Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 03:38:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927011.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_SRR927011 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927011_1.fastq.gz SRR927011_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 03:38:11 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927011.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,002,494
Mapped reads	10,767,459 / 97.86%
Unmapped reads	235,035 / 2.14%
Mapped paired reads	10,767,459 / 97.86%
Mapped reads, first in pair	5,406,334 / 49.14%
Mapped reads, second in pair	5,361,125 / 48.73%
Mapped reads, both in pair	10,638,008 / 96.69%
Mapped reads, singletons	129,451 / 1.18%
Secondary alignments	0
Supplementary alignments	309,776 / 2.82%
Read min/max/mean length	30 / 101 / 102.17
Duplicated reads (estimated)	597,435 / 5.43%
Duplication rate	4.38%
Clipped reads	4,392,724 / 39.92%

2.2. ACGT Content

Number/percentage of A's	281,884,124 / 28.63%
Number/percentage of C's	191,487,734 / 19.45%
Number/percentage of T's	286,799,215 / 29.13%
Number/percentage of G's	224,171,603 / 22.77%
Number/percentage of N's	189,597 / 0.02%

GC Percentage	42.22%

2.3. Coverage

Mean	0.3183
Standard Deviation	1.4252

2.4. Mapping Quality

Mean Mapping Quality	52.53

2.5. Insert size

Mean	327,912.55
Standard Deviation	5,565,370.49
P25/Median/P75	144 / 187 / 249

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	9,388,763
Insertions	172,698
Mapped reads with at least one insertion	1.57%
Deletions	512,324
Mapped reads with at least one deletion	4.63%
Homopolymer indels	51.74%

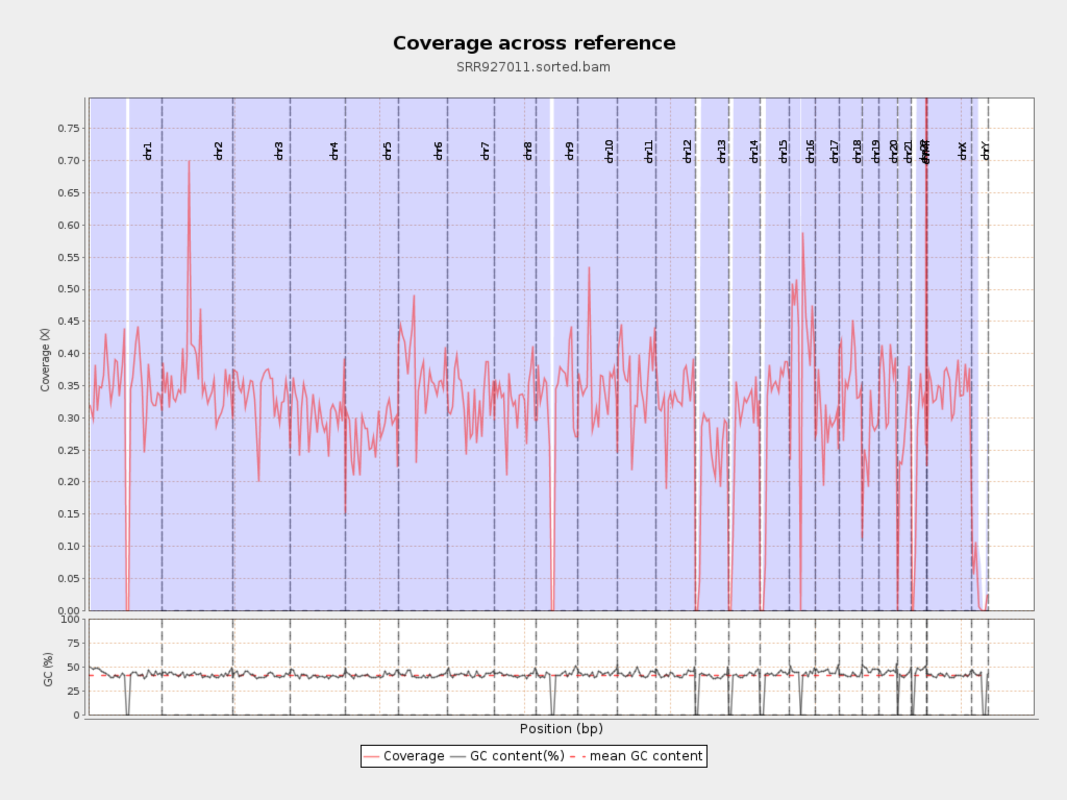
2.7. Chromosome stats

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

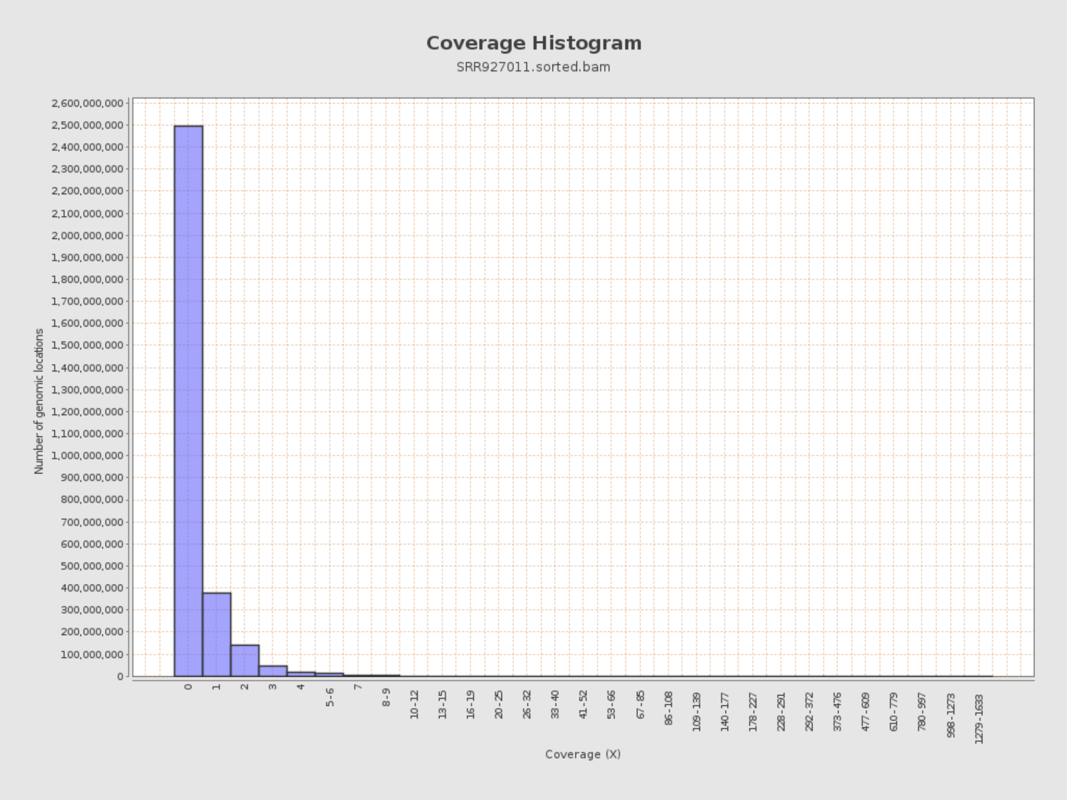
		bases	coverage	deviation
chr1	249250621	82880173	0.3325	1.8943
chr2	243199373	88790567	0.3651	2.5427
chr3	198022430	66374603	0.3352	0.8226
chr4	191154276	58832771	0.3078	1.0399
chr5	180915260	49922195	0.2759	0.7288
chr6	171115067	64134410	0.3748	1.1324
chr7	159138663	51924385	0.3263	1.077
chr8	146364022	48232306	0.3295	0.9254
chr9	141213431	43935790	0.3111	1.6592
chr10	135534747	47272818	0.3488	2.5459
chr11	135006516	48508192	0.3593	1.0982
chr12	133851895	44320846	0.3311	0.8239
chr13	115169878	25442269	0.2209	0.6458
chr14	107349540	28749266	0.2678	0.7506
chr15	102531392	29648808	0.2892	0.7784
chr16	90354753	37441609	0.4144	2.1435
chr17	81195210	23500974	0.2894	0.9423
chr18	78077248	28572934	0.366	1.5993
chr19	59128983	15493046	0.262	1.1908
chr20	63025520	22430161	0.3559	0.9012
chr21	48129895	12386849	0.2574	1.2188
chr22	51304566	11319484	0.2206	0.7192
chrMT	16571	53866	3.2506	3.3807
chrX	155270560	53192282	0.3426	0.9231

chrY	59373566	1930865	0.0325	1.3012

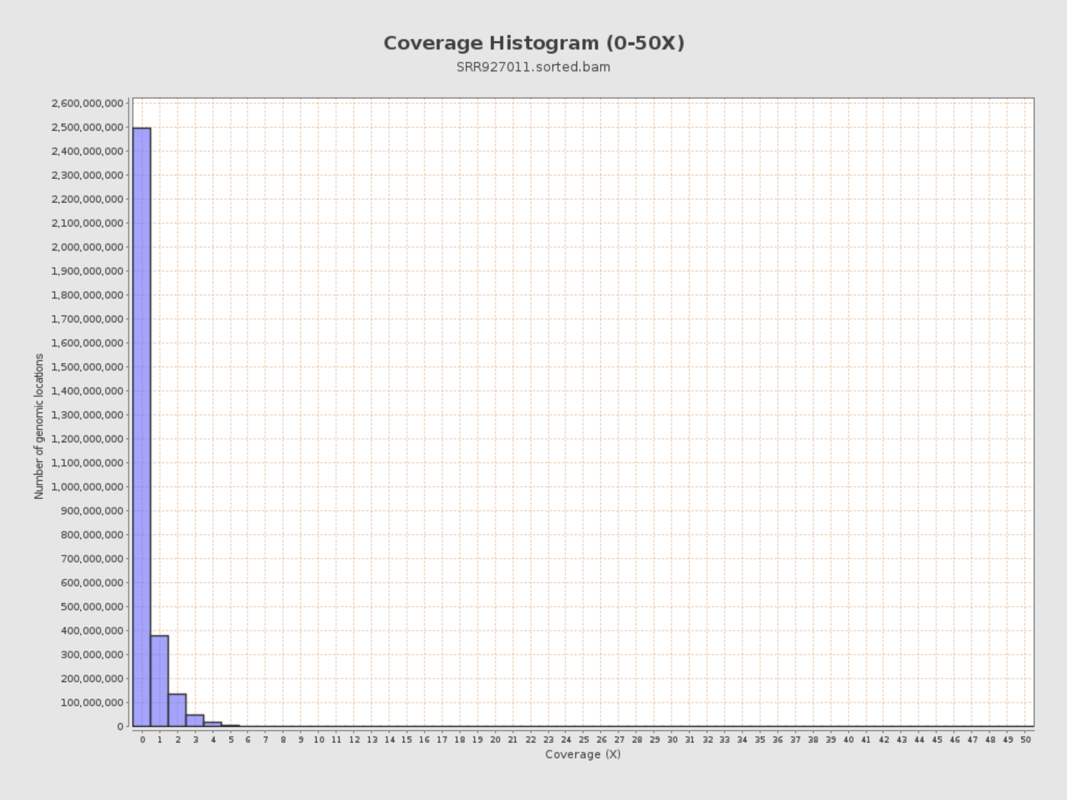
3. Results : Coverage across reference



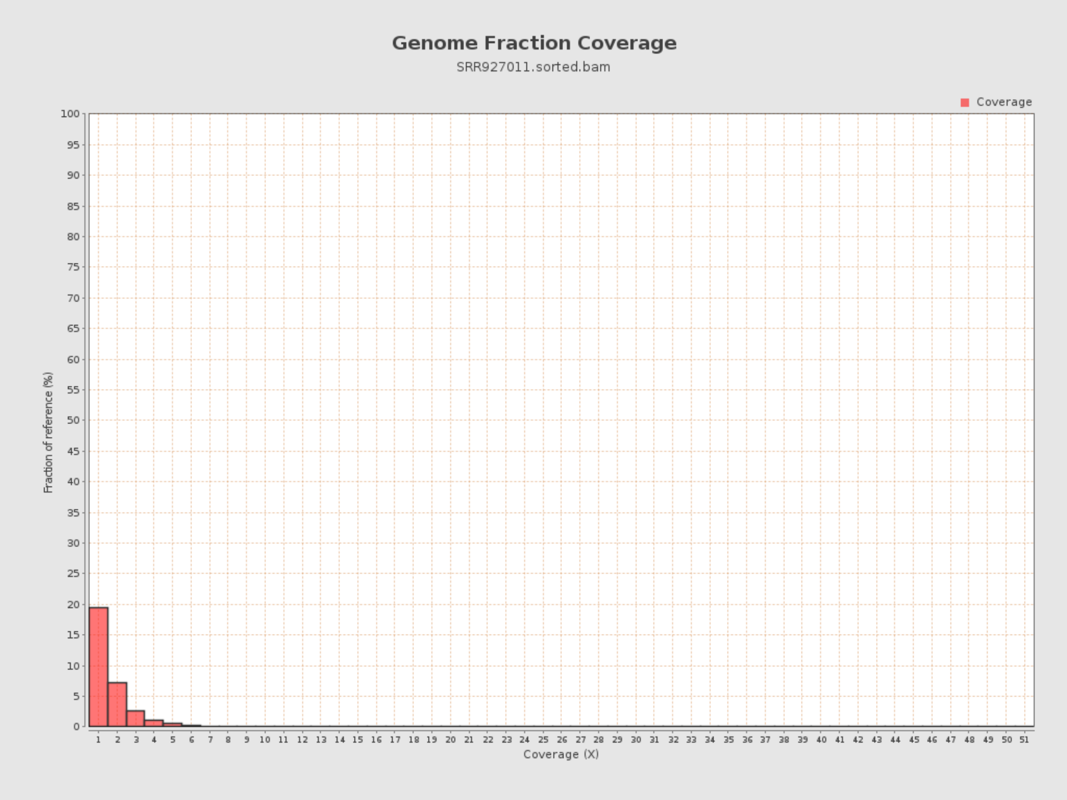
4. Results : Coverage Histogram



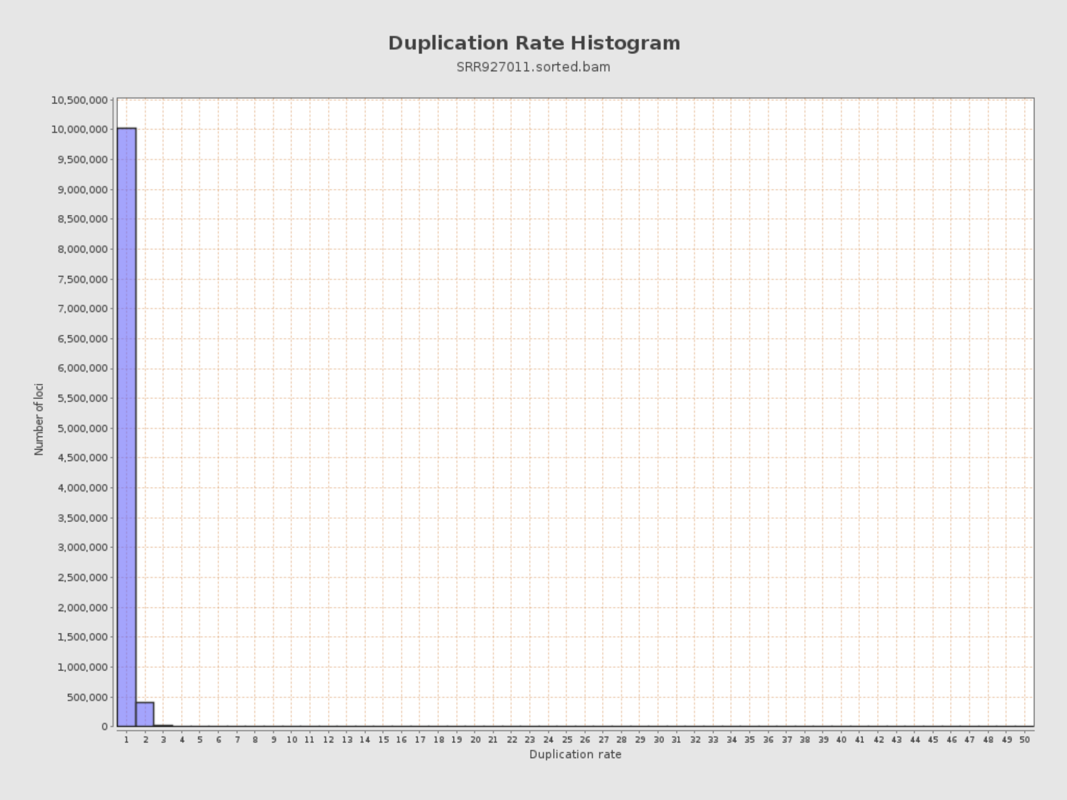
5. Results : Coverage Histogram (0-50X)



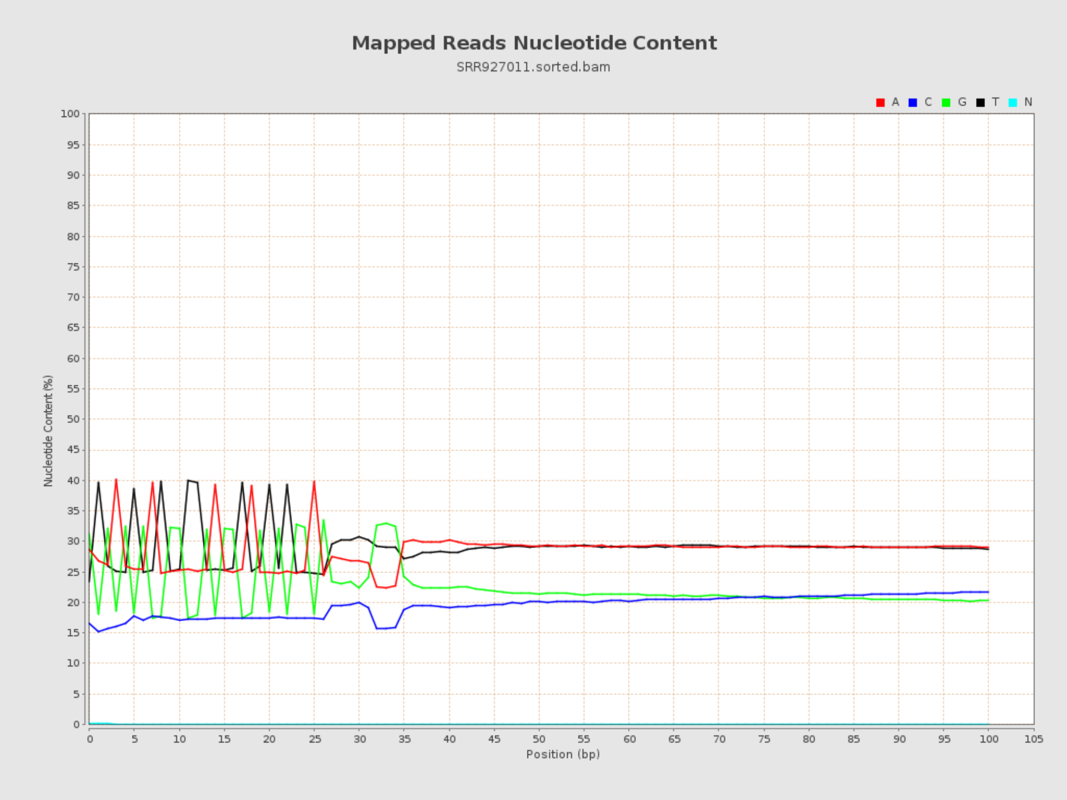
6. Results : Genome Fraction Coverage



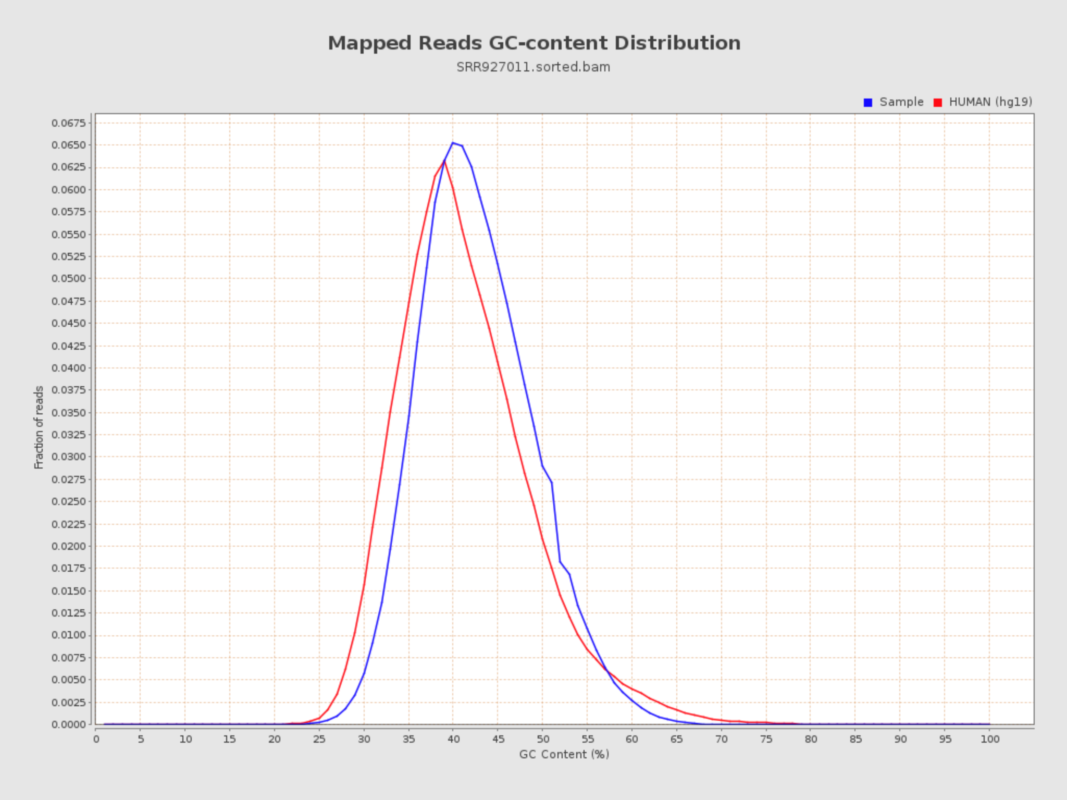
7. Results : Duplication Rate Histogram



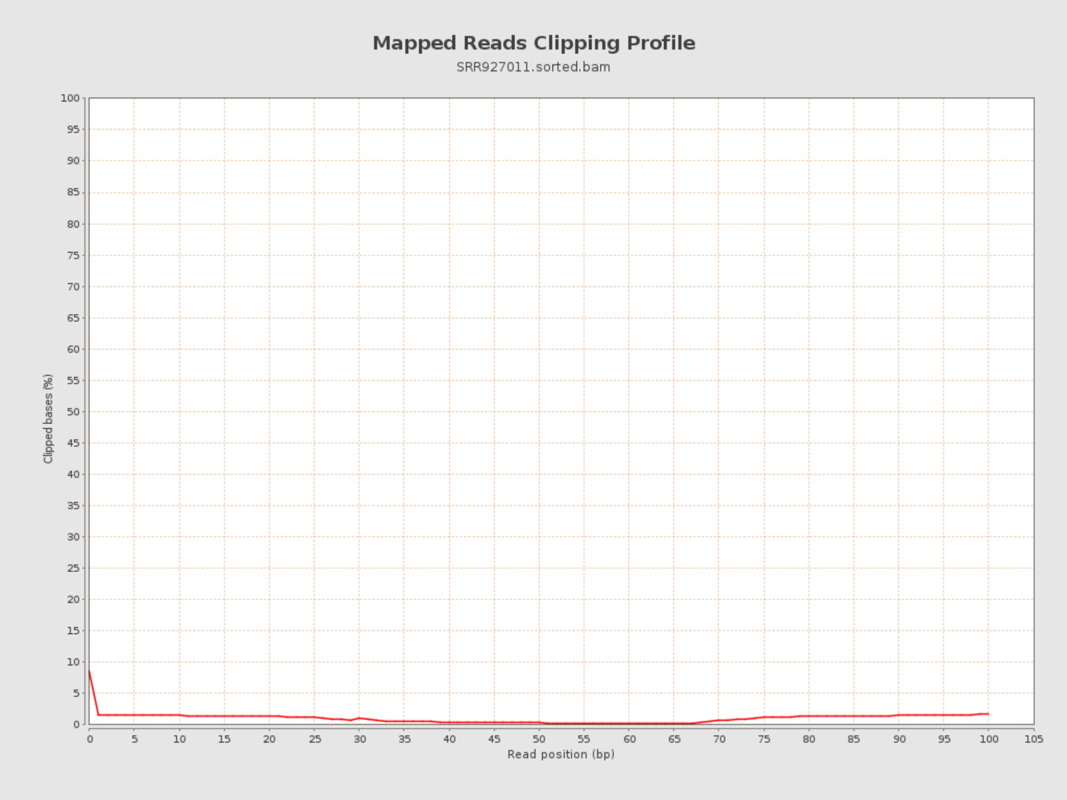
8. Results : Mapped Reads Nucleotide Content



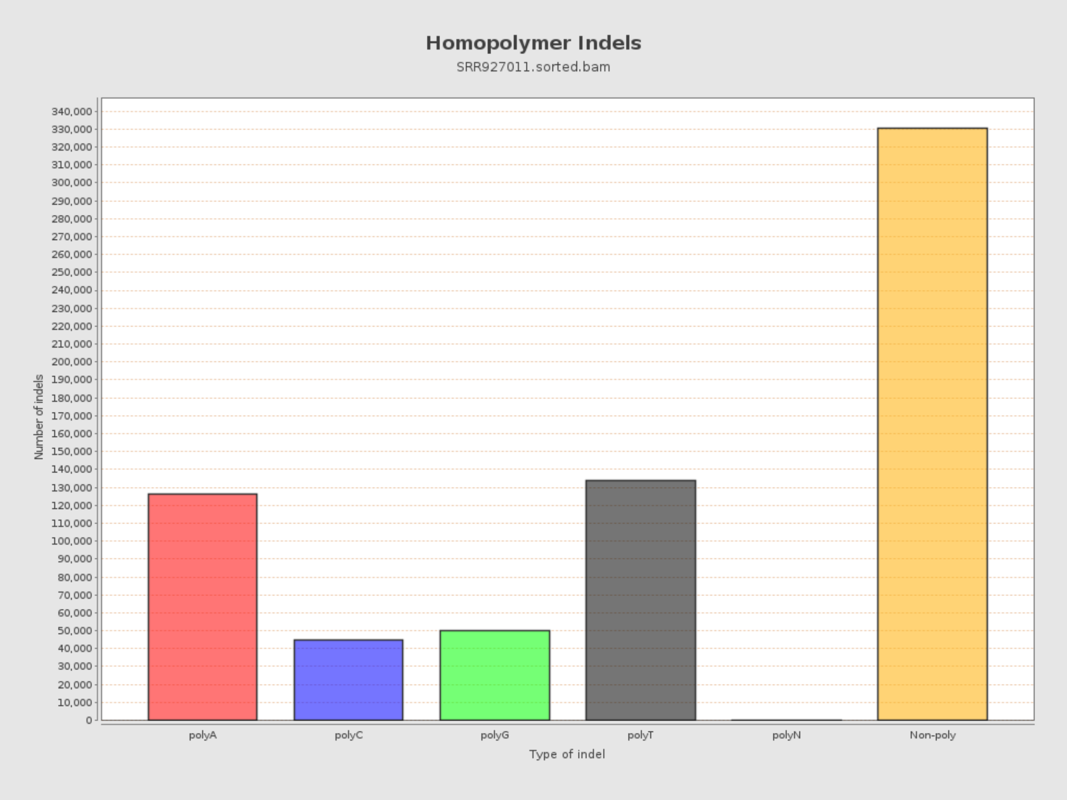
9. Results : Mapped Reads GC-content Distribution



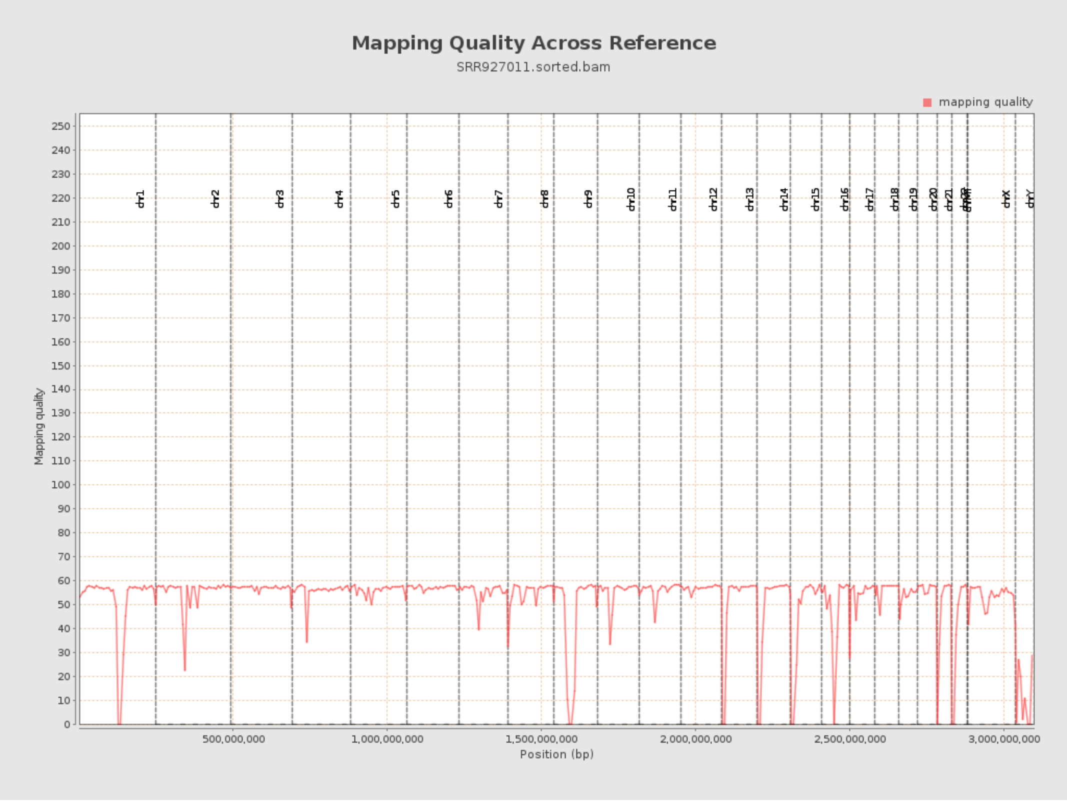
10. Results : Mapped Reads Clipping Profile



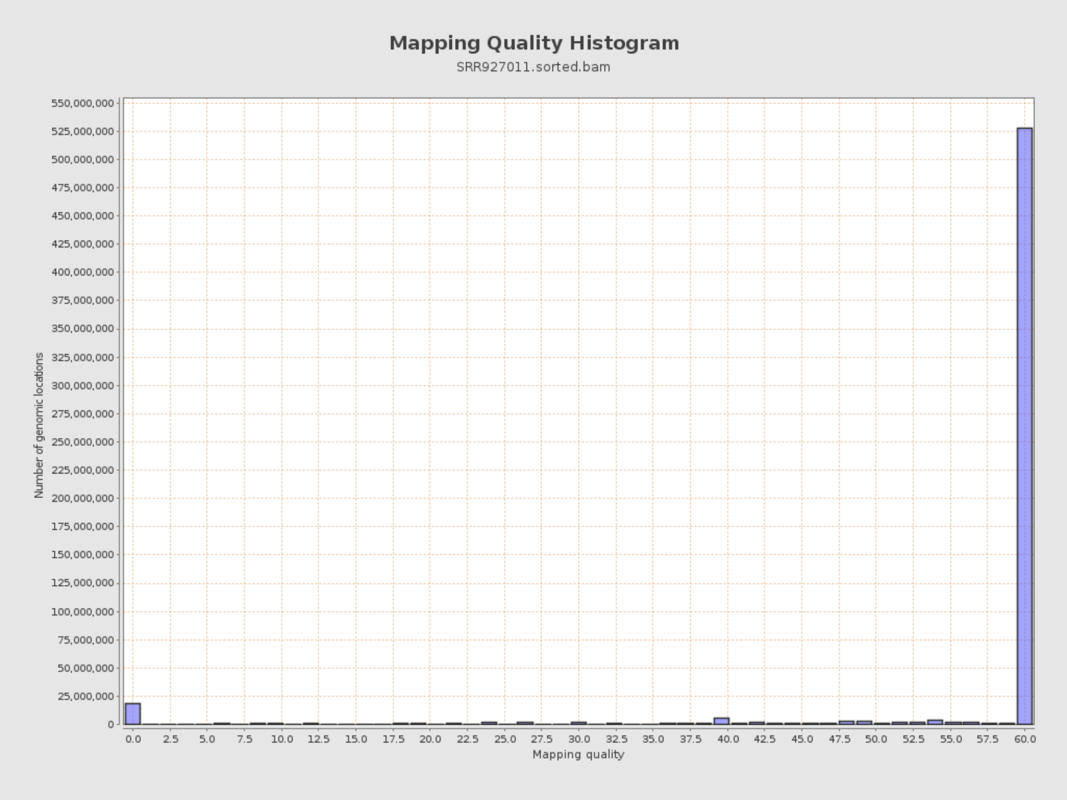
11. Results : Homopolymer Indels



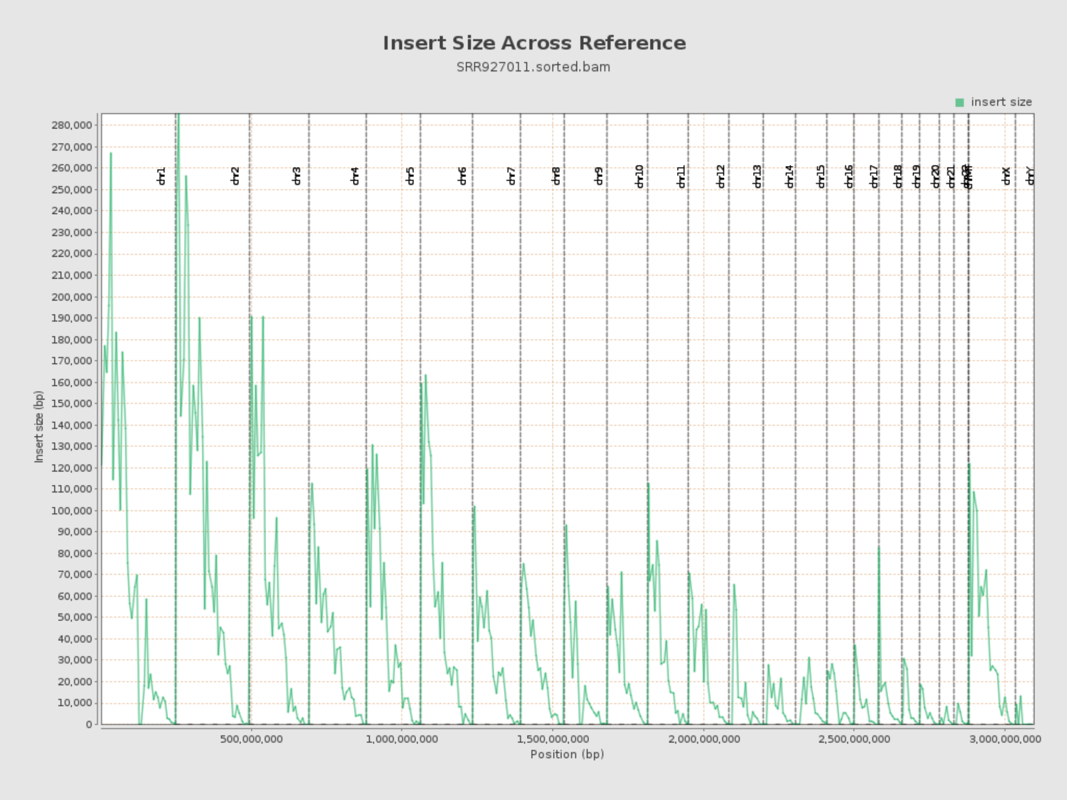
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram