Supplemental Figure S6: Quantitative real time RT-PCR experiments performed with samples from vegetative organs (a mixture of equal amounts of RNA from roots, stems, leaves, sepals and petals) and stigmas/styles (S/S). The RNA samples used for the experiments above are a simulation of the samples used for the preparation of the negative and positive cDNA probes used in the macroarray analysis and the results obtained show that in each case, the stigma/style expression is at least 2 fold higher than the expression in the vegetative organs, with the exception of cluster S010A10. The relative expression levels are represented in arbitrary units (A.U.) normalized to the expression level of the β-actin gene, used as reference, in each RNA sample. Observe the scales used for the detection of the expression levels of each of these genes.