

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:51:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173864.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_SRR10173864 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173864_1.fastq.gz SRR10173864_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:51:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173864.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,386,552
Mapped reads	2,315,506 / 97.02%
Unmapped reads	71,046 / 2.98%
Mapped paired reads	2,315,506 / 97.02%
Mapped reads, first in pair	1,160,183 / 48.61%
Mapped reads, second in pair	1,155,323 / 48.41%
Mapped reads, both in pair	2,270,156 / 95.12%
Mapped reads, singletons	45,350 / 1.9%
Secondary alignments	0
Supplementary alignments	244,509 / 10.25%
Read min/max/mean length	30 / 133 / 128.24
Duplicated reads (estimated)	1,792,206 / 75.1%
Duplication rate	63.57%
Clipped reads	1,020,102 / 42.74%

2.2. ACGT Content

Number/percentage of A's	81,965,231 / 30.16%
Number/percentage of C's	53,040,007 / 19.52%
Number/percentage of T's	81,713,758 / 30.07%
Number/percentage of G's	55,039,853 / 20.25%
Number/percentage of N's	2,938 / 0%

GC Percentage	39.77%
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2.3. Coverage

Mean	0.0878
Standard Deviation	1.4514

2.4. Mapping Quality

Mean Mapping Quality	52.75
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2.5. Insert size

Mean	1,203,084.89
Standard Deviation	9,950,387.16
P25/Median/P75	142 / 202 / 294

2.6. Mismatches and indels

General error rate	1.14%
Mismatches	2,995,484
Insertions	32,114
Mapped reads with at least one insertion	1.33%
Deletions	65,827
Mapped reads with at least one deletion	2.77%
Homopolymer indels	42.72%

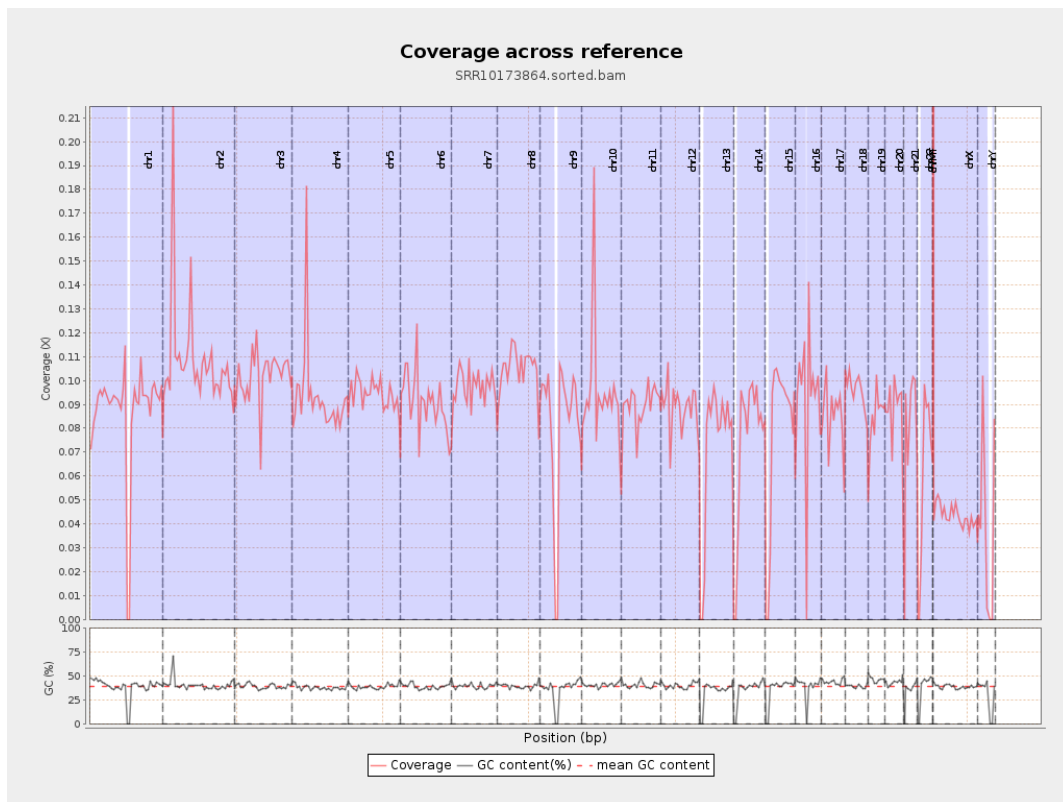
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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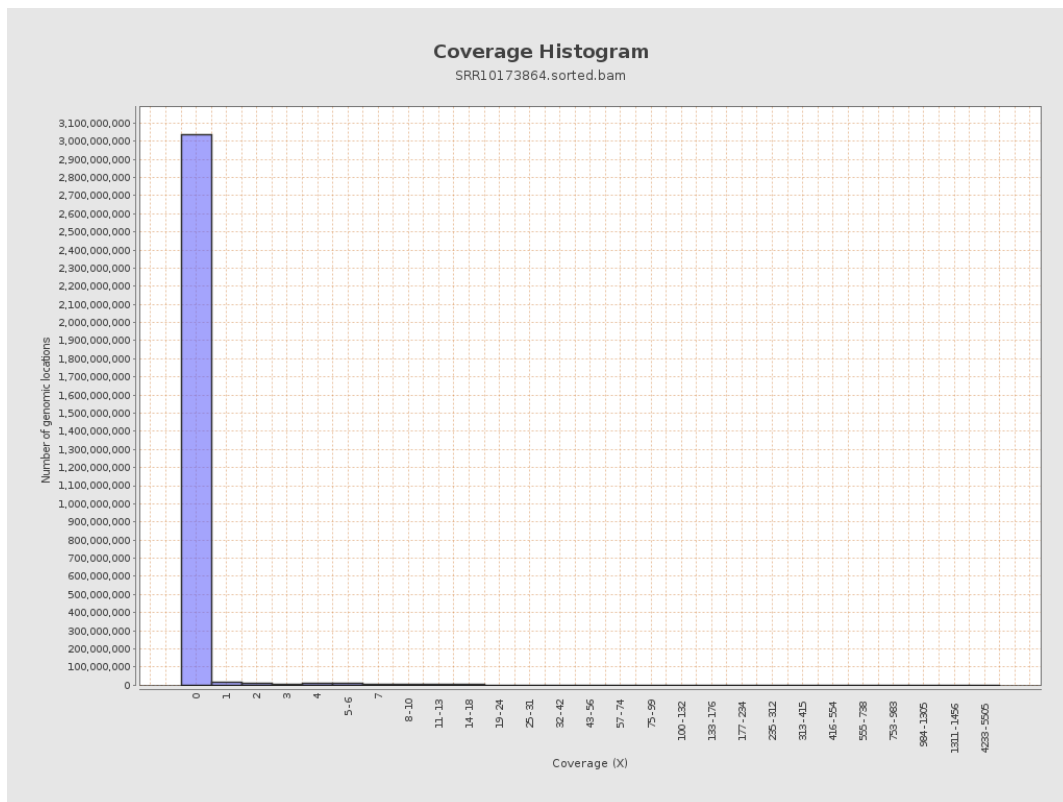
		bases	coverage	deviation
chr1	249250621	21717451	0.0871	1.0497
chr2	243199373	26318843	0.1082	3.9457
chr3	198022430	20175763	0.1019	0.9199
chr4	191154276	17807216	0.0932	1.0806
chr5	180915260	17043972	0.0942	0.8817
chr6	171115067	15615503	0.0913	0.9262
chr7	159138663	15435755	0.097	1.092
chr8	146364022	15344838	0.1048	1.2285
chr9	141213431	11581417	0.082	1.0132
chr10	135534747	12874668	0.095	1.2675
chr11	135006516	12072830	0.0894	0.8732
chr12	133851895	11899297	0.0889	0.8568
chr13	115169878	8249274	0.0716	0.7711
chr14	107349540	8076433	0.0752	0.7851
chr15	102531392	7854917	0.0766	0.7819
chr16	90354753	8257533	0.0914	1.0185
chr17	81195210	6992313	0.0861	0.864
chr18	78077248	7496295	0.096	1.4562
chr19	59128983	5023878	0.085	0.9427
chr20	63025520	5588013	0.0887	0.8794
chr21	48129895	3874717	0.0805	1.0865
chr22	51304566	3088069	0.0602	0.7404
chrMT	16571	356427	21.5091	17.2568
chrX	155270560	6758128	0.0435	0.592

chrY	59373566	2426640	0.0409	0.7866
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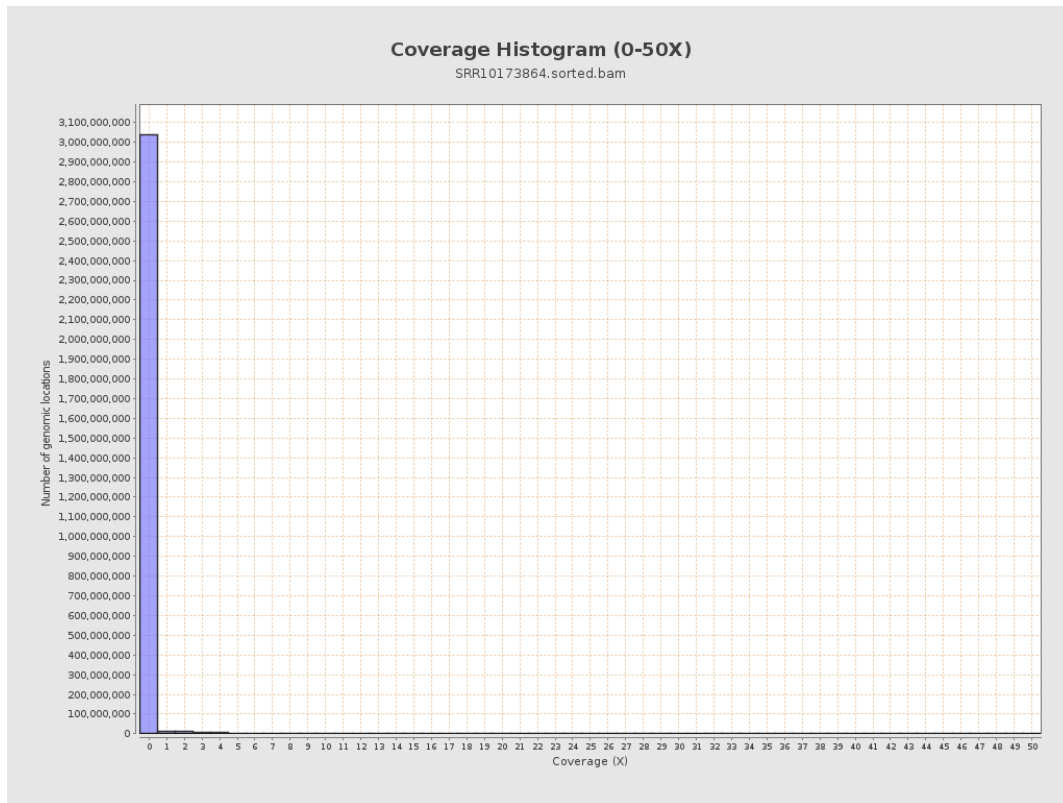
3. Results : Coverage across reference



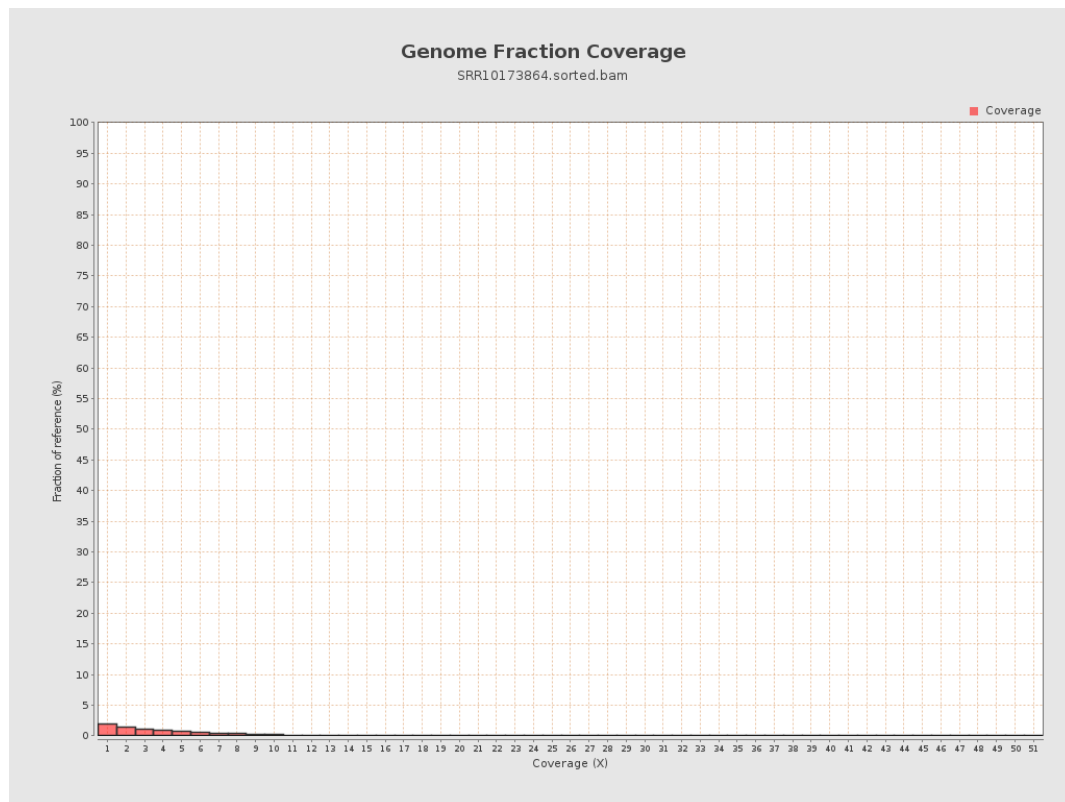
4. Results : Coverage Histogram



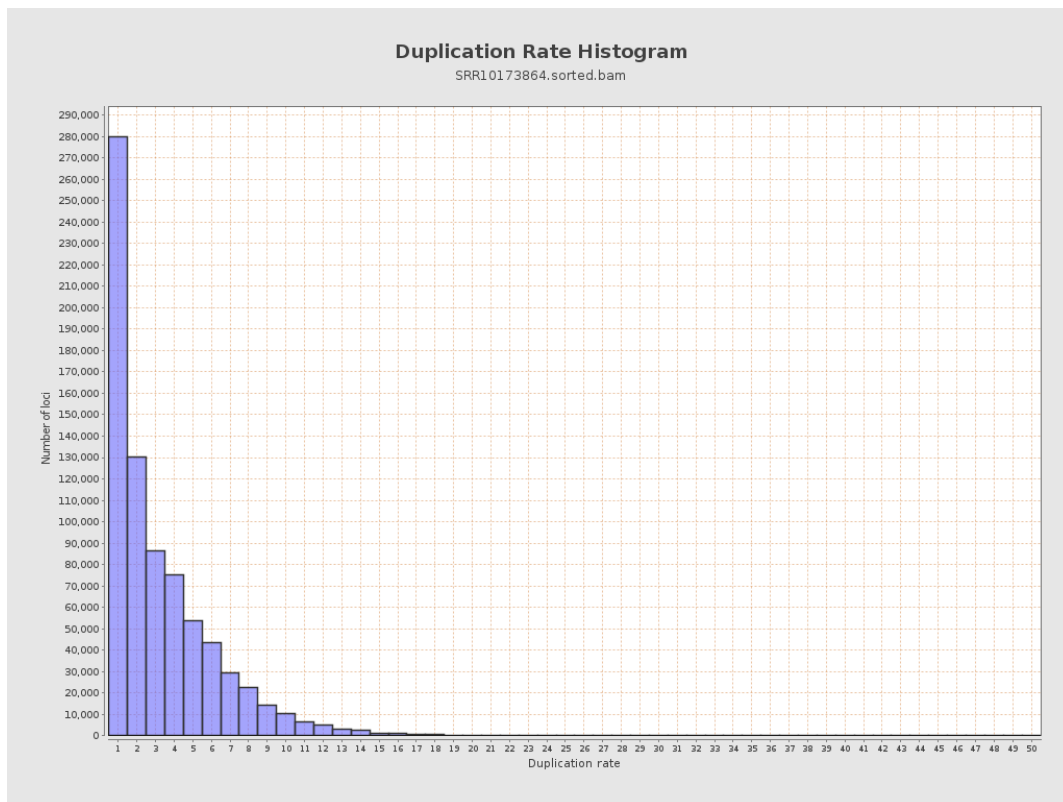
5. Results : Coverage Histogram (0-50X)



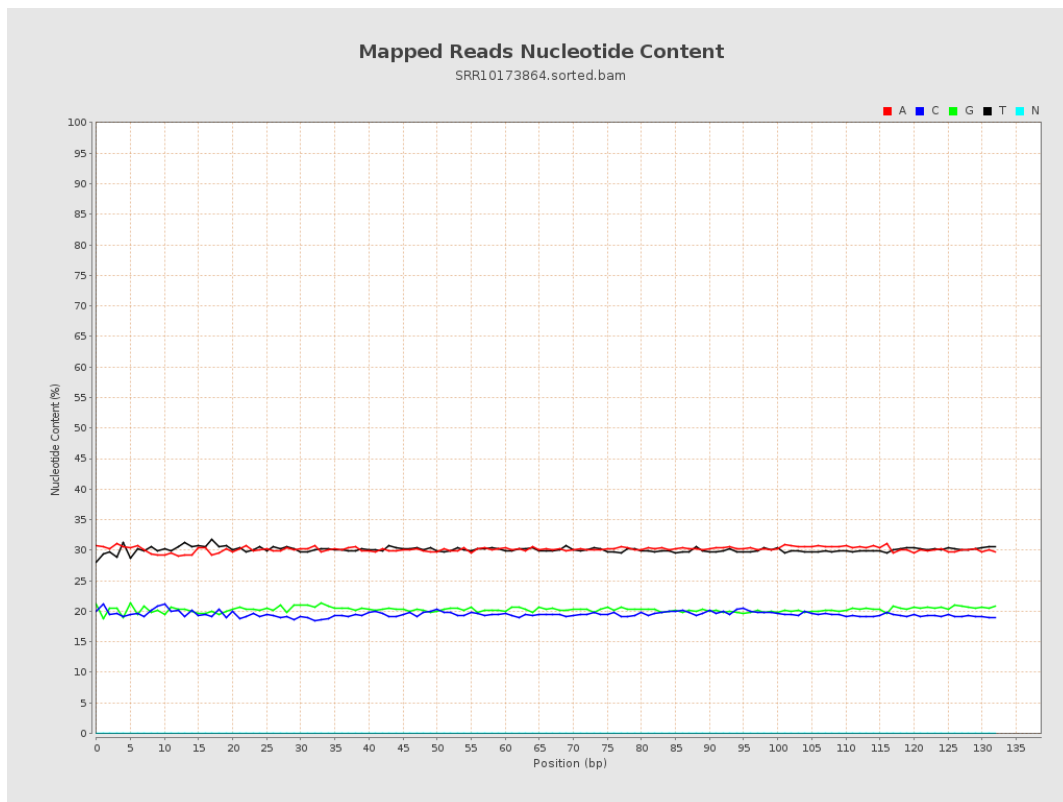
6. Results : Genome Fraction Coverage



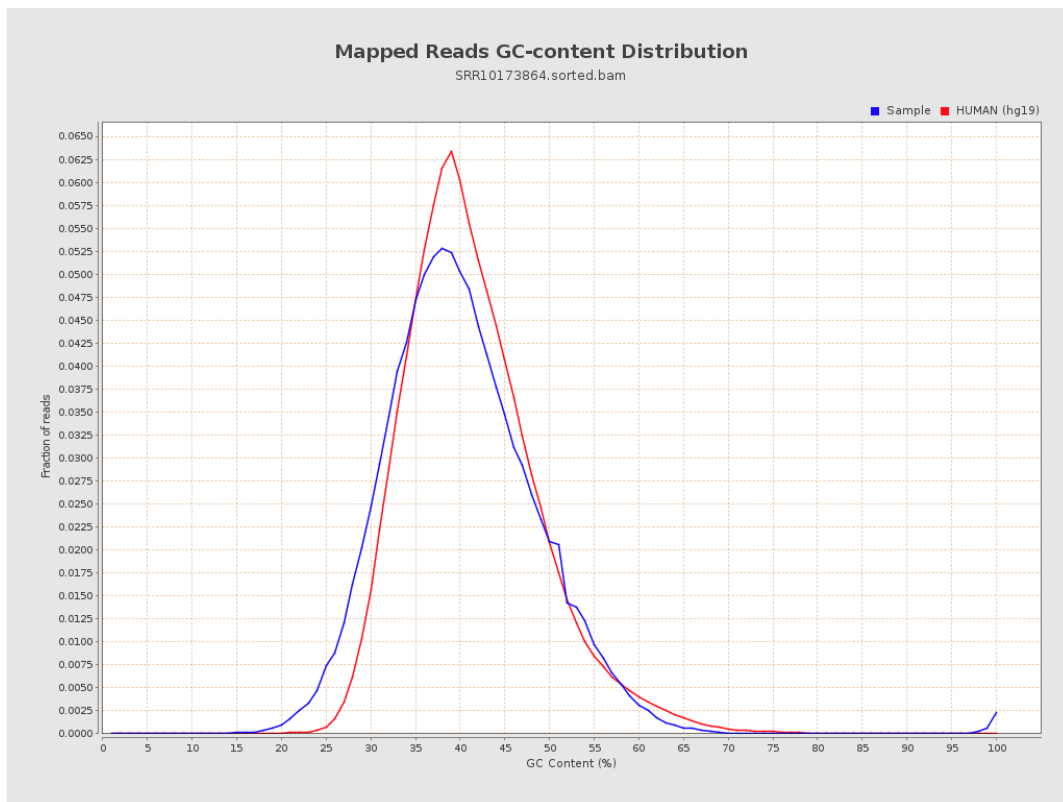
7. Results : Duplication Rate Histogram



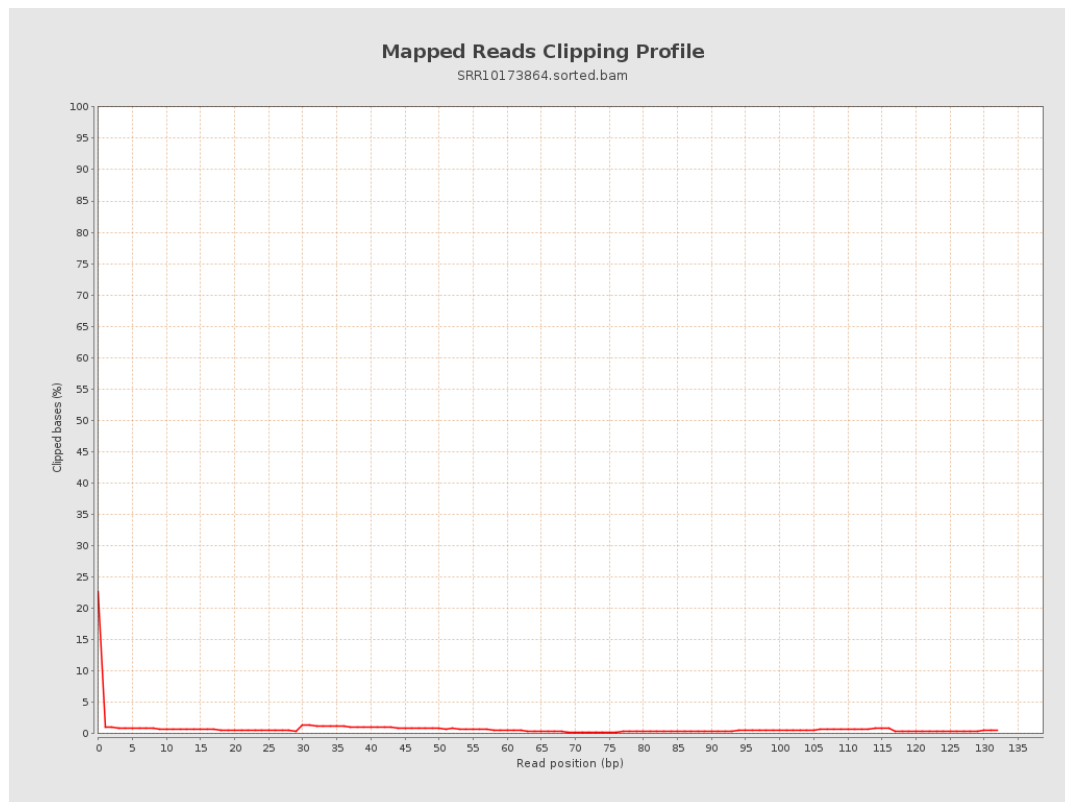
8. Results : Mapped Reads Nucleotide Content



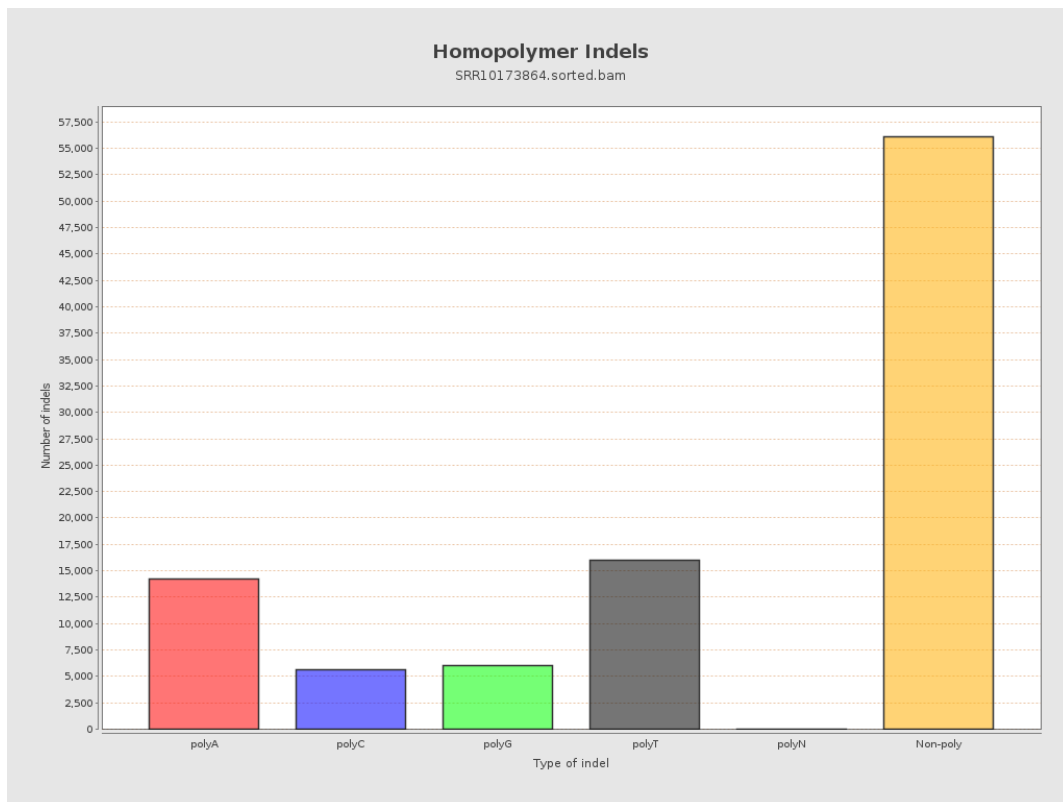
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



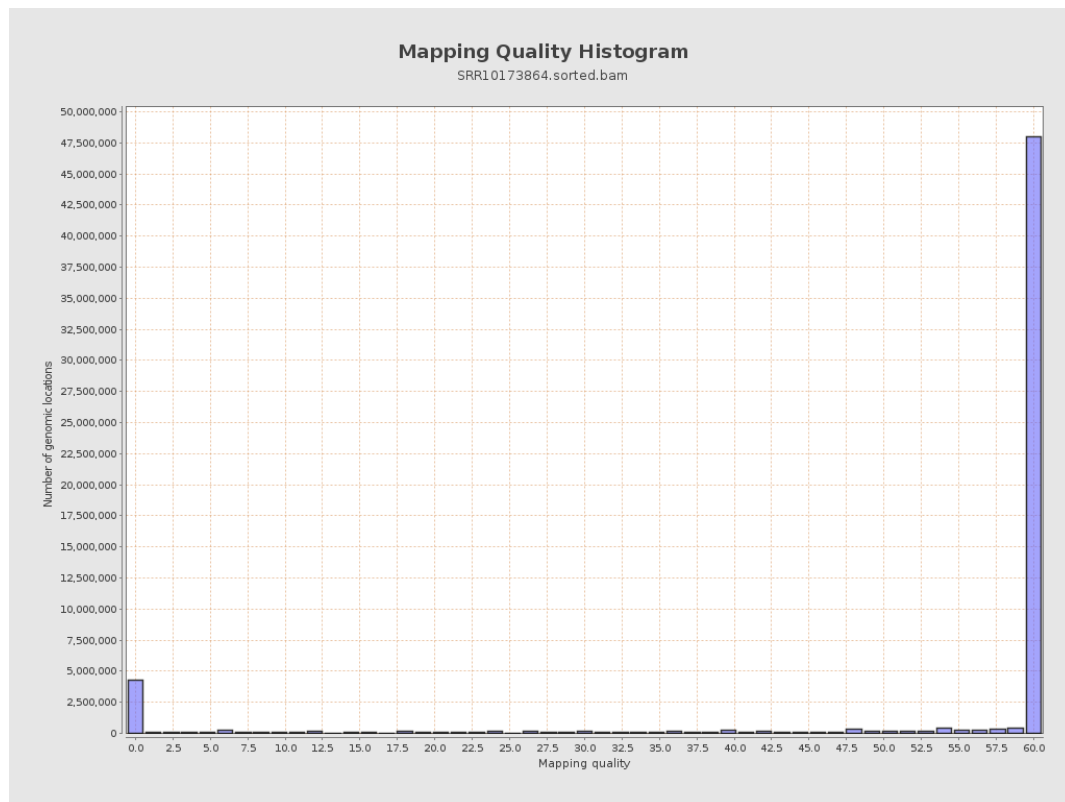
11. Results : Homopolymer Indels



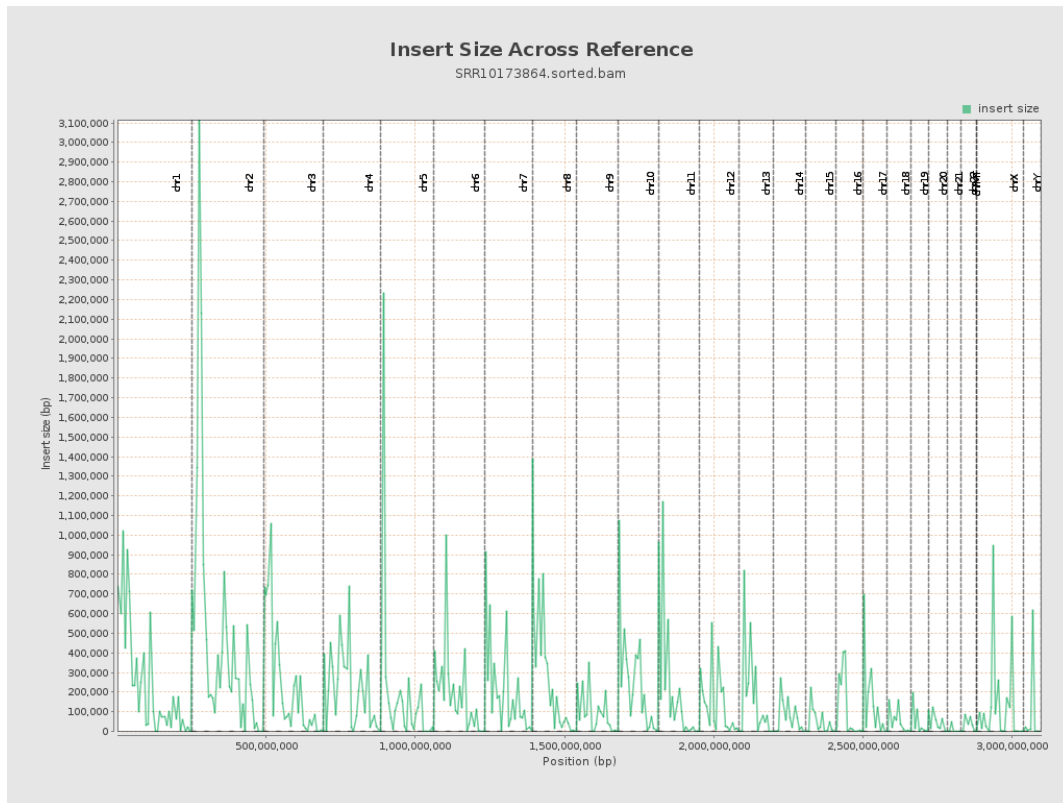
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

