

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 06:52:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173917.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_SRR10173917 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173917_1.fastq.gz SRR10173917_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 06:52:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173917.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,812,644
Mapped reads	5,649,829 / 97.2%
Unmapped reads	162,815 / 2.8%
Mapped paired reads	5,649,829 / 97.2%
Mapped reads, first in pair	2,828,496 / 48.66%
Mapped reads, second in pair	2,821,333 / 48.54%
Mapped reads, both in pair	5,535,606 / 95.23%
Mapped reads, singletons	114,223 / 1.97%
Secondary alignments	0
Supplementary alignments	614,291 / 10.57%
Read min/max/mean length	30 / 133 / 128.79
Duplicated reads (estimated)	4,461,533 / 76.76%
Duplication rate	65.18%
Clipped reads	2,414,417 / 41.54%

2.2. ACGT Content

Number/percentage of A's	199,859,185 / 29.95%
Number/percentage of C's	131,091,673 / 19.65%
Number/percentage of T's	199,860,260 / 29.95%
Number/percentage of G's	136,415,623 / 20.44%
Number/percentage of N's	8,126 / 0%

GC Percentage	40.09%
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2.3. Coverage

Mean	0.2157
Standard Deviation	3.2421

2.4. Mapping Quality

Mean Mapping Quality	52.52
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2.5. Insert size

Mean	1,031,533.64
Standard Deviation	9,398,378.34
P25/Median/P75	148 / 207 / 301

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	6,994,083
Insertions	70,604
Mapped reads with at least one insertion	1.21%
Deletions	161,168
Mapped reads with at least one deletion	2.78%
Homopolymer indels	42.7%

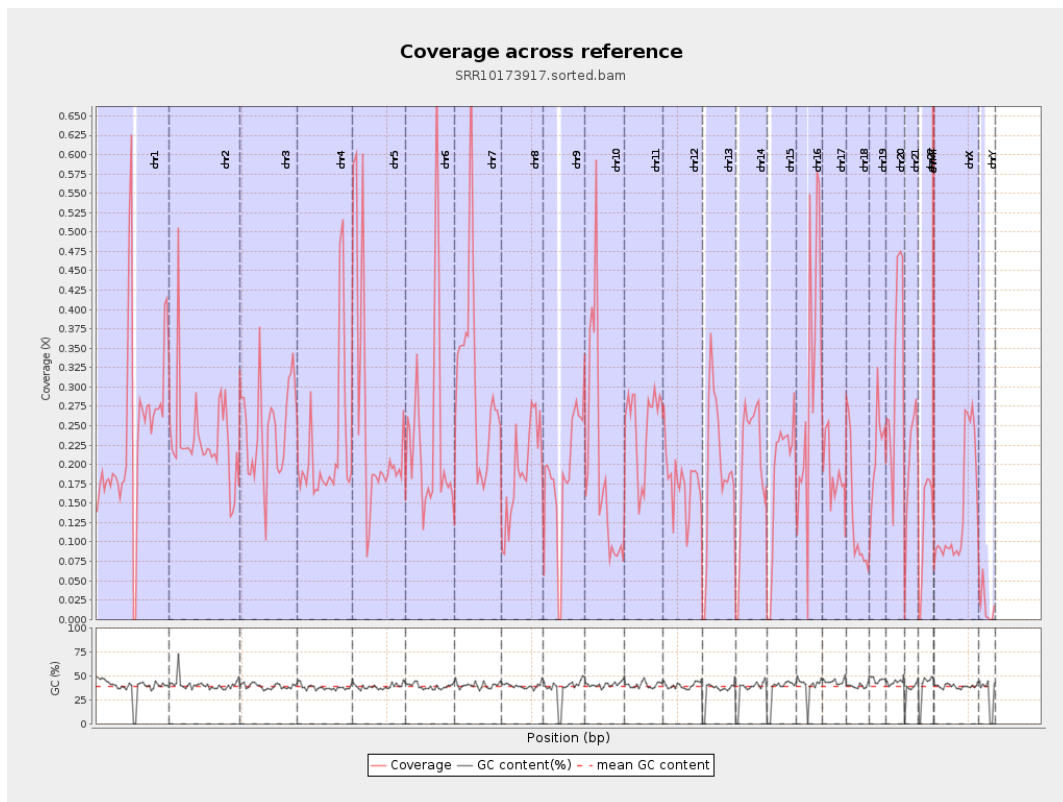
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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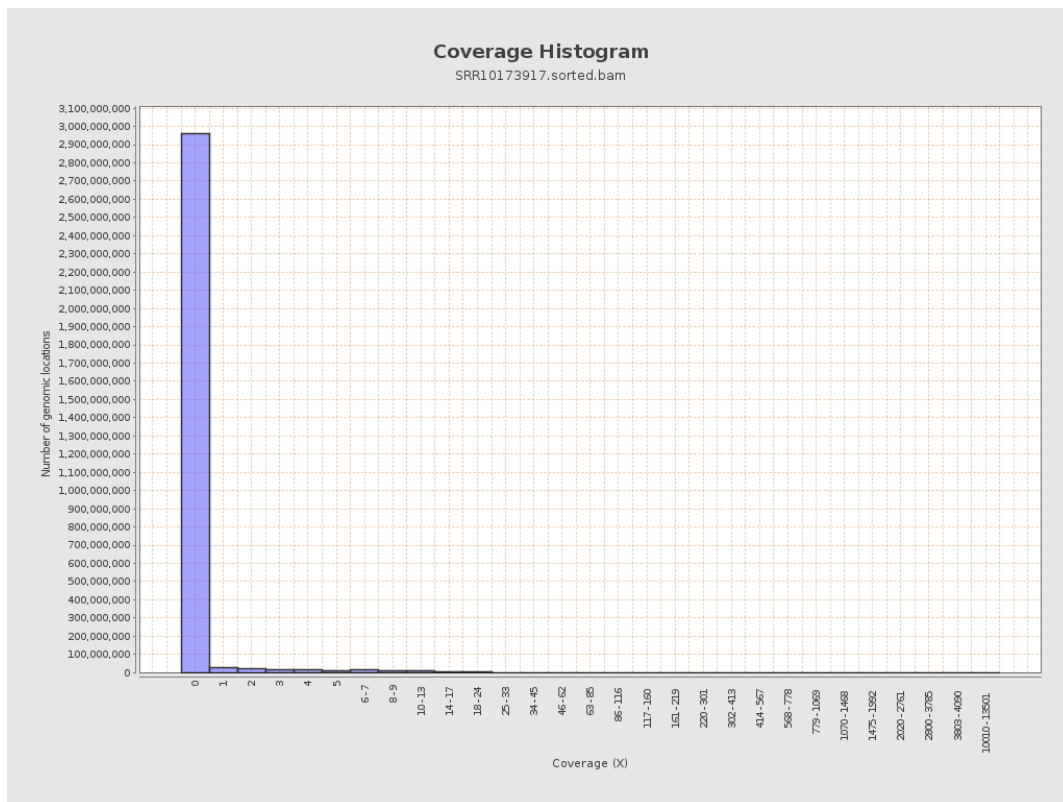
		bases	coverage	deviation
chr1	249250621	59365004	0.2382	2.7021
chr2	243199373	56091968	0.2306	9.4244
chr3	198022430	48705019	0.246	1.4391
chr4	191154276	41215477	0.2156	1.7323
chr5	180915260	45700837	0.2526	1.4675
chr6	171115067	41116805	0.2403	1.485
chr7	159138663	48402672	0.3042	3.4377
chr8	146364022	28262397	0.1931	1.509
chr9	141213431	26806258	0.1898	1.6135
chr10	135534747	26230629	0.1935	3.2178
chr11	135006516	33658675	0.2493	1.4772
chr12	133851895	23713404	0.1772	1.22
chr13	115169878	22234527	0.1931	1.2886
chr14	107349540	21324733	0.1986	1.3138
chr15	102531392	19054412	0.1858	1.2374
chr16	90354753	27345187	0.3026	2.5187
chr17	81195210	14938492	0.184	1.4748
chr18	78077248	10246033	0.1312	2.2803
chr19	59128983	12856029	0.2174	2.8422
chr20	63025520	20477996	0.3249	1.6737
chr21	48129895	9706643	0.2017	1.3959
chr22	51304566	6229444	0.1214	0.9628
chrMT	16571	1359044	82.0134	65.7717
chrX	155270560	21656954	0.1395	1.0786

chrY	59373566	926012	0.0156	0.7537
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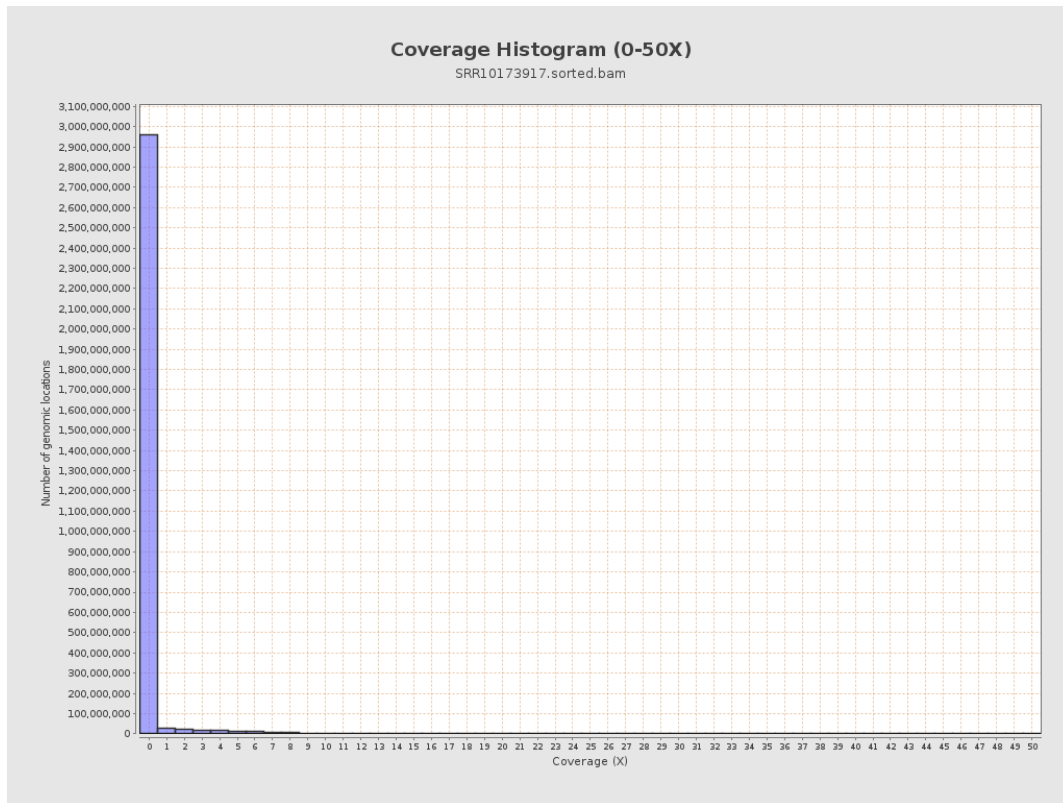
3. Results : Coverage across reference



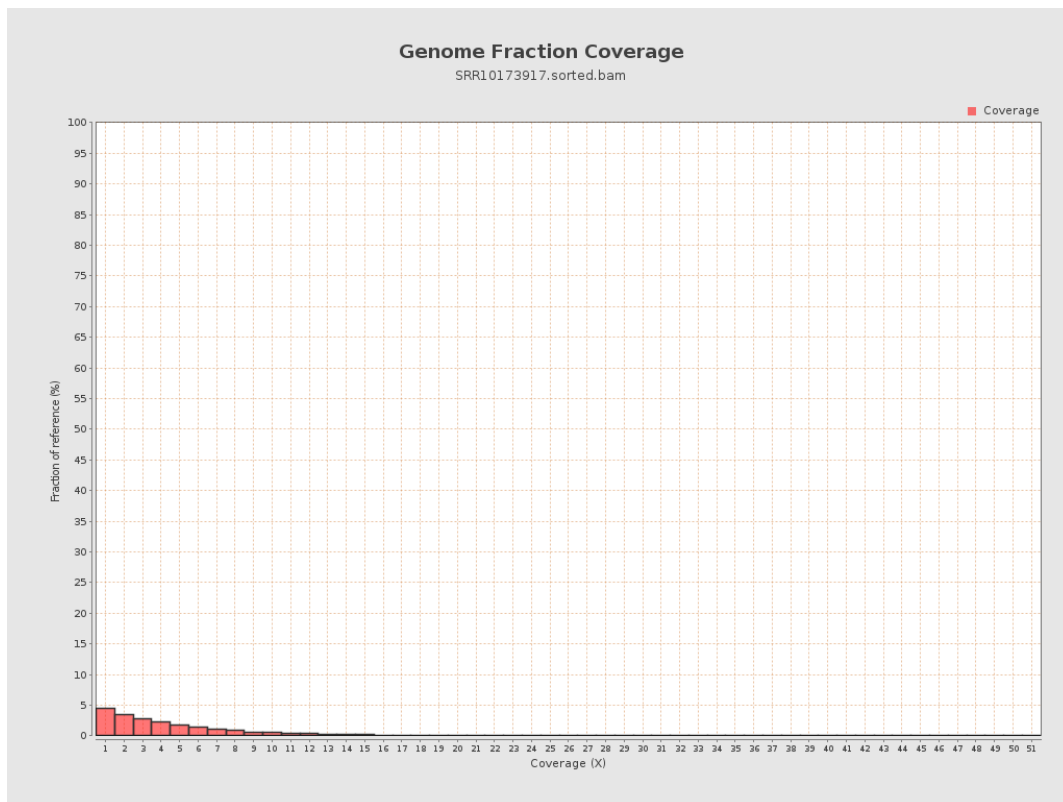
4. Results : Coverage Histogram



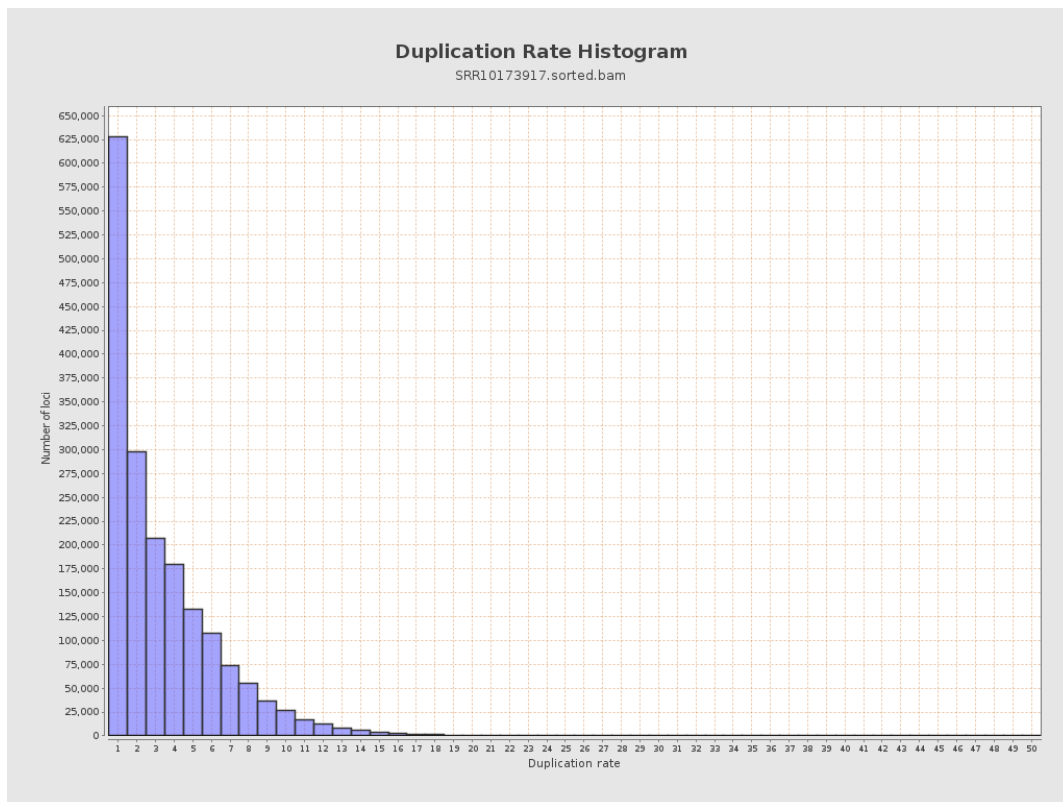
5. Results : Coverage Histogram (0-50X)



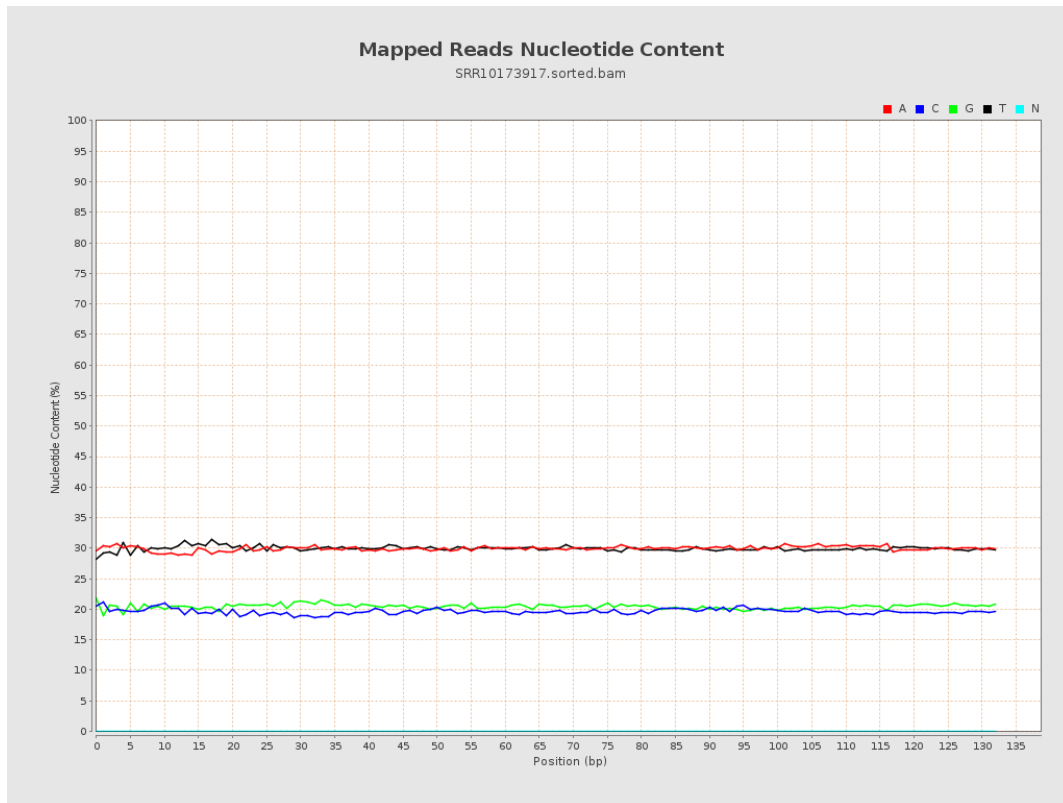
6. Results : Genome Fraction Coverage



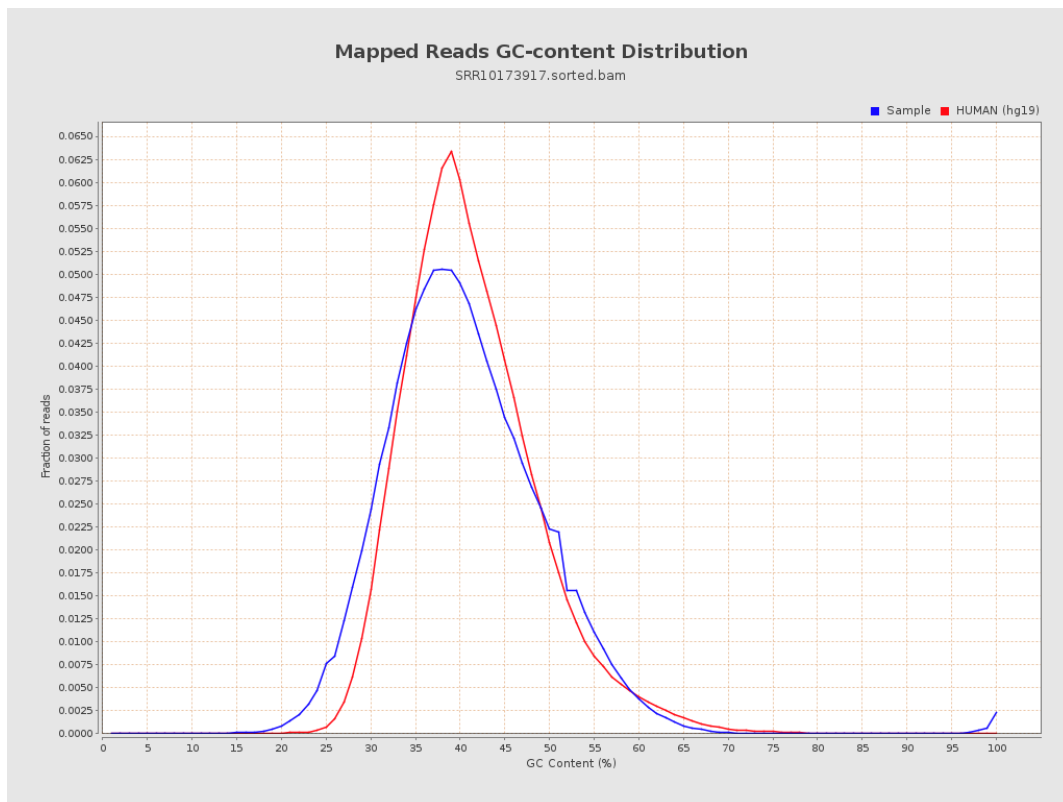
7. Results : Duplication Rate Histogram



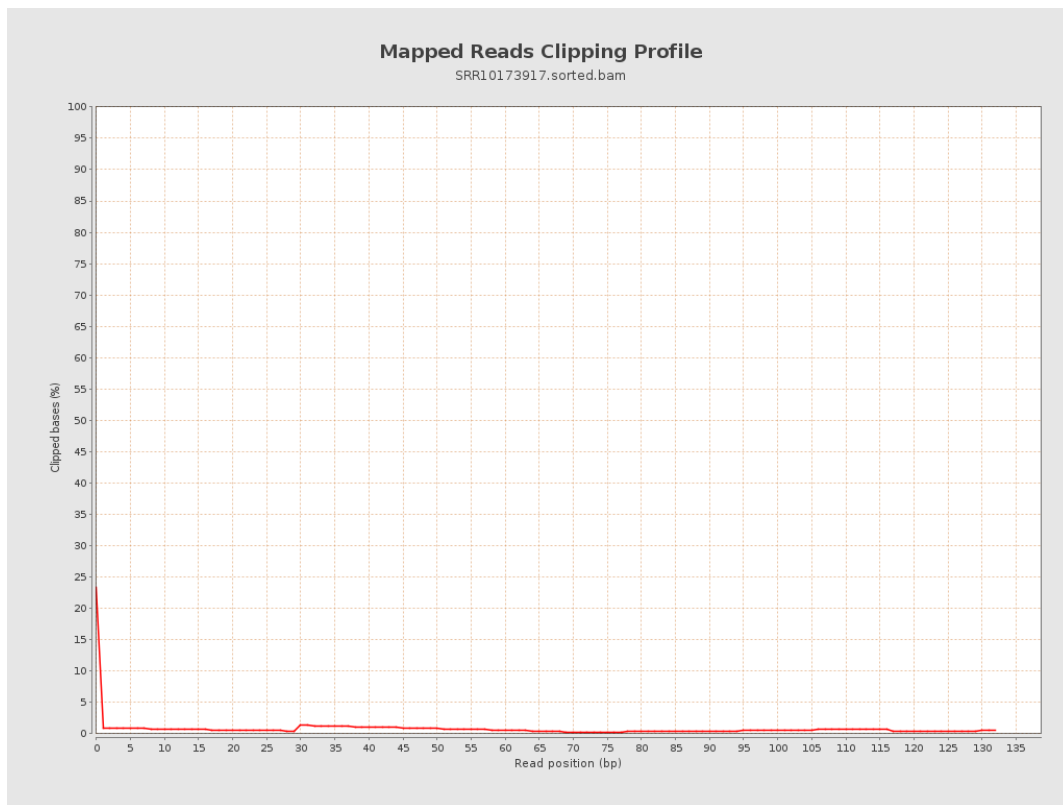
8. Results : Mapped Reads Nucleotide Content



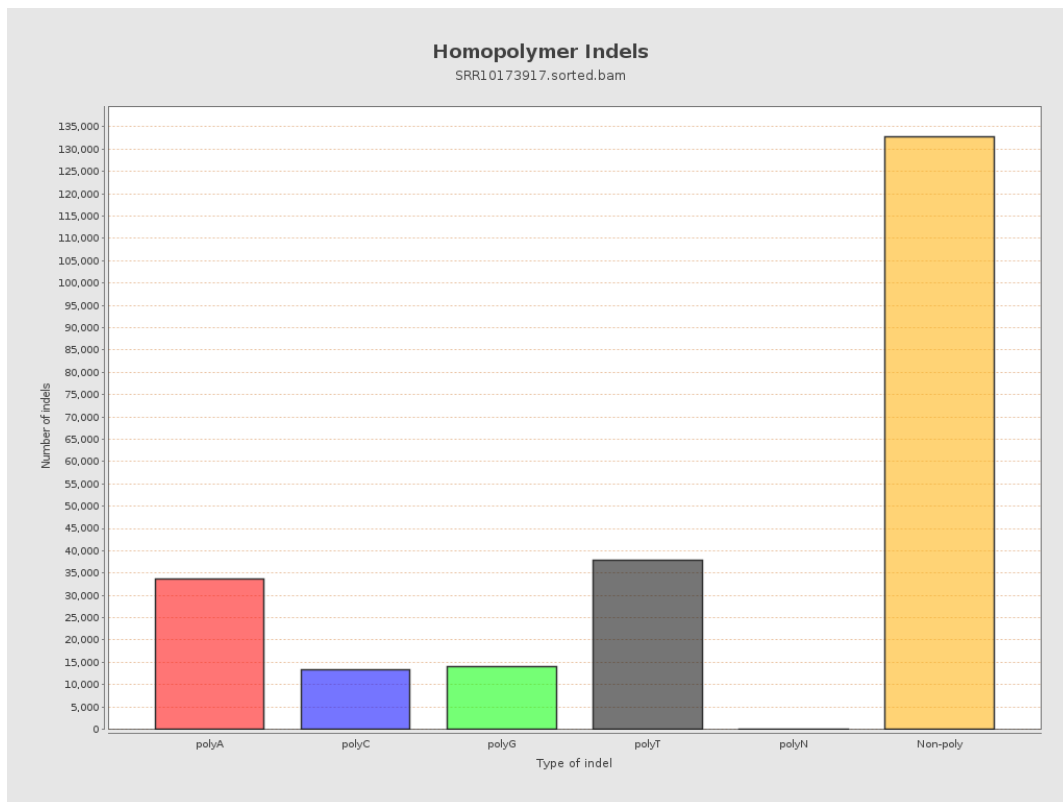
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



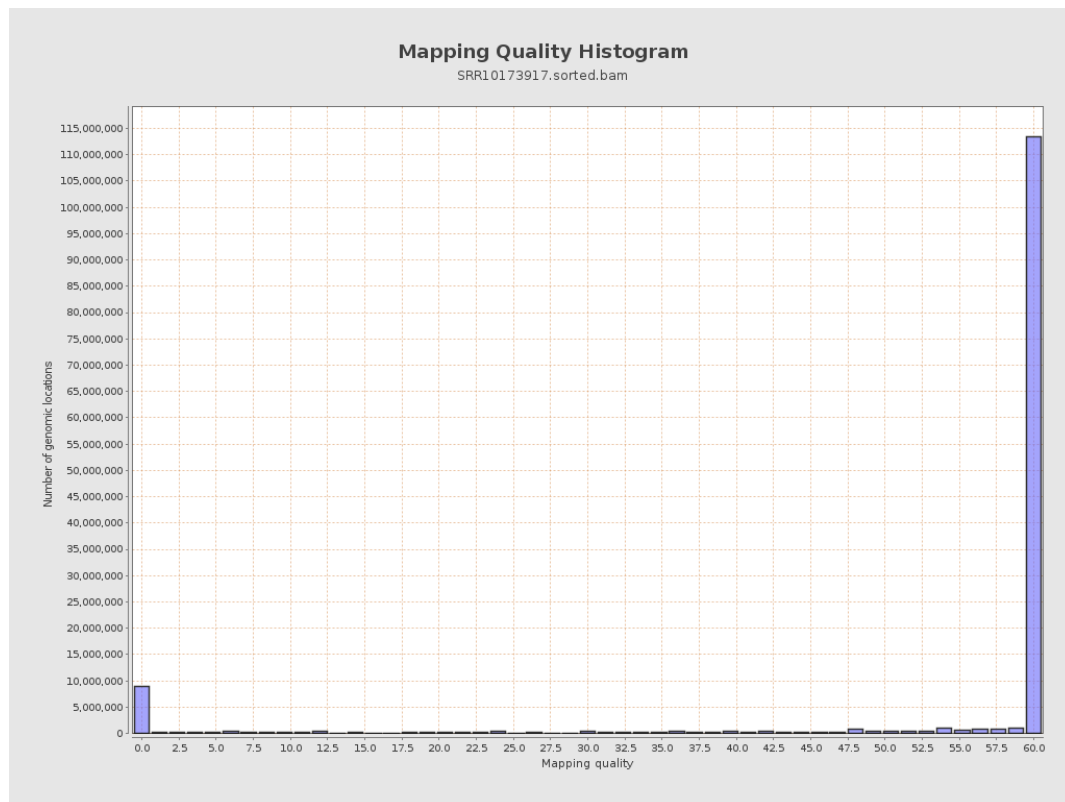
11. Results : Homopolymer Indels



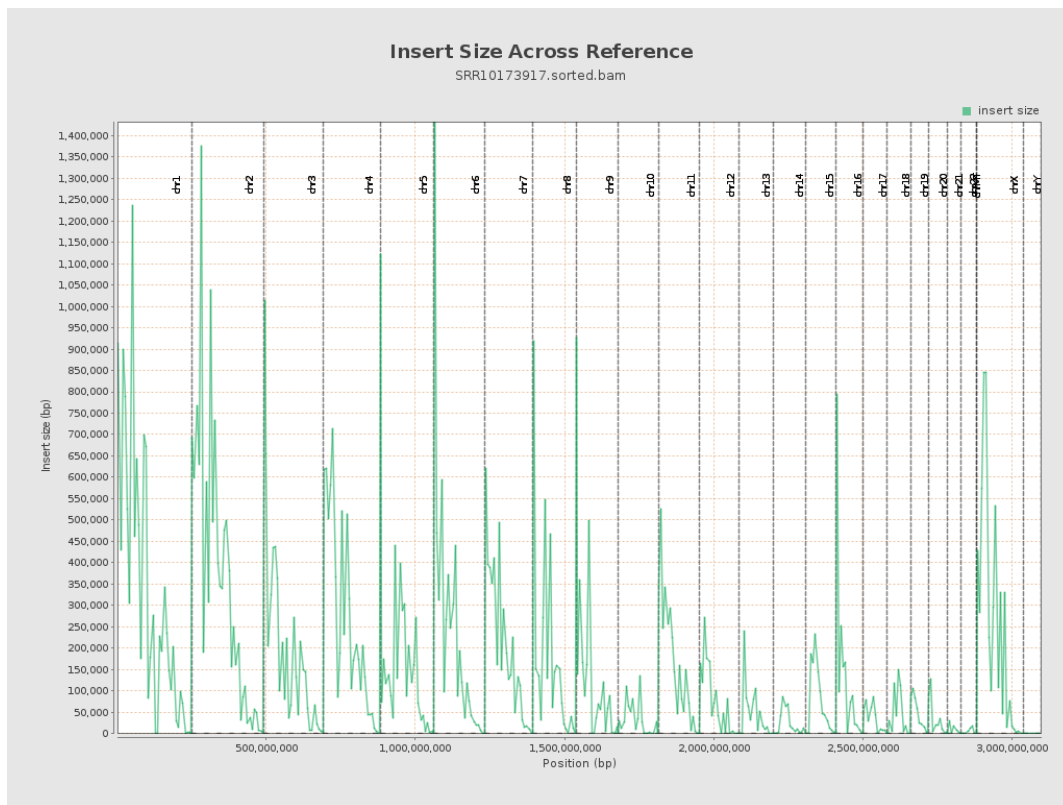
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

