Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 02:30:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927008.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_SRR927008 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927008_1.fastq.gz SRR927008_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 02:30:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927008.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,677,748
Mapped reads	8,481,141 / 97.73%
Unmapped reads	196,607 / 2.27%
Mapped paired reads	8,481,141 / 97.73%
Mapped reads, first in pair	4,261,077 / 49.1%
Mapped reads, second in pair	4,220,064 / 48.63%
Mapped reads, both in pair	8,355,298 / 96.28%
Mapped reads, singletons	125,843 / 1.45%
Secondary alignments	0
Supplementary alignments	217,304 / 2.5%
Read min/max/mean length	30 / 101 / 102.04
Duplicated reads (estimated)	393,624 / 4.54%
Duplication rate	3.74%
Clipped reads	3,317,513 / 38.23%

2.2. ACGT Content

Number/percentage of A's	222,122,989 / 28.55%
Number/percentage of C's	151,962,202 / 19.54%
Number/percentage of T's	226,195,143 / 29.08%
Number/percentage of G's	177,455,649 / 22.81%
Number/percentage of N's	150,239 / 0.02%

GC Percentage	42.35%

2.3. Coverage

Mean	0.2515
Standard Deviation	1.0926

2.4. Mapping Quality

Mean Mapping Quality	52.62

2.5. Insert size

Mean	296,206.35
Standard Deviation	5,352,082.14
P25/Median/P75	146 / 190 / 255

2.6. Mismatches and indels

General error rate	0.97%
Mismatches	7,307,065
Insertions	134,000
Mapped reads with at least one insertion	1.55%
Deletions	400,596
Mapped reads with at least one deletion	4.6%
Homopolymer indels	51.85%

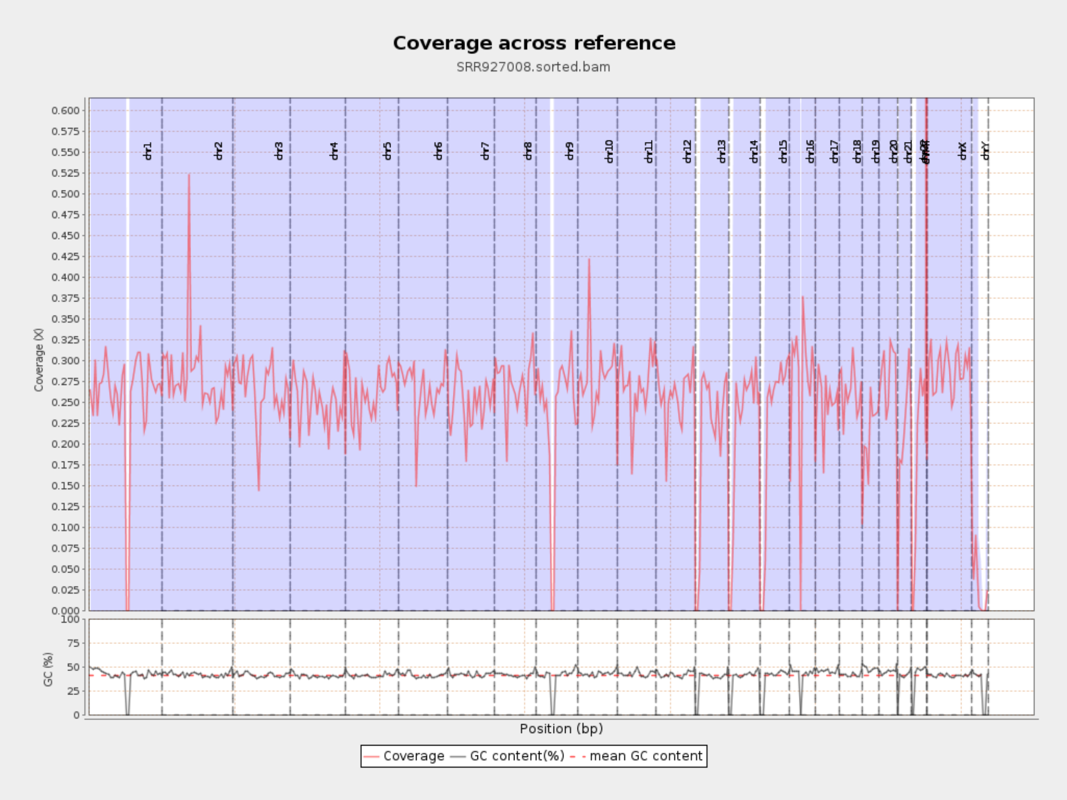
2.7. Chromosome stats

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

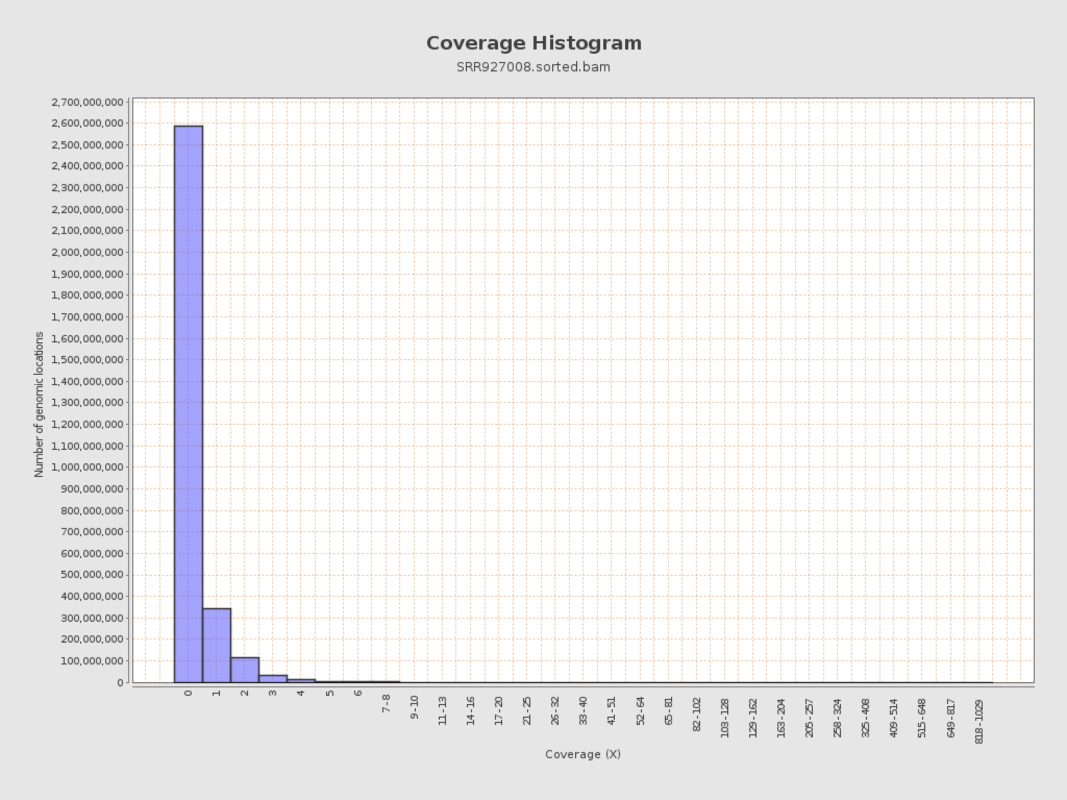
		bases	coverage	deviation
chr1	249250621	63219637	0.2536	1.3228
chr2	243199373	68973924	0.2836	1.9424
chr3	198022430	52597856	0.2656	0.6934
chr4	191154276	47979870	0.251	0.8983
chr5	180915260	47092313	0.2603	0.6816
chr6	171115067	45582992	0.2664	0.8109
chr7	159138663	39876257	0.2506	0.8512
chr8	146364022	40022367	0.2734	0.7876
chr9	141213431	33348110	0.2362	1.312
chr10	135534747	38396839	0.2833	1.9063
chr11	135006516	36353368	0.2693	0.8526
chr12	133851895	34541235	0.2581	0.6988
chr13	115169878	23971778	0.2081	0.6073
chr14	107349540	23241382	0.2165	0.6374
chr15	102531392	22549544	0.2199	0.6412
chr16	90354753	24523612	0.2714	1.4137
chr17	81195210	20134124	0.248	0.8122
chr18	78077248	20596538	0.2638	1.2944
chr19	59128983	12566893	0.2125	0.8775
chr20	63025520	17817580	0.2827	0.75
chr21	48129895	9985498	0.2075	0.8933
chr22	51304566	9107431	0.1775	0.5931
chrMT	16571	70996	4.2844	3.8891
chrX	155270560	44389171	0.2859	0.7746

chrY	59373566	1537889	0.0259	1.0191

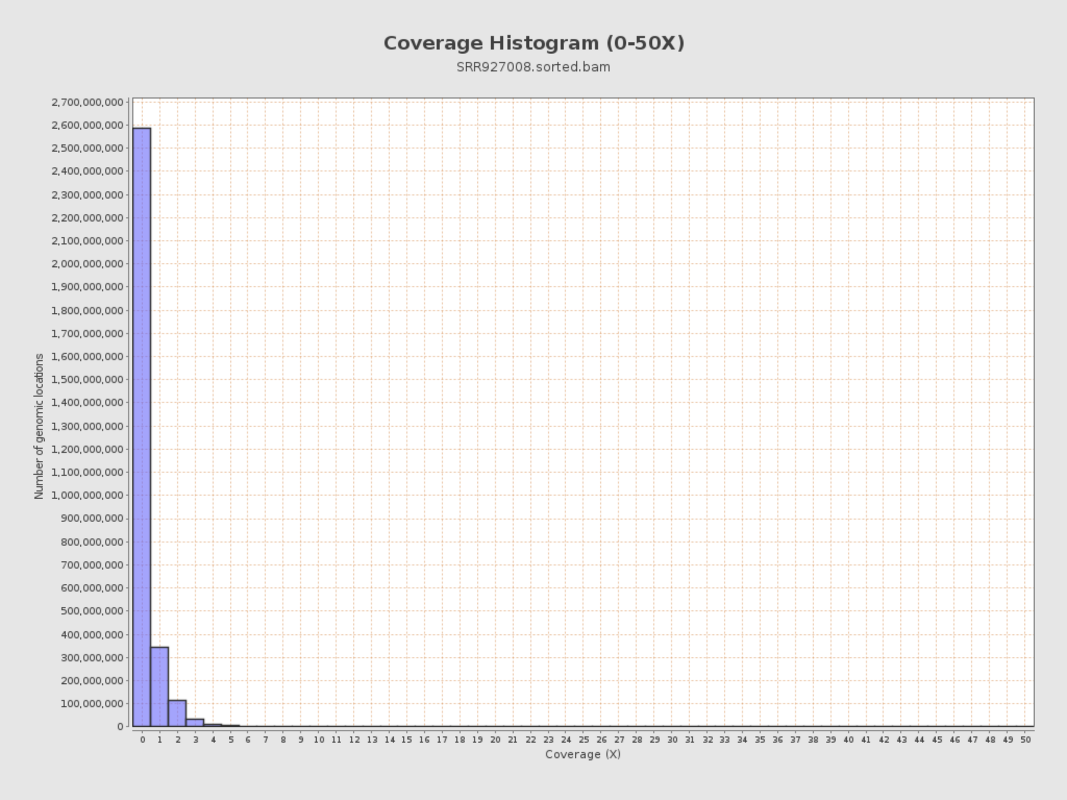
3. Results : Coverage across reference



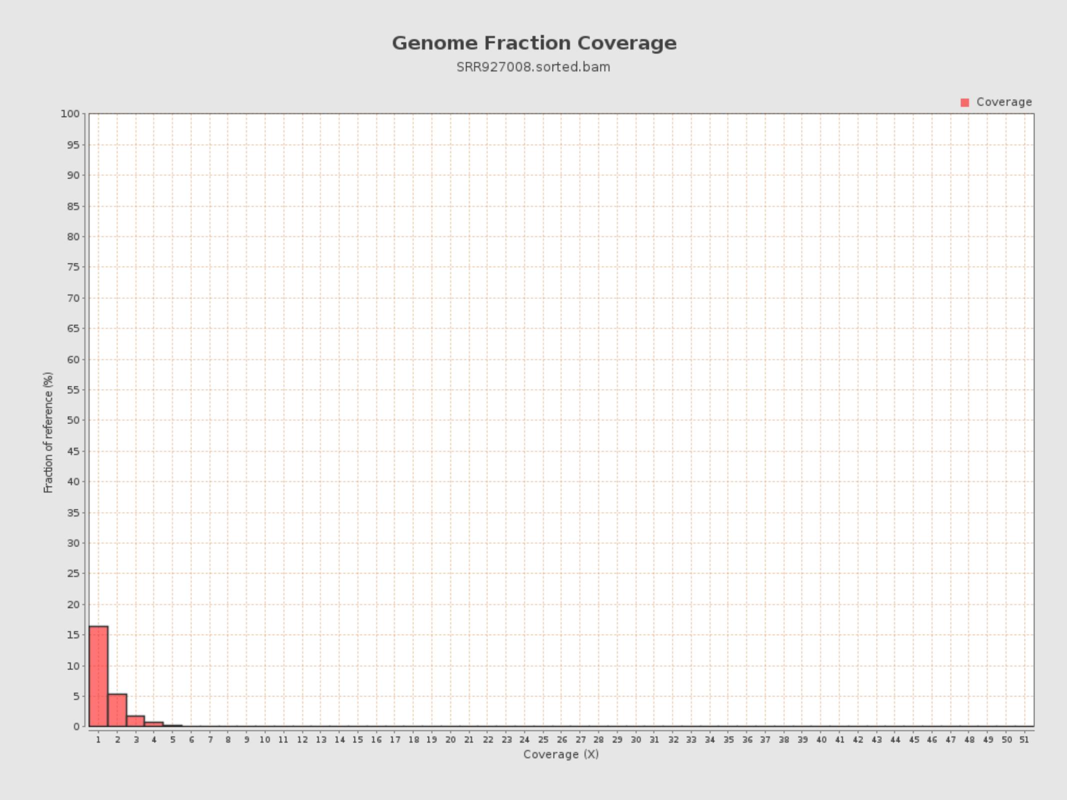
4. Results : Coverage Histogram



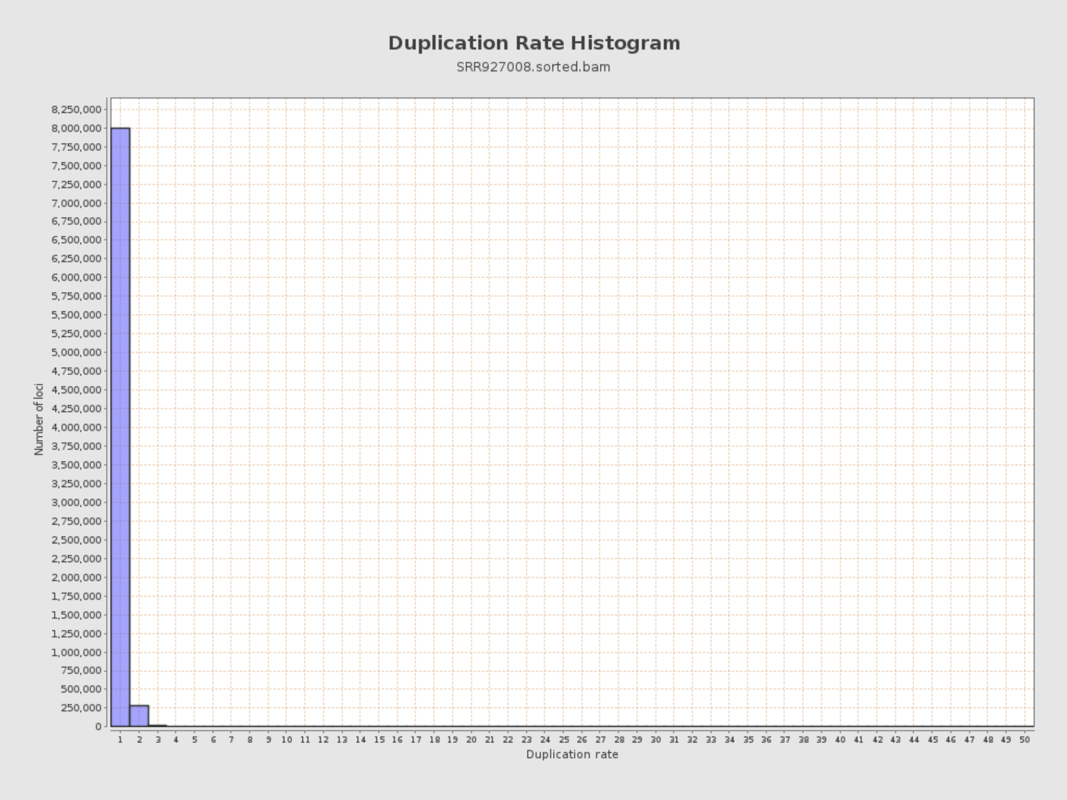
5. Results : Coverage Histogram (0-50X)



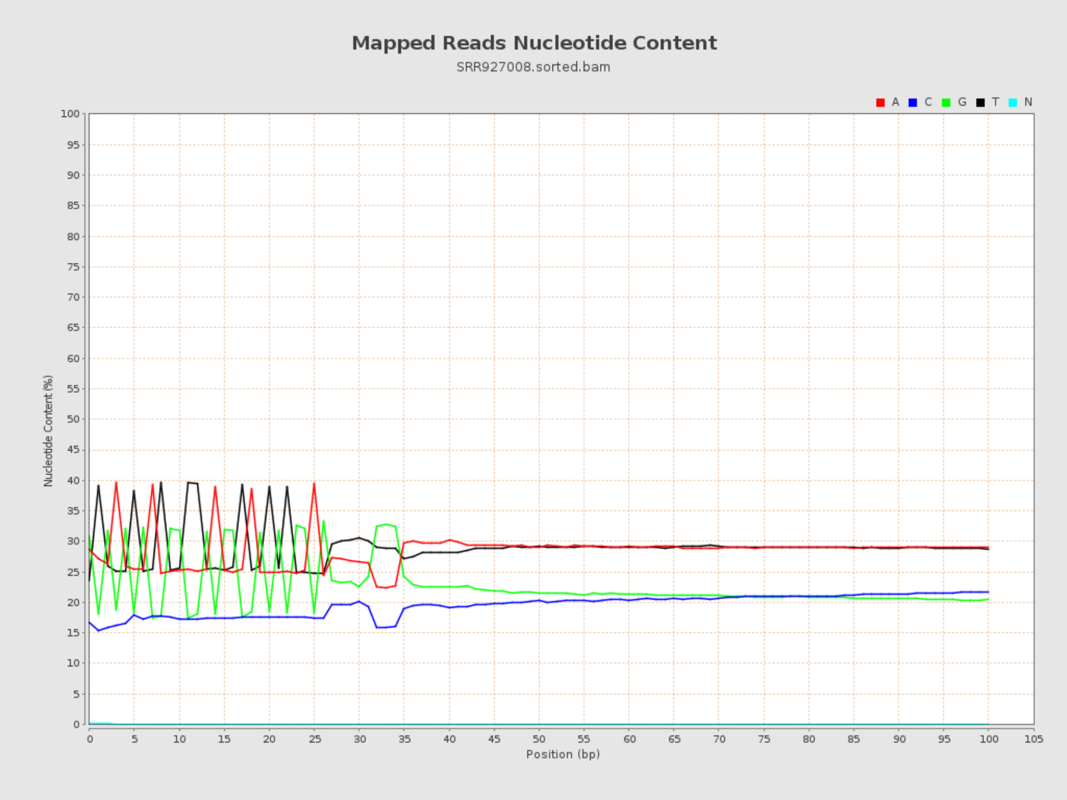
6. Results : Genome Fraction Coverage



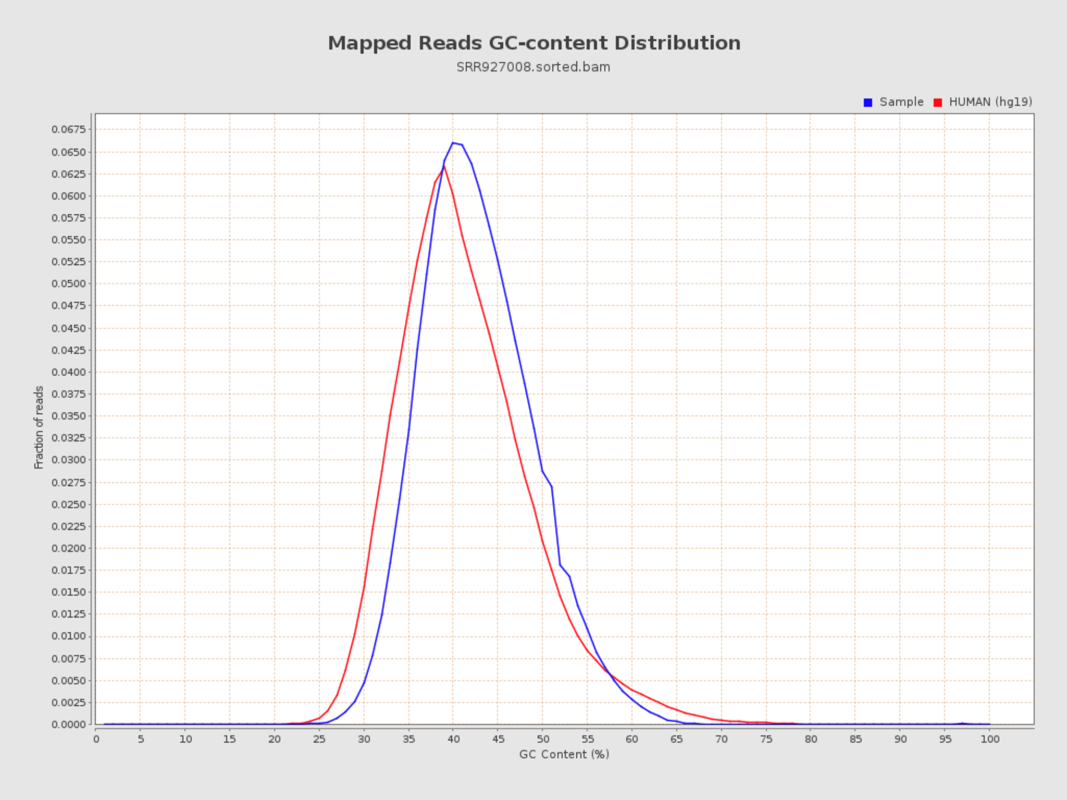
7. Results : Duplication Rate Histogram



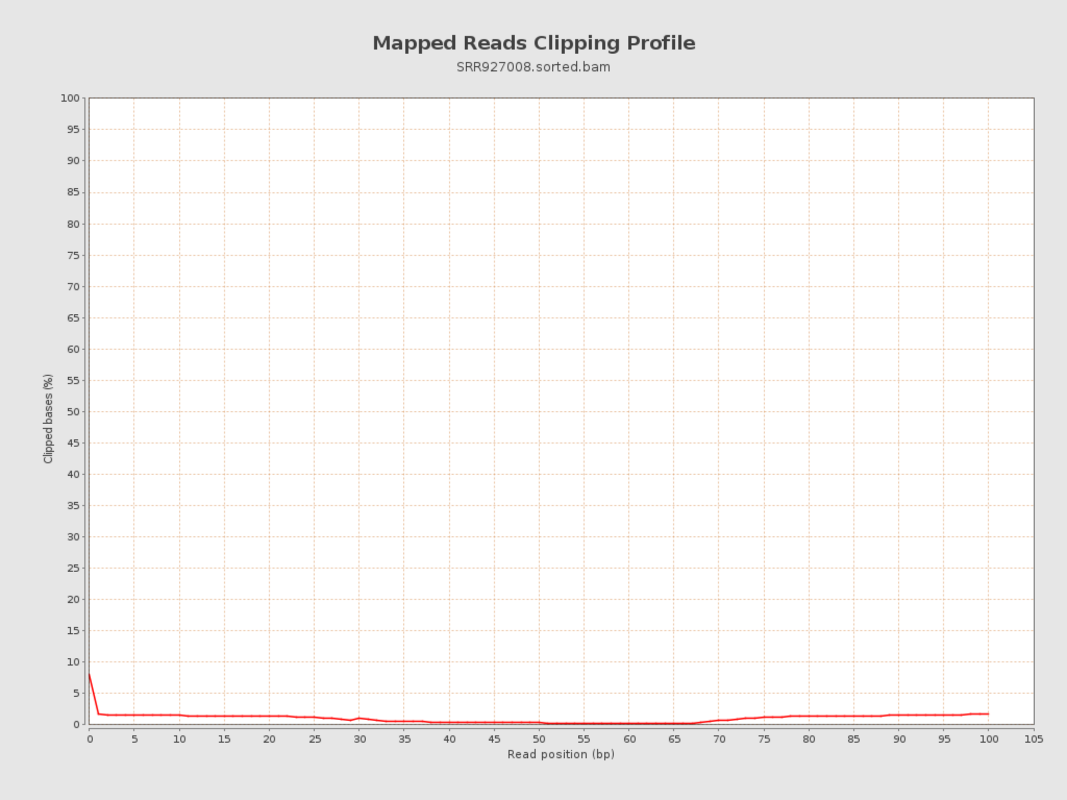
8. Results : Mapped Reads Nucleotide Content



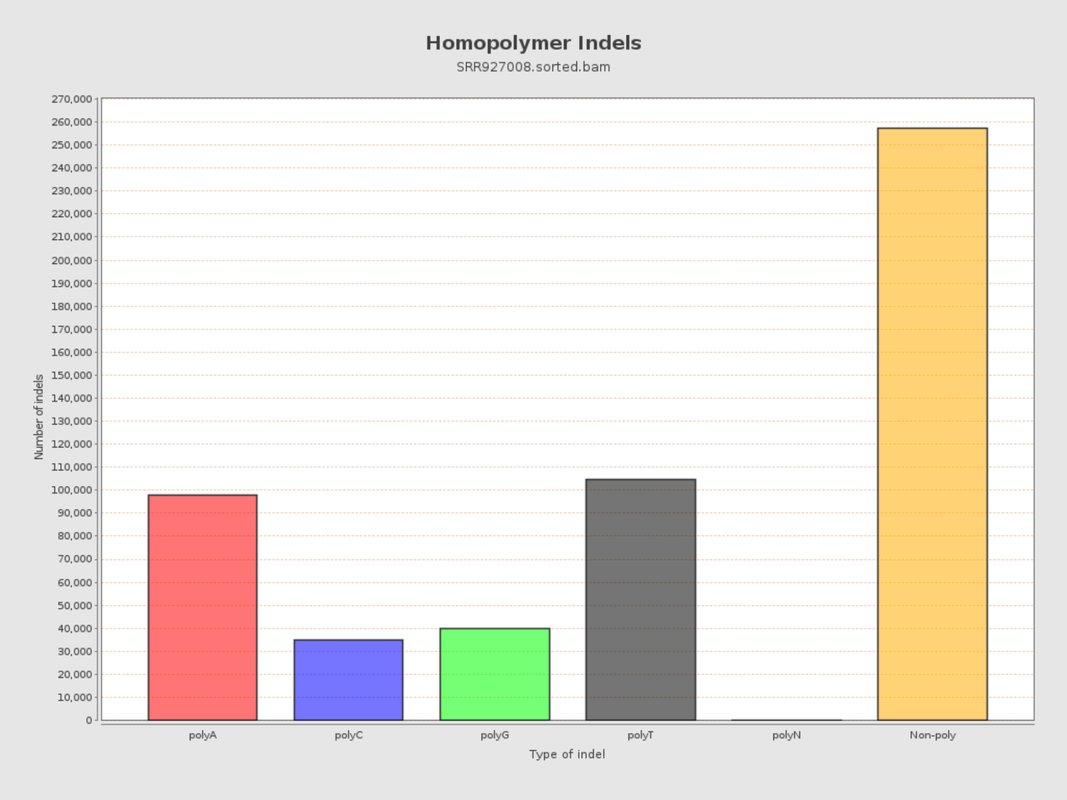
9. Results : Mapped Reads GC-content Distribution



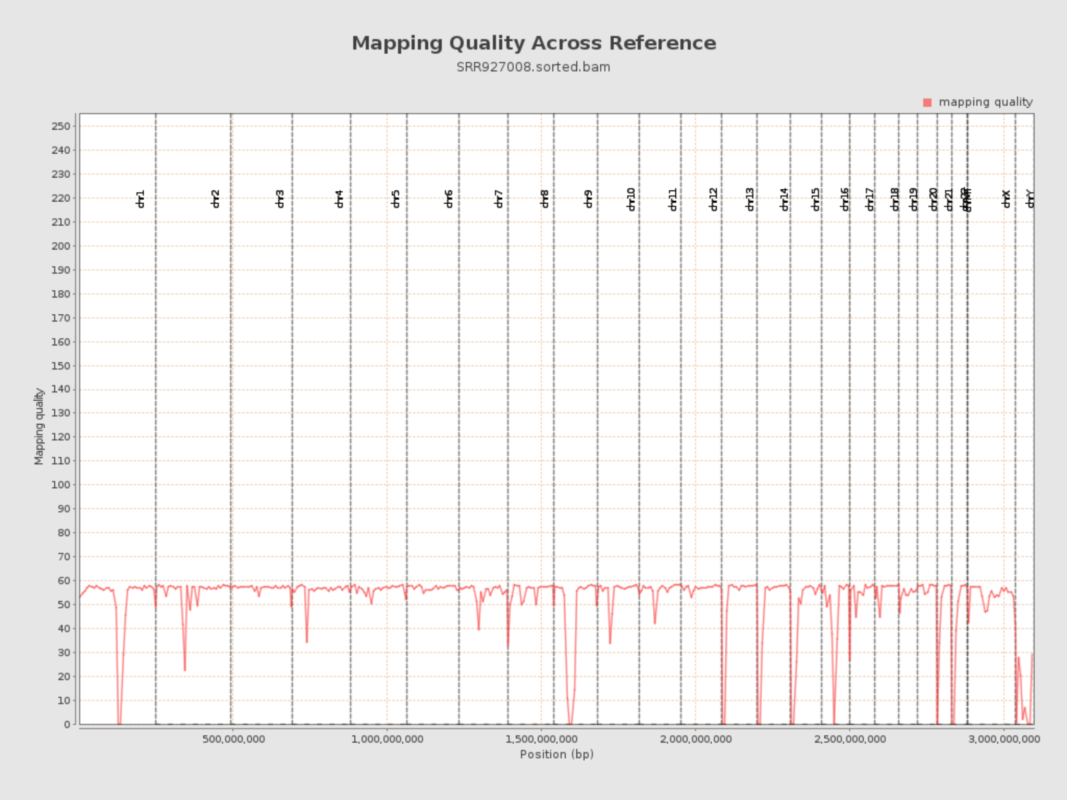
10. Results : Mapped Reads Clipping Profile



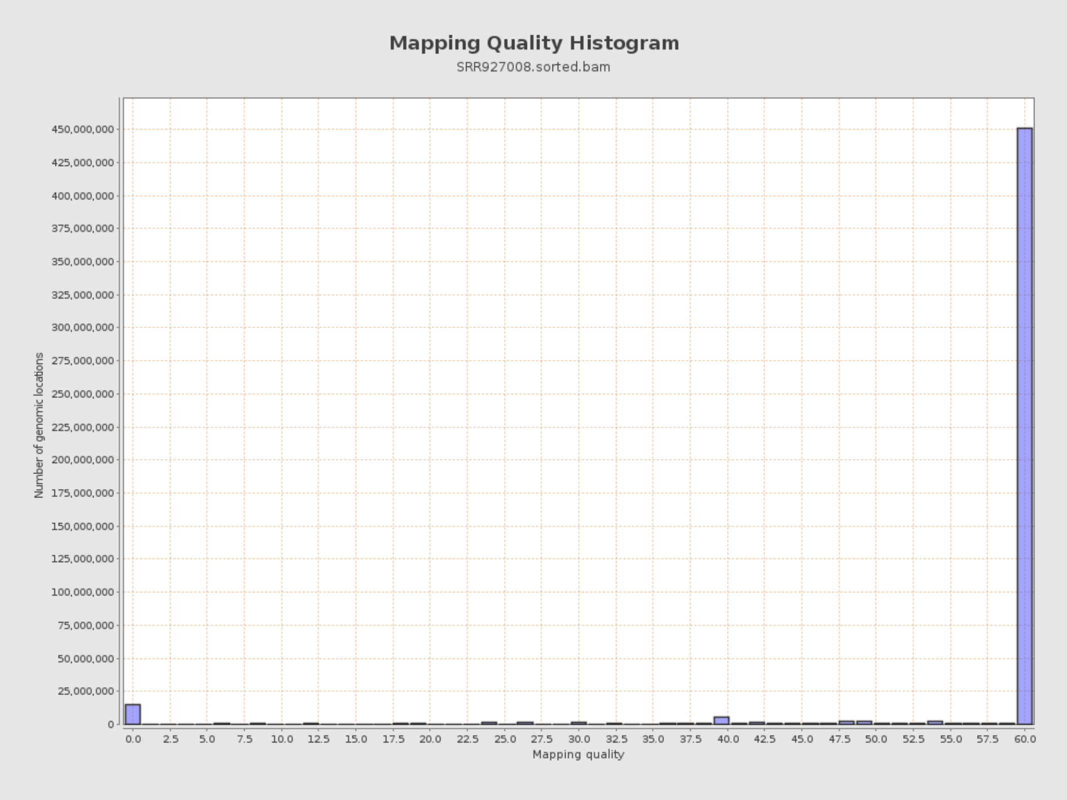
11. Results : Homopolymer Indels



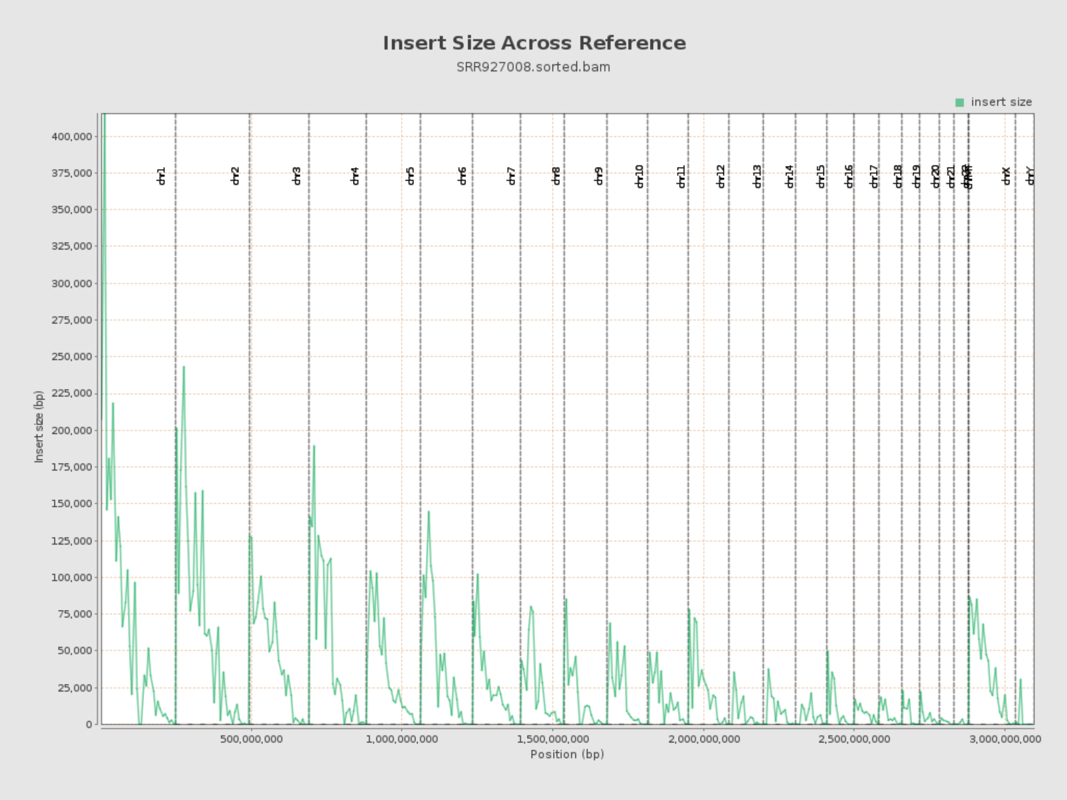
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram