Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 23:03:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927000.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_SRR927000 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927000_1.fastq.gz SRR927000_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 23:03:43 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927000.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,861,206
Mapped reads	11,549,701 / 97.37%
Unmapped reads	311,505 / 2.63%
Mapped paired reads	11,549,701 / 97.37%
Mapped reads, first in pair	5,786,676 / 48.79%
Mapped reads, second in pair	5,763,025 / 48.59%
Mapped reads, both in pair	11,356,920 / 95.75%
Mapped reads, singletons	192,781 / 1.63%
Secondary alignments	0
Supplementary alignments	287,023 / 2.42%
Read min/max/mean length	30 / 101 / 102
Duplicated reads (estimated)	702,167 / 5.92%
Duplication rate	5%
Clipped reads	4,654,614 / 39.24%

2.2. ACGT Content

Number/percentage of A's	302,992,792 / 28.73%
Number/percentage of C's	204,849,160 / 19.42%
Number/percentage of T's	307,342,364 / 29.14%
Number/percentage of G's	239,405,273 / 22.7%
Number/percentage of N's	201,028 / 0.02%

GC Percentage	42.12%

2.3. Coverage

Mean	0.341
Standard Deviation	1.4036

2.4. Mapping Quality

Mean Mapping Quality	52.85

2.5. Insert size

Mean	241,077.29
Standard Deviation	4,802,071.75
P25/Median/P75	138 / 183 / 250

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	10,098,643
Insertions	178,473
Mapped reads with at least one insertion	1.52%
Deletions	548,956
Mapped reads with at least one deletion	4.63%
Homopolymer indels	52.01%

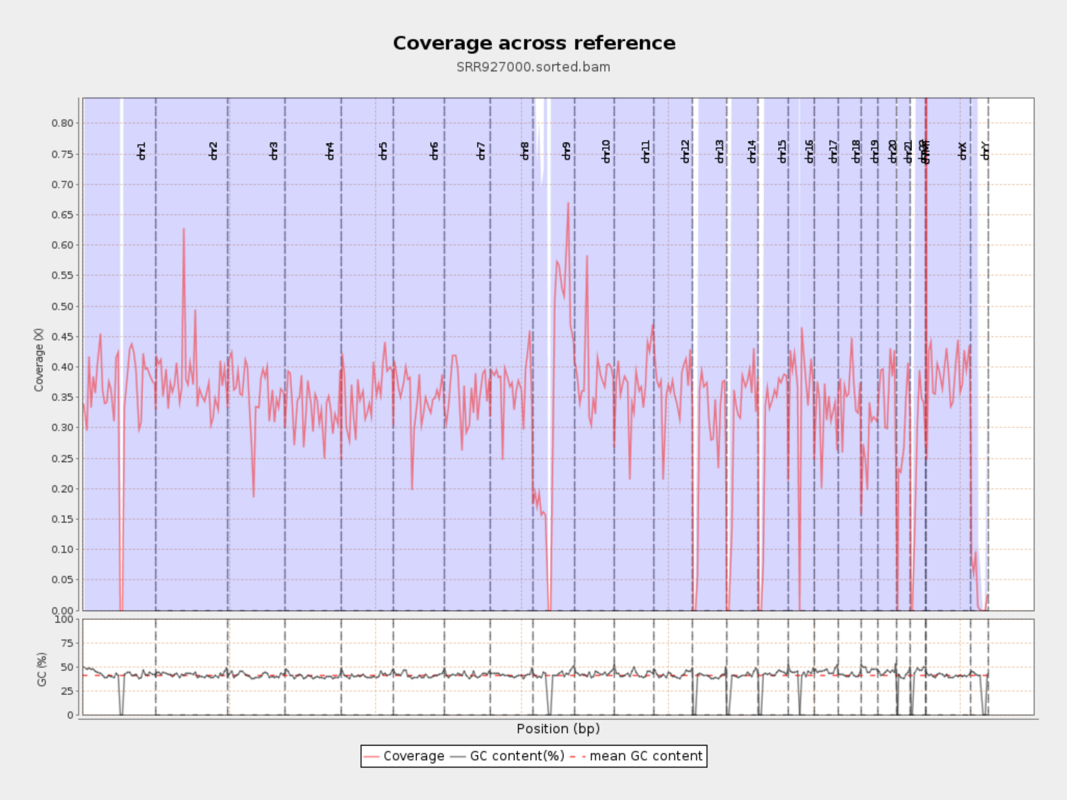
2.7. Chromosome stats

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

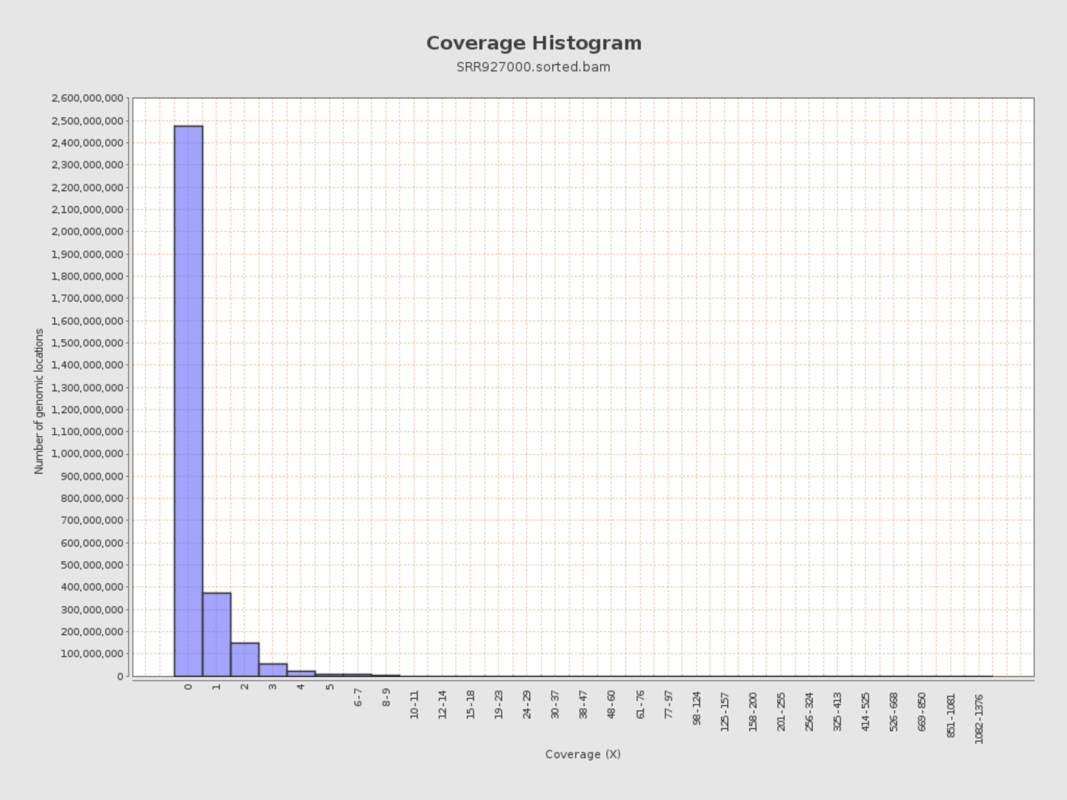
		bases	coverage	deviation
chr1	249250621	87892691	0.3526	1.7263
chr2	243199373	92314780	0.3796	2.3715
chr3	198022430	70203526	0.3545	0.8692
chr4	191154276	63607797	0.3328	1.0049
chr5	180915260	64814863	0.3583	0.8713
chr6	171115067	59894849	0.35	0.9959
chr7	159138663	56090630	0.3525	1.1971
chr8	146364022	54397570	0.3717	0.9776
chr9	141213431	48208170	0.3414	1.4566
chr10	135534747	51625963	0.3809	2.8633
chr11	135006516	49881336	0.3695	1.0936
chr12	133851895	48982337	0.3659	0.8981
chr13	115169878	32289669	0.2804	0.7657
chr14	107349540	32180792	0.2998	0.8115
chr15	102531392	29700074	0.2897	0.7869
chr16	90354753	32033428	0.3545	1.9053
chr17	81195210	26088490	0.3213	1.0481
chr18	78077248	27777823	0.3558	1.3534
chr19	59128983	16631091	0.2813	1.1296
chr20	63025520	23293423	0.3696	0.9267
chr21	48129895	13063725	0.2714	1.2378
chr22	51304566	12132704	0.2365	0.7792
chrMT	16571	413563	24.957	23.5734
chrX	155270560	60132830	0.3873	1.0084

chrY	59373566	1941623	0.0327	1.3464

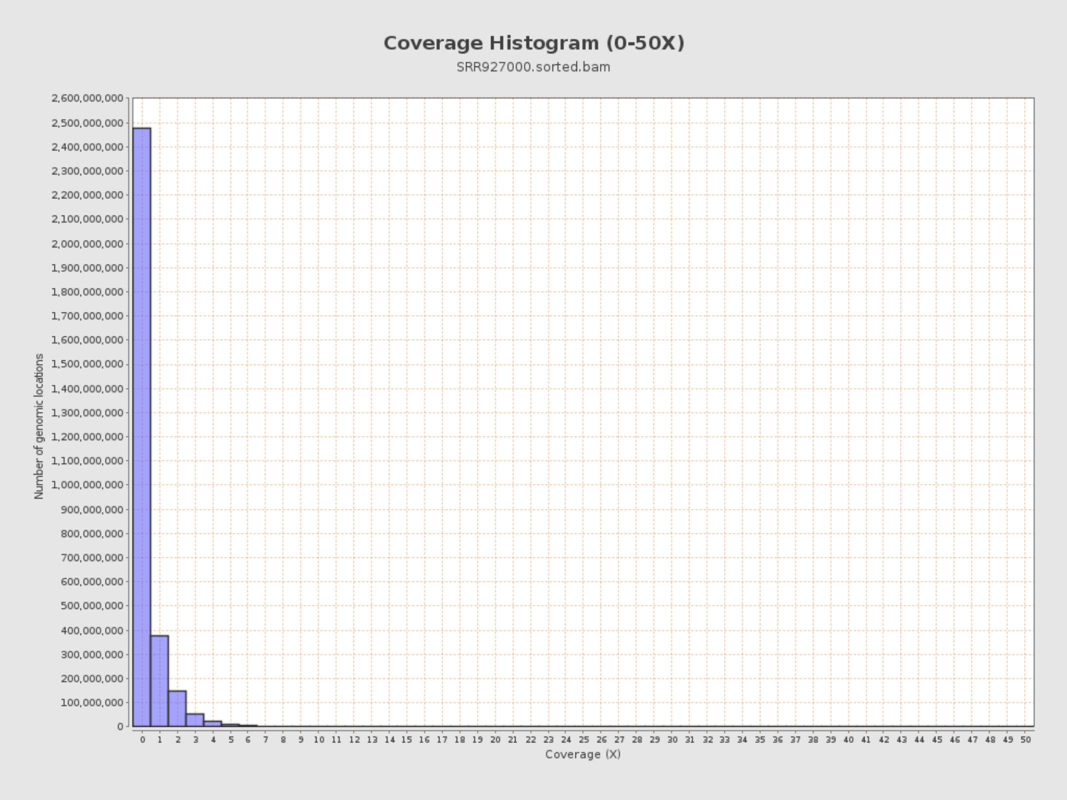
3. Results : Coverage across reference



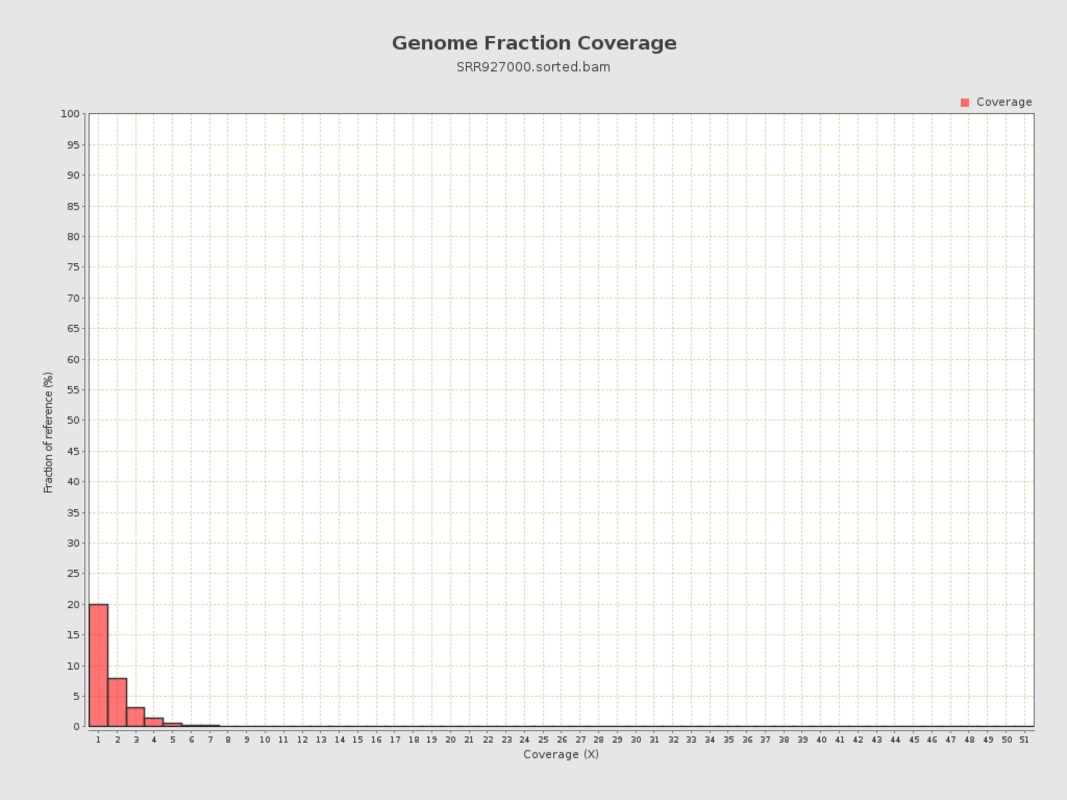
4. Results : Coverage Histogram



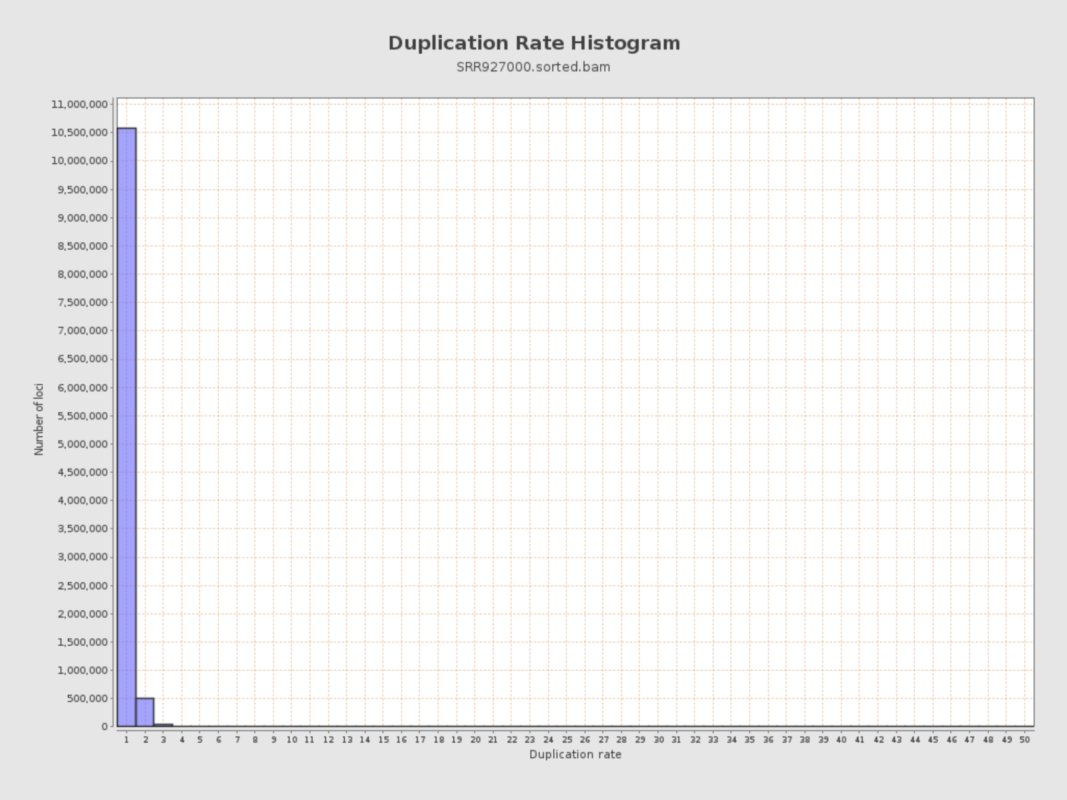
5. Results : Coverage Histogram (0-50X)



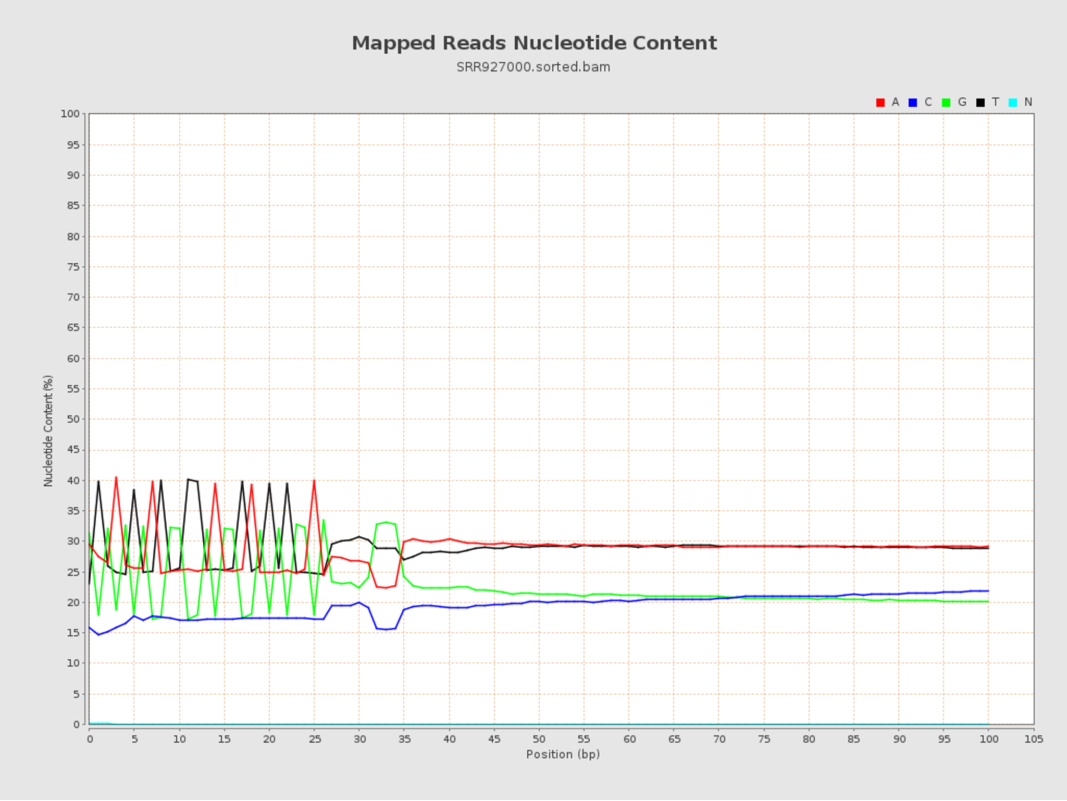
6. Results : Genome Fraction Coverage



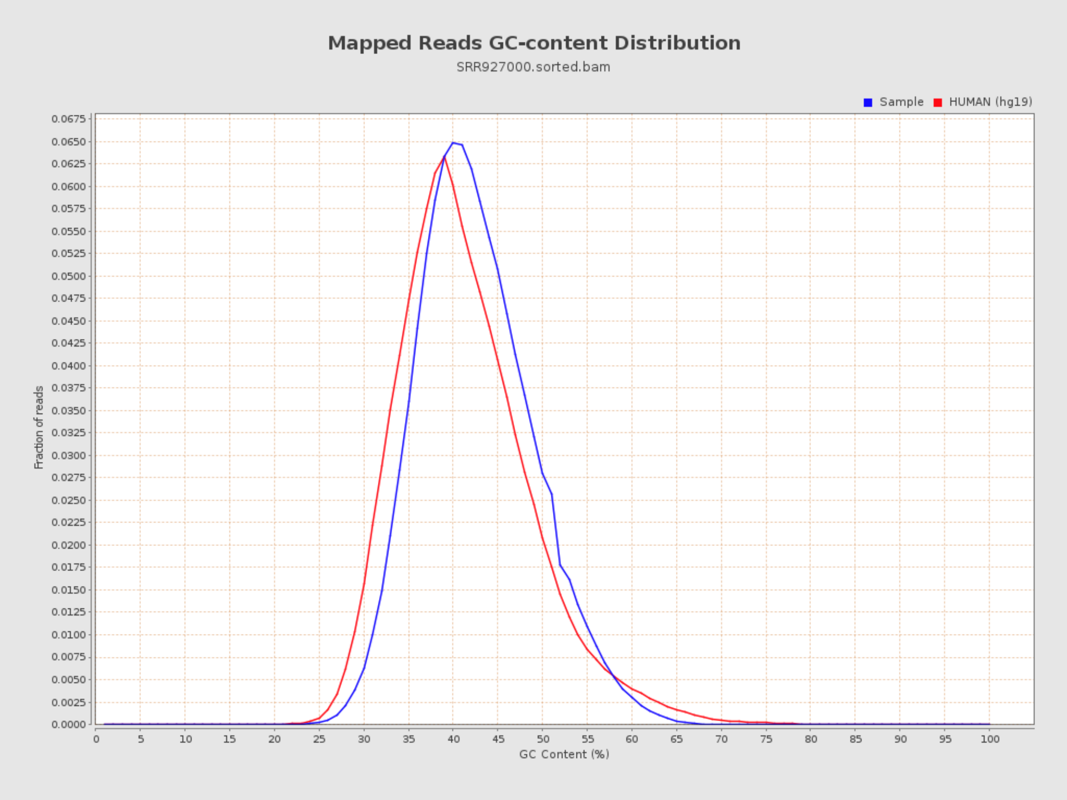
7. Results : Duplication Rate Histogram



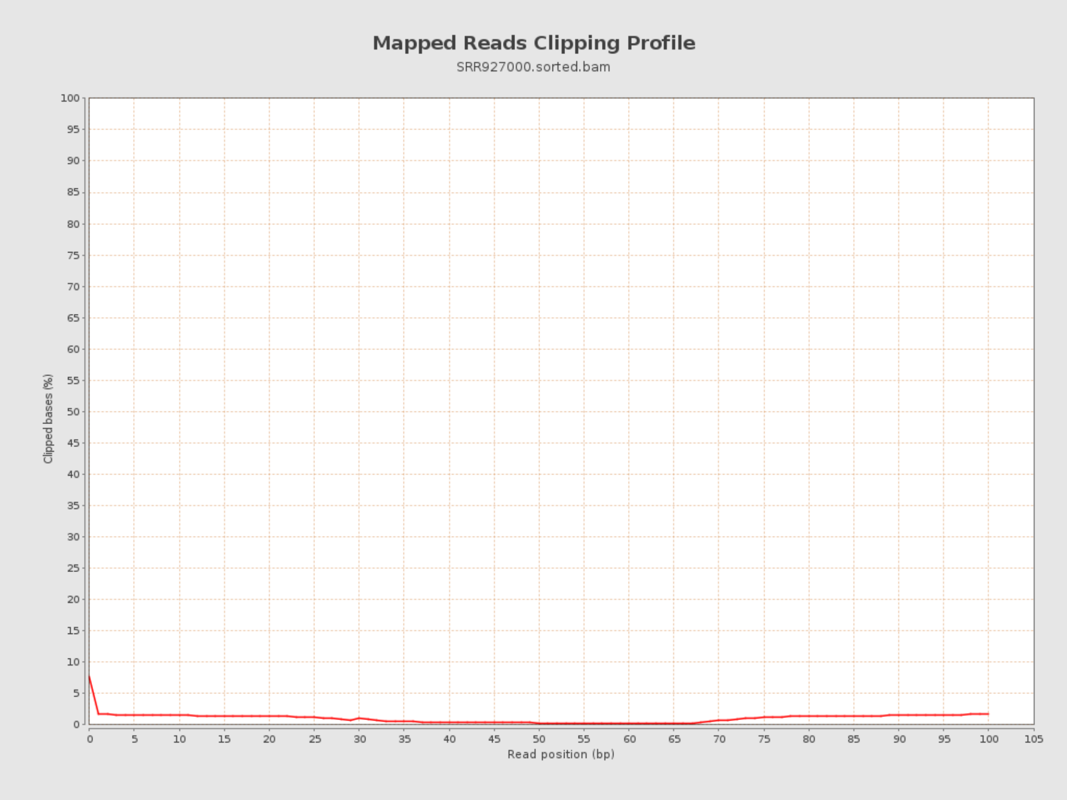
8. Results : Mapped Reads Nucleotide Content



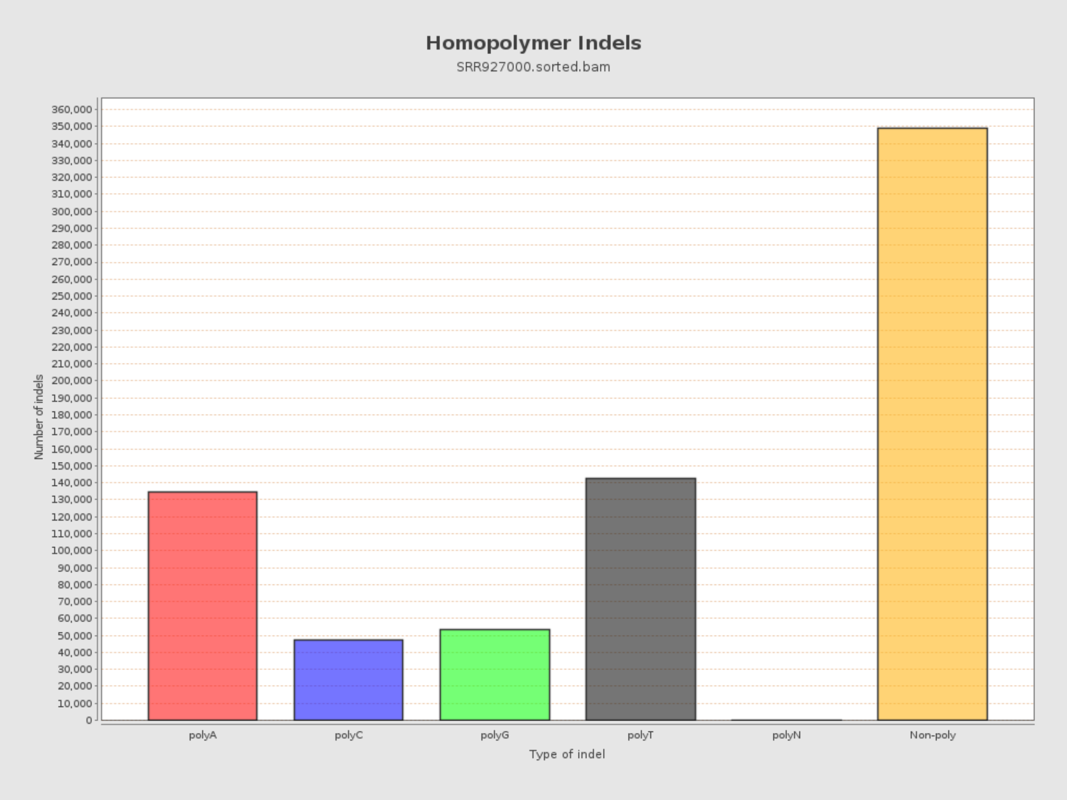
9. Results : Mapped Reads GC-content Distribution



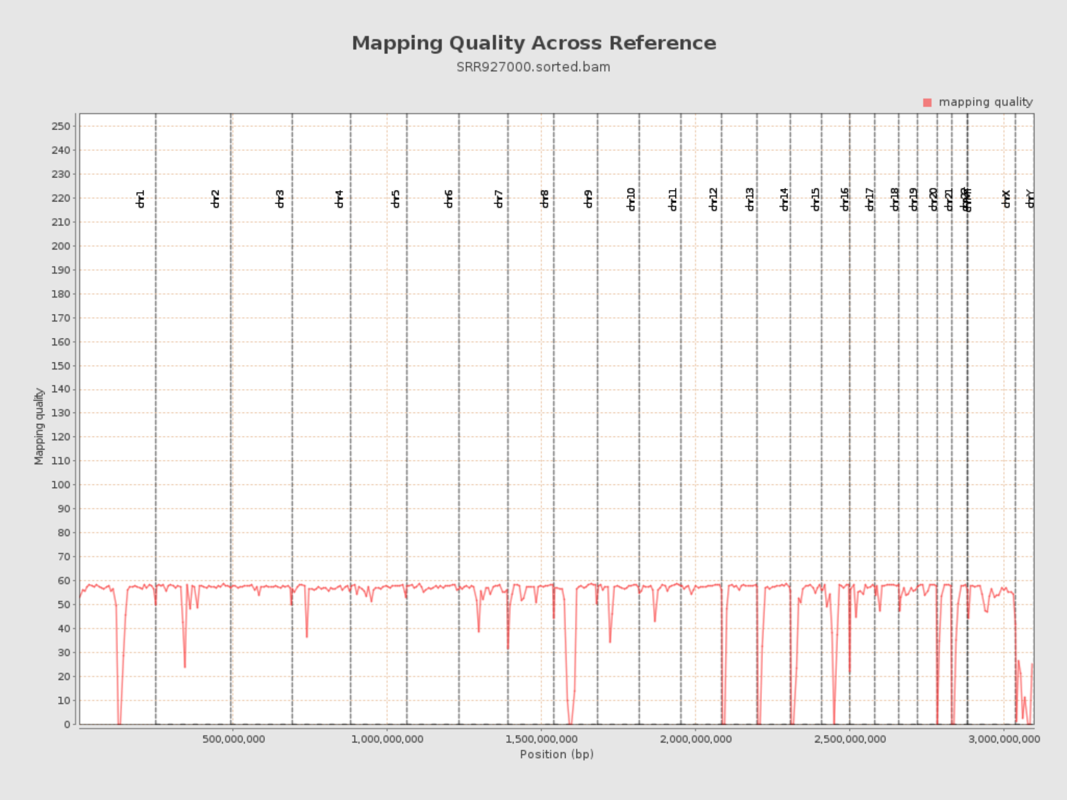
10. Results : Mapped Reads Clipping Profile



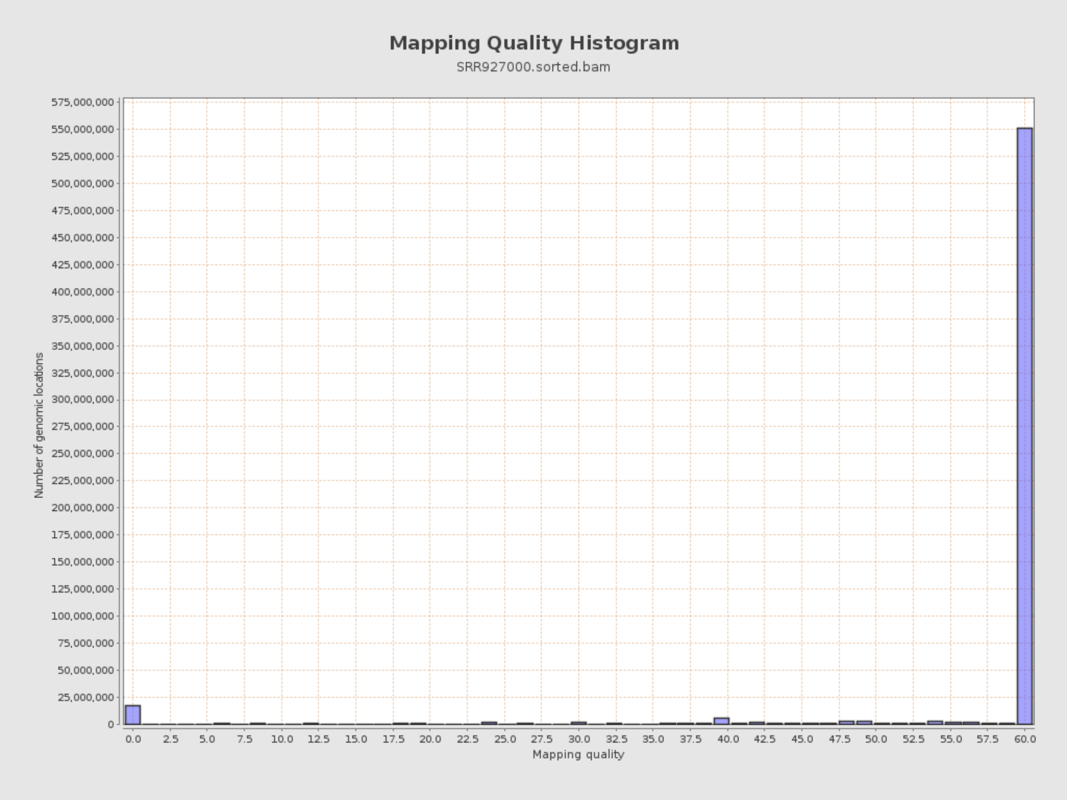
11. Results : Homopolymer Indels



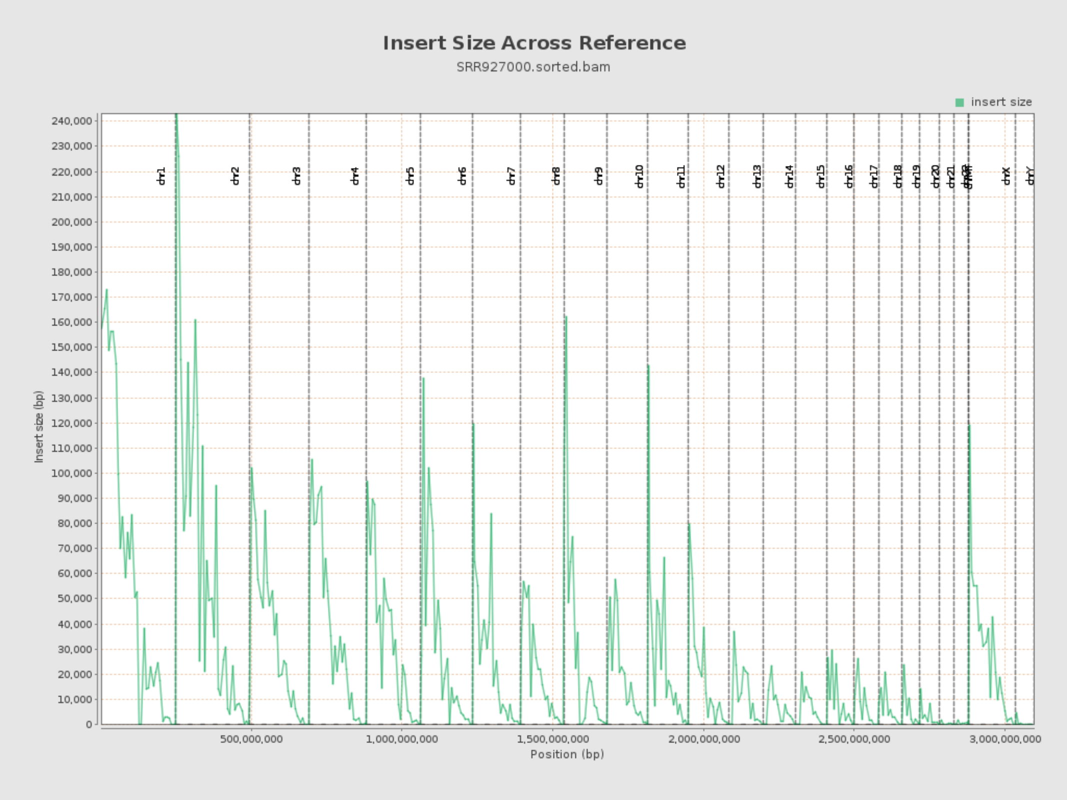
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram