

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 09:38:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173939.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_SRR10173939 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173939_1.fastq.gz SRR10173939_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 09:38:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173939.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,496,252
Mapped reads	7,322,688 / 97.68%
Unmapped reads	173,564 / 2.32%
Mapped paired reads	7,322,688 / 97.68%
Mapped reads, first in pair	3,661,887 / 48.85%
Mapped reads, second in pair	3,660,801 / 48.84%
Mapped reads, both in pair	7,213,716 / 96.23%
Mapped reads, singletons	108,972 / 1.45%
Secondary alignments	0
Supplementary alignments	994,515 / 13.27%
Read min/max/mean length	30 / 133 / 125.69
Duplicated reads (estimated)	5,954,206 / 79.43%
Duplication rate	65.09%
Clipped reads	3,905,630 / 52.1%

2.2. ACGT Content

Number/percentage of A's	246,593,129 / 29.75%
Number/percentage of C's	165,152,106 / 19.92%
Number/percentage of T's	244,717,897 / 29.52%
Number/percentage of G's	172,410,069 / 20.8%
Number/percentage of N's	6,156 / 0%

GC Percentage	40.73%
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2.3. Coverage

Mean	0.2679
Standard Deviation	4.972

2.4. Mapping Quality

Mean Mapping Quality	52.54
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2.5. Insert size

Mean	1,055,736.83
Standard Deviation	9,548,252.72
P25/Median/P75	105 / 154 / 238

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	7,239,445
Insertions	91,317
Mapped reads with at least one insertion	1.2%
Deletions	247,228
Mapped reads with at least one deletion	3.29%
Homopolymer indels	40.94%

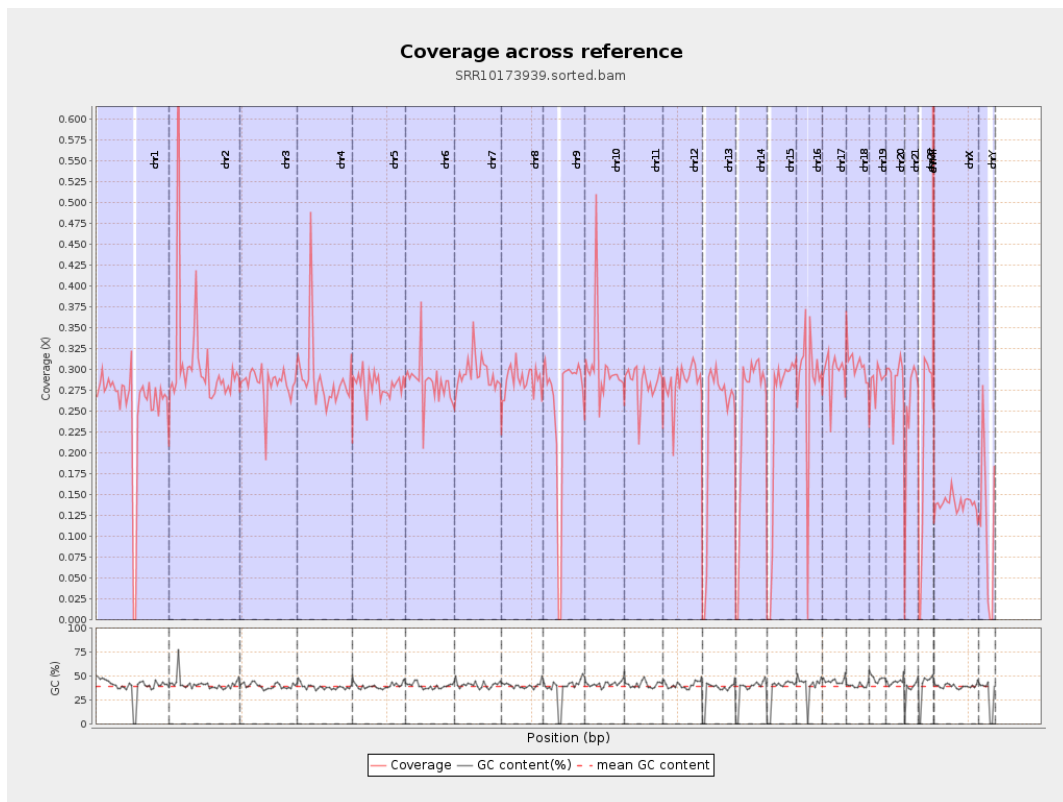
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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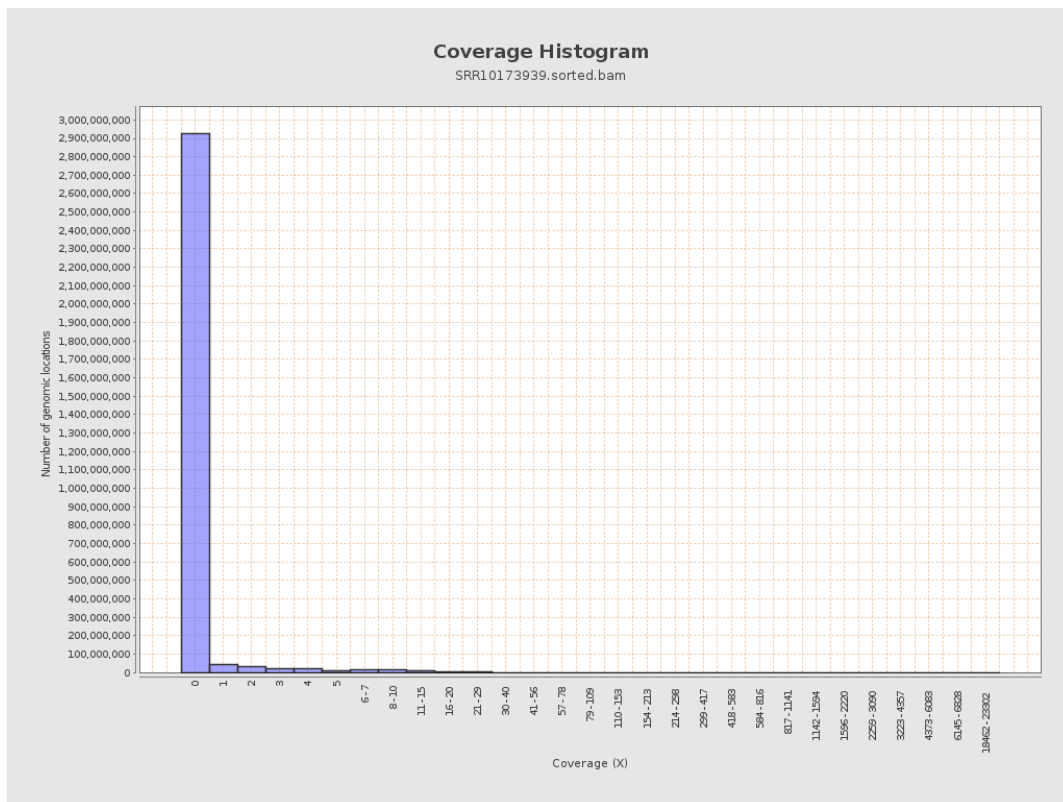
		bases	coverage	deviation
chr1	249250621	63645898	0.2553	2.3538
chr2	243199373	75039194	0.3086	16.2868
chr3	198022430	55909902	0.2823	1.6308
chr4	191154276	55068881	0.2881	2.3025
chr5	180915260	50738729	0.2805	1.6295
chr6	171115067	48502147	0.2834	1.9341
chr7	159138663	47026092	0.2955	2.5374
chr8	146364022	41974536	0.2868	2.5796
chr9	141213431	36107761	0.2557	2.2095
chr10	135534747	41003841	0.3025	2.6589
chr11	135006516	38262323	0.2834	1.6945
chr12	133851895	38100794	0.2846	1.7308
chr13	115169878	26823762	0.2329	1.4843
chr14	107349540	26528935	0.2471	1.5583
chr15	102531392	24299244	0.237	1.5281
chr16	90354753	25516625	0.2824	2.0807
chr17	81195210	23951178	0.295	1.8445
chr18	78077248	23930540	0.3065	3.1079
chr19	59128983	16886348	0.2856	1.9655
chr20	63025520	18077719	0.2868	1.7228
chr21	48129895	12001338	0.2494	2.0041
chr22	51304566	10666698	0.2079	1.6916
chrMT	16571	1468116	88.5955	76.3359
chrX	155270560	21565577	0.1389	1.1521

chrY	59373566	6368688	0.1073	1.6956
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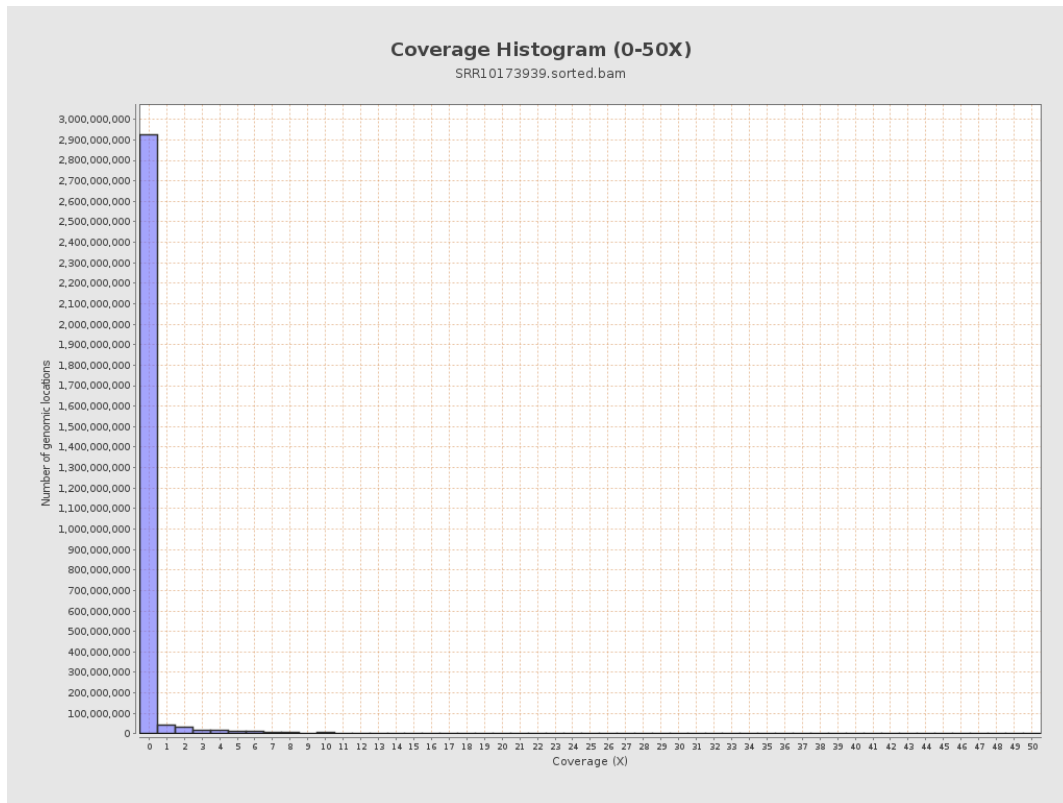
3. Results : Coverage across reference



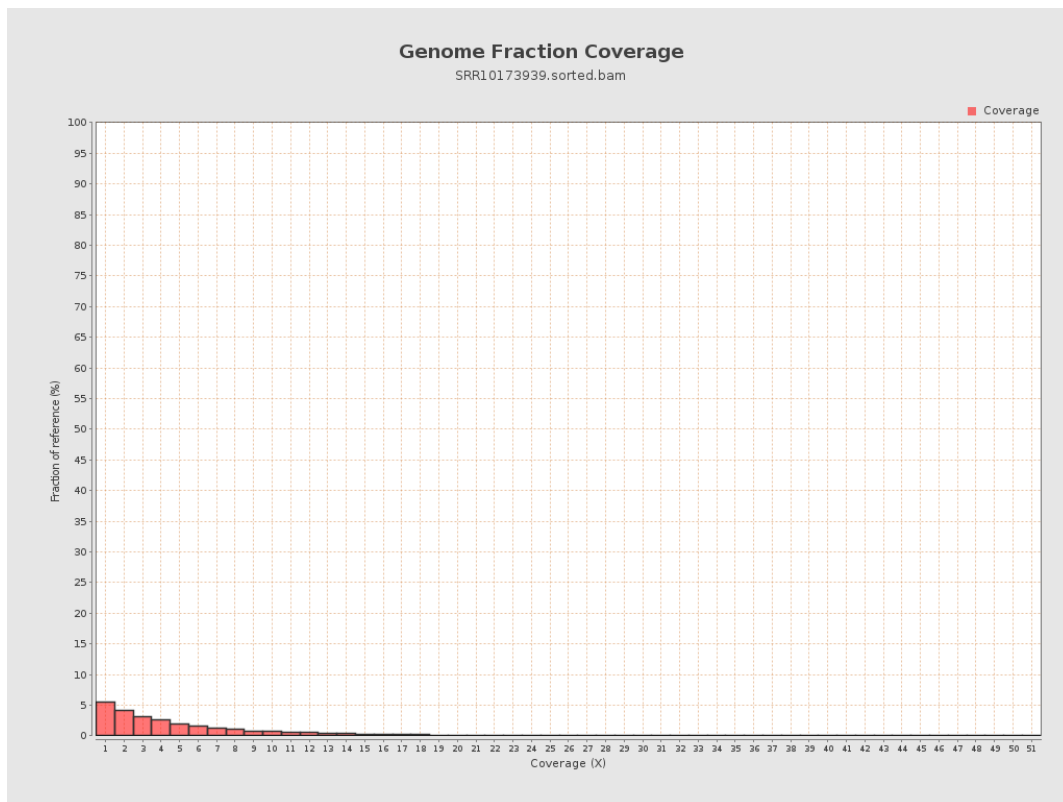
4. Results : Coverage Histogram



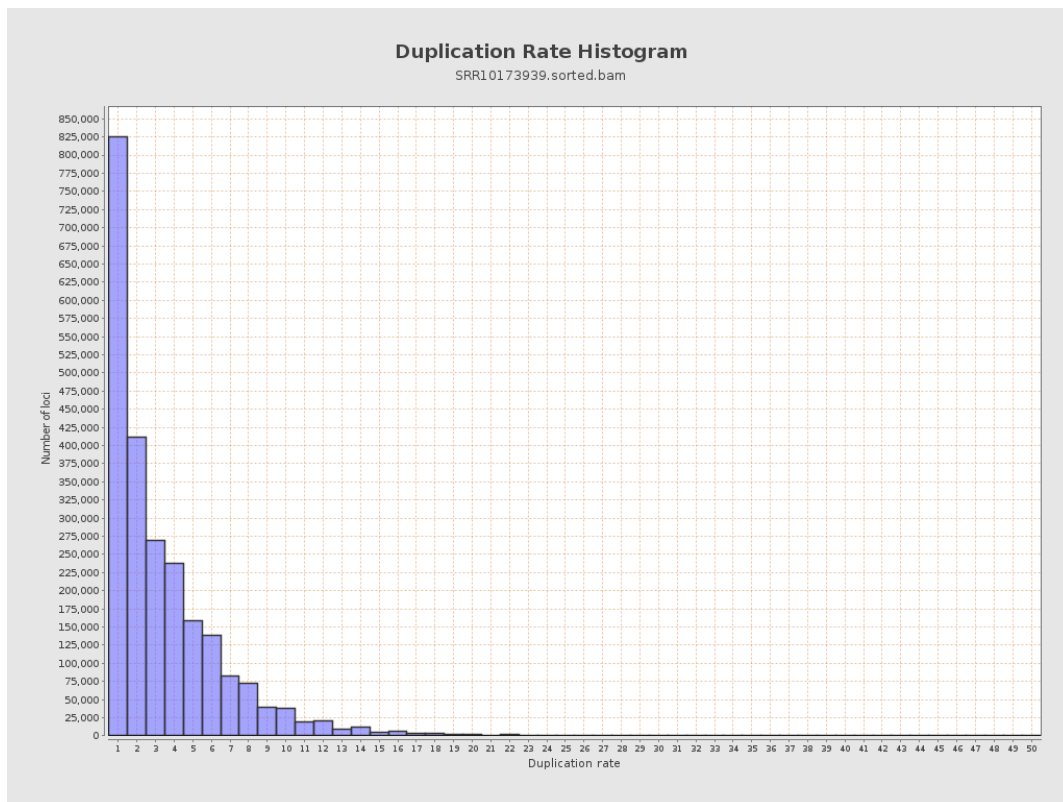
5. Results : Coverage Histogram (0-50X)



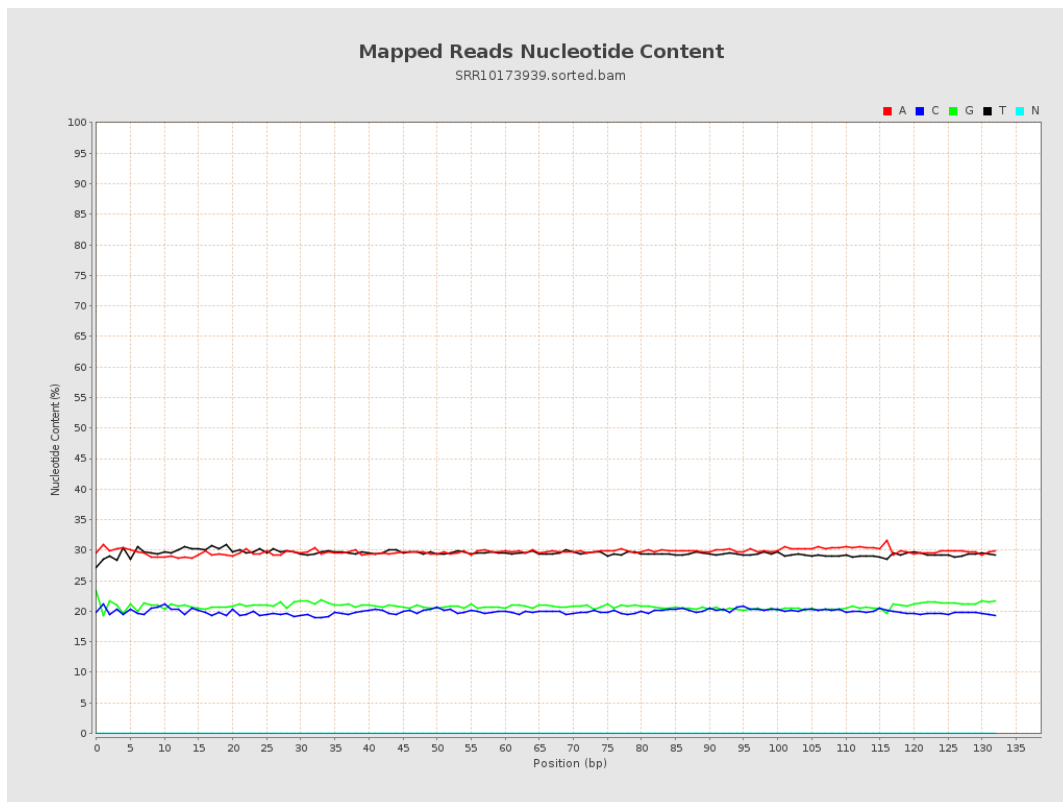
6. Results : Genome Fraction Coverage



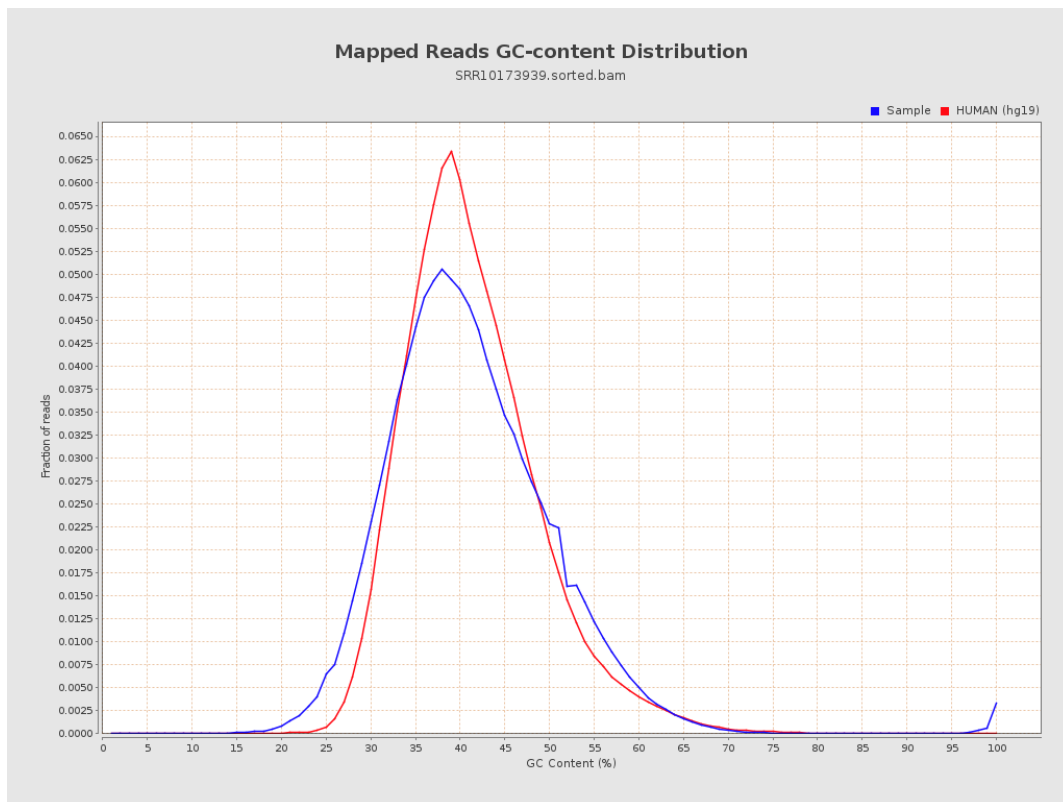
7. Results : Duplication Rate Histogram



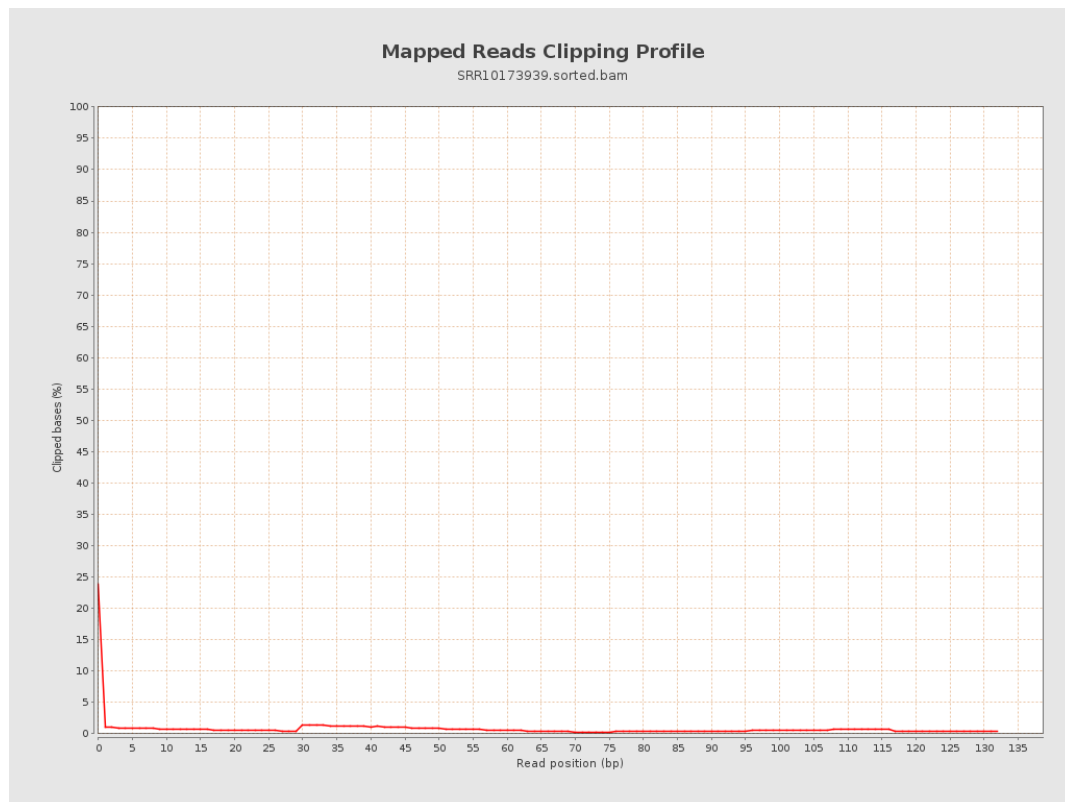
8. Results : Mapped Reads Nucleotide Content



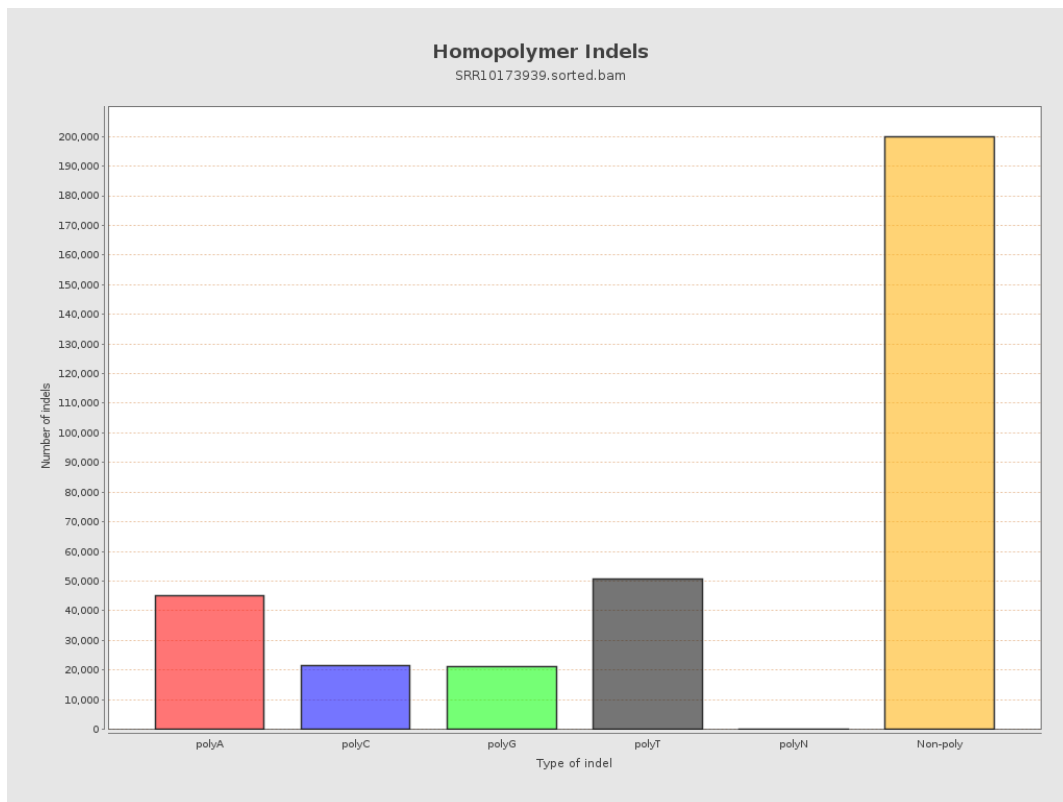
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



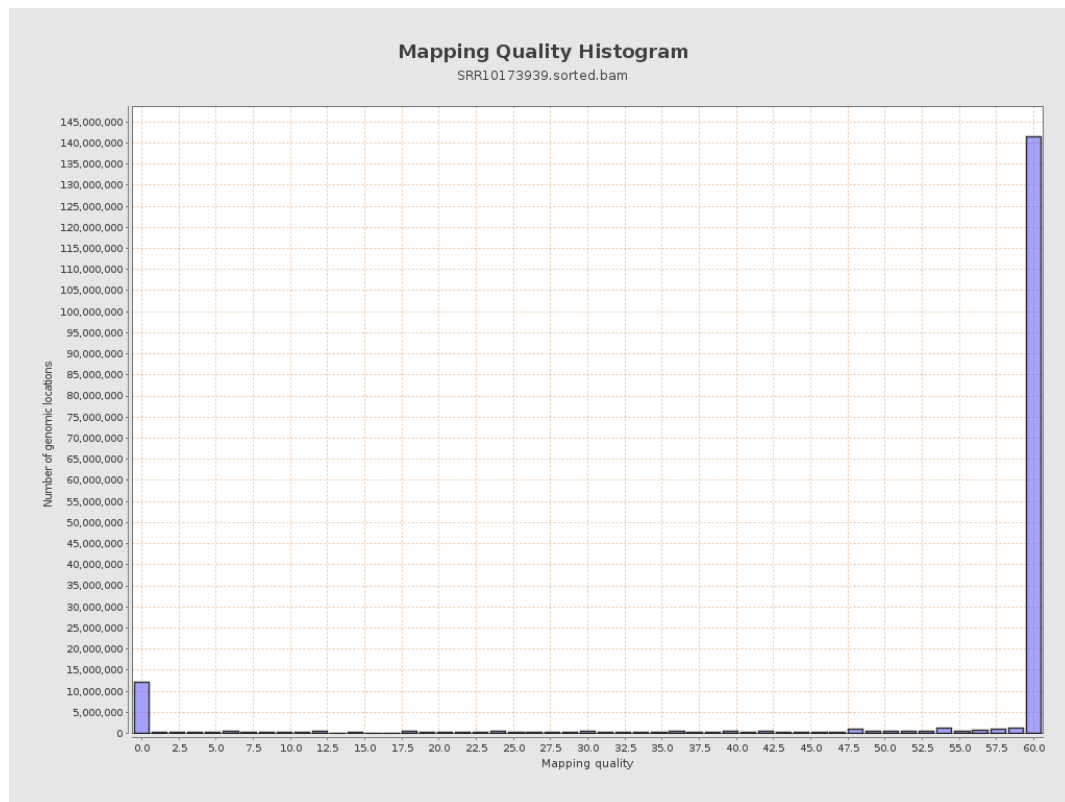
11. Results : Homopolymer Indels



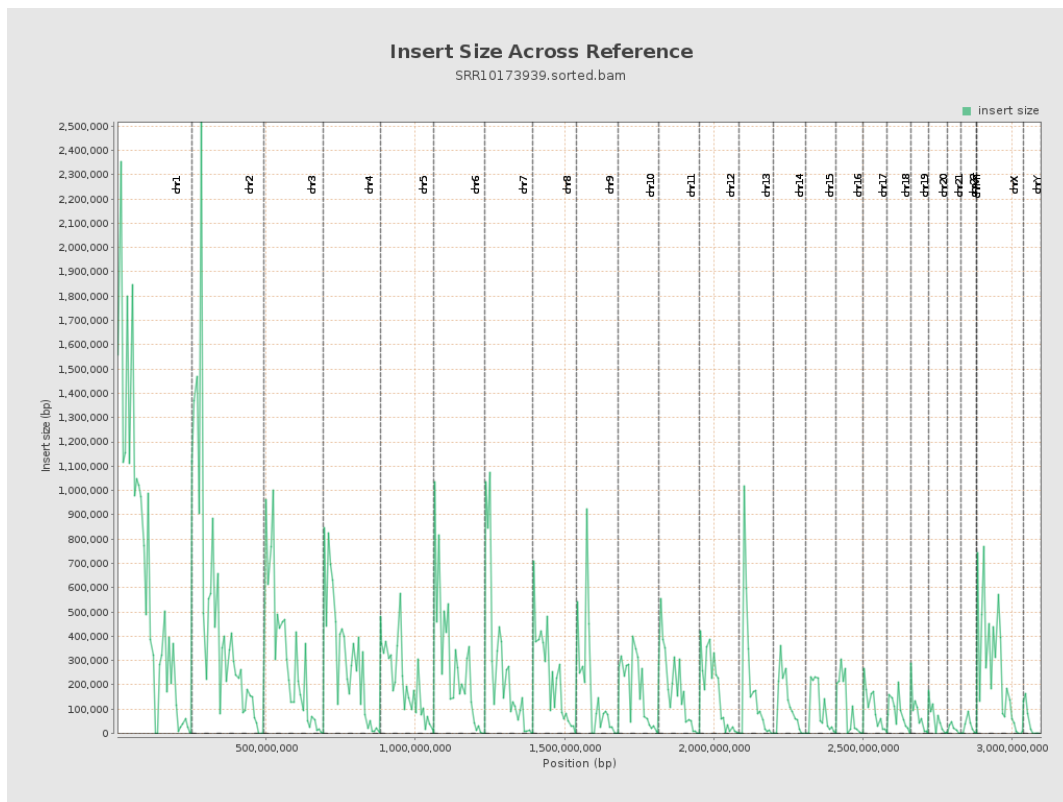
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

