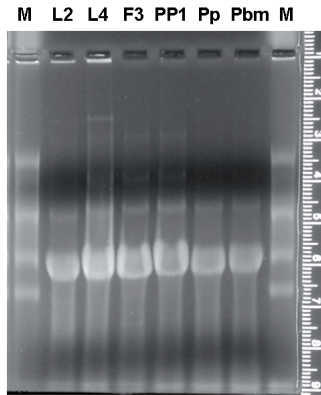
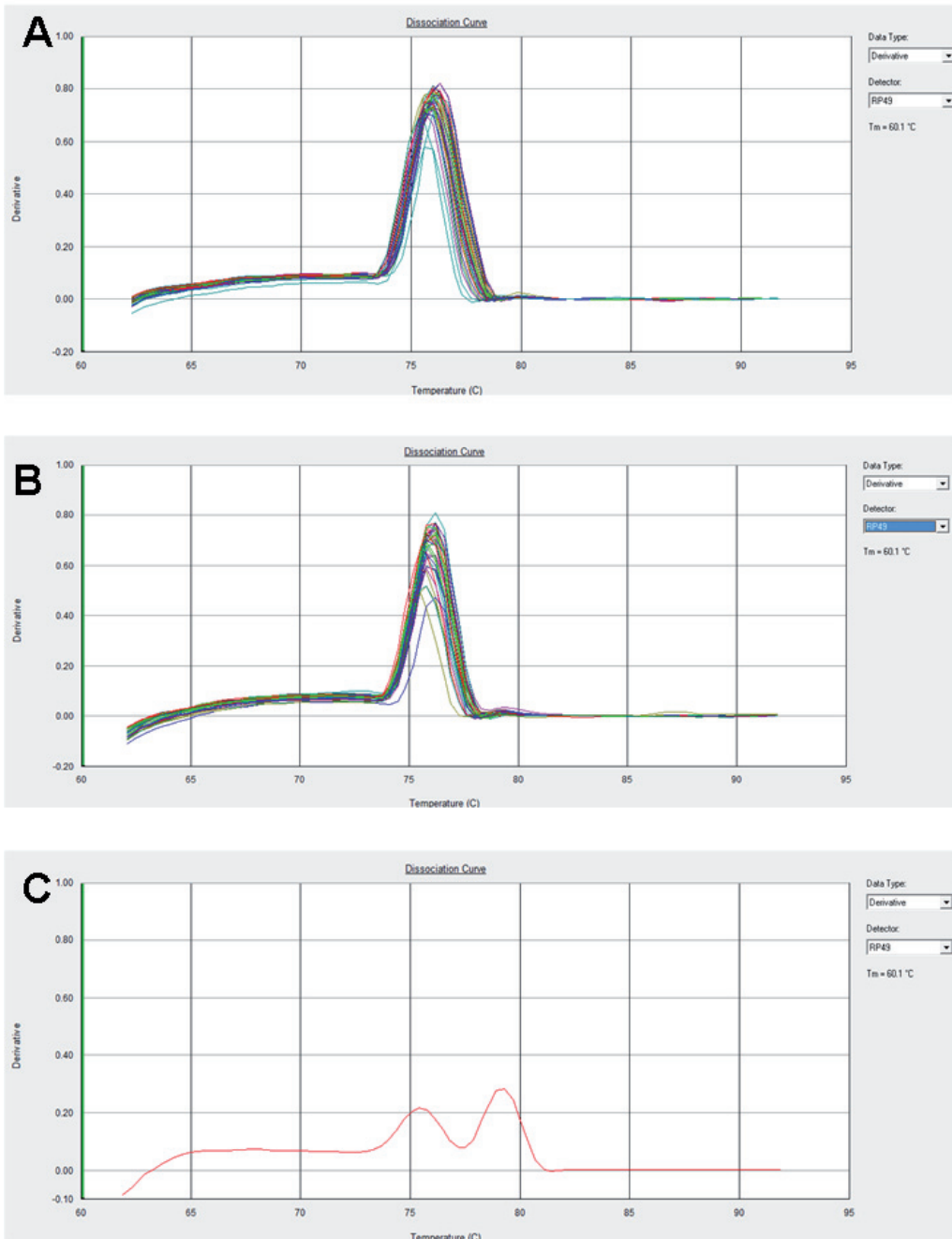


Online Material

SUPPLEMENTARY MATERIALS

Supplementary Figure 1. Analysis of RNA integrity by denaturing formaldehyde agarose gel (1.2%) electrophoresis. 40 μ g total RNA of six samples were loaded and stained with Ethidium Bromide. Note that this figure reports only some samples, however all samples were tested for this criterion.



Supplementary Figure 2. Graphs showing dissociation curves after real time PCR for *rp49*. A and B represent curves from analyses of developmental stages (A) and tissues and hormone treatments (B). Graph C shows a curve for a sample (not from this study) where both cDNA and genomic fragments are amplified. Note that two peaks occur in such a case, one corresponding to the cDNA fragment (76 °C), also shown in graphics A and B, and other one to a genomic fragment (78 °C).

Supplementary Table I. Results of sample integrity: Intrinsic Variation [InVar] based on selected House-keeping Genes; InVar index for each sample is highlighted in gray.

Samples from development analysis								
	n	BestKeeper	InVar. [± CP]	InVar. [± % CP]	InVar. [± x-fold]	InVar. [± CP]	InVar. [± % CP]	InVar. [± x-fold]
sample 1	4	17.46	±0.55	±3.11	±0.44	0.55	3.11	0.44
sample 2	4	17.29	±0.84	±4.82	±0.65	0.84	4.82	0.65
sample 3	4	17.48	±0.6	±3.34	±0.45	0.6	3.34	0.45
sample 4	4	16.92	±0.52	±3.06	±0.27	0.52	3.06	0.27
sample 5	4	17.04	±0.62	±3.57	±0.31	0.62	3.57	0.31
sample 6	4	17.49	±0.45	±2.59	±0.32	0.45	2.59	0.32
sample 7	4	18.48	±0.38	±1.67	±0.45	0.38	1.67	0.45
sample 8	4	18.41	±0.44	±2.01	±0.53	0.44	2.01	0.53
sample 9	4	17.57	±0.11	±0.6	±0.09	0.11	0.6	0.09
sample 10	4	17.5	±0.06	±0.32	±0.05	0.06	0.32	0.05
sample 11	4	17.18	±0.2	±1.13	±0.13	0.2	1.13	0.13
sample 12	4	16.73	±0.62	±3.32	±0.26	0.62	3.32	0.26
sample 13	4	17.2	±1.11	±6.22	±1.01	1.11	6.22	1.01
sample 14	4	17.08	±0.78	±4.37	±0.52	0.78	4.37	0.52
sample 15	4	17.13	±0.36	±1.9	±0.19	0.36	1.9	0.19
sample 16	4	17.83	±0.61	±3.5	±0.77	0.61	3.5	0.77
sample 17	4	17.23	±0.53	±2.89	±0.33	0.53	2.89	0.33
Samples from tissues analysis								
	n	BestKeeper	InVar. [± CP]	InVar. [± % CP]	InVar. [± x-fold]	InVar. [± CP]	InVar. [± % CP]	InVar. [± x-fold]
sample 1	4	18.82	±0.09	±0.31	±0.03	0.09	0.31	0.03
sample 2	4	18.94	±0.13	±0.7	±0.07	0.13	0.7	0.07
sample 3	4	19.21	±0.72	±3.55	±0.58	0.72	3.55	0.58
sample 4	4	18.76	±0.09	±0.25	±0.03	0.09	0.25	0.03
sample 5	4	18.82	±0.25	±1.28	±0.13	0.25	1.28	0.13
sample 6	4	18.93	±0.25	±1.4	±0.14	0.25	1.4	0.14
sample 7	4	19.26	±0.34	±1.76	±0.25	0.34	1.76	0.25
sample 8	4	19.11	±0.27	±1.32	±0.16	0.27	1.32	0.16
sample 9	4	19.23	±0.54	±2.89	±0.46	0.54	2.89	0.46
sample 10	4	20.2	±0.6	±3.13	±0.8	0.6	3.13	0.8
sample 11	4	20.48	±0.56	±2.84	±0.9	0.56	2.84	0.9
sample 12	4	20.26	±0.64	±3.29	±0.91	0.64	3.29	0.91
Samples from hormone treatment analysis								
	n	BestKeeper	InVar. [± CP]	InVar. [± % CP]	InVar. [± x-fold]	InVar. [± CP]	InVar. [± % CP]	InVar. [± x-fold]
sample 1	4	19.69	±0.16	±0.79	±0.11	0.16	0.79	0.11
sample 2	4	20.08	±0.46	±2.54	±0.5	0.46	2.54	0.5
sample 3	4	19.59	±0.21	±1.03	±0.13	0.21	1.03	0.13
sample 4	4	19.49	±0.16	±0.89	±0.09	0.16	0.89	0.09
sample 5	4	19.79	±0.2	±1.05	±0.15	0.2	1.05	0.15
sample 6	4	20.23	±0.14	±0.8	±0.14	0.14	0.8	0.14