

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 13:24:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173960.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_SRR10173960 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173960_1.fastq.gz SRR10173960_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 13:24:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173960.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,155,866
Mapped reads	31,313,814 / 97.38%
Unmapped reads	842,052 / 2.62%
Mapped paired reads	31,313,814 / 97.38%
Mapped reads, first in pair	15,672,860 / 48.74%
Mapped reads, second in pair	15,640,954 / 48.64%
Mapped reads, both in pair	30,751,418 / 95.63%
Mapped reads, singletons	562,396 / 1.75%
Secondary alignments	0
Supplementary alignments	4,831,563 / 15.03%
Read min/max/mean length	30 / 133 / 127.29
Duplicated reads (estimated)	26,247,909 / 81.63%
Duplication rate	66.44%
Clipped reads	17,847,166 / 55.5%

2.2. ACGT Content

Number/percentage of A's	1,052,451,620 / 29.62%
Number/percentage of C's	711,544,858 / 20.03%
Number/percentage of T's	1,045,153,844 / 29.42%
Number/percentage of G's	743,511,232 / 20.93%
Number/percentage of N's	25,922 / 0%

GC Percentage	40.96%
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2.3. Coverage

Mean	1.1484
Standard Deviation	18.8799

2.4. Mapping Quality

Mean Mapping Quality	52.17
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2.5. Insert size

Mean	1,465,327.05
Standard Deviation	11,109,355.42
P25/Median/P75	108 / 164 / 263

2.6. Mismatches and indels

General error rate	0.93%
Mismatches	31,842,410
Insertions	418,386
Mapped reads with at least one insertion	1.28%
Deletions	1,030,821
Mapped reads with at least one deletion	3.21%
Homopolymer indels	41.07%

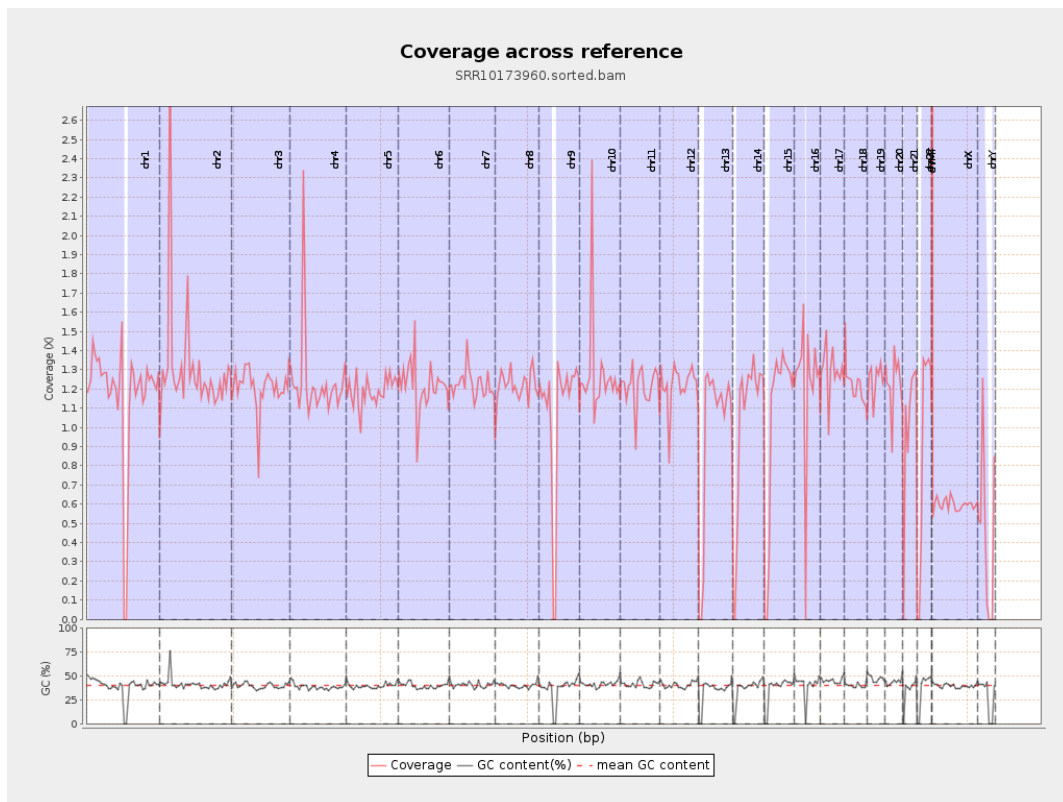
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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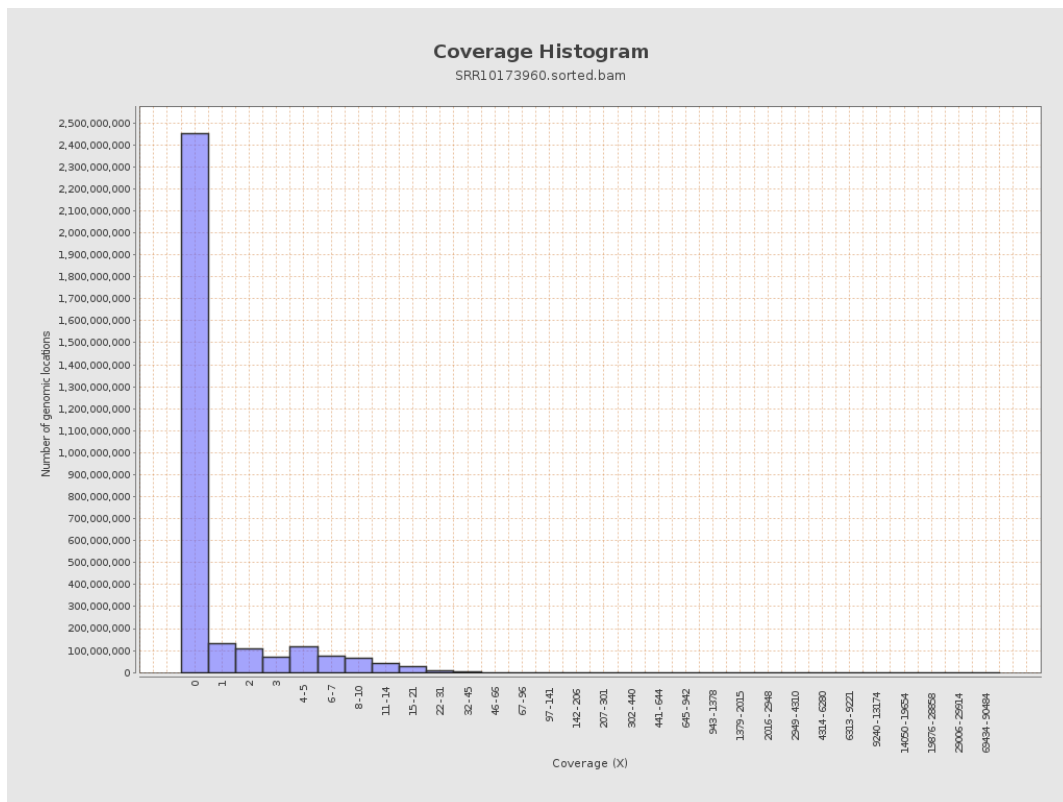
		bases	coverage	deviation
chr1	249250621	293803482	1.1787	10.7229
chr2	243199373	320605099	1.3183	62.9413
chr3	198022430	239389661	1.2089	3.4732
chr4	191154276	235379384	1.2314	9.0082
chr5	180915260	214876228	1.1877	3.4566
chr6	171115067	208689318	1.2196	5.7868
chr7	159138663	194978924	1.2252	7.4851
chr8	146364022	179491813	1.2263	9.4474
chr9	141213431	151351527	1.0718	8.4293
chr10	135534747	173661492	1.2813	10.7115
chr11	135006516	164149257	1.2159	4.3932
chr12	133851895	163314817	1.2201	4.4023
chr13	115169878	113726500	0.9875	3.1043
chr14	107349540	110879894	1.0329	3.5365
chr15	102531392	105898643	1.0328	3.8263
chr16	90354753	111156966	1.2302	6.194
chr17	81195210	104748301	1.2901	4.9766
chr18	78077248	94943198	1.216	11.0376
chr19	59128983	73687143	1.2462	6.8583
chr20	63025520	77582866	1.231	4.5749
chr21	48129895	50164447	1.0423	6.0271
chr22	51304566	46973678	0.9156	4.1145
chrMT	16571	5285811	318.9796	207.3454
chrX	155270560	92623386	0.5965	2.7134

chrY	59373566	27761360	0.4676	7.6737
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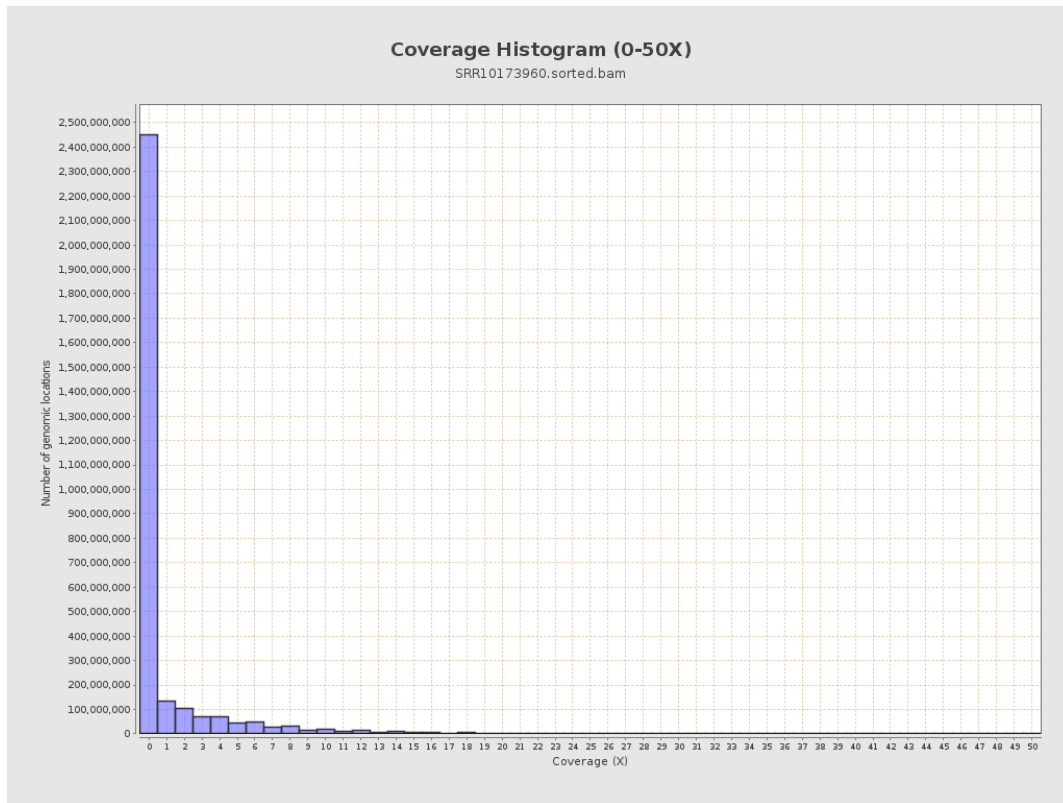
3. Results : Coverage across reference



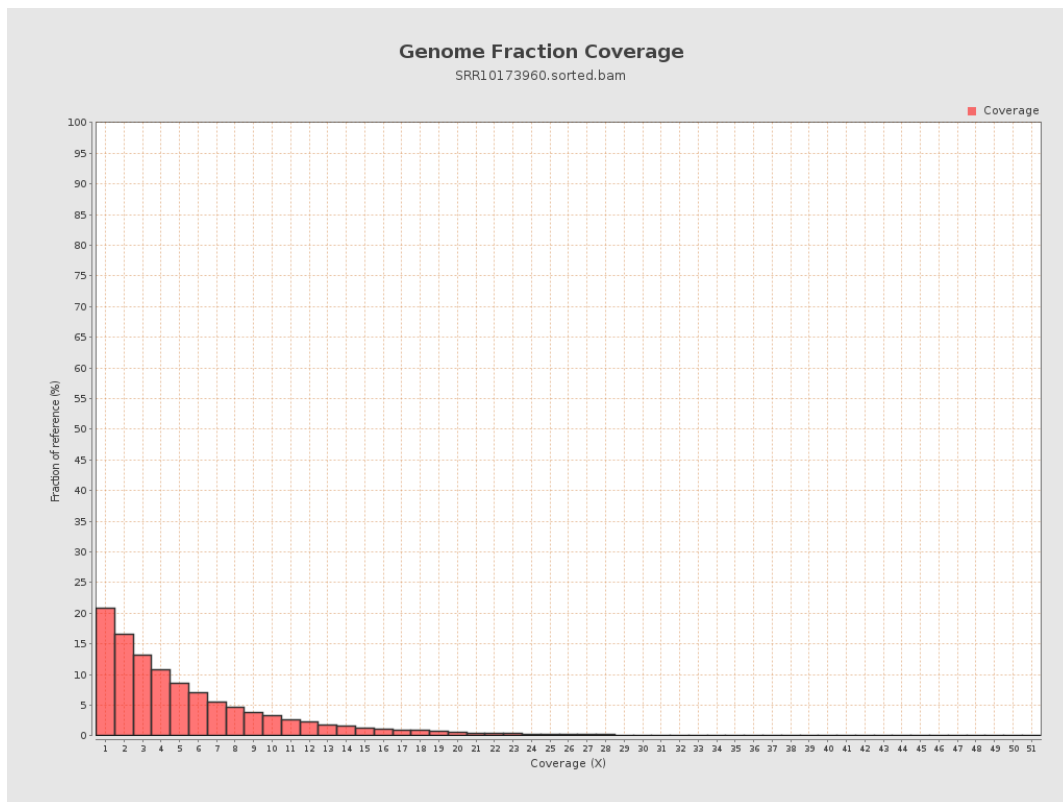
4. Results : Coverage Histogram



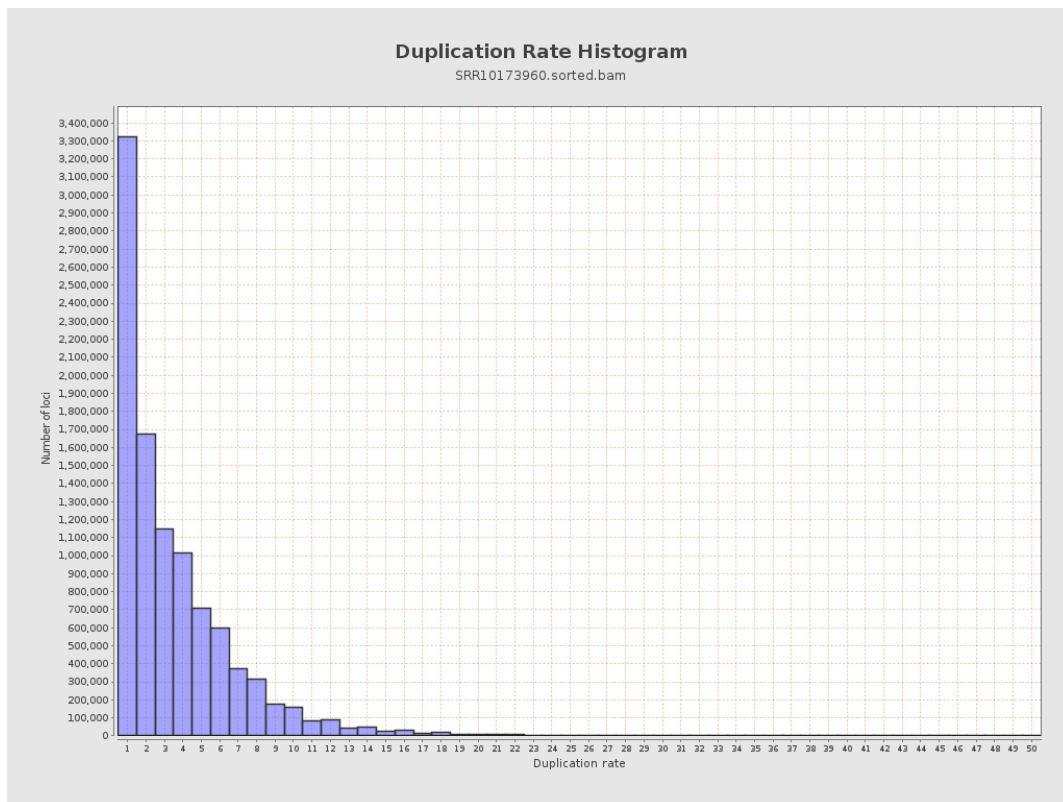
5. Results : Coverage Histogram (0-50X)



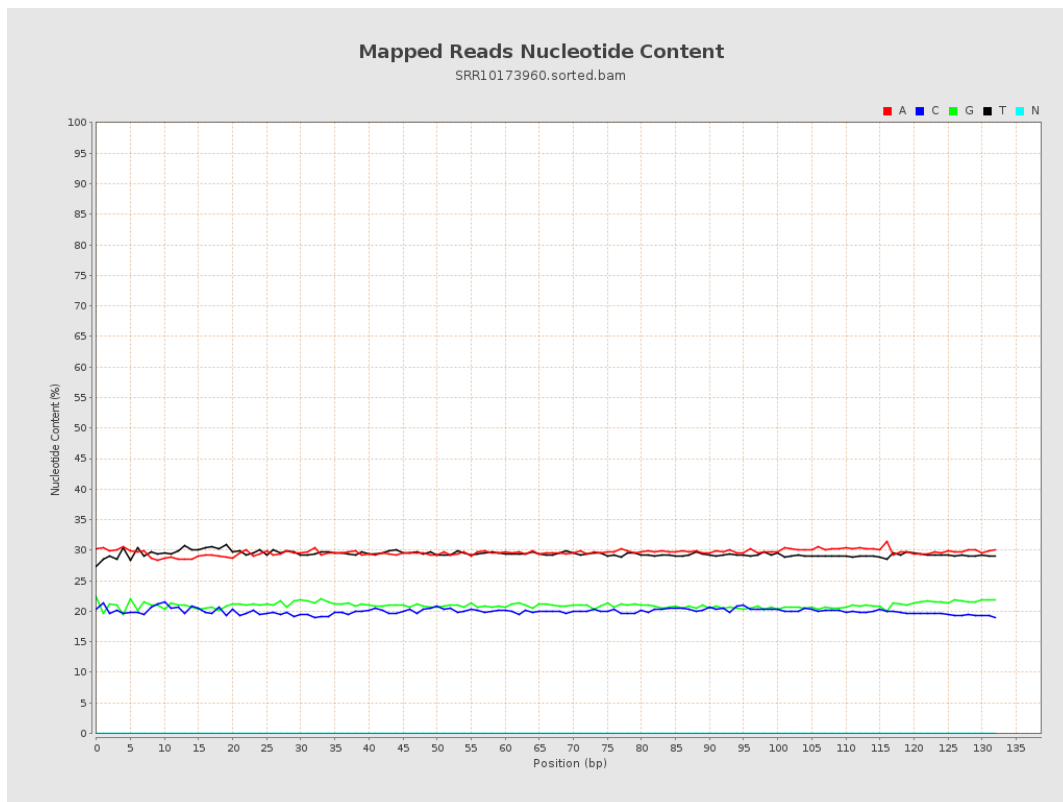
6. Results : Genome Fraction Coverage



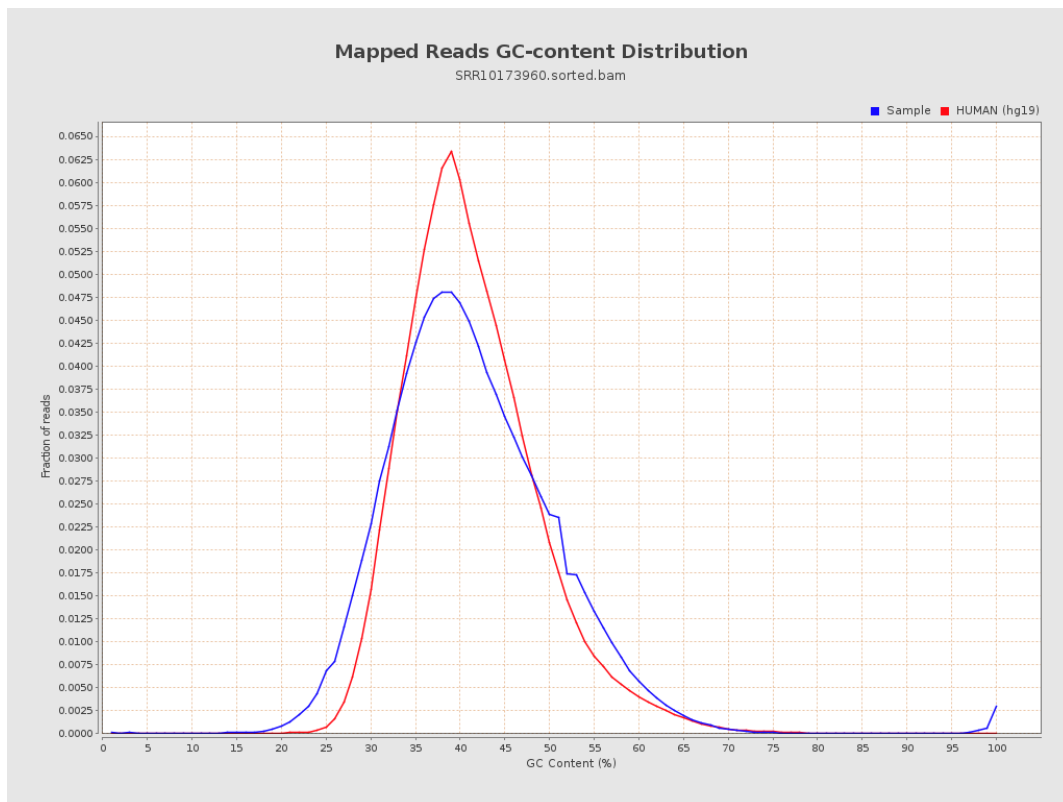
7. Results : Duplication Rate Histogram



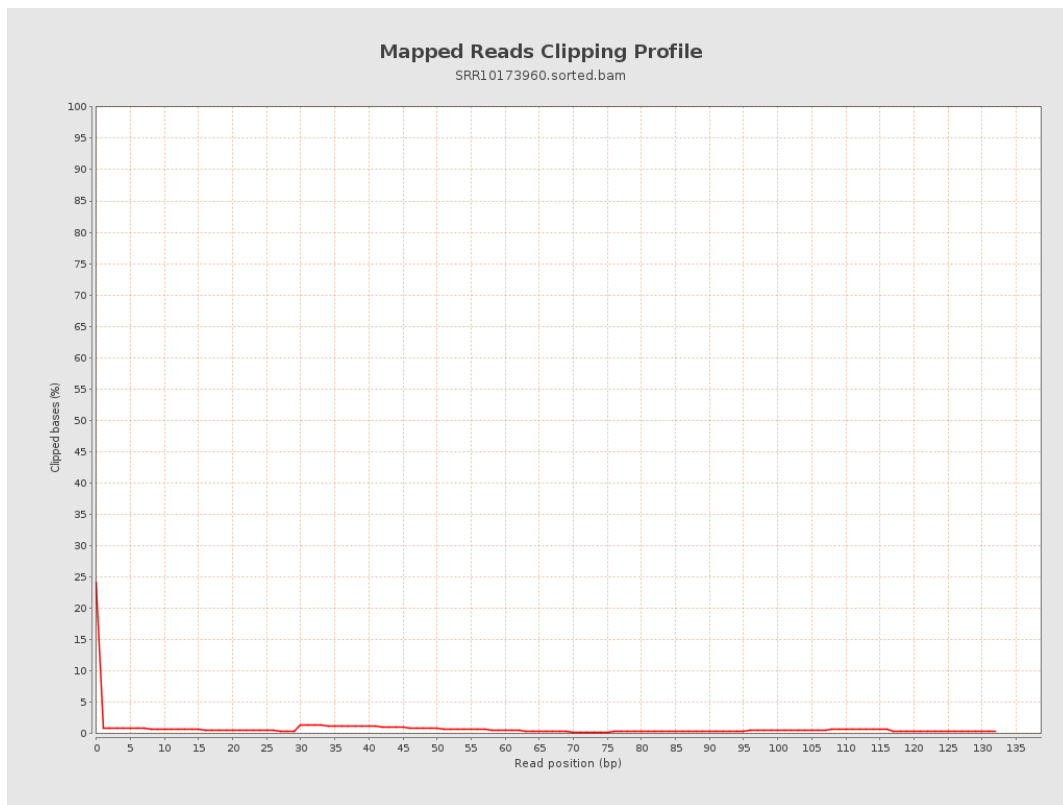
8. Results : Mapped Reads Nucleotide Content



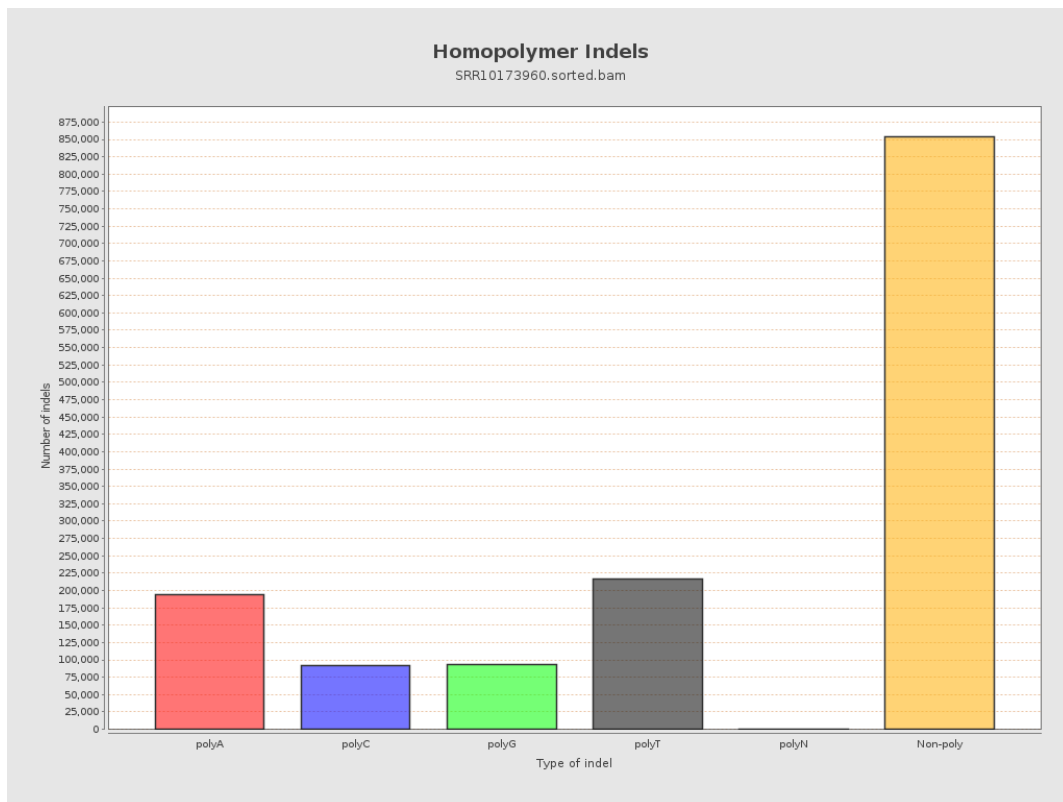
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



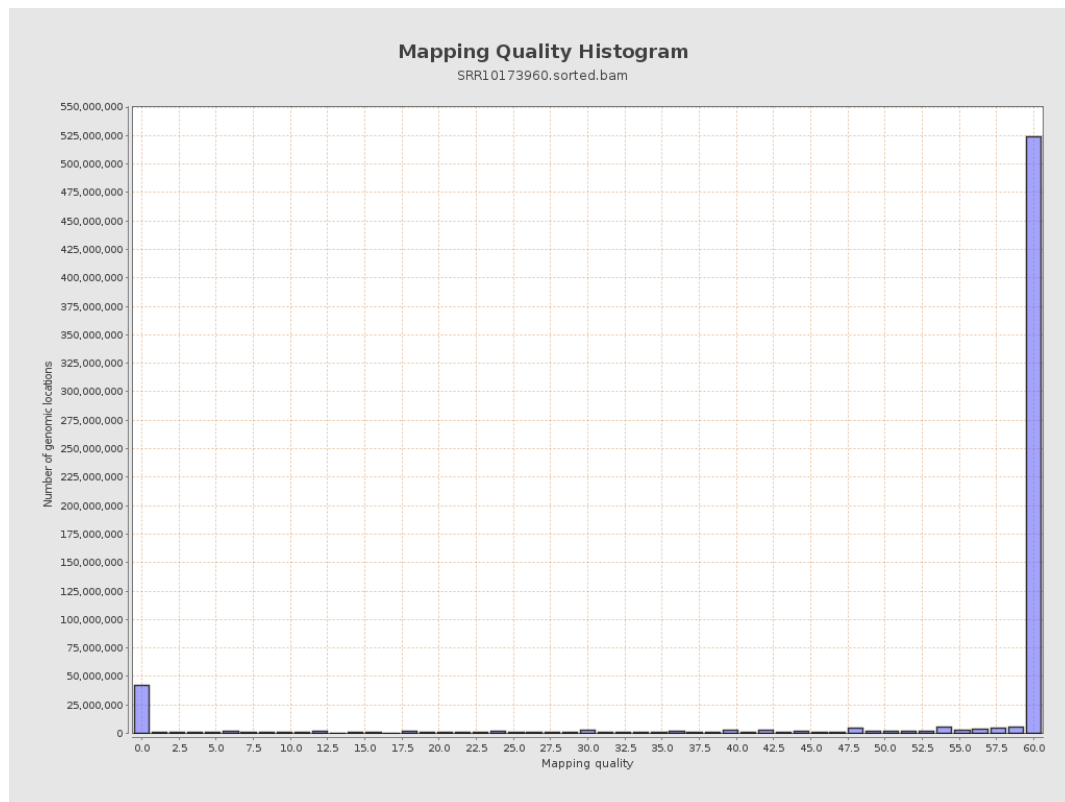
11. Results : Homopolymer Indels



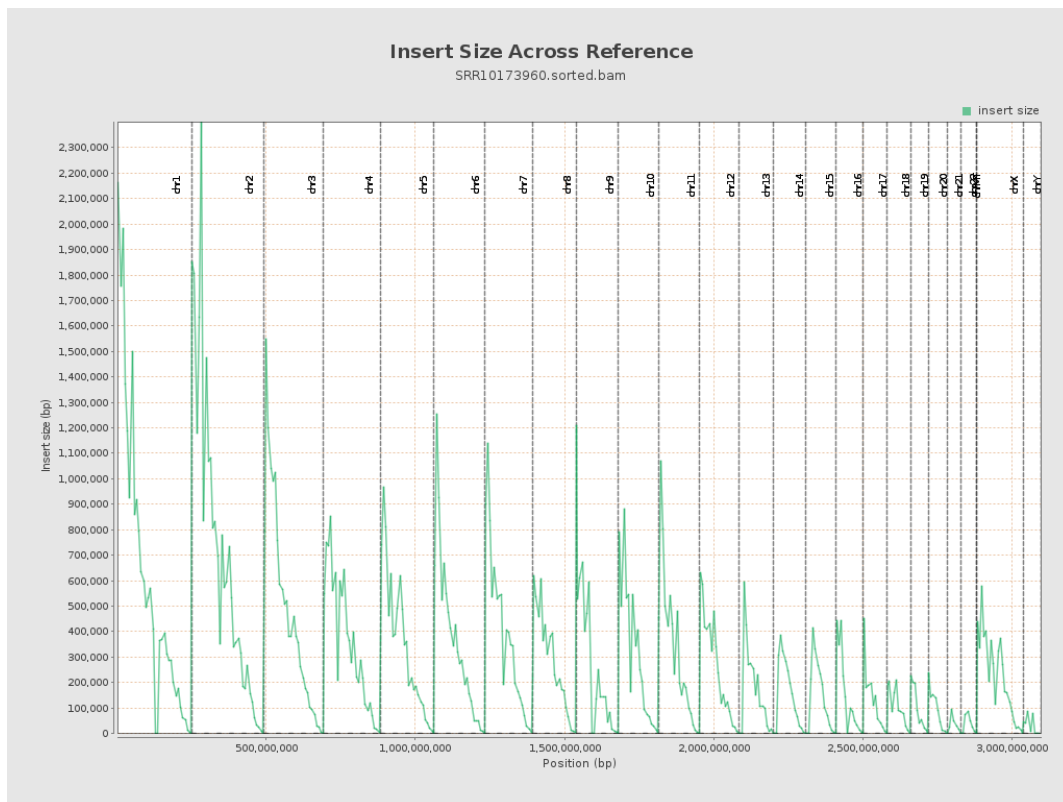
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

