

A simple and efficient in planta transformation method based on the active regeneration capacity of plants

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1 **A simple and efficient *in planta* transformation method based on the**
2 **active regeneration capacity of plants**

3
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12

13

14 **Abstract**

15 Plant genetic transformation strategies serve as essential tools for the genetic
16 engineering and advanced molecular breeding of plants. However, the complicated
17 operational protocol and low efficiency of the current transformation strategies restrict
18 the genetic modification of most plant species. This paper describes the development
19 of a Regenerative Activity-dependent *in* Planta Injection Delivery (RAPID) method
20 based on the active regeneration capacity of plants. In this method, *Agrobacterium*
21 *tumefaciens* was delivered to plant meristems via injection for inducing transfected
22 reascent tissues. Stable transgenic plants were obtained by subsequent vegetative
23 propagation of the positive reascent tissues. The method was successfully applied for
24 the transformation of plants with strong regeneration capacity, including different
25 genotypes of sweet potato (*Ipomoea batatas*), potato (*Solanum tuberosum*), and
26 bayhops (*I. pes-caprae*). Compared to the traditional transformation methods, RAPID
27 has a markedly high transformation efficiency (up to 40%), shorter duration (less than
28 4 weeks), and does not require tissue culture procedures. The RAPID method therefore
29 overcomes the limitations of traditional methods for achieving rapid *in planta*
30 transformation, and can be potentially applied to a wide range of plant species that are
31 capable of active regeneration.

32

33 **Main**

34 The emerging strategies in biotechnology, including genome editing and high-
35 throughput sequencing, immensely promote the progress of modern agriculture, and are
36 widely employed for improving the agronomic traits of crop plants^{1,2}. The accuracy of
37 genetic modification primarily relies on plant transformation, which is difficult to
38 achieve in most plant species³. To date, gene editing based on traditional transformation
39 strategies has been successfully realized in only a limited number of representative
40 crops⁴. The functional analysis of genes, exploration of the mechanism underlying
41 important traits, and the genetic improvement of potentially valuable plant species face
42 several challenges owing to the lack of a universal transformation technology.

43 The existing methods for the genetic transformation of plants primarily include
44 particle bombardment, viral vector delivery, and delivery of *Agrobacterium* sp (*A. sp.*)
45 for transferring synthetic exogenous information into genomes. Of these, the *A. sp.*-
46 mediated transformation of plants is mostly employed owing to its high efficiency and
47 reliability⁵⁻⁷. Following inflorescence infection, *A. tumefaciens* directly contacts germ
48 cells of the model plant, *Arabidopsis thaliana*, to induce the formation of the
49 transformed progeny^{8,9}. Although the floral dip strategy is ideal for plant transformation,
50 the method is unsuitable for other flowering plants. Most plant transformation methods
51 involve the conversion of *A. sp.*-infected dedifferentiated calli into regenerated plantlets
52 through tissue culture⁵. However, this strategy is primarily limited by numerous factors,
53 including the plant species, culture conditions, several genetic and technical
54 instabilities¹⁰, expensive and complicated processes for culturing transformed cells,
55 high time consumption¹¹, and low transformation efficiency.

56 Several advances have been made in plant genetic transformation technologies in
57 recent years, based on tissue culture method or nonsterile conditions. In one strategy,
58 RNA viruses and mobile elements were used to guide dsRNA components into plant
59 meristems. This method elevates the efficiency of heritable gene editing but possibly
60 requires a tissue culture procedure for generating the primary Cas9 transgenic plant¹².
61 In another strategy, meristem identity regulators were used to promote the regeneration

62 of transformed tissues without sterile operation procedures¹³. In a recent study, *A.*
63 *rhizogenes* was used for directly inducing the regeneration of transgenic organs¹⁴.
64 Additionally, numerous studies have employed various delivery intermediaries,
65 including viruses, nanomaterials, or grafting for plant transformation^{6,15,16}. These
66 transformation strategies offer different solutions for improving the transformation
67 efficiency of plants. However, it is necessary to develop novel transformation strategies
68 that can be easily and universally applied in various plant species for overcoming the
69 technological limitations and challenges arising from plant diversity.

70 This paper describes an efficient, easy-to-use *A. tumefaciens*-mediated
71 transformation system, denoted as Regenerative Activity-dependent in Planta Injection
72 Delivery (RAPID), which has the advantages of a high transformation rate, short
73 duration, user-friendly operational protocol, and no requirement for tissue culture. The
74 study confirmed that the RAPID method significantly promoted the genetic
75 transformation of plants with strong regeneration capacities, including sweet potatoes,
76 potatoes, and bayhops. The RAPID strategy can therefore serve as a potentially
77 powerful tool for the genetic modification of plants that propagate vegetatively.

78

79 **Results**

80 **Implementation of a simple and effective *in planta* transformation delivery system** 81 **in sweet potato**

82 Owing to the natural regeneration capacity, plants can be propagated from excised
83 organs, including leaves, stems, and roots¹⁷⁻¹⁹. It is therefore possible to obtain
84 independent transformants by *in planta* regeneration instead of tissue culture. Sweet
85 potato (*Ipomoea batatas* L.), a well-known tuberous crop with strong vegetative
86 propagation capacity in the stems and roots²⁰, was selected in this study for developing
87 the tissue culture-free transformation approach. Various methods, including soaking,
88 vacuum infiltration, injecting, and other strategies, were tested for delivering *A.*
89 *tumefaciens* into various plant tissues, including the leaves, stems, flowers, and roots.
90 The transformation efficacy of various combinations of post-transfection culture

91 substrates, including water, nutrient solution, sand, and solid media, was also evaluated.
92 The findings revealed that the direct injection of stem segments with a subsequent
93 culture in the soil substrate achieved an effective and stable transformation (**Fig. 1**).

94 The protocol of the stem-injection delivery strategy is depicted in **Fig. 1a**. Healthy
95 sweet potato stems bearing several nodes were excised, and each node was injected
96 upward until the injection liquid oozed from the other pinholes and excised ends. The
97 injected stems were subsequently planted into the soil substrate (**Fig. 1a**), and
98 adventitious roots spontaneously sprouted within 1 week after soil cutting (**Fig. 1b**).
99 The positive transformants were rapidly detected from the adventitious roots. *GUS* (β -
100 *glucuronidase*) was selected as the reporter gene for evaluating the transformation of
101 the reascent roots (**Fig. 1b**). Continuous cultivation of the stem cuttings generated
102 transgenic reascent leaves, lateral buds, and tubers from the adventitious roots, and the
103 positive signal was detected in these tissues (**Supplementary Fig. 1**). The independent
104 transgenic plants were obtained by subsequent vegetative propagation of the positive
105 lateral shoots within a short term, or from the buds that sprouted from the positive tubers
106 (**Fig. 1c**). The study therefore preliminarily established an effective *in planta*
107 transformation method by taking advantage of the active regeneration capacity of sweet
108 potato plants.

109

110 **Optimization of the *in planta* transformation system**

111 The offspring that were vegetatively propagated from the positive reascent shoots and
112 tubers were genotyped, and the results demonstrated that the examined plant tissues
113 were also positive (**Fig. 1c**). The finding suggested that the transgenic events produced
114 by the *in planta* method are stable and have a low chimeric rate. We subsequently aimed
115 to improve the transformation efficiency of the stem injection method. To this end, we
116 first screened different strains of *A. sp.* commonly used for plant transformation,
117 including the AGL1, GV3101, EHA105, and LBA4404 strains of *A. tumefaciens*, and
118 the K599 strain of *A. rhizogenes*^{9,21,22}. Following transfection, the reascent
119 adventitious roots were selected for GUS staining, and the positive rate (ratio of positive

120 roots per positive plant \times ratio of positive plants in all the injected plants) was
121 determined for evaluating the transformation efficiency (**Supplementary Table 1**). The
122 results demonstrated that the AGL1 strain of *A. tumefaciens* had the highest
123 transformation efficiency (28%), followed by the GV3101 and EHA105 strains (19%),
124 while transformation with the LBA4404 strain did not generate any positive roots. The
125 K599 strain of *A. rhizogenes* had a weak transformation efficiency of $< 2\%$ (**Fig. 2a**).
126 Therefore, the AGL1 strain of *A. tumefaciens* was found to be most suitable for the
127 transformation of sweet potato using this system.

128 The optimal optical density (OD), which is another important variable for *A.sp.-*
129 mediated transformation, was subsequently determined. The AGL1 strain was cultured
130 and diluted to generate a series of concentrations with OD values ranging from 0.01 to
131 0.80, and the cultures were subsequently injected into sweet potato stems for
132 investigating the GUS-positive roots. The findings revealed that 0.5 was the optimal
133 OD for transformation (**Fig. 2b, Supplementary Table 1**). Previous studies reported
134 that chemical additives, including Silwet-L77 and acetosyringone, can significantly
135 promote the transformation rates of the floral dip method for the transformation of
136 *Arabidopsis* and the tissue culture-based transformation methods in some plants^{8,23}. The
137 initial infecting solution for injection, containing 0.01% Silwet-L77 and 100 μM
138 acetosyringone, was prepared as previously described (**Fig. 2c**)⁸. Different
139 combinations of these two additives were compared, and the results demonstrated that
140 the transformation failed in the absence of Silwet-L77, which indicated that the
141 surfactant component, Silwet-L77 (S), is critical for successful transformation.
142 Acetosyringone (A) also had a prominent effect in promoting the transformation
143 efficiency. Notably, the findings revealed that the transformation efficiency was
144 significantly improved to 37% when 0.02% Silwet-L77 and 100 μM acetosyringone
145 (2S+A) were added to the solution (**Fig. 2c**).

146 To improve the screening throughput, we attempted to select multiple explants
147 using herbicides and antibiotics (**Fig. 2d, Supplementary Fig. 2**). The successful
148 transformants carrying resistance genes can resist the damages caused by externally

149 applied compounds, and these positive plants were further confirmed by genotyping
150 **(Fig. 2e, Supplementary Fig. 2).**

151 The present study describes the development of a novel method for plant
152 transformation that does not require a sterile operation strategy. The transformation rate
153 of the method was subsequently elevated to nearly 40% and the period was shortened
154 to only 1 month via multiple optimization steps. The method described herein exhibited
155 remarkable superiority over the traditional tissue culture method used for sweet potato
156 **(Table 1)**²⁴⁻²⁶. The transformation method developed in this study was denoted as the
157 Regenerative Activity-dependent *in Planta* Injection Delivery (RAPID) method.

158

159 **The RAPID method can deliver multiple reporter vectors and is a reliable gene** 160 **editing tool**

161 In order to verify the applicability of the RAPID system, diverse reporter genes were
162 selected for verifying the transformation. The application of fluorescent reporters can
163 aid in examining the transformation of plants in a living state; however, the interference
164 of spontaneous biological fluorescence needs to be considered as well²⁷. We determined
165 the spontaneous fluorescence spectra of sweet potato tissues using a confocal
166 microscope **(Supplementary Fig. 3)**. In order to evade the interference due to
167 spontaneous biological fluorescence, the mScarlet red fluorescent protein (the
168 excitation and emission wavelengths were at 569 nm and 593 nm, respectively) was
169 selected as the transformation reporter. As expected, most of the positive nascent
170 tissues identified by polymerase chain reaction (PCR) exhibited an obvious red
171 fluorescence. Furthermore, the strong fluorescence signals were maintained in the
172 leaves of the individual transgenic plants regenerated from the transformants **(Fig. 3a)**,
173 suggesting that mScarlet is a suitable fluorescence reporter for studying the
174 transformation of sweet potato. The RUBY reporter system was subsequently tested in
175 this study. RUBY can produce visible red accumulation in living plants, and is also used
176 for monitoring transformation events under non-invasive conditions²⁸. The RUBY
177 transformants in our delivery system were similar to those reported in other species^{28,29},

178 and exhibited an obvious red phenotype in the positive sweet potato plants (**Fig. 3b**).

179 Gene editing systems serve as important tools for plant genetic research. To verify
180 whether the RAPID system can be compatible with gene editing tools, the *phytoene*
181 *desaturase* (*PDS*) homolog gene (g31261) of sweet potato was knocked out by
182 CRISPR-Cas9. The loss of *PDS* function produces distinct albino phenotypes in
183 different plants³⁰, and the transgenic reascent shoots gradually developed an obvious
184 albino phenotype in this study (**Fig. 3c**). Taken together, the results suggested that the
185 RAPID method is reliable for the delivery of diverse report vectors and application in
186 studies on gene editing.

187

188 **RAPID produces positive reascent tissues by inducing the successful transfection** 189 **of meristematic cells**

190 RAPID is an efficient method for plant transformation, and has a high transformation
191 efficiency; however, certain transient transfection methods, including virus-induced
192 gene silencing (VIGS) and leaf-agroinfiltration, can also produce a high transformation
193 rate³¹. The key difference between these methods and RAPID is that the latter can
194 generate stable regenerative transgenic plants. Lateral buds and adventitious roots are
195 known to develop from the meristematic cells of phloem tissues^{18,19,32}; we therefore
196 speculated that the RAPID method might induce the transfection of tissues with
197 regeneration capacity. In order to test this hypothesis, mScarlet was selected as the
198 reporter gene for analyzing the stem biopsies following transfection. The untreated
199 plants in the control group exhibited a spontaneous fluorescence in the epidermal layer
200 of the stems. Interestingly, the transformants exhibited obvious fluorescence signals in
201 the interior cross-section of the stem (**Fig 4a**). Further observations revealed that these
202 signals were primarily localized in the meristematic regions of the phloem, including
203 the cambium and endodermis, which are involved in the differentiation of lateral buds
204 and adventitious roots in sweet potato (**Fig 4b**)^{20,33}. Consistently, the lateral buds and
205 adventitious roots exhibited strong positive signals (**Supplementary Fig. 4**), and
206 regenerated transgenic offspring. These observations suggested that the RAPID method

207 can induce the transfection of the meristematic zone via the phloem *in planta*, and
208 generate stable regenerated plants from the lateral and tuber buds (**Fig. 4c**). The period
209 between injection and the generation of individual transgenic plants from the lateral
210 buds and tuber buds was 3–4 weeks and 6–8 weeks, respectively. All the positive lines
211 obtained from the tuber buds were non-chimeric and supported the notion that the
212 transgene originated from one or a few meristematic cells.

213

214 **RAPID is applicable to different plant species**

215 In order to evaluate the applicability of the RAPID method to different genetic
216 backgrounds, we first tested its efficacy in different varieties of sweet potato, including
217 the major cultivars (Guangshu87, Pushu32, Longshu9, and Jishu26), a cultivar with
218 high anthocyanin content (Guangzishu8), and a genome-sequenced cultivar
219 (Taizhong6)³⁴ (**Fig. 5a**). To detect the transgenic materials on a large scale, the artificial
220 light source method was employed for detecting the GFP signals³⁵. The stems were
221 peeled to nullify the interference due to the spontaneous biological fluorescence of the
222 epidermis. Strong green fluorescence was observed in the peeled stems of the GFP
223 transformants, suggesting that the RAPID method can be applied for the transformation
224 of sweet potato plants with different genetic backgrounds. Additionally, the
225 transformation rate of the RAPID method was high in sweet potato (12.5–37.5%; **Fig.**
226 **5a**).

227 The present study also determined whether the RAPID method can be applied to
228 other plant species. Bayhops (*I. pes-caprae* L.) is a coastal plant with strong adaptation
229 to barren and saline conditions, and has a high potential for application in
230 vegetation repair. In this study, bayhops was selected for analyzing whether the RAPID
231 method can be applied for the transformation of this plant species. Bayhops and sweet
232 potato belong to the Convolvulaceae family; however, unlike sweet potato, the
233 vegetative propagation of bayhops occurs via stolons rather than via storage roots.
234 There are no established transformation systems for bayhops to date. In this study, the
235 stems of bayhops plants were excised and transformed using the RAPID system by

236 transferring the *Bar* gene. PCR detection revealed that out of the 30 plants transfected
237 in this study, the nascent shoots of 8 plants were positive, and most of the regenerated
238 transgenic plants that developed from these shoots exhibited herbicide resistance (**Fig.**
239 **5b**). Taken together, the findings suggested that bayhops can be efficiently transformed
240 using the RAPID method.

241 Potato (*Solanum tuberosum*. L) is the fourth largest food crop in the world and it
242 exhibits a strong ability of vegetative propagation via tubers³⁶. This feature enables the
243 application of the RAPID method for the transformation of potato plants. In order to
244 determine the transformation efficacy of the RAPID method in potato, the detached
245 stems of potato plants were initially infected by injections and cultured in the soil.
246 However, the efficacy could not be precisely determined owing to the unstable survival
247 rate of the stem cuttings of potato. The tubers were subsequently selected as the
248 transformation receptor owing to their stronger natural regeneration capacity compared
249 to stems. We injected *A. sp.* mixed with exogenous growth regulators of 6-BA (6-
250 benzyladenine) and NAA (naphthylacetic acid) into the skin of the tuber around the
251 buds. The growth regulators induced sprouting without causing any undesirable genetic
252 alterations (**Supplementary Fig. 5**). Nascent shoots emerged from the tubers after
253 1–2 weeks, and the transformants exhibited strong phenotypes of mScarlet and RUBY
254 in the leaves and stems (**Fig. 5c**). The transformation rate was nearly 40%, which was
255 markedly higher than that of the traditional transformation method for potato (<1%)³⁷.

256 Taken together, the above findings revealed that by using selectively targeted
257 tissues and optimized conditions, the RAPID method can be widely applied for the
258 genetic transformation of various plant species to generate transformants with active
259 regeneration capacity.

260

261 **Discussion**

262 The existing methods for plant transformation commonly deliver exogenous genes into
263 plants by infecting with *A. sp.*, and the majority of these strategies rely on tissue culture
264 procedures³⁸. However, the methods for plant transformation often have low

265 transformation efficiency and are highly time-consuming owing to the limitations of
266 the culture conditions, challenges in different plant species, and issues during technical
267 operation, which poses as bottlenecks in plant genetic research and application efforts.
268 In this study, we developed a simple *in planta* transformation strategy, denoted as
269 RAPID, that delivers genes by directly injecting *A. tumefaciens* into plants. The RAPID
270 method overcomes some of the main limitations of the current transformation strategies
271 as described hereafter. First, the RAPID method does not require tissue culture, special
272 induction strategies, or treatments that are necessary in the existing plant transformation
273 methods^{12,13}. Successful transformation with the RAPID method only relies on the
274 active regeneration capacity of plants, which substantially increases the transformation
275 efficiency, shortens the duration, and reduces the possibility of genetic mutations
276 caused by cellular dedifferentiation and redifferentiation. Furthermore, RAPID is
277 compatible with different genetic modification strategies, including ectopic expression
278 or gene editing, and with different strains of *A. sp.*; therefore, transformation with
279 RAPID is relatively simple, flexible, and can be employed for diverse purposes. For
280 instance, *A. rhizogenes* has been used for achieving plant transformation under non-
281 sterile conditions. Several recent transformation strategies have also employed *A.*
282 *rhizogenes* for inducing the regeneration of plant organs^{14,39}. However, *A. rhizogenes*
283 potentially causes persistent abnormal plant growth owing to the presence of *rol* genes
284 that are randomly inserted into the genome⁴⁰⁻⁴². RAPID can use *A. tumefaciens* as the
285 mediator of infection, and the issues with *A. rhizogenes* can therefore be evaded.
286 Additionally, there is no limitation of specific explants, and the method has a
287 widespread regeneration capacity across different plant species. Theoretically, RAPID
288 can be successfully applied to other plants, besides those tested in this study.

289 The floral dip method is typically used for the transformation of plants such as
290 *Arabidopsis*, in which the transfected germ cells act as precursors that pass the
291 transgenic information to seeds to generate transgenic plants⁸. RAPID is similar to the
292 floral dip method in that the meristematic cells are transfected via direct contact with
293 *A. sp.*, which subsequently leads to the regeneration of positive reascent tissues and

294 transgenic offspring via vegetative propagation. It has been reported that bacteria and
295 viruses can spread through the phloem channels after entering the cortex⁴³, which
296 enables direct contact between meristematic cells and *A. sp.* (**Fig. 4**). The RAPID
297 system delivers *A. sp.* into the phloem to ensure that the core cells can be fully
298 transfected *in planta*, and may be one of the reasons underlying the high transformation
299 rate of this method. This hypothesis is also supported by the fact that the Silwet-L77
300 surfactant is critical for successful transformation using RAPID (**Fig. 2c**). However, the
301 chimeric rate of the regenerated tissues is very low owing to asexual succession (**Fig.**
302 **1c**). The germ cells of the secondary plants may carry the genetic information and
303 possibly allow the isolation of genetic information via sexual reproduction.

304 The strong vegetative propagation ability of plants is the key for obtaining
305 regenerated transgenic plants with the RAPID method. Vegetative propagation is
306 achieved via meristematic cells that actively divide by mitosis and allow the widespread
307 and rapid primary growth of plants, which results in the production of specialized,
308 permanent plant tissue systems for regeneration⁴⁴. These findings indicate that RAPID
309 can be theoretically applied to all plant species that develop into independent plants via
310 vegetative propagation. The chimeric rate is potentially reduced by the regeneration
311 from positive adventitious organs. Because the tubers of sweet potato develop from
312 adventitious roots originating from one or a few meristematic cells in the cortex, all the
313 transgenic plants that regenerated from the tubers were positive in this study. However,
314 further studies are necessary for confirming whether this also occurs in other plant
315 species.

316 In conclusion, a simple and efficient *A. sp.*-mediated transformation system was
317 developed, which overcomes the technical limitations of the existing transformation
318 strategies. The potential wide application of the method for the transformation of
319 different plant species can be achieved via the specific optimization of the strain of *A.*
320 *sp.* used, tissues infected, culture conditions, and other factors.

321
322

323 **Methods**

324 **Plant materials and growth conditions**

325 The materials of sweet potato (*I. batatas* L.), potato (*S. tuberosum* L.), and bayhops (*I.*
326 *pes-caprae* L.) used in this study were grown under normal conditions (28°C, 10-h/14-
327 h light/dark cycle, and light intensity of ~200 $\mu\text{mol m}^{-2} \text{s}^{-1}$).

328

329 **Vector construction**

330 The cloned DNA was amplified and assembled using the Phanta Max Super-Fidelity
331 DNA Polymerase (P505, Vazyme, China) and a ClonExpress II One Step Cloning Kit
332 (C112, Vazyme, China). pCambia1301 was used for the GUS reporter vector
333 (*35S:GUS*). The coding region of *GUS* contained a modified *Catalase* intron from
334 castor bean to ensure that the gene was only expressed under the *35S* promoter of the
335 transformed plant and not expressed in *A. sp.* The coding sequence (CDS) of *mScarlet*
336 was cloned into the pTF101 plasmid⁴⁵ for generating the *35S:mScarlet* reporter vector.
337 The GFP reporter was expressed under the *35S* promoter using the *35S:mGFP* plant
338 binary plasmid, as previously described⁴⁶. The RUBY reporter vector was supported by
339 the *DR5:RUBY* plant binary plasmid, as previously described²⁸. The *PDS*-CRISPR
340 construct was generated using the CRISPR-Cas9 system, as previously described⁴⁷. The
341 synthetic guide RNA (sgRNA) targeted the *Ipomoea batatas phytoene desaturase* gene
342 (*IbPDS*; g31261, <https://sweetpotao.com/gRNAdesigner>) was inserted into the
343 CRISPR-Cas9 binary vector, which was driven by the *AtU6* promoter, while *Cas9* was
344 driven by the *35S* promoter. The sequences of the corresponding vectors are available
345 at <https://www.addgene.org>, and the template and primers used for vector construction
346 are listed in **Supplementary Table 2**.

347

348 **RAPID system**

349 ***A. sp.* culture and activation**

350 The AGL1, GV3101, EHA105, and LBA4404 strains of *A. tumefaciens*, and the K599
351 strain of *A. rhizogenes*⁴⁸ carrying the target plasmids were plated on Luria-Bertani (LB)

352 solid medium supplemented with the corresponding antibiotics, and cultured from a
353 single bacterial colony at 28°C for 2–3 days. The freshly grown *A. sp.* was gently
354 washed off from the medium with a wash buffer (10 mM MgCl₂ and 100 μM
355 acetylsyringone; pH 5.6) and centrifuged at 3000 g for 5 min for collecting the bacteria.
356 The collected *A. sp.* was subsequently diluted to an OD₆₀₀ of 0.5 with an infiltration
357 buffer (1/4 Murashige & Skoog (MS), 0.1 % sucrose (w/v), 100 μM acetylsyringone,
358 and 0.02% Silwet L-77 (v/v); pH 5.6), and prepared for subsequent analyses.

359

360 **Transformation of sweet potato**

361 Stem segments, approximately 10 cm long, and bearing 3–4 nodes and 2–3 mature
362 leaves, were excised from healthy sweet potato plants. The infiltration buffer containing
363 the activated *A. sp.* was drawn into a 1-mL syringe and injected into the lower excised
364 end of the stem segment until the solution oozed from the upper end. The infiltration
365 buffer was subsequently injected upwards into each node with the syringe until the
366 solution oozed from the adjacent pinholes, to ensure that the infection solution was
367 completely distributed in the stem segments. The injected stem segments were
368 transplanted in sandy soil and cultured in a growth chamber for 1–2 days under dark
369 conditions, and subsequently returned to normal conditions under a light cycle (28°C,
370 10-h/14-h light/dark cycle, and light intensity of ~200 μmol m⁻² s⁻¹). The nascent shoots
371 and adventitious roots derived from the stem cuttings after 2–4 weeks were selected for
372 identifying the positive transformants by molecular detection studies and phenotypic
373 selection. The positive tubers were harvested after 8–10 weeks and sprouted for
374 obtaining the independent transgenic lines by vegetative propagation.

375

376 **Transformation of bayhops**

377 The process of transformation of bayhops was similar to that used for sweet potatoes.
378 Approximately 10 cm-long stem segments bearing several nodes and mature leaves
379 were excised and transplanted in sandy soil following injection with *A. sp.* using a 1-
380 mL syringe. The nascent shoots were obtained after 2–3 weeks and used for determining

381 the positive shoots and phenotypic selection. The independent transformants were
382 obtained by vegetative propagation.

383

384 **Transformation of potato**

385 The previously described method of pretreatment with *A. sp.* was used for the
386 transformation of potato plants; however, the growth regulators NAA (2.5 mg/L) and
387 6-BA (0.5 mg/L) were added to the infiltration buffer used for the transformation of
388 potato. The fresh tubers of potato were cut, and holes were pricked in the epidermis
389 with the needle of a 1-mL syringe. The infiltration buffer was aspirated with a
390 needleless syringe and the buffer was injected beneath the skin of the tubers, close to
391 the regions around the buds. The injected tuber segments were transplanted in sandy
392 soil. The new buds were unearthed after 1–2 weeks for the detection of positive tubers
393 and phenotypic analyses. The positive tubers were harvested after 6–8 weeks and
394 propagated for developing independent transgenic lines by vegetative propagation.

395

396 **Selection of transformants**

397 Phosphinothricin (Basta[®], 0.002%, v/v, CB2471, Coolaber, China) and hygromycin (50
398 µg/mL, H370, Phytotech, USA) were sprayed and applied to the aboveground parts for
399 resistance screening. The treated plants were selected after 72 h, and the leaves of the
400 non-transformed plants appeared wilted and yellow, while the positive plants were less
401 affected.

402

403 **GUS staining**

404 The GUS staining assay was performed as previously described⁴⁹. The adventitious
405 roots were immersed in the work solution (50 mM Na₂PO₄, 0.5 mM K₃Fe(CN)₆, 0.5
406 mM K₄Fe(CN)₆, and 2 mM X-Gluc; pH 7.0) under vacuum for 5 min and subsequently
407 allowed to react at 37°C for 4–6 h. The immersed tissues were placed in a decolorization
408 solution (70% ethanol and 30% acetic acid) for 2–3 times for decolorizing the tissues.
409 The decolorized samples were biopsied and observed under a stereoscope (M165C,

410 Leica, Germany).

411

412 **Fluorescence detection**

413 The fluorescence of the mScarlet reporter in the live transgenic tissues was observed
414 under a fluorescent stereoscope (M205 FA, Leica, Germany) with a red fluorescence
415 filter (Exc 540–580 nm, Em 593–667 nm). The spontaneous fluorescence spectra of
416 sweet potato were observed under a confocal microscope (SP8 STED 3X, Leica,
417 Germany). One-week-old adventitious roots were freshly selected for testing the root
418 samples, and the third mature leaf of the nascent shoots was selected for testing the leaf
419 samples. The materials of transgenic sweet potato containing the GFP reporter were
420 observed using the dual-wavelength fluorescent protein excitation light source (Exc 440
421 nm, Em 500 nm, 3415RG, LUYOR, China). The regions near the phloem at the base of
422 the stems were peeled for nullifying the spontaneous biological fluorescence of the
423 epidermis, and the whole plant was irradiated by a light source under dark conditions.
424 Green fluorescence was detected in the inner region of the stems of positively
425 transformed plants.

426

427 **Statistical analyses**

428 To evaluate the transformation efficacy, at least 10 biological replicates were performed,
429 and the numbers of replicates are depicted in the figures. For molecular biology analysis,
430 at least three individual samples were mixed with three biological replicates, and the
431 number of replicates is presented in the figures. The standard deviation (SD) and P
432 values were determined using Student's *t*-test.

433

434 **Reference**

- 435 1. Zhang, J., Zeng, P., Yu, H., Meng, X. & Li, J. *De novo* domestication of polyploid
436 rice: a novel breeding strategy and future prospects. *SCIENTIA SINICA Vitae* **51**,
437 1467-1476 (2021).
- 438 2. Gao, C. Genome engineering for crop improvement and future agriculture. *Cell* **184**,
439 1621-1635 (2021).

- 440 3. Mao, Y., Botella, J. R., Liu, Y. & Zhu, J. K. Gene editing in plants: progress and
441 challenges. *Natl. Sci. Rev.* **6**, 421-437 (2019).
- 442 4. Jing, H., Tian, Z., Chong, K. & Li, J. Progress and perspective of molecular design
443 breeding. *SCIENTIA SINICA Vitae* **51**, 1356-1365 (2021).
- 444 5. Krenek, P. et al. Transient plant transformation mediated by *Agrobacterium*
445 *tumefaciens*: principles, methods and applications. *Biotechnol. Adv.* **33**, 1024-1042
446 (2015).
- 447 6. Ma, X., Zhang, X., Liu, H. & Li, Z. Highly efficient DNA-free plant genome editing
448 using virally delivered CRISPR-Cas9. *Nat. Plants* **6**, 773-779 (2020).
- 449 7. Kjemtrup, S. et al. Gene silencing from plant DNA carried by a Geminivirus. *Plant*
450 *J.* **14**, 91-100 (1998).
- 451 8. Clough, S. J. & Bent, A. F. Floral dip: a simplified method for *Agrobacterium*-
452 mediated transformation of *Arabidopsis thaliana*. *Plant J.* **16**, 735-743 (1998).
- 453 9. Lazo, G. R., Stein, P. A. & Ludwig, R. A. A DNA Transformation-Competent
454 *Arabidopsis* Genomic Library in *Agrobacterium*. *Bio/Technology* **9**, 963-967 (1991).
- 455 10. Phillips, R. L., Kaeppler, S. M. & Olhofs, P. Genetic instability of plant tissue
456 cultures: breakdown of normal controls. *Proc. Natl. Acad. Sci. U. S. A.* **91**, 5222-
457 5226 (1994).
- 458 11. Filipecki, M. & Malepszy, S. Unintended consequences of plant transformation: A
459 molecular insight. *J. Appl. Genet.* **47**, 277-286 (2006).
- 460 12. Maher, M. F. et al. Plant gene editing through de novo induction of meristems. *Nat.*
461 *Biotechnol.* **38**, 84-89 (2020).
- 462 13. Lian, Z. et al. Application of developmental regulators to improve *in planta* or *in*
463 *vitro* transformation in plants. *Plant Biotechnol. J.* **20**, 1622-1635 (2022).
- 464 14. Cao, X. et al. Cut-dip-budding delivery system enables genetic modifications in
465 plants without tissue culture. *Innovation (Camb)* **4**, 100345 (2022).
- 466 15. Ellison, E. E. et al. Multiplexed heritable gene editing using RNA viruses and
467 mobile single guide RNAs. *Nat. Plants* **6**, 620-624 (2020).
- 468 16. Yang, L., Machin, F., Wang, S., Saploura, E. & Kragler, F. Heritable transgene-
469 free genome editing in plants by grafting of wild-type shoots to transgenic donor
470 rootstocks. *Nat. Biotechnol.* (2023) <https://doi.org/10.1038/s41587-022-01585-8>.
- 471 17. Bar, M. & Ori, N. Leaf development and morphogenesis. *Development* **141**, 4219-
472 4230 (2014).

- 473 18. Wang, B., Smith, S. M. & Li, J. Genetic regulation of shoot architecture. *Annu. Rev.*
474 *Plant Biol.* **69**, 437-468 (2018).
- 475 19. Omary, M. et al. A conserved superlocus regulates above and belowground root
476 initiation. *Science* **375**, eabf4368 (2022).
- 477 20. Ma, J. et al. Adventitious root primordia formation and development in stem nodes
478 of 'Georgia Jet' sweet potato, *Ipomoea batatas*. *Am. J. Bot.* **102**, 1040-1049 (2015).
- 479 21. RA, J., TA, K. & MW, B. GUS fusions: beta-glucuronidase as a sensitive and
480 versatile gene fusion marker. *EMBO J.* **6**, 3901-3907 (1987).
- 481 22. Hellens, R., Mullineaux, P. & Klee, H. Technical Focus: a guide to *Agrobacterium*
482 binary Ti vectors. *Trends Plant Sci.* **5**, 446-451 (2000).
- 483 23. Mayavan, S. et al. *Agrobacterium tumefaciens*-mediated *in planta* seed
484 transformation strategy in sugarcane. *Plant Cell Rep.* **32**, 1557-1574 (2013).
- 485 24. Choi, H. J., Chandrasekhar, T., Lee, H.-Y. & Kim, K.-M. Production of herbicide-
486 resistant transgenic sweet potato plants through *Agrobacterium tumefaciens* method.
487 *Plant Cell, Tissue Organ Cult.* **91**, 235-242 (2007).
- 488 25. Yu, B. et al. Efficient *Agrobacterium tumefaciens*-mediated transformation using
489 embryogenic suspension cultures in sweet potato, *Ipomoea batatas* (L.) Lam. *Plant*
490 *Cell, Tissue Organ Cult.* **90**, 265-273 (2007).
- 491 26. Yang, J. et al. Efficient embryogenic suspension culturing and rapid transformation
492 of a range of elite genotypes of sweet potato (*Ipomoea batatas* [L.] Lam.). *Plant Sci.*
493 **181**, 701-711 (2011).
- 494 27. Shaner, N. C., Steinbach, P. A. & Tsien, R. Y. A guide to choosing fluorescent
495 proteins. *Nat. Methods* **2**, 905-909 (2005).
- 496 28. He, Y., Zhang, T., Sun, H., Zhan, H. & Zhao, Y. A reporter for noninvasively
497 monitoring gene expression and plant transformation. *Hortic. Res.* **7**, 152 (2020).
- 498 29. Chen, K. et al. High-Efficient and Transient Transformation of Moso Bamboo
499 (*Phyllostachys edulis*) and Ma Bamboo (*Dendrocalamus latiflorus* Munro). *J. Plant*
500 *Biol.* **91**, 684-699 (2021).
- 501 30. Kumagai, M. H. et al. Cytoplasmic inhibition of carotenoid biosynthesis with virus-
502 derived RNA. *Proc. Natl. Acad. Sci. U. S. A.* **92**, 1679-1683 (1995).
- 503 31. Ruiz, M. T., Voinnet, O. & Baulcombe, D. C. Initiation and maintenance of virus-
504 induced gene silencing. *Plant Cell* **10**, 937-946 (1998).
- 505 32. Sugimoto, K., Jiao, Y. & Meyerowitz, E. M. *Arabidopsis* regeneration from

- 506 multiple tissues occurs via a root development pathway. *Dev. Cell* **18**, 463-471 (2010).
- 507 33. Belehu, T., Hammes, P. S. & Robbertse, P. J. The origin and structure of
508 adventitious roots in sweet potato (*Ipomoea batatas*). *Aust J Bot.* **52**, 551-558 (2004).
- 509 34. Liu, X. et al. Natural allelic variation confers high resistance to sweet potato
510 weevils in sweet potato. *Nat. Plants* **8**, 1233-1244 (2022).
- 511 35. Yuan, G. et al. Expanding the application of a UV-visible reporter for transient gene
512 expression and stable transformation in plants. *Hortic. Res.* **8**, 234 (2021).
- 513 36. Tang, D. et al. Genome evolution and diversity of wild and cultivated potatoes.
514 *Nature* **606**, 535-541 (2022).
- 515 37. Vinterhalter, D., Miti, N., Cingel, A., Raspor, M. & Ninkovi, S. Protocols for
516 *Agrobacterium*-mediated transformation of potato. *Fruit, Vegetable and Cereal*
517 *Science and Biotechnology* **2**, 1-15 (2008).
- 518 38. Ji, X., Yang, B. & Wang, D. Achieving plant genome editing while bypassing tissue
519 culture. *Trends Plant Sci.* **25**, 427-429 (2020).
- 520 39. Zhang, W. et al. Fast track to obtain heritable transgenic sweet potato inspired by
521 its evolutionary history as a naturally transgenic plant. *Plant Biotechnol. J.* (2022).
522 <https://doi.org/10.1111/pbi.13986>.
- 523 40. Tepfer, D. Transformation of several species of higher plants by *Agrobacterium*
524 *rhizogenes*: sexual transmission of the transformed genotype and phenotype. *Cell* **37**,
525 959-967 (1984).
- 526 41. Dehio, C., Grossmann, K., Schell, J. & Schmülling, T. Phenotype and hormonal
527 status of transgenic tobacco plants overexpressing the *rolA* gene of *Agrobacterium*
528 *rhizogenes* T-DNA. *Plant Mol. Biol.* **23**, 1199-1210 (1993).
- 529 42. Kumlehn, J., Serazetdinova, L., Hensel, G., Becker, D. & Loerz, H. Genetic
530 transformation of barley (*Hordeum vulgare* L.) via infection of androgenetic pollen
531 cultures with *Agrobacterium tumefaciens*. *Plant Biotechnol. J.* **4**, 251-261 (2006).
- 532 43. Lewis, J. D., Knoblauch, M. & Turgeon, R. The phloem as an arena for plant
533 pathogens. *Annu. Rev. Phytopathol.* **60**, 77-96 (2022).
- 534 44. Bailey, R. Types of vegetative propagation. ThoughtCo.
535 <https://www.thoughtco.com/vegetative-propagation-4138604> (2020).
- 536 45. Li, X. et al. Overcoming the genetic compensation response of soybean florigens
537 to improve adaptation and yield at low latitudes. *Curr. Biol.* **31**, 3755-3767 (2021).
- 538 46. Liu, X. et al. The NF-YC-RGL2 module integrates GA and ABA signalling to

- 539 regulate seed germination in *Arabidopsis*. *Nat. Commun.* **7**, 12768 (2016).
- 540 47. Wang, Z. et al. Optimized paired-sgRNA/Cas9 cloning and expression cassette
541 triggers high-efficiency multiplex genome editing in kiwifruit. *Plant Biotechnol. J.*
542 **16**, 1424-1433 (2018).
- 543 48. Bahramnejad, B., Naji, M., Bose, R. & Jha, S. A critical review on use of
544 *Agrobacterium rhizogenes* and their associated binary vectors for plant
545 transformation. *Biotechnol Adv.* **37**, 107405 (2019).
- 546 49. Ohta, S., Hattori, T., Morikami, A. & Nakamura, K. High-level expression of a
547 sweet potato sporamin gene promoter. *Mol. Gen. Genet.* **225**, 369-378 (1991).

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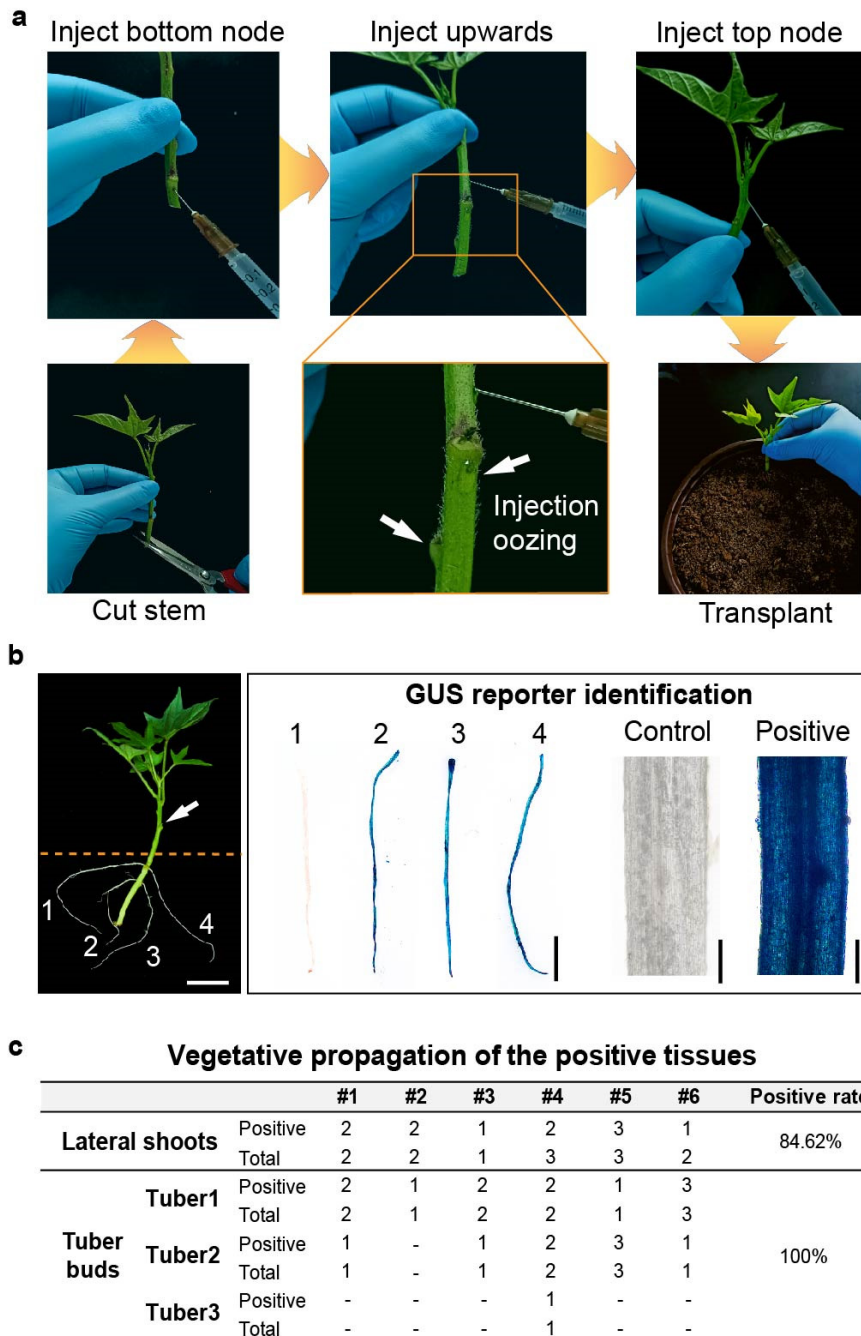
558 **Author contributions**

559 G.M., X.L. and X.H. designed the experiments. G.M., A.C., Y.W., S.L. and M.W.
560 performed the experiments. G.M. and X.L. performed the data analysis. G.M., X.L. and
561 X.H. wrote the manuscript.

562 **Competing interests**

563 The authors declare no competing interests.

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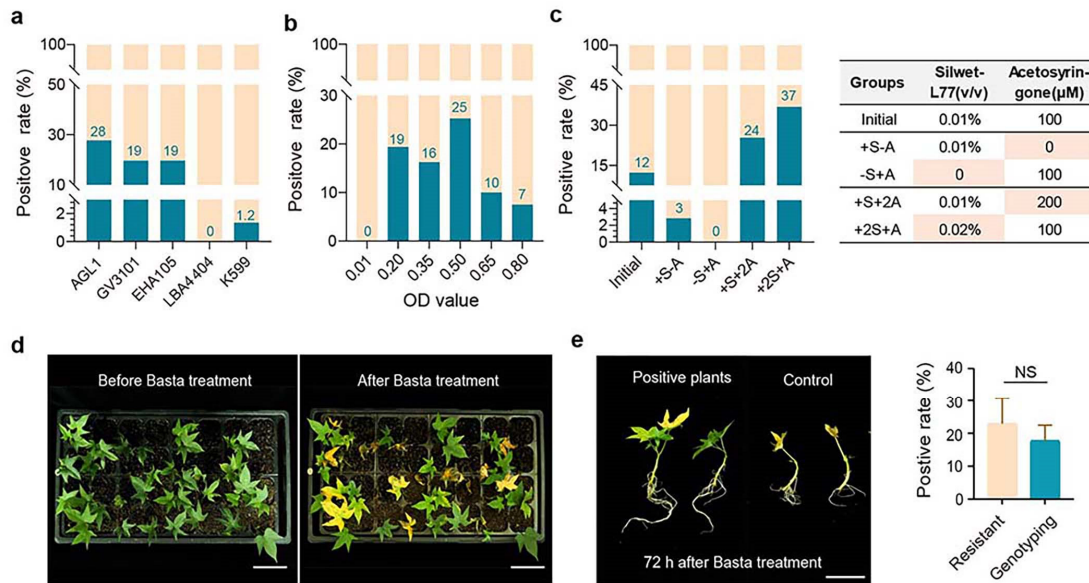


567

568 **Fig. 1 Operating procedure of the stem-injection delivery system**

569 **a**, The operating procedure of the stem-injection delivery system. The healthy stems of
 570 sweet potato plants with several nodes were excised, and each node was injected
 571 upwards until the solution oozed from the adjacent pinholes and excised end. The
 572 injected stems were planted into the soil substrate. **b**, Evaluation of the transformation
 573 of nascent roots. The adventitious roots sprouted spontaneously under the soil within

574 1 week (below the yellow line) and were selected for GUS staining. Scale bar, 1 cm
 575 (left), 0.5 cm (middle), 0.5 mm (right). **c**, Vegetative propagation of the positive tissues.
 576 Independent transgenic plants were further obtained by the vegetative propagation of
 577 the positive lateral shoots, or from the buds that sprouted from the positive tubers.
 578 Positive rate = average (positive/total) × 100%.
 579

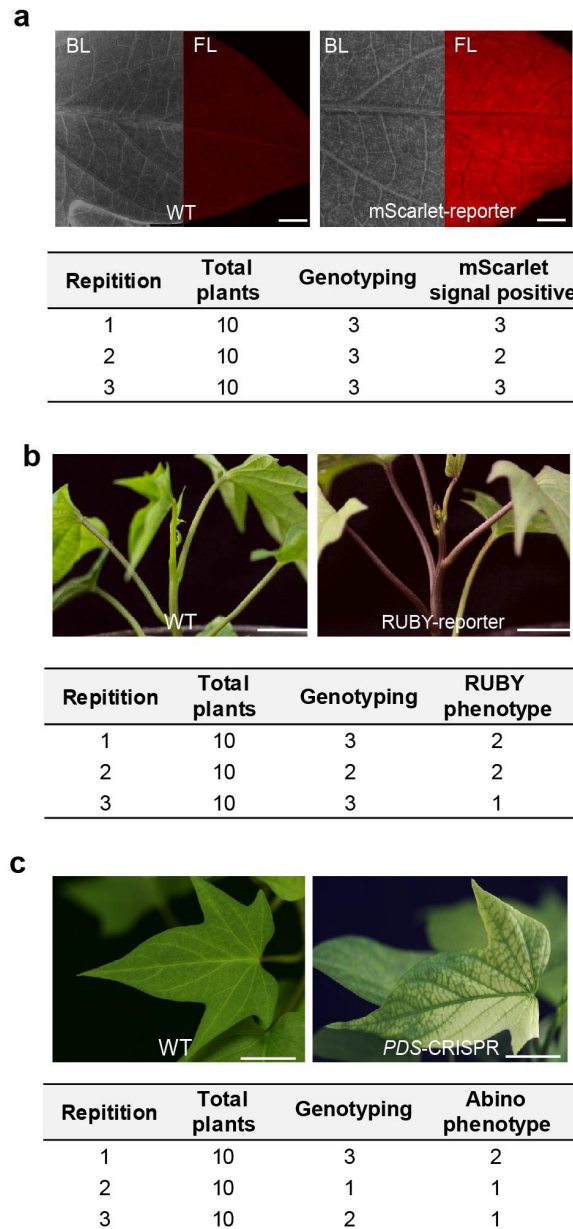


580

581 **Fig. 2 Optimization of the stem-injection delivery system**

582 **a**, Transformation efficiency of different *A. sp.* strains. **b**, Transformation efficiency of
 583 *A. sp.* strains at different OD values. **c**, Transformation efficiency following the addition
 584 of different additives. Positive rate = [average (positive roots/total number of roots per
 585 positive plant)] × (number of positive plants/total number of injected plants) × 100%.
 586 **d**, Bulk selection of transgenic materials based on phosphinothricin (Basta) resistance.
 587 The phenotype of the injected plants before and after spraying Basta. **e**, Comparison of
 588 the morphology of the positive plants and wild-type (WT) after 72 h of spraying Basta.
 589 The bar chart shows the positive rate of Basta resistance and genotyping of the screened
 590 plants. Positive rate = number of positive plants/total number of plants (%). The data
 591 are presented as the mean ± SD of 10 biological replicates (two-tailed Student's *t*-test,
 592 NS, no significance, $P > 0.05$). Scale bar, 5 cm in **d**, 5 cm in **e**.

593



594

595 **Fig. 3 Transformation applicability of reporter vectors and gene editing tools in**

596 **RAPID**

597 **a**, Applicability of the mScarlet reporter in transformation. Scale bar, 0.5 cm. The table

598 depicts the statistics of the transformation results obtained from three independent

599 replicates. BL, bright light; FL fluorescent light. **b**, The applicability of the RUBY

600 reporter in transformation. Scale bar, 2 cm. The table depicts the statistics of the

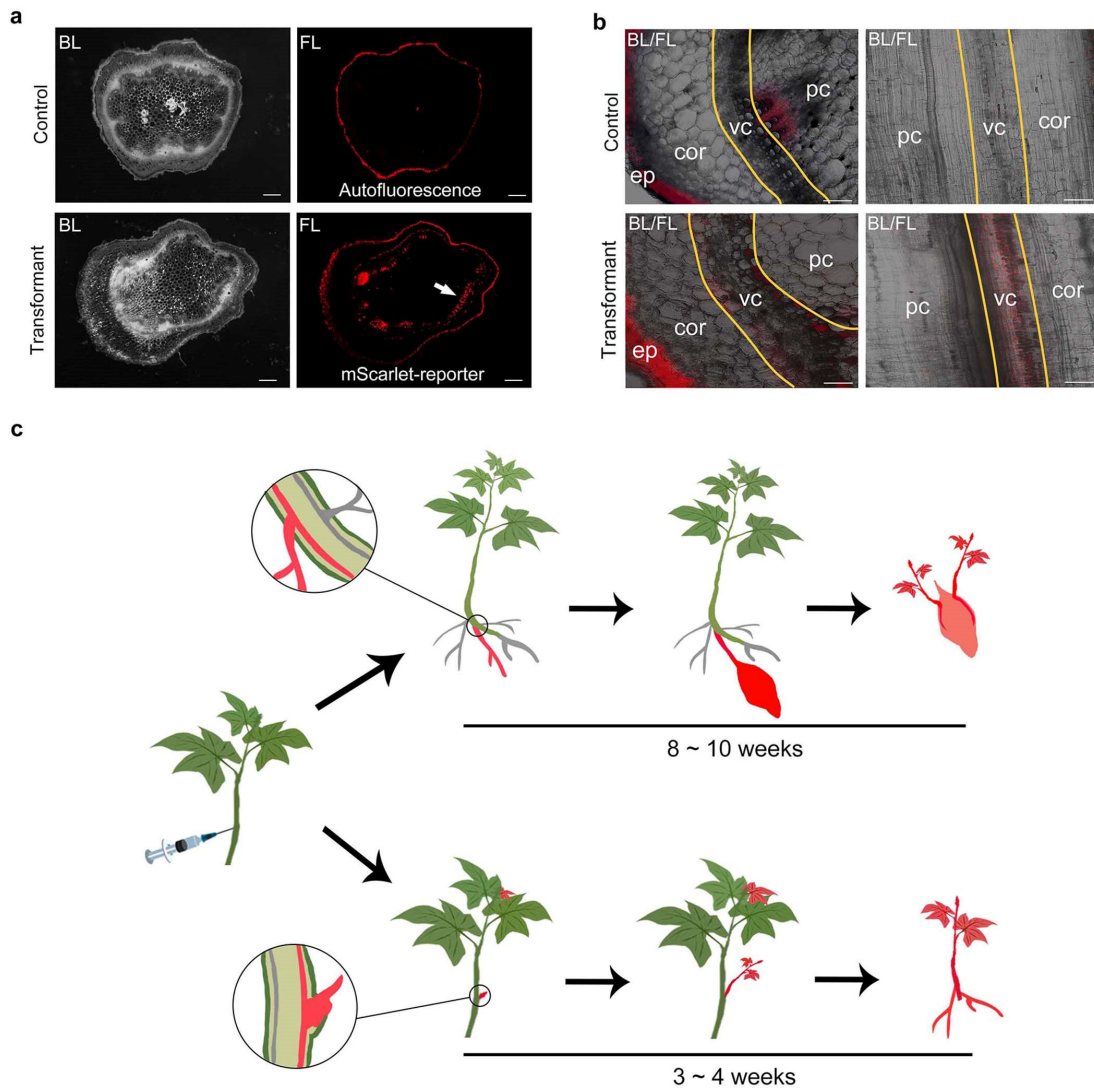
601 transformation results obtained from three independent replicates. **c**, The applicability

602 of the CRISPR-Cas9 tool in transformation following *PDS* knockout. Scale bar, 2 cm.

603 The statistics of the transformation results obtained from three independent replicates

604 are depicted in the table.

605



606

607 **Fig. 4 *A. sp.* was directly delivered to the phloem in the RAPID system**

608 **a**, Fluorescence due to mScarlet in the cross-section of sweet potato stems. The white

609 arrow indicates the obvious fluorescence signal in the transformant tissue. Scale bar,

610 0.5 mm; bright light, BL; fluorescent light, FL. **b**, Histological observation of the signal

611 due to the mScarlet reporter. The area within the yellow lines in the transverse (left) and

612 longitudinal sections (right) of the stems depict the signal due to mScarlet in the

613 transformant; scale bar, 0.1 mm. Vascular cell, vc; parenchymal cell, pc; cortex, cor;

614 epidermis, ep. **c**, Working model of the acquired transformed generations following

615 direct transfection with the RAPID system.

616

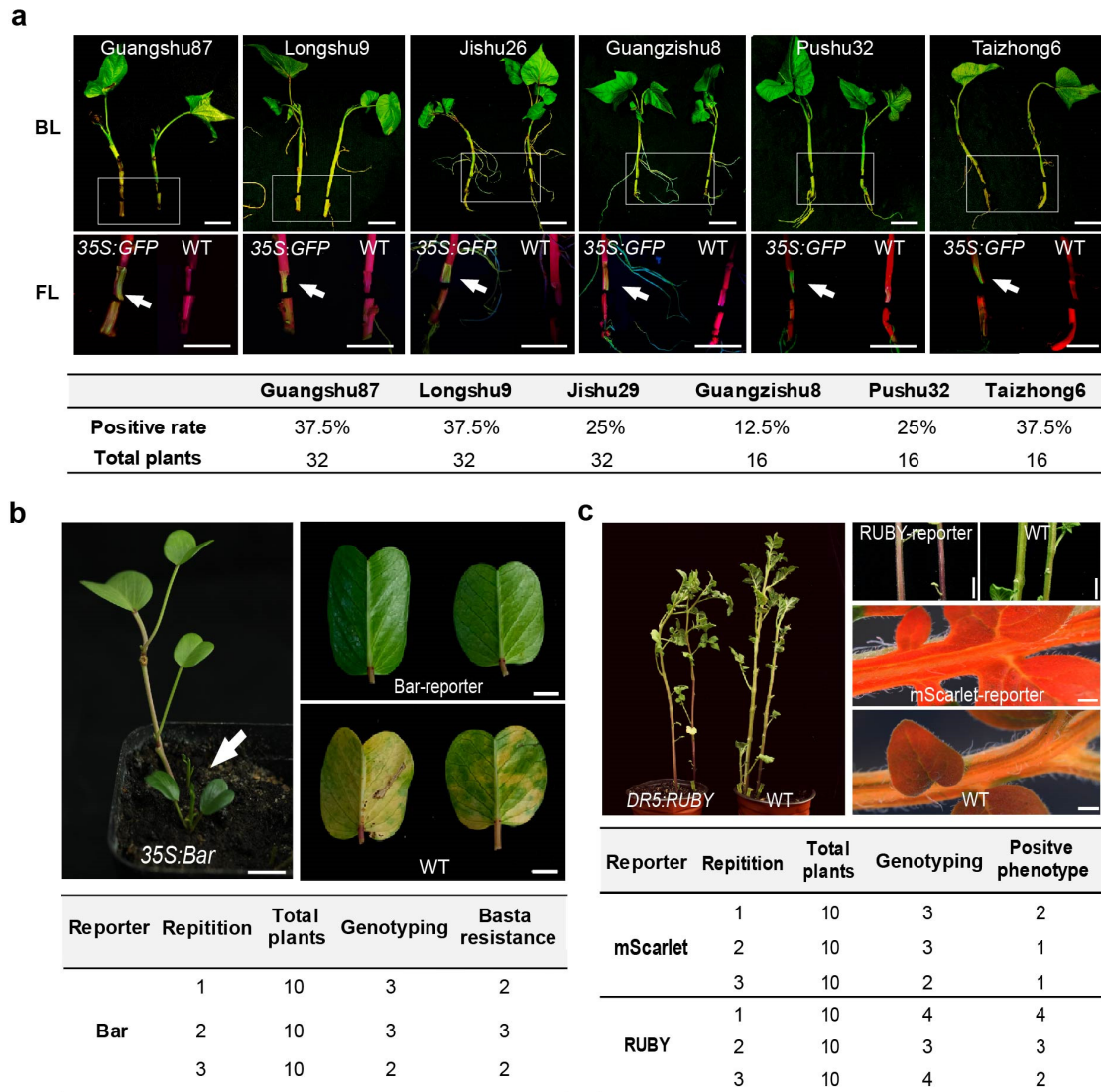


Fig. 5 Application of the RAPID system in other plant species

a, Transformation of different varieties of sweet potato using the RAPID method. The stem was peeled and observed under light and dark conditions (within the box). The arrow indicates the green fluorescence due to the GFP reporter (*35S:GFP*). Positive rate = number of positive plants/total number of plants (%). Scale bar, 2 cm; bright light, BL; fluorescent light, FL. **b**, Transformation of bayhops. The white arrow indicates the reascent shoots from the transformed stems. The leaves from the transgenic shoots carrying the *Bar* gene (*35S:Bar*) retained the green fluorescence under phosphinothricin (Basta) treatment compared to the WT. Scale bar, 2 cm (left), 1 cm (right). The table depicts the statistics of transformation results obtained from three independent replicates. **c**, Transformation of potato. The transgenic materials carrying the RUBY

629 (*DR5:RUBY*) and mScarlet (*35S: mScarlet*) reporters exhibited positive phenotypes.
 630 Scale bar, 2 cm (upper), 0.5 cm (lower). The table depicts the two statistics of
 631 transformation results obtained from three independent replicates.

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 637

Table 1 Comparison of RAPID and traditional tissue culture method in sweet

Methods		Transformation process			Culture condition	Period	Transformant acquisition rate	Reference
RAPID	Operations	Injection		Soil cultivation	Non-sterile	3-10 weeks	28-40% ^a	In this study
	Time	1 day		3-10 weeks				
	Efficiency	35-40%		80-100%				
Tissue culture	Operations	Embryonic callus induction	Subculture and co-culture	Re-generation	Sterile	24-40 weeks	0.004-0.2% ^b	Choi <i>et al.</i> , 2007 ²⁴ ; Yu <i>et al.</i> , 2007 ²⁵ ; Yang <i>et al.</i> , 2011 ²⁶
	Time	4-6 weeks	12-24 weeks	8-10 weeks				
	Efficiency	1-5%	1-5%	40-80%				

638 **potato**

639

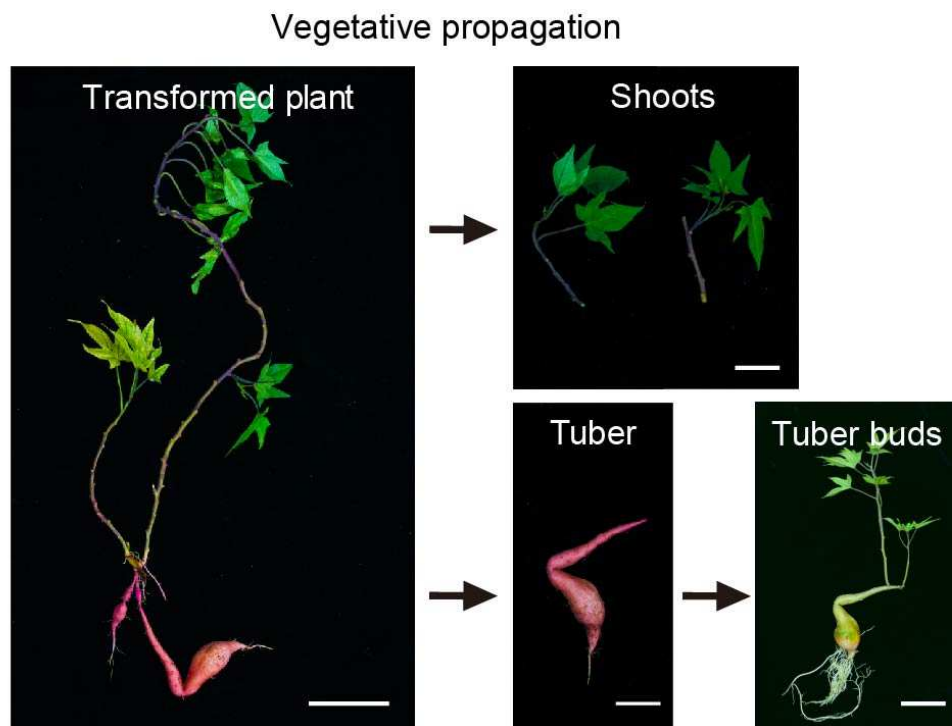
640 ^a Transformant acquisition rate of RAPID = injection efficiency × soil cultivation
 641 efficiency.

642 ^b Transformant acquisition rate of tissue culture = embryonic callus induction efficiency
 643 × subculture and co-culture efficiency × regeneration efficiency.

644

645 **Supplementary Figures**

646



Identification of the transformed plants

Shoots	1	2	3	4	5	6	7	8	9	10
Positive lines	0	0	0	0	0	0	1	2	0	0
Total samples	3	1	1	2	3	2	2	2	1	1

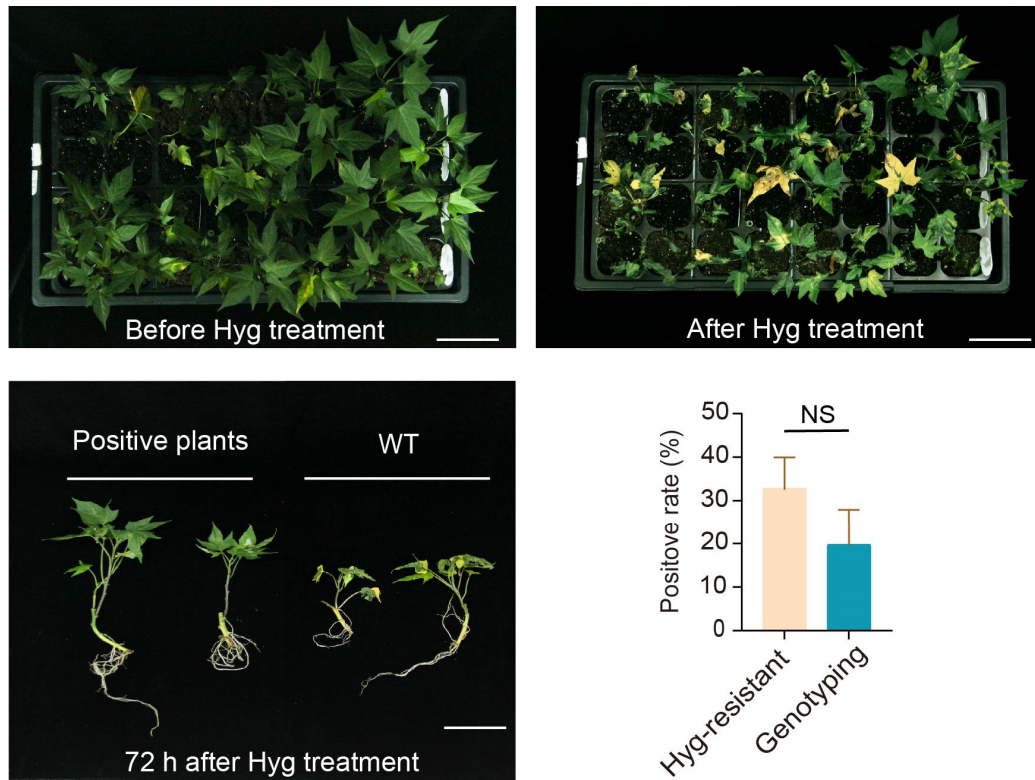
Tuber buds	1	2	3	4	5	6	7	8	9	10	11	12
Positive lines	0	0	0	0	0	0	0	2	1	3	0	0
Total buds	3	4	7	1	1	4	1	2	1	3	2	2
Total samples	10 plants											

647

648 **Supplementary Fig. 1 Generation of transformed offspring of sweet potato**

649 The stem cuttings generated transgenic renascent leaves, lateral shoots, and tubers
 650 developed from adventitious roots. The table depicts the identification of these tissues
 651 by genotyping and GUS staining. Scale bar, 5 cm (left), 2 cm (right).

652



653

654 **Supplementary Fig. 2 Bulk selection of transgenic materials by hygromycin**
 655 **resistance**

656 Phenotypes of the injected plants before and after hygromycin (Hyg) treatment.

657 Comparison of the morphology of the positive and WT plants after 72 h of applying

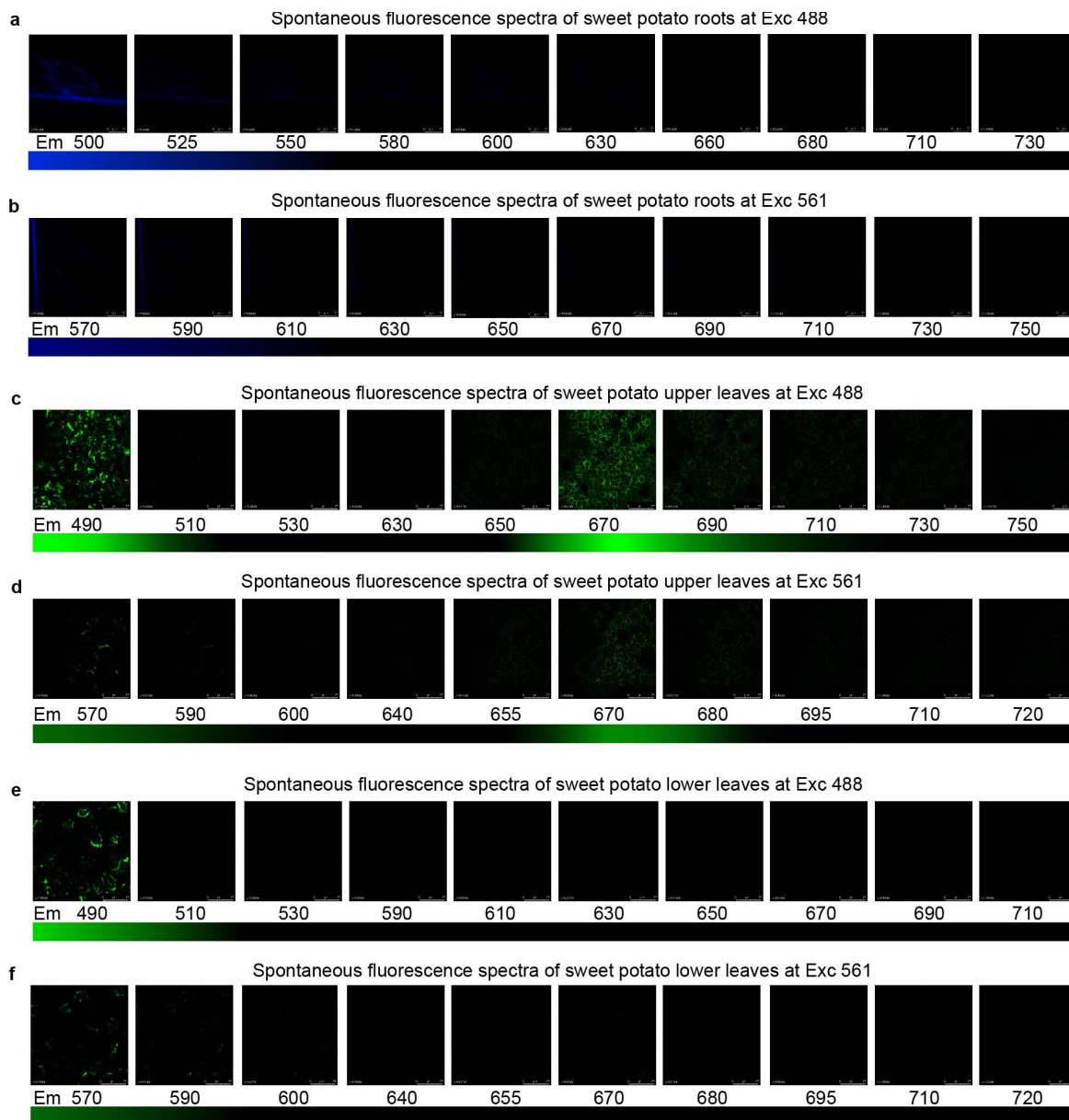
658 Hyg. The bar chart depicts the positive rate of resistance and results of genotyping of

659 screened plants. Positive rate = number of positive plants/total number of plants (%).

660 The data are presented as the mean \pm SD of ten biological replicates (two-tailed

661 Student's *t*-test, NS, no significance, $P > 0.05$). Scale bar, 5 cm.

662

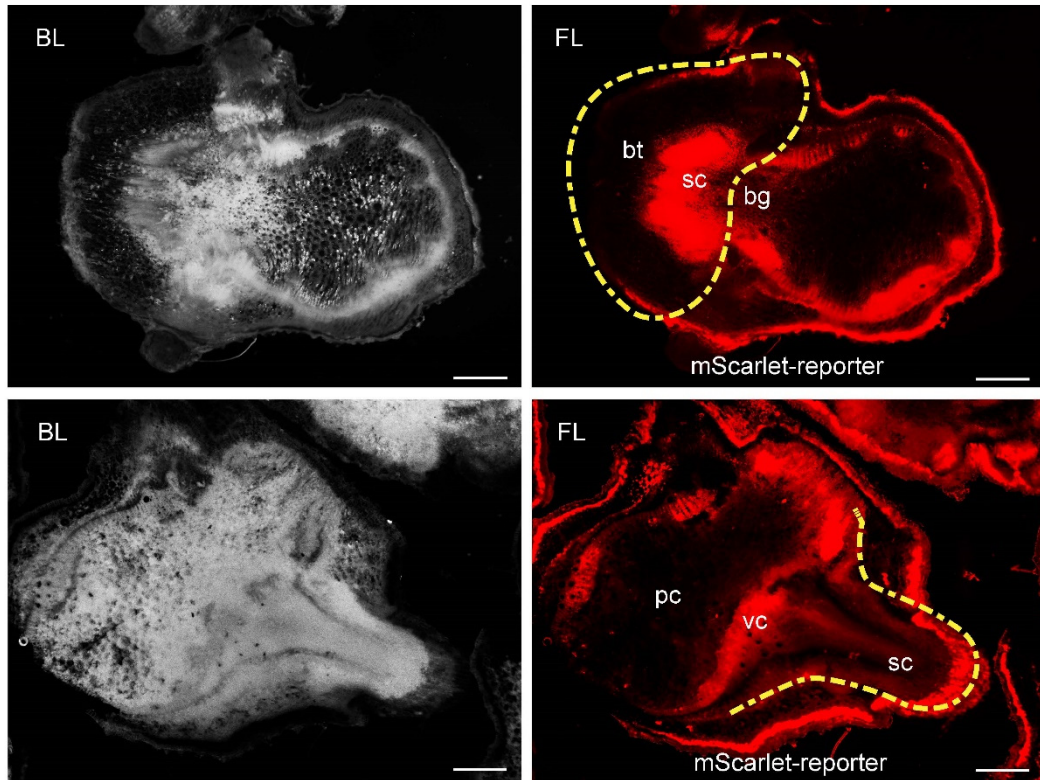


663

664 **Supplementary Fig. 3 Spontaneous fluorescence spectra of sweet potato tissues**

665 Spontaneous fluorescence spectra of the adventitious roots of sweet potato at **a**, Exc
 666 488 nm and **b**, Exc 561 nm. Spontaneous fluorescence spectra of the upper leaves of
 667 sweet potato at **c**, Exc 488 nm and **d**, Exc 561 nm. Spontaneous fluorescence spectra of
 668 the lower leaves at **e**, Exc 488 nm and **f**, Exc 561 nm.

669



670

671

672 **Supplementary Fig. 4 Fluorescence signals due to mScarlet in the transfected**
 673 **renascence tissues**

674 The signals due to mScarlet in the cross-section of the lateral buds (upper) and

675 adventitious roots (lower) of the transfected plants. The yellow line depicts the

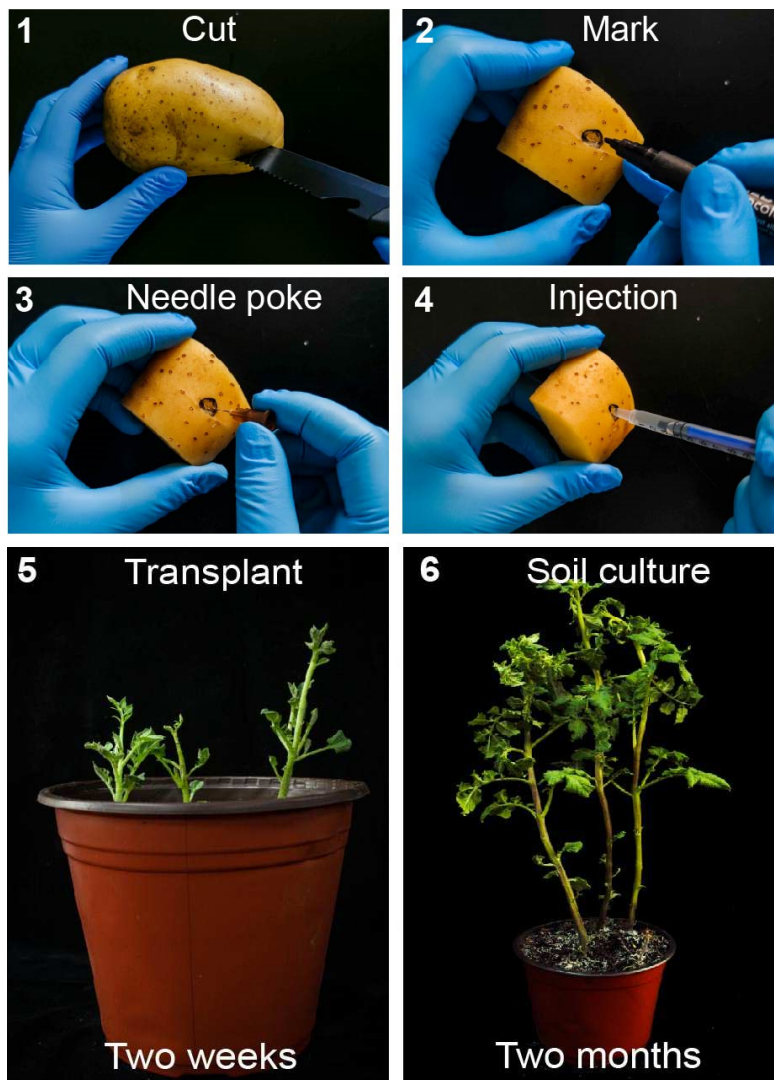
676 approximate area of the renascence tissues. The approximate spatial position of the

677 lateral bud primordium was located between branch trace (bt) and branch gap (bg); stem

678 cell, sc. The vascular cells (vc) are connected to the root primordium; parenchymal cell,

679 pc; bright light, BL; fluorescent light, FL. Scale bar, 1 mm.

680



681

682 **Supplementary Fig. 5 Transformation procedure of potato by RAPID**

683 The fresh tubers of potato were cut and marked around the budding point. The tubers
684 were poked with a needle, and the needle was inserted into the epidermis for injection.

685 The transformed segments of tuber were transplanted in sandy soil. The new buds were
686 unearthed after 1–2 weeks and subjected to further analysis for determining the positive
687 transformants and phenotypic observations. The positive tubers were harvested after 6–
688 8 weeks for subculture and mass propagation.

689