

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:47:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173863.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_SRR10173863 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173863_1.fastq.gz SRR10173863_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:47:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173863.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,207,840
Mapped reads	2,145,352 / 97.17%
Unmapped reads	62,488 / 2.83%
Mapped paired reads	2,145,352 / 97.17%
Mapped reads, first in pair	1,076,351 / 48.75%
Mapped reads, second in pair	1,069,001 / 48.42%
Mapped reads, both in pair	2,104,652 / 95.33%
Mapped reads, singletons	40,700 / 1.84%
Secondary alignments	0
Supplementary alignments	203,817 / 9.23%
Read min/max/mean length	30 / 133 / 127.82
Duplicated reads (estimated)	1,655,123 / 74.97%
Duplication rate	63.88%
Clipped reads	845,591 / 38.3%

2.2. ACGT Content

Number/percentage of A's	76,242,373 / 30.13%
Number/percentage of C's	49,479,256 / 19.55%
Number/percentage of T's	76,038,993 / 30.05%
Number/percentage of G's	51,303,755 / 20.27%
Number/percentage of N's	2,989 / 0%

GC Percentage	39.82%
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2.3. Coverage

Mean	0.0818
Standard Deviation	1.3452

2.4. Mapping Quality

Mean Mapping Quality	53.01
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2.5. Insert size

Mean	1,096,641.24
Standard Deviation	9,723,519.84
P25/Median/P75	146 / 205 / 291

2.6. Mismatches and indels

General error rate	1.13%
Mismatches	2,782,724
Insertions	28,417
Mapped reads with at least one insertion	1.28%
Deletions	59,939
Mapped reads with at least one deletion	2.72%
Homopolymer indels	42.65%

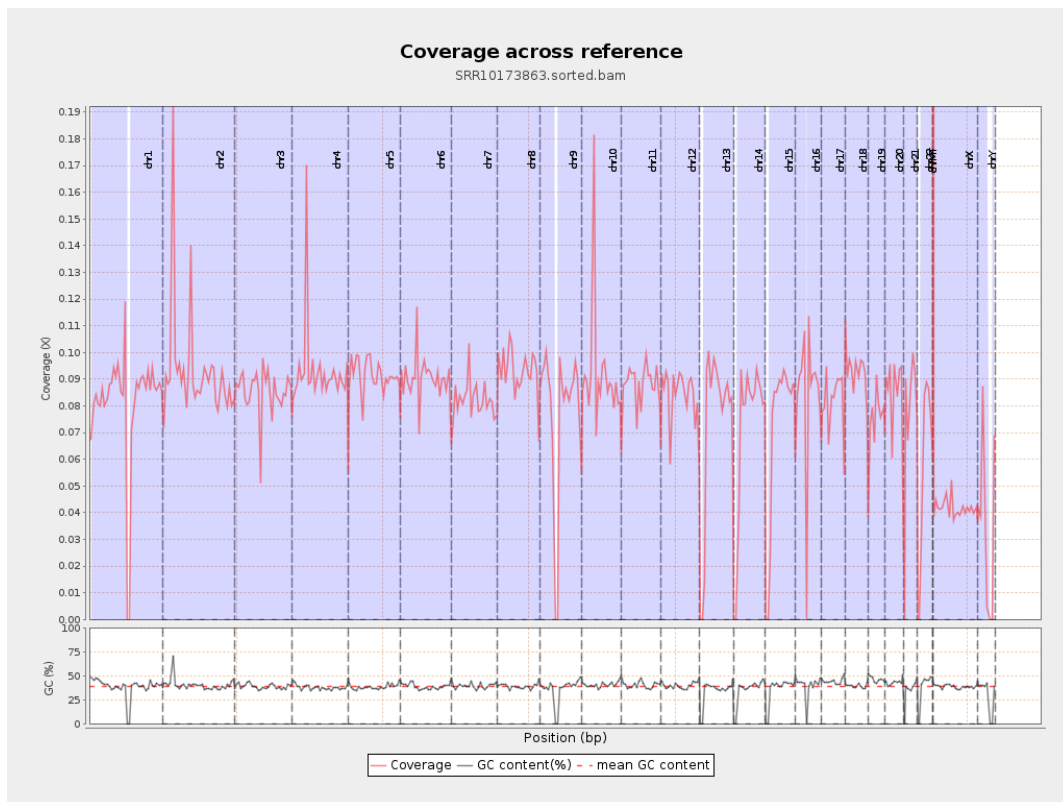
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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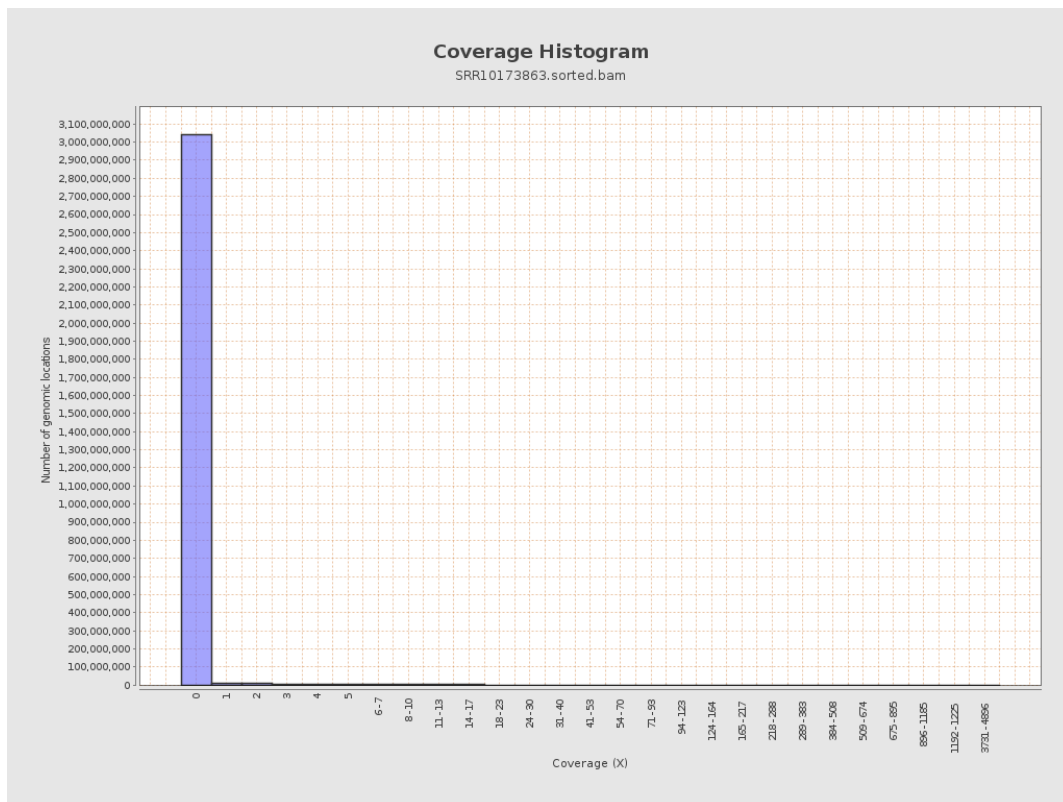
		bases	coverage	deviation
chr1	249250621	20294155	0.0814	1.1624
chr2	243199373	22589621	0.0929	3.5057
chr3	198022430	16884502	0.0853	0.8418
chr4	191154276	17827629	0.0933	1.0846
chr5	180915260	16467953	0.091	0.8766
chr6	171115067	15460490	0.0904	0.9269
chr7	159138663	13035308	0.0819	0.9475
chr8	146364022	13611152	0.093	1.2424
chr9	141213431	10947609	0.0775	0.9856
chr10	135534747	12424798	0.0917	1.2045
chr11	135006516	11847438	0.0878	0.8735
chr12	133851895	11334246	0.0847	0.84
chr13	115169878	8455881	0.0734	0.7889
chr14	107349540	7740806	0.0721	0.7697
chr15	102531392	7180650	0.07	0.7434
chr16	90354753	7490065	0.0829	0.9517
chr17	81195210	6718518	0.0827	0.8251
chr18	78077248	7278509	0.0932	1.264
chr19	59128983	4479418	0.0758	0.931
chr20	63025520	5406158	0.0858	0.8569
chr21	48129895	3756028	0.078	0.9458
chr22	51304566	2952659	0.0576	0.7041
chrMT	16571	445072	26.8585	23.8866
chrX	155270560	6472246	0.0417	0.593

chrY	59373566	2116410	0.0356	0.6916
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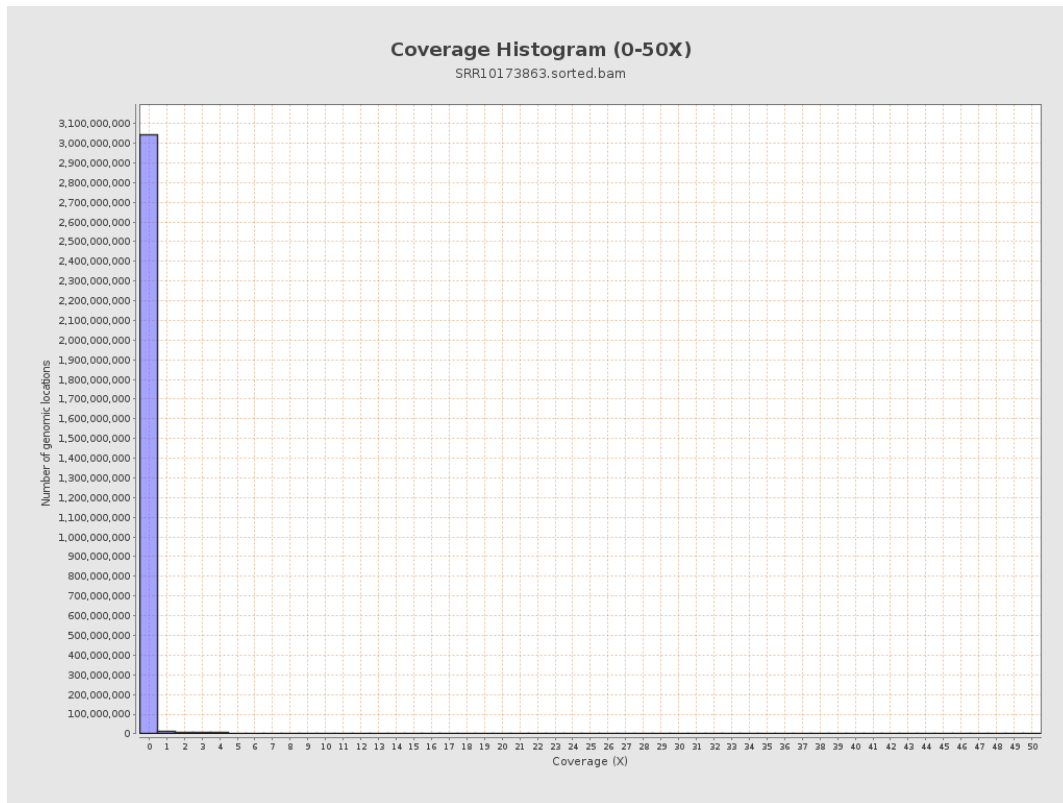
3. Results : Coverage across reference



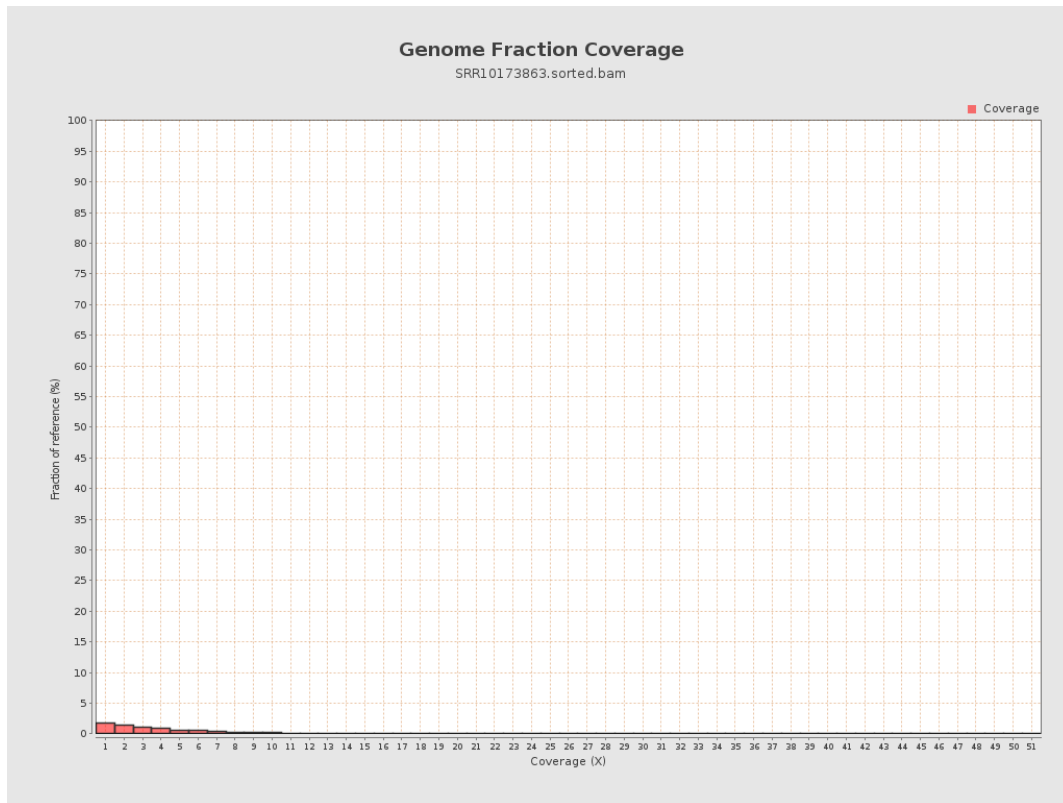
4. Results : Coverage Histogram



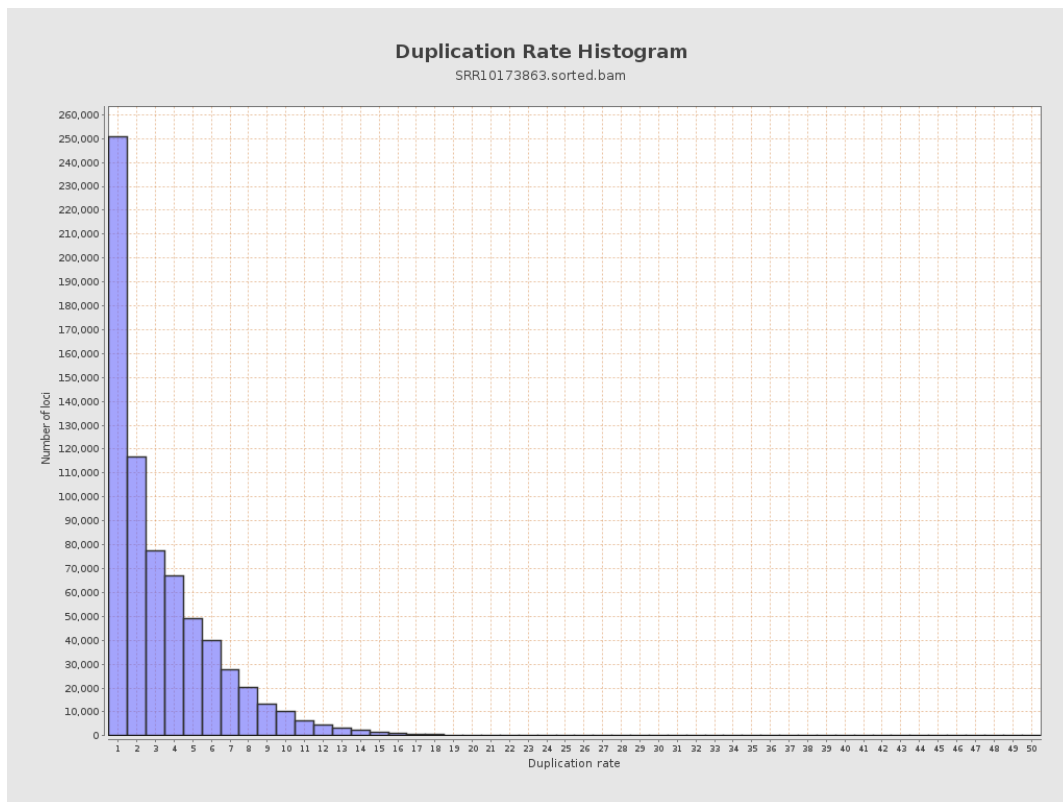
5. Results : Coverage Histogram (0-50X)



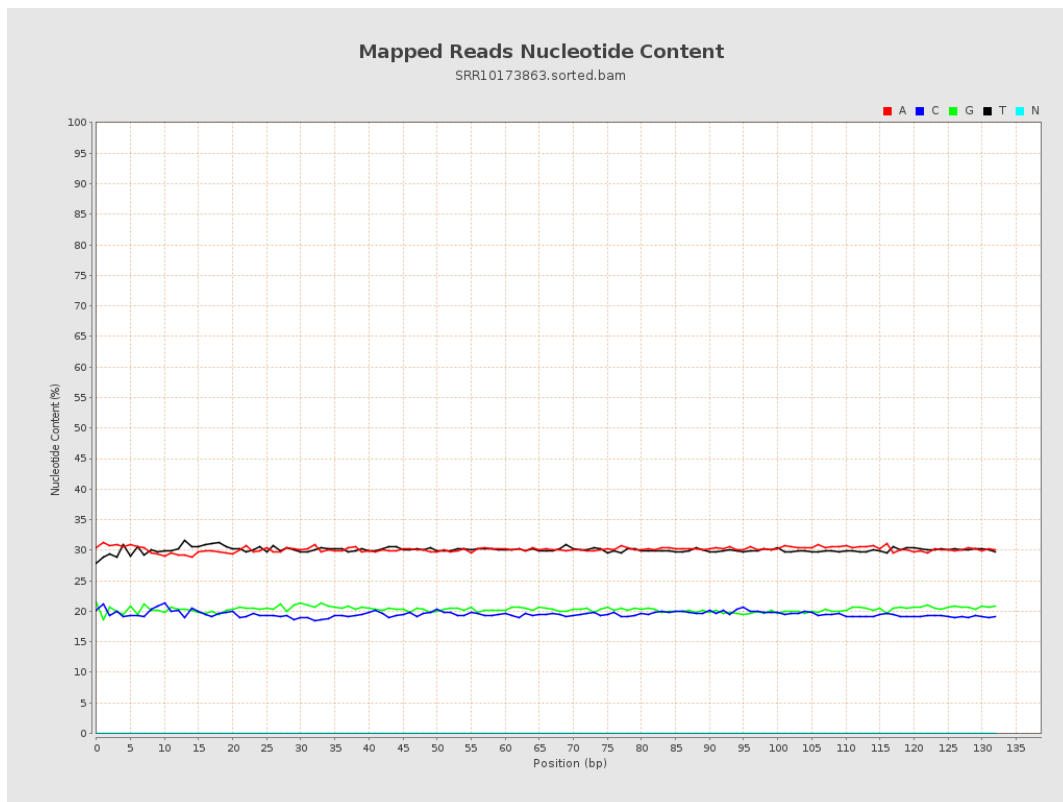
6. Results : Genome Fraction Coverage



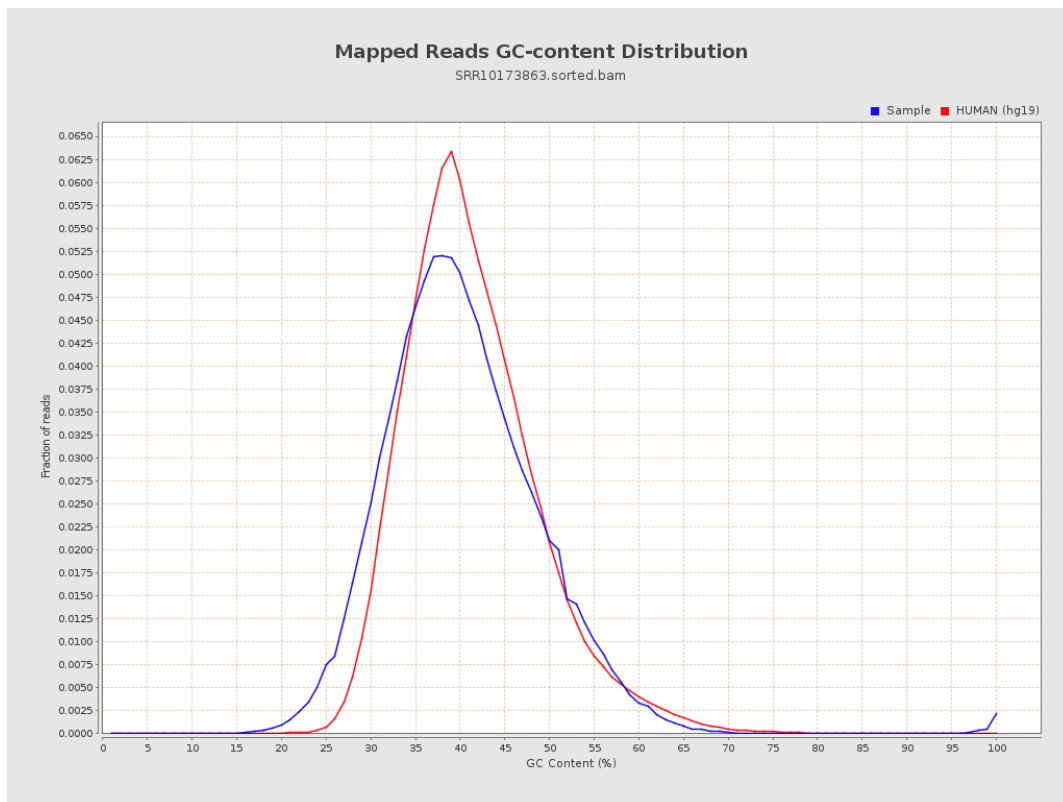
7. Results : Duplication Rate Histogram



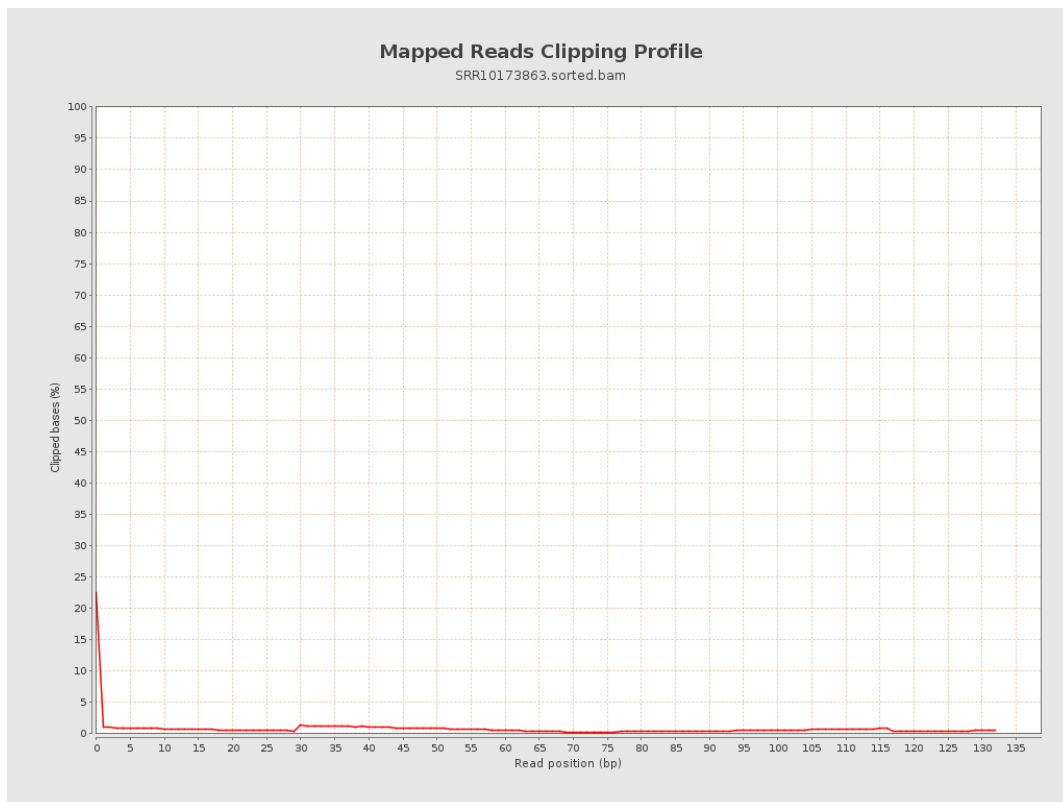
8. Results : Mapped Reads Nucleotide Content



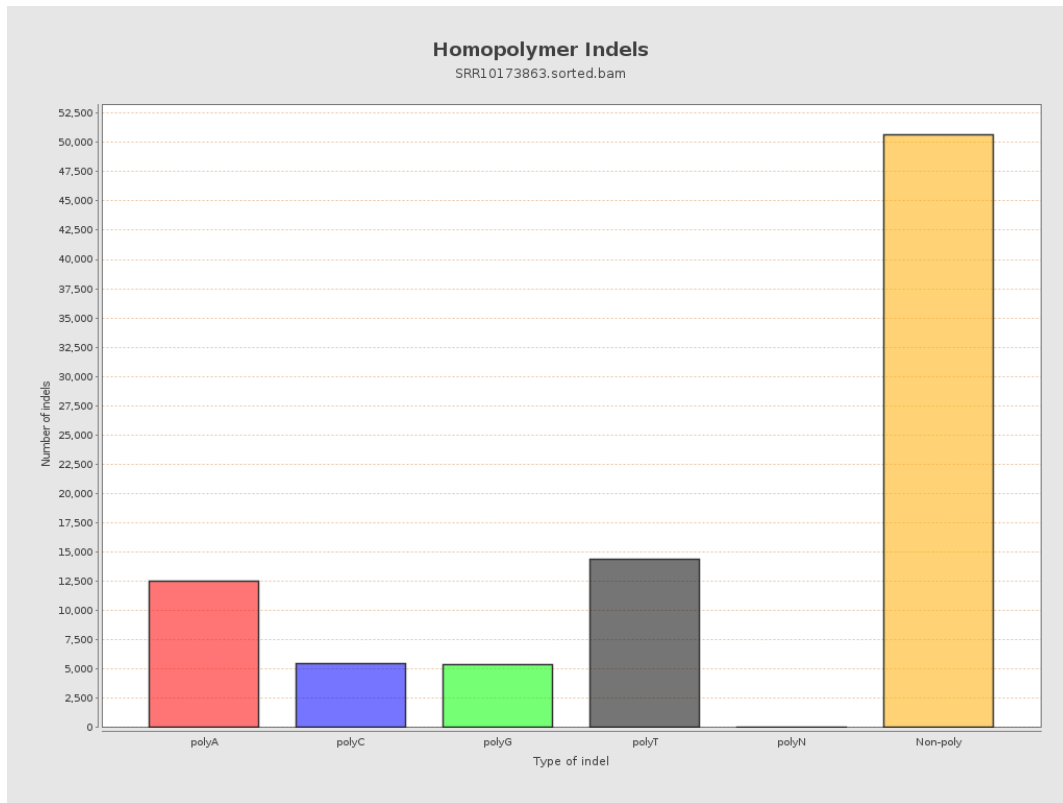
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



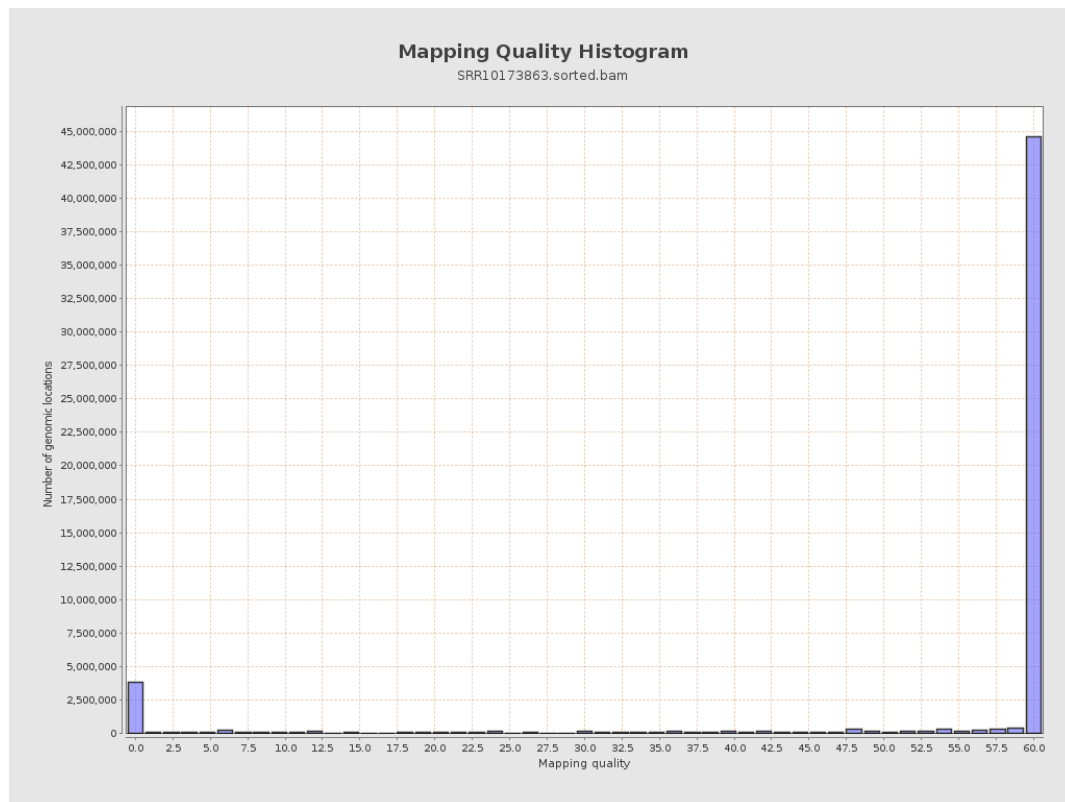
11. Results : Homopolymer Indels



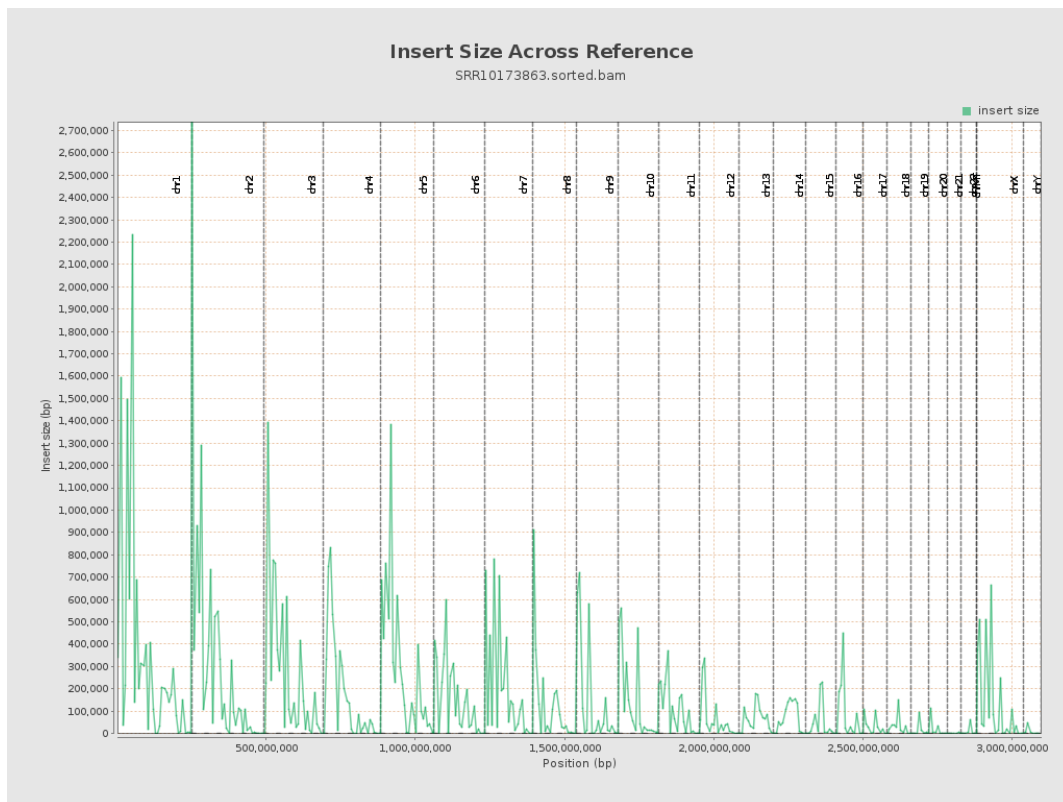
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

