Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 11:24:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927029.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_SRR927029 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927029_1.fastq.gz SRR927029_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 11:24:20 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927029.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,063,604
Mapped reads	22,518,355 / 97.64%
Unmapped reads	545,249 / 2.36%
Mapped paired reads	22,518,355 / 97.64%
Mapped reads, first in pair	11,297,194 / 48.98%
Mapped reads, second in pair	11,221,161 / 48.65%
Mapped reads, both in pair	22,216,168 / 96.33%
Mapped reads, singletons	302,187 / 1.31%
Secondary alignments	0
Supplementary alignments	641,174 / 2.78%
Read min/max/mean length	30 / 101 / 102.15
Duplicated reads (estimated)	1,709,918 / 7.41%
Duplication rate	6.06%
Clipped reads	8,794,769 / 38.13%

2.2. ACGT Content

Number/percentage of A's	586,296,754 / 28.32%
Number/percentage of C's	413,297,582 / 19.97%
Number/percentage of T's	595,503,935 / 28.77%
Number/percentage of G's	474,619,102 / 22.93%
Number/percentage of N's	279,812 / 0.01%

GC Percentage	42.89%

2.3. Coverage

Mean	0.6692
Standard Deviation	2.4534

2.4. Mapping Quality

Mean Mapping Quality	52.85

2.5. Insert size

Mean	292,318.26
Standard Deviation	5,287,043.54
P25/Median/P75	138 / 182 / 246

2.6. Mismatches and indels

General error rate	1.11%
Mismatches	22,345,875
Insertions	347,806
Mapped reads with at least one insertion	1.52%
Deletions	1,067,527
Mapped reads with at least one deletion	4.62%
Homopolymer indels	51.7%

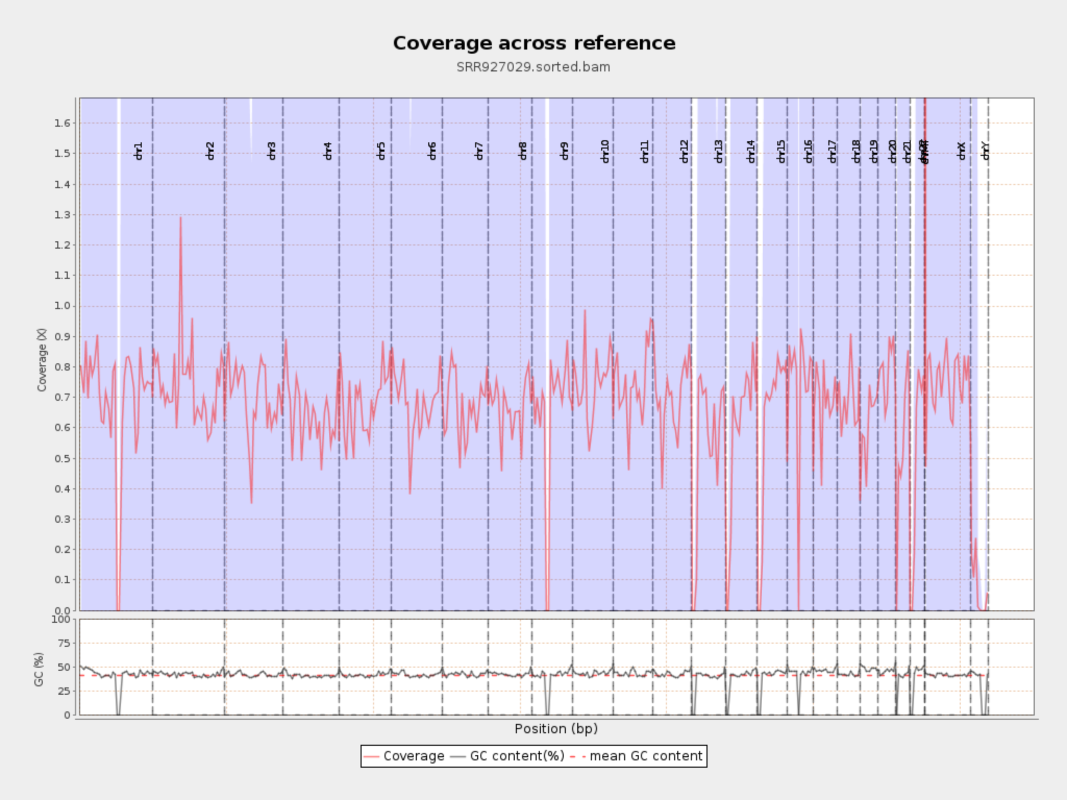
2.7. Chromosome stats

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

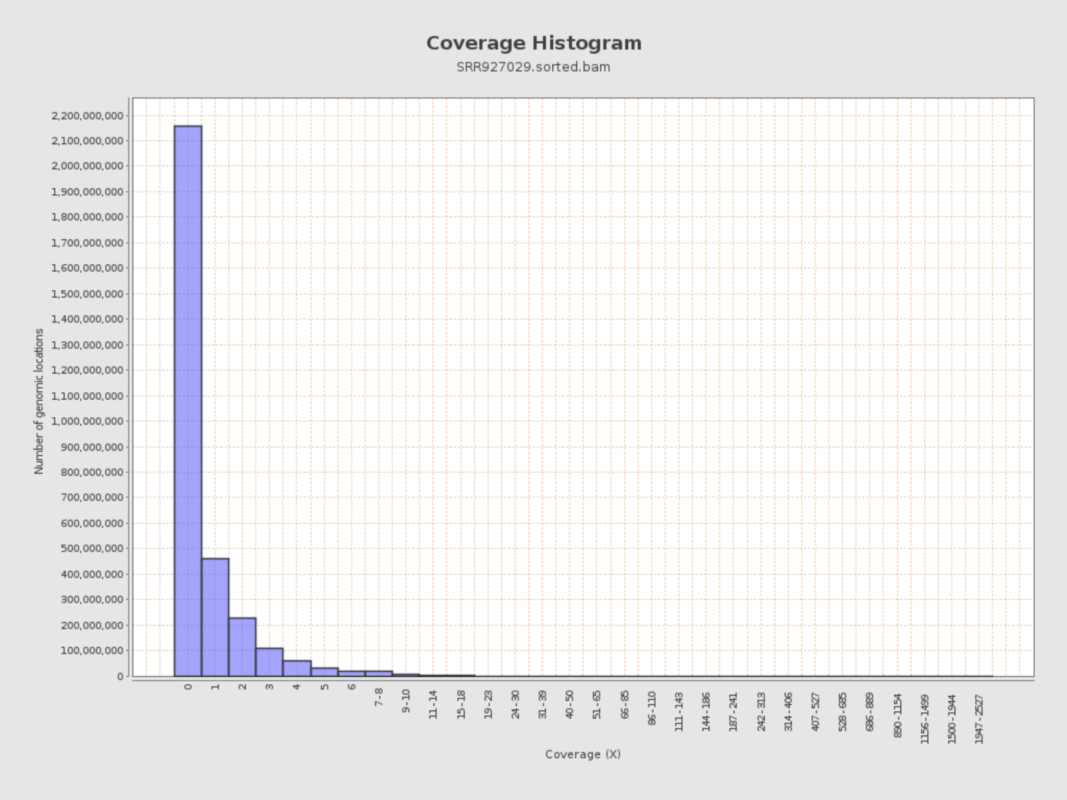
		bases	coverage	deviation
chr1	249250621	172908561	0.6937	3.0871
chr2	243199373	180461976	0.742	4.4453
chr3	198022430	139088338	0.7024	1.4523
chr4	191154276	123713213	0.6472	2.2232
chr5	180915260	123888001	0.6848	1.4277
chr6	171115067	117576431	0.6871	1.4472
chr7	159138663	107089224	0.6729	1.8567
chr8	146364022	98014394	0.6697	1.6765
chr9	141213431	91433184	0.6475	2.8786
chr10	135534747	101876896	0.7517	3.7724
chr11	135006516	100161582	0.7419	2.3017
chr12	133851895	94105083	0.7031	1.4717
chr13	115169878	61876514	0.5373	1.2653
chr14	107349540	62553345	0.5827	1.3799
chr15	102531392	61492701	0.5997	1.3722
chr16	90354753	65969040	0.7301	3.2896
chr17	81195210	55940439	0.689	1.8102
chr18	78077248	54886375	0.703	3.0052
chr19	59128983	36033236	0.6094	2.047
chr20	63025520	49774277	0.7897	1.7034
chr21	48129895	26512554	0.5509	2.0999
chr22	51304566	25324076	0.4936	1.3637
chrMT	16571	542749	32.7529	24.41
chrX	155270560	116149227	0.748	1.6611

chrY	59373566	4182243	0.0704	3.021

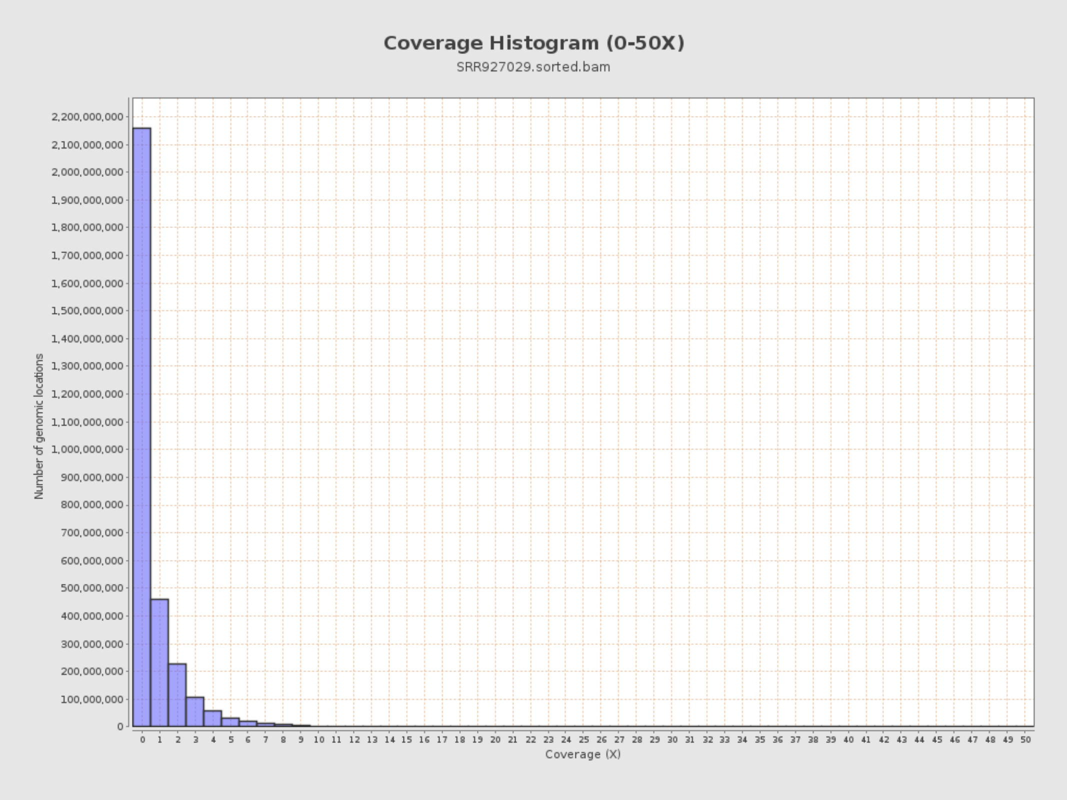
3. Results : Coverage across reference



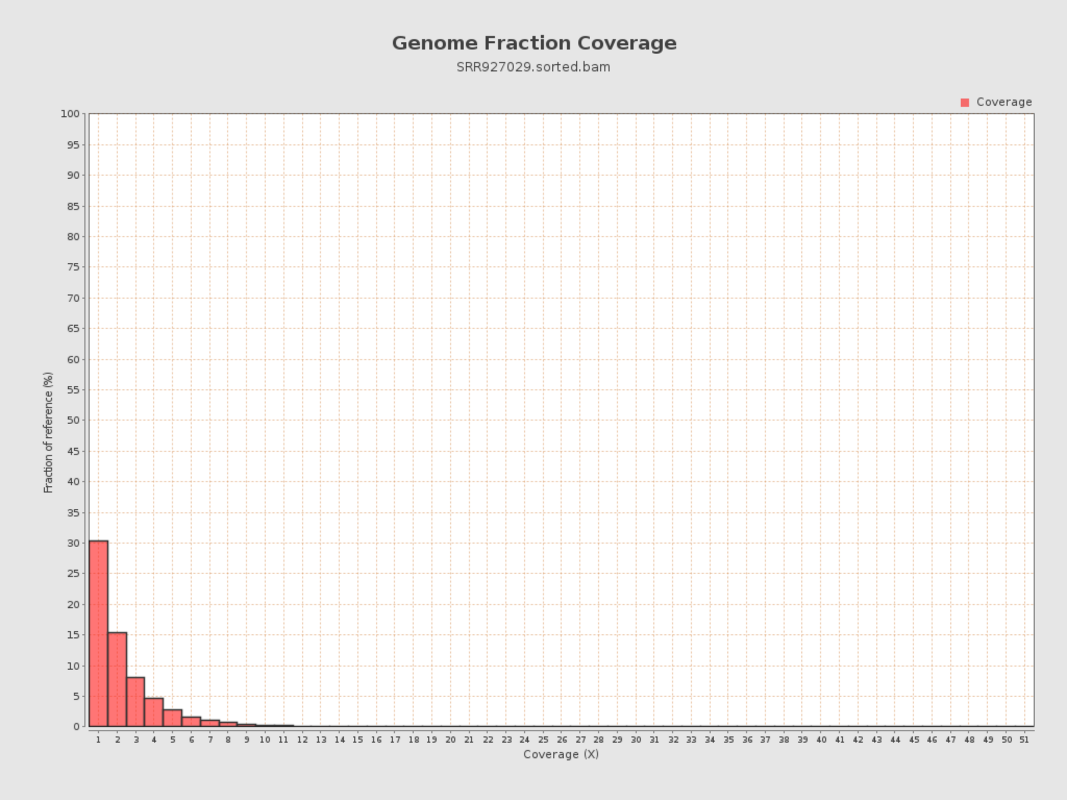
4. Results : Coverage Histogram



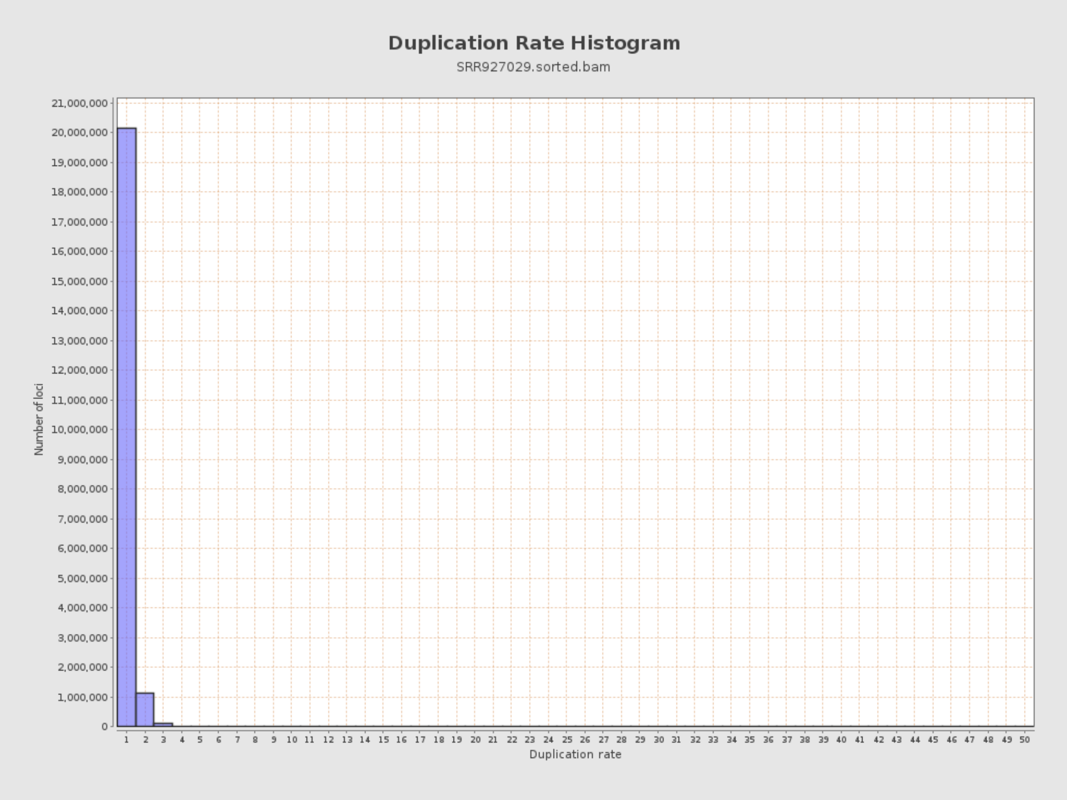
5. Results : Coverage Histogram (0-50X)



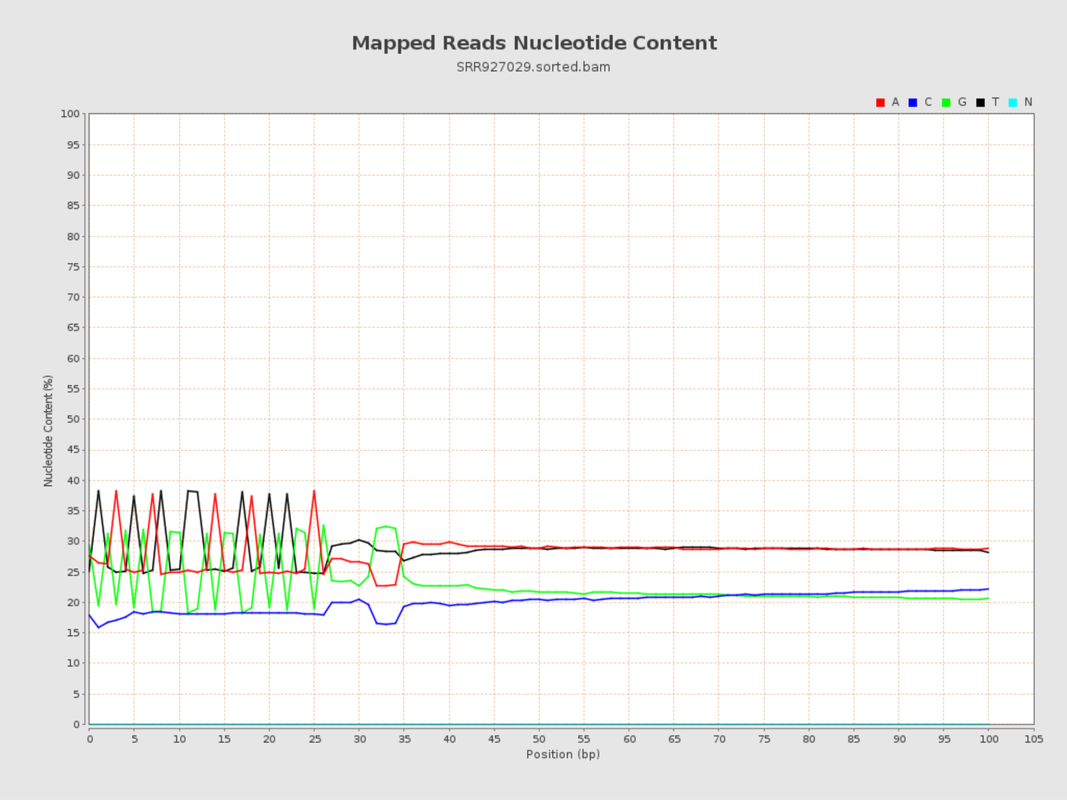
6. Results : Genome Fraction Coverage



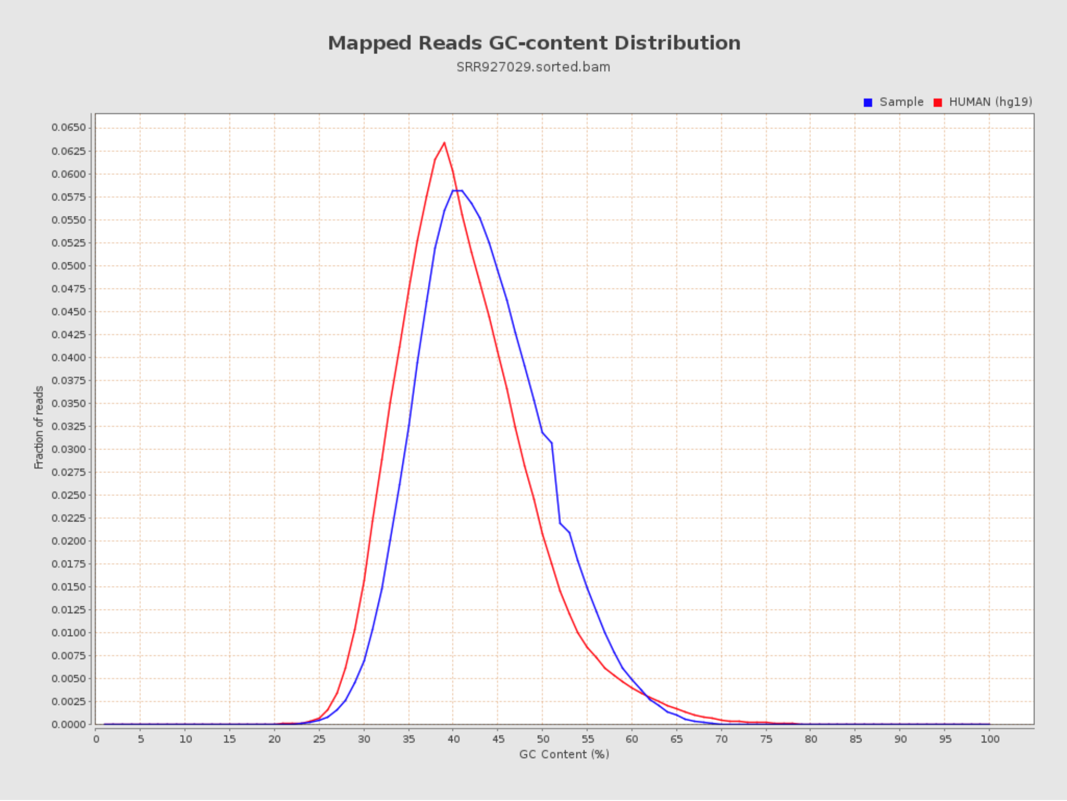
7. Results : Duplication Rate Histogram



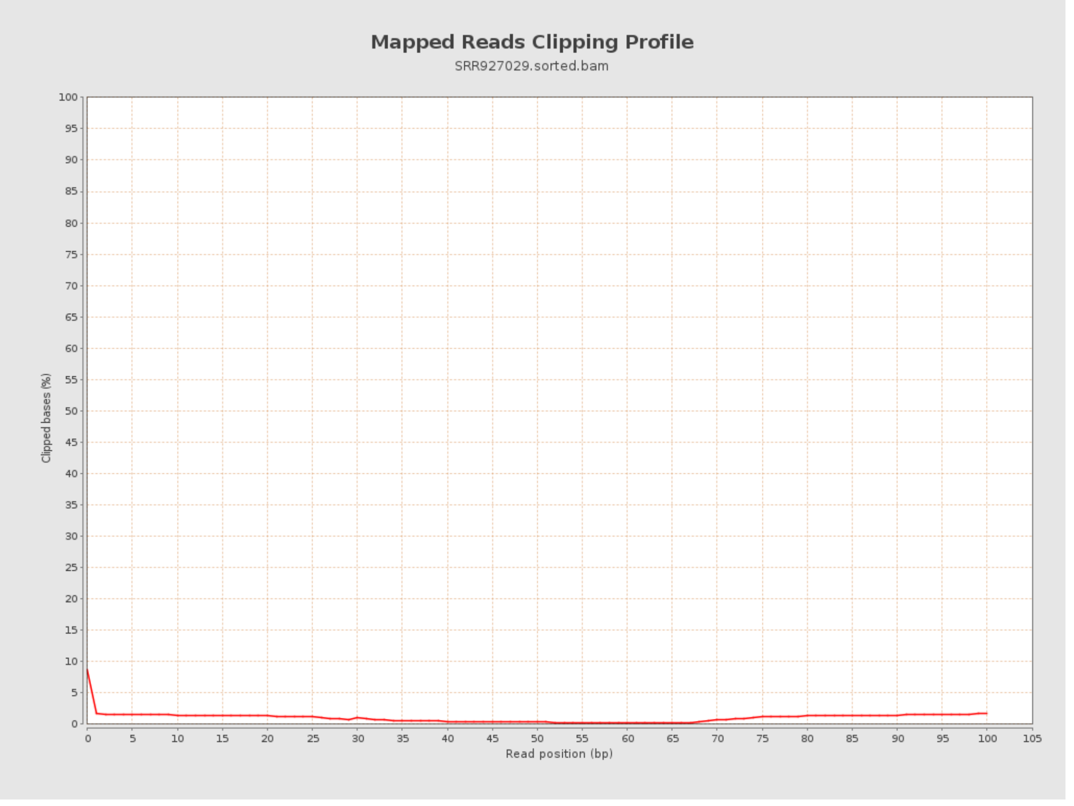
8. Results : Mapped Reads Nucleotide Content



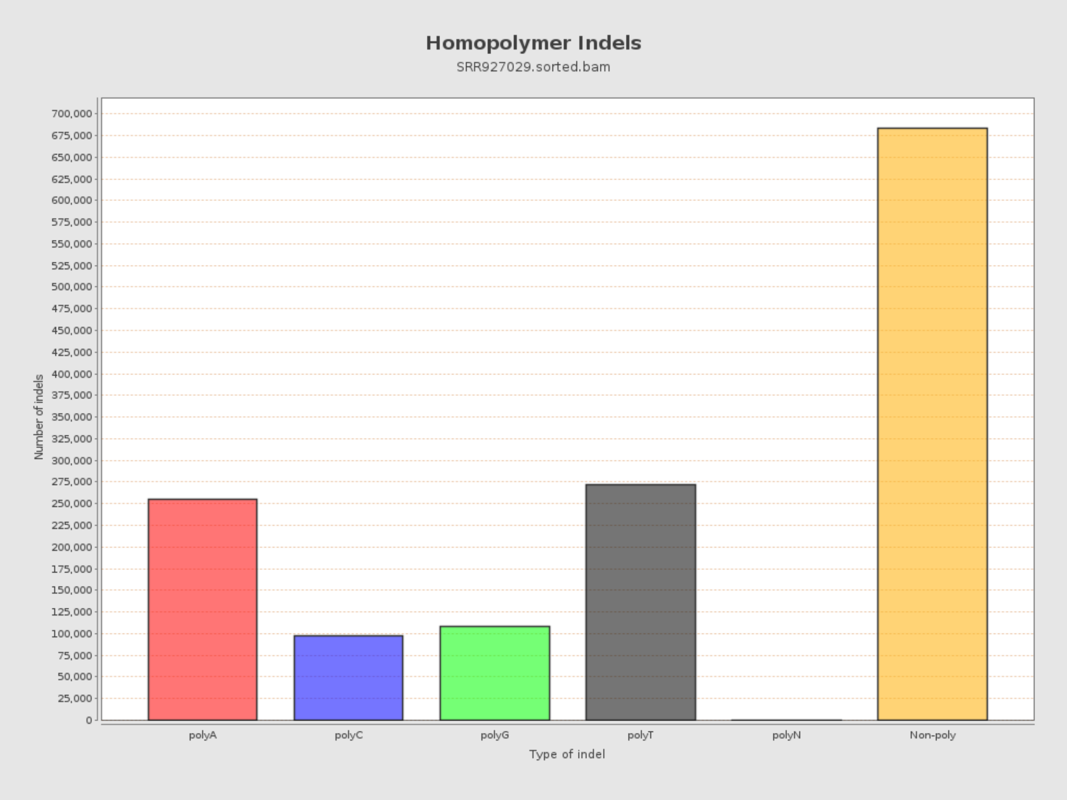
9. Results : Mapped Reads GC-content Distribution



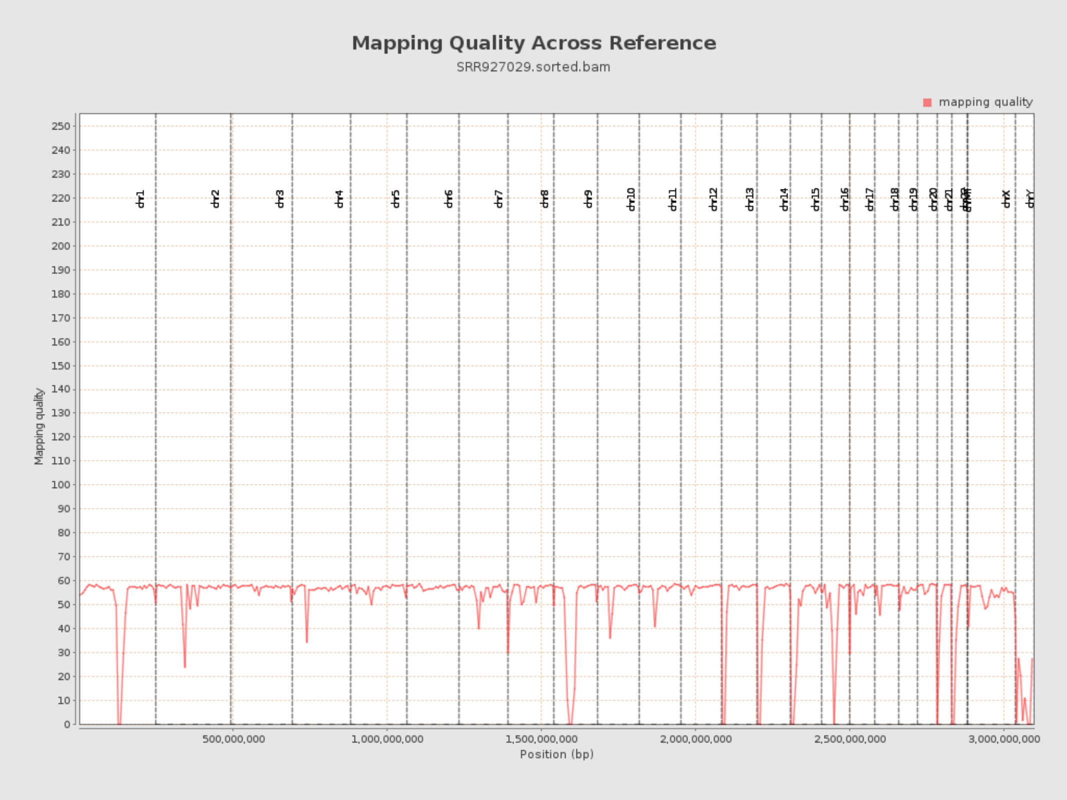
10. Results : Mapped Reads Clipping Profile



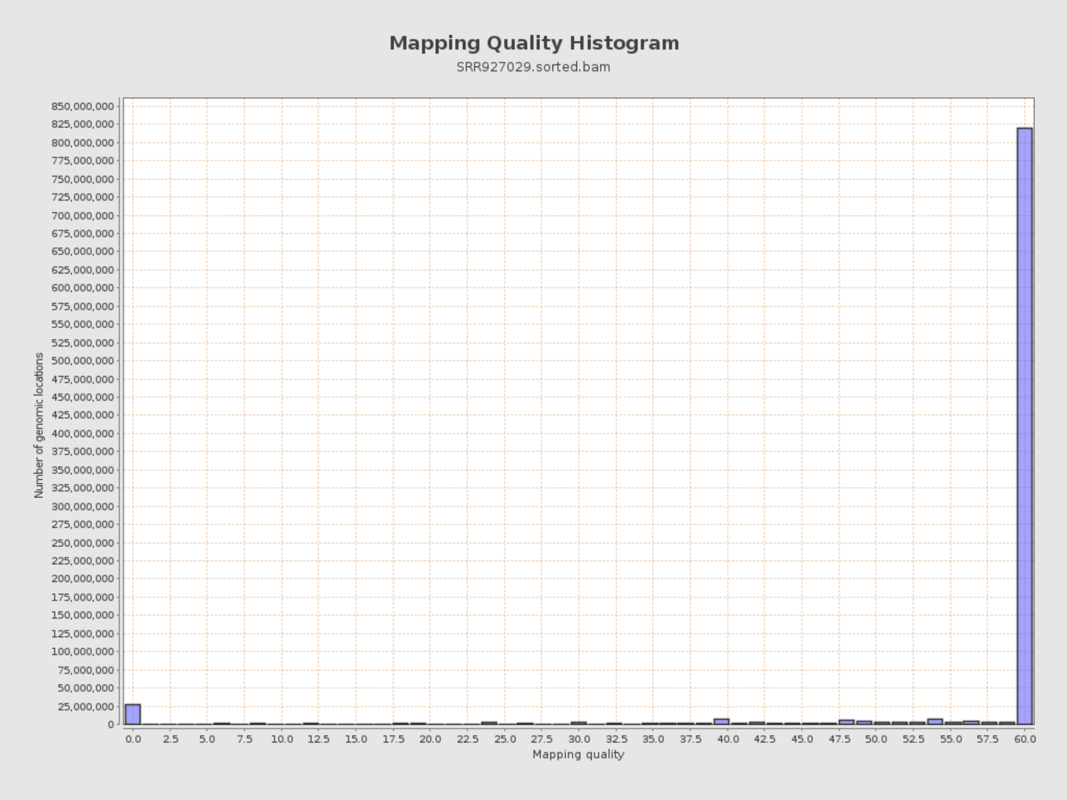
11. Results : Homopolymer Indels



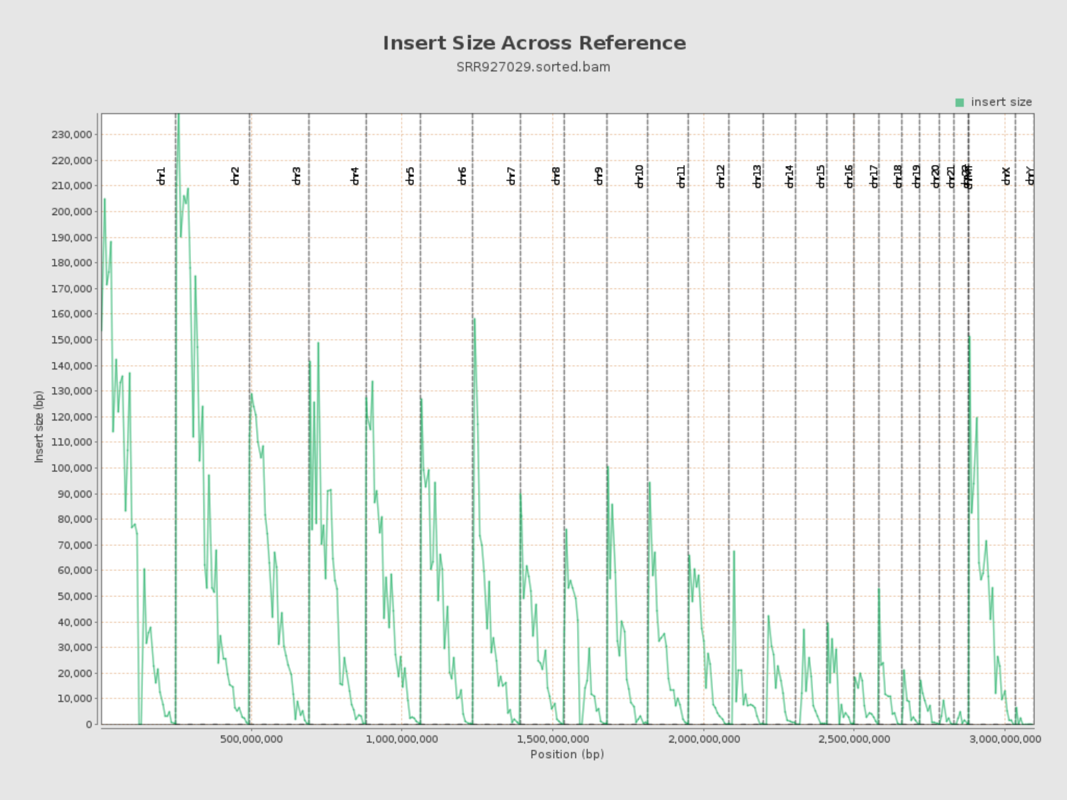
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram