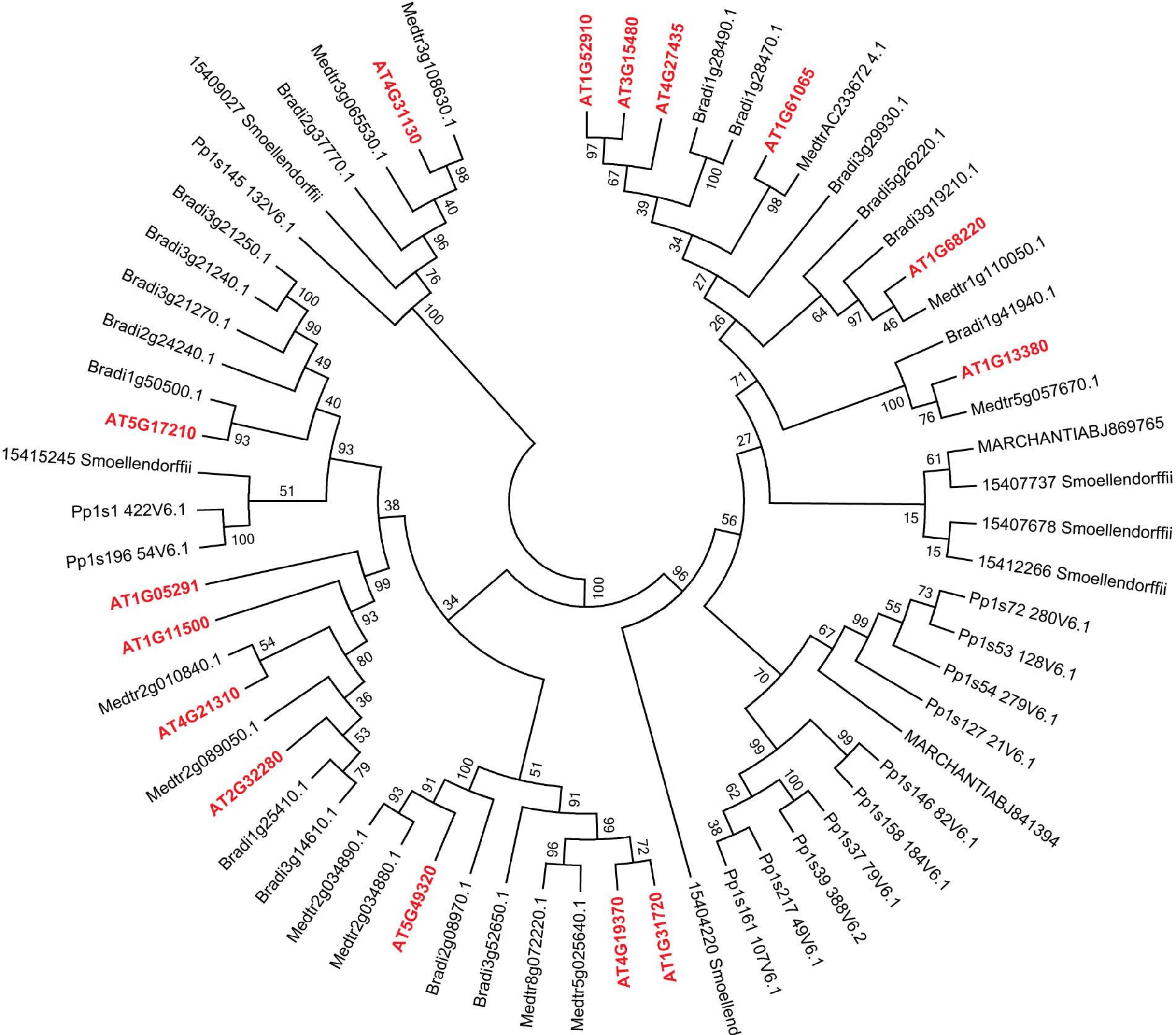
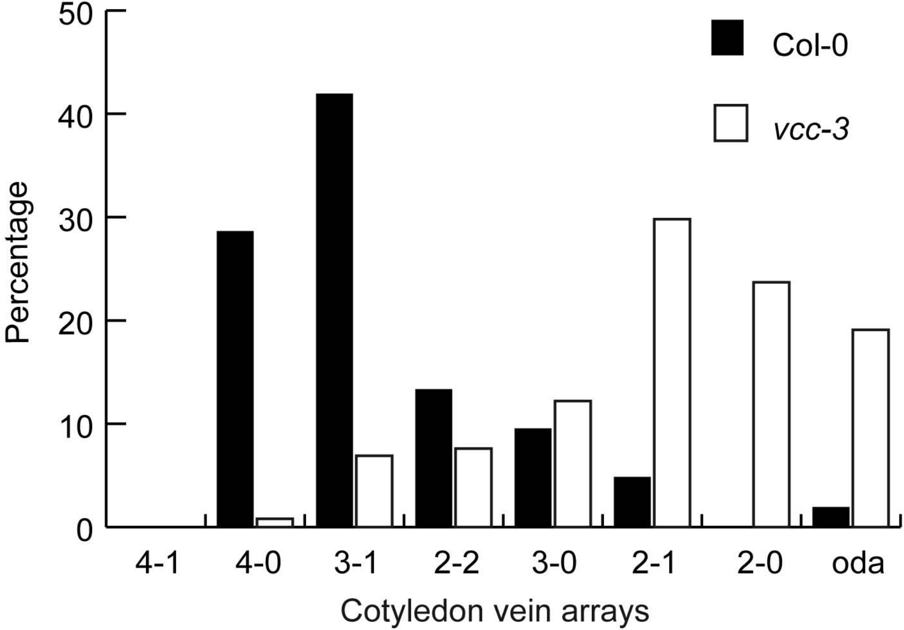
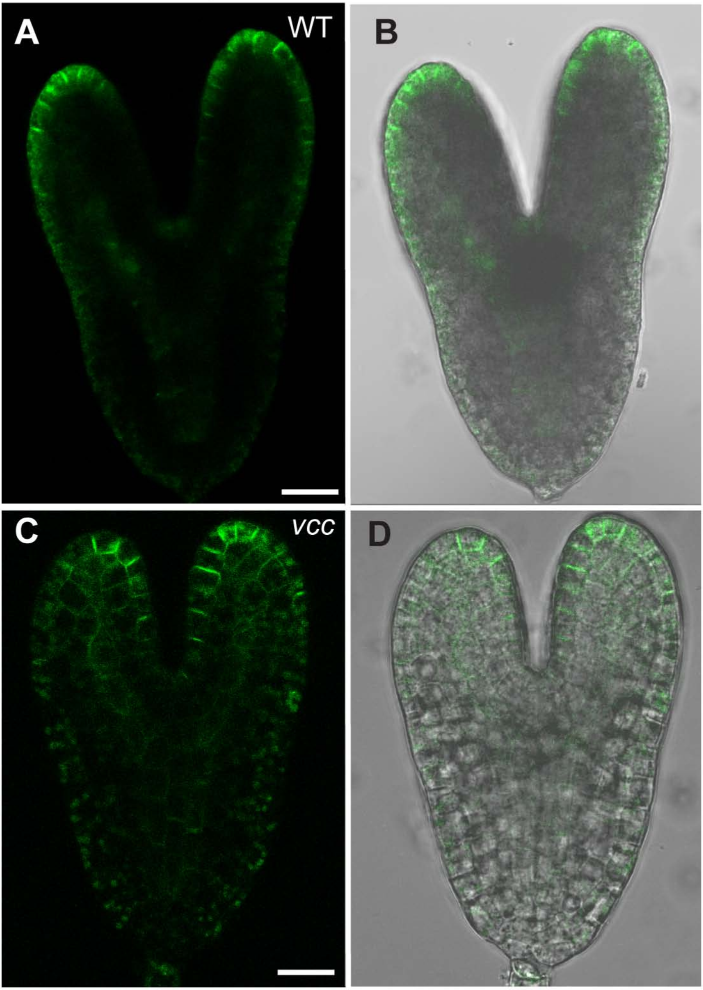


Supplemental Figure S1. Molecular phylogenetic analysis based on Maximum Likelihood. Values for bootstrap consensus tree inferred from 500 replicates are shown. Arabidopsis proteins are highlighted in red. Phylogenetic tree calculation was performed using MEGA5 (Tamura et al., 2011).

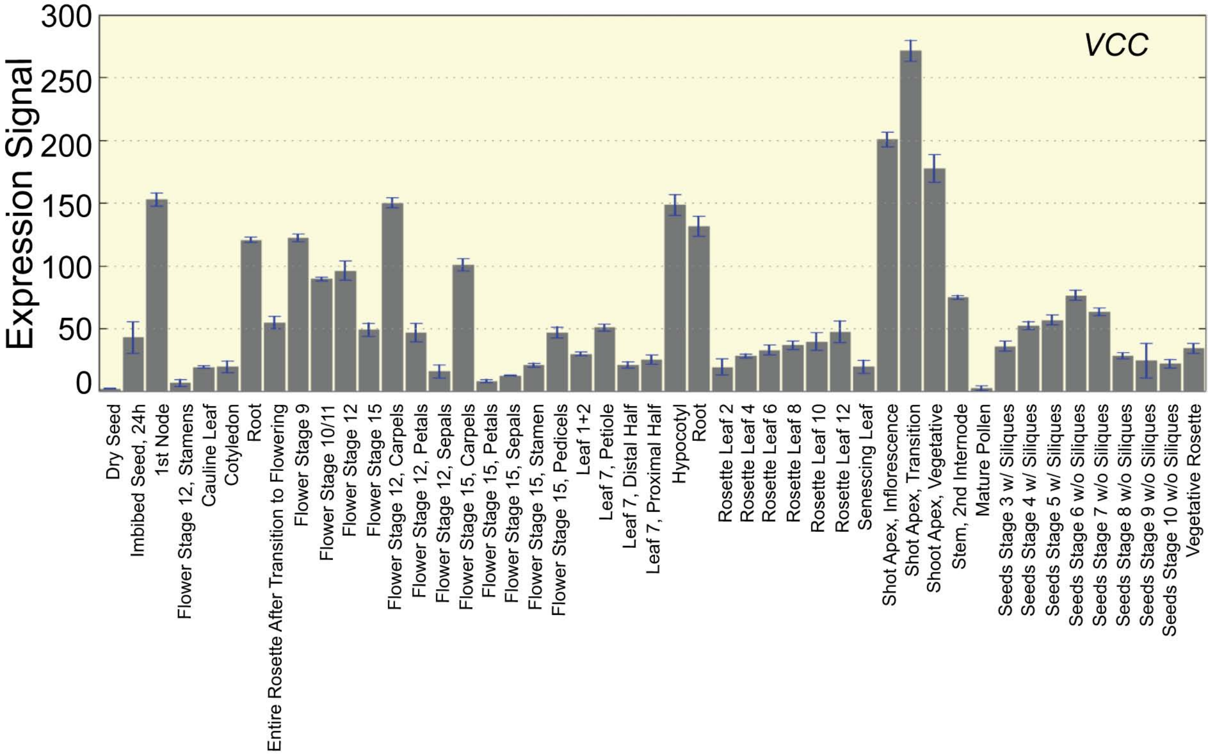


Supplemental Figure S2. *vcc* embryos show abnormal cotyledon vein complexity. Isolated dry seed embryos were stained to detect iron distribution. The graph shows vein complexity categories and frequency of oda in WT and *vcc-3* cotyledons (n=105 for WT and n=131 for *vcc-3*).

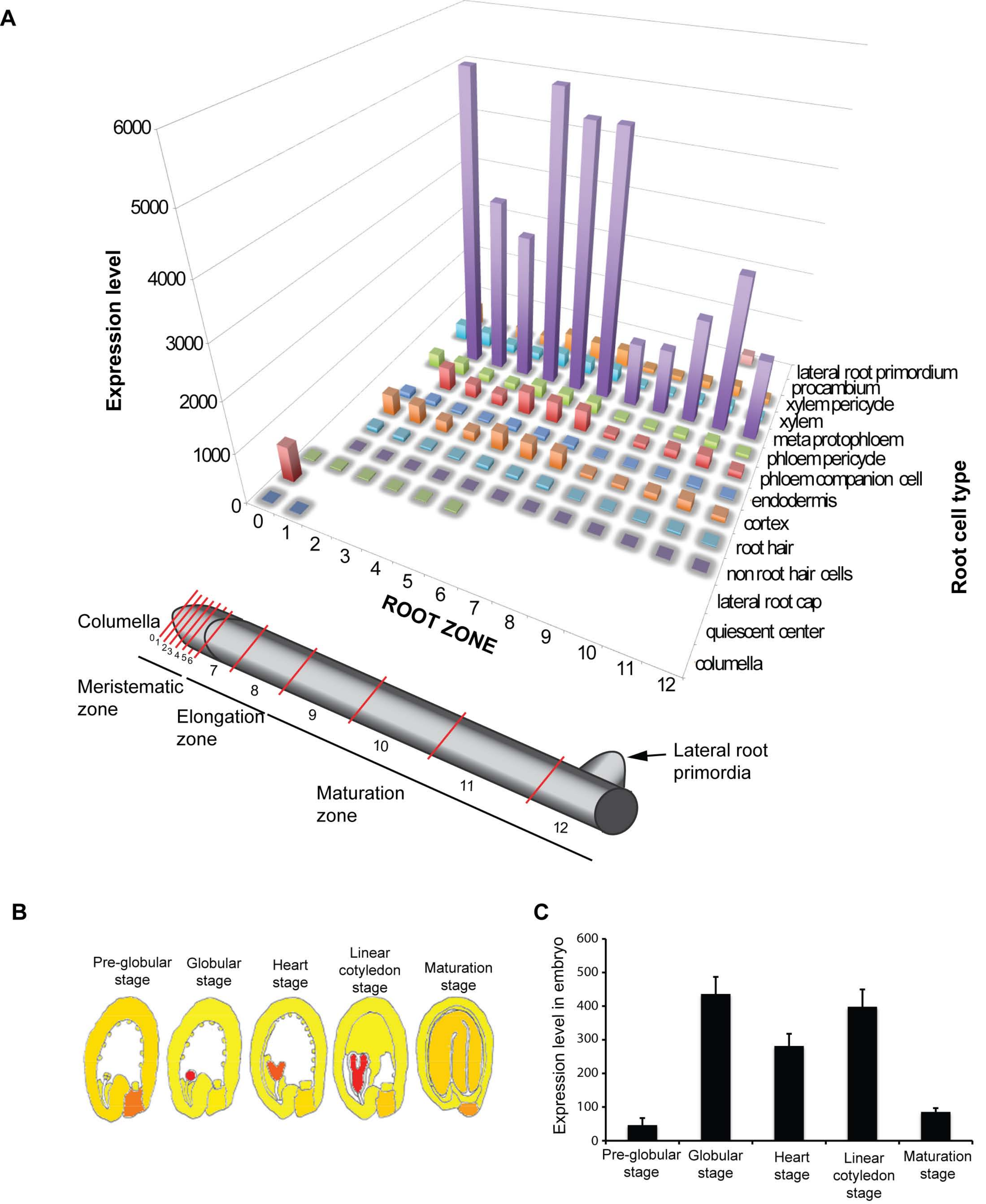
pPIN1:PIN1-GFP



Supplemental Figure S3. PIN1-GFP localization in WT (A and B) and *vcc* mutant (C and D) embryos. A and C, PIN1-GFP; B and D, merged PIN1-GFP and bright field. Bars = 20 µm.



Supplemental Figure S4. Expression pattern of *VCC*. Expression values and standard deviation in different tissues/developmental stages was extracted from eFPBrowser (http://bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi).



Supplemental Figure S5. Expression of *VCC* in root and embryo. A, Expression pattern of *VCC* in root according to Brady et al., 2007. B and C, Expression pattern of *VCC* during embryo development. Expression values and standard deviation in different developmental stages were extracted from eFPBrowser (http://bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi).

Supplemental Table 1: Quantitative analysis of vascular network complexity and connectivity in several lines shown Fig. 2 and Fig. 6.

		4-1	**4-0**	**3-1**	**2-2**	**3-0**	**2-1**	**2-0**	**oda**	**others**	**N**
Col-0	**n**	2	17	31	12	3	3	0	0	4	72
Col-0	**%**	2.78	23.61	43.06	16.67	4.17	4.17	0.00	0.00	5.56	

		4-1	**4-0**	**3-1**	**2-2**	**3-0**	**2-1**	**2-0**	**oda**	**others**	**N**
***vcc-1* SALK_023737C**	**n**	0	1	10	9	12	66	120	86	0	304
***vcc-2* SALK_047972C**	**n**	0	3	5	12	86	61	134	64	0	365
***vcc-3* SAIL_237_C09**	**n**	0	1	6	17	21	72	59	45	0	221
***vcc-1* SALK_023737C**	**%**	0.00	0.30	3.30	3.00	4.00	21.70	39.50	28.30	0.00	
***vcc-2* SALK_047972C**	**%**	0.00	0.80	1.40	3.30	23.60	16.70	36.70	17.50	0.00	
***vcc-3* SAIL_237_C09**	**%**	0.0	0.5	2.7	7.7	9.5	32.6	26.7	20.4	0.0	

		4-1	**4-0**	**3-1**	**2-2**	**3-0**	**2-1**	**2-0**	**oda**	**others**	**N**
***ops-3* salk_089722C**	**n**	0	1	8	10	7	21	15	14	6	82
***ops-4* salk_042563C**	**n**	0	2	1	9	6	39	42	20	3	122
***ops-3* salk_089722C**	**%**	0.00	1.22	9.76	12.20	8.54	25.61	18.29	17.07	7.32	
***ops-4* salk_042563C**	**%**	0.00	1.64	0.82	7.38	4.92	31.97	34.43	16.39	2.46	

		4-1	**4-0**	**3-1**	**2-2**	**3-0**	**2-1**	**2-0**	**oda**	**others**	**N**
***vcc-3 ops-4* Plant1**	**n**	0	0	0	0	1	19	53	140	0	213
***vcc-3 ops-4* Plant21**	**n**	0	0	0	0	0	8	37	66	0	111
***vcc-3 ops-4* Plant1**	**%**	0.00	0.00	0.00	0.00	0.47	8.92	24.88	65.73	0.00	
***vcc-3 ops-4* Plant21**	**%**	0.00	0.00	0.00	0.00	0.00	7.21	33.33	59.46	0.00	

		4 (1)*	**4 (2)**	**3-1 (1)**	**3-1 (2)**	**2-2 (1)**	**2-2 (2)**	**3 (1)**	**3 (2)**	**2-1 (1)**	**2-1 (2)**	**2 (1)**	**2 (2)**	**Fragmented veins**	**N**
vcc-3	n	0	0	2	0	1	0	5	1	20	2	68	14	1	114
ops-4	n	0	0	6	0	1	0	5	0	4	0	3	0	0	19
vcc-3 ops4	n	2	0	7	0	6	0	6	0	17	0	7	0	0	45
vcc-3	%	4.4	0.0	15.6	0.0	13.3	0.0	13.3	0.0	37.8	0.0	15.6	0.0	0.0	
ops-4	%	0.0	0.0	31.6	0.0	5.3	0.0	26.3	0.0	21.1	0.0	15.8	0.0	0.0	
vcc-3 ops4	%	0.0	0.0	1.8	0.0	0.9	0.0	4.4	0.9	17.5	1.8	59.6	12.3	0.9	

Numbers of oda/cotyledon are between parentheses

Supplemental Table 2: Quantitative analysis (in percentages) of vascular network complexity and connectivity in control and *VCC*-overexpressing lines. P-values obtained for t-test analysis between the frequencies of vascular arrays in control and VCC-overexpressing lines are included at the bottom of the table.

	4-1	**4**	**3-1**	**2-2**	**3**	**2-1**	**2**	**oda**	**others**	**N**
pBI121 1	0.00	22.47	30.34	19.10	7.87	14.61	3.37	2.25	0.00	89
pBI121 2	0.00	20.17	16.81	31.93	11.76	11.76	3.36	4.20	0.00	119
pBI121 3	0.00	19.47	30.97	23.89	5.31	11.50	7.96	0.88	0.00	113
pBI121 4	0.86	17.24	30.17	23.28	7.76	15.52	2.59	2.59	0.00	116
pBI121 5	0.00	21.78	31.68	21.78	7.92	10.89	3.96	1.98	0.00	101
pBI121 6	0.00	25.84	38.20	17.98	10.11	3.37	1.12	3.37	0.00	89
pBI121 7	0.74	25.19	35.56	21.48	5.93	8.89	1.48	0.74	0.00	135
average	**0.23**	**21.74**	**30.53**	**22.78**	**8.09**	**10.93**	**3.41**	**2.29**	**0.00**	
SD	**0.39**	**3.09**	**6.76**	**4.56**	**2.24**	**4.02**	**2.26**	**1.25**	**0.00**	

	4-1	**4**	**3-1**	**2-2**	**3**	**2-1**	**2**	**oda**	**others**	**N**
35S:VCC 1	0.00	34.21	35.53	11.84	6.58	7.89	1.32	1.32	1.32	76
35S:VCC 2	0.00	25.37	33.58	18.66	10.45	9.70	2.24	0.00	0.00	134
35S:VCC 3	0.79	30.16	34.92	15.08	6.35	9.52	1.59	0.79	0.79	126
35S:VCC 4	1.06	35.11	24.47	10.64	18.09	9.57	0.00	1.06	0.00	94
35S:VCC 5	0.00	26.74	36.05	18.60	5.81	9.30	2.33	1.16	0.00	86
35S:VCC 6	1.16	29.07	27.91	20.93	5.81	12.79	0.00	1.16	1.16	86
35S:VCC 7	0.70	45.07	29.58	9.15	9.15	4.23	0.00	0.00	2.11	142
35S:VCC 8	0.00	30.39	38.24	11.76	8.82	7.84	2.94	0.00	0.00	102
35S:VCC 9	0.00	18.35	30.28	18.35	18.35	10.09	4.59	0.00	0.00	109
average	**0.41**	**30.50**	**32.28**	**15.00**	**9.94**	**8.99**	**1.67**	**0.61**	**0.60**	
SD	**0.51**	**7.40**	**4.48**	**4.28**	**4.97**	**2.29**	**1.56**	**0.60**	**0.79**	
p-values		0.00555		0.00174				0.00156		