		29d	35d	42d	57d		Plant Cell 23:873 Cluster
AT4G21980		**60.8**	60.2	85.5	118.2	ATG8A	U1
AT4G04620		**73.7**	81.5	106.3	83.4	ATG8B	U1
AT4G11910		**12.7**	**82.7**	126.4	120.5	SGR2	U1
AT2G29350		0.3	**2.8**	**79.5**	198.9	SAG13	U2
AT4G22920		**37.4**	**101.4**	141.0	149.2	SGR1	U2
AT5G05410		**17.5**	**64.7**	78.5	30.2	DREB2A	U2
AT5G51070		**407.4**	**592.4**	823.7	705.4	ERD1	U2
AT5G66400		**163.5**	**191.7**	71.0	36.3	RAB18	U2
AT5G13080		**0.5**	**4.6**	25.0	204.1	WRKY75	U3
AT3G25760		**2.7**	**124.9**	239.6	54.2	AOC1	U3
AT1G19180		**64.9**	**556.4**	801.1	483.4	JAZ1	U3
AT2G06050		**6.1**	**440.6**	445.7	146.8	OPR3	U3
AT1G72450		**105.0**	**350.0**	558.0	263.3	JAZ6	U3
AT2G33380		30.3	**44.8**	**140.8**	193.3	RD20	U3
AT4G32810		0.1	**4.4**	**26.5**	38.3	CCD8	U5
AT5G04200		2.3	2.0	**3.1**	**6.0**	MC9	U5
AT5G64810		0.1	0.0	**3.2**	**15.6**	WRKY51	U6
AT5G45890		0.0	0.2	**4.7**	**72.5**	SAG12	U7

Supplemental Table 3. RPKM values (mean of three replicates) are shown along with the up-regulation cluster that was assigned in Breeze et al., 2011, which analyzed leaf 7. Bold RPKM values show the largest fold-change, except in the case of the first two genes in which initial RPKM values were high. U1 were up-regulated by the first time point (19d), and are also up-regulated at the first time point in the RNA-seq data. U2 (21d) and U3 (23d) are mostly up-regulated (9/11) in the first time interval (29-35d), although some (2/11) showed a greater fold-induction in the second interval (35-42d). U5 (27d), U6 (29d) and U7 (31d) were expressed late in leaf senescence, and showed a similar pattern in the RNA-seq data with highest values at 57d. The RNA-seq data generally follow the developmental leaf senescence data previously described, however with less temporal refinement.