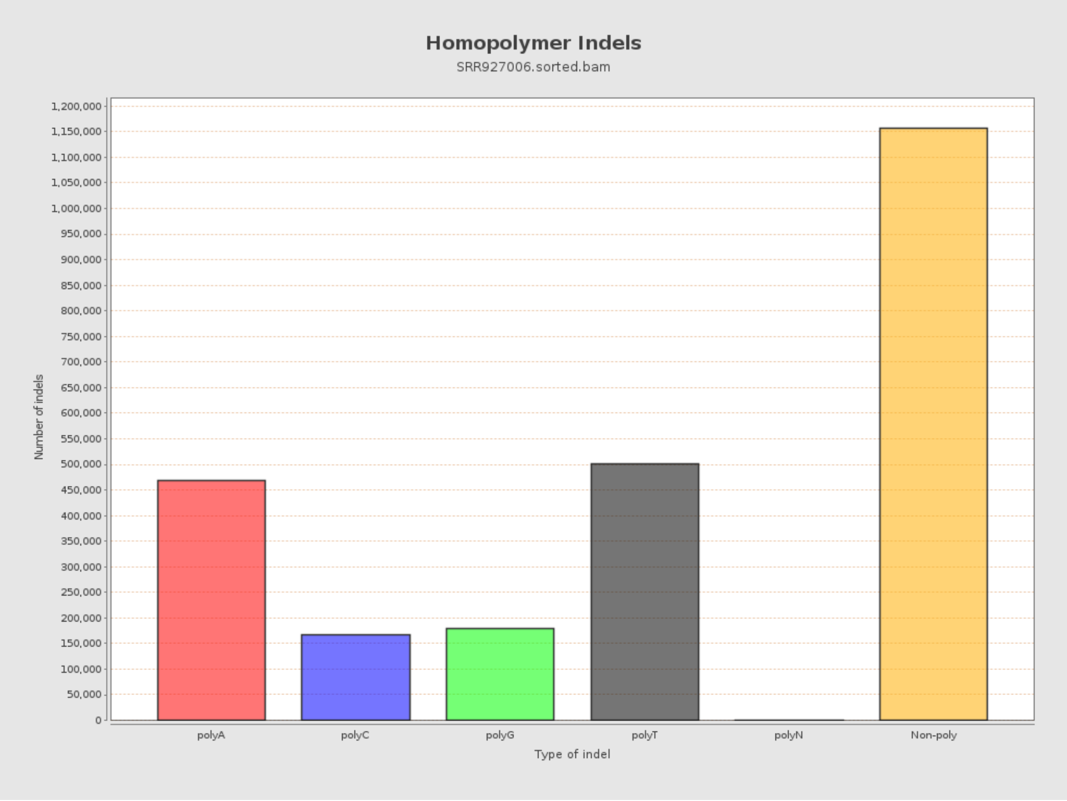
9. Results : Mapped Reads GC-content Distribution



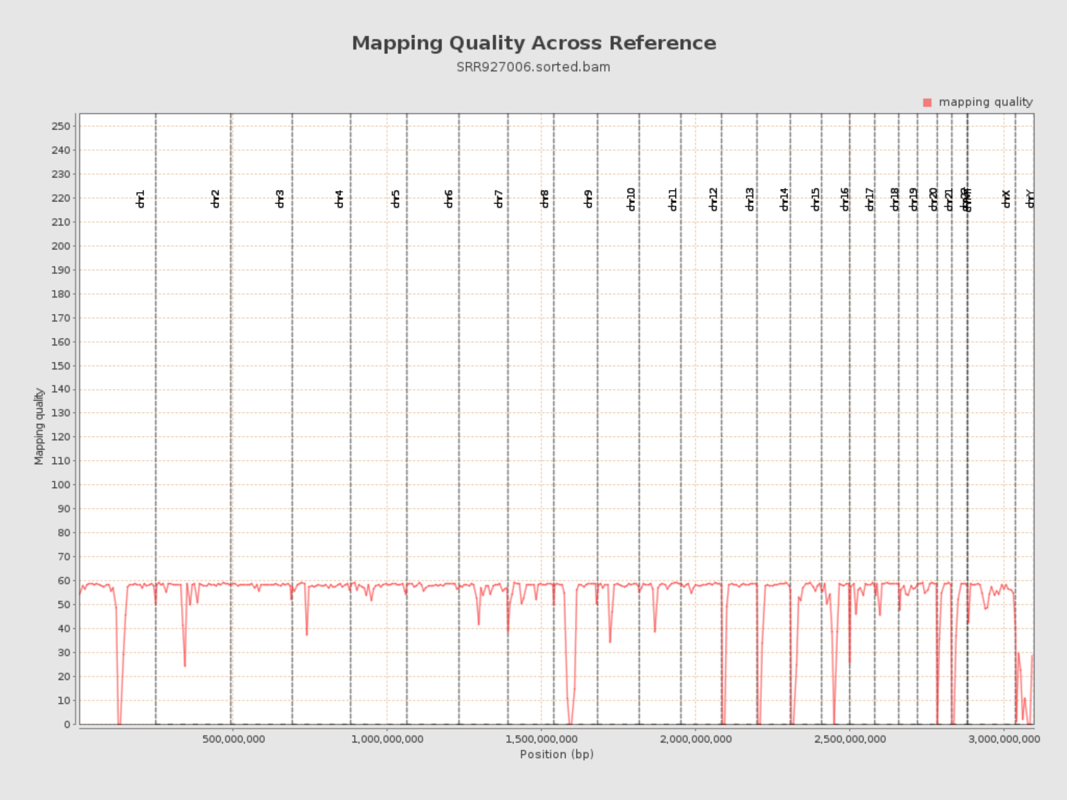
10. Results : Mapped Reads Clipping Profile



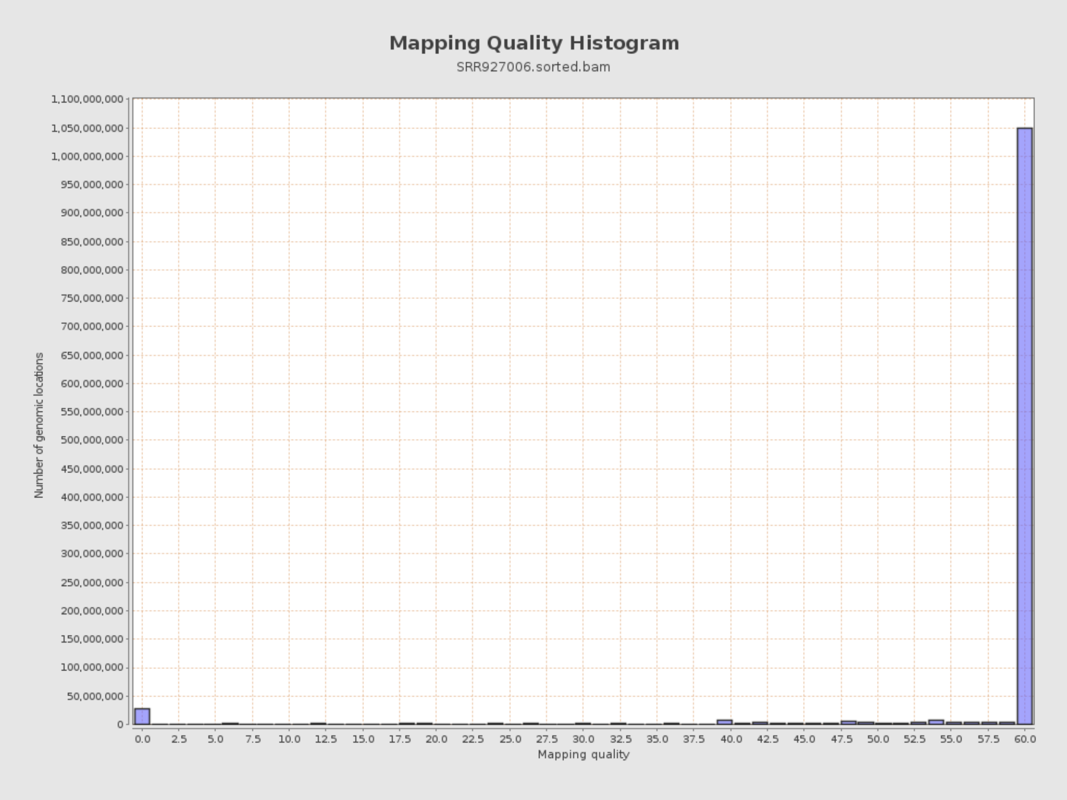
11. Results : Homopolymer Indels



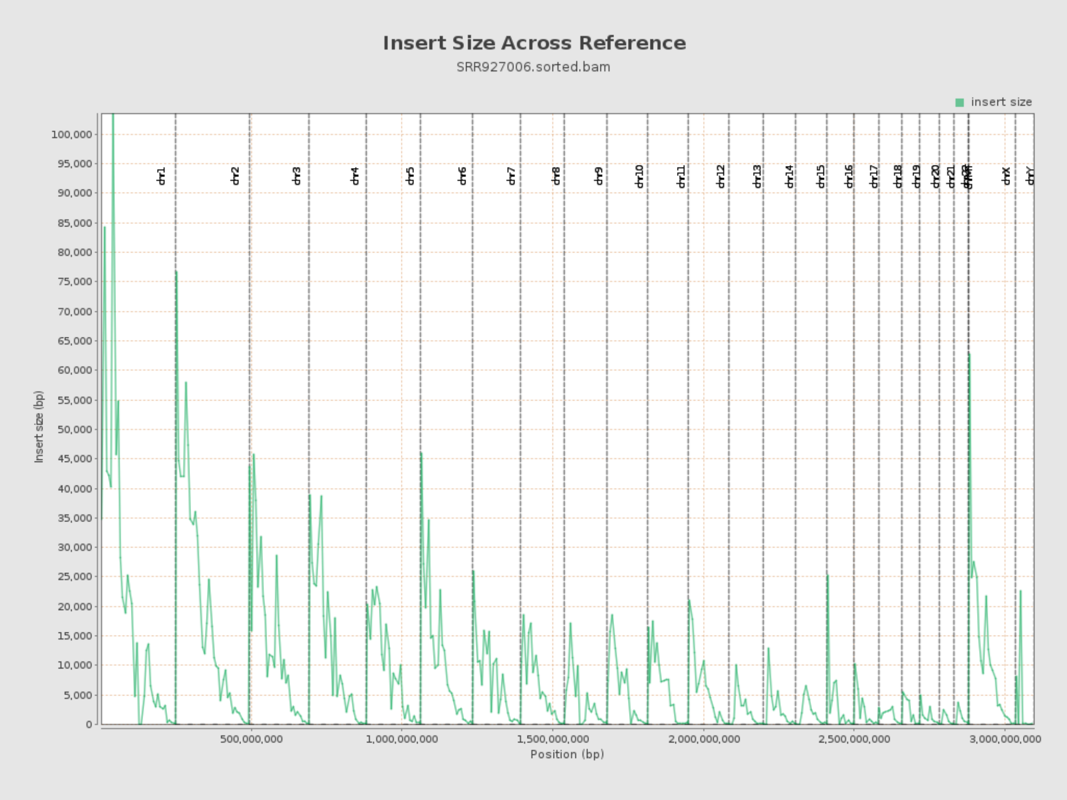
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram