

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 22:33:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173853.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_SRR10173853 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173853_1.fastq.gz SRR10173853_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 22:32:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173853.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,803,276
Mapped reads	9,541,517 / 97.33%
Unmapped reads	261,759 / 2.67%
Mapped paired reads	9,541,517 / 97.33%
Mapped reads, first in pair	4,781,052 / 48.77%
Mapped reads, second in pair	4,760,465 / 48.56%
Mapped reads, both in pair	9,365,138 / 95.53%
Mapped reads, singletons	176,379 / 1.8%
Secondary alignments	0
Supplementary alignments	953,854 / 9.73%
Read min/max/mean length	30 / 133 / 128.23
Duplicated reads (estimated)	7,335,410 / 74.83%
Duplication rate	64.75%
Clipped reads	3,951,633 / 40.31%

2.2. ACGT Content

Number/percentage of A's	340,907,340 / 30.28%
Number/percentage of C's	218,048,197 / 19.37%
Number/percentage of T's	340,488,859 / 30.25%
Number/percentage of G's	226,230,434 / 20.1%
Number/percentage of N's	13,805 / 0%

GC Percentage	39.47%
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2.3. Coverage

Mean	0.3638
Standard Deviation	5.1185

2.4. Mapping Quality

Mean Mapping Quality	52.72
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2.5. Insert size

Mean	815,473.81
Standard Deviation	8,183,374.77
P25/Median/P75	145 / 202 / 288

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	11,401,377
Insertions	115,655
Mapped reads with at least one insertion	1.17%
Deletions	250,636
Mapped reads with at least one deletion	2.56%
Homopolymer indels	43.22%

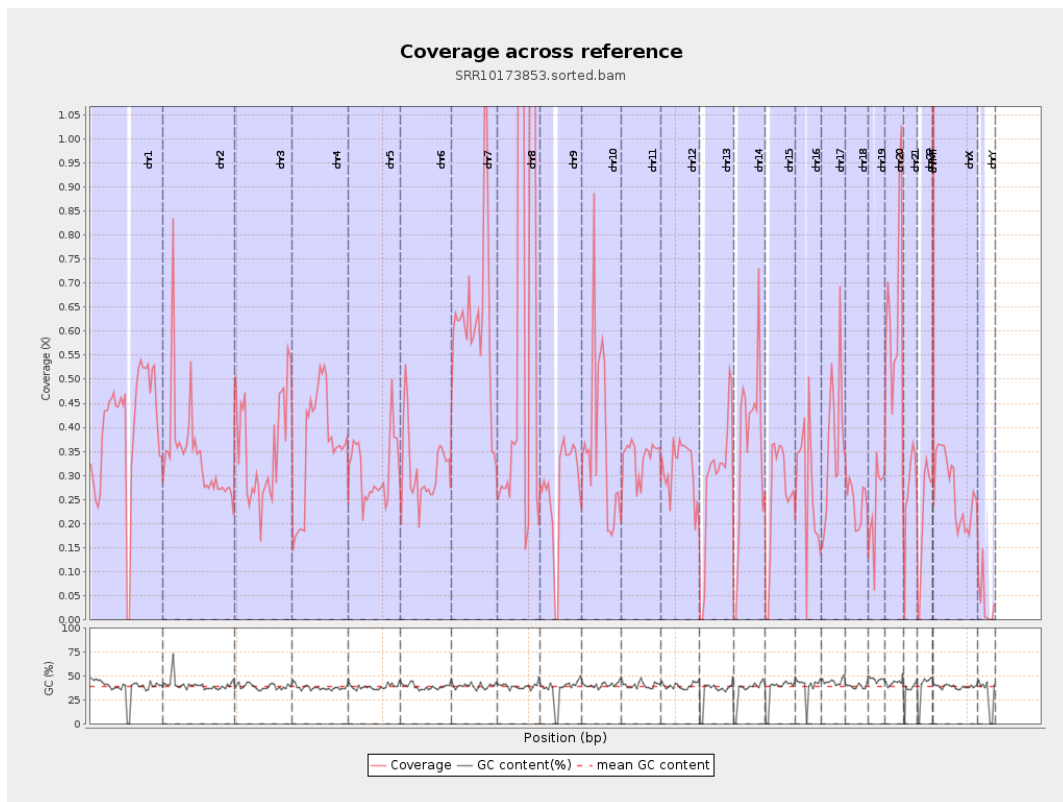
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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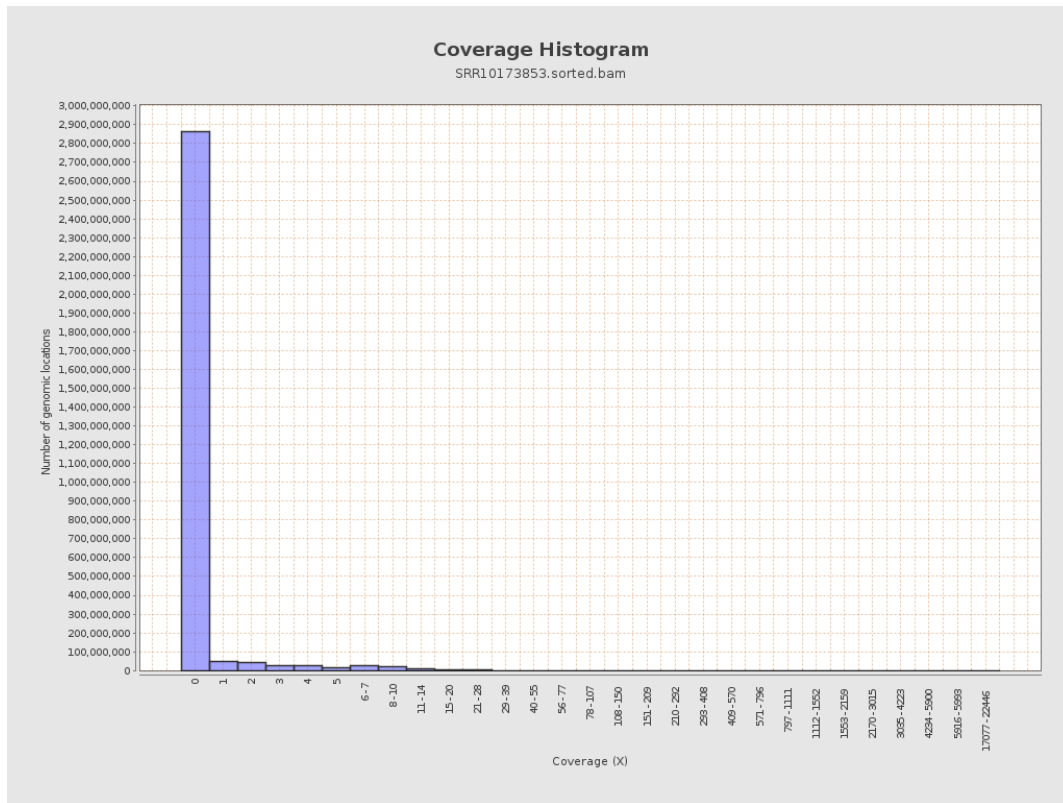
		bases	coverage	deviation
chr1	249250621	99134456	0.3977	2.6753
chr2	243199373	82521953	0.3393	15.6382
chr3	198022430	71150729	0.3593	1.7042
chr4	191154276	69734971	0.3648	2.4749
chr5	180915260	56077336	0.31	1.5612
chr6	171115067	53816073	0.3145	1.7214
chr7	159138663	97521227	0.6128	5.1808
chr8	146364022	120837643	0.8256	3.8777
chr9	141213431	38768734	0.2745	2.1959
chr10	135534747	49881867	0.368	5.9828
chr11	135006516	45531588	0.3373	1.739
chr12	133851895	42088910	0.3144	1.6051
chr13	115169878	33860039	0.294	1.5381
chr14	107349540	38995703	0.3633	1.74
chr15	102531392	26172920	0.2553	1.4243
chr16	90354753	24868630	0.2752	2.3934
chr17	81195210	29538688	0.3638	2.0712
chr18	78077248	19430574	0.2489	2.9421
chr19	59128983	14172880	0.2397	2.1702
chr20	63025520	41495390	0.6584	2.3697
chr21	48129895	13016563	0.2704	1.7766
chr22	51304566	11068046	0.2157	1.2582
chrMT	16571	2741142	165.418	109.4946
chrX	155270560	41755682	0.2689	1.489

chrY	59373566	2128112	0.0358	1.4413
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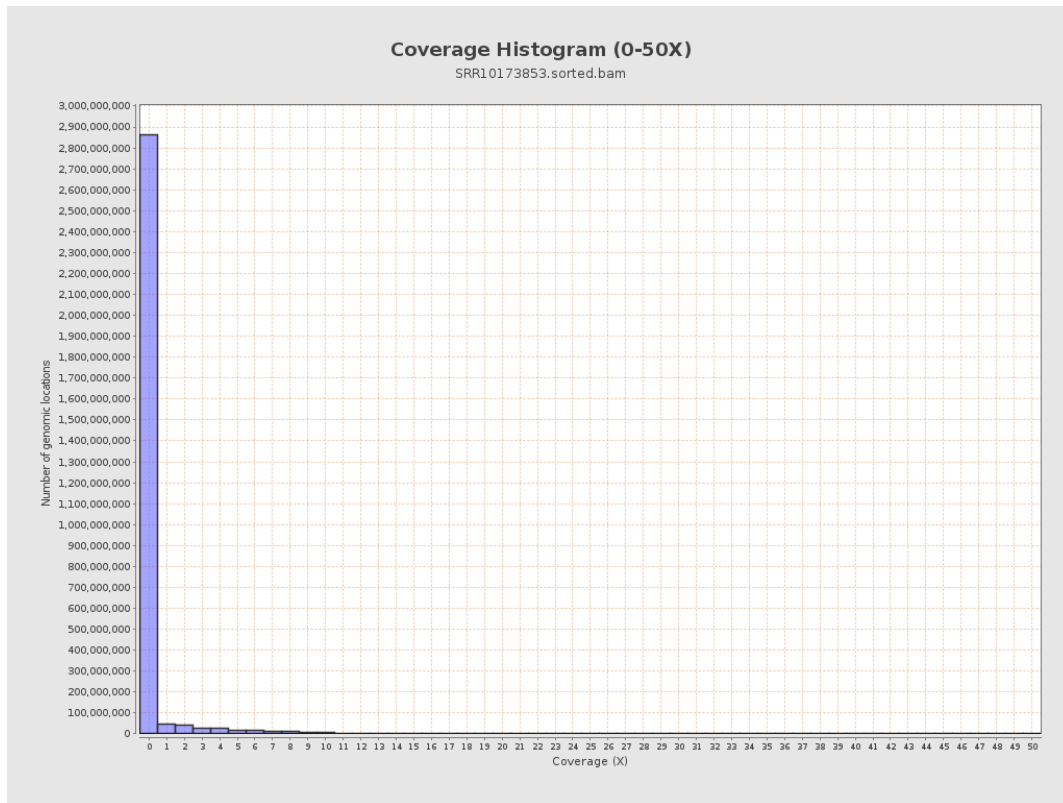
3. Results : Coverage across reference



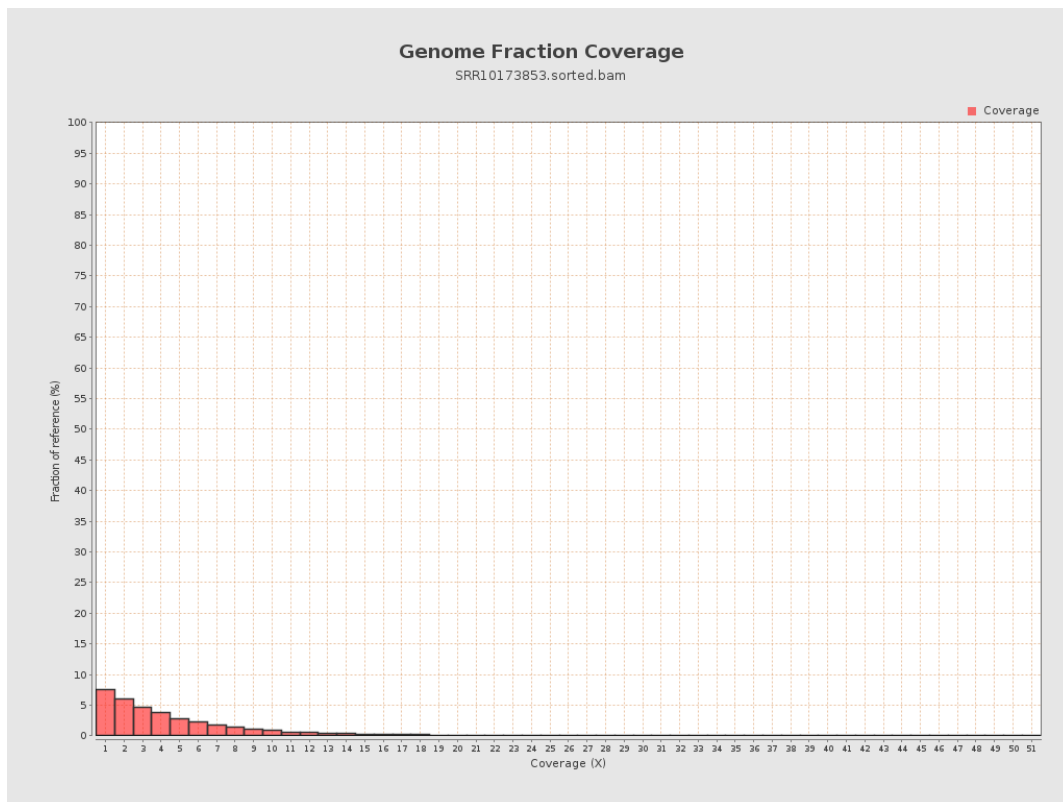
4. Results : Coverage Histogram



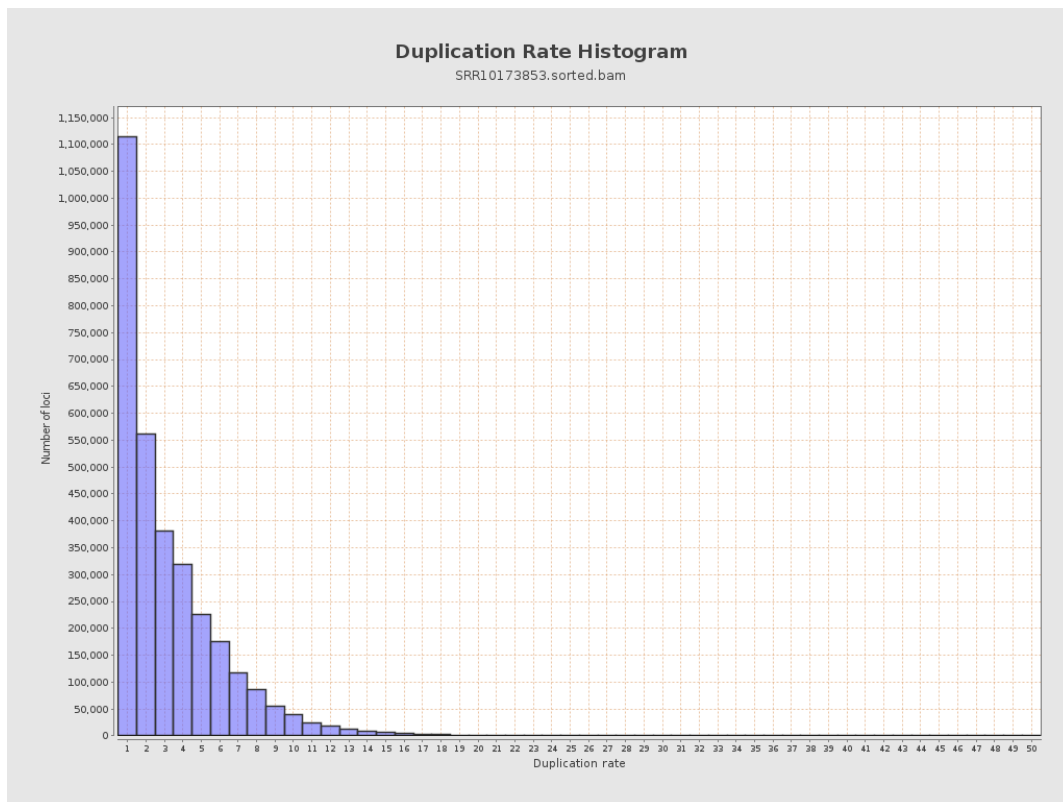
5. Results : Coverage Histogram (0-50X)



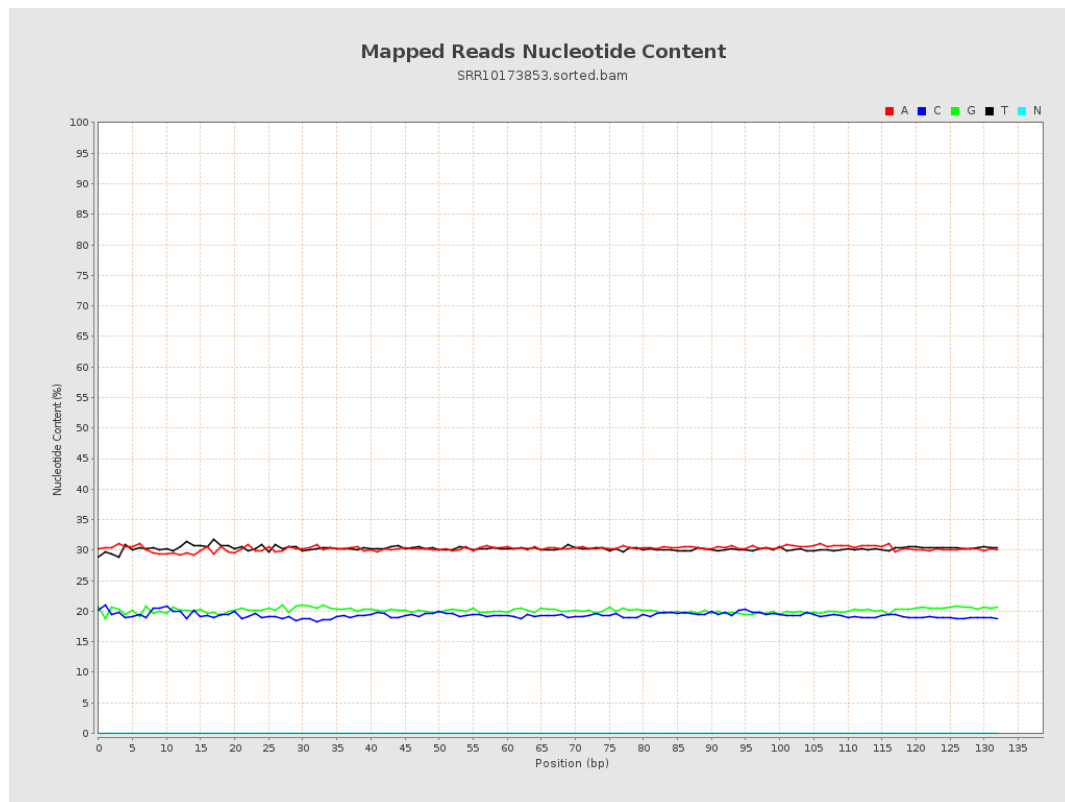
6. Results : Genome Fraction Coverage



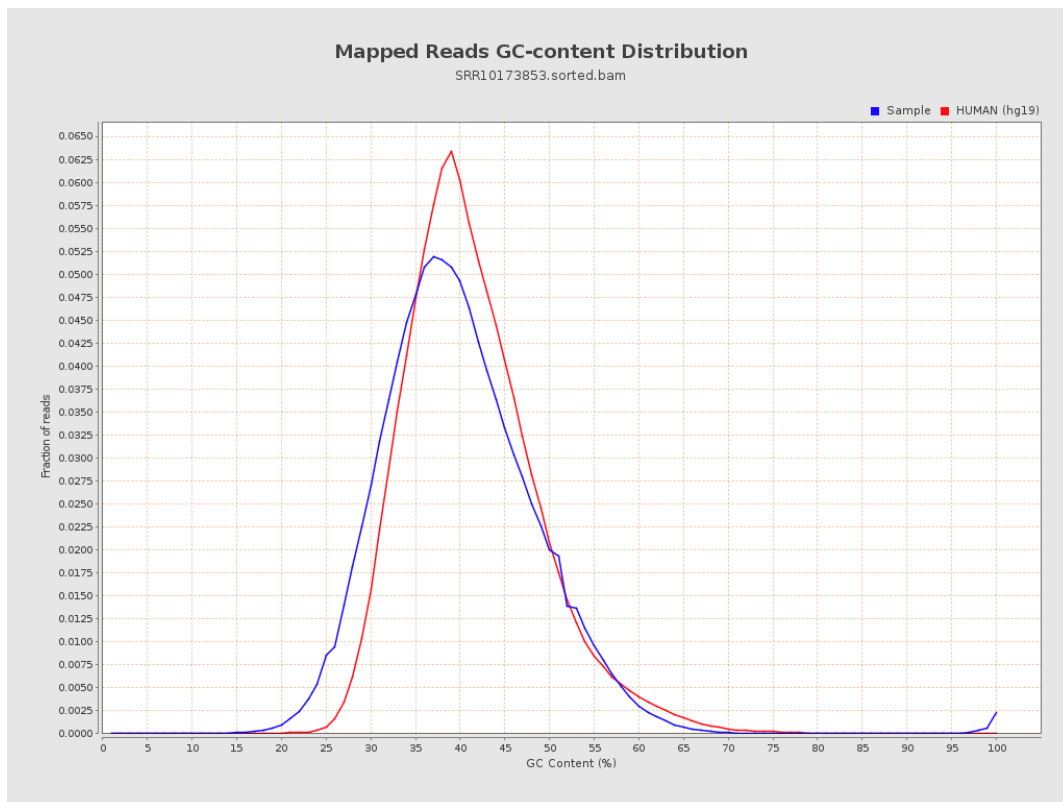
7. Results : Duplication Rate Histogram



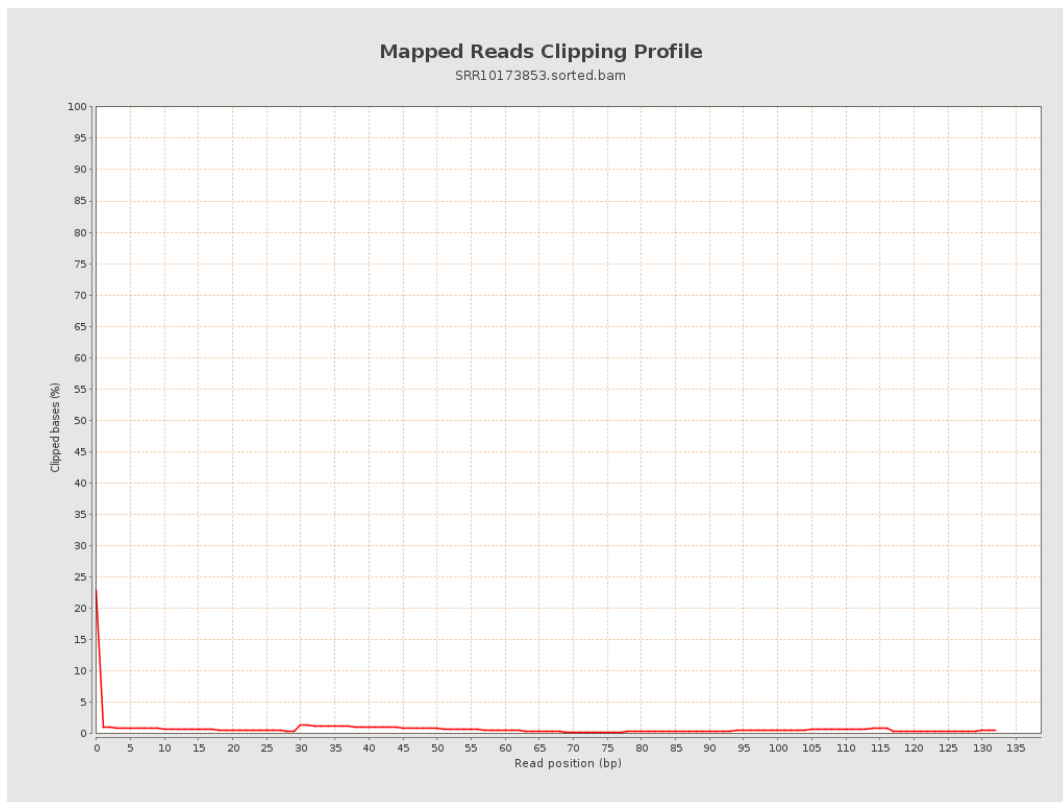
8. Results : Mapped Reads Nucleotide Content



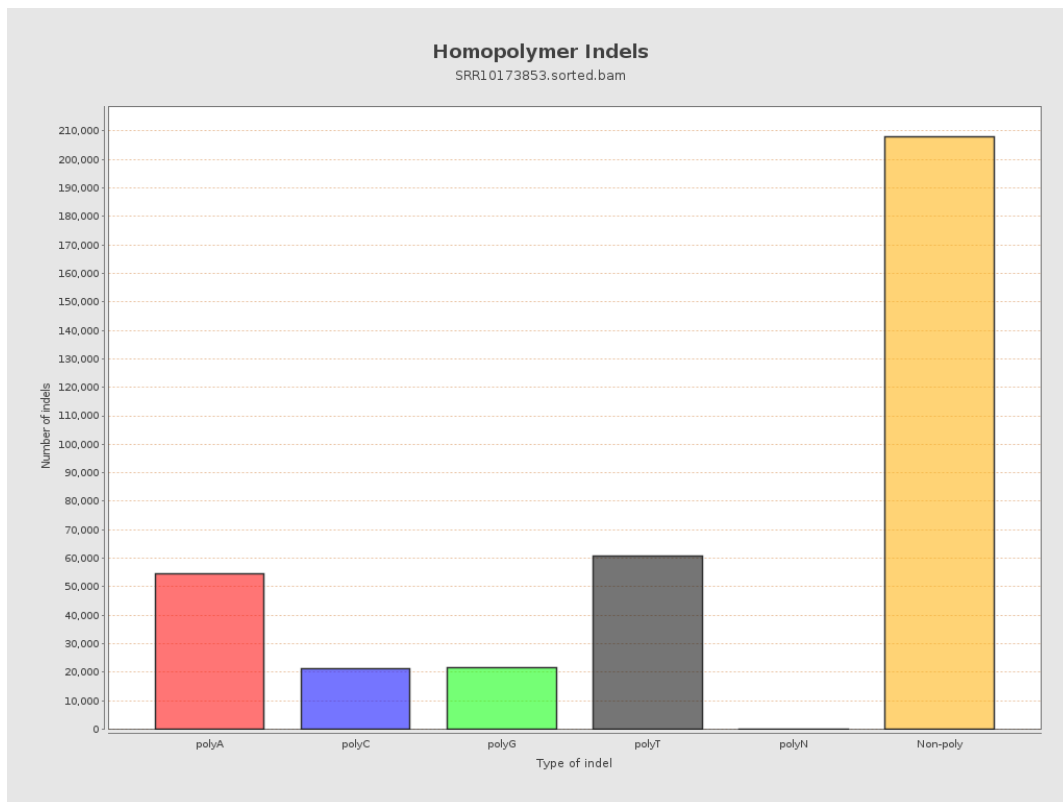
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



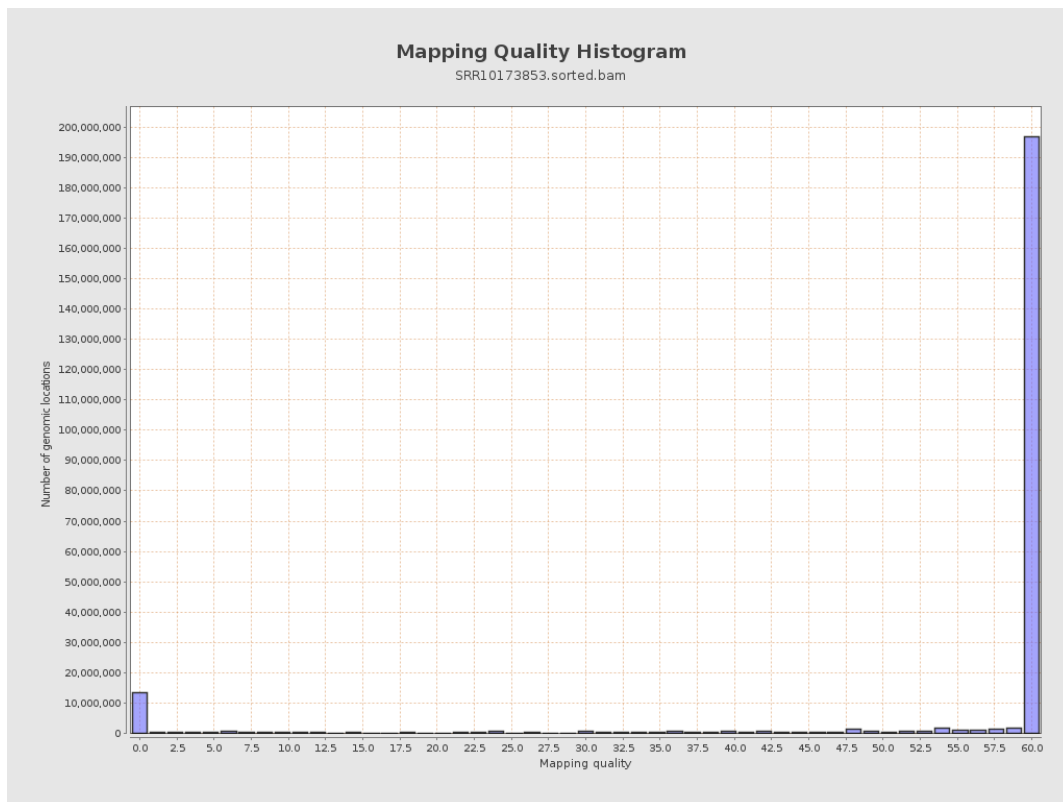
11. Results : Homopolymer Indels



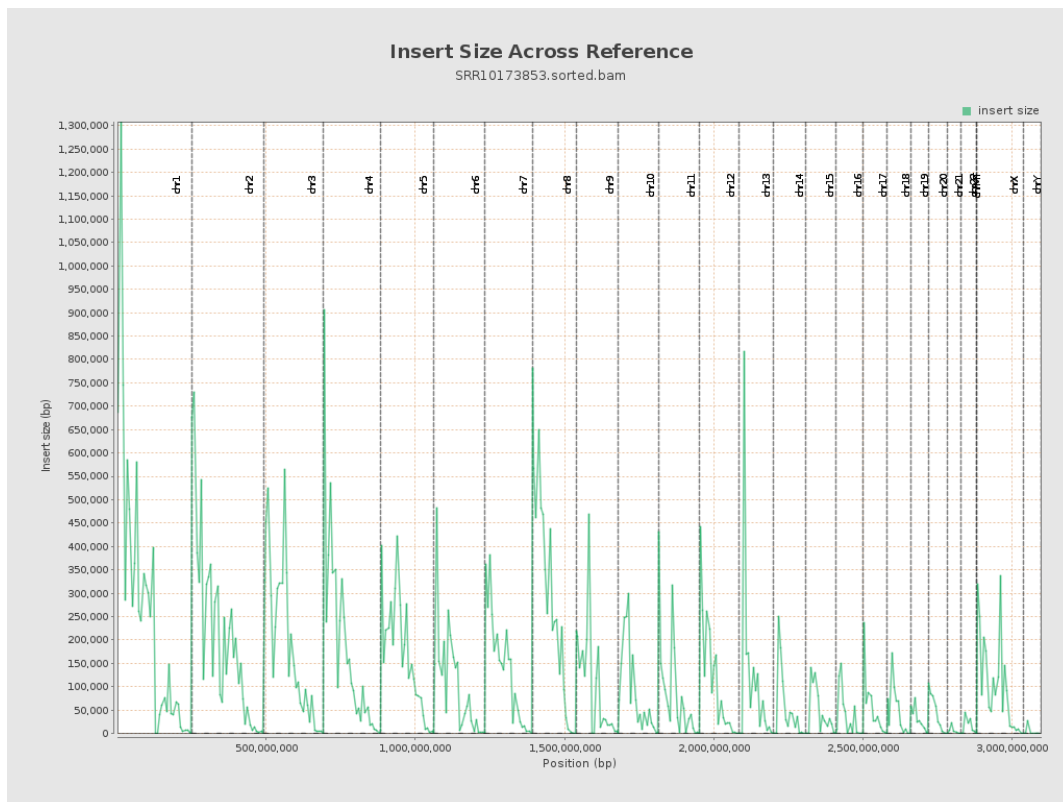
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

