Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 22:57:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927050.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_SRR927050 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927050_1.fastq.gz SRR927050_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 22:57:41 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927050.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	33,383,154
Mapped reads	32,465,735 / 97.25%
Unmapped reads	917,419 / 2.75%
Mapped paired reads	32,465,735 / 97.25%
Mapped reads, first in pair	16,332,554 / 48.92%
Mapped reads, second in pair	16,133,181 / 48.33%
Mapped reads, both in pair	31,932,692 / 95.66%
Mapped reads, singletons	533,043 / 1.6%
Secondary alignments	0
Supplementary alignments	661,386 / 1.98%
Read min/max/mean length	30 / 101 / 101.82
Duplicated reads (estimated)	2,800,988 / 8.39%
Duplication rate	6.89%
Clipped reads	11,848,156 / 35.49%

2.2. ACGT Content

Number/percentage of A's	834,160,803 / 27.91%
Number/percentage of C's	606,536,352 / 20.29%
Number/percentage of T's	850,454,336 / 28.46%
Number/percentage of G's	697,095,390 / 23.32%
Number/percentage of N's	412,090 / 0.01%

GC Percentage	43.62%

2.3. Coverage

Mean	0.9661
Standard Deviation	3.2677

2.4. Mapping Quality

Mean Mapping Quality	53.14

2.5. Insert size

Mean	216,006.41
Standard Deviation	4,589,008.01
P25/Median/P75	143 / 184 / 245

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	31,473,280
Insertions	465,934
Mapped reads with at least one insertion	1.41%
Deletions	1,469,515
Mapped reads with at least one deletion	4.42%
Homopolymer indels	52.02%

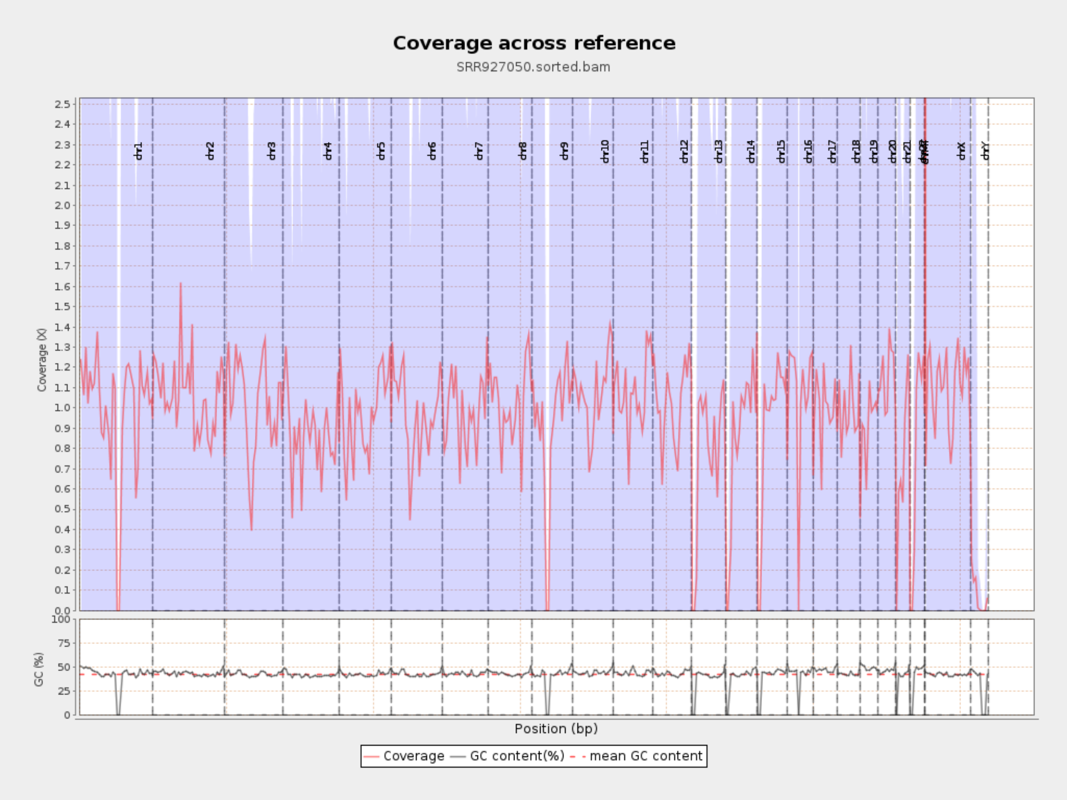
2.7. Chromosome stats

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

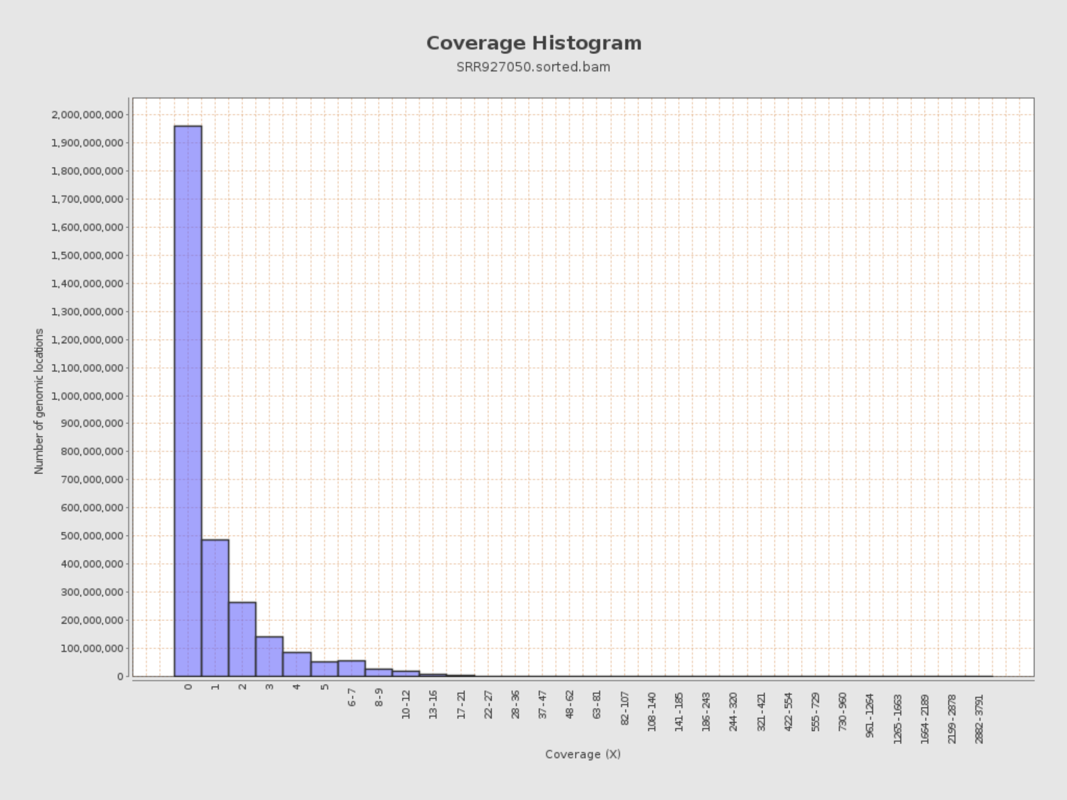
		bases	coverage	deviation
chr1	249250621	246475190	0.9889	3.961
chr2	243199373	259834444	1.0684	5.934
chr3	198022430	202397994	1.0221	1.9779
chr4	191154276	166836736	0.8728	2.1637
chr5	180915260	177080736	0.9788	1.93
chr6	171115067	165520051	0.9673	1.9306
chr7	159138663	155661555	0.9782	2.3112
chr8	146364022	149743287	1.0231	2.1856
chr9	141213431	128787586	0.912	3.0579
chr10	135534747	146410493	1.0802	3.3117
chr11	135006516	145337421	1.0765	3.1932
chr12	133851895	137357005	1.0262	2.0088
chr13	115169878	87952420	0.7637	1.68
chr14	107349540	89480485	0.8335	1.8665
chr15	102531392	91398299	0.8914	1.9412
chr16	90354753	94481872	1.0457	3.8528
chr17	81195210	81214496	1.0002	2.3269
chr18	78077248	78433343	1.0046	2.9607
chr19	59128983	54152293	0.9158	2.7159
chr20	63025520	73193987	1.1613	2.2587
chr21	48129895	36157981	0.7513	2.3782
chr22	51304566	41097312	0.801	1.9864
chrMT	16571	7540533	455.0439	344.6648
chrX	155270560	169953635	1.0946	2.3272

chrY	59373566	4277891	0.0721	2.0393

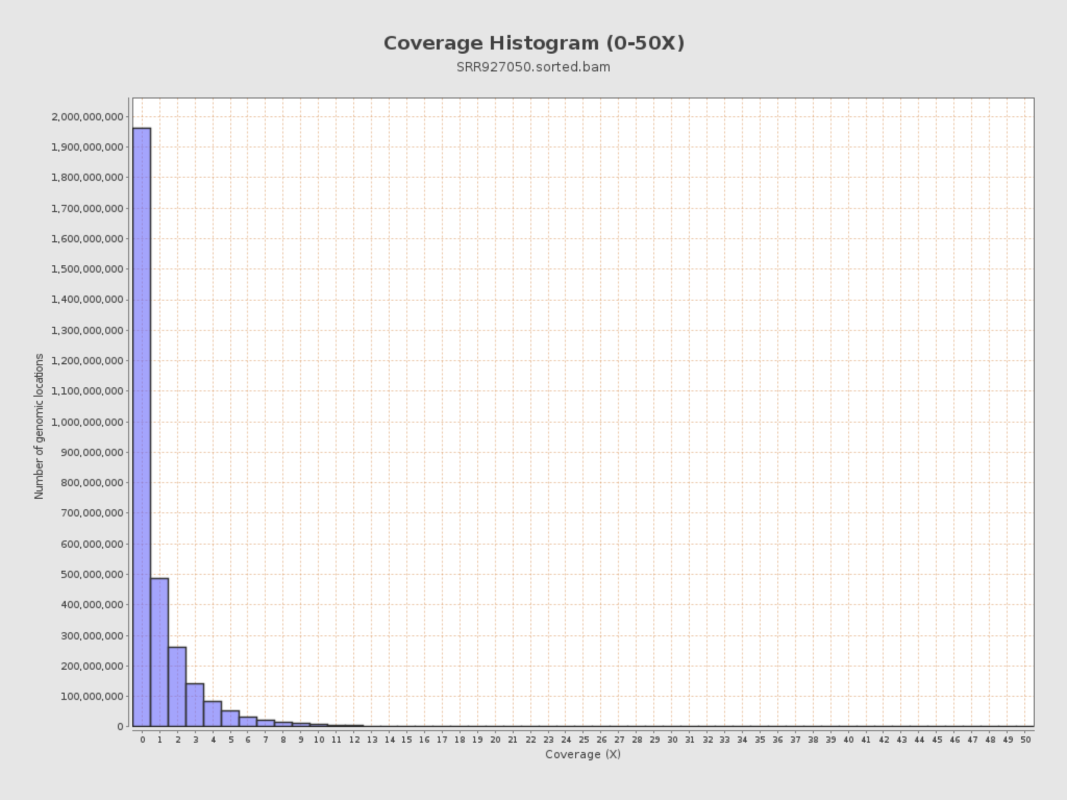
3. Results : Coverage across reference



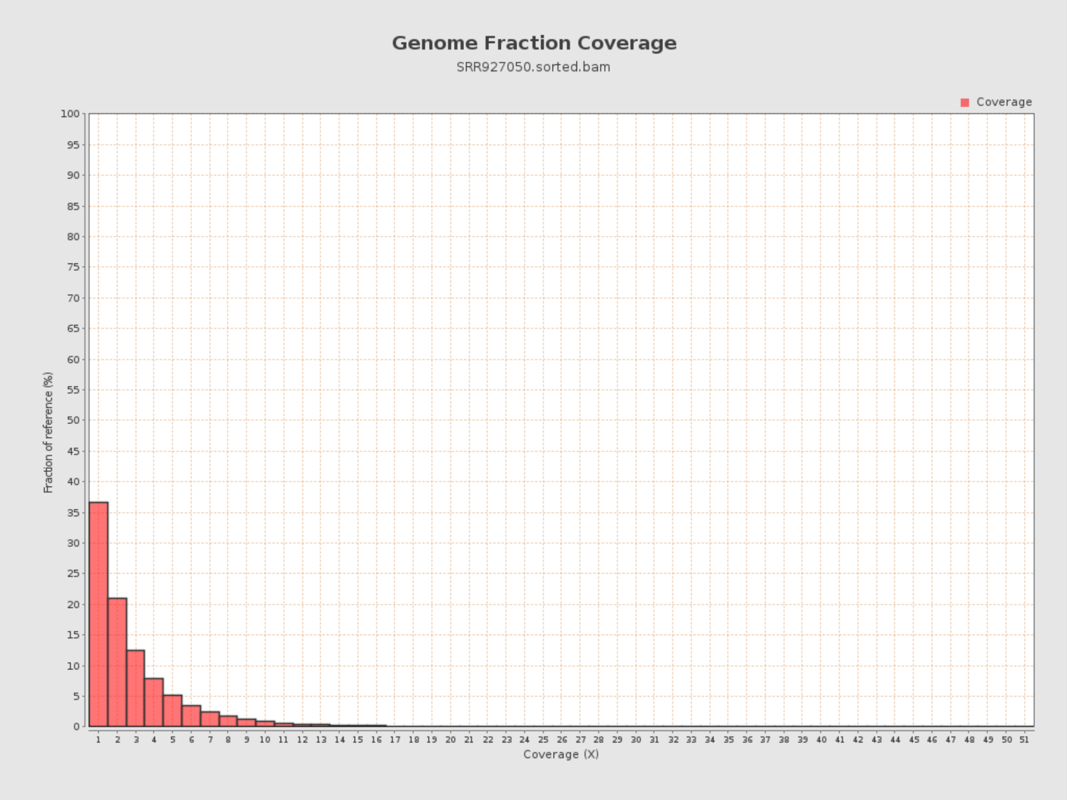
4. Results : Coverage Histogram



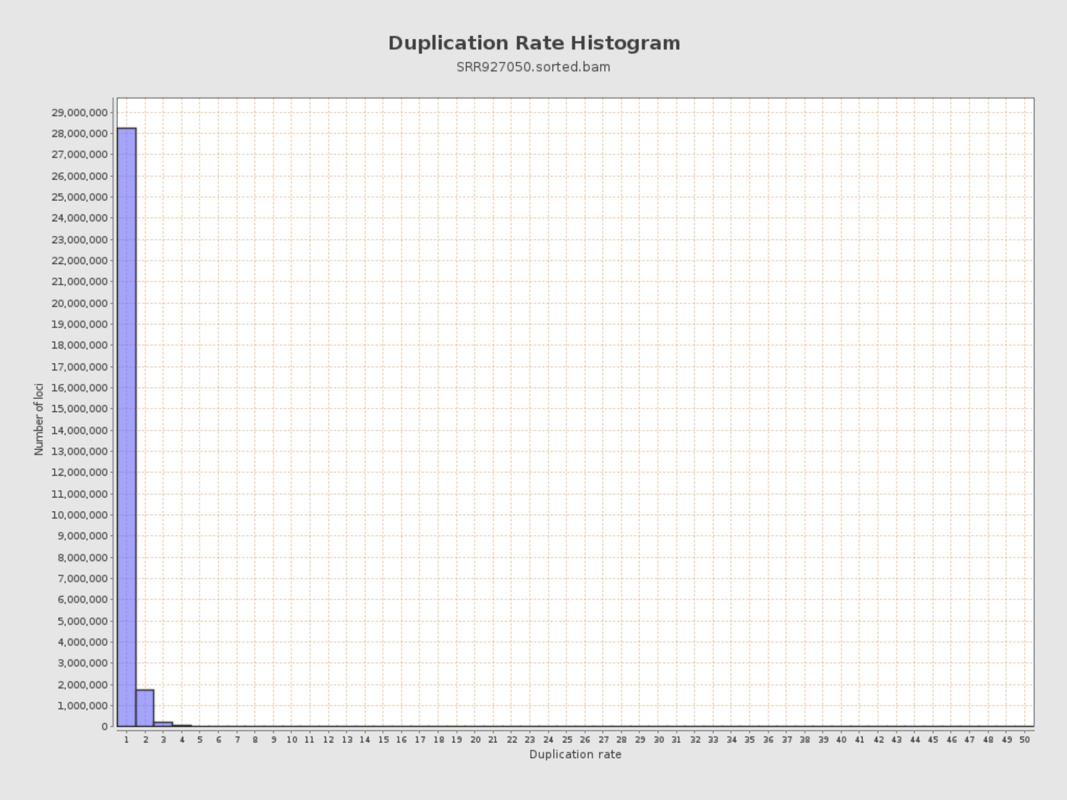
5. Results : Coverage Histogram (0-50X)



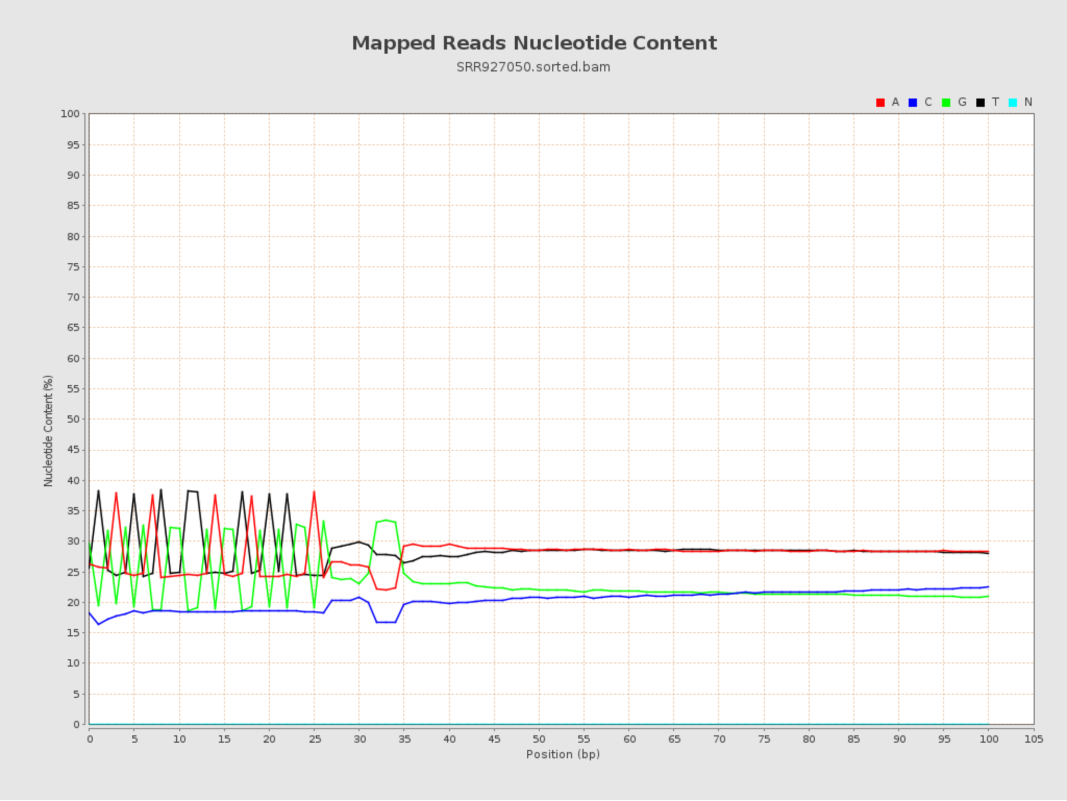
6. Results : Genome Fraction Coverage



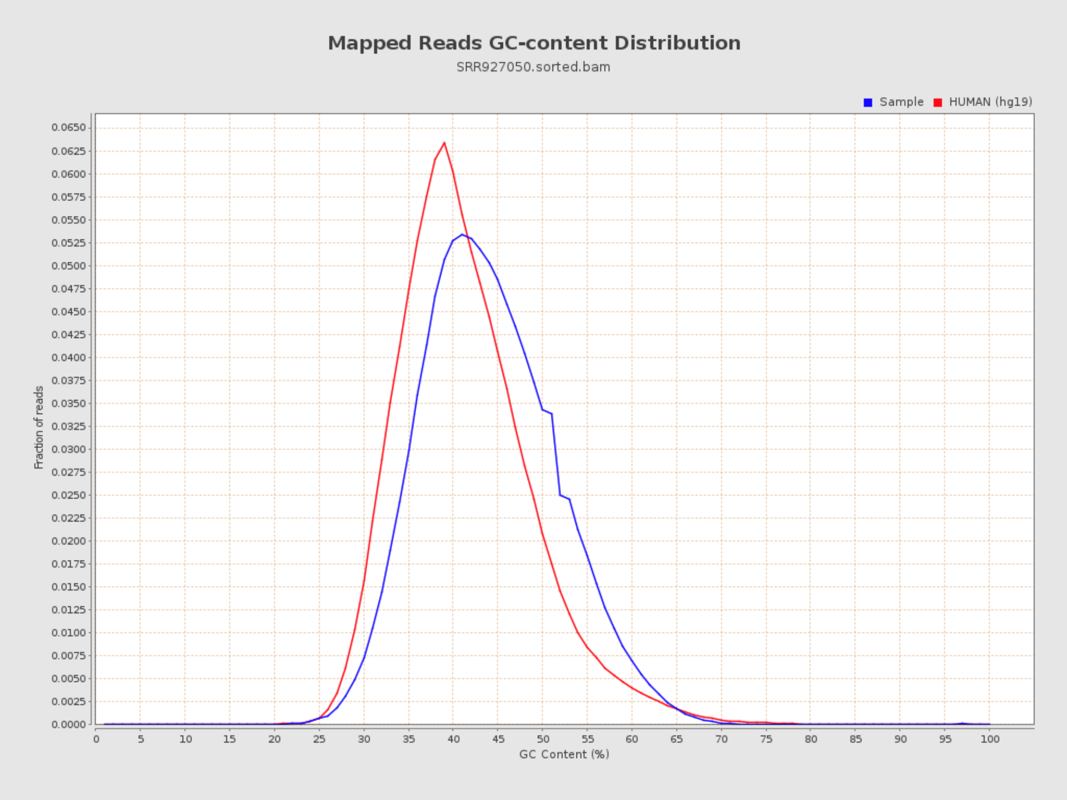
7. Results : Duplication Rate Histogram



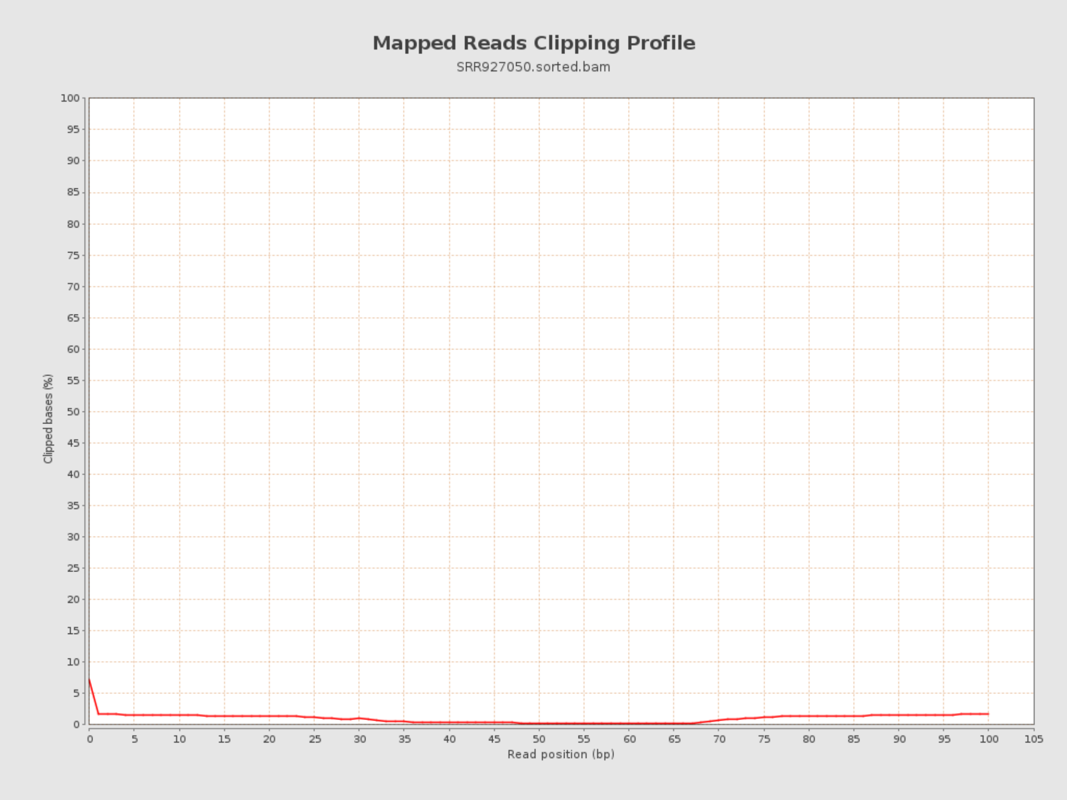
8. Results : Mapped Reads Nucleotide Content



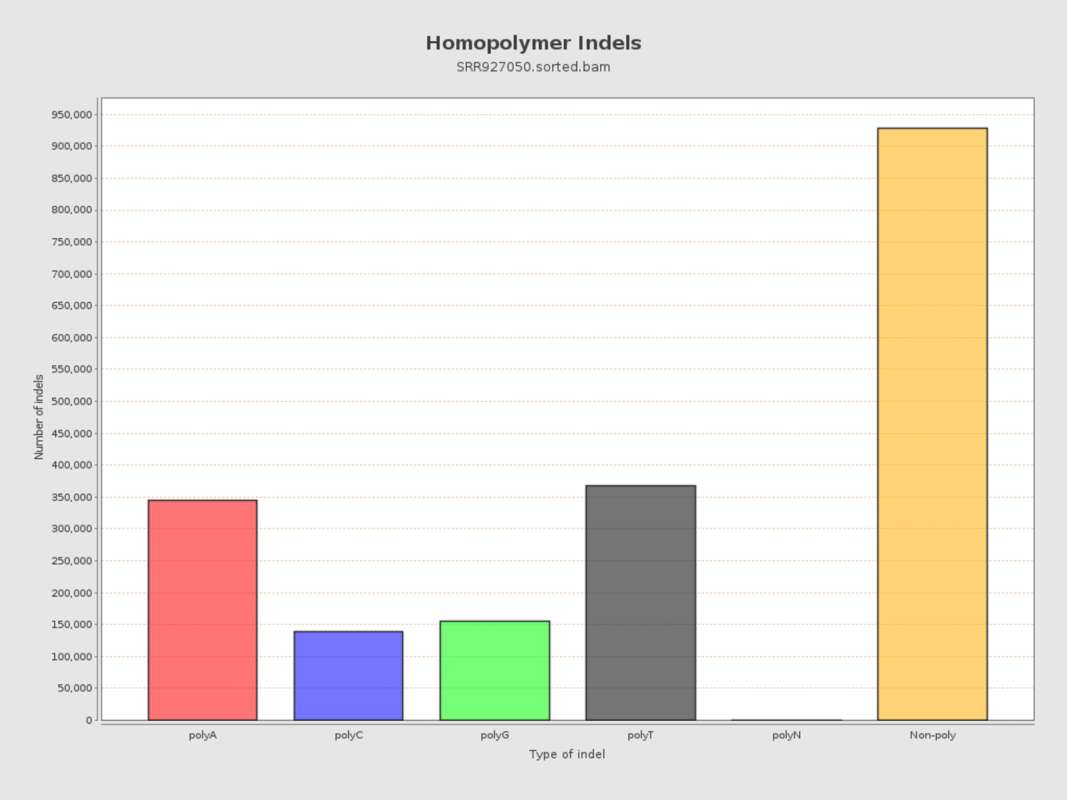
9. Results : Mapped Reads GC-content Distribution



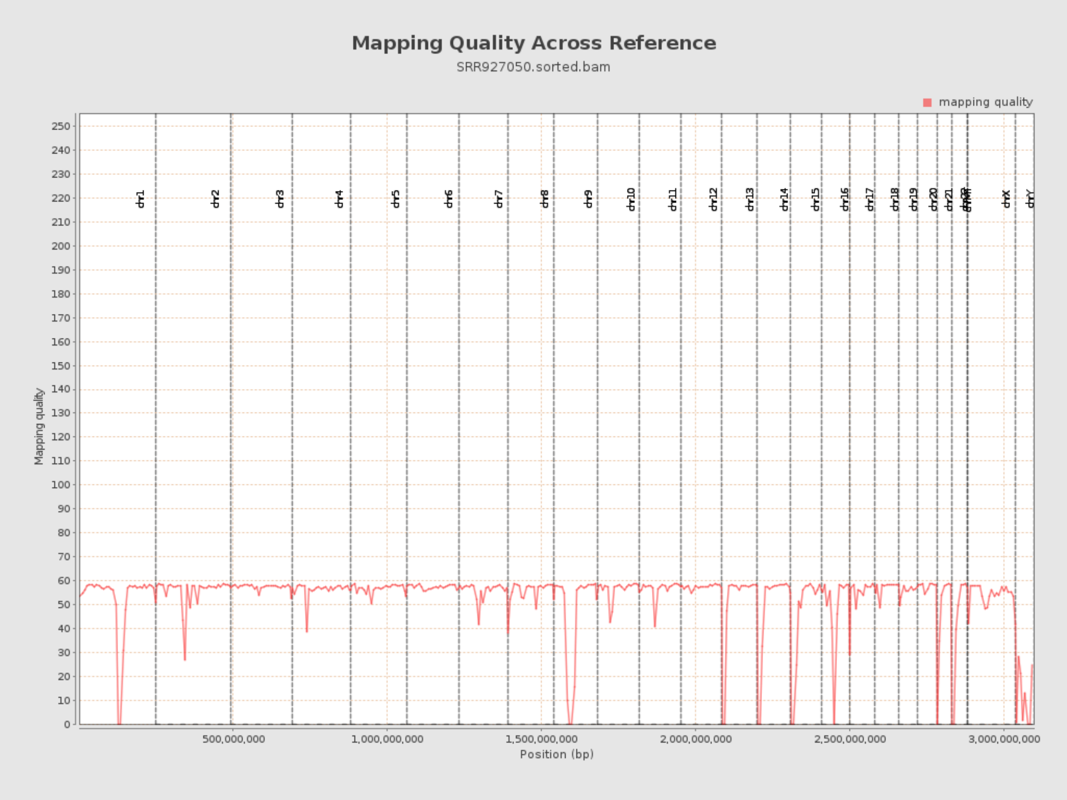
10. Results : Mapped Reads Clipping Profile



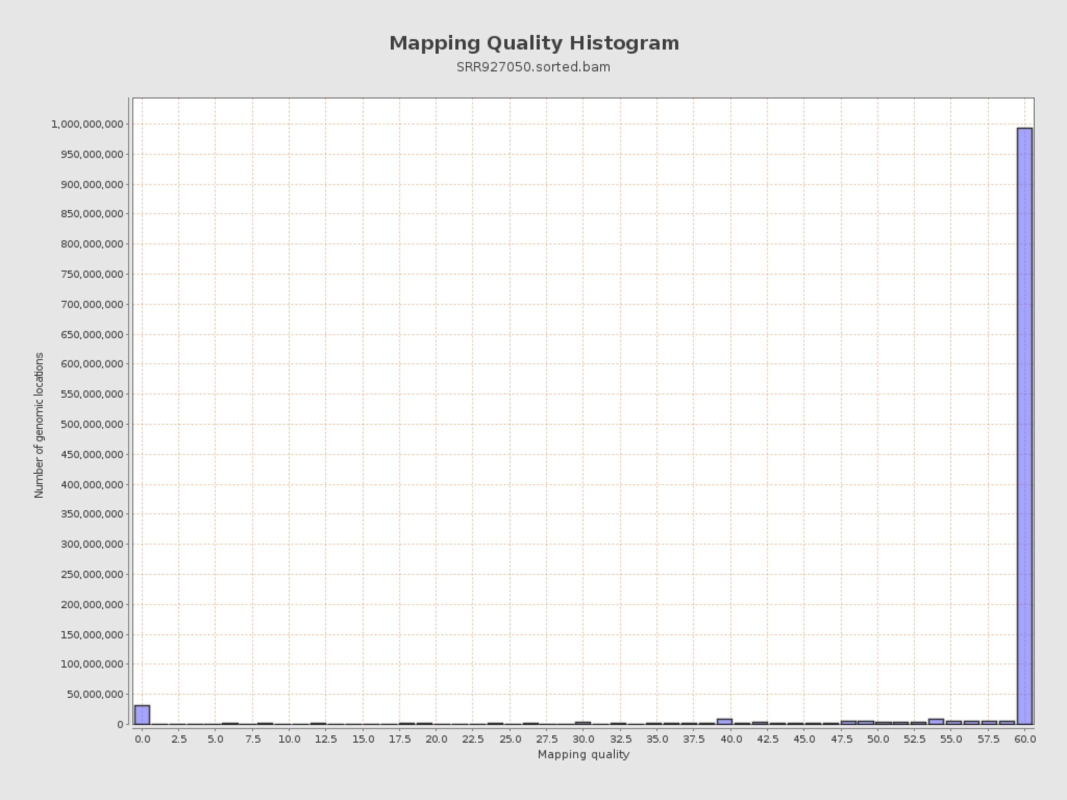
11. Results : Homopolymer Indels



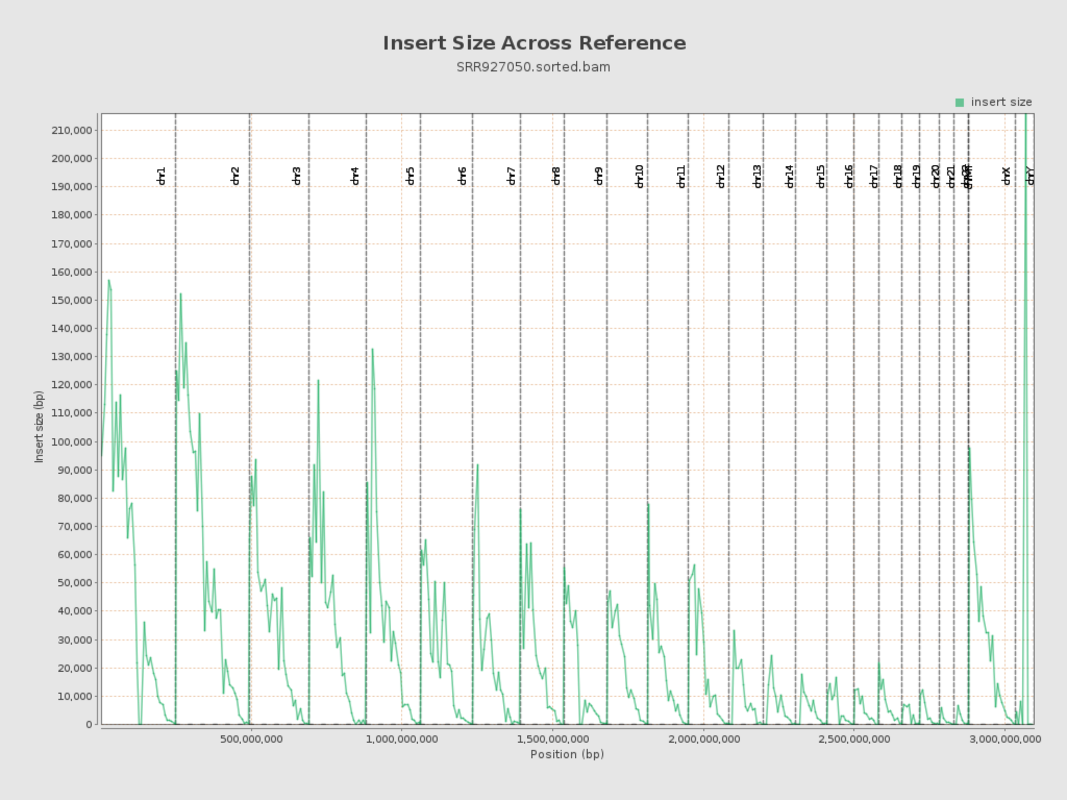
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram