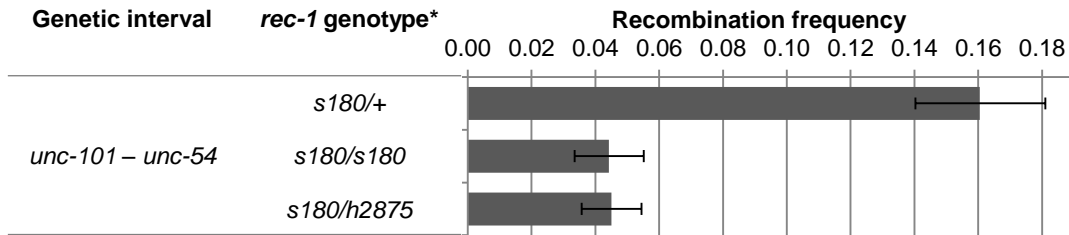


# Supplemental Figures

## Supplemental Figure 1

Chung\_SuppFig1

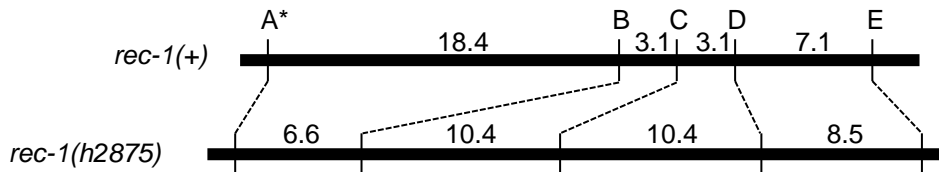


Supplemental Figures  
**Supplemental Figure 2**

**A**

Gamete type	Genotype at					Numbers observed in	
	Site A*	Site B	Site C	Site D	Site E	<i>rec-1(+)</i>	<i>rec-1(h2875)</i>
i	<i>B</i>	<i>B</i>	<i>B</i>	<i>B</i>	<i>B</i>	38	27
ii	<i>H</i>	<i>H</i>	<i>H</i>	<i>H</i>	<i>H</i>	29	41
iii	<i>B</i>	<i>H</i>	<i>H</i>	<i>H</i>	<i>H</i>	8	5
iv	<i>H</i>	<i>B</i>	<i>B</i>	<i>B</i>	<i>B</i>	10	2
v	<i>B</i>	<i>B</i>	<i>H</i>	<i>H</i>	<i>H</i>	1	6
vi	<i>H</i>	<i>H</i>	<i>B</i>	<i>B</i>	<i>B</i>	2	5
vii	<i>B</i>	<i>B</i>	<i>B</i>	<i>H</i>	<i>H</i>	2	4
viii	<i>H</i>	<i>H</i>	<i>H</i>	<i>B</i>	<i>B</i>	1	7
ix	<i>B</i>	<i>B</i>	<i>B</i>	<i>B</i>	<i>H</i>	4	4
x	<i>H</i>	<i>H</i>	<i>H</i>	<i>H</i>	<i>B</i>	3	5
with >1 crossover	(not observed)					0	0
Total						98	106

**B**



# Supplemental Figures

## Supplemental Figure 3

Chung\_SuppFig3

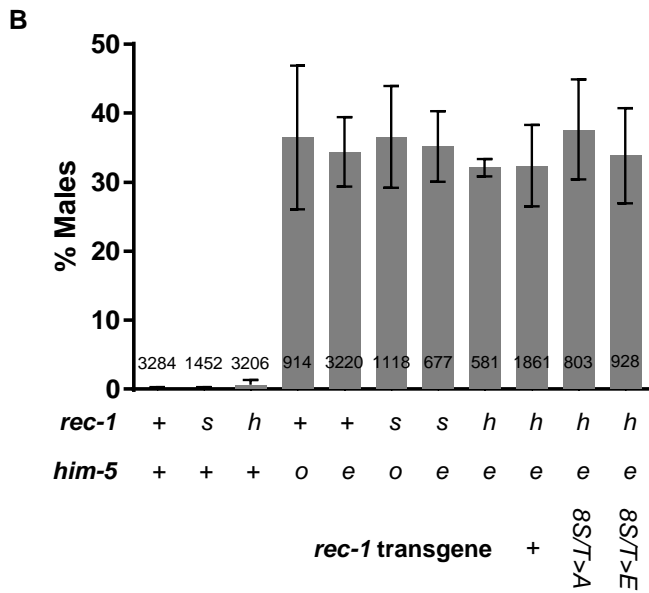
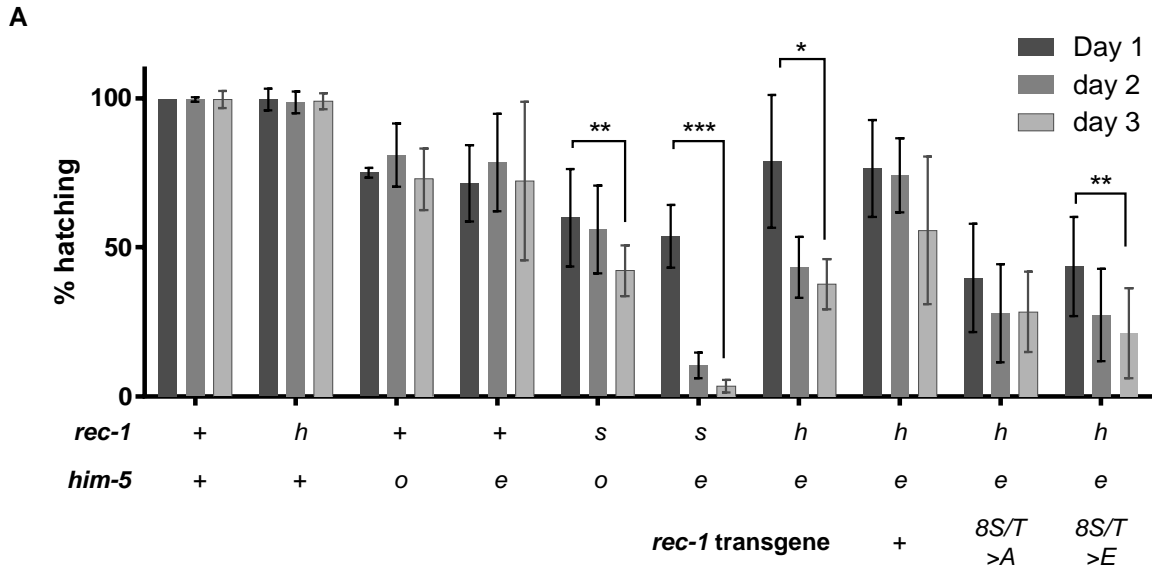
CLUSTAL 2.1 multiple sequence alignment

```
Celeg_rec-1-N  MFGNDDIVMLSDIIVADLRREIASRPVIFDRRPGYVPTPWVNCWKEIIEIWSDDSEDD 60
Crem_rec-1-N  MEDDDDLIEITDEQHAREIRATIGKRF--FDH---LRLDLQLSDSEHRCESSESEDD 55
               * .:***: ::** * :* *..** :**: : : . .* . *::****

Celeg_rec-1-N  DGD-----VITGSQEAQLKR 75
Crem_rec-1-N  EGGELFYKRNTLRVITVQEAATKR 80
               :* . * * :*** :**
```

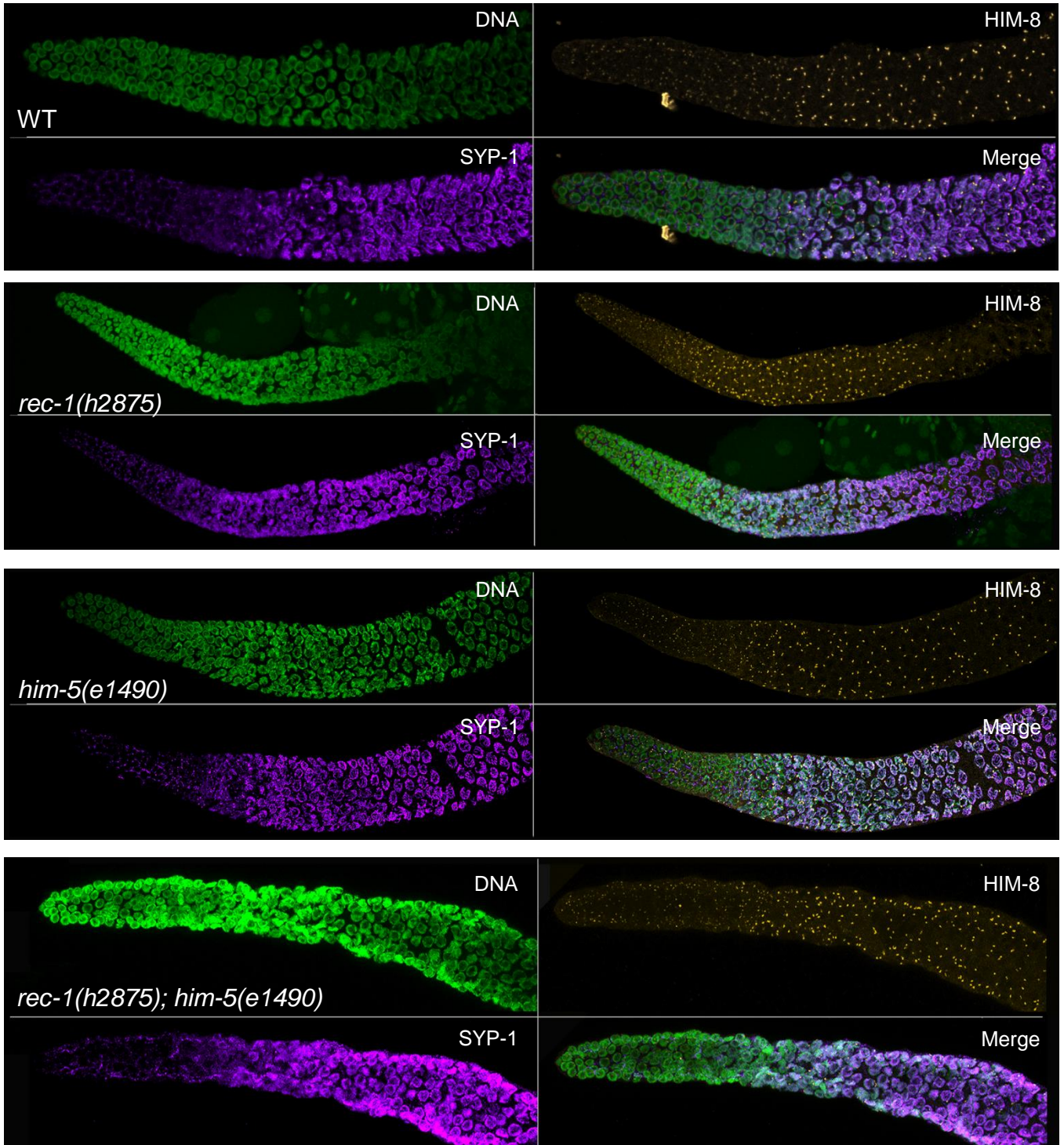
Supplemental Figures  
**Supplemental Figure 4**

Chung\_SuppFig4



Supplemental Figures  
Supplemental Figure 5

Chung\_SuppFig5



Supplemental Figures  
Supplemental Figure 6

Chung\_SuppFig6

