Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 10:55:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927028.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_SRR927028 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927028_1.fastq.gz SRR927028_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 10:55:30 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927028.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,378,786
Mapped reads	27,962,928 / 98.53%
Unmapped reads	415,858 / 1.47%
Mapped paired reads	27,962,928 / 98.53%
Mapped reads, first in pair	14,022,121 / 49.41%
Mapped reads, second in pair	13,940,807 / 49.12%
Mapped reads, both in pair	27,719,268 / 97.68%
Mapped reads, singletons	243,660 / 0.86%
Secondary alignments	0
Supplementary alignments	229,668 / 0.81%
Read min/max/mean length	30 / 101 / 101.33
Duplicated reads (estimated)	1,846,288 / 6.51%
Duplication rate	4.95%
Clipped reads	6,771,862 / 23.86%

2.2. ACGT Content

Number/percentage of A's	767,185,550 / 28.98%
Number/percentage of C's	521,751,080 / 19.71%
Number/percentage of T's	775,431,457 / 29.29%
Number/percentage of G's	582,449,607 / 22%
Number/percentage of N's	579,039 / 0.02%

GC Percentage	41.71%

2.3. Coverage

Mean	0.8558
Standard Deviation	4.0371

2.4. Mapping Quality

Mean Mapping Quality	53.55

2.5. Insert size

Mean	87,059
Standard Deviation	2,883,633.05
P25/Median/P75	157 / 202 / 268

2.6. Mismatches and indels

General error rate	0.95%
Mismatches	24,350,650
Insertions	426,431
Mapped reads with at least one insertion	1.5%
Deletions	1,406,190
Mapped reads with at least one deletion	4.9%
Homopolymer indels	53.16%

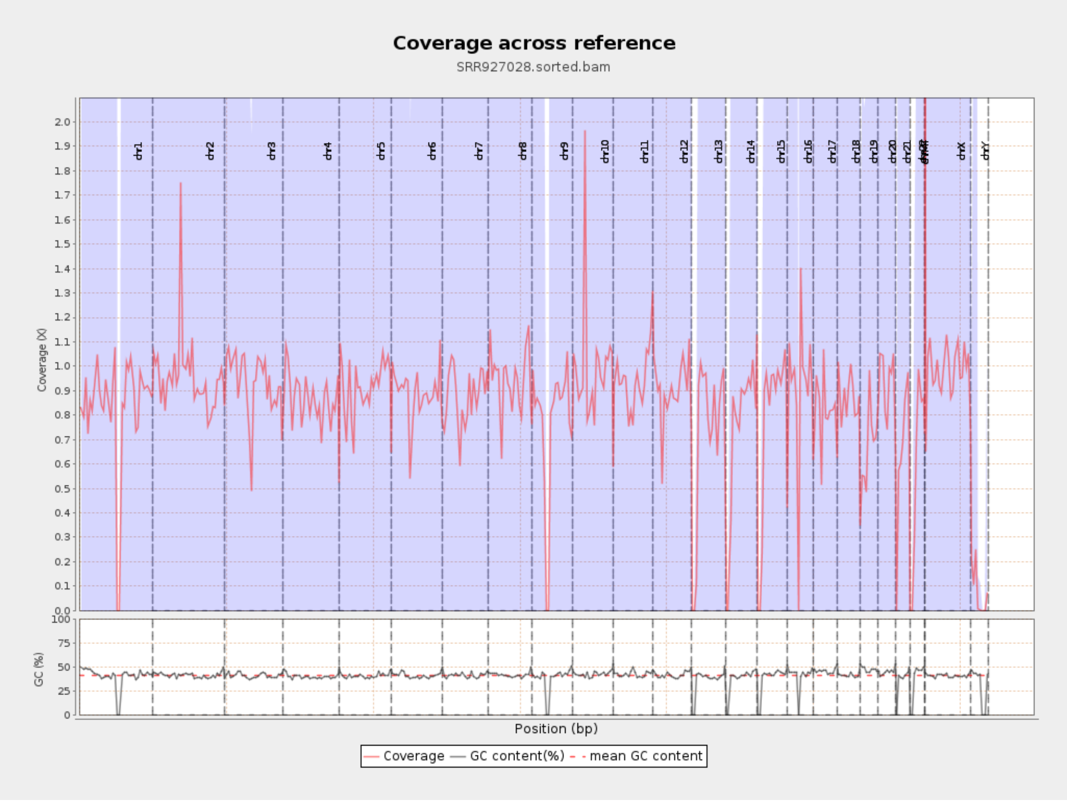
2.7. Chromosome stats

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

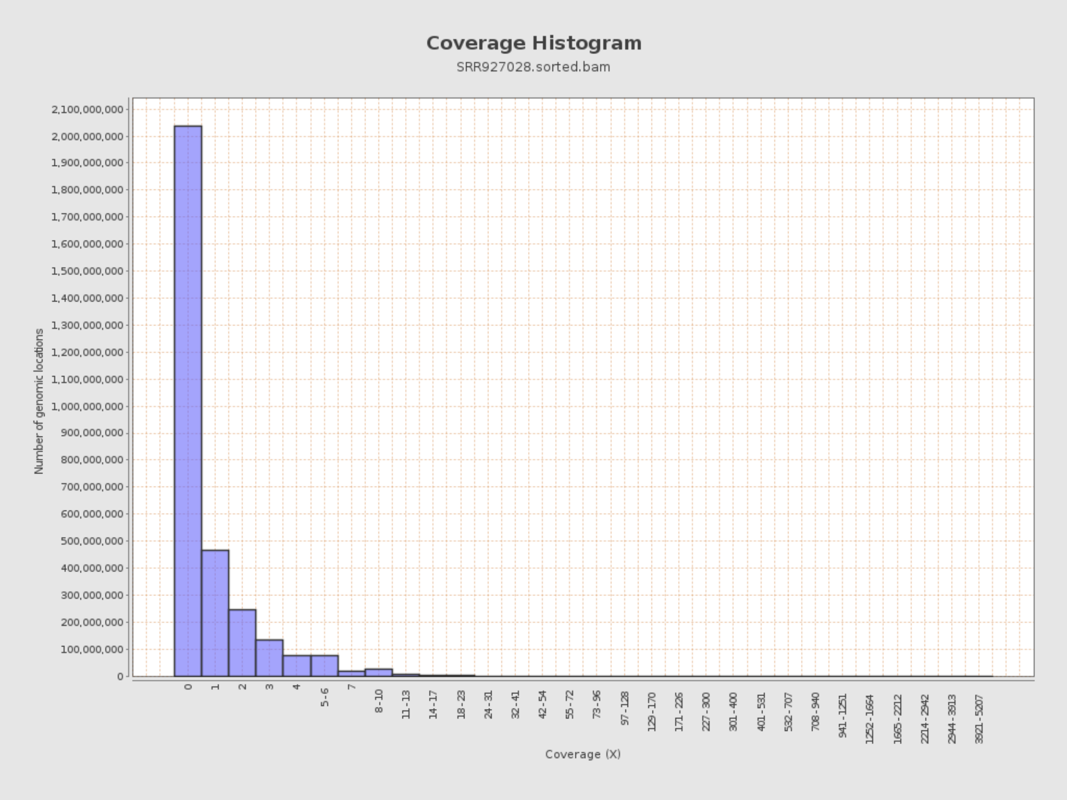
		bases	coverage	deviation
chr1	249250621	208326481	0.8358	5.6486
chr2	243199373	233897435	0.9618	5.99
chr3	198022430	184395809	0.9312	1.8475
chr4	191154276	165984702	0.8683	2.6059
chr5	180915260	165280835	0.9136	1.7717
chr6	171115067	152560530	0.8916	1.7993
chr7	159138663	138917180	0.8729	2.494
chr8	146364022	138310071	0.945	2.1425
chr9	141213431	106781309	0.7562	4.5267
chr10	135534747	136139300	1.0045	10.6541
chr11	135006516	125434961	0.9291	4.2243
chr12	133851895	121383051	0.9068	1.7839
chr13	115169878	83028091	0.7209	1.5587
chr14	107349540	78498426	0.7312	1.6458
chr15	102531392	78424011	0.7649	1.6729
chr16	90354753	80310721	0.8888	5.0909
chr17	81195210	65706354	0.8092	2.2584
chr18	78077248	68770938	0.8808	4.9546
chr19	59128983	39165470	0.6624	3.1158
chr20	63025520	58783196	0.9327	1.9836
chr21	48129895	32161238	0.6682	2.3455
chr22	51304566	30010193	0.5849	1.5426
chrMT	16571	135843	8.1976	6.5795
chrX	155270560	152523096	0.9823	2.2408

chrY	59373566	4451501	0.075	2.3287

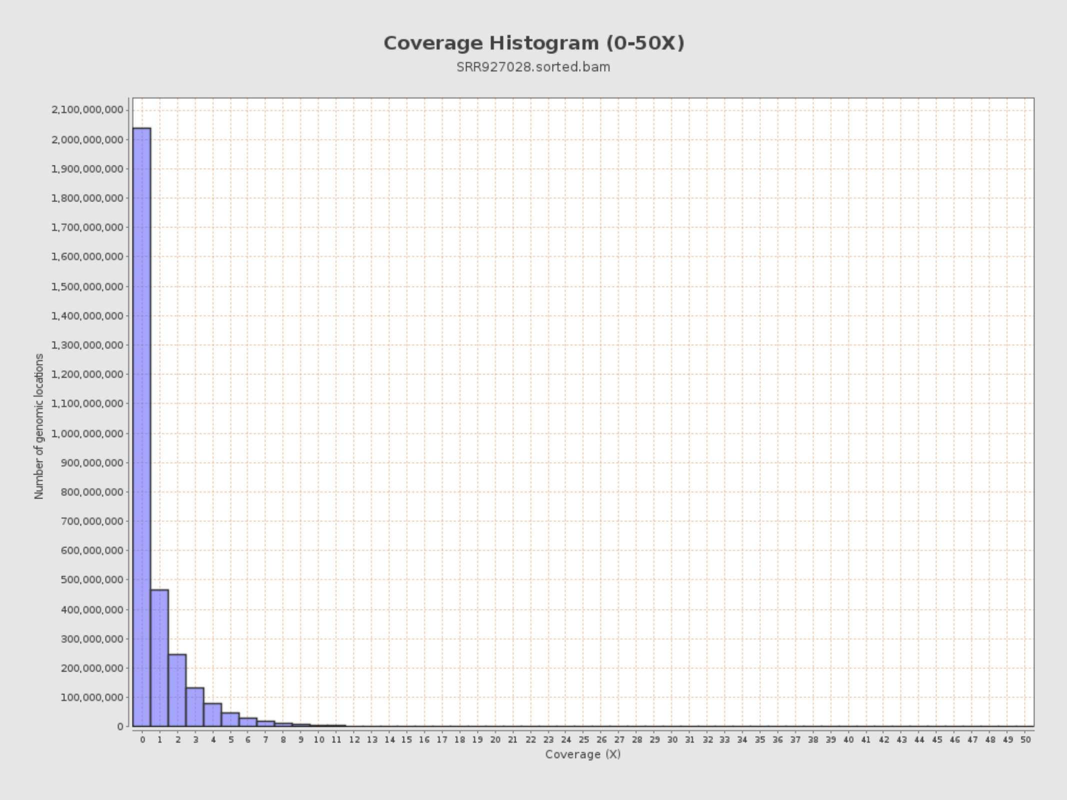
3. Results : Coverage across reference



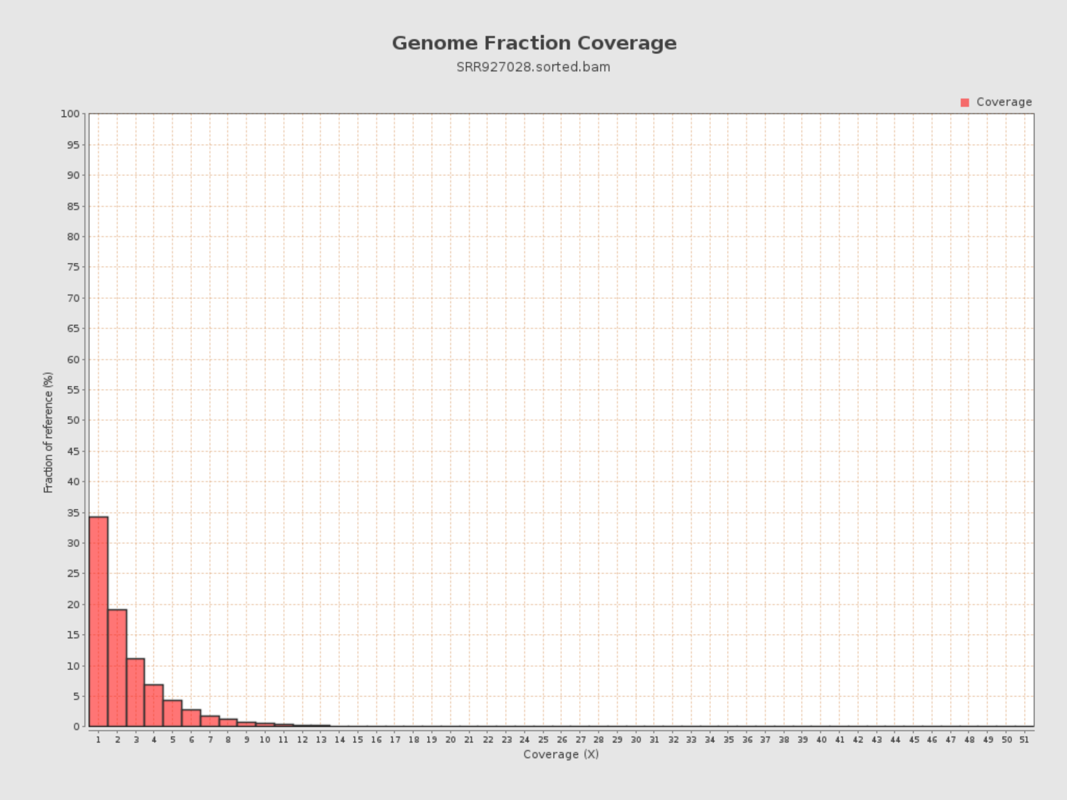
4. Results : Coverage Histogram



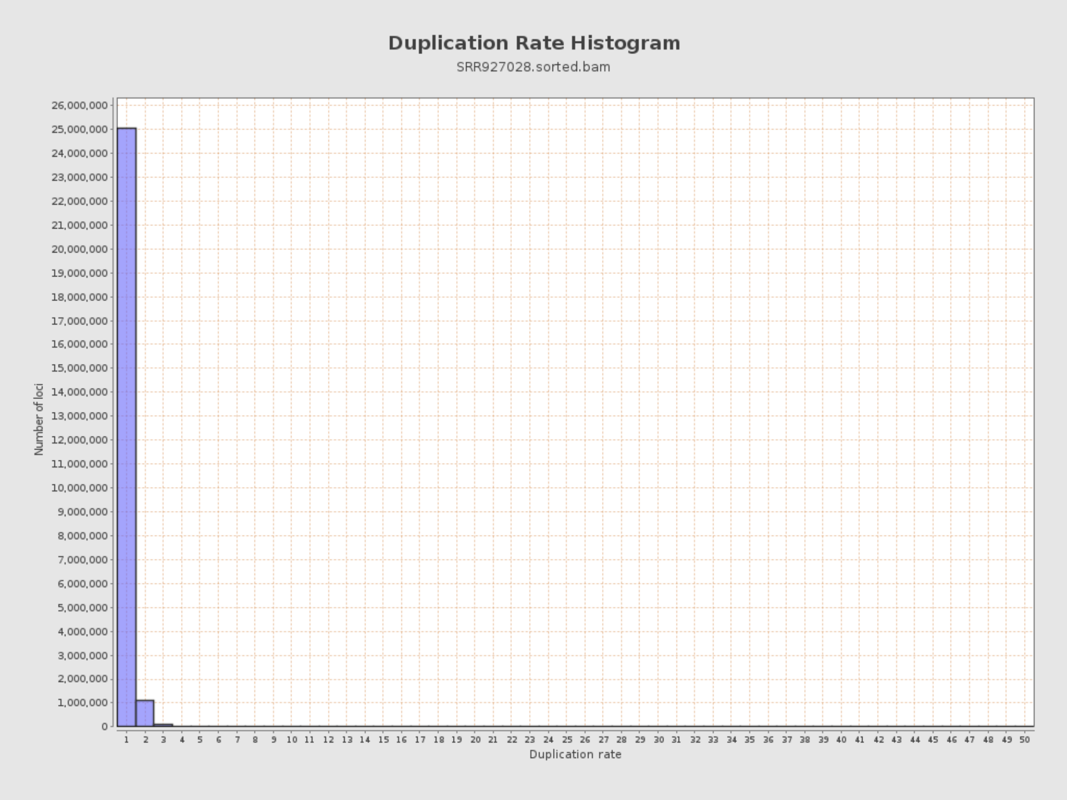
5. Results : Coverage Histogram (0-50X)



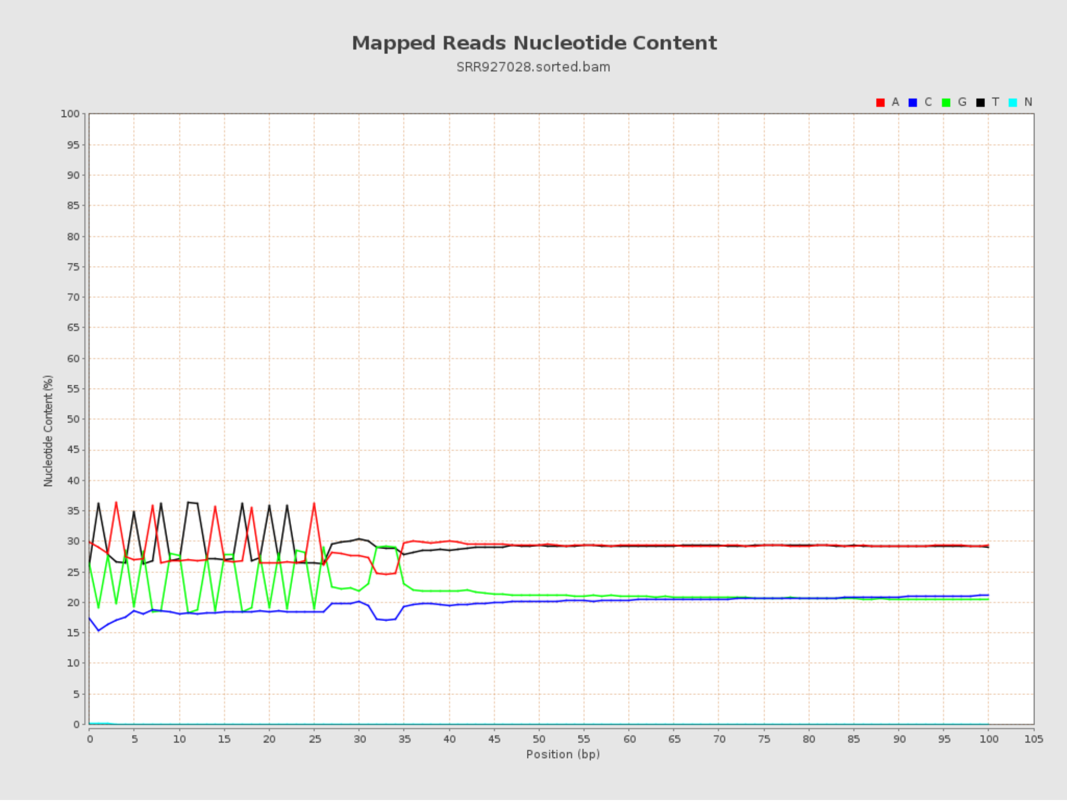
6. Results : Genome Fraction Coverage



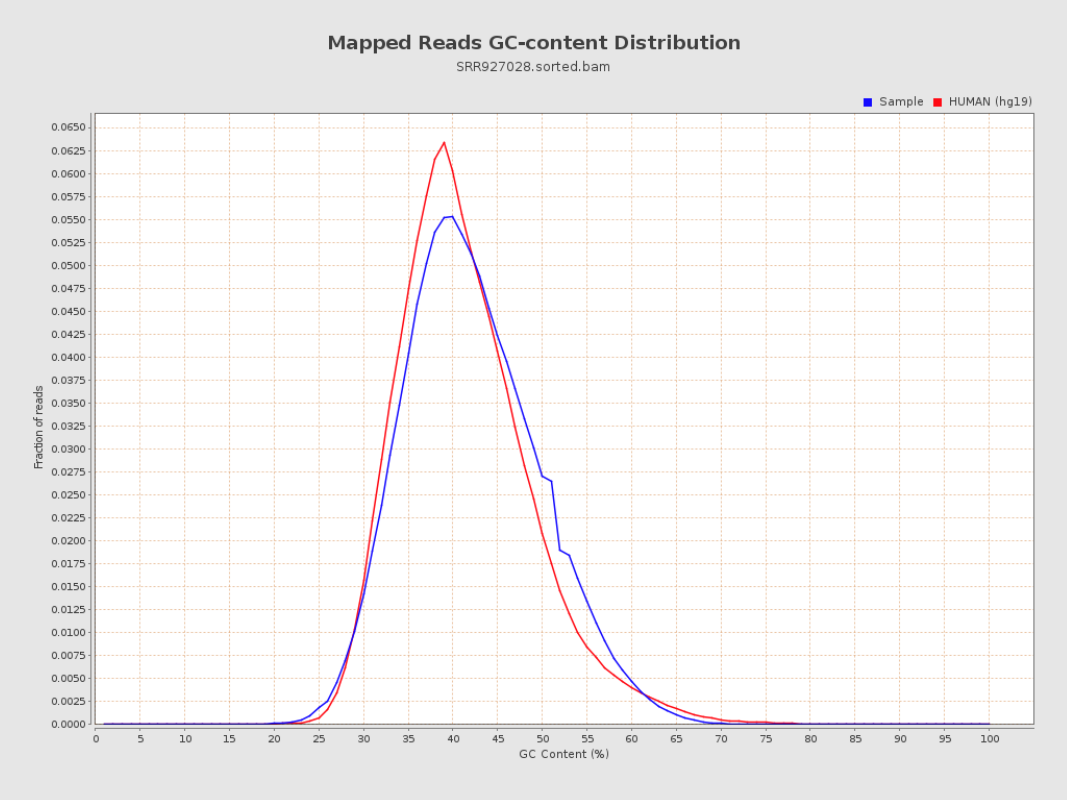
7. Results : Duplication Rate Histogram



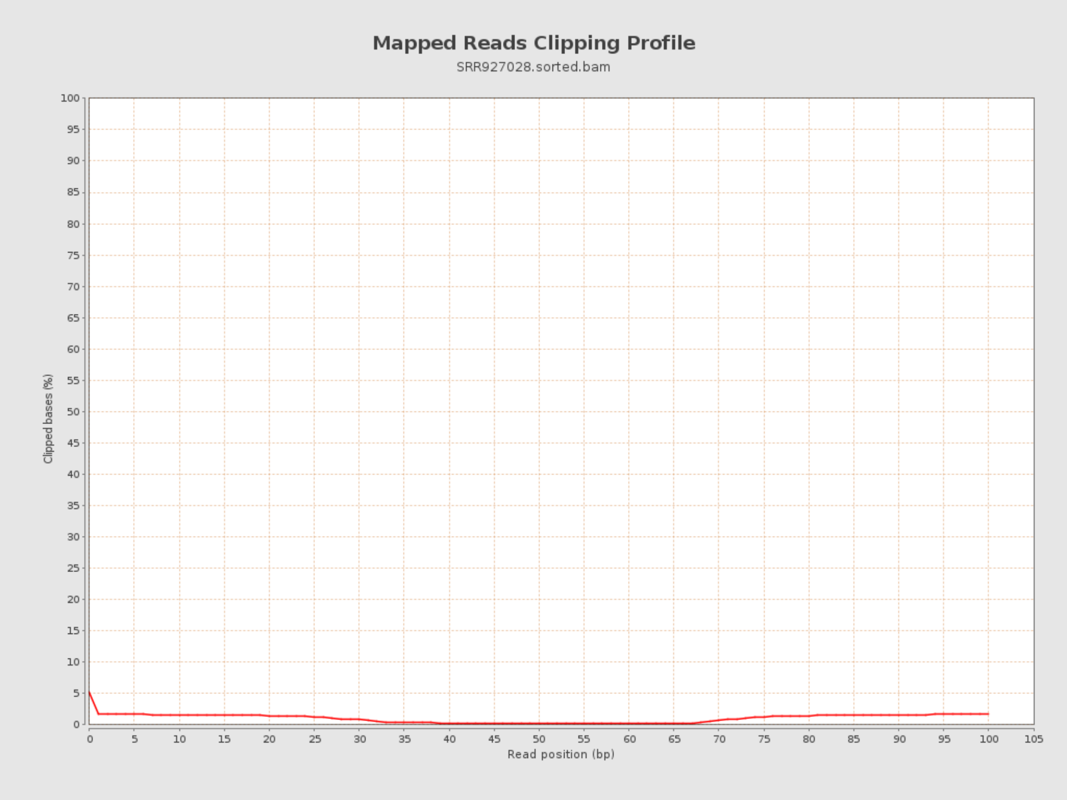
8. Results : Mapped Reads Nucleotide Content



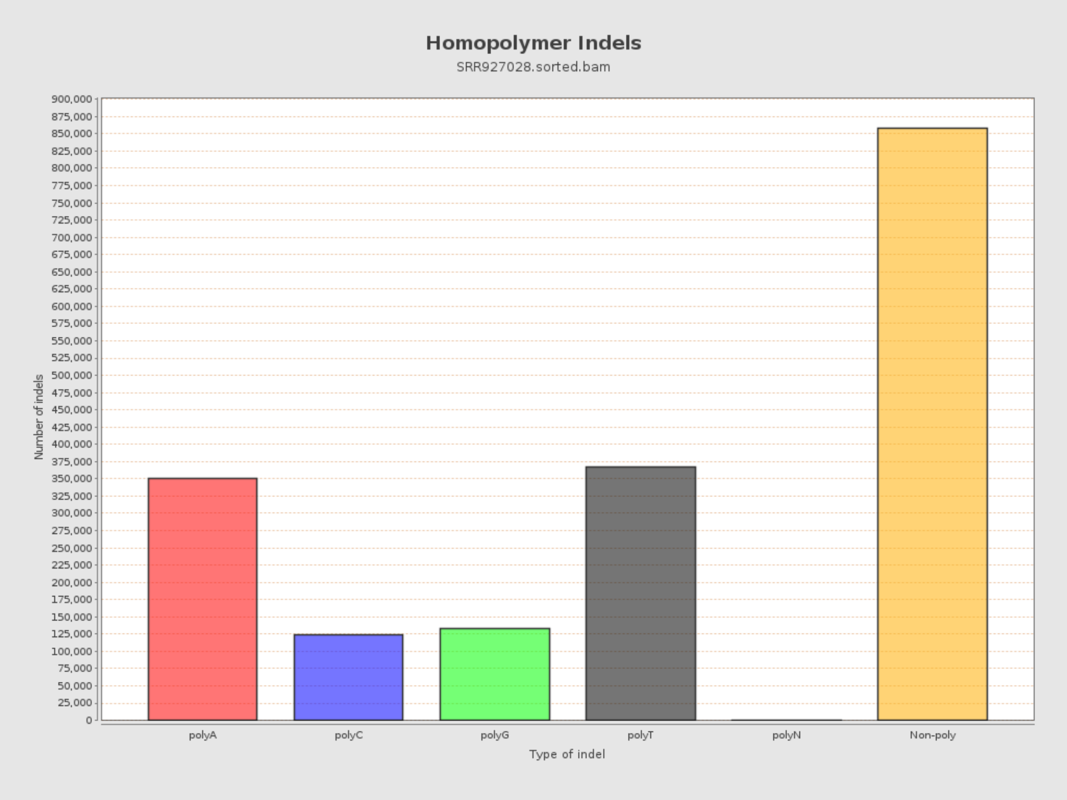
9. Results : Mapped Reads GC-content Distribution



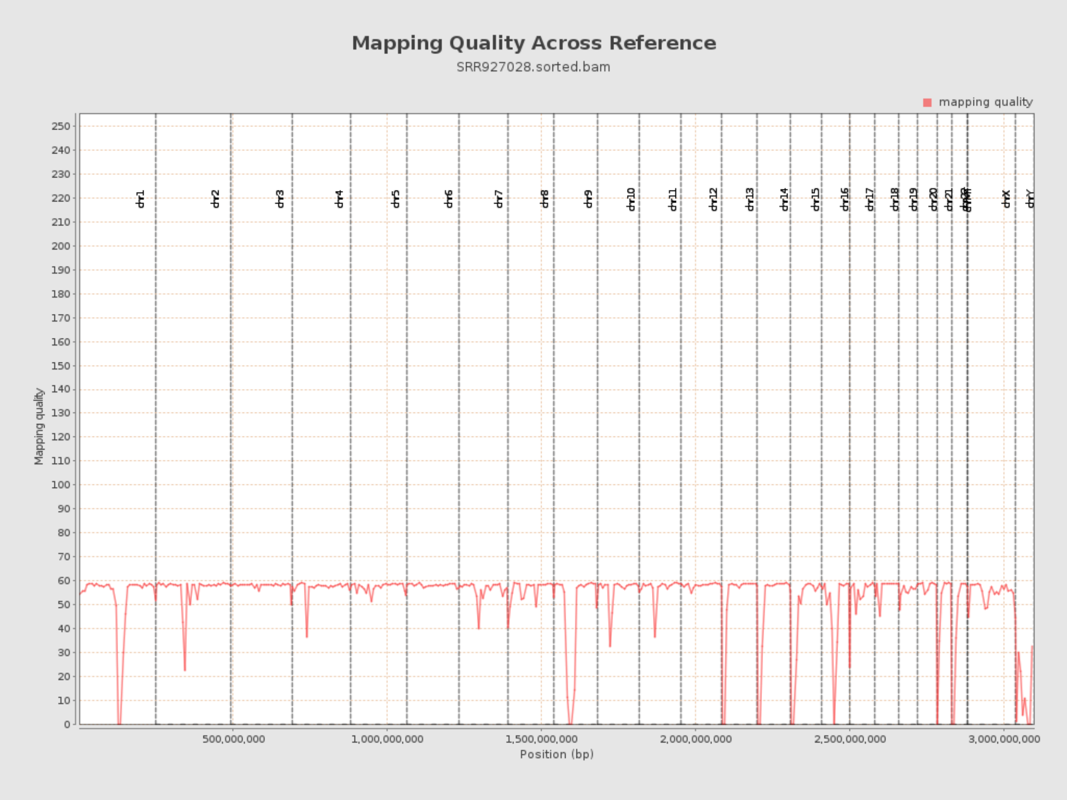
10. Results : Mapped Reads Clipping Profile



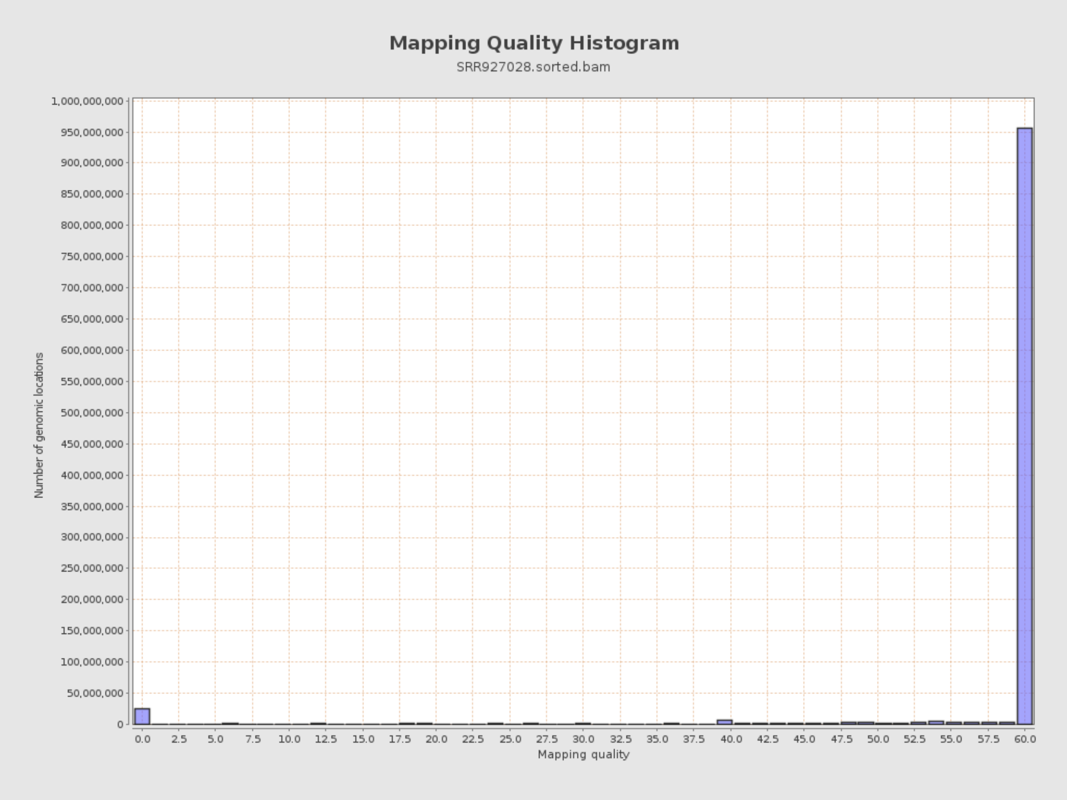
11. Results : Homopolymer Indels



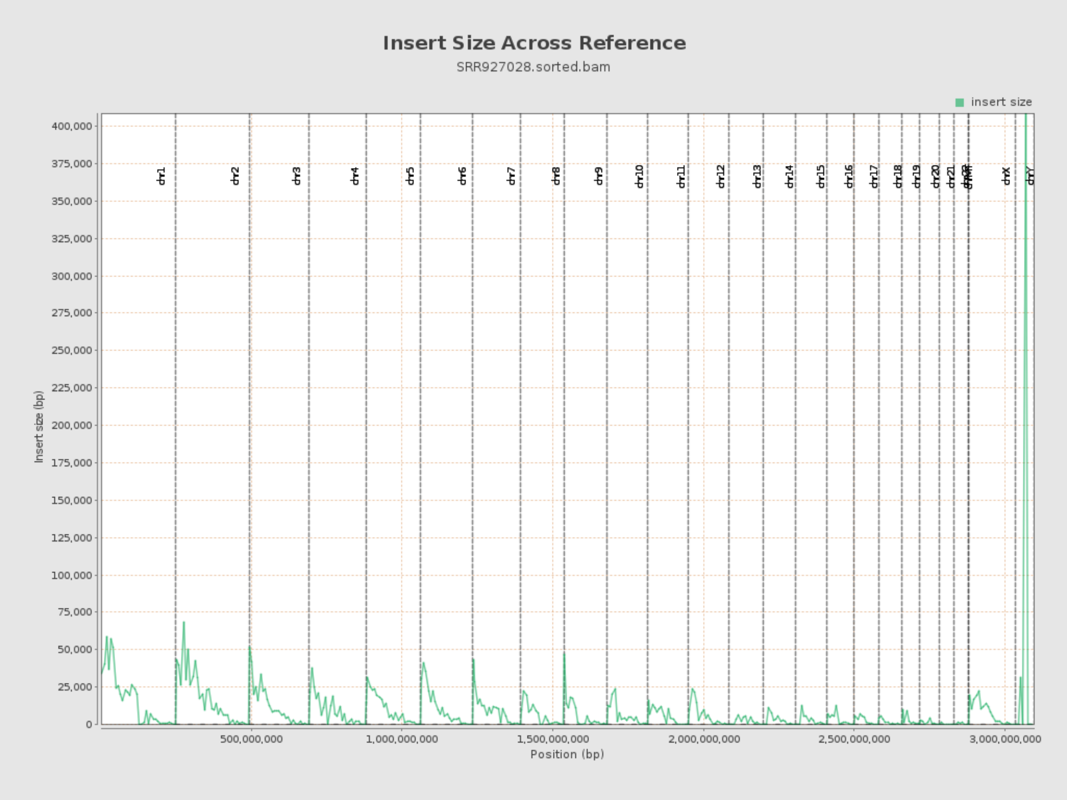
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram