

Table S1. Age-related changes in the expression level of Yki target genes.

Gene	Sex	Age (days)	Mean (dCt)	Standard Error	p-value
<i>CycE</i>	♂	10	11.6	0.2	0.0001
	♂	20	12.7	0.1	
<i>dally</i>	♂	10	7.2	0.2	0.0409
	♂	20	7.8	0.1	
<i>Diap1</i>	♂	10	2.8	0.2	0.0316
	♂	20	3.4	0.1	
<i>E2f1</i>	♂	10	4.3	0.1	0.2499
	♂	20	4.0	0.1	
<i>myc</i>	♂	10	7.2	0.3	0.2122
	♂	20	6.8	0.1	
<i>vn</i>	♂	10	8.2	0.3	0.2864
	♂	20	7.9	0.1	
<i>wg</i>	♂	10	7.5	0.4	0.1902
	♂	20	7.9	0.3	
<i>Yki</i>	♂	10	4.9	0.2	0.7089
	♂	20	4.8	0.1	
<i>CycE</i>	♀	10	8.7	0.2	0.0000
	♀	20	10.3	0.1	
<i>dally</i>	♀	10	7.8	0.1	0.0000
	♀	20	8.8	0.1	
<i>Diap1</i>	♀	10	4.7	0.1	0.8341
	♀	20	4.7	0.1	
<i>E2f1</i>	♀	10	5.1	0.1	0.7278
	♀	20	5.1	0.1	
<i>myc</i>	♀	10	6.2	0.1	0.0373
	♀	20	6.6	0.1	
<i>vn</i>	♀	10	9.1	0.1	0.5022
	♀	20	9.2	0.1	
<i>wg</i>	♀	10	9.9	0.4	0.0013
	♀	20	9.3	0.3	
<i>Yki</i>	♀	10	5.4	0.1	0.1415
	♀	20	5.1	0.1	

♂ – males, ♀ – females; dCt – delta Ct (cycle thresholds) values were calculated as the differences in Ct values for target genes and reference genes (*β-Tubulin* and *RpL32*). The Ct values are inversely proportional to the mRNA transcript levels. Higher dCt values represent a lower expression level. p-value – significance was determined by two-way ANOVA followed by post-hoc Duncan test.