Supporting Information

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SI Materials and Methods

Plant Material and Growth Conditions. The 88 *Arabidopsis thaliana* (L.) Heynh. accessions (N22660) (Fig. 1 and Table S1) and 86 recombinant inbred lines (RILs) from a cross between Nok-3 and Ga-0 (N717142) were obtained from the Nottingham *Arabidopsis* Stock Centre. The *receptor-like protein kinase1-1* (*rpk1-1*) and *rpk1-5* mutants and the *pRPK1::RPK1-GFP* line, all in Columbia-0 (Col-0) background (1), were provided by Frans Tax (University of Arizona, Tucson, AZ). The *rpk1-1* mutant has an exonic transfer DNA insertion 502 bp downstream of the translation start and downstream of the leucine-rich repeat; no full-length transcripts are detected in this line (1). The *rpk1-5* mutant has been identified in a population generated by targeting induced local lesions in genomes and has a nonsense mutation that is predicted to result in an early premature stop codon in the leucine-rich repeat (1). Seeds were sterilized by fumigation for 4 h in a desiccator jar with chlorine gas generated by adding 5 mL concentrated HCl to 100 mL 5% (vol/vol) NaOCl. Sterilized seeds were sown on square Petri dishes with basal medium [BM; Gamborg's B5 salts, 0.05% 2-(4-morpholino-)ethane sulfonic acid, pH 5.8, 2% (wt/vol) glucose, 0.7% agar]. After a cold treatment for 3 d at 4 °C, the plates were placed vertically in a growth chamber at 22 °C under a 16-/8-h light-to-dark photoperiod (45 μmol m^{-2} s^{-1} light irradiance from cool white fluorescent tungsten tubes). Shoot regeneration from root explants was as described (2) with modifications: 7-mm-long apical root segments were taken from 7-d-old seedlings and placed on callus-inducing medium (BM supplemented with 2.2 μM 2,4-dichlorophenoxy acetic acid and 0.2 μM kinetin) for 4 d. Explants were transferred to shoot-inducing medium (SIM; BM supplemented with 10 μM 2-isopentenyl adenine and 0.86 μM 3-indoleacetic acid). Hormones were dissolved in DMSO and supplied to the medium after autoclaving.

Correlation Study. Shoots, primordia, roots, callus, and greenness were monitored for root explants of 88 *Arabidopsis* accessions at different time points during SIM incubation (7, 11, 14, and 21 d). The number of shoots after 7 d of SIM incubation was not included, because almost no shoots were formed at that time point. Formation of primordia, shoots, and roots was quantified by counting the number of developmental events. Developing structures were counted as primordia when they were green or purple and dome-shaped or spherical with a smooth surface and a clearly organized cellular patterning and eventually had leaf primordia (as represented in Fig. 2*A*). For a developing structure to be counted as shoot, it had to originate from a primordium and have side structures that were clearly identifiable as trichome-bearing leaves emerging from a single meristem (as represented in Fig. 2*B*). Explant greening and callus development were defined within five classes ranging from class 0 to class 4 for the absence of the response to the strongest response among all explants of all accessions (Fig. 2 *C* and *D*). Pairwise correlations between the different parameters were calculated with the Spearman's rank correlation coefficient. The correlation coefficients were clustered based on Euclidean distances, whereas intercluster distance was measured by complete linkage clustering. These analyses were done with the R software package, version 2.10.1 (www.r-project.org/).

Linkage Mapping. The genotypes for the Nok-3 × Ga-0 RILs at each of 75 markers are available at http://www.jic.ac.uk/staff/ian-bancroft/arabidopsis.htm. From 94 RILs available, NG1, NG33, NG36, NG40, NG49, NG68, NG71, and NG88 were not used. The regeneration rate (i.e., the number of explants producing at least one shoot) among 20 explants was measured at 14 and 21 d for each of the 86 RILs. The experiment was done in triplicate. Because data were binomial, probit-transformed data were used for quantitative trait loci (QTL) analysis as implemented in GenStat, version 14 (3), comprising a preliminary search for QTL by means of a simple interval mapping followed by a composite interval mapping and a backward selection. Mapping was conducted with an interval size of 5 cM at a genome-wide type I error rate of 5%. Thresholds to identify significant QTL were calculated as described (4).

Association Mapping. The shoot regeneration rate among 30 explants was assessed after 14 and 21 d of SIM incubation for 88 accessions. Six biological replicates of the experiment were done sequentially in time. Analogously to the linkage mapping, data were probit-transformed. SNP–trait associations for 250,000 SNPs (https://cynin.gmi.oeaw.ac.at/home/resources/atpolydb) (5), considering a minor allelic frequency of 5%, were evaluated by fitting a linear mixed model to the probit-transformed data, controlling for the population structure as described (6), and testing the null hypothesis of no association by means of a Wald test. The association mapping with 62 full-sequenced accessions at the time of analysis (January of 2012; http://signal.salk.edu/atg1001) was done in a similar way as described above considering a minor allelic frequency of 10%. Fitting linear mixed models using REML and Wald testing was done with GenStat, version 14 (3). The genotype and linkage disequilibrium plots were constructed at the Genome Variation Server (http://gvs.gs.washington.edu/GVS137/).

Quantitative Complementation Test. The shoot regeneration rate among explants was assessed after 14 d threefold for four genotypes (Nok-3/*rpk1-5*, Ga-0/*rpk1-5*, Nok-3/Col-0, and Ga-0/Col-0) and their reciprocal crosses. The experiment was replicated two times, totaling the number of experimental units to 48. A probit regression model of the form $y = \beta_0 + \beta_1 EXP + \beta_2 P_1 + \beta_3 P_2 + \beta_4 P_1 \cdot P_2 + \varepsilon$ was fitted to the binomial data, where y represents the probit-transformed binomial data; EXP is the experiment (two levels), and P_1 and P_2 are two dummies with Nok-3 and Ga-0 and *rpk1-5* and Col-0 as levels, respectively. One single observation was left out of the analysis because of its large standardized residual. The interaction between the mutated *rpk1* allele and the RPK1 QTL alleles was evaluated by an analysis of deviance, with the dispersion parameter fixed at one, as implemented in the generalized linear model framework in Genstat, version 14 (3).

***rpk1* Regeneration.** Data were collected from three (Col-0 and *rpk1-5*) or two (*rpk1-1*) time-independent replicates, with three plates per repeat and genotype and on average, at least 18 (Col-0 and *rpk1-5*) or 10 (*rpk1-1*) explants per plate. A generalized linear model, as implemented in GenStat, version 14 (3), was fitted to probit-transformed data. Differences were assessed by an analysis of deviance.

Microscopy. For confocal microscopy, explants were mounted in propidium iodide (10 μg/mL) or half-strength liquid Murashige and Skoog medium under glass coverslips. Confocal laser-scanning microscopy was done with an inverted Axiovert 100M (Zeiss) microscope and an argon ion laser to generate 488-nm light for GFP excitation and 543-nm light for propidium iodide fluorescence. Images were captured with the LSM510 image acquisition software (Zeiss).

1. Nodine MD, Yadegari R, Tax FE (2007) *RPK1* and *TOAD2* are two receptor-like kinases redundantly required for *Arabidopsis* embryonic pattern formation. *Dev Cell* 12(6): 943–956.
2. Valvekens D, Van Montagu M, Van Lijsebettens M (1988) *Agrobacterium tumefaciens*-mediated transformation of *Arabidopsis thaliana* root explants by using kanamycin selection. *Proc Natl Acad Sci USA* 85(15):5536–5540.
3. Payne RW (2011) *Genstat Release 14 Reference Manual, Part 3 Procedure Library PL20* (VSN International, Hemel Hempstead, United Kingdom).
4. Li J, Ji L (2005) Adjusting multiple testing in multilocus analyses using the eigenvalues of a correlation matrix. *Heredity (Edinb)* 95(3):221–227.
5. Kim S, et al. (2007) Recombination and linkage disequilibrium in *Arabidopsis thaliana*. *Nat Genet* 39(9):1151–1155.
6. Zhao K, et al. (2007) An *Arabidopsis* example of association mapping in structured samples. *PLoS Genet* 3(1):e4.

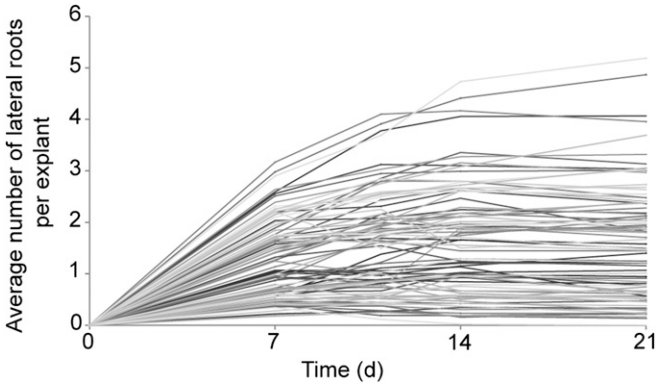

Fig. S1. Root formation on root explants of 88 *Arabidopsis* accessions throughout SIM incubation.

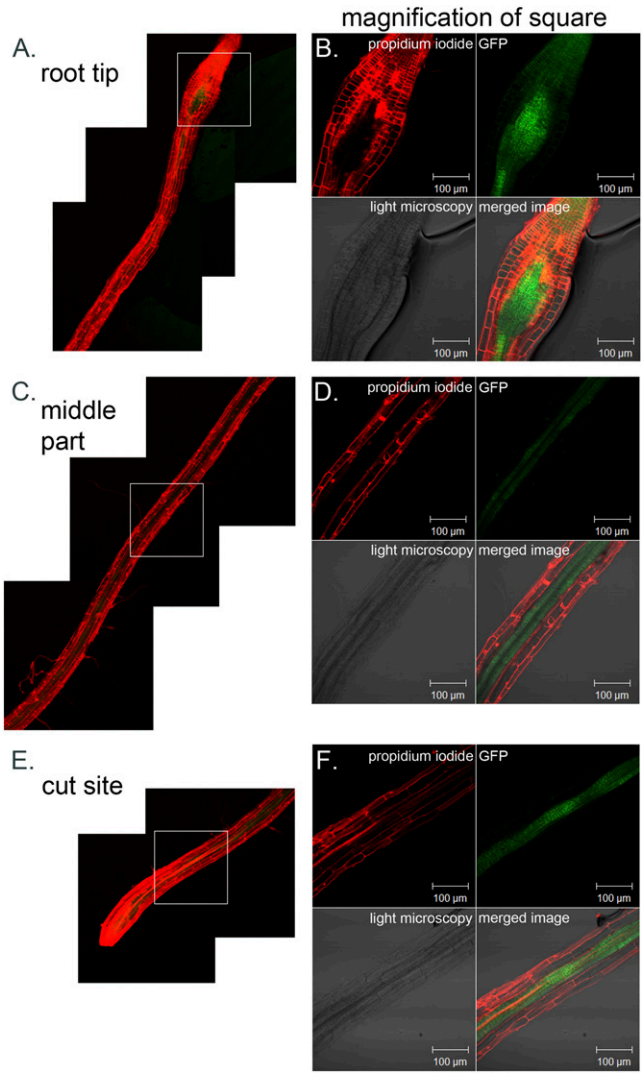

Fig. S2. Confocal images of *pRPK1::RPK1-GFP* expression in a root explant after 4 d of incubation on callus-inducing medium. Root explant at the (*A* and *B*) root tip, (*C* and *D*) middle part, and (*E* and *F*) cut site. (*B*, *D*, and *F*) Magnification of the areas indicated by the squares in *A*, *C*, and *E*, respectively.

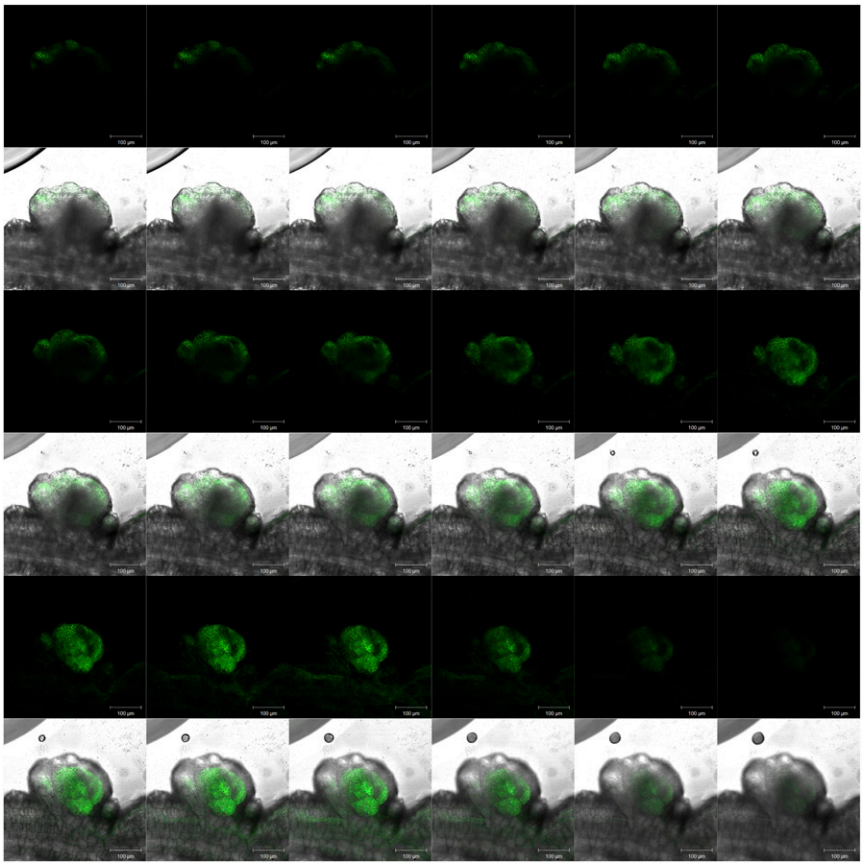

Fig. S3. *Z* stack (2.8-μm slices) of the primordium in Fig. 5*E* (11 d after SIM incubation) showing (*Upper*) the *pRPK1::RPK1-GFP* fluorescence and (*Lower*) the merged images with light microscopy.

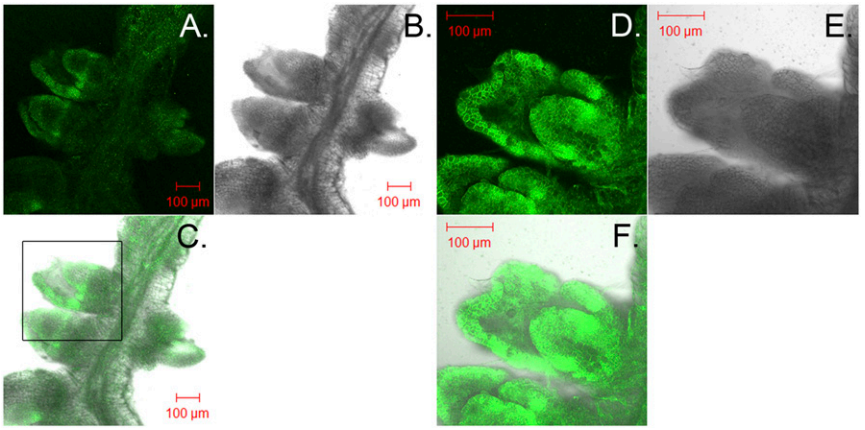

Fig. S4. *pRPK1::RPK1-GFP* expression in developing shoots after 11 d of SIM incubation. (*A* and *D*) GFP fluorescence, (*B* and *E*) light microscopy, and (*C* and *F*) merged images. (*D–F*) Magnifications of the area indicated by the square in *C*.

Table S1. Data of different phenotypical responses evaluated at different time points during the incubation on SIM for 88 *Arabidopsis* accessions

	No. of shoots/explant								No. of primordia/explant								Callus class								Greenness class								No. of roots/explant							
Accession	7 d	SEM	11 d	SEM	14 d	SEM	21 d	SEM	7 d	SEM	11 d	SEM	14 d	SEM	21 d	SEM	7 d	SEM	11 d	SEM	14 d	SEM	21 d	SEM	7 d	SEM	11 d	SEM	14 d	SEM	21 d	SEM	7 d	SEM	11 d	SEM	14 d	SEM	21 d	SEM
Ag-0	0	0	0.9	0.641	1.044	0.703	1.233	0.696	0.044	0.036	2.056	1.189	3.044	1.97	3.122	1.49	0.211	0.132	0.678	0.241	1.311	0.179	1.267	0.211	0.556	0.279	1.889	0.405	2.2	0.672	1.922	0.502	1.578	0.173	1.578	0.173	1.656	0.074	1.578	0.118
An-1	0	0	0	0	0.178	0.079	0.333	0.087	0	0	0.422	0.305	0.544	0.31	0.689	0.392	0	0	0.156	0.074	0.244	0.149	0.533	0.22	0.144	0.04	0.444	0.096	0.767	0.291	0.778	0.209	1.411	0.078	1.411	0.078	1.878	0.196	2.122	0.292
Bay-0	0	0	0.011	0.009	0.113	0.049	0.306	0.107	0	0	0.749	0.442	1.983	1.072	1.629	0.999	0.482	0.265	1.089	0.073	0.917	0.185	1.193	0.017	1.265	0.176	2.078	0.153	2.181	0.102	1.948	0.122	2.203	0.347	2.203	0.347	2.616	0.394	2.366	0.081
Bil-5	0	0	0.522	0.203	3.856	1.753	4.122	1.725	0.111	0.065	9.122	4.556	11.42	2.237	11	3.019	0.467	0.125	1.178	0.199	1.556	0.543	1.822	0.485	1.189	0.089	2.389	0.146	2.378	0.498	2.678	0.377	0.644	0.343	0.644	0.343	1.222	0.101	1.222	0.155
Bor-1	0	0	0.311	0.254	2.133	1.459	2.289	1.518	0.011	0.009	2.344	1.341	2.678	1.155	3.567	1.68	0.033	0.016	0.656	0.229	1.422	0.331	1.378	0.269	0.689	0.159	1.867	0.031	2	0.113	2.044	0.143	1.256	0.195	1.256	0.195	2.467	0.096	1.822	0.379
Bor-4	0	0	1.101	0.776	7.841	1.277	7.163	1.756	1.768	1.293	23.04	9.333	17.05	3.32	16.56	3.147	0.567	0.181	1.778	0.373	1.644	0.242	1.656	0.236	1.411	0.235	2.922	0.302	2.478	0.199	2.489	0.205	0.211	0.055	0.211	0.055	0.233	0.094	0.233	0.094
Br-0	0	0	0	0	0.211	0.122	0.333	0.163	0.022	0.018	0.767	0.357	0.6	0.354	0.267	0.144	0.389	0.218	0.478	0.161	1.222	0.169	1.856	0.373	0.889	0.209	1.978	0.377	2.267	0.083	2.878	0.241	0.933	0.262	0.933	0.262	0.844	0.322	0.811	0.363
Bur-0	0	0	0	0	0.011	0.009	0.133	0.057	0	0	0	0	0.056	0.045	0.133	0.109	0.622	0.131	0.889	0.146	1.444	0.12	1.522	0.059	1.144	0.092	1.989	0.073	2.911	0.433	2.167	0.103	1.267	0.098	1.267	0.098	2.178	0.091	2.033	0.126
C24	0	0	3.289	1.302	11.52	4.59	11.73	4.46	0.822	0.338	28.98	8.755	18.19	7.445	18.77	7.149	0.478	0.251	2.067	0.594	2.9	0.544	3.067	0.412	1	0.22	2.967	0.283	3.378	0.38	3.544	0.249	1.711	0.428	1.711	0.428	1.922	0.364	1.867	0.34
CIBC-17	0	0	0	0	0	0	0	0	0	0	0.056	0.045	0	0	0.244	0.2	0.678	0.092	0.556	0.181	0.6	0.137	1.144	0.203	0.244	0.11	0.533	0.15	0.556	0.155	1.067	0.315	1.044	0.102	1.044	0.102	0.989	0.476	0.944	0.358
CIBC-5	0	0	0.333	0.22	0.733	0.507	1.156	0.794	0	0	1.289	0.781	1.311	0.949	1.422	0.739	0.511	0.22	0.989	0.196	1.289	0.4	1.3	0.257	0.833	0.155	2.3	0.319	2.656	0.549	2.233	0.315	1.622	0.421	1.622	0.421	2.656	0.451	2.4	0.573
Col-0	0	0	1.178	0.558	4.367	1.789	4.611	1.794	0	0	3.244	1.32	4.467	1.98	3.678	1.643	0.478	0.27	0.778	0.263	0.856	0.303	1.278	0.059	0.322	0.116	1.722	0.478	1.656	0.154	2.033	0.228	0.5	0.181	0.5	0.181	0.567	0.175	0.567	0.129
CS22491	0	0	0.011	0.009	0.156	0.101	0.222	0.131	0	0	0.967	0.613	1.478	1.02	1.089	0.783	0.5	0.087	0.944	0.211	1.4	0.242	1.622	0.27	1.089	0.182	1.833	0.042	1.844	0.236	2.167	0.424	0.689	0.221	0.689	0.221	1.022	0.386	1.067	0.49
Ct-1	0	0	0.056	0.033	0.322	0.196	0.544	0.349	0.022	0.018	0.3	0.205	0.289	0.141	0.544	0.297	0.644	0.192	1.167	0.103	1.411	0.268	1.689	0.087	0.922	0.118	2.367	0.257	2.367	0.341	2.178	0.107	1.478	0.189	1.478	0.189	2.111	0.048	2.278	0.105
Cvi-0	0	0	0.978	0.348	3	1.34	3.522	1.134	0	0	8.456	3.378	11.92	4.278	11.26	4.585	0.078	0.024	0.689	0.351	1.3	0.126	1.311	0.157	0.422	0.126	1.6	0.291	1.878	0.018	2.422	0.359	0.456	0.018	0.456	0.018	0.422	0.071	0.478	0.024
Eden-1	0	0	0	0	0.035	0.001	0.413	0.114	0.011	0.009	0.297	0.06	1.093	0.717	1.255	0.413	0.491	0.225	0.915	0.282	1.45	0.167	1.784	0.245	0.864	0.207	2.129	0.259	2.064	0.181	2.863	0.358	0.554	0.192	0.554	0.192	1.66	0.371	1.491	0.456
Edi-0	0	0	0.011	0.009	0.011	0.009	0.011	0.009	0.022	0.018	0.133	0.016	0.1	0.047	0.267	0.063	0.122	0.1	0.344	0.149	0.1	0.068	0.789	0.256	0.678	0.19	2.4	0.425	2.067	0.765	2.133	0.251	0.922	0.095	0.922	0.095	0.922	0.205	0.911	0.184
Ei-2	0	0	0.1	0.068	0.5	0.22	0.844	0.294	0	0	1.189	0.339	2.867	0.968	3.111	0.617	0.222	0.168	0.7	0.177	0.978	0.196	1.2	0.123	0.622	0.244	1.633	0.152	1.767	0.125	1.878	0.079	1.244	0.299	1.244	0.299	0.978	0.137	0.844	0.149
Est-1	0	0	0.089	0.073	2.622	1.471	2.8	1.417	0.544	0.064	12.17	4.038	10.58	3.874	9.011	3.479	0.978	0.033	1.578	0.285	1.744	0.415	2.156	0.229	2.511	0.245	2.978	0.018	2.978	0.167	3.067	0.096	2.556	0.574	2.556	0.574	3.1	0.3	3.033	0.382
Fab-4	0	0	0.024	0.019	1.144	0.622	4.149	0.71	0	0	1.43	0.367	3.041	0.415	8.414	3.72	0.632	0.151	0.813	0.163	1.315	0.239	2.351	0.207	1.193	0.249	1.701	0.179	2.298	0.288	2.982	0.411	0.868	0.269	0.868	0.269	1.921	0.219	1.704	0.295
Fei-0	0	0	0.422	0.167	2.689	0.591	2.811	0.482	0.189	0.154	18.18	9.796	20.34	5.59	19.77	5.819	0.444	0.241	1.544	0.546	2.1	0.581	2.311	0.488	1.233	0.382	2.511	0.318	3.033	0.345	3.122	0.308	0.389	0.153	0.389	0.153	0.189	0.081	0.222	0.102
Ga-0	0	0	0.011	0.009	0.1	0.047	0.344	0.229	0	0	0.356	0.11	1.4	0.656	1.4	0.946	0.156	0.079	0.989	0.127	1.244	0.283	1.467	0.206	0.433	0.181	1.8	0.191	2.267	0.257	2.344	0.27	1.067	0.284	1.067	0.284	1.133	0.216	0.567	0.098
Got-22	0	0	0.011	0.009	0.067	0.027	0.811	0.345	0	0	0.167	0.072	1.289	0.848	3.267	1.482	0.056	0.033	0.233	0.137	0.222	0.11	0.378	0.107	0.022	0.018	0.622	0.168	0.933	0.206	0.844	0.168	0.722	0.282	0.722	0.282	1.789	0.158	1.944	0.045
Got-7	0	0	0.011	0.009	0.133	0.083	0.367	0.123	0	0	0.178	0.071	0.722	0.296	2.167	0.933	0.067	0.054	0.356	0.277	0.233	0.087	0.367	0.098	0.033	0.016	0.156	0.114	0.267	0.152	0.867	0.123	0.722	0.296	0.722	0.296	1.889	0.157	1.8	0.098
Gu-0	0	0	0.022	0.018	0.189	0.095	0.189	0.089	0	0	0.967	0.395	1.044	0.606	1.244	0.745	0.356	0.177	0.433	0.189	0.4	0.178	0.311	0.146	0.511	0.167	0.411	0.074	1.211	0.471	0.9	0.193	0.222	0.101	0.222	0.101	0.344	0.161	0.333	0.218
Gy-0	0	0	0.114	0.068	0.806	0.311	1.326	0.417	0	0	0.91	0.448	2.407	0.558	1.681	0.523	0.235	0.068	0.332	0.217	0.582	0.198	0.775	0.11	0.067	0.027	0.942	0.362	1.211	0.111	1.325	0.058	0.374	0.14	0.374	0.14	0.305	0.066	0.317	0.091
HR-10	0.017	0.012	3.217	0.766	5.033	0.236	5.133	0.094	3.65	1.19	4.411	2.066	7.717	1.992	6.389	2.828	0.689	0.285	1.067	0.446	1.322	0.553	1.367	0.562	1.067	0.475	1.778	0.743	2.111	0.867	2.367	0.966	0.378	0.161	0.378	0.161	0.178	0.073	0.133	0.057
HR-5	0	0	0	0	0.05	0.035	0.617	0.436	0	0	0.033	0.024	0.067	0.047	0.45	0.318	0.367	0.047	0.567	0.401	1.1	0.165	0.7	0.212	0.95	0.035	1.533	0.283	1.767	0.283	2.783	0.012	1.017	0.177	1.017	0.177	1.15	0.295	1.4	0.236
Kas-1	0	0	0	0	0.044	0.009	0.133	0.047	0	0	0.278	0.04	0.556	0.11	0.478	0.195	0.622	0.194	1.3	0.286	1.4	0.15	1.522	0.195	1.244	0.1	2.822	0.516	2.5	0.242	3.444	0.214	2.978	0.508	2.978	0.508	4.411	0.135	4.867	0.247
Kin-0	0	0	0.444	0.187	1.233	0.519	1.411	0.496	0.178	0.107	2.722	0.87	5.033	2.23	4.167	2.592	0.056	0.033	0.667	0.235	1.133	0.14	1.189	0.229	0.289	0.018	1.467	0.178	2.033	0.262	2.189	0.398	1.844	0.425	1.844	0.425	2.611	0.074	2.478	0.213
Knox-10	0	0	0.4	0.212	1.517	0.672	1.983	0.483	0	0	5.583	0.012	11.57	3.936	9.55	5.032	0.117	0.035	0.8	0.189	1.1	0.024	1.233	0.047	0.7	0.236	2.1	0.094	2.333	0.236	3.183	0.247	0.65	0.247	0.65	0.247	1.017	0.224	0.767	0.071
Knox-18	0	0	0.356	0.277	1.378	1.044	1.633	1.143	0	0	0.889	0.553	1.289	0.699	1.433	1.048	0.522	0.213	1.044	0.324	1.356	0.203	1.567	0.129	1.1	0.047	2.078	0.081	2.089	0.059	2.133	0.063	2.389	0.553	2.389	0.553	3.156	0.731	2.967	0.717
Kondara	0	0	0.011	0.009	1.116	0.409	1.673	0.468	0	0	2.122	0.897	4.8	2.231	4.196	2.06	0.48	0.239	1.031	0.144	1.587	0.497	1.729	0.373	0.98	0.034	1.791	0.037	2.336	0.354	2.631	0.292	2.511	0.458	2.511	0.458	2.991	0.46	3.008	0.393
KZ-1	0	0	0.011	0.009	0.044	0.009	0.044	0.009	0	0	0.033	0.027	0.078	0.051	0.033	0.027	0.478	0.217	1.133	0.129	1.133	0.123	1.322	0.187	0.7	0.287	2.022	0.079	2.2	0.181	2.489	0.319	2.589	0.574	2.589	0.574	4.056	0.487	4.067	0.648
KZ-9	0	0	3.633	1.748	18.68	6.069	18.68	6.069	0.189	0.154	36.56	8.965	33.61	6.865	33.61	6.865	0.3	0.181	2.144	0.134	1.878	0.508	1.878	0.508	0.622	0.024	2.689	0.118	3.078	0.078	3.078	0.078	1.622	0.467	1.622	0.467	1.444	0.342	1.444	0.342
Ler-1	0	0	0.075	0.048	0.213	0.135	0.213	0.135	0	0	0.267	0.119	0.626	0.266	0.487	0.282	0.057	0.032	0.959	0.065	0.696	0.255	1.466	0.282	1.003	0.13	1.511	0.4	2.38	0.392	2.153	0.054	0.99	0.346	0.99	0.346	2.126	0.303	1.868	0.148
LL-0	0	0	0.144	0.059	0.933	0.418	2.511	1.033	0.033	0.027	2.711	1.18	9.842	3.71	8.026	3.48	0.203	0.07	0.944	0.134	1.302	0.247	1.576	0.061	0.656	0.141	1.873	0.117	2.03	0.147	2.943	0.165	0.873	0.36	0.873	0.36	1.204	0.492	1.207	0.664
Lov-1	0	0	0	0	0.048	0.039	0.751	0.319	0	0	1.724	1.301	3.045	0.885	2.457	1.335	0.198	0.142	0.995	0.356	0.579	0.196	1.004	0.178	0.328	0.204	0.945	0.254	1.097	0.145	0.833	0.079	1.314	0.634	1.314	0.634	2.101	0.592	2.403	0.658
Lp2-2	0	0	0.8	0.342	5.233	0.826	5.533	0.749	0	0	12.32	2.255	10.08	2.42	9.9	2.827	0.189	0.018	1.067	0.042	1.544	0.22	1.478	0.172	0.589	0.202	2	0.031	2.522	0.252	2.422	0.183	0.956	0.469	0.956	0.469	1.289	0.521	1.244	0.487
Lp2-6	0	0	0.022	0.009	0.133	0.063	0.156	0.055	0	0	0.167	0.087	0.122	0.051	0.111	0.055	0.289	0.101	0.633	0.247	0.878	0.168	1.522	0.203	0.6	0.11	2.178	0.358	2.622	0.146	2.278	0.282	2.033	0.031	2.033	0.031	2.244	0.078	2.178	0.074
Lz-0	0	0	0.1	0.057	1.233	0.435	1.344	0.481	0	0	4.722	2.218	8.267	3.943	8.311	3.855	0.611	0.153	1.122	0.045	1.144	0.036	1.822	0.269	1.022	0.033	2.322	0.277	2.778	0.286	3.2	0.098	0.722	0.081	0.722	0.081	0.667	0.072	0.611	0.024
Mr-0	0	0	0.489	0.111	2.589	1.277	2.956	1.203	2.3	1.73	10.87	4.661	4.056	1.173	4.211	1.132	0.789	0.096	2.278	0.31	2.422	0.349	2.467	0.196	1.622	0.223	3.211	0.303	3.144	0.189	3.056	0.036	2.156	0.527	2.156	0.527	2.6	0.568	2.733	0.578
Mrk-0	0	0	0.1	0.082	0.289	0.222	0.8	0.653	0.022	0.018	0.811	0.568	1.5	1.102	1.333	0.943	0.622	0.255	1.133	0.453	1.533	0.087	1.367	0.247	1.311	0.186	1.9	0.432	2.133	0.654	1.756	0.57	1.322	0.213	1.322	0.213	1.244	0.122	1.156	0.127
Ms-0	0	0	2.589	0.834	6.989	1.979	6.944	1.996	6.189	4.631	17.58	4.515	11.77	5.642	12.01	5.526	0.8	0.087	2.311	0.333	2.689	0.552	2.711	0.535	1.622	0.22	2.822	0.247	3.233	0.314	3.256	0.299	1.733	0.386	1.733	0.386	1.856	0.395	1.867	0.398
Mt-0	0	0	0.8	0	1.533	0	1.733	0	1	0	2.022	1.651	3.733	0	1.311	1.071	0.144	0.118	0.633	0.517	0.733	0.599	0.711	0.581	0.622	0.508	0.878	0.717	1.011	0.826	0.9	0.735	0.9	0.735	0.9	0.735	0.956	0.78	0.767	0.626
Mz-0	0	0	0.3	0.245	0.556	0.454	0.533	0.435	0.278	0.146	0.678	0.553	0.933	0.722	0.711	0.554	0.4	0.247	1.211	0.173	1.378	0.114	1.711	0.165	0.744	0.244	2.667	0.461	2.778	0.486	2.367	0.222	0.556	0.229	0.556	0.229	0.933	0.155	0.644	0.048
Nd-1	0	0	0.256	0.018	0.956	0.277	0.978	0.349	0.144	0.04	1.967	0.134	1.589	0.455	2.111	0.843	0.878	0.101	1.3	0.159	1.478	0.214	1.622	0.218	1.333	0.178	2.144	0.071	2.578	0.299	2.144	0.286	1.656	0.078	1.656	0.078	1.811	0.089	1.911	0.04
NFA-10	0	0	2	0	6.5	0	6.5	0	0.5	0	24.45	16.59	95.5	0	29.89	14.55	0.691	0.252	1.805	0.677	1.575	0.575	1.575	0.575	1.205	0.433	2.119	0.784	2.264	0.819	2.264	0.819	2.2	1.087	2.2	1.087	1.973	0.772	1.973	0.772
NFA-8	0	0	1.244	0.411	2.989	0.786	3.711	0.649	0.267	0.204	4.4	0.669	8.967	0.889	8.556	0.925	0.456	0.181	0.956	0.081	0.822	0.199	1.056	0.167	0.733	0.068	1.8	0.144	2.233	0.201	2.344	0.247	0.356	0.155	0.356	0.155	0.156	0.074	0.244	0.095
Nok-3	0	0	1.933	0.589	4.456	1.022	4.733	0.8	3.867	2.306	27.67	2.943	43.02	10.55	43.13	10.49	0.722	0.137	1.411	0.389	1.9	0.22	1.844	0.255	1.178	0.159	2.578	0.223	2.389	0.291	2.4	0.291	0.656	0.189	0.656	0.189	0.622	0.279	0.511	0.19
Omo2-1	0	0	0.122	0.1	0.122	0.1	0.236	0.112	0	0	0.156	0.114	0.178	0.096	0.038	0.019	0.711	0.135	0.867	0.096	0.831	0.219	1.113	0.057	0.98	0.046	1.933	0.031	2.1	0.082	2.776	0.303	1.136	0.534	1.136	0.534	1.742	0.579	2.08	0.317
Omo2-3	0	0	0.044	0.036	1.189	0.199	1.678	0.383	0	0	7.856	3.019	12.19	4.631	13.79	6.101	0.056	0.033	0.4	0.181	0.678	0.143	0.911	0.105	0.467	0.094	1.789	0.354	1.911	0.312	1.778	0.281	1.889	0.492	1.889	0.492	3.356	0.641	3.133	0.645
Oy-0	0	0	0.044	0.024	0.774	0.419	1.548	0.25	0	0	1.407	0.623	3.104	1.419	2.111	1.724	0.033	0.027	0.648	0.101	0.885	0.233	1.037	0.109	0.211	0.159	1.278	0.078	1.648	0.17	1.926	0.199	2.637	0.132	2.637	0.132	3.274	0.202	3.319	0.281
Pna-10	0	0	0.044	0.024	0.611	0.22	1.211	0.39	0	0	2.567	1.203	3.356	1.212	2.378	1.02	0.033	0.016	0.544	0.105	0.989	0.225	1.189	0.2	0.467	0.249	2	0.638	1.744	0.181	2.333	0.126	0.6	0.134	0.6	0.134	0.789	0.217	0.767	0.223
Pna-17	0	0	0.022	0.018	0.189	0.04	0.333	0.159	0.122	0.1	7.622	0.666	11.16	2.925	4.433	1.565	0.156	0.114	1.156	0.479	1.822	0.254	2.422	0.448	0.478	0.128	2.344	0.342	2.367	0.094	2.878	0.255	3.167	0.508	3.167	0.508	4.167	0.299	3.956	0.398
Pu2-23	0	0	0.124	0.051	1.298	0.491	1.833	0.781	0	0	4.902	0.553	8.436	0.969	7.854	1.357	0.023	0.019	0.575	0.24	0.911	0.045	1.023	0.071	0.751	0.054	2.153	0.278	2.33	0.452	2.379	0.312	0.418	0.104	0.418	0.104	0.543	0.156	0.543	0.156

Table S1. Cont.

	No. of shoots/explant								No. of primordia/explant								Callus class								Greenness class								No. of roots/explant							
Accession	7 d	SEM	11 d	SEM	14 d	SEM	21 d	SEM	7 d	SEM	11 d	SEM	14 d	SEM	21 d	SEM	7 d	SEM	11 d	SEM	14 d	SEM	21 d	SEM	7 d	SEM	11 d	SEM	14 d	SEM	21 d	SEM	7 d	SEM	11 d	SEM	14 d	SEM	21 d	SEM
Pu2-7	0	0	0.111	0.048	0.467	0.063	1.167	0.257	0.011	0.009	2.167	0.328	4.678	1.111	4.433	0.815	0.167	0.098	0.456	0.149	0.744	0.277	1.233	0.063	0.689	0.236	1.589	0.186	2.378	0.671	2.433	0.354	1.767	0.469	1.767	0.469	2.8	0.083	2.478	0.135
Ra-0	0	0	0.022	0.018	0.133	0.068	0.556	0.184	0	0	0.222	0.096	0.778	0.181	0.233	0.063	0.833	0.216	1.244	0.164	1.644	0.342	1.944	0.159	1.178	0.102	1.7	0.278	2.544	0.488	2.444	0.29	0.711	0.134	0.711	0.134	0.5	0.22	0.744	0.096
Ren-1	0	0	0.122	0.087	0.344	0.089	0.533	0.15	0.289	0.236	1.044	0.018	1.222	0.357	1	0.228	0.478	0.235	1.011	0.395	1.744	0.301	1.733	0.191	1.578	0.406	2.256	0.209	2.456	0.157	2.344	0.181	2.267	0.206	2.267	0.206	2.6	0.094	2.544	0.161
Rmx-A02	0	0	0	0	0.121	0.073	0.414	0.272	0	0	0.068	0.041	0.948	0.231	0.442	0.133	0.011	0.009	0.23	0.047	0.651	0.067	0.677	0.019	0.047	0.019	1.356	0.264	2.149	0.071	2.27	0.1	0.701	0.165	0.701	0.165	0.954	0.237	0.643	0.217
Rmx-A180	0	0	0.1	0.042	0.444	0.12	1.078	0.091	0	0	0.722	0.205	0.767	0.279	1.189	0.716	0.222	0.018	0.711	0.249	0.989	0.134	0.967	0.079	0.656	0.194	1.756	0.389	1.622	0.244	1.856	0.187	0.4	0.137	0.4	0.137	0.422	0.169	0.378	0.105
RRS-10	0	0	0.056	0.033	1.084	0.288	1.508	0.372	0.011	0.009	1.644	0.595	4.594	1.859	4.592	0.674	0.022	0.018	0.511	0.209	0.549	0.265	0.752	0.198	0.236	0.072	1.185	0.341	1.572	0.206	2.367	0.205	0.791	0.239	0.791	0.239	0.468	0.299	0.289	0.195
RRS-7	0	0	0	0	0	0	0.022	0.018	0	0	0.011	0.009	0.167	0.123	0.033	0.016	0.267	0.218	0.511	0.209	0.778	0.222	1.133	0.096	0.567	0.119	1.278	0.225	1.378	0.235	1.144	0.415	1.478	0.458	1.478	0.458	1.967	0.372	1.822	0.354
Se-0	0	0	0	0	0	0	0.033	0.016	0	0	0	0	0.1	0.082	0.2	0.072	0.011	0.009	0.444	0.225	0.489	0.203	0.3	0.141	0.456	0.214	1.033	0.031	1.067	0.027	1.211	0.323	0.511	0.262	0.511	0.262	0.956	0.227	0.633	0.216
Shah	0	0	0	0	0.011	0.009	0.022	0.009	0	0	0	0	0.044	0.024	0.044	0.036	0.389	0.181	0.944	0.033	0.989	0.065	0.967	0.201	0.967	0.164	1.889	0.048	1.578	0.081	1.978	0.078	2.9	0.123	2.9	0.123	4.733	0.542	5.189	0.232
Sorbo	0	0	0	0	0.033	0.024	0.383	0.106	0	0	0.033	0.027	0.133	0.047	0.011	0.009	0	0	0.089	0.073	0.1	0.082	0.289	0.119	0.011	0.009	0.256	0.105	0.6	0.257	0.811	0.357	0.178	0.132	0.178	0.132	0.189	0.087	0.167	0.068
Spr1-6	0	0	2	1.414	5.75	3.712	7.25	2.652	0	0	19.5	14.91	22.75	11.84	19.17	9.322	0	0	0.667	0.544	1.167	0.593	1.333	0.593	0.5	0.408	0.833	0.491	1.5	0.707	2	0.816	2	0.85	2	0.85	1.5	0.624	1.667	0.68
Sq-1	0	0	0.056	0.045	0.656	0.202	0.833	0.247	0	0	1.922	0.528	1.922	0.672	1.6	0.65	0.756	0.251	1.511	0.333	2.389	0.285	2.522	0.169	1.389	0.202	2.589	0.273	2.856	0.255	3.311	0.194	0.411	0.173	0.411	0.173	0.589	0.26	0.456	0.181
Sq-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.089	0.024	0.633	0.15	0.922	0.373	0.578	0.2	0.156	0.055	0.844	0.159	1.4	0.201	0.889	0.346	1.522	0.342	1.522	0.342	2.289	0.49	2.156	0.523
Tamm-2	0	0	0	0	0	0	0.044	0.036	0	0	0	0	0.193	0.089	0.078	0.051	0.239	0.118	1.073	0.248	1.058	0.093	1.676	0.259	0.674	0.112	1.498	0.15	1.509	0.186	1.998	0.265	2.148	0.332	2.148	0.332	3.079	0.064	3.69	0.185
Tamm-27	0	0	0	0	0	0	0	0	0	0	0	0	0.067	0.054	0	0	0.122	0.055	0.589	0.211	1.056	0.369	1.2	0.109	0.356	0.127	1.556	0.229	1.7	0.287	1.389	0.251	2.1	0.587	2.1	0.587	2.778	0.413	3.022	0.255
Ts-1	0	0	0.033	0.027	0.189	0.04	0.556	0.209	0	0	0.978	0.581	0.989	0.527	0.611	0.39	0.222	0.091	0.922	0.426	1.089	0.04	0.844	0.181	0.367	0.218	1.778	0.221	1.789	0.593	1.167	0.178	0.467	0.103	0.467	0.103	0.533	0.098	0.467	0.103
Ts-5	0	0	0	0	0.053	0.007	0.223	0.08	0	0	0.189	0.054	0.407	0.212	0.533	0.103	0.539	0.107	0.852	0.279	1.325	0.189	1.533	0.196	0.896	0.031	1.763	0.243	1.812	0.088	1.568	0.273	1.542	0.167	1.542	0.167	1.707	0.106	1.478	0.176
Tsu-1	0	0	0.011	0.009	0.244	0.2	0.878	0.581	0.033	0.016	0.456	0.182	1.589	0.76	1.244	0.535	0.4	0.15	1.189	0.127	1.156	0.059	1.156	0.2	1.267	0.235	2.356	0.211	2.044	0.221	1.789	0.217	1.944	0.451	1.944	0.451	2.722	0.358	3.056	0.454
Ull2-3	0	0	0	0	0.056	0.033	0.833	0.478	0	0	0.333	0.259	2.956	2.332	3.078	1.647	0.333	0.144	0.367	0.211	1.033	0.016	1.111	0.064	0.4	0.247	0.978	0.449	1.411	0.247	1.411	0.209	1.422	0.55	1.422	0.55	2.178	0.566	2.378	0.322
Ull2-5	0	0	0	0	0.583	0.295	1.283	0.059	0	0	0.778	0.481	0.583	0.412	1.233	1.007	0.078	0.051	0.689	0.292	0.7	0.294	0.778	0.318	0.089	0.073	0.9	0.368	1.3	0.531	1.122	0.461	0.278	0.143	0.278	0.143	0.367	0.191	0.233	0.098
Uod-1	0	0	0.111	0.04	0.4	0.119	2.111	0.76	0	0	3.344	1.241	6.511	3.199	8.267	4.334	0.367	0.245	0.589	0.244	0.944	0.189	1.144	0.073	0.967	0.22	2	0.063	2.378	0.513	2.333	0.113	1.756	0.485	1.756	0.485	1.933	0.397	2	0.354
Uod-7	0	0	0	0	0	0	0	0	0	0	0.067	0.031	0.056	0.045	0.011	0.009	0.1	0.047	0.556	0.184	0.911	0.149	0.789	0.114	0.2	0.082	1.9	0.087	2.444	0.288	2.033	0.441	1.689	0.323	1.689	0.323	1.556	0.357	1.456	0.495
Van-0	0	0	0	0	0	0	1.578	0.213	0	0	0.1	0.082	0.379	0.088	2.486	0.949	0.189	0.141	0.586	0.182	0.967	0.377	1.789	0.218	0.624	0.167	1.56	0.226	2.273	0.327	2.446	0.1	0.773	0.291	0.773	0.291	1.289	0.205	1.219	0.126
Wa-1	0	0	0.011	0.009	0.011	0.009	0.1	0.042	0	0	0.044	0.024	0.1	0.047	0.2	0.103	0.311	0.132	0.8	0.354	0.589	0.205	1.411	0.433	0.233	0.068	1.378	0.107	1.422	0.105	2.4	0.423	0.611	0.252	0.611	0.252	0.956	0.102	1.011	0.149
Wei-0	0	0	0.258	0.106	1.383	0.431	1.847	0.336	0.067	0.054	2.392	0.189	3.525	0.962	3.2	0.638	0.5	0.236	1.022	0.119	1.328	0.176	1.347	0.158	0.85	0.178	2.064	0.265	2.047	0.094	2.458	0.223	1.717	0.175	1.717	0.175	2.011	0.195	2.036	0.127
Ws-0	0	0	0.677	0.236	2.68	1.06	2.925	0.934	0.137	0.086	10.22	3.513	19.85	8.626	22.9	6.755	0.183	0.122	0.772	0.335	1.938	0.356	1.993	0.31	0.817	0.312	2.191	0.197	2.879	0.128	2.723	0.255	0.559	0.307	0.559	0.307	0.757	0.198	0.613	0.228
Ws-2	0	0	0.203	0.103	0.889	0.176	2.068	0.745	0	0	1.796	0.595	8.079	1.958	10.75	1.356	1.067	0.038	1.667	0.177	2.074	0.192	1.853	0.198	1.675	0.136	3.061	0.113	2.944	0.239	3.355	0.234	2.315	0.156	2.315	0.156	2.647	0.224	2.392	0.106
Wt-5	0	0	0.922	0.264	1.878	0.134	2.1	0.283	0.333	0.259	3.244	0.292	2.344	1.266	2.444	1.324	0.356	0.29	1.167	0.345	1.189	0.423	1.267	0.425	1.067	0.273	2.356	0.275	3.067	0.206	2.811	0.35	2.244	0.564	2.244	0.564	2.8	0.558	2.633	0.558
Yo-0	0	0	7.107	2.265	30.42	3.622	27.99	4.542	1.538	0.774	28.2	4.711	28.41	9.482	26.4	11.07	0.688	0.214	2.423	0.28	2.62	0.145	1.698	0.706	1.444	0.227	3.017	0.248	3.4	0.249	2.333	0.981	0.341	0.146	0.341	0.146	0.022	0.018	0	0
Zdr-1	0	0	2.267	0.66	5.3	0.471	5.45	0.389	2.317	1.615	6.367	1.768	6.267	2.192	7.083	1.615	0.383	0.271	0.65	0.247	0.683	0.106	0.65	0.13	0.767	0.424	1.517	0.153	1.35	0.295	1.467	0.354	0.6	0.283	0.6	0.283	0.583	0.13	0.533	0.094
Zdr-6	0	0	0.278	0.153	3.556	1.428	4.344	1.173	0.233	0.191	11.67	4.522	16.99	5.075	14.58	4.102	0.089	0.059	0.656	0.268	0.633	0.247	0.744	0.209	0.478	0.153	1.333	0.272	1.611	0.25	1.667	0.144	2.211	0.192	2.211	0.192	2.667	0.253	2.678	0.254

All data are averages of three repeats, with 30 explants per repeat. The classes of callus and greenness of the explants are defined in Fig. 2 *A* and *B*. Classification of callus formation: class 0, no callus; class 1, callus is present at the ends of the explant; class 2, callus is present and covers a maximum of one-third of the explant; class 3, callus is abundant but does not cover the whole explant; class 4, thick callus covers the whole explant. Classification of greenness of the explants, excluding shoots: class 0, explant is white; class 1, explant is yellow; class 2, explant is (partially) pale green; class 3, complete explant is green; class 4, complete explant is dark green.

Table S2. Spearman's rank correlation coefficients (*r*) between different phenotypical responses accompanying shoot regeneration at different time points of SIM incubation

	7 d				11 d					14 d					21 d				
	Roots	Callus	Greenness	Primordia	Roots	Callus	Greenness	Primordia	Shoots	Roots	Callus	Greenness	Primordia	Shoots	Roots	Callus	Greenness	Primordia	Shoots
7 d																			
Roots	1.000	0.049	0.150	0.007*	0.769	0.122	0.163	−0.070	−0.070	0.719	0.049	0.048	−0.088	−0.116	0.679	0.175	0.123	−0.068	−0.073
Callus	0.049	1.000	0.493	0.225	0.032	0.401	0.331	0.143	0.174	0.006*	0.384	0.305	0.104	0.148	0.051	0.340	0.192	0.081	0.036
Greenness	0.150	0.493	1.000	0.289	0.118	0.503	0.539	0.276	0.236	0.082	0.453	0.446	0.163	0.220	0.142	0.392	0.307	0.071	0.050
Primordia	0.007*	0.225	0.289	1.000	−0.036	0.245	0.222	0.316	0.431	−0.088	0.209	0.189	0.176	0.296	−0.010*	0.102	0.086	0.075	0.089
11 d																			
Roots	0.769	0.032	0.118	−0.036	1.000	0.070	0.144	−0.090	−0.102	0.847	0.042	0.068	−0.099	−0.129	0.806	0.147	0.091	−0.063	−0.087
Callus	0.122	0.401	0.503	0.245	0.070	1.000	0.596	0.388	0.325	0.032	0.532	0.454	0.255	0.318	0.099	0.436	0.326	0.076	0.083
Greenness	0.163	0.331	0.539	0.222	0.144	0.596	1.000	0.429	0.297	0.075	0.517	0.608	0.293	0.323	0.157	0.469	0.430	0.113	0.102
Primordia	−0.070	0.143	0.276	0.316	−0.090	0.388	0.429	1.000	0.519	−0.145	0.364	0.406	0.670	0.737	−0.056	0.176	0.266	0.436	0.459
Shoots	−0.070	0.174	0.236	0.431	−0.102	0.325	0.297	0.519	1.000	−0.167	0.252	0.262	0.312	0.583	−0.048	0.049	0.119	0.168	0.280
14 d																			
Roots	0.719	0.006*	0.082	−0.088	0.847	0.032	0.075	−0.145	−0.167	1.000	0.127	0.147	0.020	−0.006*	0.863	0.111	0.068	−0.068	−0.077
Callus	0.049	0.384	0.453	0.209	0.042	0.532	0.517	0.364	0.252	0.127	1.000	0.633	0.374	0.422	0.227	0.529	0.377	0.128	0.137
Greenness	0.048	0.305	0.446	0.189	0.068	0.454	0.608	0.406	0.262	0.147	0.633	1.000	0.434	0.432	0.213	0.426	0.522	0.221	0.197
Primordia	−0.088	0.104	0.163	0.176	−0.099	0.255	0.293	0.670	0.312	0.020	0.374	0.434	1.000	0.618	0.126	0.182	0.296	0.475	0.541
Shoots	−0.116	0.148	0.220	0.296	−0.129	0.318	0.323	0.737	0.583	−0.006*	0.422	0.432	0.618	1.000	0.163	0.127	0.224	0.319	0.586
21 d																			
Roots	0.679	0.051	0.142	−0.010*	0.806	0.099	0.157	−0.056	−0.048	0.863	0.227	0.213	0.126	0.163	1.000	0.084	0.042	−0.106	−0.131
Callus	0.175	0.340	0.392	0.102	0.147	0.436	0.469	0.176	0.049	0.111	0.529	0.426	0.182	0.127	0.084	1.000	0.516	0.105	0.150
Greenness	0.123	0.192	0.307	0.086	0.091	0.326	0.430	0.266	0.119	0.068	0.377	0.522	0.296	0.224	0.042	0.516	1.000	0.228	0.301
Primordia	−0.068	0.081	0.071	0.075	−0.063	0.076	0.113	0.436	0.168	−0.068	0.128	0.221	0.475	0.319	−0.106	0.105	0.228	1.000	0.428
Shoots	−0.073	0.036	0.050	0.089	−0.087	0.083	0.102	0.459	0.280	−0.077	0.137	0.197	0.541	0.586	−0.131	0.150	0.301	0.428	1.000

Numbers of shoots, primordia, and lateral roots and classes for callus and greenness are presented. Data were collected for 88 different *Arabidopsis* accessions using three repeats with each time, 30 explants per accession. Because almost no shoots were observed after 7 d of SIM incubation, this parameter was not included. All correlations were significant at $P < 0.05$, except for the indicated correlations.
*Not significant.

Table S3. Regeneration QTLs identified by using an Nok-3 × Ga-0 inbred population

					Percent explained variation			
					Single trait		Multitrait	
QTL	Trait*	Origin positive allele	Chromosome	Position (cM/Mb)	14 d	21 d	14 d	21 d
REG-1	14, 21, multi	Nok-3	1	91/25.9	31.8	23.8	30.6	27.8
REG-2	21, multi	Ga-0	2	23/7	—	12.4	4.9	22.2
REG-3	14	Ga-0	2	70/18	14.3	—	—	—
REG-4	21	Nok-3	3	25/7.7	—	7.4	—	—
REG-5	14, multi	Nok-3	3	84/23	12.1	—	11.7	9.6

*Single trait analysis for regeneration-responsive explants after 14 or 21 d of SIM incubation is indicated by 14 or 21, respectively; multi indicates multitrait analysis for responsive explants after 14 and 21 d of SIM incubation.