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## Genome-Scale Analysis of Metazoan Replication Origins Reveals their Organization in Specific but Flexible Sites Defined by Conserved Features

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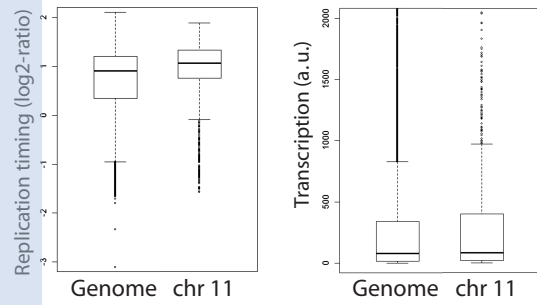
Submitted on 27 Oct 2011

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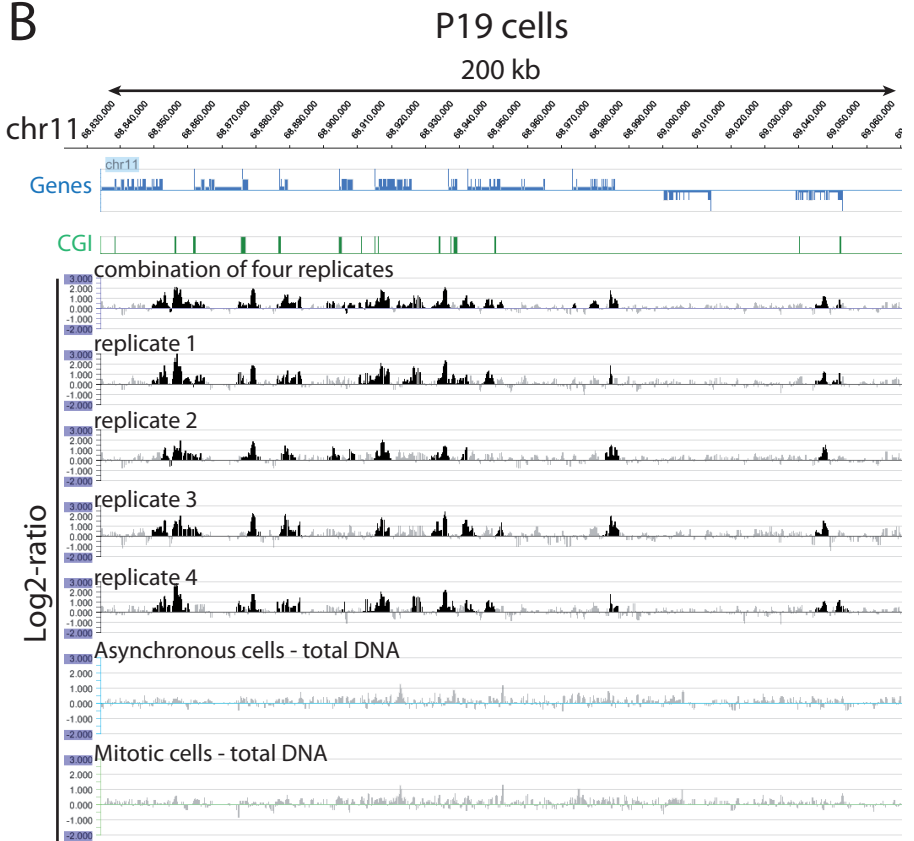
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# Supplementary Figure 1

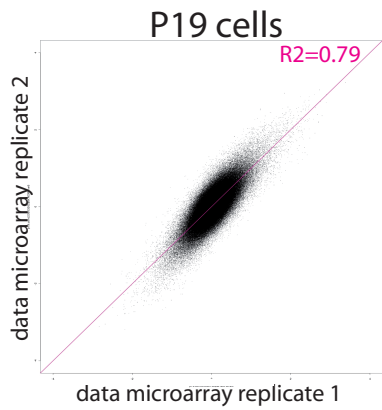
**A**



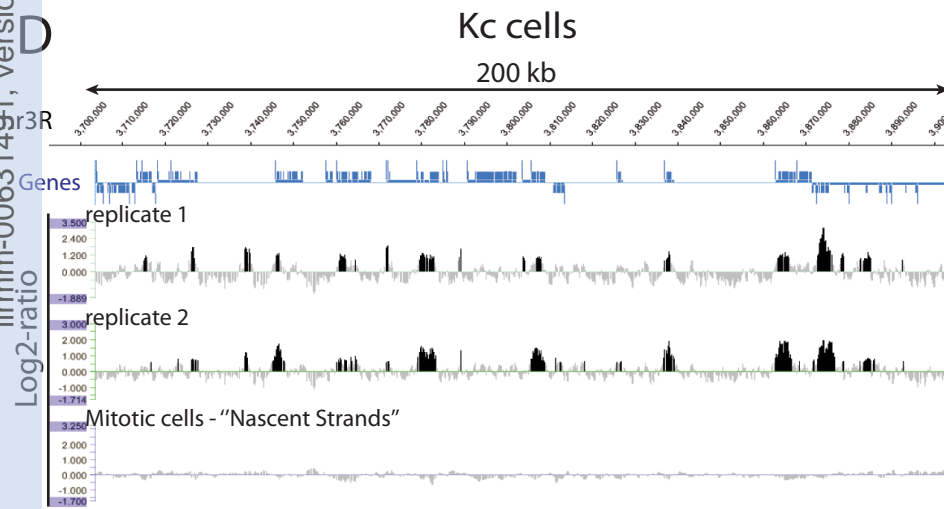
**B**



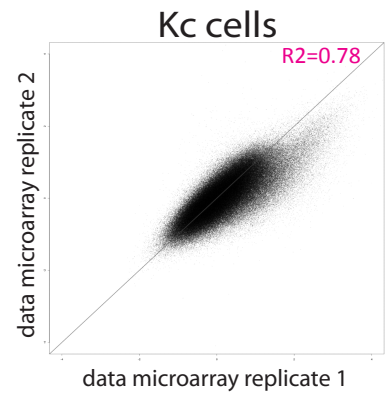
**C**



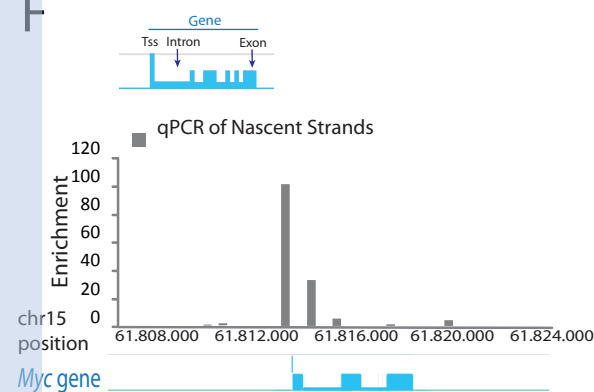
**D**



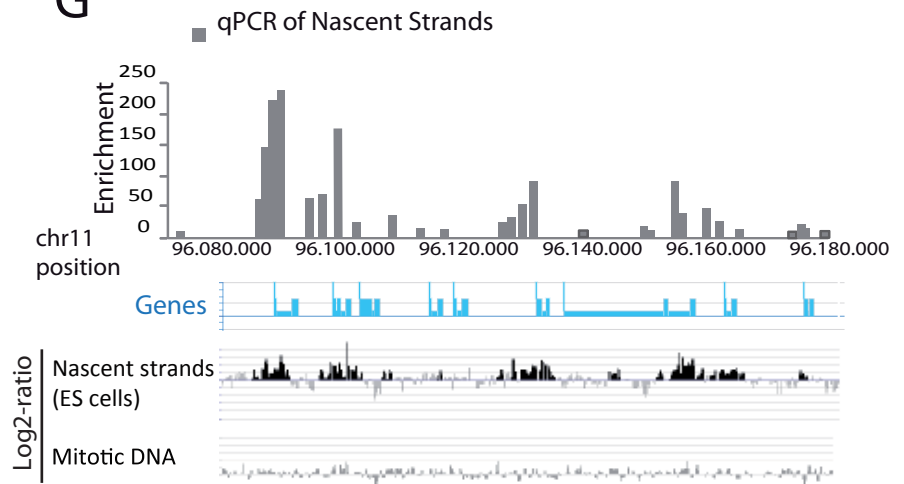
**E**



**F**

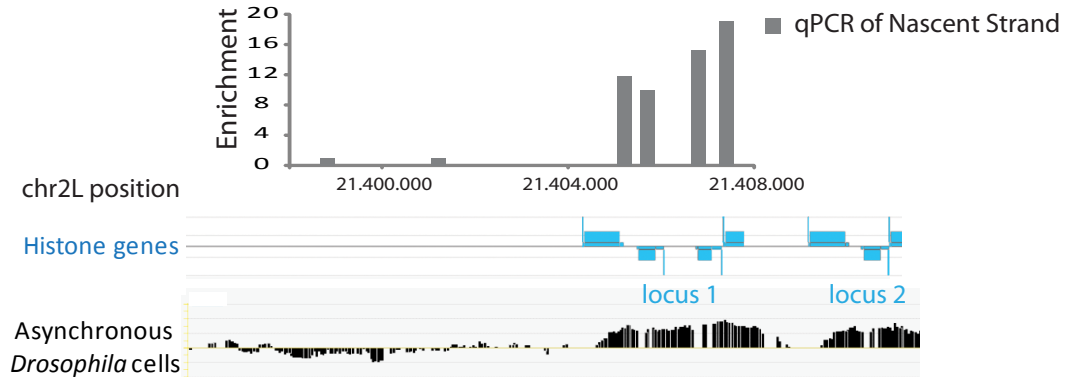


**G**

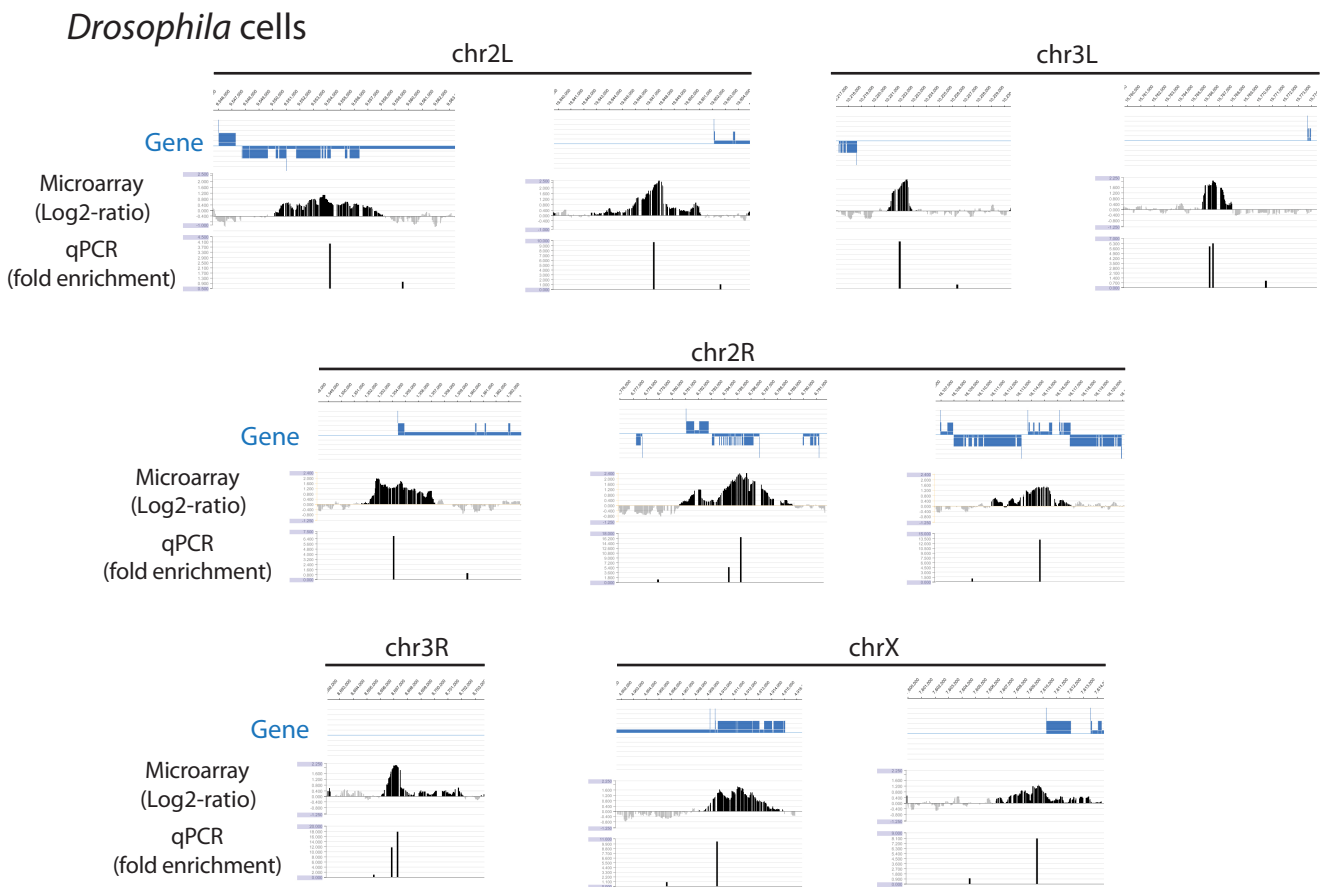


# Supplementary Figure 2

**A**

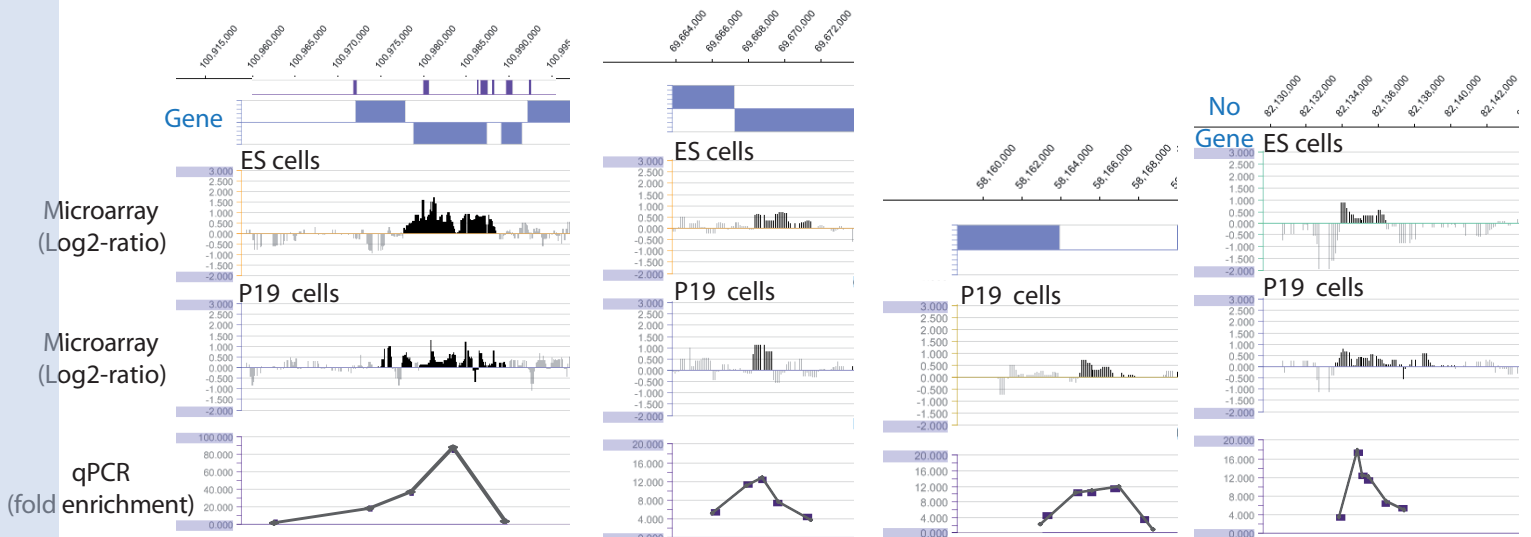


**B**



**C**

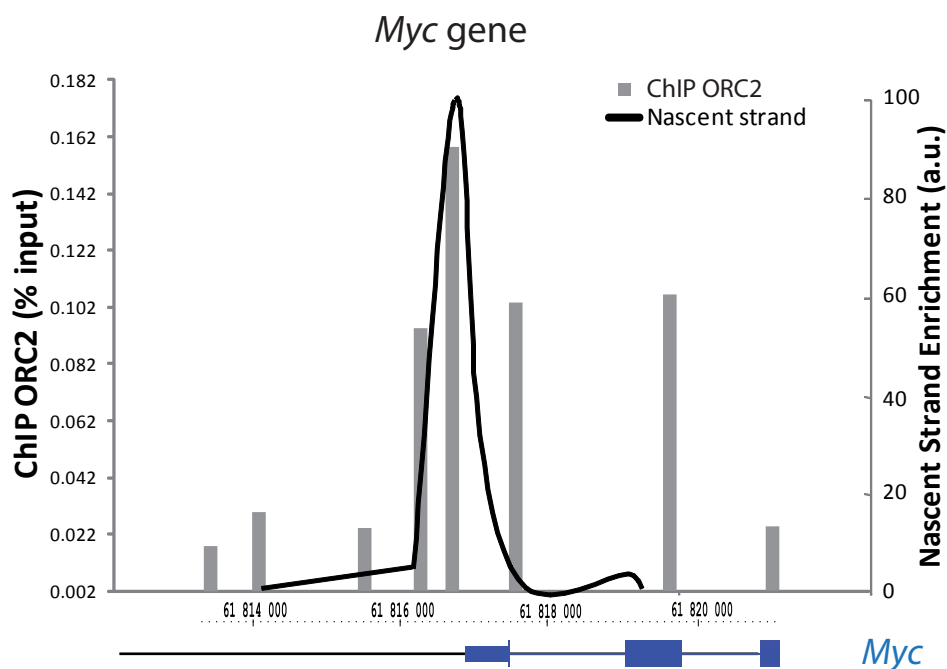
Mouse cells



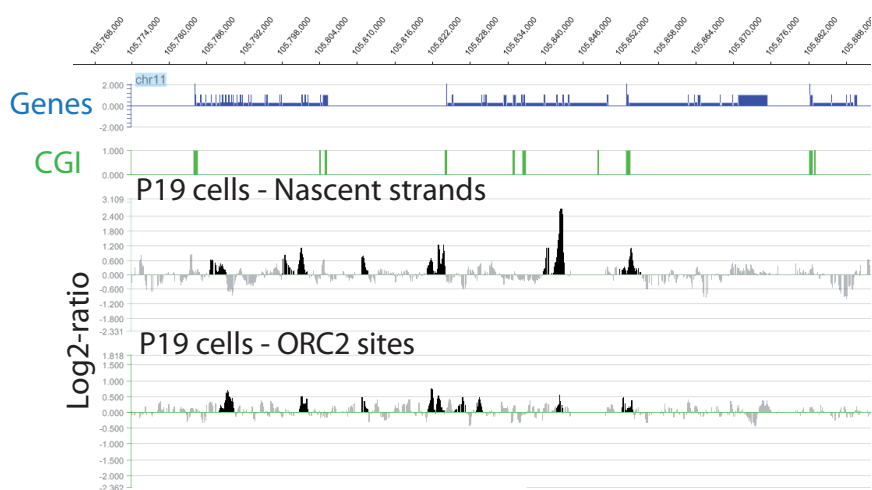
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# Supplementary Figure 3

## A

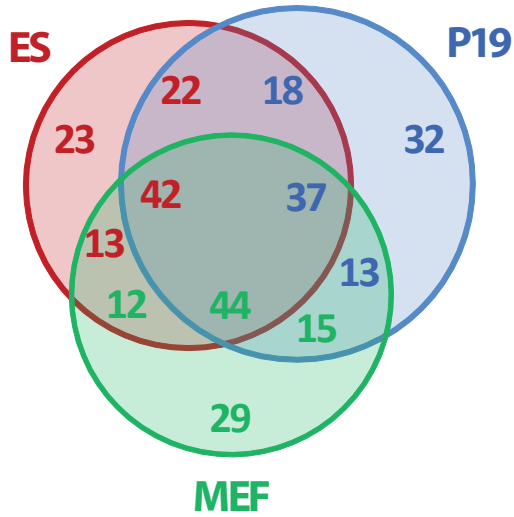


## B

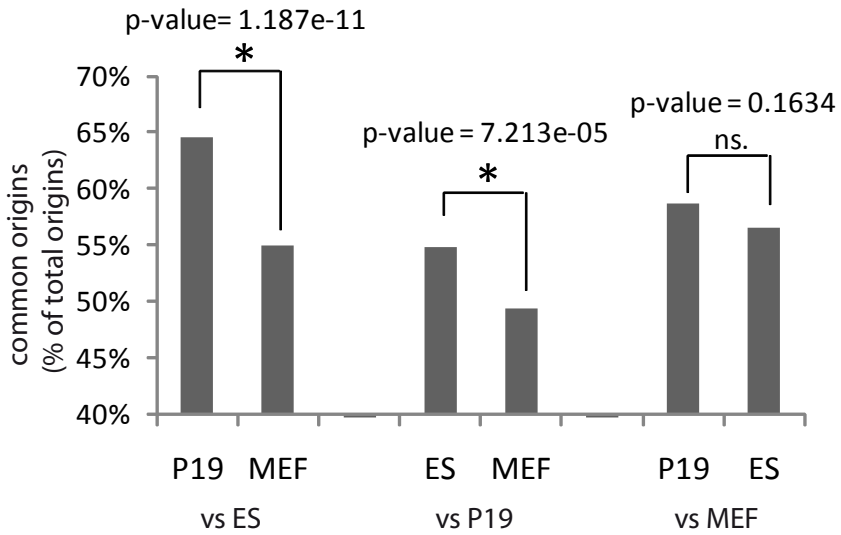


# Supplementary Figure 4

A

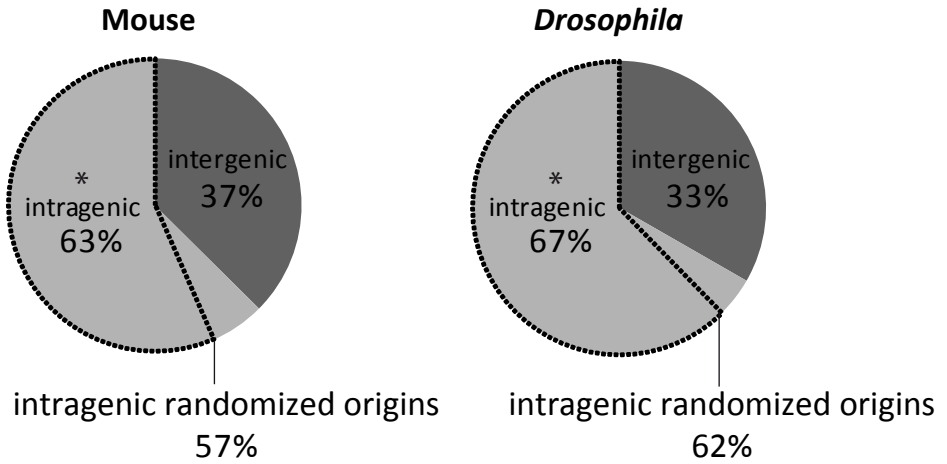


B

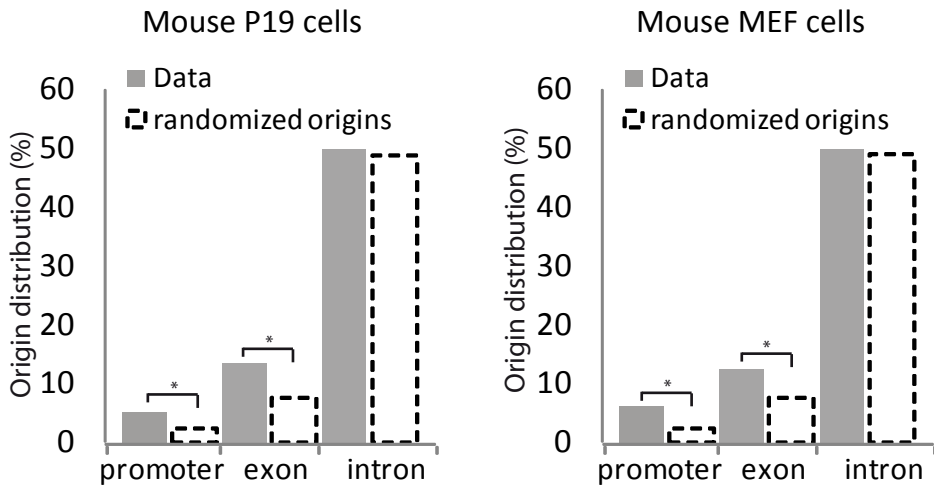


# Supplementary Figure 5

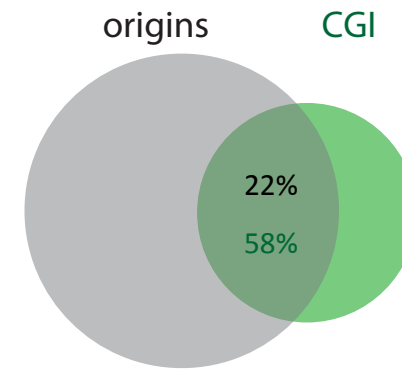
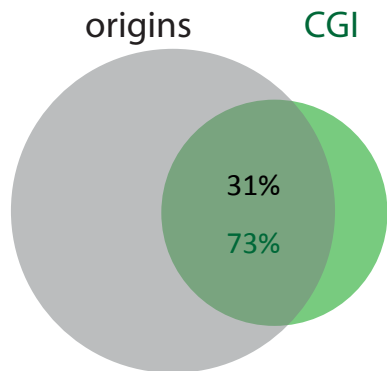
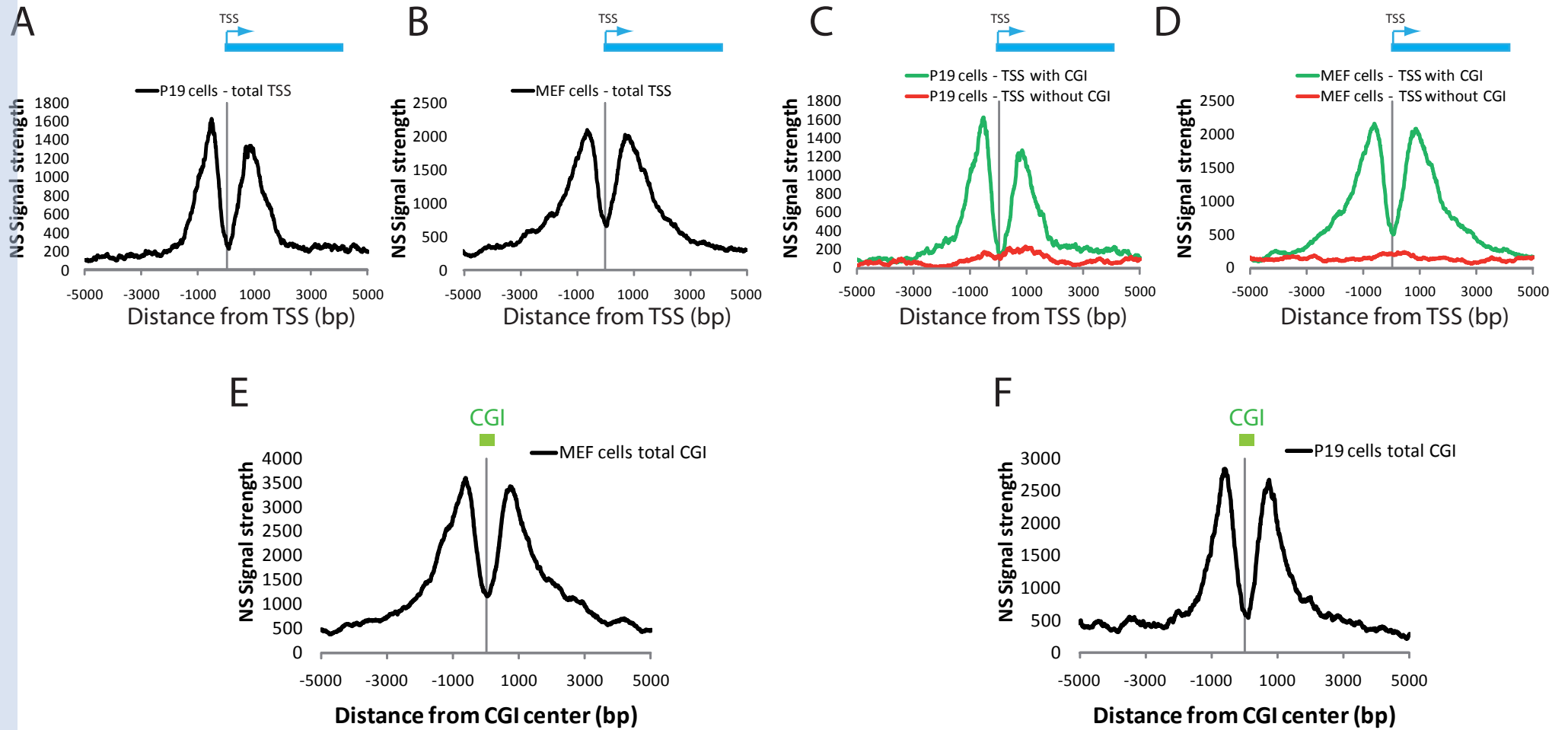
A



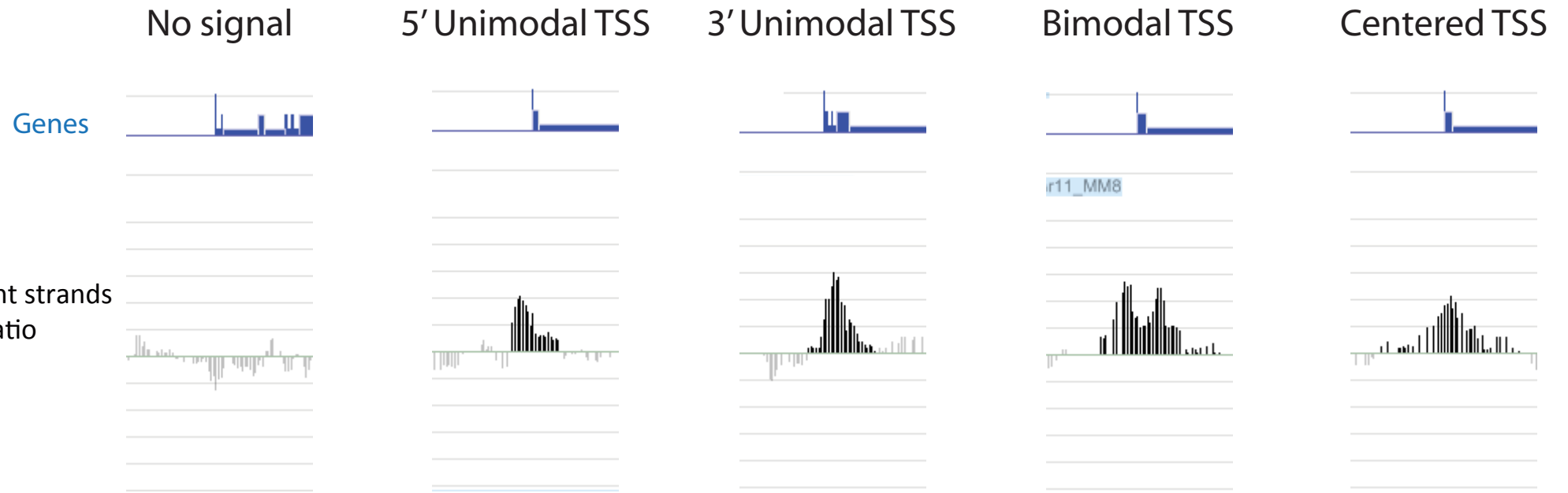
B



# Supplementary Figure 6



# Supplementary Figure 7

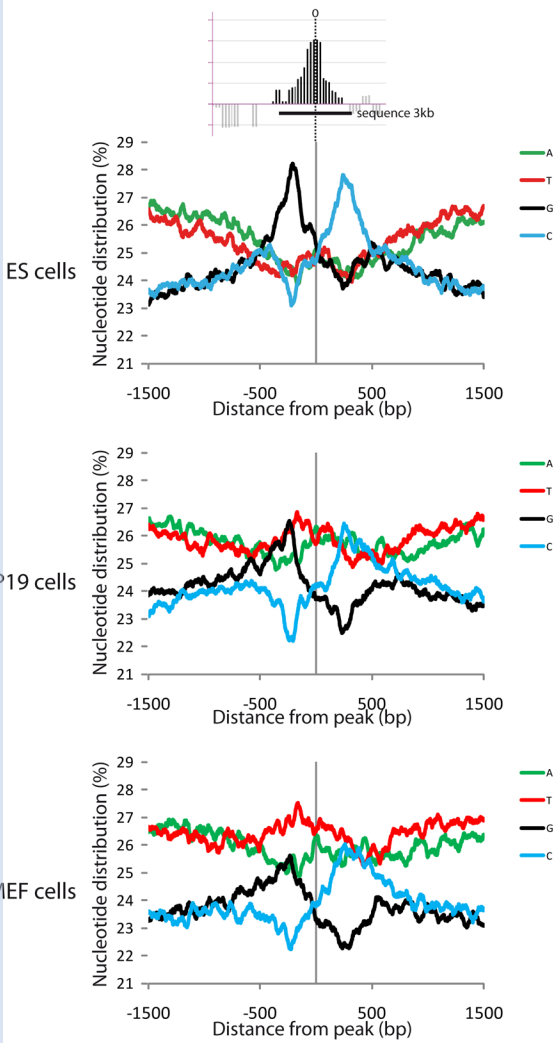


<b>MEF</b>	-	10.5%	8.3%	76.9%	4.2%
<b>P19</b>	-	9.1%	9.9%	76.8%	4.2%



# Supplementary Figure 8

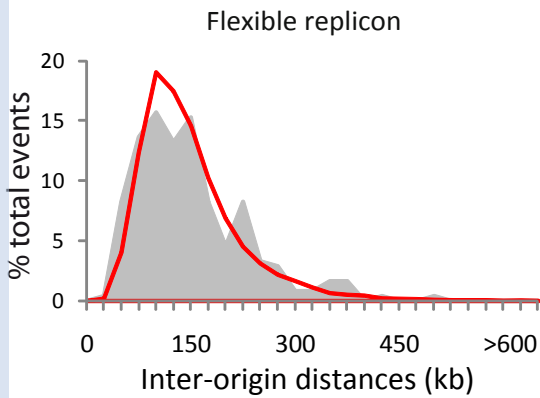
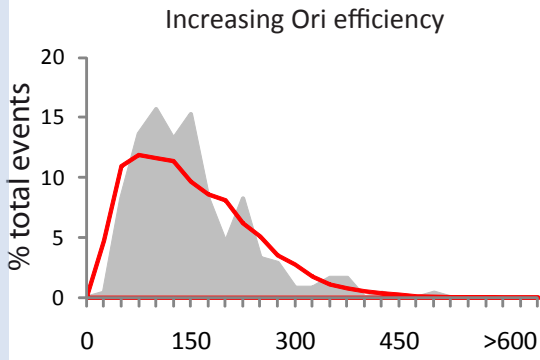
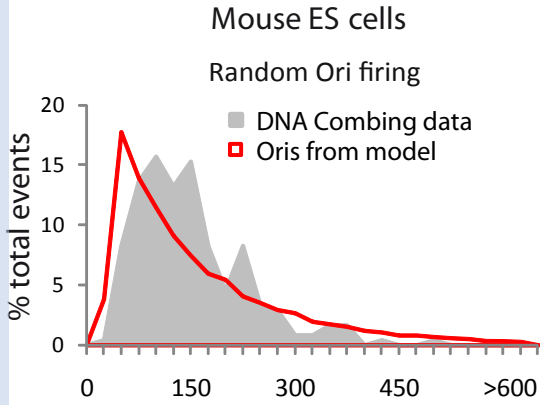
A



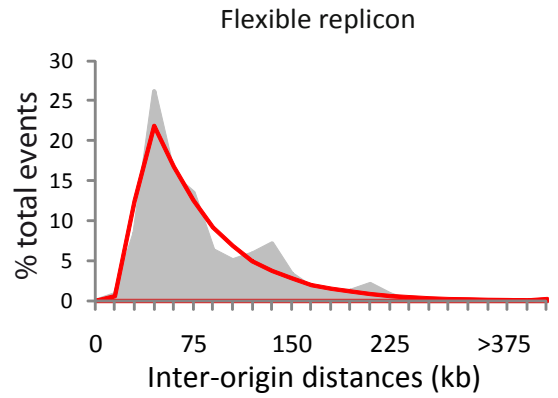
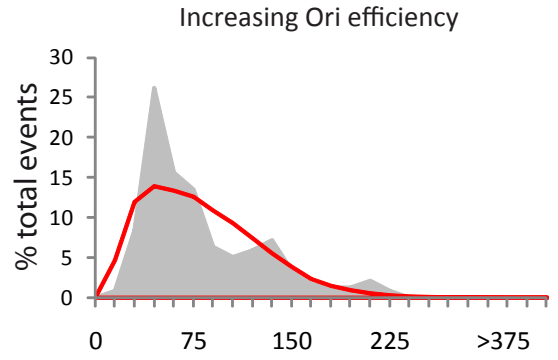
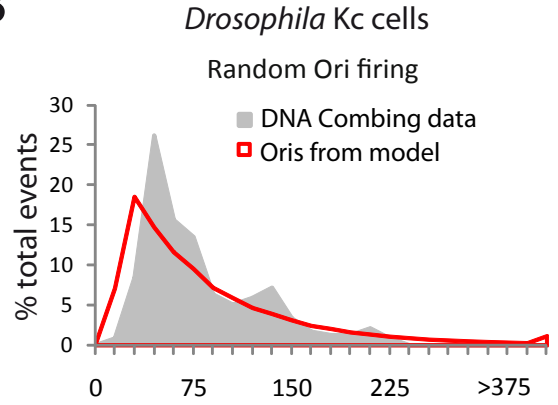
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# Supplementary Figure 9

## A

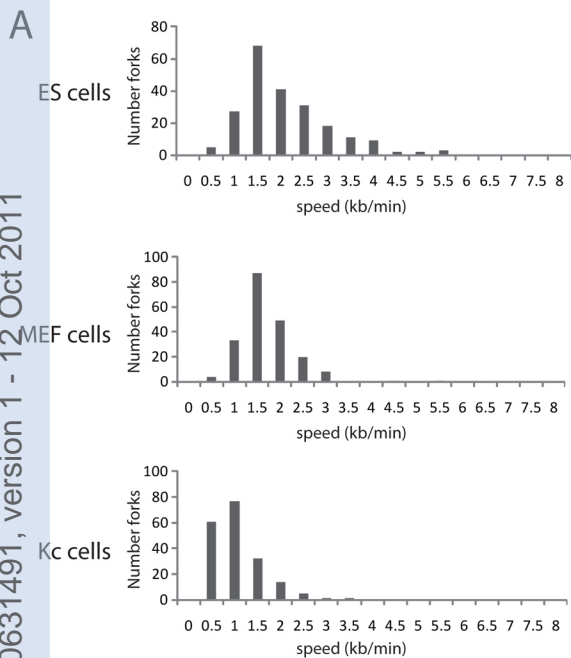


## B



# Supplementary Figure 10

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Speed Fork (kb/min)	ES cells		MEF cells		Kc cells	
	Mean	Median	Mean	Median	Mean	Median
	<b>1.47</b>	<b>1.37</b>	<b>1.77</b>	<b>1.57</b>	<b>0.81</b>	<b>0.66</b>

