Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 04:21:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927013.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_SRR927013 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927013_1.fastq.gz SRR927013_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 04:21:55 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927013.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,699,628
Mapped reads	18,228,353 / 97.48%
Unmapped reads	471,275 / 2.52%
Mapped paired reads	18,228,353 / 97.48%
Mapped reads, first in pair	9,127,685 / 48.81%
Mapped reads, second in pair	9,100,668 / 48.67%
Mapped reads, both in pair	17,968,016 / 96.09%
Mapped reads, singletons	260,337 / 1.39%
Secondary alignments	0
Supplementary alignments	575,048 / 3.08%
Read min/max/mean length	30 / 101 / 102.28
Duplicated reads (estimated)	1,234,553 / 6.6%
Duplication rate	5.25%
Clipped reads	7,767,668 / 41.54%

2.2. ACGT Content

Number/percentage of A's	473,911,307 / 28.52%
Number/percentage of C's	324,109,769 / 19.51%
Number/percentage of T's	483,171,098 / 29.08%
Number/percentage of G's	379,908,462 / 22.87%
Number/percentage of N's	311,118 / 0.02%

GC Percentage	42.37%

2.3. Coverage

Mean	0.5371
Standard Deviation	2.3336

2.4. Mapping Quality

Mean Mapping Quality	52.52

2.5. Insert size

Mean	316,723.39
Standard Deviation	5,472,548.19
P25/Median/P75	140 / 182 / 244

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	15,879,683
Insertions	289,765
Mapped reads with at least one insertion	1.56%
Deletions	873,899
Mapped reads with at least one deletion	4.67%
Homopolymer indels	51.8%

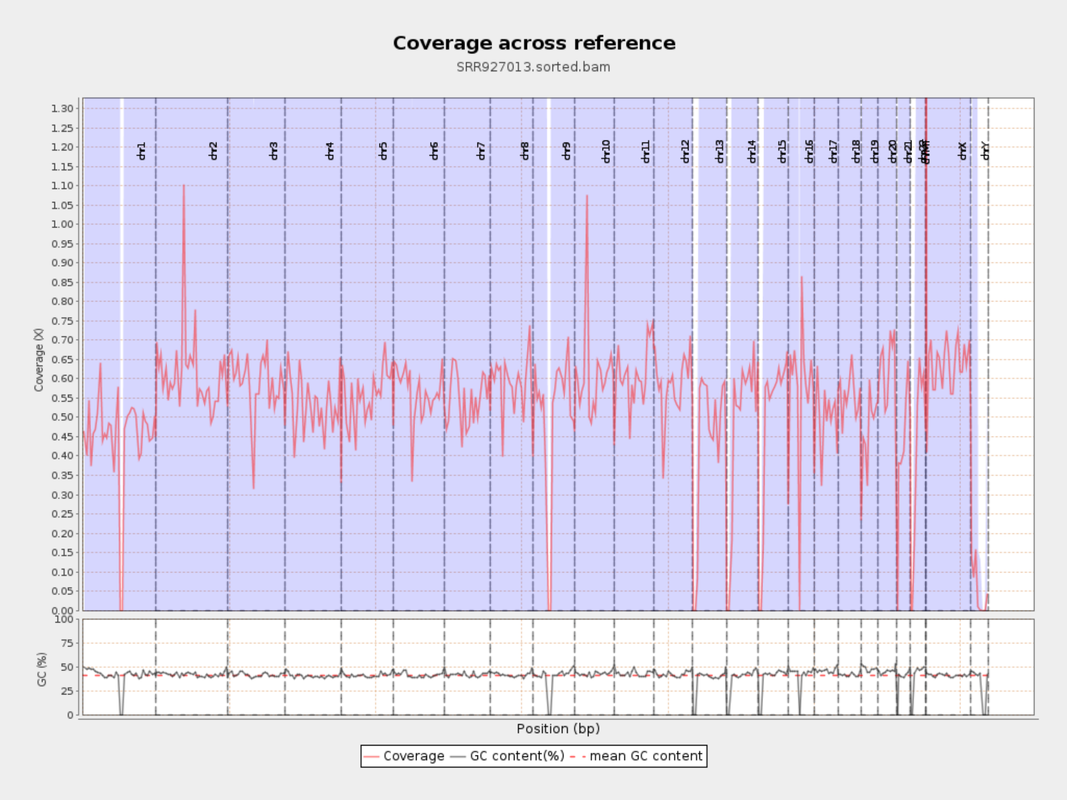
2.7. Chromosome stats

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

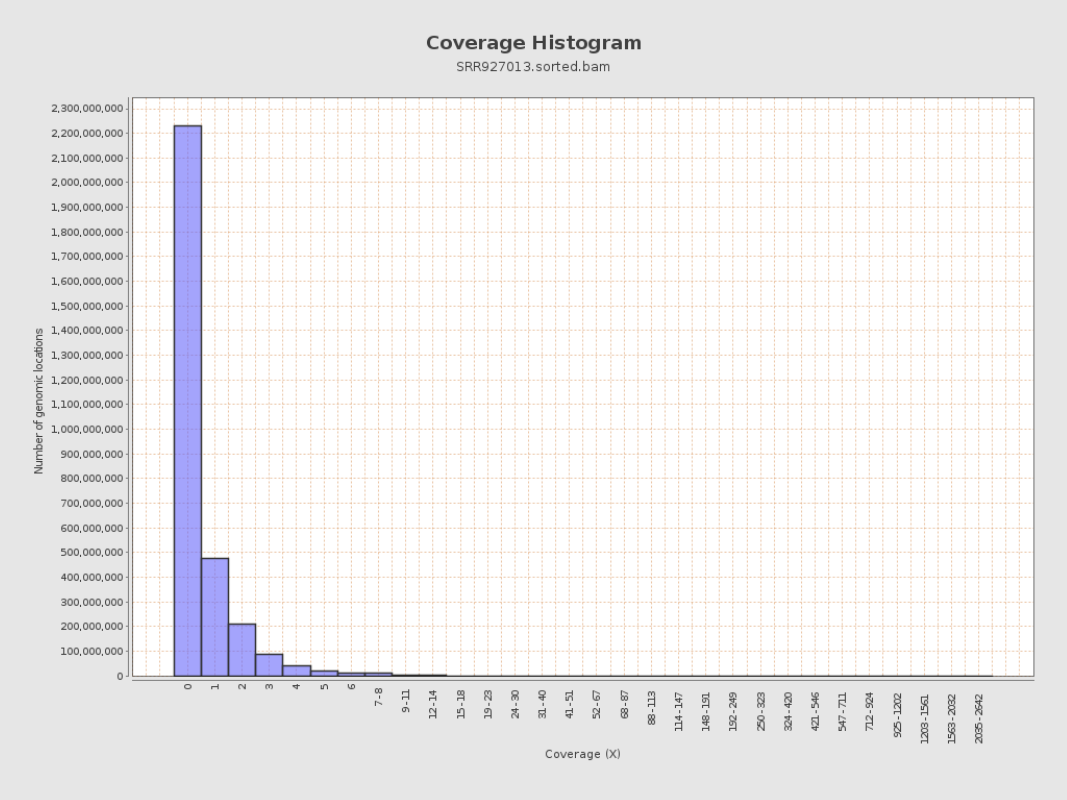
		bases	**coverage**	**deviation**
chr1	249250621	111529745	0.4475	2.8505
chr2	243199373	149418856	0.6144	3.7773
chr3	198022430	116223719	0.5869	1.2184
chr4	191154276	102395758	0.5357	1.9668
chr5	180915260	101214904	0.5595	1.1583
chr6	171115067	96407259	0.5634	1.4106
chr7	159138663	86920606	0.5462	1.6688
chr8	146364022	86554920	0.5914	1.4342
chr9	141213431	71173910	0.504	2.6855
chr10	135534747	82668794	0.6099	5.3039
chr11	135006516	82235721	0.6091	2.48
chr12	133851895	78517088	0.5866	1.2385
chr13	115169878	50482302	0.4383	1.0215
chr14	107349540	51593045	0.4806	1.1244
chr15	102531392	49176421	0.4796	1.1077
chr16	90354753	50867518	0.563	3.2289
chr17	81195210	41141565	0.5067	1.4017
chr18	78077248	43452445	0.5565	2.7442
chr19	59128983	27742611	0.4692	1.9385
chr20	63025520	39842149	0.6322	1.3707
chr21	48129895	20801475	0.4322	1.5549
chr22	51304566	20639665	0.4023	1.077
chrMT	16571	98483	5.9431	5.9106
chrX	155270560	98536209	0.6346	1.4625

chrY	59373566	3062415	0.0516	1.7827

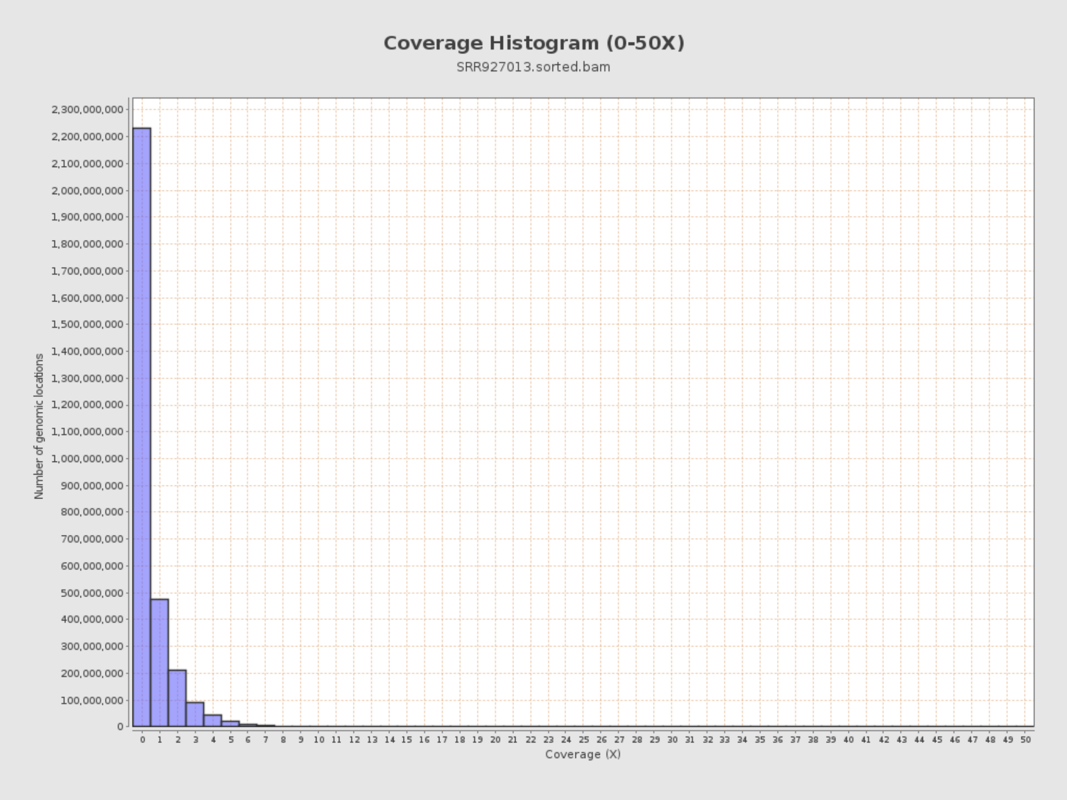
3. Results : Coverage across reference



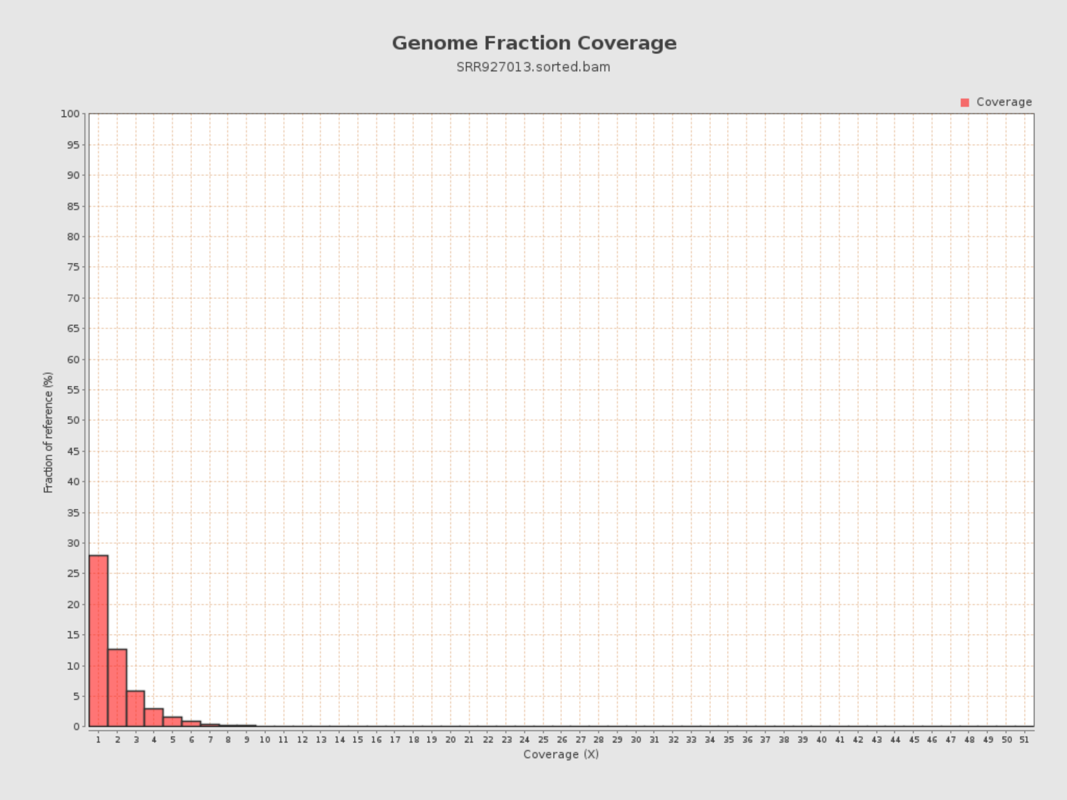
4. Results : Coverage Histogram



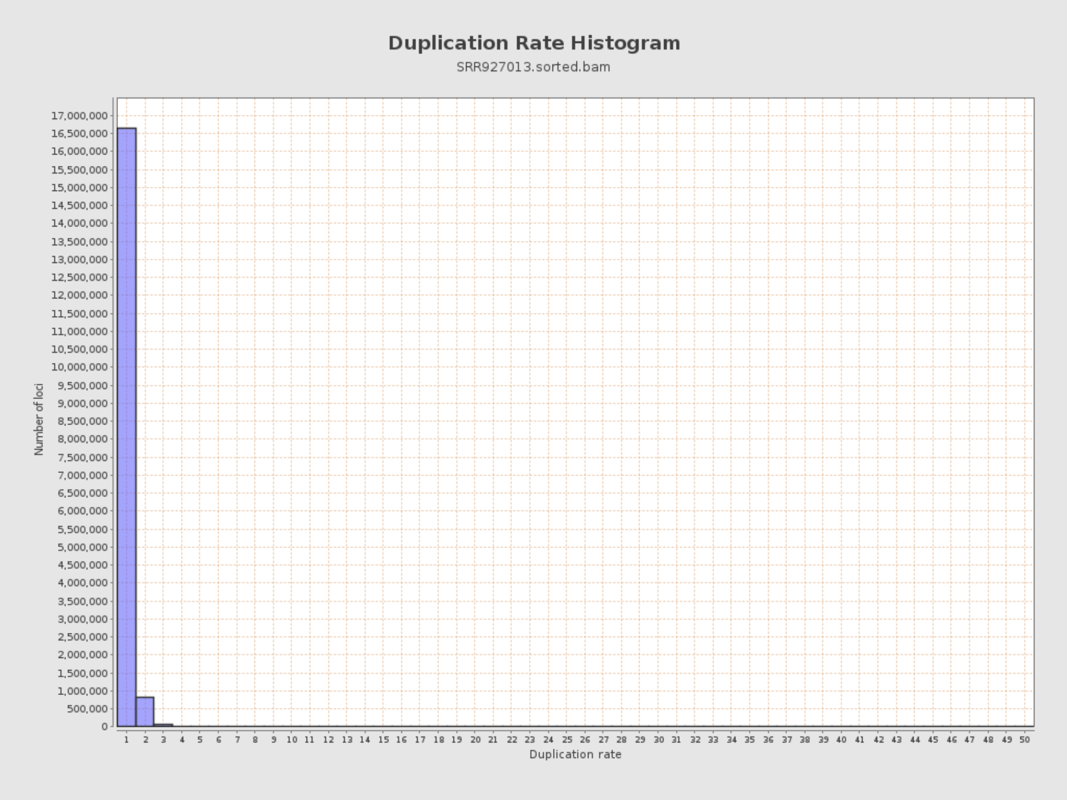
5. Results : Coverage Histogram (0-50X)



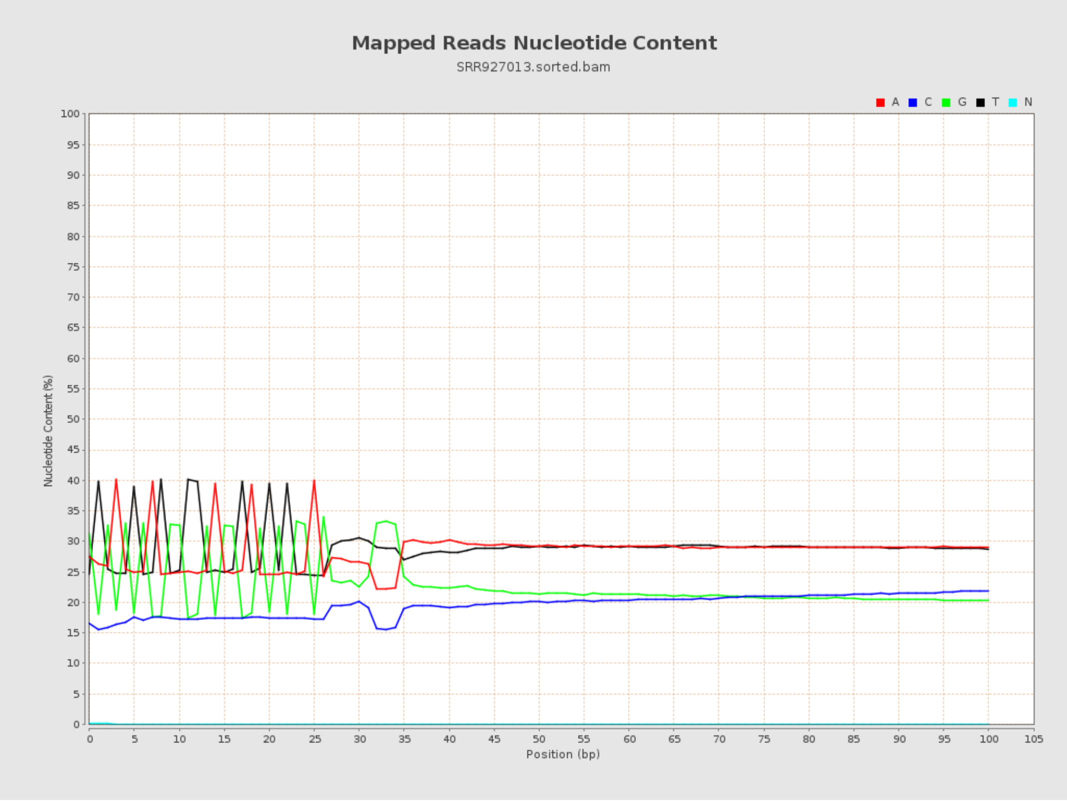
6. Results : Genome Fraction Coverage



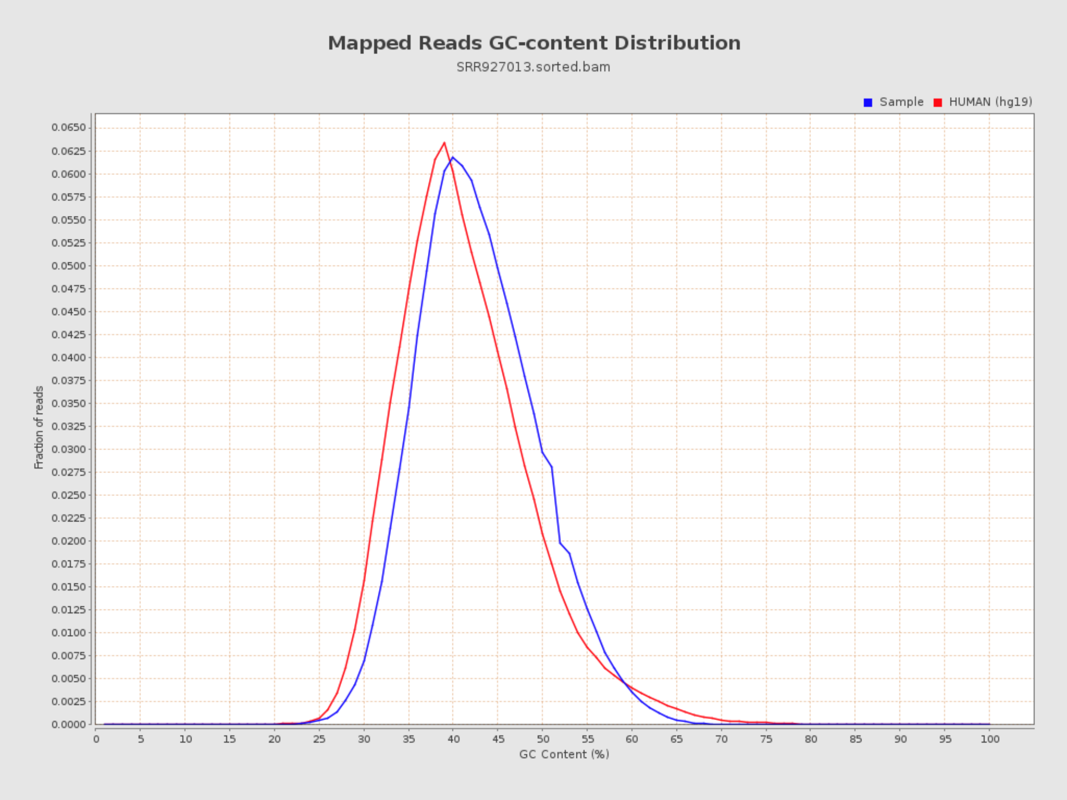
7. Results : Duplication Rate Histogram



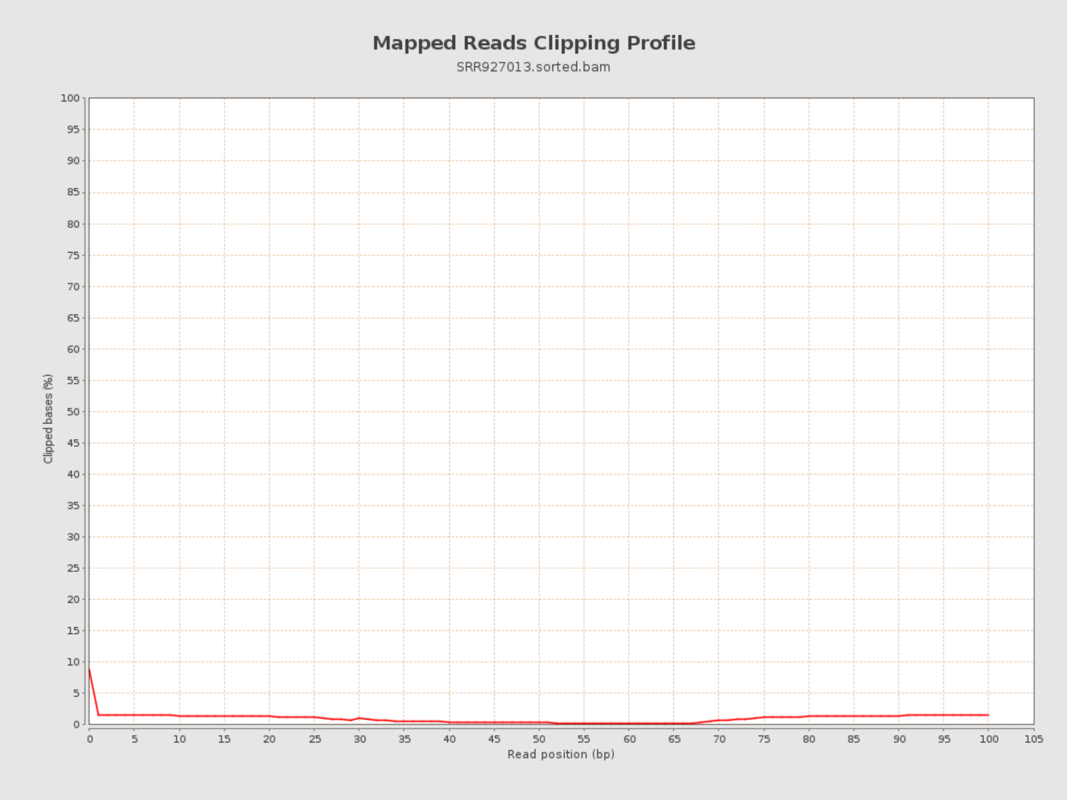
8. Results : Mapped Reads Nucleotide Content



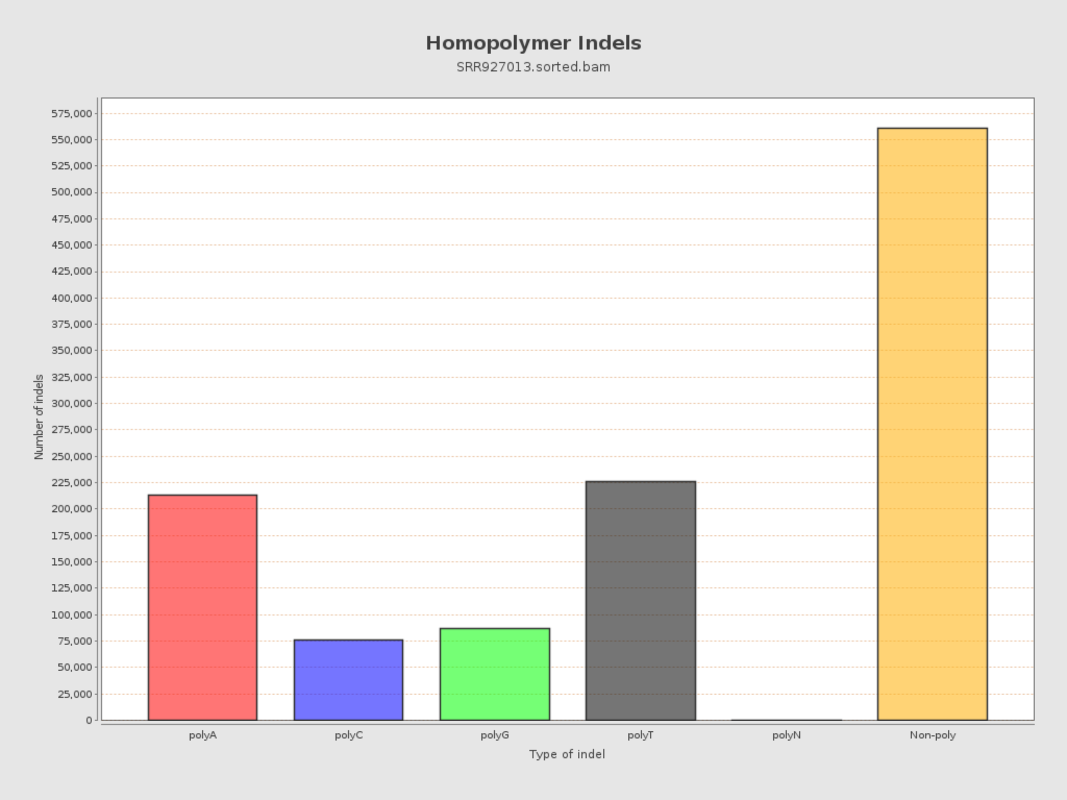
9. Results : Mapped Reads GC-content Distribution



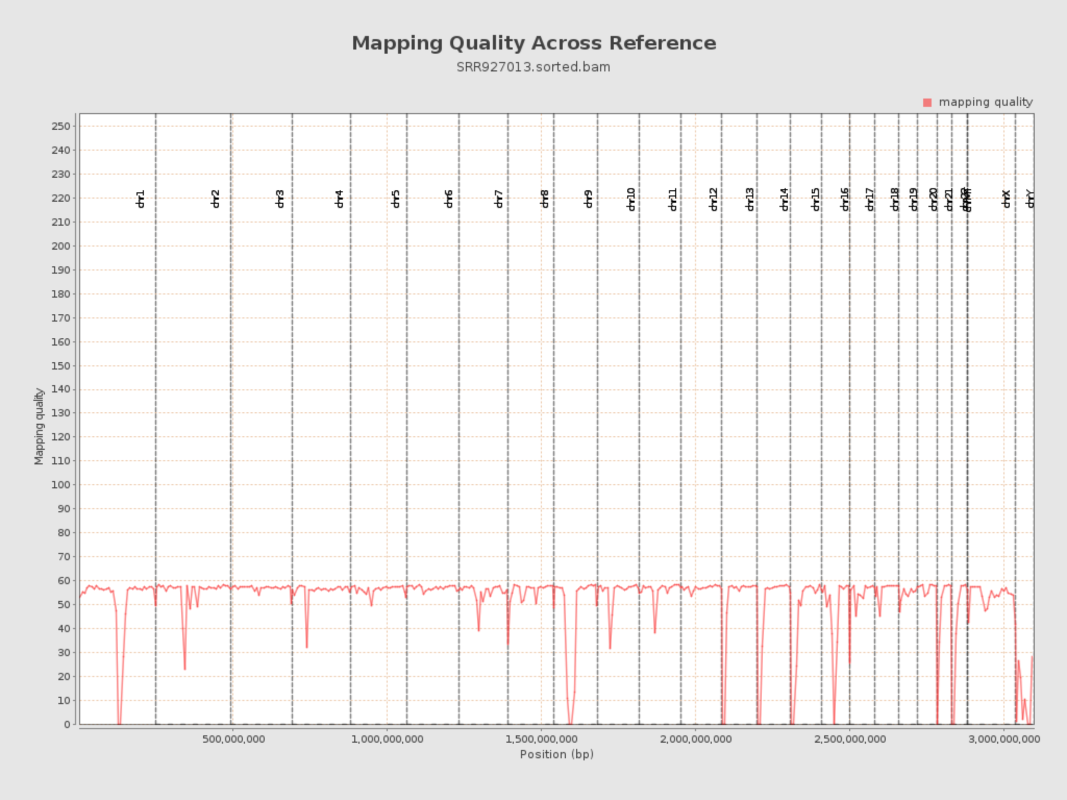
10. Results : Mapped Reads Clipping Profile



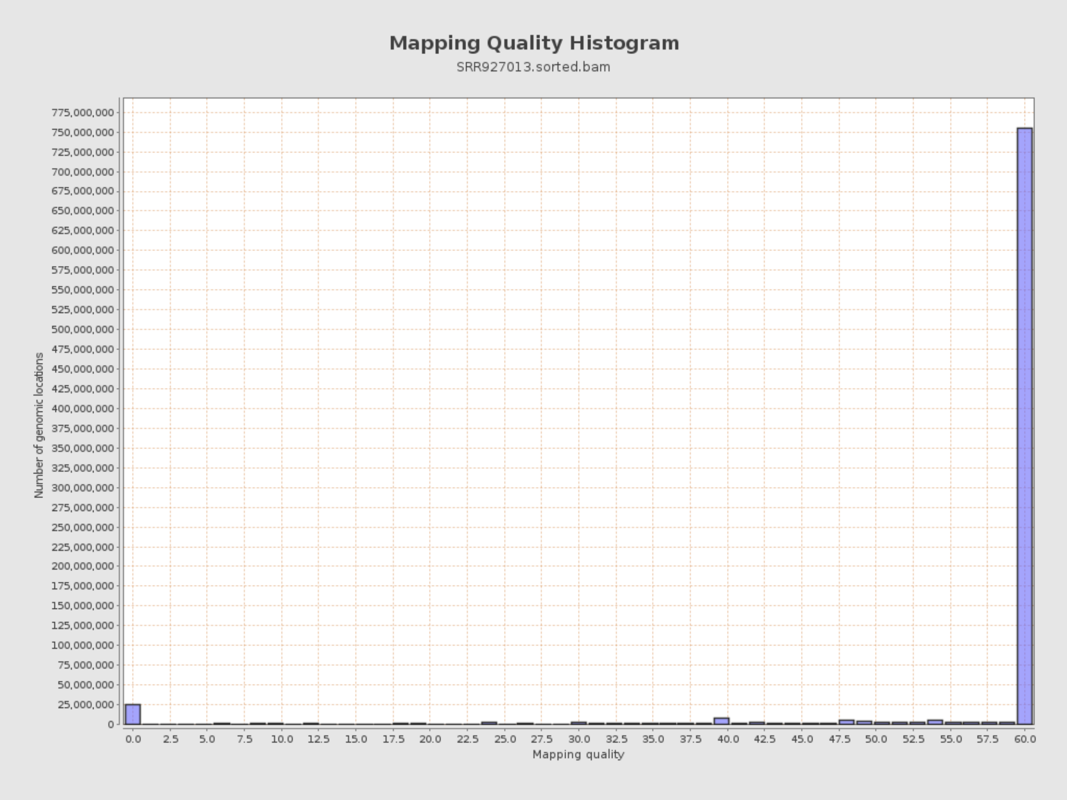
11. Results : Homopolymer Indels



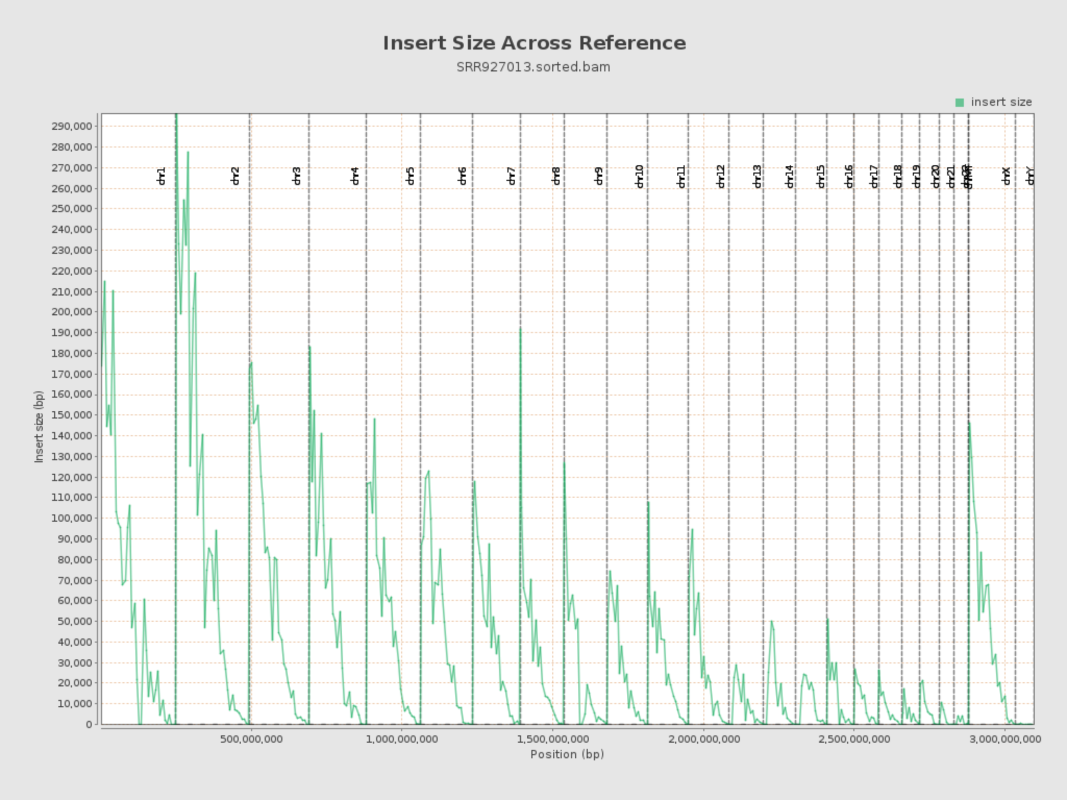
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram