

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 22:18:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173852.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_SRR10173852 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173852_1.fastq.gz SRR10173852_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 22:18:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173852.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,157,506
Mapped reads	6,951,462 / 97.12%
Unmapped reads	206,044 / 2.88%
Mapped paired reads	6,951,462 / 97.12%
Mapped reads, first in pair	3,481,359 / 48.64%
Mapped reads, second in pair	3,470,103 / 48.48%
Mapped reads, both in pair	6,816,476 / 95.24%
Mapped reads, singletons	134,986 / 1.89%
Secondary alignments	0
Supplementary alignments	728,728 / 10.18%
Read min/max/mean length	30 / 133 / 127.95
Duplicated reads (estimated)	5,285,096 / 73.84%
Duplication rate	63.87%
Clipped reads	2,978,087 / 41.61%

2.2. ACGT Content

Number/percentage of A's	245,092,266 / 30.07%
Number/percentage of C's	160,014,666 / 19.63%
Number/percentage of T's	244,469,228 / 29.99%
Number/percentage of G's	165,462,772 / 20.3%
Number/percentage of N's	8,996 / 0%

GC Percentage	39.93%
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2.3. Coverage

Mean	0.2635
Standard Deviation	3.8309

2.4. Mapping Quality

Mean Mapping Quality	52.66
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2.5. Insert size

Mean	859,401.29
Standard Deviation	8,362,981.99
P25/Median/P75	138 / 194 / 280

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	8,528,935
Insertions	86,523
Mapped reads with at least one insertion	1.2%
Deletions	216,847
Mapped reads with at least one deletion	3.04%
Homopolymer indels	41.68%

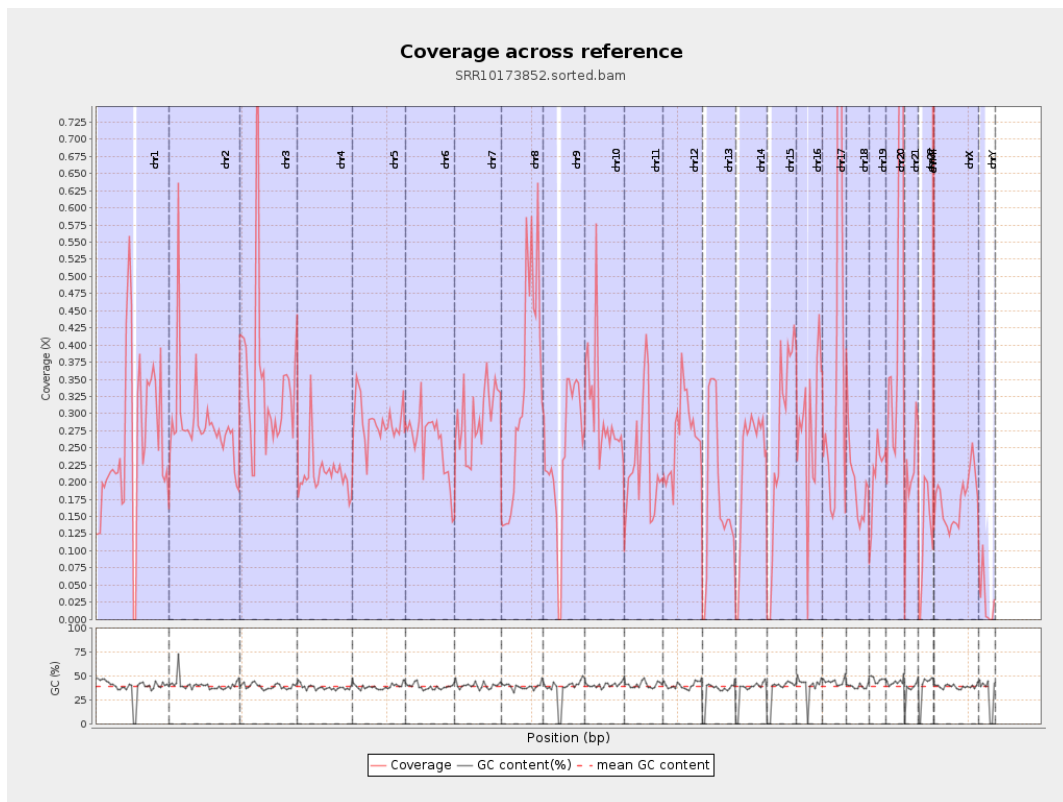
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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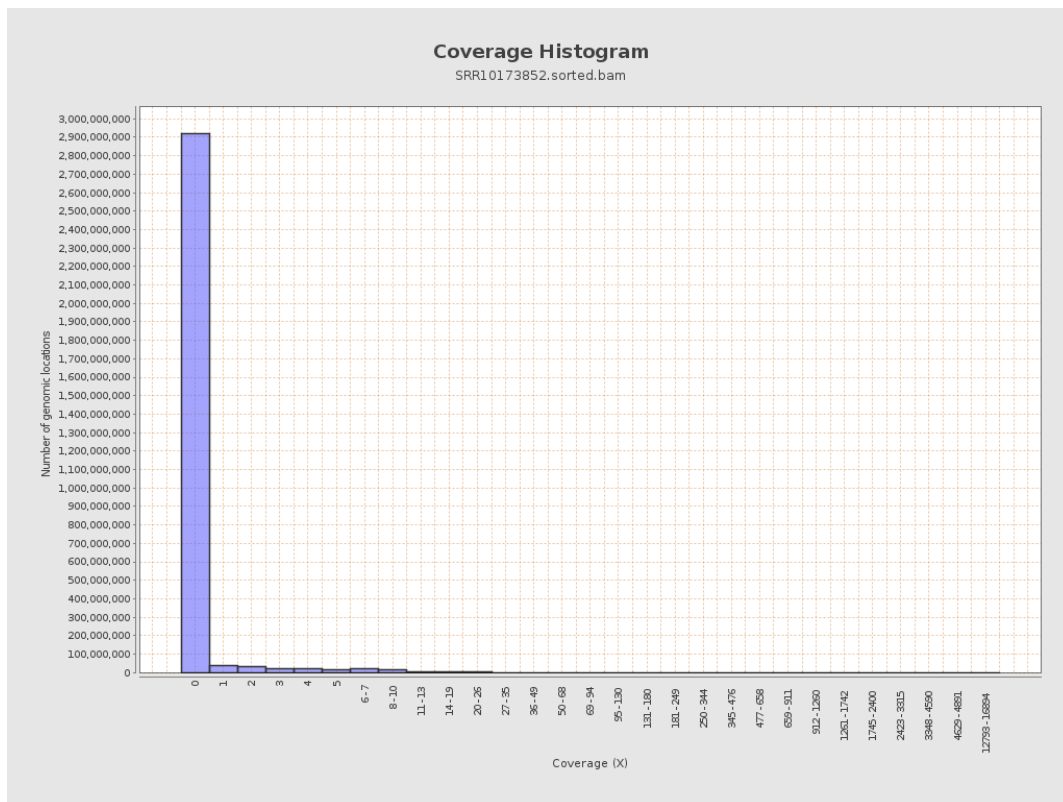
		bases	coverage	deviation
chr1	249250621	63436409	0.2545	2.638
chr2	243199373	69162592	0.2844	11.8218
chr3	198022430	68086547	0.3438	1.674
chr4	191154276	40497824	0.2119	1.7183
chr5	180915260	52189938	0.2885	1.4973
chr6	171115067	43883210	0.2565	1.69
chr7	159138663	46891078	0.2947	2.3992
chr8	146364022	48280346	0.3299	2.73
chr9	141213431	33943601	0.2404	1.7502
chr10	135534747	40924643	0.3019	3.4506
chr11	135006516	31009246	0.2297	1.4061
chr12	133851895	35925519	0.2684	1.4627
chr13	115169878	20437642	0.1775	1.1815
chr14	107349540	24661236	0.2297	1.355
chr15	102531392	27090744	0.2642	1.4401
chr16	90354753	25680926	0.2842	2.0978
chr17	81195210	33147083	0.4082	2.0266
chr18	78077248	15618860	0.2	2.6333
chr19	59128983	12654268	0.214	2.0092
chr20	63025520	35672244	0.566	2.3921
chr21	48129895	10282161	0.2136	1.4295
chr22	51304566	6057971	0.1181	0.9306
chrMT	16571	1519475	91.6948	65.5945
chrX	155270560	26929649	0.1734	1.1701

chrY	59373566	1600906	0.027	1.0411
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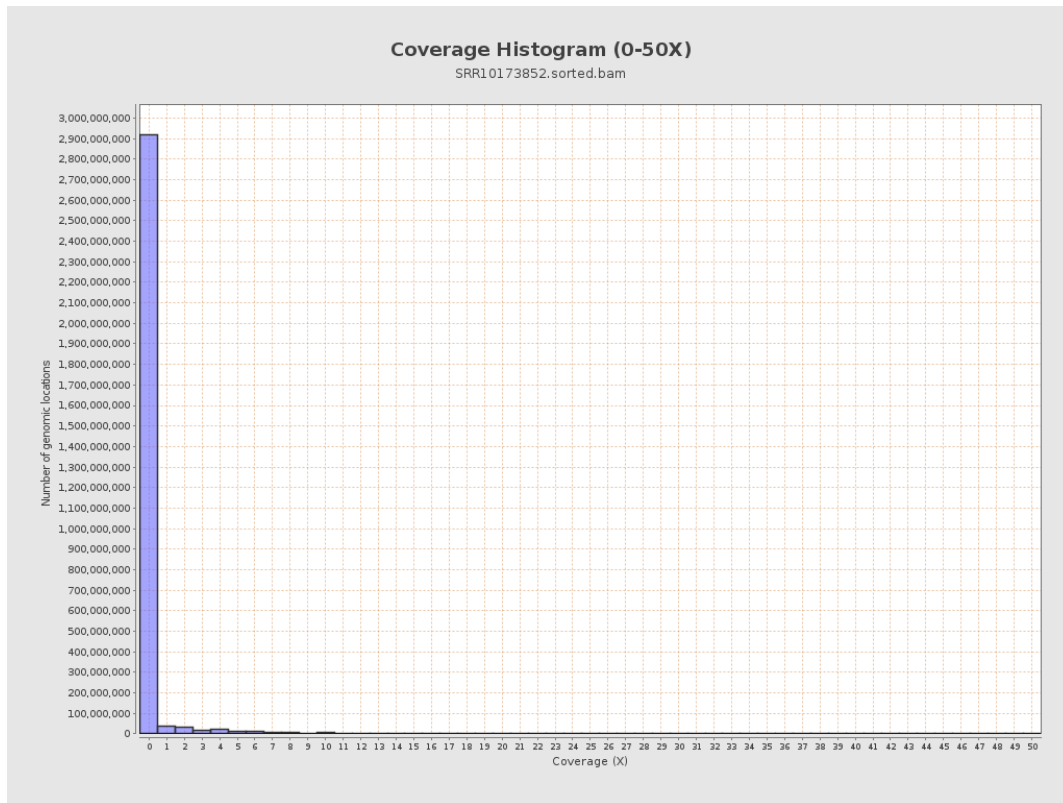
3. Results : Coverage across reference



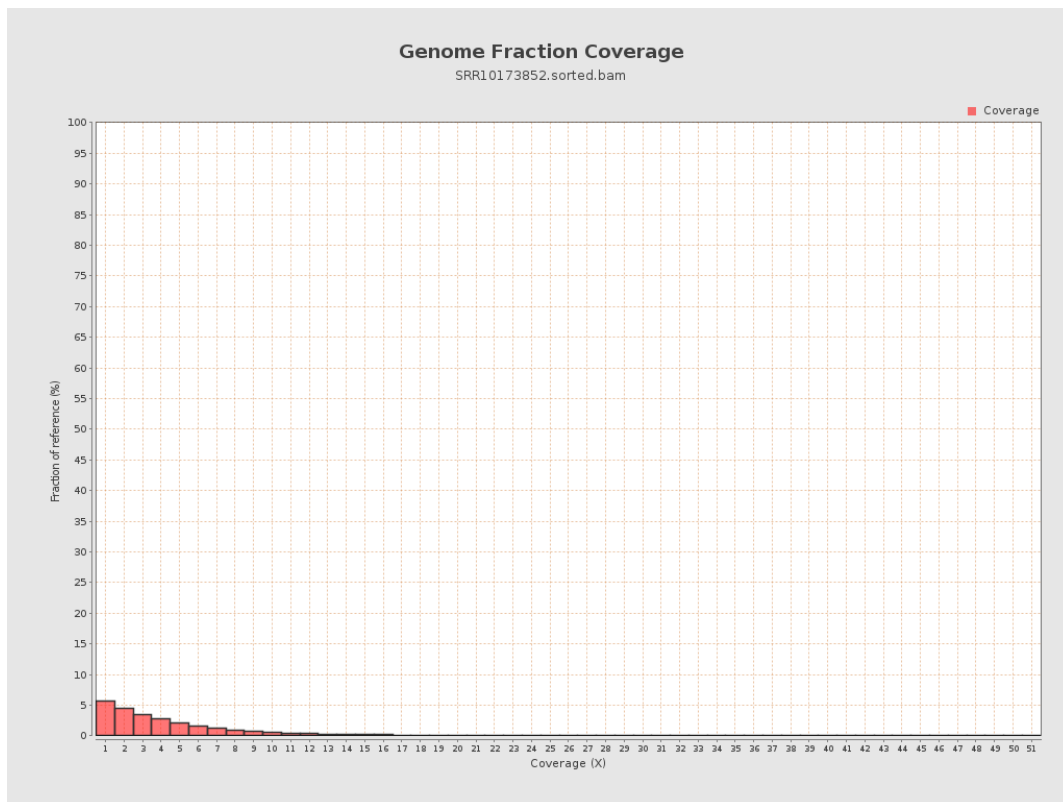
4. Results : Coverage Histogram



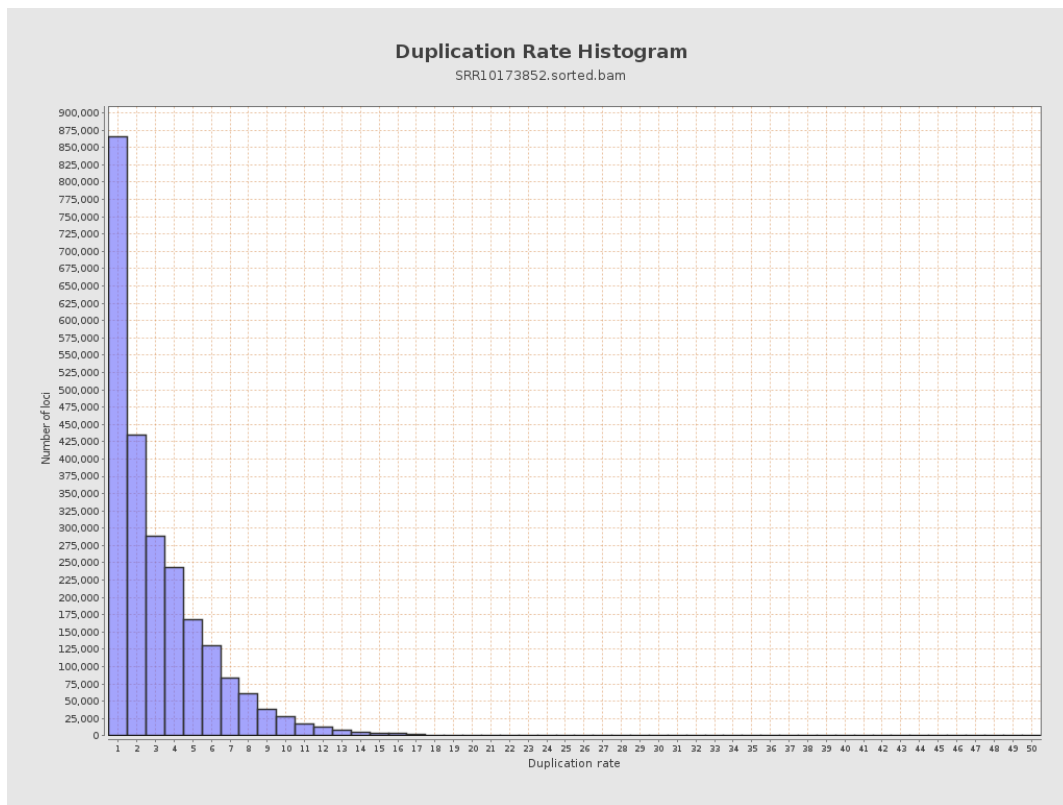
5. Results : Coverage Histogram (0-50X)



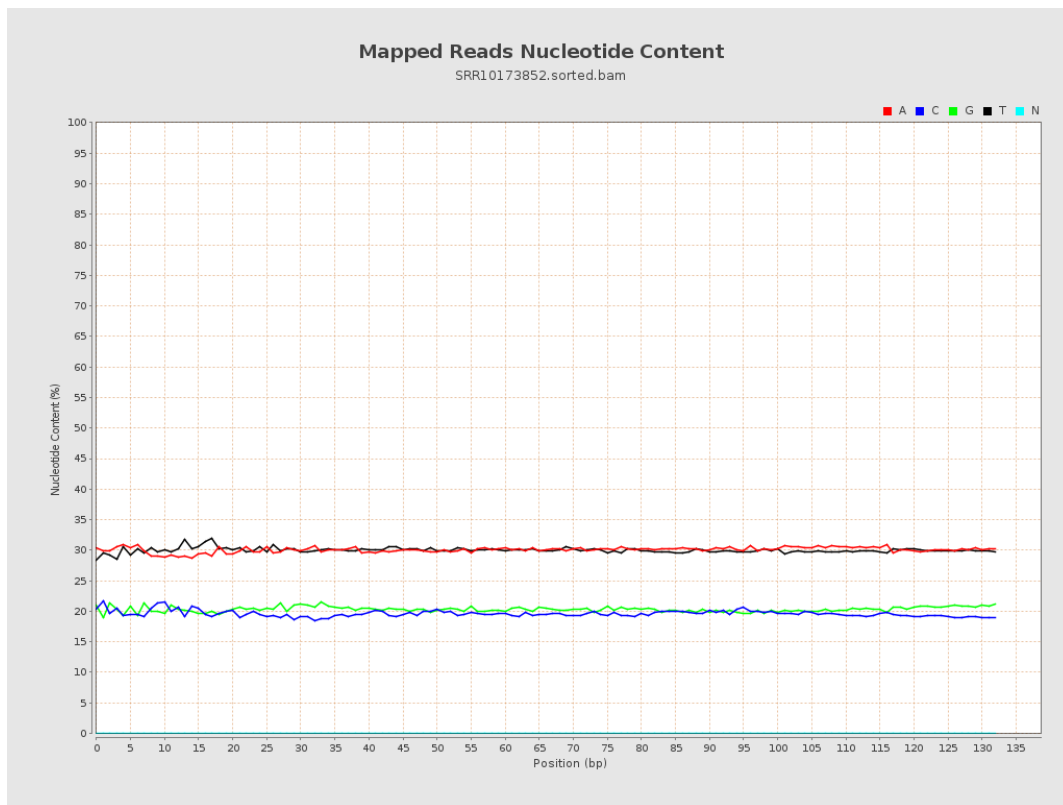
6. Results : Genome Fraction Coverage



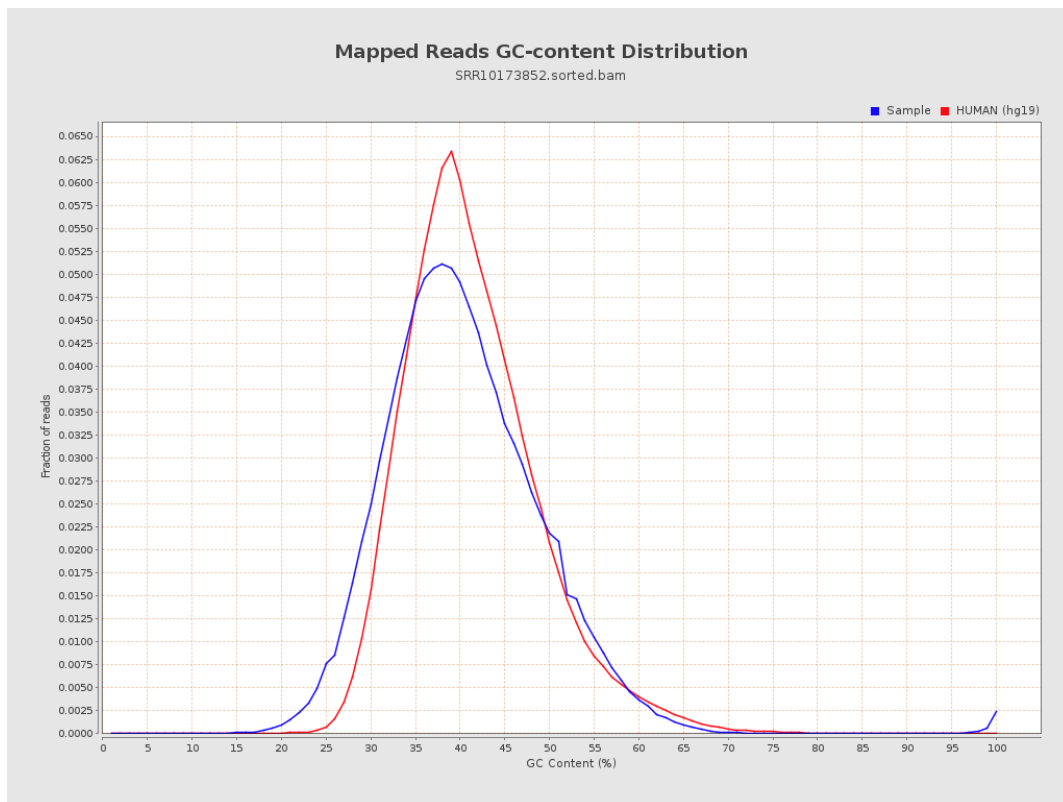
7. Results : Duplication Rate Histogram



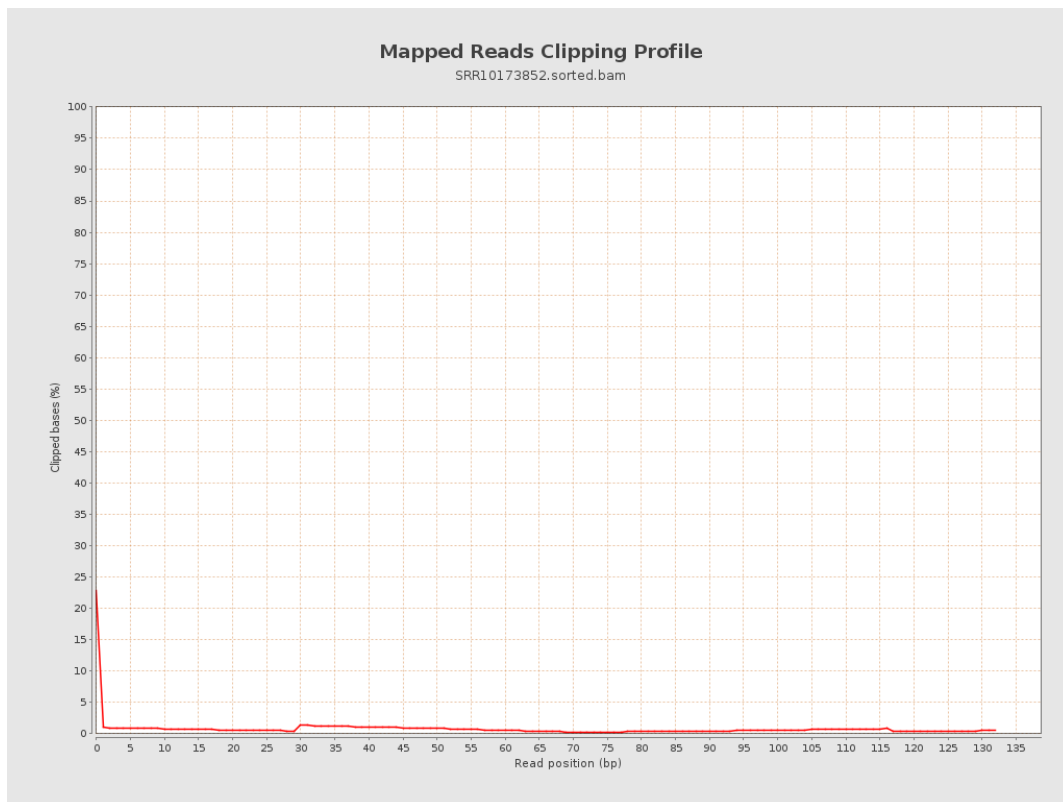
8. Results : Mapped Reads Nucleotide Content



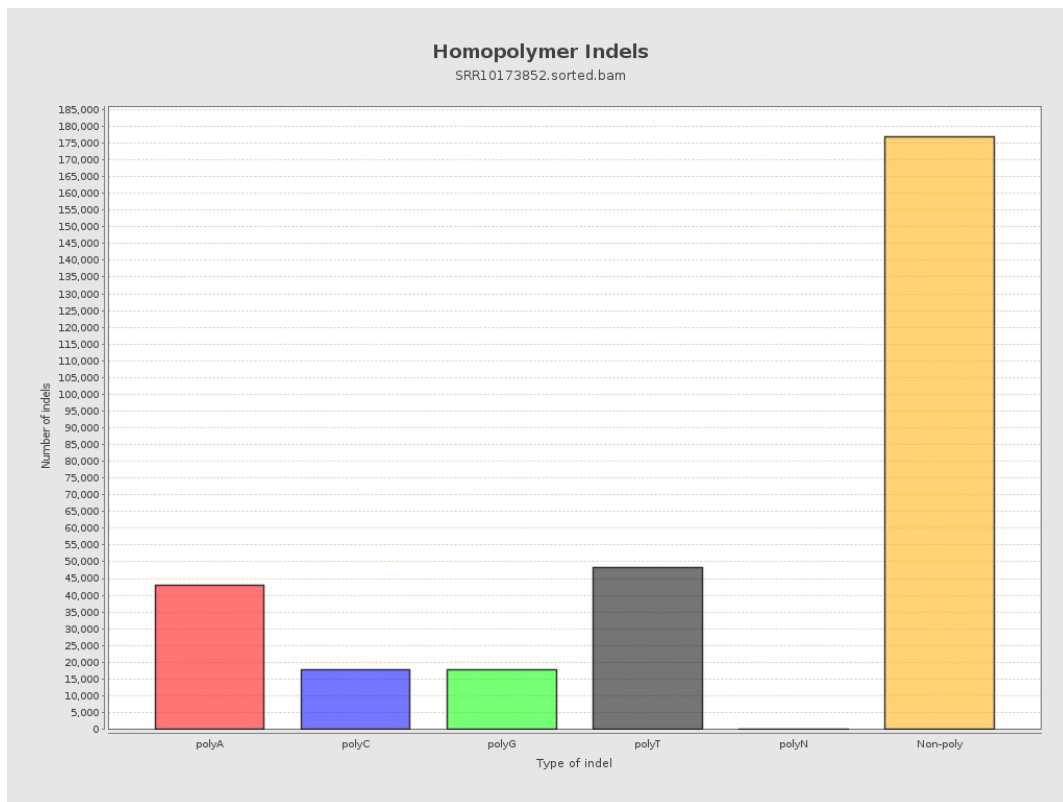
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



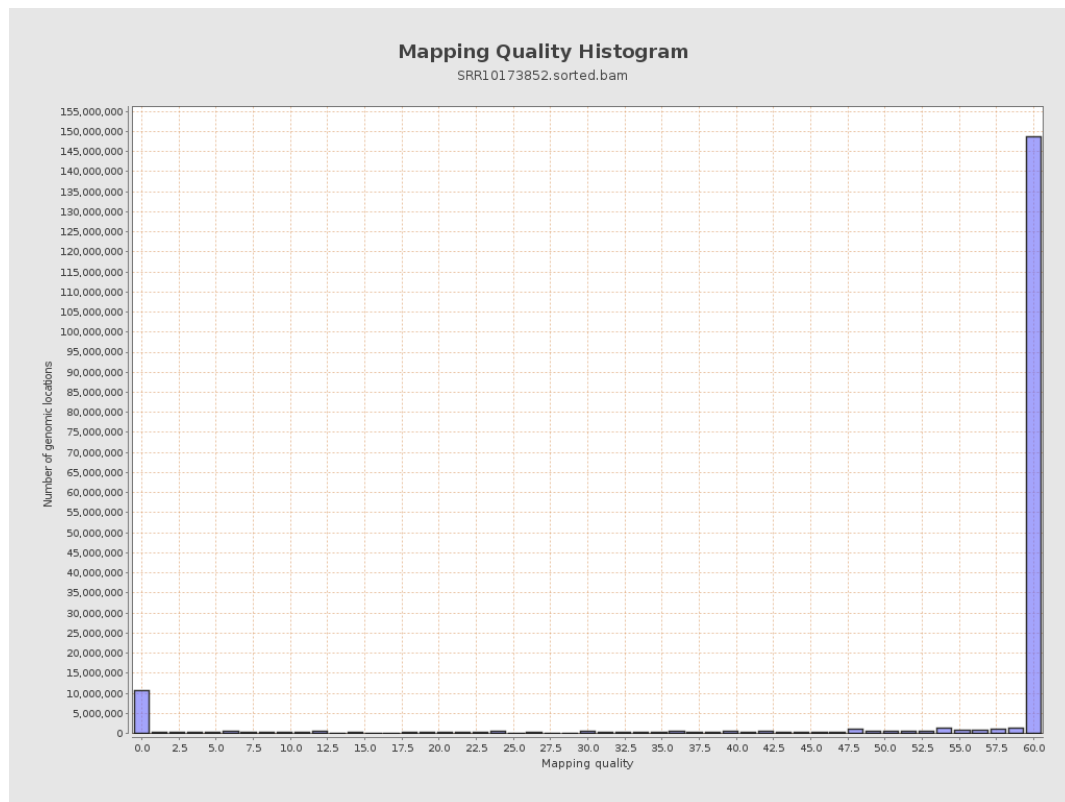
11. Results : Homopolymer Indels



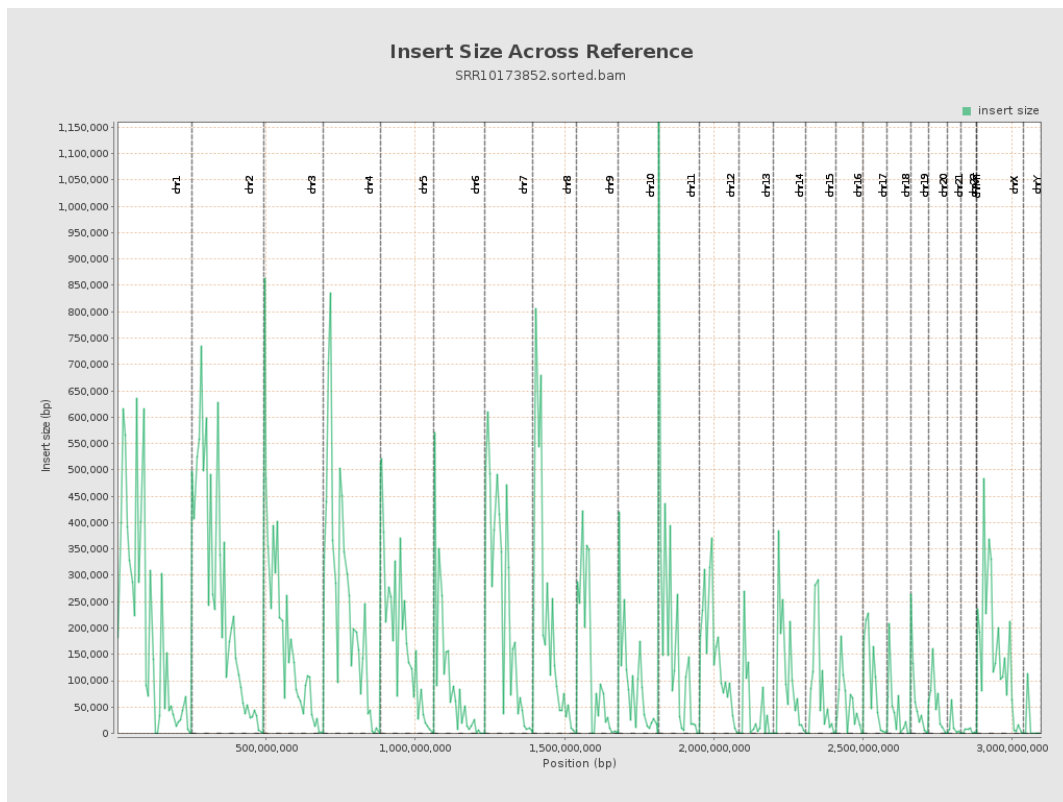
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

