SUPPLEMENTAL TABLES

Table S1. *Pairwise comparison of PRO_{INO}:INO/YAB3 with PRO_{INO}:III*

Genotype[a]	PRO_{INO}:[b] Transgene	P-value[c]	Adjusted Alpha Value[d]	Significantly Different
INO sup-5		4.40×10^{-18}	8.33×10^{-04}	Yes
ino-1 SUP		9.19×10^{-13}	9.09×10^{-04}	Yes
	333	1.91×10^{-11}	1.00×10^{-03}	Yes
	333i	1.67×10^{-09}	1.11×10^{-03}	Yes
	33I	4.44×10^{-09}	1.25×10^{-03}	Yes
	I33	9.59×10^{-08}	1.43×10^{-03}	Yes
	3I3	1.72×10^{-06}	1.67×10^{-03}	Yes
	I3I	2.51×10^{-04}	2.00×10^{-03}	Yes
Wild type		2.69×10^{-03}	2.50×10^{-03}	No
	3II	5.09×10^{-02}	3.33×10^{-03}	No
	II3	5.20×10^{-02}	5.00×10^{-03}	No
	III3	3.67×10^{-01}	1.00×10^{-02}	No

[a]Ovules were examined in wild-type, *ino-1*, or *sup-5* mutant plants. [b]Transgenes were constructed as transcriptional fusions of the listed coding sequence with PRO_{INO} and examined in an *ino-1* mutant background. [c]The phenotypic class distribution of each set was calculated using Fisher's Exact Test to determine the p-value. [d]Alpha values were adjusted by applying the modified Bonferroni adjustment to the alpha value ($\alpha = 0.01$).

Table S2. *Pairwise comparison of PRO_{INO}:INO/YAB3 with PRO_{INO}:333*

Genotype[a]	PRO_{INO}:[b] Transgene	P-value[c]	Adjusted Alpha Value[d]	Significantly Different
Wild type		$7.10x10^{-13}$	$8.33x10^{-04}$	Yes
ino-1 SUP		$7.10x10^{-13}$	$8.33x10^{-04}$	Yes
INO sup-5		$2.24x10^{-12}$	$1.00x10^{-03}$	Yes
	III	$1.91x10^{-11}$	$1.11x10^{-03}$	Yes
	III3	$6.14x10^{-10}$	$1.25x10^{-03}$	Yes
	3II	$2.01x10^{-09}$	$1.43x10^{-03}$	Yes
	3I3	$2.54x10^{-07}$	$1.67x10^{-03}$	Yes
	II3	$2.75x10^{-07}$	$2.00x10^{-03}$	Yes
	I33	$6.02x10^{-04}$	$2.50x10^{-03}$	Yes
	33I	$3.00x10^{-03}$	$3.33x10^{-03}$	Yes
	I3I	$5.20x10^{-03}$	$5.00x10^{-03}$	Yes[e]
	333i	$5.89x10^{-02}$	$1.00x10^{-02}$	No

[a]Ovules were examined in wild-type, *ino-1*, or *sup-5* mutant plants. [b]Transgenes were constructed as transcriptional fusions of the listed coding sequence with PRO_{INO} and examined in an *ino-1* mutant background. [c]The phenotypic class distribution of each set was calculated using Fisher's Exact Test to determine the p-value. [d]Alpha values were adjusted by applying the modified Bonferroni adjustment to the alpha value ($\alpha = 0.01$). [e]For PRO_{INO}:*I3I* versus PRO_{INO}:*333*, although the p-value>alpha value, the difference observed is considered significant due to the closeness of these values and the presence of ten wild-type individuals containing PRO_{INO}:*I3I* while PRO_{INO}:*333* individuals never appeared wild-type.

Table S3. *Pairwise comparison of PRO_{INO}:INO/YAB5 with PRO_{INO}:III*

Genotype[a]	PRO_{INO}:[b] Transgene	P-value[c]	Adjusted Alpha Value[d]	Significantly Different
INO sup-5		$4.40x10^{-18}$	$1.00x10^{-03}$	Yes
ino-1 SUP		$9.19x10^{-13}$	$1.11x10^{-03}$	Yes
	555	$2.55x10^{-09}$	$1.25x10^{-03}$	Yes
	5I5	$2.05x10^{-08}$	$1.43x10^{-03}$	Yes
	I5I	$6.66x10^{-07}$	$1.67x10^{-03}$	Yes
	I55	$1.50x10^{-06}$	$2.00x10^{-03}$	Yes
	5II	$1.90x10^{-06}$	$2.50x10^{-03}$	Yes
	55I	$1.30x10^{-03}$	$3.33x10^{-03}$	Yes
Wild type		$2.69x10^{-03}$	$5.00x10^{-03}$	Yes
	II5	$1.59x10^{-02}$	$1.00x10^{-02}$	No

[a]Ovules were examined in wild-type, *ino-1*, or *sup-5* mutant plants. [b]Transgenes were constructed as transcriptional fusions of the listed coding sequence with PRO_{INO} and examined in an *ino-1* mutant background. [c]The phenotypic class distribution of each set was calculated using Fisher's Exact Test to determine the p-value. [d]Alpha values were adjusted by applying the modified Bonferroni adjustment to the alpha value ($\alpha = 0.01$).

Table S4. *Pairwise comparison of PRO_{INO}:INO/YAB5 with PRO_{INO}:555*

Genotype[a]	PRO_{INO}:[b] Transgene	P-value[c]	Adjusted Alpha Value[d]	Significantly Different
Wild type		$1.44x10^{-13}$	$1.00x10^{-03}$	Yes
INO sup-5		$4.97x10^{-13}$	$1.11x10^{-03}$	Yes
	III	$2.55x10^{-09}$	$1.25x10^{-03}$	Yes
	I5I	$1.76x10^{-07}$	$1.43x10^{-03}$	Yes
	5II	$8.31x10^{-07}$	$1.67x10^{-03}$	Yes
	II5	$3.83x10^{-06}$	$2.00x10^{-03}$	Yes
	5I5	$8.19x10^{-06}$	$2.50x10^{-03}$	Yes
	55I	$6.47x10^{-05}$	$3.33x10^{-03}$	Yes
	I55	$1.74x10^{-04}$	$5.00x10^{-03}$	Yes
ino-1 SUP		$8.76x10^{-02}$	$1.00x10^{-02}$	No

[a]Ovules were examined in wild-type, *ino-1*, or *sup-5* mutant plants. [b]Transgenes were constructed as transcriptional fusions of the listed coding sequence with PRO_{INO} and examined in an *ino-1* mutant background. [c]The phenotypic class distribution of each set was calculated using Fisher's Exact Test to determine the p-value. [d]Alpha values were adjusted by applying the modified Bonferroni adjustment to the alpha value ($\alpha = 0.01$).

Table S5. *Pairwise comparison of PRO_{INO}:INO/CCC with PRO_{INO}:III*

Genotype[a]	PRO_{INO}:[b] Transgene	P-value[c]	Adjusted Alpha Value[d]	Significantly Different
INO sup-5		4.40×10^{-18}	1.67×10^{-03}	Yes
	CCC	4.30×10^{-14}	2.00×10^{-03}	Yes
ino-1 SUP		9.19×10^{-13}	2.50×10^{-03}	Yes
	CCCi	1.36×10^{-08}	3.33×10^{-03}	Yes
	IIIc	1.94×10^{-05}	5.00×10^{-03}	Yes
Wild type		2.69×10^{-03}	1.00×10^{-02}	Yes

[a]Ovules were examined in wild-type, *ino-1*, or *sup-5* mutant plants. [b]Transgenes were constructed as transcriptional fusions of the listed coding sequence with PRO_{INO} and examined in an *ino-1* mutant background. [c]The phenotypic class distribution of each set was calculated using Fisher's Exact Test to determine the p-value. [d]Alpha values were adjusted by applying the modified Bonferroni adjustment to the alpha value ($\alpha = 0.01$).

Table S6. *Pairwise comparison of PRO_{INO}:INO/CCC with PRO_{INO}:CCC*

Genotype[a]	PRO_{INO}:[b] Transgene	P-value[c]	Adjusted Alpha Value[d]	Significantly Different
Wild type		$1.58x10^{-14}$	$1.67x10^{-03}$	Yes
	III	$4.30x10^{-14}$	$2.00x10^{-03}$	Yes
ino-1 SUP		$4.11x10^{-13}$	$2.50x10^{-03}$	Yes
INO sup-5		$8.95x10^{-08}$	$3.33x10^{-03}$	Yes
	IIIc	$1.87x10^{-04}$	$5.00x10^{-03}$	Yes
	CCCi	$4.61x10^{-04}$	$1.00x10^{-02}$	Yes

[a]Ovules were examined in wild-type, *ino-1*, or *sup-5* mutant plants. [b]Transgenes were constructed as transcriptional fusions of the listed coding sequence with PRO_{INO} and examined in an *ino-1* mutant background. [c]The phenotypic class distribution of each set was calculated using Fisher's Exact Test to determine the p-value. [d]Alpha values were adjusted by applying the modified Bonferroni adjustment to the alpha value ($\alpha = 0.01$).