Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 21:48:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927048.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_SRR927048 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927048_1.fastq.gz SRR927048_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 21:48:05 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927048.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,666,820
Mapped reads	21,098,859 / 97.38%
Unmapped reads	567,961 / 2.62%
Mapped paired reads	21,098,859 / 97.38%
Mapped reads, first in pair	10,590,046 / 48.88%
Mapped reads, second in pair	10,508,813 / 48.5%
Mapped reads, both in pair	20,770,910 / 95.87%
Mapped reads, singletons	327,949 / 1.51%
Secondary alignments	0
Supplementary alignments	644,764 / 2.98%
Read min/max/mean length	30 / 101 / 102.24
Duplicated reads (estimated)	1,902,428 / 8.78%
Duplication rate	7.04%
Clipped reads	11,005,915 / 50.8%

2.2. ACGT Content

Number/percentage of A's	538,212,793 / 28.68%
Number/percentage of C's	356,056,458 / 18.97%
Number/percentage of T's	555,863,489 / 29.62%
Number/percentage of G's	426,374,614 / 22.72%
Number/percentage of N's	211,669 / 0.01%

GC Percentage	41.69%

2.3. Coverage

Mean	0.6067
Standard Deviation	2.5113

2.4. Mapping Quality

Mean Mapping Quality	52.63

2.5. Insert size

Mean	319,399.36
Standard Deviation	5,513,679.93
P25/Median/P75	132 / 173 / 235

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	19,462,214
Insertions	317,552
Mapped reads with at least one insertion	1.48%
Deletions	933,644
Mapped reads with at least one deletion	4.31%
Homopolymer indels	51.41%

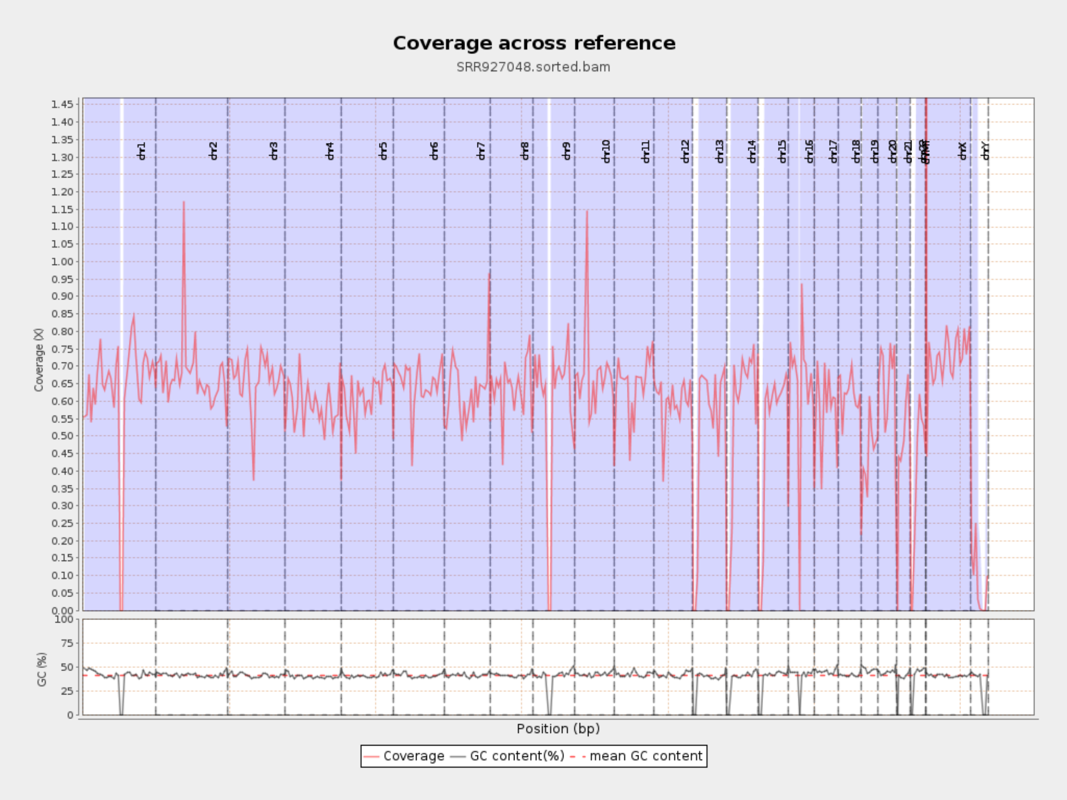
2.7. Chromosome stats

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

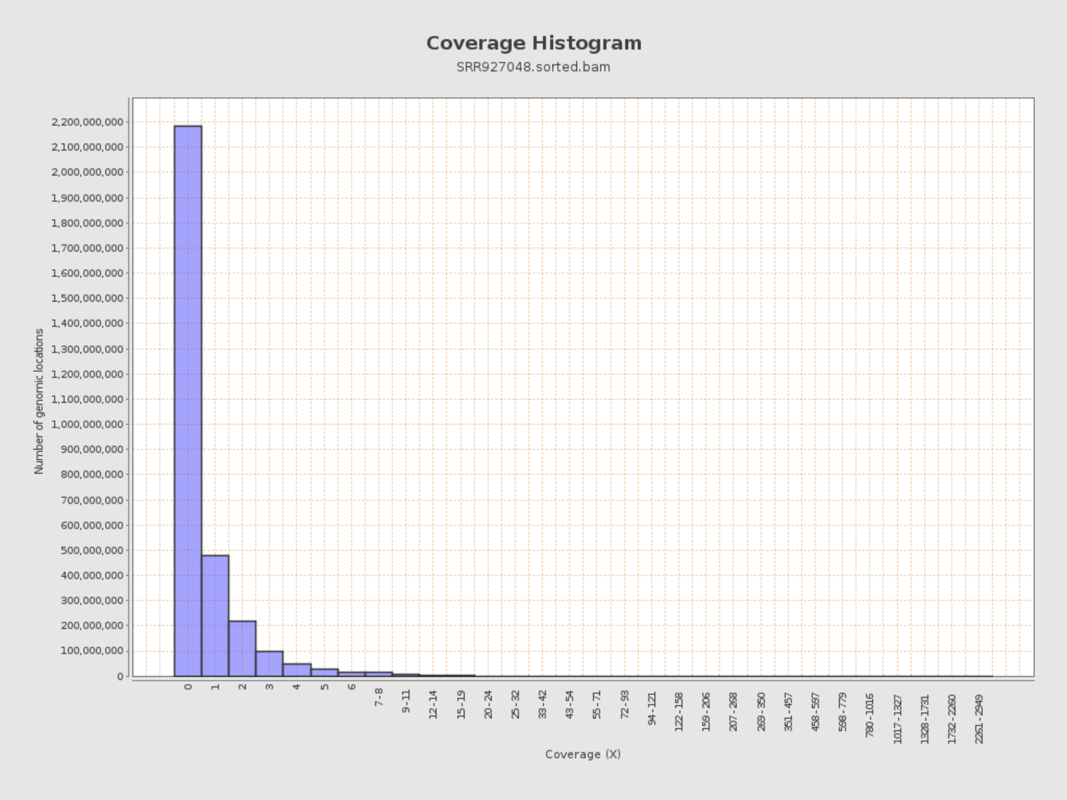
		bases	coverage	deviation
chr1	249250621	157747870	0.6329	3.1922
chr2	243199373	165269846	0.6796	3.9318
chr3	198022430	131067962	0.6619	1.4051
chr4	191154276	113400306	0.5932	2.0738
chr5	180915260	111459997	0.6161	1.3
chr6	171115067	111677898	0.6526	1.432
chr7	159138663	100310904	0.6303	2.0239
chr8	146364022	93688291	0.6401	1.6395
chr9	141213431	84268821	0.5967	3.221
chr10	135534747	91671705	0.6764	5.4896
chr11	135006516	87493313	0.6481	2.0173
chr12	133851895	80044834	0.598	1.2964
chr13	115169878	59724144	0.5186	1.2075
chr14	107349540	59504885	0.5543	1.3495
chr15	102531392	51202777	0.4994	1.2014
chr16	90354753	56370348	0.6239	3.2305
chr17	81195210	47512974	0.5852	1.7379
chr18	78077248	48420701	0.6202	3.2171
chr19	59128983	26474521	0.4477	1.9303
chr20	63025520	41871935	0.6644	1.4824
chr21	48129895	22800253	0.4737	1.7455
chr22	51304566	19323520	0.3766	1.1016
chrMT	16571	153044	9.2357	5.6374
chrX	155270560	112026117	0.7215	1.6114

chrY	59373566	4605339	0.0776	2.8302

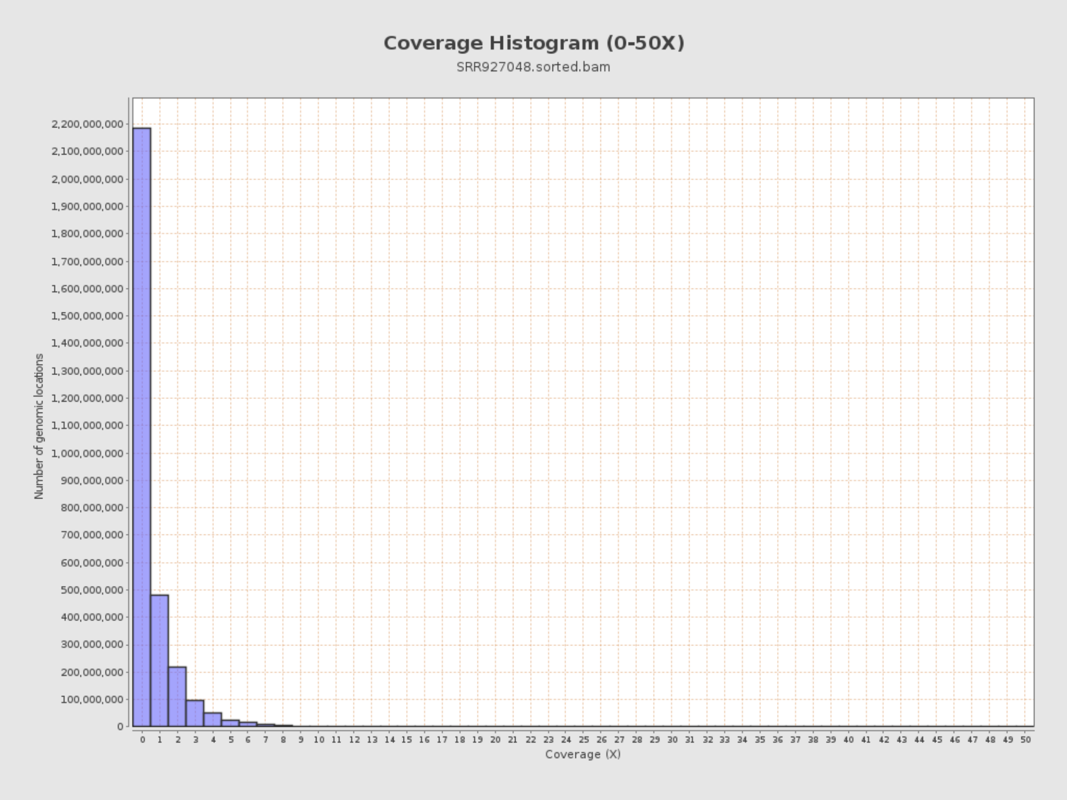
3. Results : Coverage across reference



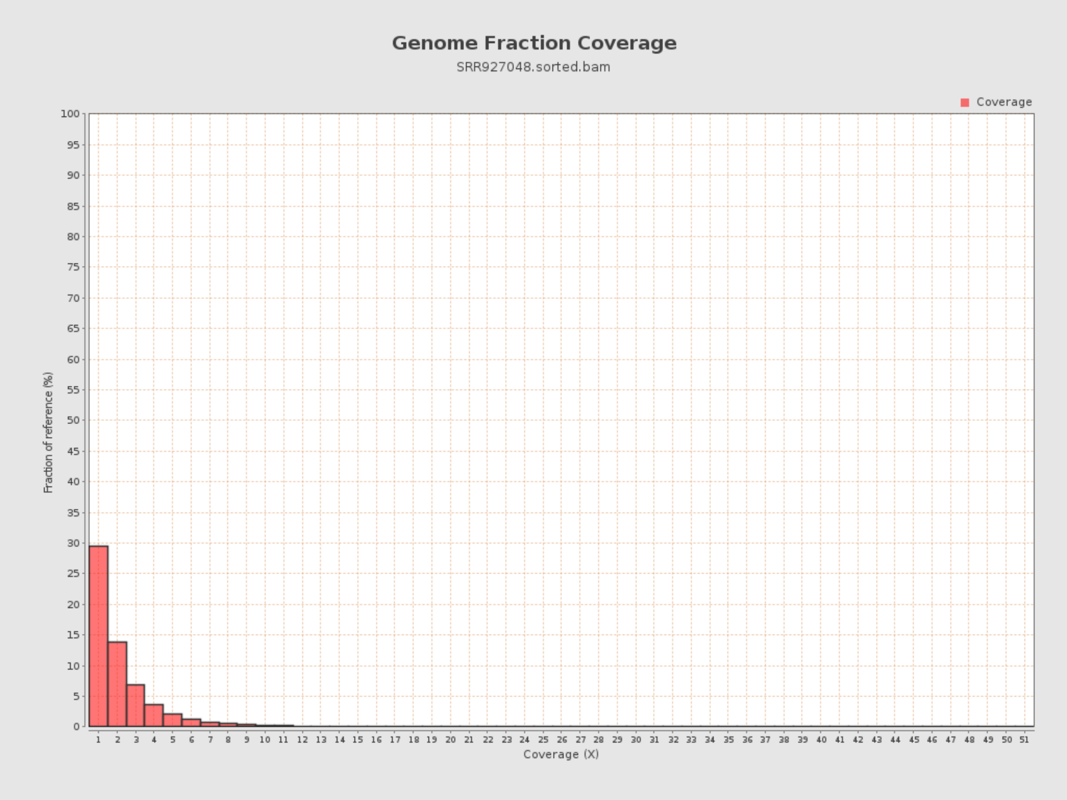
4. Results : Coverage Histogram



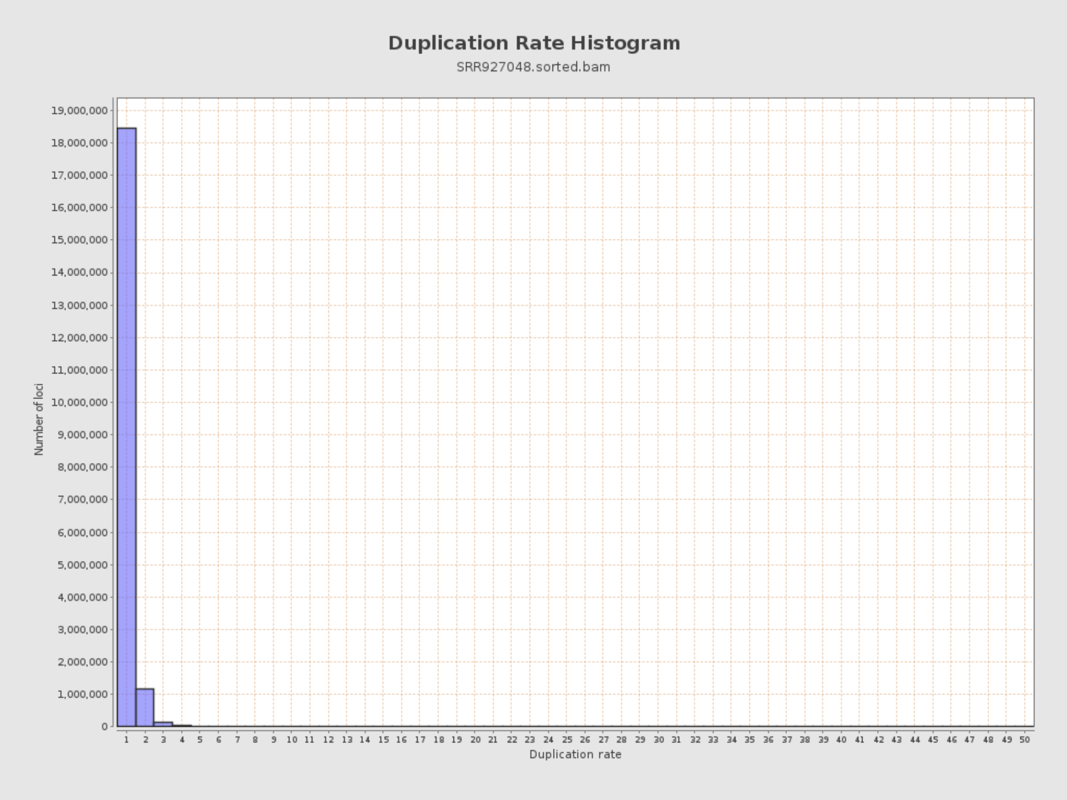
5. Results : Coverage Histogram (0-50X)



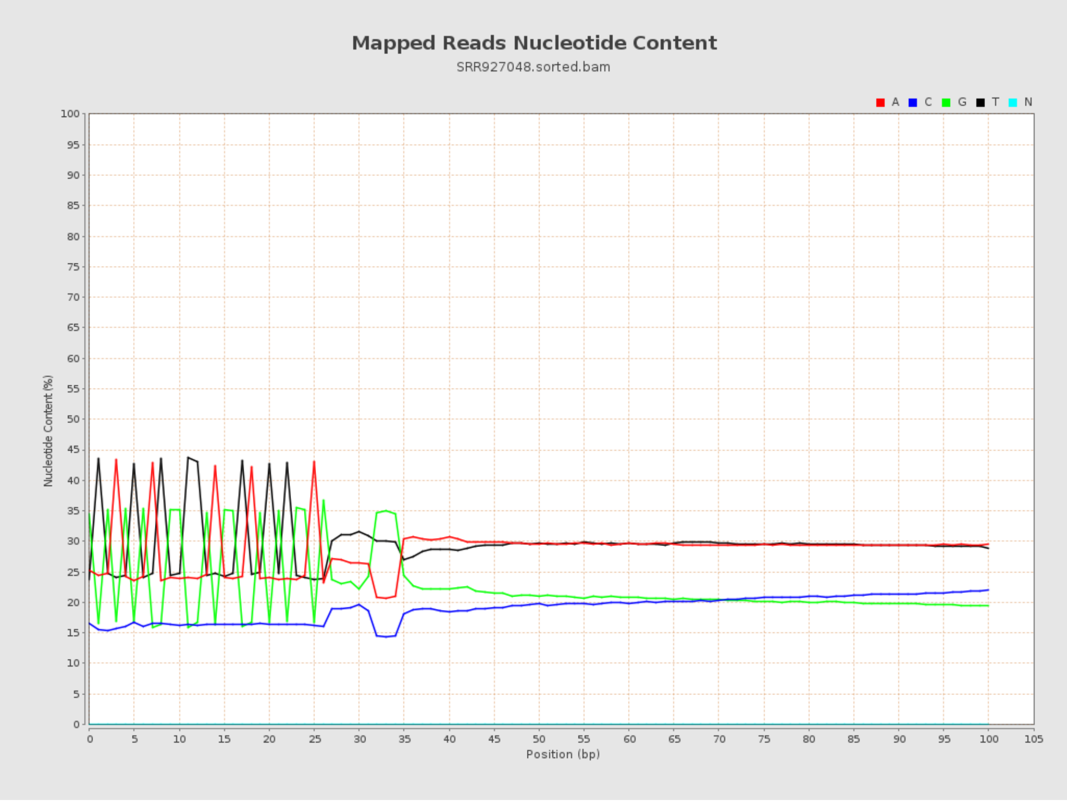
6. Results : Genome Fraction Coverage



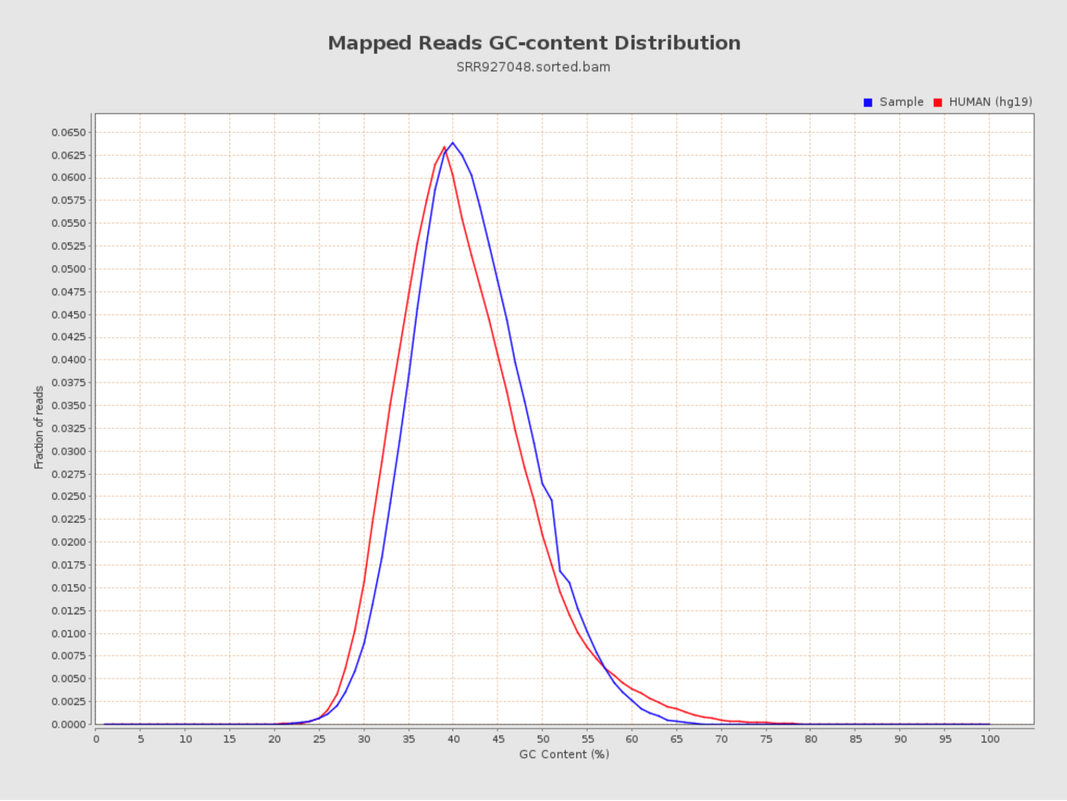
7. Results : Duplication Rate Histogram



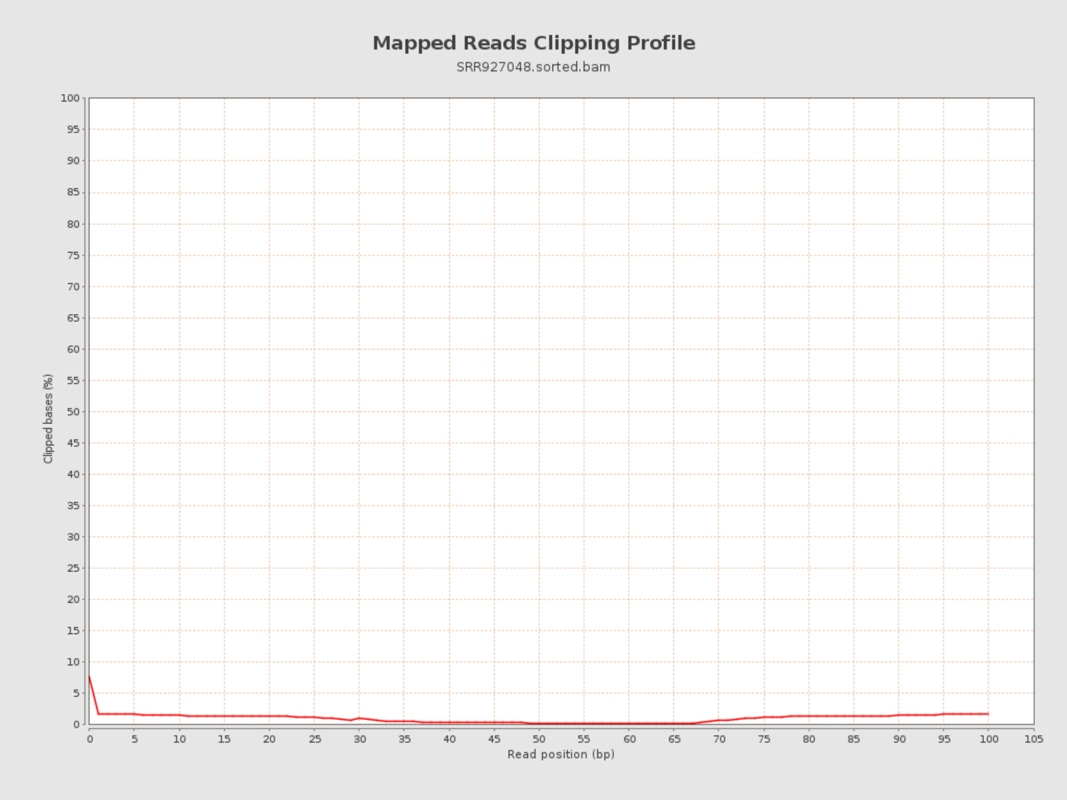
8. Results : Mapped Reads Nucleotide Content



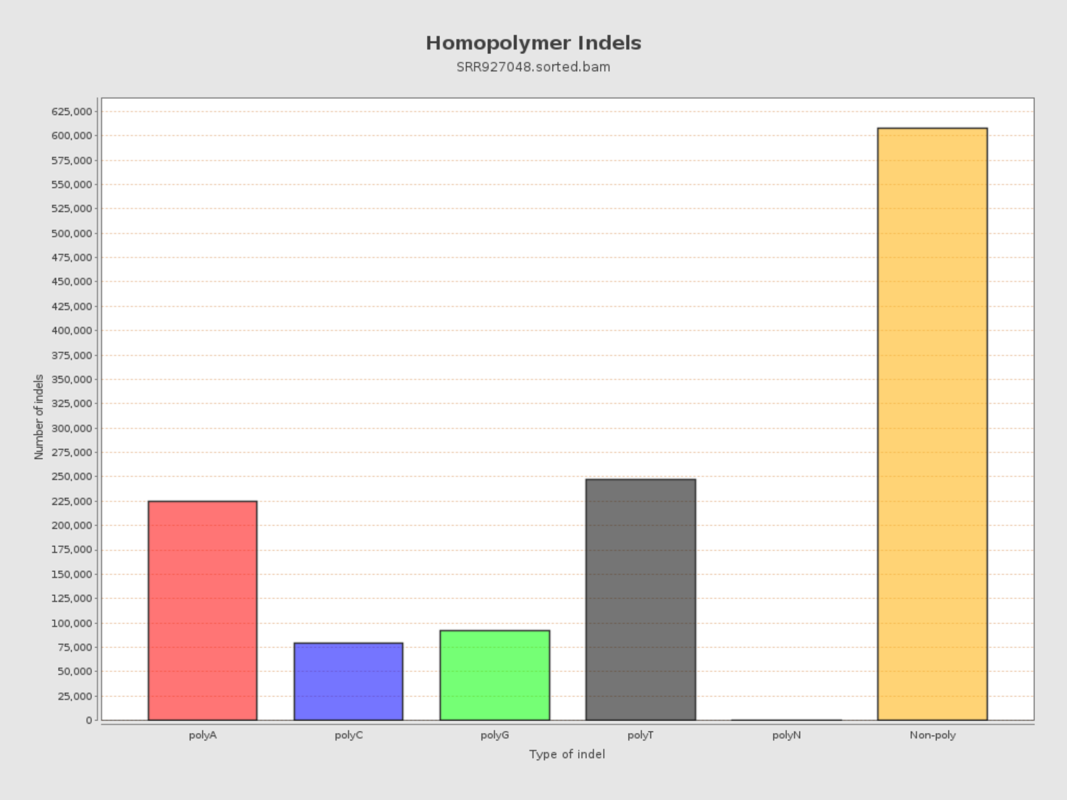
9. Results : Mapped Reads GC-content Distribution



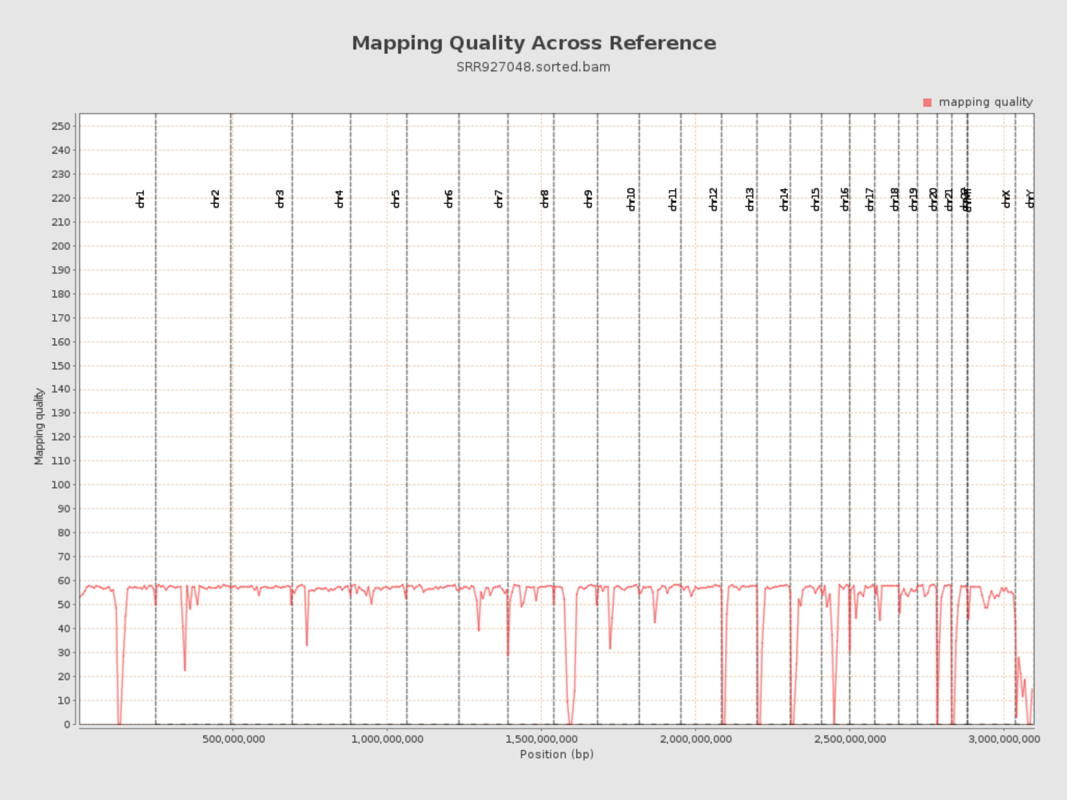
10. Results : Mapped Reads Clipping Profile



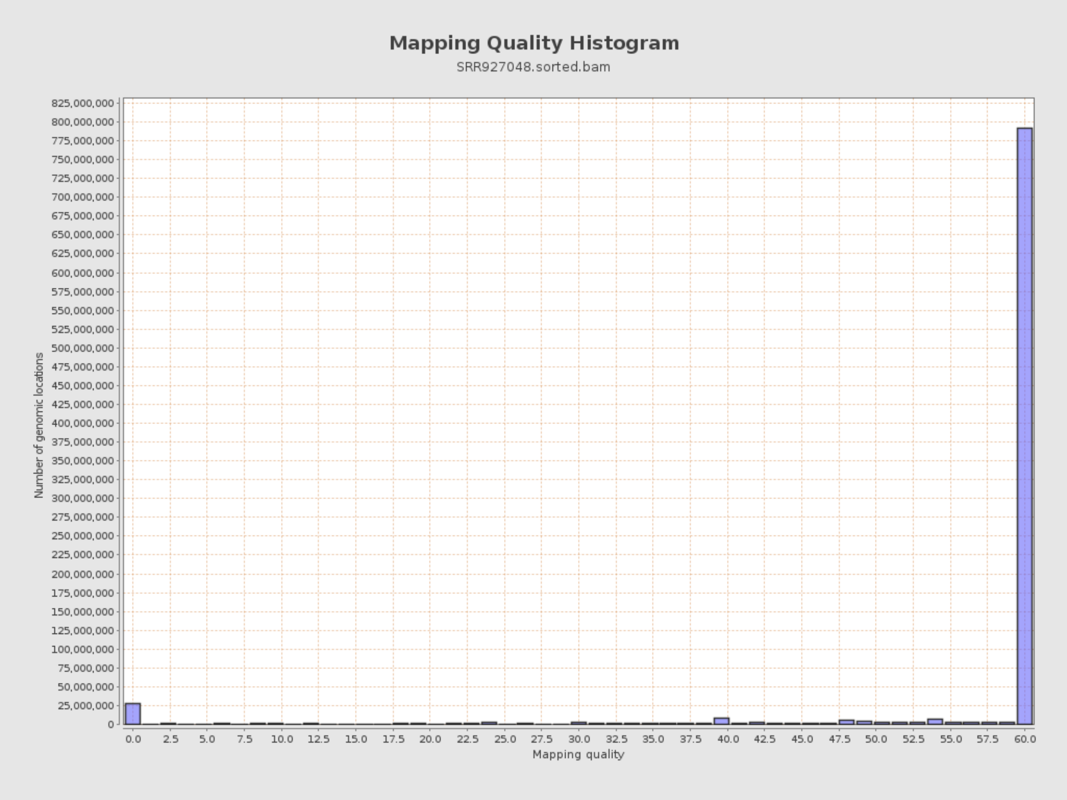
11. Results : Homopolymer Indels



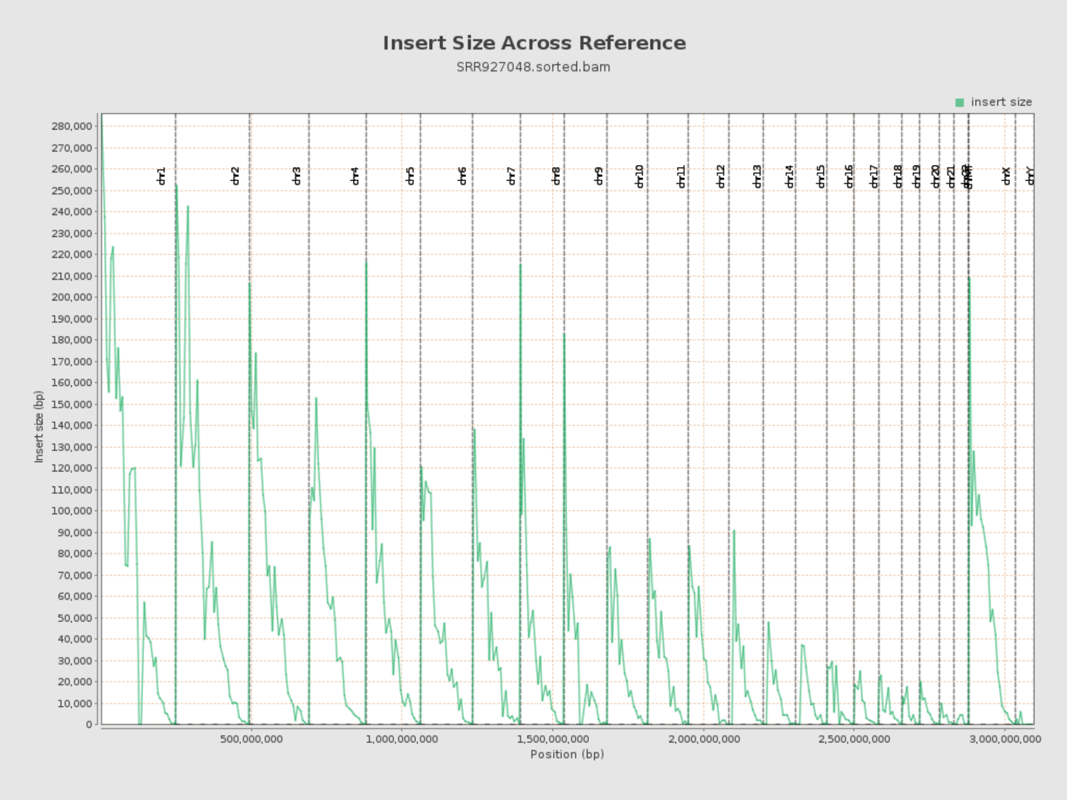
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram