Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 19:41:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927044.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_SRR927044 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927044_1.fastq.gz SRR927044_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 19:41:13 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927044.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,989,054
Mapped reads	30,301,839 / 97.78%
Unmapped reads	687,215 / 2.22%
Mapped paired reads	30,301,839 / 97.78%
Mapped reads, first in pair	15,198,930 / 49.05%
Mapped reads, second in pair	15,102,909 / 48.74%
Mapped reads, both in pair	29,895,192 / 96.47%
Mapped reads, singletons	406,647 / 1.31%
Secondary alignments	0
Supplementary alignments	586,199 / 1.89%
Read min/max/mean length	30 / 101 / 101.79
Duplicated reads (estimated)	2,918,620 / 9.42%
Duplication rate	7.35%
Clipped reads	11,386,208 / 36.74%

2.2. ACGT Content

Number/percentage of A's	786,898,392 / 28.33%
Number/percentage of C's	548,648,879 / 19.75%
Number/percentage of T's	804,823,576 / 28.98%
Number/percentage of G's	636,827,022 / 22.93%
Number/percentage of N's	371,968 / 0.01%

GC Percentage	42.68%

2.3. Coverage

Mean	0.8979
Standard Deviation	3.7807

2.4. Mapping Quality

Mean Mapping Quality	53.12

2.5. Insert size

Mean	201,155.98
Standard Deviation	4,436,025.32
P25/Median/P75	145 / 190 / 258

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	28,798,317
Insertions	477,149
Mapped reads with at least one insertion	1.54%
Deletions	1,472,372
Mapped reads with at least one deletion	4.73%
Homopolymer indels	52.13%

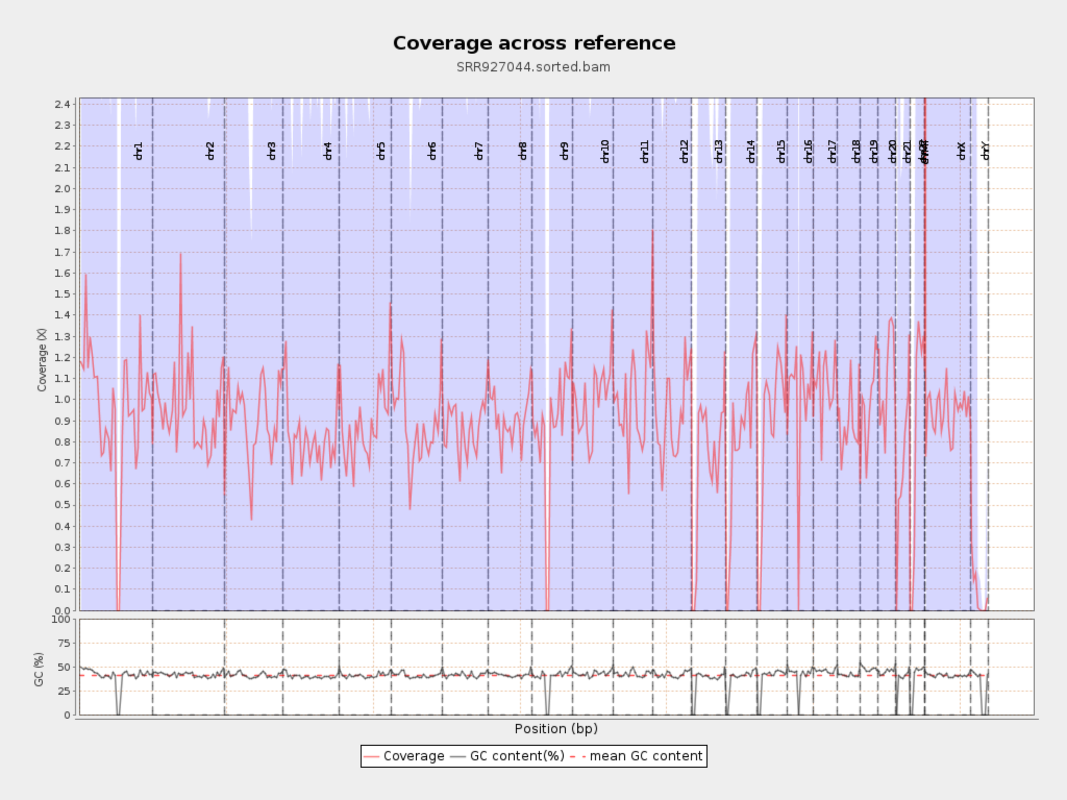
2.7. Chromosome stats

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

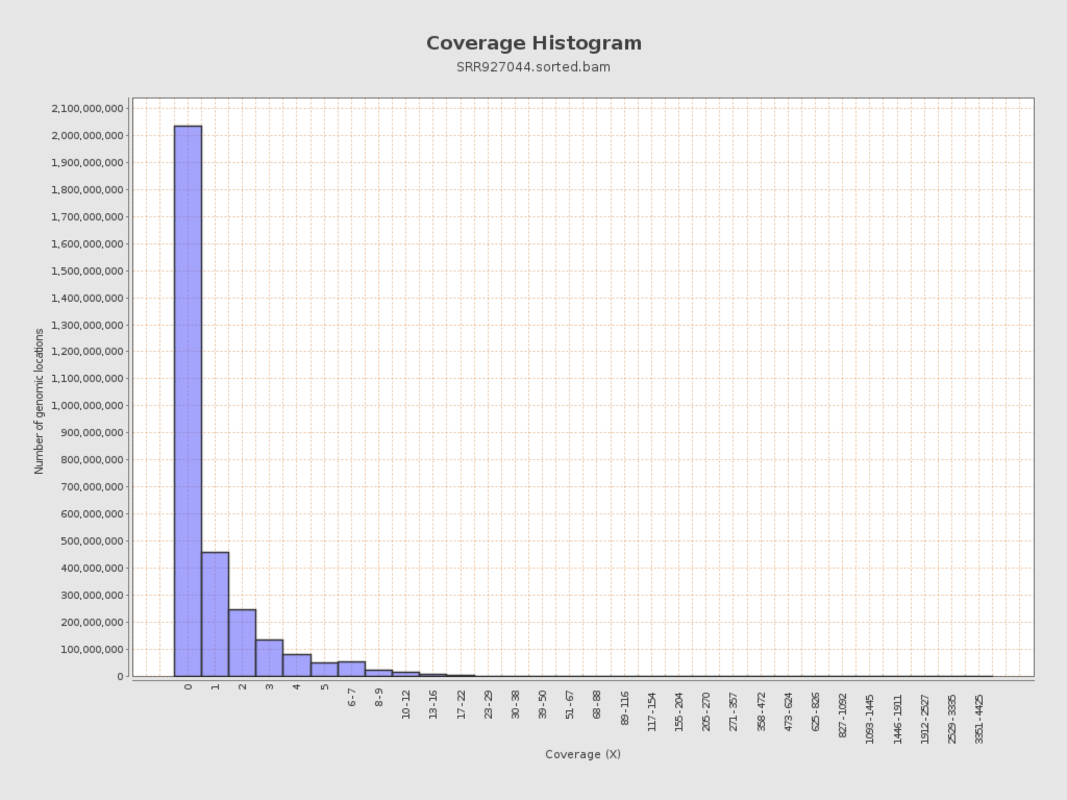
		bases	coverage	deviation
chr1	249250621	237214156	0.9517	3.7352
chr2	243199373	235281414	0.9674	5.5656
chr3	198022430	180249918	0.9103	1.8473
chr4	191154276	156404157	0.8182	2.4187
chr5	180915260	162435101	0.8979	1.8496
chr6	171115067	151186071	0.8835	1.8383
chr7	159138663	138859118	0.8726	2.159
chr8	146364022	132870632	0.9078	2.21
chr9	141213431	121660379	0.8615	3.6987
chr10	135534747	135342073	0.9986	4.2148
chr11	135006516	133557830	0.9893	2.9397
chr12	133851895	124185089	0.9278	1.9366
chr13	115169878	79578527	0.691	1.5996
chr14	107349540	84683145	0.7889	1.8385
chr15	102531392	87067175	0.8492	1.9223
chr16	90354753	91350772	1.011	4.734
chr17	81195210	87635246	1.0793	2.6983
chr18	78077248	69602937	0.8915	3.6927
chr19	59128983	58564978	0.9905	2.6729
chr20	63025520	70875179	1.1245	2.3197
chr21	48129895	34006910	0.7066	2.2623
chr22	51304566	43957184	0.8568	2.1374
chrMT	16571	12739114	768.7595	598.495
chrX	155270560	145694750	0.9383	2.1163

chrY	59373566	4702695	0.0792	2.4825

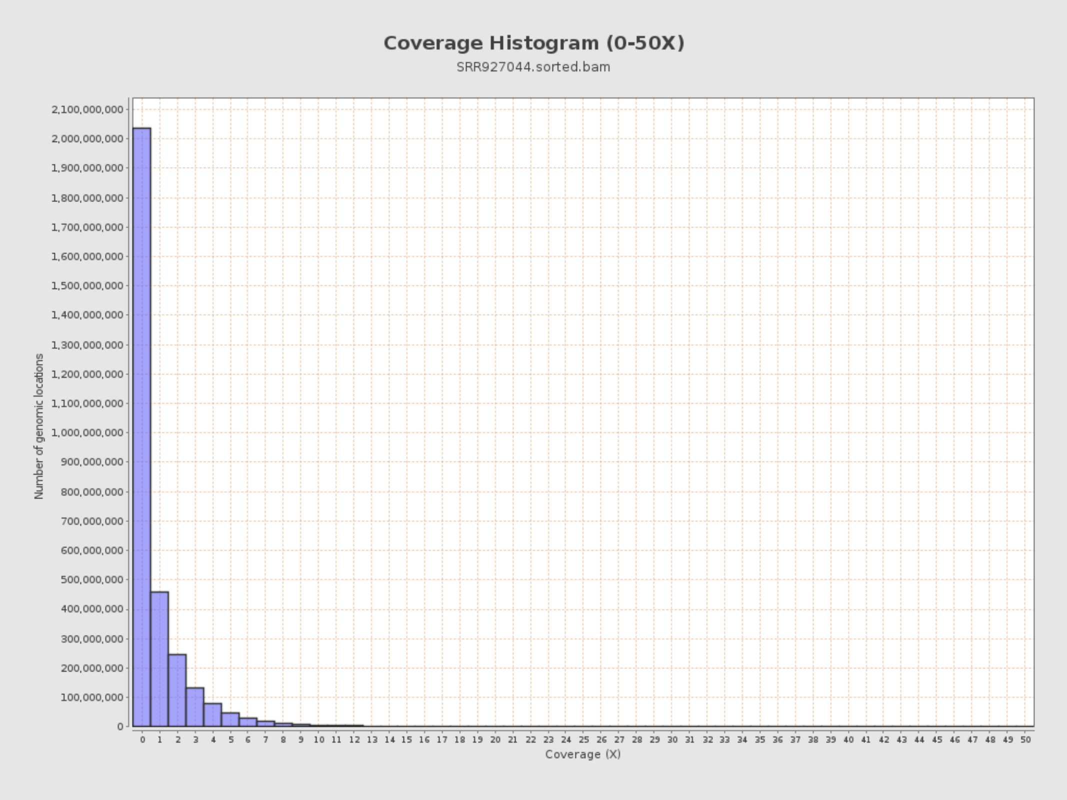
3. Results : Coverage across reference



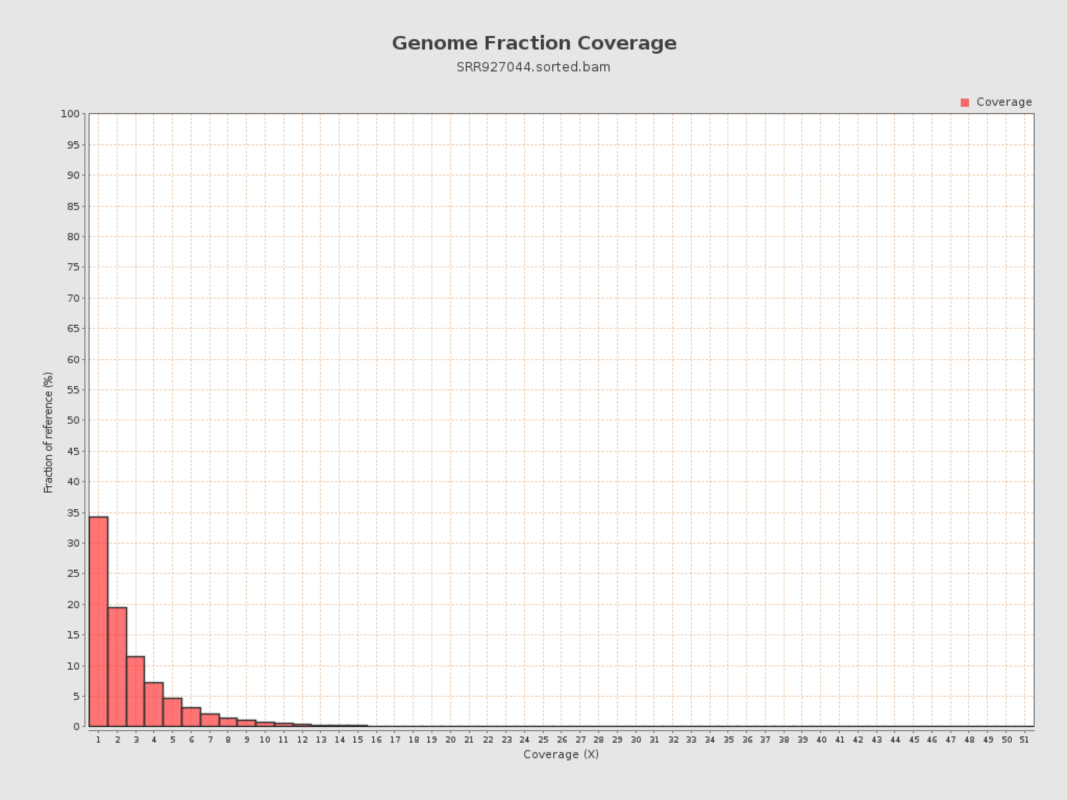
4. Results : Coverage Histogram



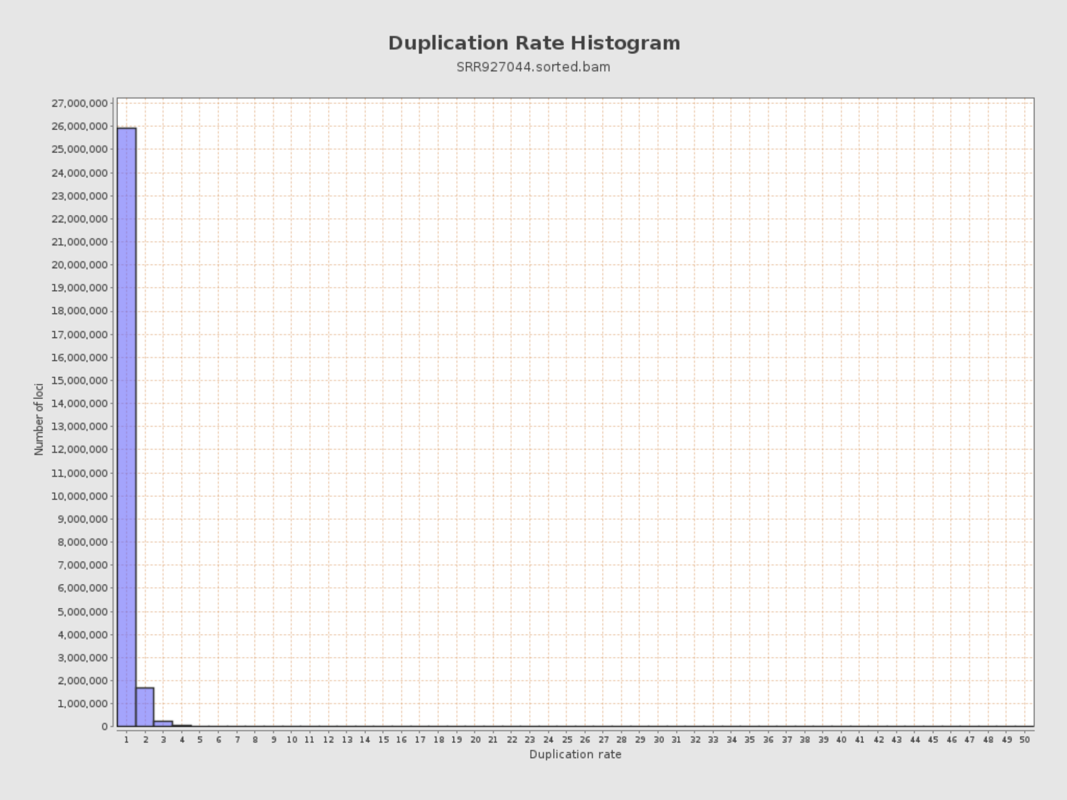
5. Results : Coverage Histogram (0-50X)



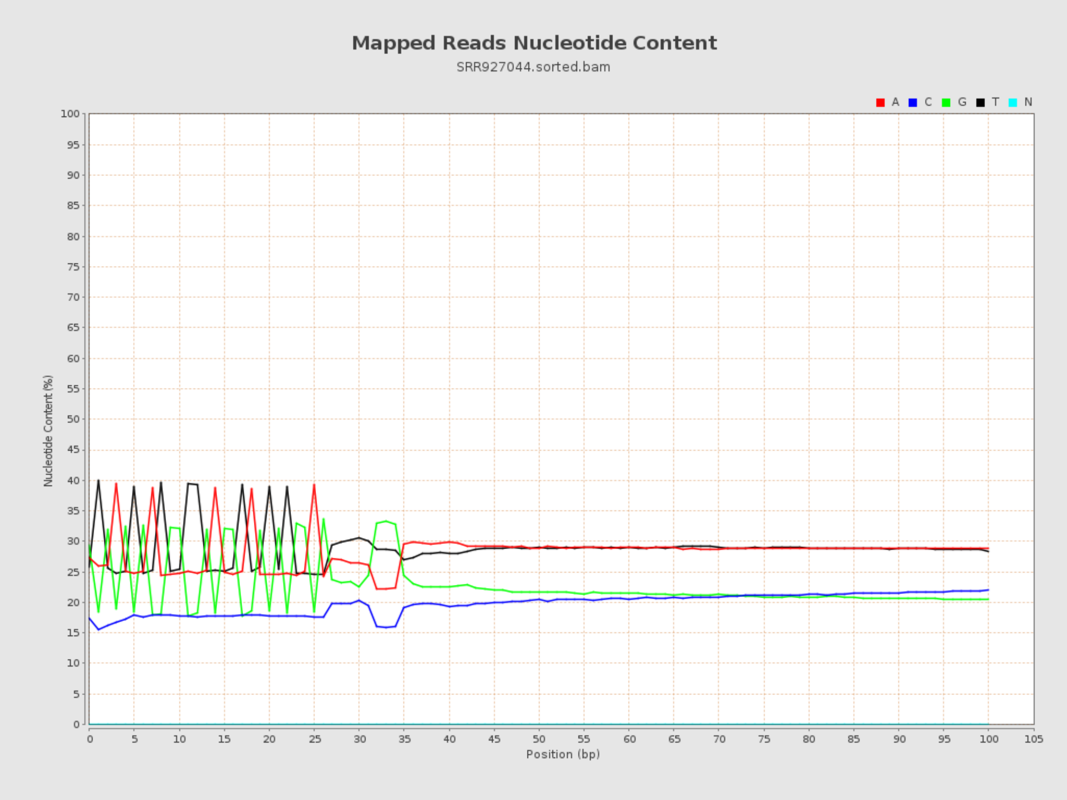
6. Results : Genome Fraction Coverage



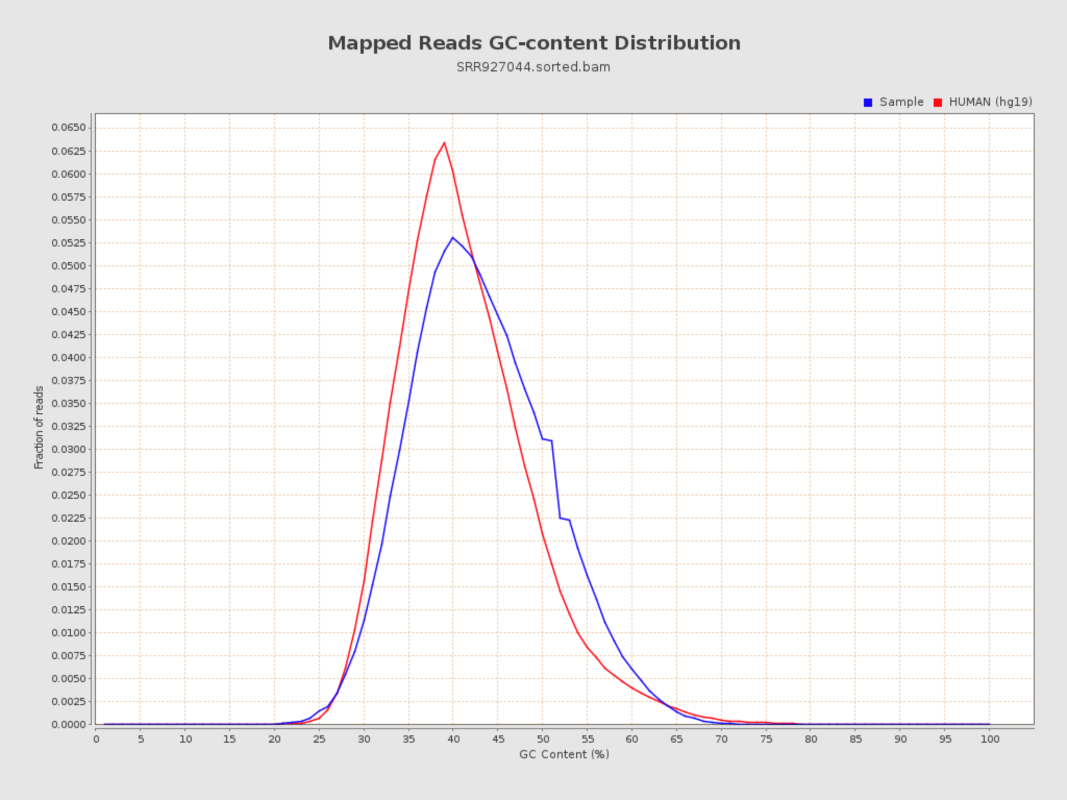
7. Results : Duplication Rate Histogram



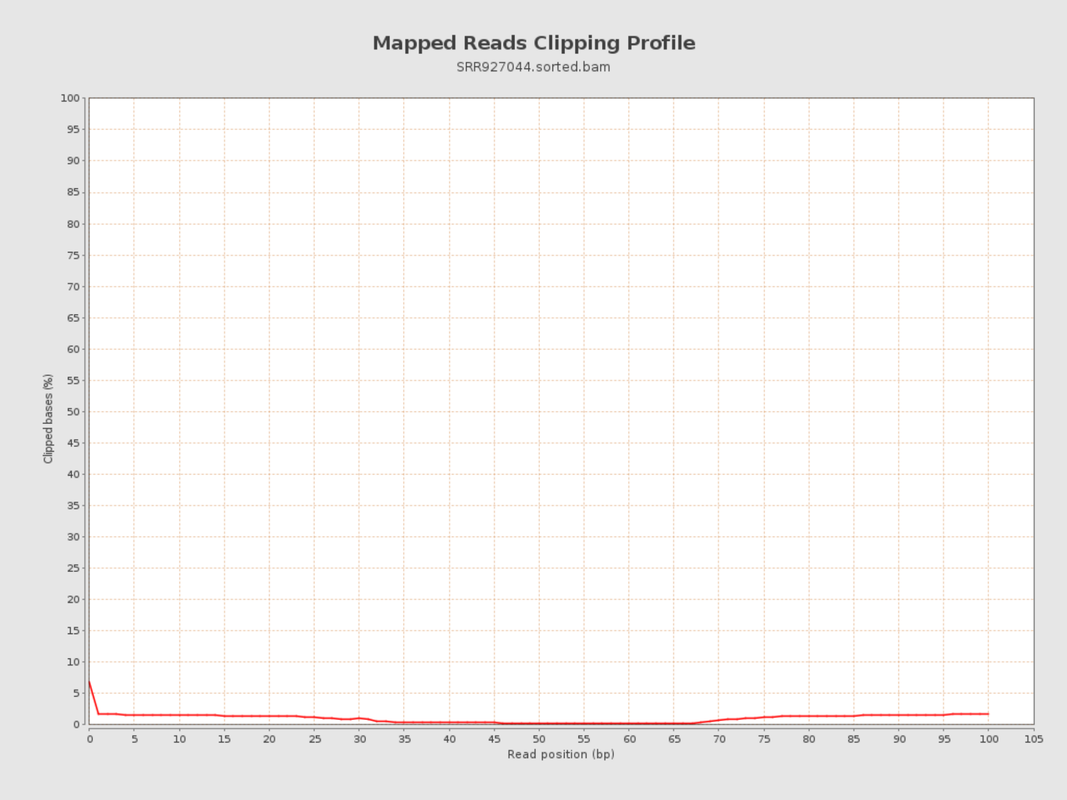
8. Results : Mapped Reads Nucleotide Content



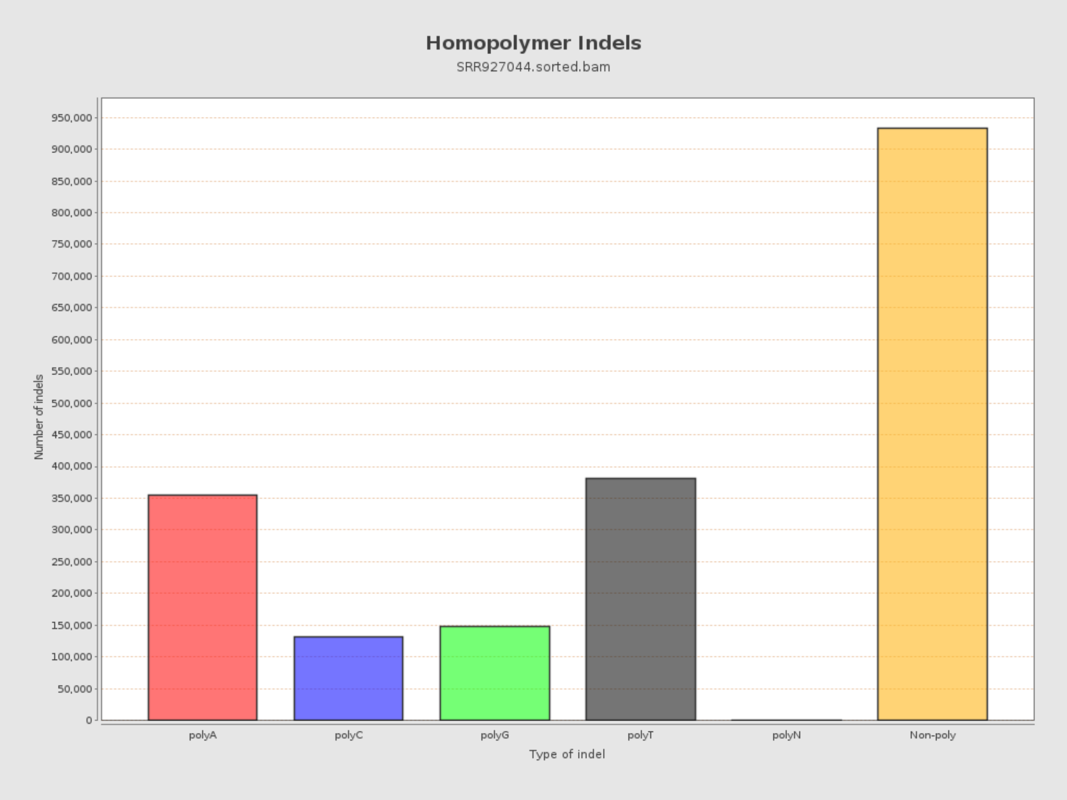
9. Results : Mapped Reads GC-content Distribution



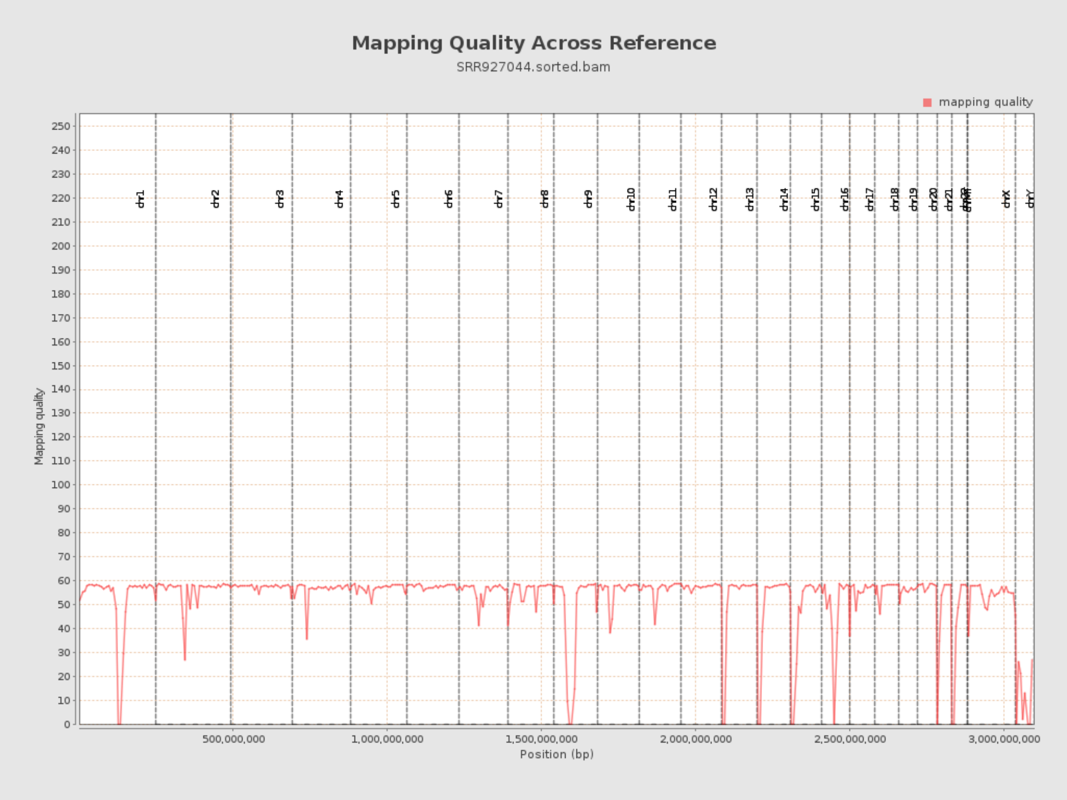
10. Results : Mapped Reads Clipping Profile



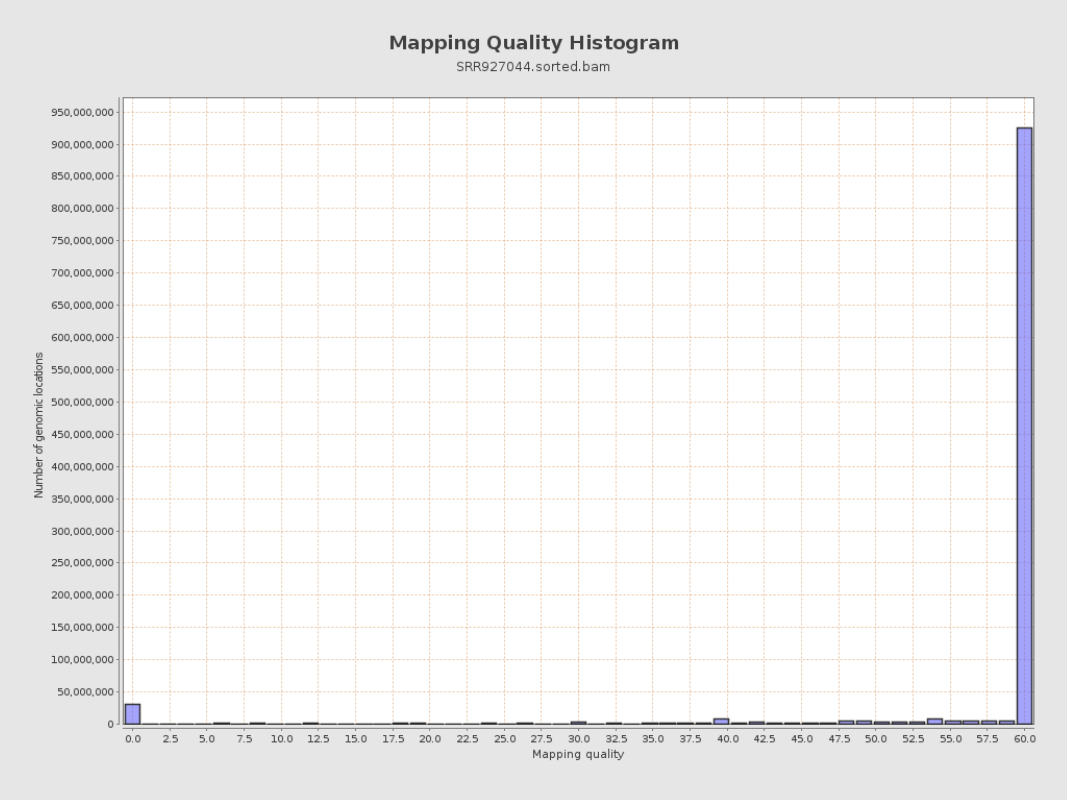
11. Results : Homopolymer Indels



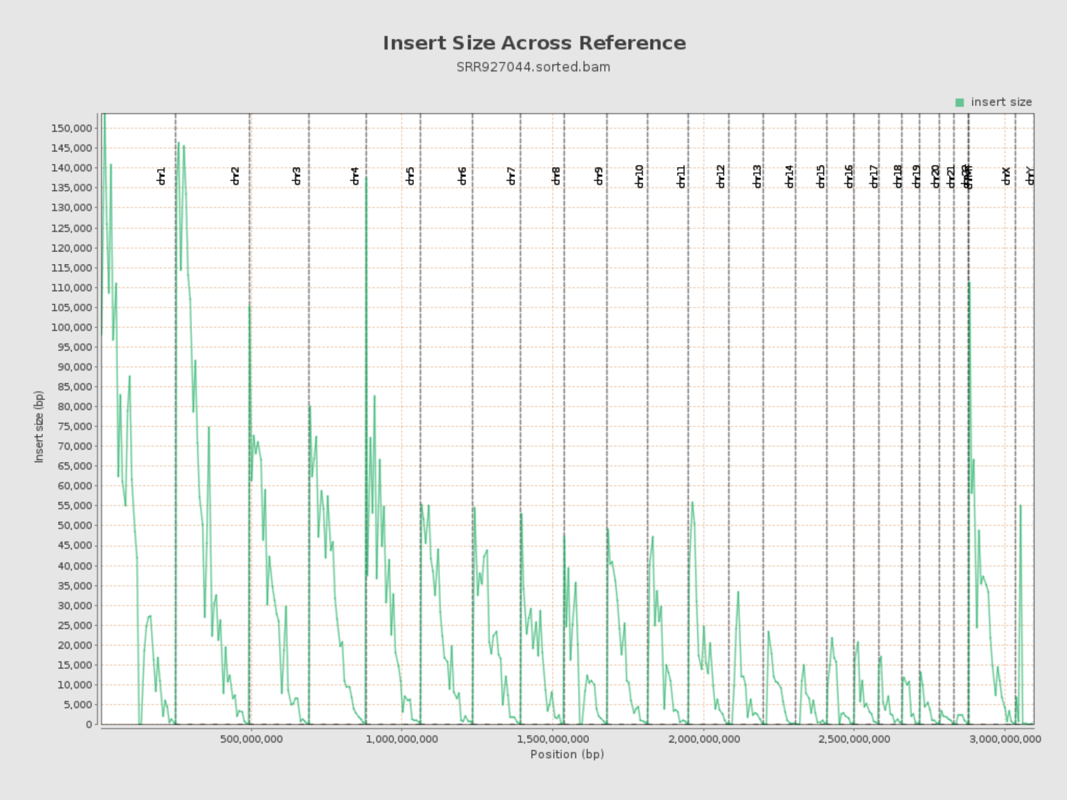
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram