

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 14:42:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173968.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_SRR10173968 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173968_1.fastq.gz SRR10173968_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 14:42:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173968.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,872,014
Mapped reads	2,811,643 / 97.9%
Unmapped reads	60,371 / 2.1%
Mapped paired reads	2,811,643 / 97.9%
Mapped reads, first in pair	1,406,181 / 48.96%
Mapped reads, second in pair	1,405,462 / 48.94%
Mapped reads, both in pair	2,774,740 / 96.61%
Mapped reads, singletons	36,903 / 1.28%
Secondary alignments	0
Supplementary alignments	353,137 / 12.3%
Read min/max/mean length	30 / 133 / 124.62
Duplicated reads (estimated)	2,231,306 / 77.69%
Duplication rate	65.24%
Clipped reads	1,390,455 / 48.41%

2.2. ACGT Content

Number/percentage of A's	95,317,810 / 30.02%
Number/percentage of C's	62,722,048 / 19.75%
Number/percentage of T's	94,554,994 / 29.78%
Number/percentage of G's	64,937,431 / 20.45%
Number/percentage of N's	2,420 / 0%

GC Percentage	40.2%
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2.3. Coverage

Mean	0.1026
Standard Deviation	1.9809

2.4. Mapping Quality

Mean Mapping Quality	52.59
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2.5. Insert size

Mean	1,075,426.79
Standard Deviation	9,580,399.4
P25/Median/P75	104 / 150 / 227

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	2,695,645
Insertions	36,257
Mapped reads with at least one insertion	1.24%
Deletions	95,279
Mapped reads with at least one deletion	3.31%
Homopolymer indels	41.36%

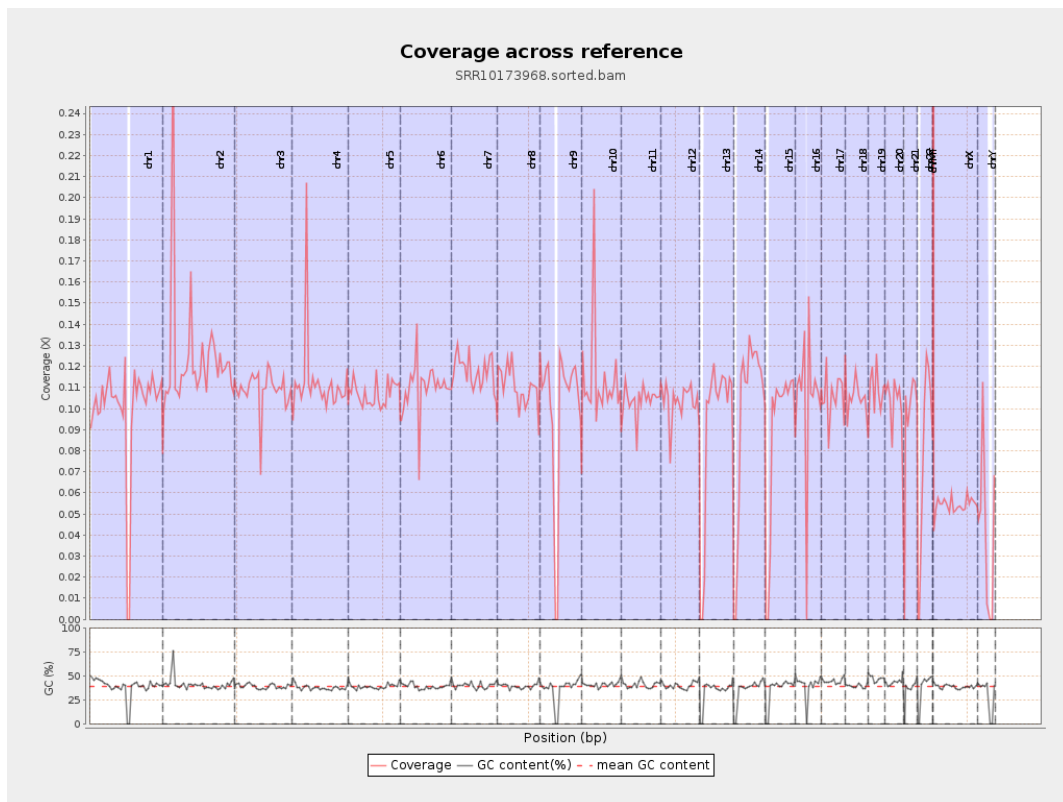
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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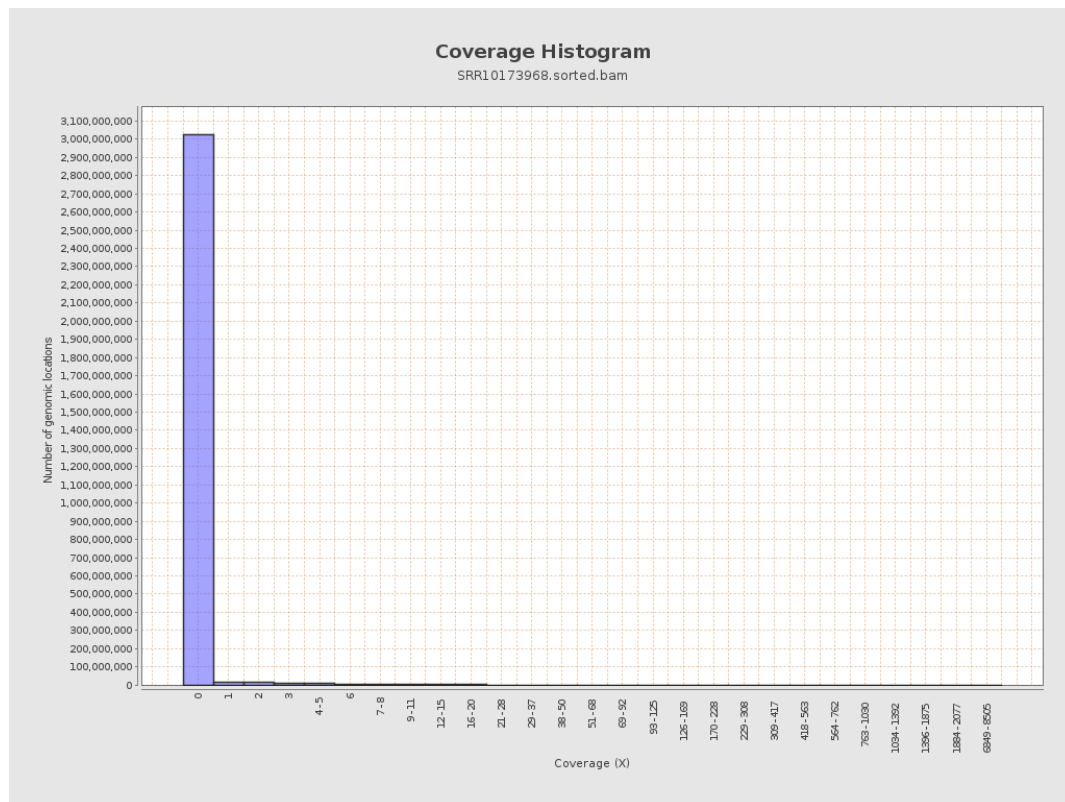
		bases	coverage	deviation
chr1	249250621	24890631	0.0999	1.1381
chr2	243199373	30074944	0.1237	5.9962
chr3	198022430	21600591	0.1091	0.989
chr4	191154276	21494920	0.1124	1.2526
chr5	180915260	19351855	0.107	0.9805
chr6	171115067	18830293	0.11	1.0714
chr7	159138663	18688635	0.1174	1.2047
chr8	146364022	16117348	0.1101	1.4635
chr9	141213431	14122848	0.1	1.1763
chr10	135534747	15369102	0.1134	1.3886
chr11	135006516	14018579	0.1038	0.9747
chr12	133851895	13844361	0.1034	0.9762
chr13	115169878	10537419	0.0915	0.9221
chr14	107349540	10789062	0.1005	0.9559
chr15	102531392	8880383	0.0866	0.8886
chr16	90354753	9438725	0.1045	1.0884
chr17	81195210	8609038	0.106	0.9855
chr18	78077248	8227307	0.1054	1.4086
chr19	59128983	6469597	0.1094	1.0287
chr20	63025520	6453393	0.1024	0.9792
chr21	48129895	4603066	0.0956	1.0196
chr22	51304566	4031869	0.0786	0.8793
chrMT	16571	317111	19.1365	18.8121
chrX	155270560	8435941	0.0543	0.6947

chrY	59373566	2561341	0.0431	0.8352
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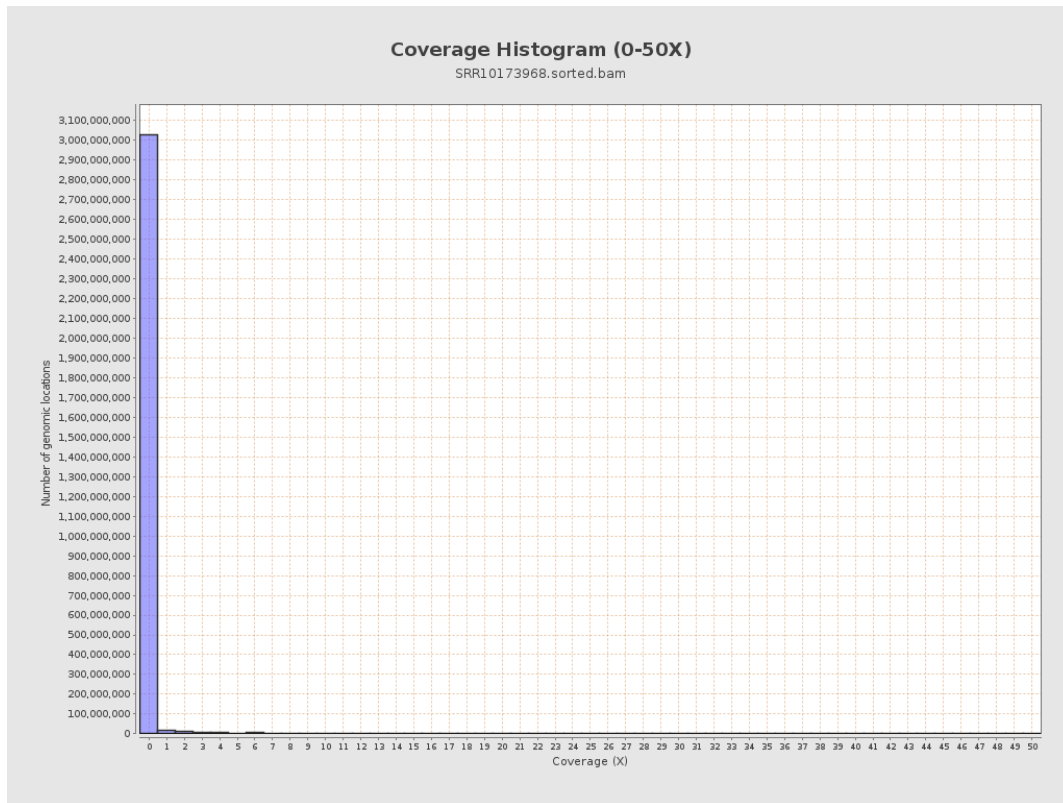
3. Results : Coverage across reference



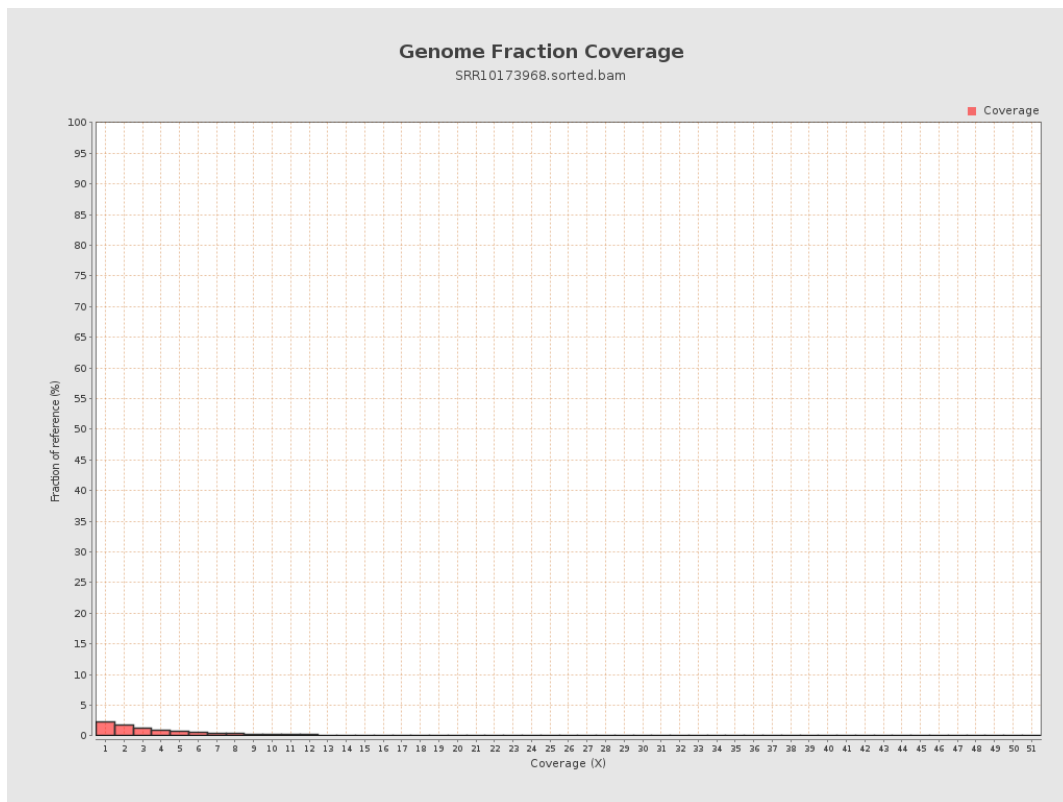
4. Results : Coverage Histogram



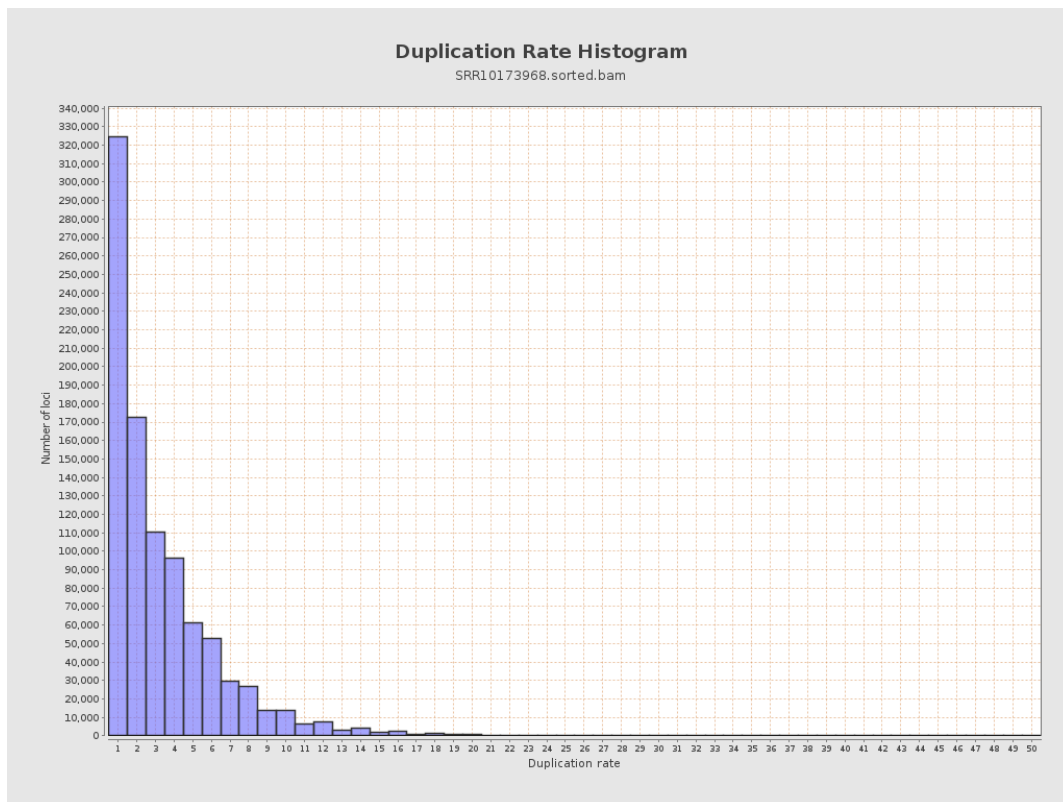
5. Results : Coverage Histogram (0-50X)



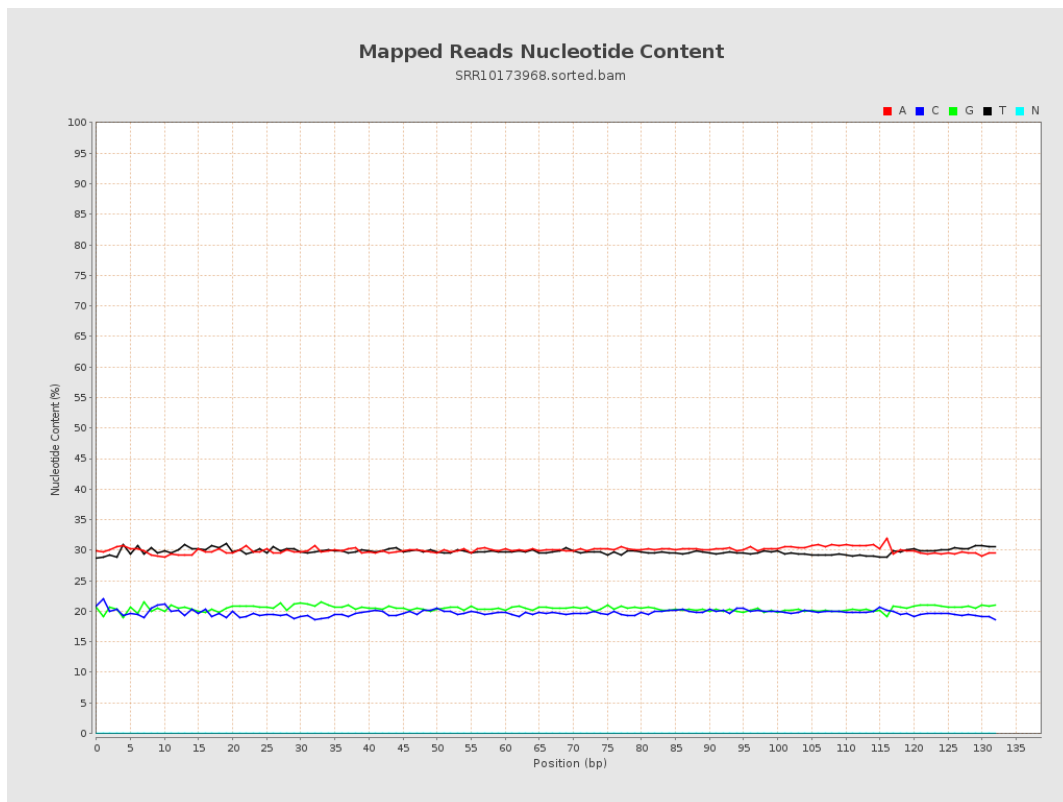
6. Results : Genome Fraction Coverage



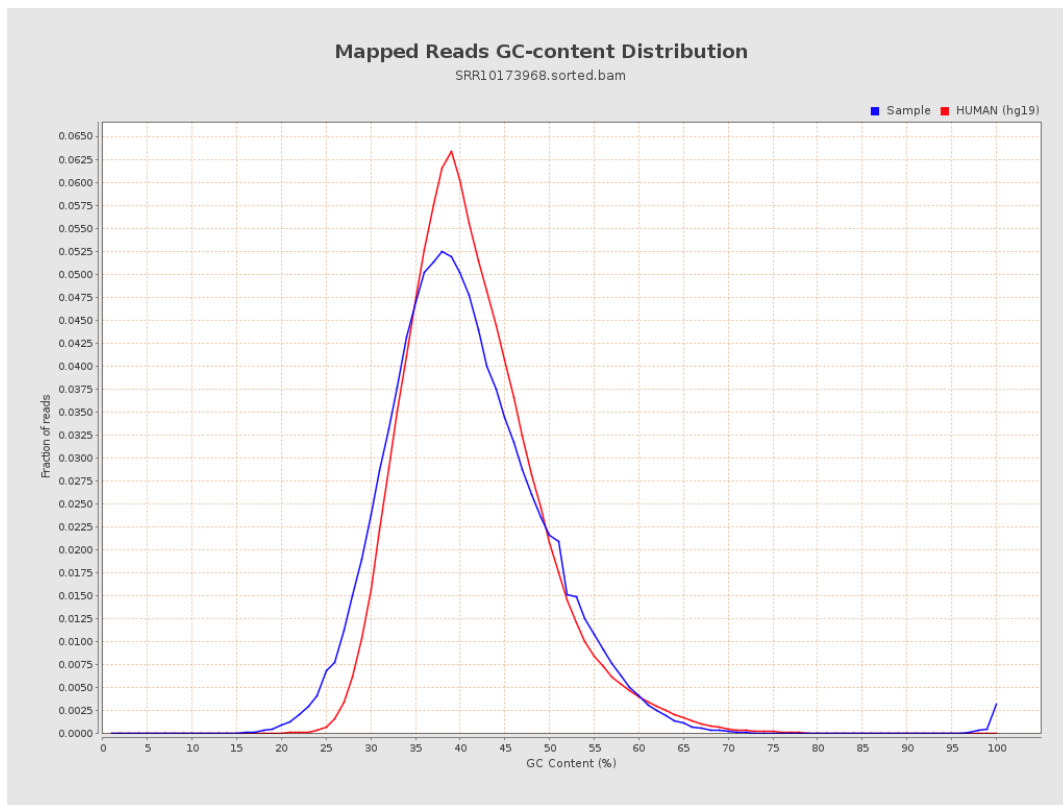
7. Results : Duplication Rate Histogram



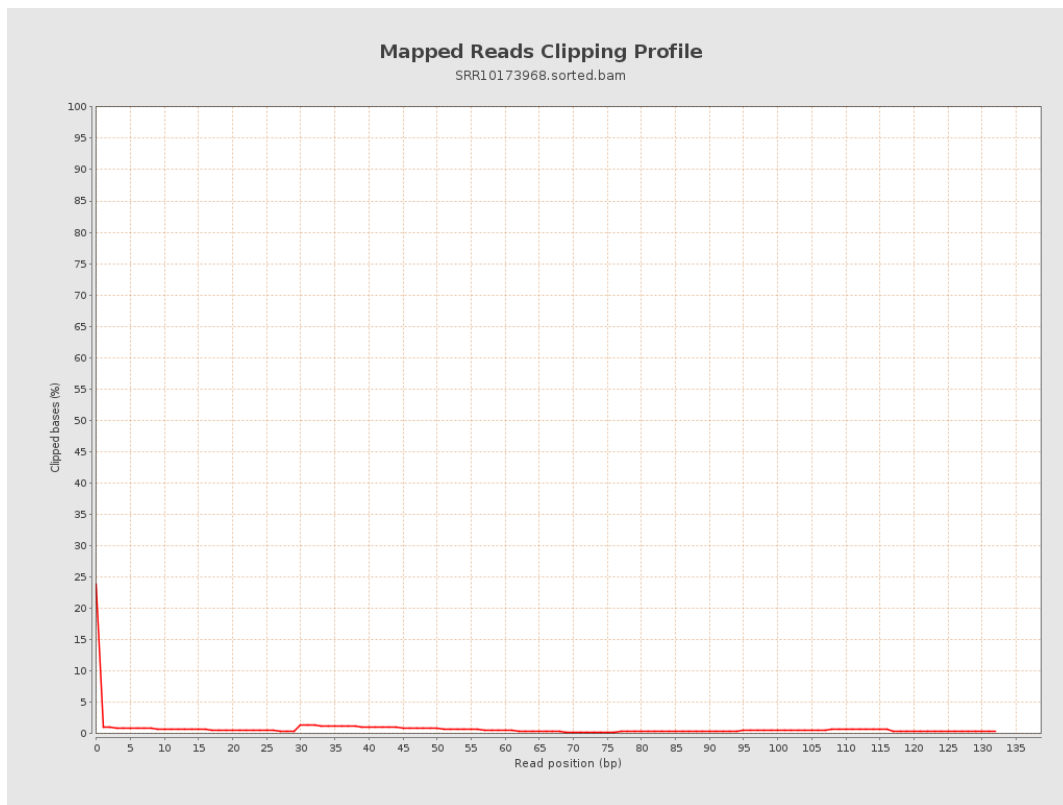
8. Results : Mapped Reads Nucleotide Content



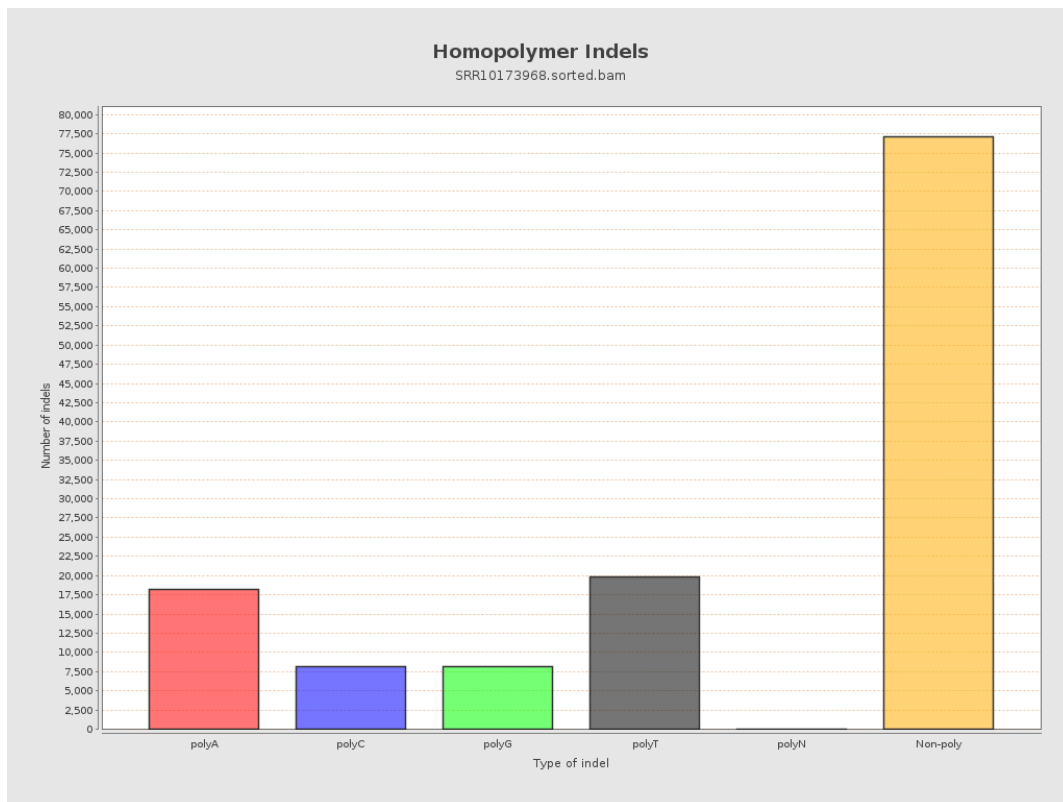
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



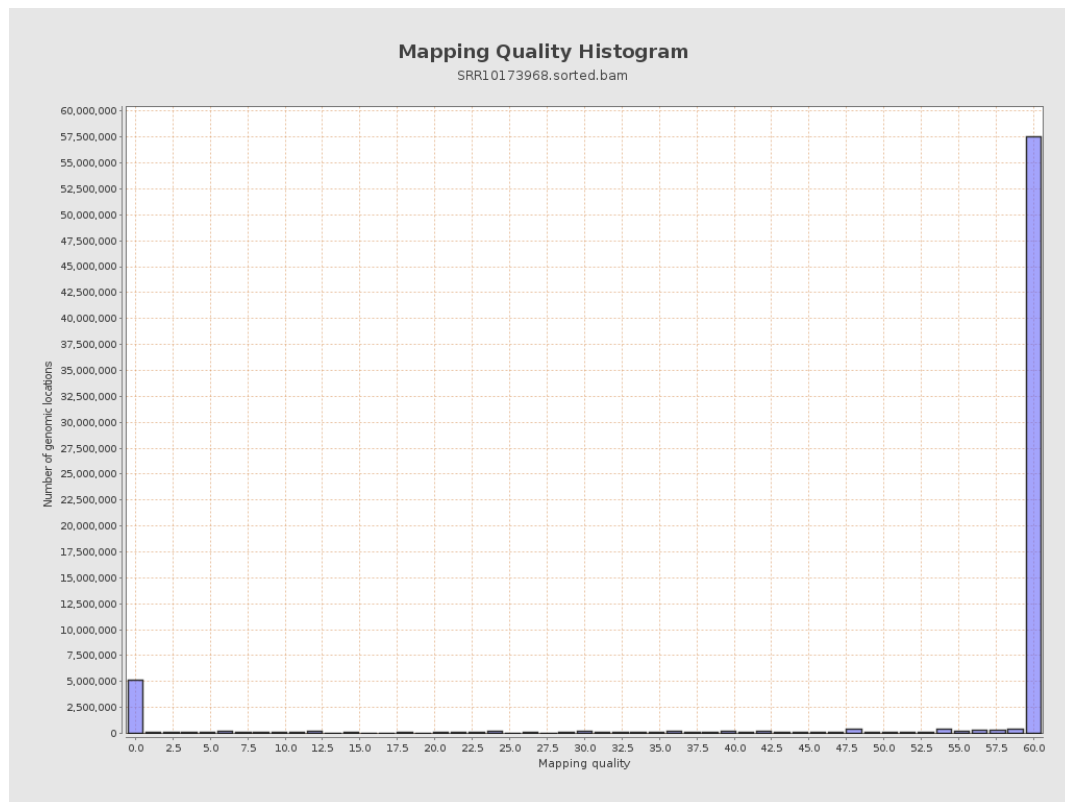
11. Results : Homopolymer Indels



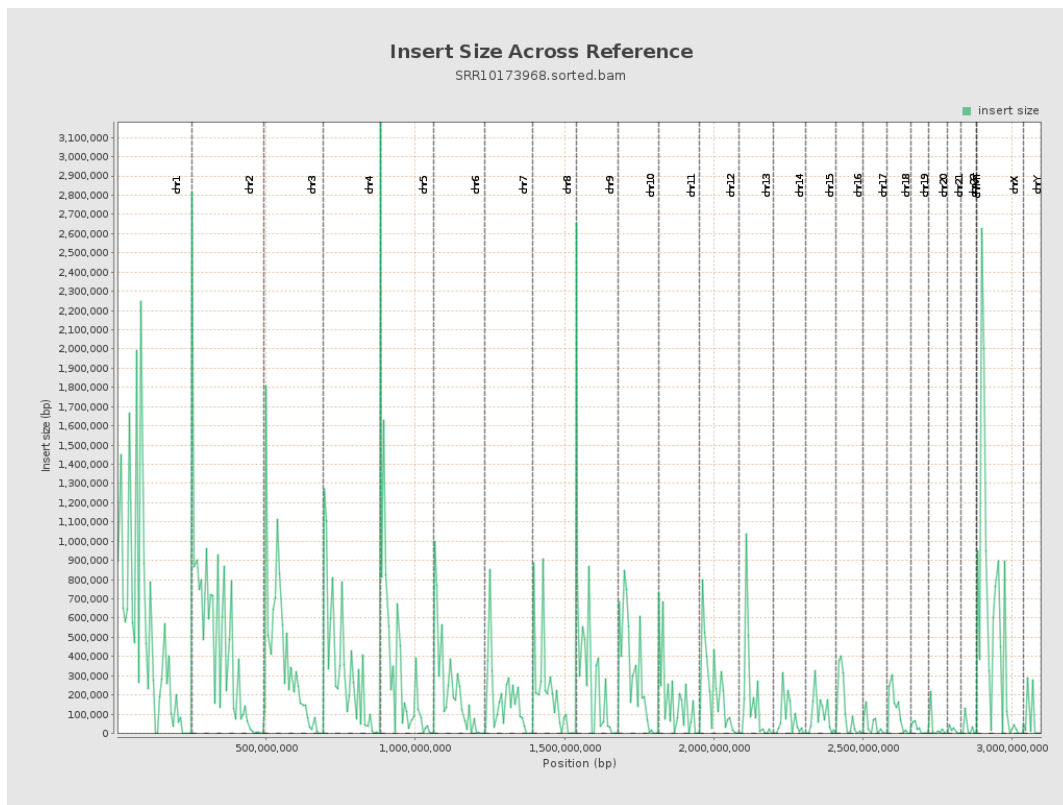
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

