An *in planta* single-cell screen to accelerate functional genetics

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Abstract

Genetic screens in whole plants are a powerful tool for functional genetics. However, elucidating gene function in highly redundant genetic programs such as signaling pathways remains challenging in both model and non-model plants. Here, we report a single-cell screening platform, PIVOT (Protoplast Isolation after Virus Overexpression *in planTa*), to accelerate identification and functional characterization of plant genes. We used *Nicotiana benthamiana* as a heterologous host to test gene libraries arrayed in a single leaf. Two elements of our system made pooled screens possible *in planta*: (1) we harnessed viral superinfection exclusion to ensure single multiplicity of infection per cell during pooled library delivery, and (2) we engineered a cell surface protein as a phenotypic marker for isolating cells of interest from a heterogeneous population. Using this system, we recovered known and new regulators of cytokinin signaling from an *Arabidopsis* open reading frame library. We anticipate PIVOT will be broadly applicable for high-throughput, single-cell functional genetic screening across the plant kingdom.

Introduction

Identifying genes that promote plant resilience and plasticity in response to biotic and abiotic stress is essential to ensure future global food security. In this context, genome-wide genetic screens are a crucial tool for gene function elucidation in plants. While whole-plant genetic screens involving a quantifiable phenotype and a population of randomly mutagenized seeds are simple in concept, these screens are notably time, resource, and labor intensive. For example, identification of *fls2*, the gene encoding the immune receptor FLAGELLIN SENSITIVE 2 (FLS2), required manual screening over 80,000 individual *Arabidopsis thaliana* seedlings[1]. Genetic screens in plants can be further complicated by polyploid genomes, self-crossing incompatibility, gene redundancy, or the long life cycles of select plants.

We anticipate that many of the challenges associated with traditional whole-plant screening methods could be overcome if screens were instead carried out using individual cells harboring genetic perturbations. In other organismal systems such as yeast and immortalized human cell lines, cell-based screens have revolutionized gene discovery and are now routine[2]. These screens have been particularly powerful for identifying genes that encode receptors responding to molecular inputs[3]. Similarly, we anticipate cell-based screens could be suitable for many plant functional genetics efforts

that do not require whole organisms, such as de-orphaning plant receptors responding to ligands involved in growth and defense[4].

Analogous single-cell screens have yet to be realized in plants primarily because plant cell culture systems are challenging to transform, passage, and select for a phenotype. Despite these limitations, recent reports of pooled screens in plants reveal the potential for high-throughput functional genetics. For example, libraries of pooled transcriptional enhancer or terminator sequences have been introduced to *Nicotiana benthamiana* leaves, and bulk RNA-sequencing has revealed new genetic elements that boost transcription[5,6]. In more rare cases, pooled libraries have been directly delivered to protoplasts (plant cells devoid of the cell wall). In one example, a cell death-based readout in transformed wheat protoplasts enabled the rapid identification of novel resistance genes and their avirulence gene partners[7].

Building on this work, we sought to develop a pooled, cell-based, genetic screening platform in plants that could be used for the functional analysis of plant proteins. In contrast to our prior work[8,9] analyzing enzyme-encoding gene sets in whole leaves without close regard to multiplicity of infection (MOI), we anticipated functional analysis of genes that encode other classes of proteins (e.g., receptors and signaling pathway components) would require assessing gene candidates individually, one per cell. Thus, to realize a cell-based genetic screening platform that moves beyond canonical “one gene query per one plant” screening, two technological advances were necessary: (1) an efficient gene delivery method that results in the expression of libraries of gene candidates with minimal MOI and (2) a cell sorting method to enable single-cell phenotypic analysis.

Here, we describe PIVOT (Protoplast Isolation after Virus Overexpression *in planTa*), a first-in-class, pooled, high-throughput *in planta* screening platform to accelerate functional genetics and protein discovery. As proof-of-concept, we tested the ability of PIVOT to identify proteins from *Arabidopsis thaliana* that function in cytokinin signaling. Our approach successfully retrieved both known activators and new cytokinin response factor (CRF) proteins involved in cytokinin signaling. Using PIVOT to recapitulate protein function in the well-characterized cytokinin pathway serves as a model for future discovery of proteins in plant signaling pathways modulated by small molecules.

Results

Designing a platform for screening pooled gene libraries in *Nicotiana benthamiana*.

We sought to develop a high-throughput genetic screening platform in plants that would enable assessment of candidate plant proteins involved in perception and transmission of small molecule-mediated signals. Many signaling pathways are widely conserved across plant species, and it has been demonstrated that molecular readouts (e.g., transcriptional reporters) for such pathways are responsive across species[10,11]. Thus, we anticipated a wide range of pathways could be assayed using a single heterologous host. To circumvent plant cell-culture transformation challenges, we leverage existing whole-plant transient expression tools widely used in the model host *Nicotiana benthamiana* and only generate protoplasts at the final screen stage (Figure 1). Our

screening strategy involves testing pools of protein-encoding gene candidates in individual cells of an intact leaf, followed by protoplast isolation for cell-level analysis to expedite phenotypic screening.

A general overview of our workflow for single-cell genetic screening in *N. benthamiana* is as follows: (1A) Select genes of interest and generate a library of barcoded constructs to perturb (overexpress or knockdown/out) protein-coding gene candidates. (1B) Construct a transcriptional reporter that consists of a cell surface-localized protein expressed under control of a biologically relevant, selectively responsive promoter. (2) Co-deliver the pooled gene library and the transcriptional reporter into *N. benthamiana* leaves. (3) Perform a biological assay in leaves (e.g., treat with an elicitor) to assess the role of candidate proteins in modulating transcription of the reporter as a molecular phenotype. (4) Isolate protoplasts, separate based on reporter activity, and sequence cell populations to identify barcoded gene perturbations that alter the reporter activity as a proxy for the phenotype of interest (Figure 1).

Exploiting viral superinfection exclusion for pooled library delivery

We first turned our attention to developing a gene delivery method that would enable pooled delivery of 10^2-10^4 gene candidates to a single *Nicotiana benthamiana* leaf with low MOI per cell (Figure 1, Steps 1 & 2). Importantly, we aimed for each cell to harbor a single gene perturbation to facilitate independent candidate assessment within a pooled screen context. Others recently reported using *Agrobacterium* (*Agro*)-mediated transient expression with canonical binary vectors to simultaneously introduce hundreds of strains in *N. benthamiana* leaves, but to maintain single infections events per cell, the optical density at 600nm (OD_{600}) used for *Agro* delivery must be very low (OD_{600} = 0.0025)[12]. An unwanted consequence of this strategy is that a majority (90%)[12] of the cells in the leaf go untransformed, reducing the experimental output and increasing the amount of infiltrated tissue necessary to ensure a complete library coverage.

Alternatively, at high *Agro* OD_{600}, we and others have observed that co-infiltration of *Agro* strain libraries results in multiple infections per cell, following a Poisson distribution, where the number of infection events correlates to the *Agro* concentration delivered to a leaf[13]. Here, we qualitatively confirmed this high MOI when using the pEAQ[14] vector (Figure 2A, top). We used a simple model wherein three *Agro* strains harboring unique fluorescent proteins (FPs) were delivered to a *N. benthamiana* leaf at a final *Agro* OD_{600} of 0.1 (high) or 0.001 (low) (Figure 2B). For the pooled pEAQ cargo delivered at high OD_{600}, we observed co-expression of multiple FPs in single *N. benthamiana* cells (Figure 2C, pEAQ, OD_{600} = 0.1), while at low OD_{600} of *Agro* delivery, we observed sparse single infection events per cell (Figure 2C, pEAQ, OD_{600} = 0.001). These data confirm that single-strain infection events per cell are achievable with pEAQ at low *Agro* OD_{600} delivery, but indeed, at the expense of diminishing the total number of transformed cells.

We wondered if we could instead use a virus that exhibits superinfection exclusion (SE) to achieve single gene perturbations per cell while maximizing infected tissue area. SE is a naturally occurring mechanism enacted by monopartite viruses to prevent secondary, competing infections in the same cell. SE has been observed for bacteria[15]-,

plant[16]-, and animal[17]-associated viruses, and notably, has been used to protect crops from viral infection, a practice known as cross-protection[18]. The SE mechanism has been reproduced in experimental settings for many viruses, including tobacco mosaic virus (TMV)[19], a single-stranded, positive-sense RNA plant virus. A TMV-derived vector, pTRBO (TMV RNA-based Overexpression), has been highly optimized for heterologous protein expression in plants and compatibility with *Agro*infiltration[20]. pTRBO contains a viral replicase, a movement protein, and an engineered 3' sub-genomic promoter to drive gene-of-interest expression (Figure 2A, bottom).

Here, we tested whether pTRBO could be used as a pooled gene delivery tool to achieve both low MOI and high coverage of transformed tissue. Compared to the pEAQ vector, when *Agro* strains harboring FPs encoded in pTRBO vectors are pooled for delivery, single MOI is maintained regardless of the *Agro* delivery OD_{600} because of viral SE (Figure 2C, pTRBO). In addition, due to the TMV movement protein that facilitates virus movement between cells, transformation is highly efficient; in this experiment, we were unable to detect any visibly untransformed cells when pTRBO was used, even at a low inoculum concentration (Figure 2C, pTRBO, OD_{600} = 0.001). These data demonstrate *Agro*-launched pTRBO is a suitable vector for pooled gene perturbation delivery that results in single-strain infection at the cellular level while maximizing the transformed cellular space available for downstream phenotypic screening.

We next explored the dynamic range of this virus-based pooled delivery tool to determine how many gene candidates introduced as a pool could uniquely be detected in a single whole leaf infiltration. We created a series of mock libraries using defined ratios of two pTRBO-FPs (mCherry and GFP) as proxies for individual gene candidates and used microscopy to visualize FPs as the virus spreads across the leaf (Figure 2D). At five days post-infiltration (DPI), *in planta* expression of two pTRBO-FPs appears to reflect the 1:100 *Agro* OD_{600} ratio (Figure 2E, left). Microscopy confirmed superinfection exclusion was maintained during pooled delivery so that each cell contains a single gene perturbation, while virus movement across the leaf generates pockets of replicates for each gene perturbation (Figure 2E, right).

When this model library was repeated with FP ratios of up to 1 in 10,000, the minority member (mCherry) could still be detected (Supplementary Figure 1), suggesting that thousands of unique gene queries could be delivered as a pool into a single leaf but assessed individually. Taken together, these results highlight that viral genome-encoding vectors like pTRBO are a suitable platform for simultaneously delivering up to 10^4 pooled gene perturbations to a single leaf with low MOI.

Candidate representation *in planta* reflects pooled virus library with ORFs of similar size

Qualitative microscopy analysis of leaves indicated single MOI and high transformation coverage using pTRBO. We next wanted to quantify library member representation via barcode sequencing. We generated a library of barcoded pTRBO-CFP constructs for pooled *Agro* transformation and delivery to an *N. benthamiana* leaf (Figure 3A). At five DPI, CFP expression maximized the area of infected leaf tissue (Figure 3B).

To assess how members of the delivered and *in planta* CFP populations compared, plasmid harvested from *Agro* pool (pre-infiltration), and the cDNA generated from infiltrated tissue were both sequenced to quantify unique post-CFP barcodes. *Agro* plasmid reads and infiltrated leaf-derived cDNA reads revealed the 67 individually barcoded CFPs comprising the library were positively correlated and scaled linearly (Figure 3C). These data indicate that an *Agro*-launched pTRBO vector can deliver a gene overexpression library to *N. benthamiana* with a predictable input-to-output (plasmid-to-*in planta*) expression ratio for equal-sized cargo.

However, a multi-member gene overexpression screen likely contains ORFs of varying size, and we surmised ORF size may affect the dynamics of virus-based delivery[21,22]. Indeed, when we assessed barcoded pTRBO constructs harboring a 2.5 kb insert with mCherry fused to the *E. coli* β-glucuronidase (GUS) ORF, the linear relationship between plasmid and in-leaf barcodes was maintained; however, this larger viral-delivered cargo did not maximize the infiltrated leaf space at five DPI (Supplementary Figure 2A, B). These data suggest that cargo size may influence the degree of viral movement.

To assess the effect of ORF size on candidate representation *in planta* for a virus-delivered library of mixed cargo length, we cloned FPs fused with varying RNA insert size into respective pTRBO vectors: CFP alone (0.7 kb); YFP plus neomycin phosphotransferase II (NPTII) (1.5 kb); and mCherry plus GUS (2.5 kb) (Figure 3D). We cloned an additional pTRBO-YFP-NPTII construct with a stop codon between YFP and NPTII (Figure 3D, “short AA”) to determine if translation size posed an additional burden on pTRBO-based expression *in planta.* Despite approximately equivalent ratios of each pTRBO-FP class in the *Agro* plasmid pool, microscopy analysis at five DPI showed that CFP dominated the *N. benthamiana* leaf space, though pockets of YFP and mCherry expression were still detectable (Figure 3E).

Quantification of barcoded-FP transcripts (Figure 3F) corroborated the microscopy analysis: for a set of varied size cargos, the extent of propagation of the viral clone is proportional to cargo length. Indeed, barcoded CFPs comprised 90% of the in-leaf library reads despite comprising only 25% of the delivered *Agro* plasmid library (Figure 3G). Nonetheless, even the longest members of our library were able to spread and be quantified. Interestingly, the two pTRBO-YFP-NPTII constructs (short and long AA) yielded comparable plasmid and in-leaf reads with respect to one another (Figure 3G), suggesting that additional translation load does not affect library member representation of pTRBO-delivered cargo.

Taken together, these results demonstrate that the in-leaf expression of similar-sized candidates can be predicted by the input library ratio, while candidate fitness is affected by cargo length when virus-encoded ORFs of mixed sizes are present in a library. Nevertheless, candidates ranging up to 1.8kb in cargo length can all be sufficiently and reproducibly detected when delivered in a mixed-size pool.

Engineered surface receptor enables plant single-cell phenotypic sorting

Genetic screening at the single-cell-level requires a method to quickly and efficiently isolate plant single cells (protoplasts) harboring a desired phenotype following gene

perturbation (Figure 1, Steps 3 & 4). While many single-cell screens in mammalian systems utilize Fluorescence-activated Cell Sorting (FACS) for facile isolation of cell populations of interest, current FACS instruments are not compatible with fragile *N. benthamiana* protoplasts sizing 20-100 µm in diameter.

We hypothesized that transient expression of an engineered receptor protein that localized to the cell membrane could enable magnetic-based pulldown of *N. benthamiana* protoplasts harboring the receptor. We chose the HaloTag protein[23] as the extracellular receptor handle due to its strong covalent interaction with diverse chloroalkane-linked substrates. Our magnetic-activated protoplast sorting (MAPS) strategy uses a biotinylated HaloTag ligand paired with streptavidin-conjugated magnetic beads to mediate pulldown of HaloTag receptor-harboring protoplasts (Figure 4A).

We built a MAPS-compatible receptor in which HaloTag is localized to the cell surface by the signal peptide from *Arabidopsis* LORELEI-Like GPI-anchored protein 1 (LLG1)[24] and anchored in the plasma membrane by a human transmembrane domain (TMD) to stabilize surface expression[25] (Figure 4B). To assess receptor localization in *N. benthamiana* cells, we *Agro*infiltrated an mCherry-linked version of our HaloTag MAPS receptor to the cauliflower mosaic virus (CaMV) 35S constitutive promoter. At four DPI, the HaloTag-mCherry reporter outlines the plasma membrane perimeter of pavement cells in leaf tissue (Figure 4B, Leaf), and in mesophyll-derived protoplasts, HaloTag-mCherry signal is concentrated at the surface compared to chlorophyll signal distributed throughout the protoplast (Figure 4B, Protoplasts). These results indicate the HaloTag reporter is properly trafficked to the plant cell surface.

To determine if MAPS is capable of separating protoplasts based on the presence of a surface-expressed HaloTag receptor, we next generated an artificial mixture of protoplasts with and without the MAPS receptor. CaMV35S-driven HaloTag-mCherry and GFP constructs in *Agrobacterium* were infiltrated into separate *N. benthamiana* leaves; protoplasts with (HaloTag) or without (GFP) the receptor were harvested and mixed at ratios of 1:1, 1:10, or 1:100, respectively, in pools of 10^6 cells total (Figure 4C).

Figure 4D displays representative images of the mixed protoplast populations before (Input) and after (Bound and Unbound) MAPS. The input images reflect the pre-sort, artificially mixed HaloTag-mCherry:GFP protoplast ratios of 1:1, 1:10, or 1:100, respectively (Figure 4E, Input). Across all input cell ratios, the MAPS bound fraction was dominated by intact HaloTag-mCherry protoplasts, with little to no GFP cells (Figure 4D, Bound). Conversely, GFP cells comprised most of the unbound fraction for the 1:10 and 1:100 ratios (Figure 4D, Unbound). The presence of some mCherry-positive cells within MAPS unbound fraction for the 1:1 ratio might reflect saturation of the magnetic beads at this cell number and ratio.

We quantified the separation capability of MAPS by calculating enrichment ratios for HaloTag-mCherry cells and GFP cells based on cell counts in the bound and unbound fractions. The bound/unbound enrichment ratios for GFP protoplasts was around zero for all input ratios, while the mean enrichment ratio ranged from 4.5 to 8.5 for HaloTag-mCherry cells (Figure 4E). Collectively, these results demonstrate that pairing a cell

surface receptor with magnetic sorting enables protoplast isolation from a mixed population when the target cells comprise between 1-50% of 10^6 total cells.

Proof-of-concept Protoplast Isolation after Virus Overexpression *in planTa* (PIVOT) screen for cytokinin activity

With pooled library delivery (pTRBO) and single-cell isolation (MAPS) methods established, we combined these tools to enable a single-cell, functional genetic screen. For our debut PIVOT screen, we chose to probe cytokinin two-component signal transduction as a test case because of broad pre-existing knowledge of key modulators of this phosphorelay pathway including histidine kinase (HK) receptors, histidine phosphorelay (HP) proteins, and response regulators (RRs)[26], but also room for functional discovery of cytokinin-related proteins (Figure 5A). Moreover, due to conservation of cytokinin signaling across the plant kingdom, we predicted that homologous proteins could integrate with existing cytokinin signaling circuits to function in a heterologous host.

To carry out the screen, we needed to generate (1) a library of genes to query their role in cytokinin signaling and (2) a mechanism to differentiate genes that activate, repress, or do not mediate cytokinin signaling. We selected ORFs from *Arabidopsis thaliana* genes with known roles directly participating in cytokinin phosphorelay, including type-A and B response regulators[26] (ARRs, A for *Arabidopsis*) (Supplementary Table 1). Further, we included candidates tangentially involved in cytokinin signaling, though not through direct phosphorelay, such as cytokinin response factors (CRFs)[27] and SOB five-like (SOFL)[28] genes. We also included circadian rhythm genes and a barcoded GFP library as negative controls, since neither should activate cytokinin signaling. Given that expression of competing pTRBO-delivered cargo is dependent on insert size (Figure 3D-G) we purposefully selected query genes of ORF size within a 1.5kb range to limit bias based on the replication capacity of pTRBO. In total, our pTRBO-ORF library contained ORFs of 57 barcoded *Arabidopsis* gene candidates and 55 barcoded GFPs (Supplementary Table 2). We cloned individual *Arabidopsis* ORFs into an intron[29]-containing pTRBO vector to limit leaky expression in *Agro* without disrupting *in planta* activity of the pTRBO-delivered cargo (Supplementary Note 1 and Supplementary Figures 4, 5).

To assess our chosen ORF library for cytokinin-related function, we generated a transcriptional reporter linking the expression of our MAPS cell-surface protein to a previously described cytokinin-sensitive synthetic promoter called TCSn (Two Component signaling Sensor new)[10]. We hypothesized that overexpression of known cytokinin signaling activators (such as type-B ARRs) would activate the TCSn promoter, leading to expression of membrane-localized HaloTag (Figure 5B, pink border), whereas overexpression of off-target ORFs would not activate the TCSn promoter (Figure 5B, black border).

Following pooled library and reporter delivery, leaf incubation, and MAPS (Figure 5B), we calculated the enrichment ratio for each ORF based on the number of ORF-specific barcodes in the MAPS bound and unbound fractions. Considering GFP should not biologically contribute to cytokinin signaling, we used the barcoded GFP library as a control group for screen data analysis. A TCSn bound/unbound ratio that is higher than

the GFP controls was interpreted to represent TCSn activation and thus extrapolated to indicate ORF-based positive modulation of cytokinin signaling. It is worth noting the *Agro* delivery strain GV3101 carries genes for cytokinin production[30], so leaf infiltration to deliver both candidate genes and the reporter construct likely coincides with the initiation of cytokinin signaling. We expected *Agro*-derived cytokinin would contribute to the absolute levels of background TCSn signaling that could then be enhanced if a pathway protein was transiently overexpressed in a given cell.

As predicted, the GFP ORFs generally did not significantly activate the TCSn reporter, and the GFP population maintained a tight distribution around a low TCSn bound/unbound enrichment ratio. The screen recapitulated the activity of some known cytokinin signaling regulators. Five of seven tested type-B (positive) ARRs (ARR1, ARR10, ARR14, ARR18, and ARR21) yielded TCSn bound/unbound ratios greater than 1 standard deviation of the GFP mean, though ARR1 and ARR21 were not statistically significant (Figure 5C). Further, the TCSn bound/unbound ratio for six of nine tested Type-A (negative) ARRs (ARR4, ARR6, ARR8, ARR9, ARR16, and ARR17) fell within or below the GFP mean. TCSn activity for all PIVOT-screened ORFs is reported in Supplementary Table 3.

Interestingly, many cytokinin response factors (CRFs) – a subset of the AP2/ERF family of transcription factors – were amongst the top hits in our screen (Figure 5C). Though CRFs are not known to directly participate in cytokinin phosphorelay, transcriptional changes typically observed following cytokinin treatment are severely altered in *Arabidopsis* CRF mutants, indicating that CRFs are important for regulating cytokinin-responsive genes[27].

Post-screen validation highlights CRFs as regulators of cytokinin phosphorelay

To complement the results of our PIVOT screen, we individually validated CRF-mediated TCSn activation. pTRBO-CRFs were co-infiltrated with a TCSn-driven mCherry reporter construct in small leaf spots that were imaged for fluorescence intensity. Initially, we investigated CRFs 3,4,5, and 10 due to their combination of high TCSn bound/unbound ratios and statistical significance compared to the control GFP population (Figure 5C). In *Arabidopsis*, CRF5 was previously known to play a role in cytokinin response[27,31], while CRFs 3 and 4 have been implicated in embryonic development[32] and response to cold[33], respectively. CRF10 controls flowering time in *Brassica napus*[34] but has not been functionally studied in *Arabidopsis*. We also included ARR18[35] and ARR22[36] – known activators and repressors of cytokinin signaling – as positive and negative ORF controls, respectively, in addition to pTRBO-GFP as a control for virus-based delivery.

At four DPI, by visual inspection, mCherry fluorescence was modest for CRFs 3 and 4 and medium strength for CRFs 5 and 10, while the positive control, ARR18, strongly activated the TCSn reporter (Figure 5D). Fluorescence quantification indicated that ARR18, CRF5, and CRF10 are stronger TCSn activators compared to GFP or TCSn reporter-only controls (Figure 5E). As an orthogonal measurement of TCSn activation, RNA harvested from each leaf spot was analyzed for TCSn-driven mCherry transcript levels by quantitative reverse transcription PCR. Fluorescence in the spot assay was

corroborated by transcript quantification, with CRF5 and ARR18 yielding significantly more mCherry transcript compared to the reporter-only infiltrated control (Figure 5F).

Though CRF2 and CRF12 were not initially included in validation screening due to borderline statistical significance and low read counts, respectively, precedence from the literature guided us to later follow up on these candidates to understand their behavior in our screen. *Arabidopsis* CRF2 has been shown to play a role in responses to cold, gravity, pathogen, and salt stress, and regulation of reproductive development[37]. Furthermore, CRF2 is the most strongly upregulated CRF in response to cytokinin treatment[31]. On the other hand, the lack of previous knowledge about *Arabidopsis* CRF12 at the time of this study piqued our interest to pursue this candidate further.

In a separate TCSn activation leaf spot assay, CRF12 demonstrated medium-strength mCherry fluorescence, corroborated by a statistically significant increase in mCherry transcript over the pTRBO-GFP control (Supplementary Figures 6A, B). Surprisingly, though CRF2 yielded the highest TCSn bound/unbound ratio in the screen, CRF2 visually and quantitatively failed to demonstrate TCSn activation in this spot assay (Supplementary Figure 6A, B). We noticed CRF2 overexpression in the spot assay resulted in visible cell death at the site of infiltration by four DPI (Supplementary Figure 6C), which could have confounded TCSn activation or our ability to detect mCherry fluorescence. These data highlight the value of cell-based screening for identifying candidates that would likely have resulted in significant toxicity if overexpressed throughout the plant (Supplementary Note 2).

CRF overexpression upregulates type-A response regulator expression

Following validation of CRFs as significant TCSn activators, we explored the role of CRFs in cytokinin signaling outside of the screen context. Current models of cytokinin signaling postulate CRFs positively regulate expression of type-A response regulators: indeed, type-A ARRs were downregulated in a quadruple *Arabidopsis crf 1,3,5,6* mutant compared to wild-type[38]. Thus, we hypothesized that heterologous expression of *At*CRFs in *N. benthamiana* may upregulate expression of endogenous Type-A *Nb*RRs.

We aimed to study the effects of CRF overexpression independent of cytokinin signaling induced by *Agro*infiltration, so we cloned select *Arabidopsis* CRF ORFs into a pTRBO vector containing a viral coat protein (pTRBOcp) that would deliver ORFs to systemic, *Agro*-naïve tissue. Thirteen days after pTRBOcp-CRFs were *Agro*infiltrated into a lower *N. benthamiana* leaf (L0), RNA from systemic tissue (L4) was harvested and analyzed to quantify expression of an endogenous *N. benthamiana* Type-A RR homolog, *Nb*RR17 (Figure 5G). Across multiple systemic leaves in independent experiments, pTRBOcp-CRF5 and pTRBOcp-ARR18 – ORFs that significantly induced TCSn activation in both the PIVOT screen and the leaf spot assay – demonstrated trends suggestive of type-A *Nb*RR upregulation, though not statistically significant (Figure 5H).

Systemic overexpression of *At*CRF2 – which yielded the highest TCSn bound/unbound ratio in the PIVOT screen – demonstrated a 10-fold increase in *Nb*RR17 transcript compared to a GFP control (Figure 5H). CRF2-induced transcriptional alteration led to a striking systemic-wide cell death response (Figure 5I). A similar phenotype was also observed when *At*CRF2 was expressed in local tissue in the leaf spot assay

(Supplementary Figure 6C). Identifying the suite of differentially regulated genes in CRF2-overexpressed plants causing this extreme phenotype is an interesting future direction.

In sum, assessing candidates individually for their role in cytokinin signaling supported the data from the screen, providing confidence for utilizing pooled screening approaches for functional genetics. Further, post-screen assays provided experimental evidence for the cytokinin signaling activity of a sequence-predicted, but not yet functionally validated CRF (*At*CRF12), and contributed new evidence supporting the role of CRFs as regulators of type-A RR expression.

Discussion

Genetic screening in plants has historically required resource-intensive whole-plant methods. In this work, we strove to develop a single-cell screening platform to rapidly increase the pace of plant functional genetics. We harnessed superinfection exclusion from TMV as a delivery mechanism for pooled gene overexpression libraries in plants that enforces single MOI per cell (Figure 2). While our overexpression screen for cytokinin activity included 112 candidates, we anticipate PIVOT can support simultaneous investigation of up to 10^4 candidates (Supplementary Figure 1), thus providing potential for genome-wide genetic screens to occur in single plants in the future (Supplementary Note 3).

In addition to establishing virus-based pooled delivery that balances single MOI with high coverage of transformed tissue, we introduce a magnetic-based sorting method for phenotyping at the single plant cell level. Magnetic-activated cell sorting (MACS) has previously been used in plant systems to isolate specific cell types by targeting natively expressed surface markers[39,40]. In a recently disclosed study, MACS was utilized to sort *N. benthamiana* nuclei following transient transformation[12]. Here, we find that cell-surfaced expressed proteins can also be used for magnetic-based sorting of protoplasts – which are too fragile or large FACS – following transient plant gene overexpression (Supplementary Note 4). We anticipate MAPS will be particularly useful for capturing activities occurring outside of the nucleus.

We integrated pooled gene delivery (pTRBO) and protoplast sorting to enable an *in planta*, pooled genetic screen. As a test case, we screened a 112-member *Arabidopsis thaliana* ORF library for cytokinin activity in the versatile heterologous expression host *N. benthamiana*. Consistent with their respective previously annotated activities[10,41–43], we found that type-B ARRs 10, 14, and 18 were TCSn activators, while type-A ARRs 4, 6, 8, 9, 16, and 17 did not significantly activate TCSn (Figure 5C, Supplementary Table 3).

Beyond type-B ARRs, cytokinin response factors (CRFs) emerged as consistent activators of the cytokinin-sensitive TCSn promoter during pooled screening (Figure 5C). In addition to cytokinin signaling, CRFs have been implicated in a variety of growth and defense processes[37]. Importantly, assigning individual function to CRFs has been difficult using traditional loss-of-function methods, as CRFs are highly redundant, often requiring triple or quadruple mutants for appreciable phenotype[38], and some mutant combinations are embryo lethal[27]. Thus, the CRF family represents a case in which

PIVOT screening technology could capture gene function that may be inaccessible using traditional mutagenesis screening.

Our work provides new evidence supporting the role of CRFs in modulating cytokinin signaling-related gene expression. Screen validation experiments determined both CRF5 and CRF12 caused significant TCSn activation (Figure 5D-F, Supplementary Figure 6). Since the TCSn synthetic promoter is derived from type B-RR binding sites, these results corroborate previous findings[27] that CRFs share downstream gene targets with Type B-RRs (Figure 5A). Notably, *At*CRF12 had not been experimentally analyzed prior to this year when a recent report annotated it as a flowering time regulator[44]. Thus, this work provides the first functional validation for the role of CRF12 in cytokinin response. Furthermore, *At*CRF2 overexpression significantly upregulated RR17, a *N. benthamiana* type-A RR (Figure 5G). These data suggest the conserved role of CRFs in cytokinin phosphorelay regulation across plant families, and that signaling proteins can function in pathways across species.

We anticipate the versatility of PIVOT elements (i.e., viral delivery vectors, MAPS-capable reporters, and host choice) will enable its widespread acceptance as a powerful platform for plant functional genetics. In addition to ORF overexpression, viral vectors can accommodate diverse cargo for eliciting gene perturbations such as guide RNAs[45], and recently, small CRISPR-like genome editors[46]. These examples present an exciting opportunity to adapt future PIVOT iterations for pooled gene knockdown/knockout screens.

Regarding the scope of biological applications, we envision PIVOT will be particularly powerful for (but certainly not limited to) assigning gene function in small molecule-mediated plant signaling pathways. A caveat of PIVOT is that our method requires both the transcriptional reporter and the gene candidates to function properly and integrate with existing signaling pathways in a heterologous host. However, we believe this cross-species screening platform will be amenable for the many signaling pathways that are conserved across the plant kingdom, as demonstrated by our proof-of-concept case investigating cytokinin phosphorelay.

Moreover, PIVOT logic and tools need not be limited to model hosts: dozens of model and crop plants alike have established protocols for protoplast generation, and many characterized, compatible viral vector-host pairs derived from naturally-occurring pathosystems[47] – including monocot hosts[48] – could be harnessed for gene delivery. The virus-based pooled gene delivery and protoplast phenotypic sorting techniques comprising the PIVOT platform provide foundational framework for the future realization of genome-wide cell-based screening in plants.

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Author Contributions
T.N.L, W.B.C., C.T., and E.S.S. contributed to project conceptualization, experimental design, and data analysis. T.N.L, W.B.C., and C.T. performed the experiments. A.E.V, C.C.C and X.J.G. provided the transmembrane domain used to engineer the MAPS-capable receptor; T.N.L. led the manuscript writing with contributions from W.B.C. and E.S.S.

Data Availability
Raw sequencing data will be made available upon publication.

Methods

Cloning Procedures
Barcoded fluorescent protein (FP) libraries: Oligo pools containing N10 random nucleotides (barcodes) flanked by primer binding sites were ordered from Integrated DNA Technologies (IDT). The barcodes were PCR-amplified for ~6 rounds using Invitrogen Platinum SuperFi II PCR Master Mix (ThermoFisher) before insertion into the respective linearized pTRBO-FP backbone using HiFi DNA assembly mix (New England Biolabs). The barcoded pTRBO-FP library was transformed into DH10-beta competent *E. coli* cells (New England Biolabs) and plated on multiple LB-agar plates with 50 ug/mL kanamycin for overnight growth at 37 °C. The next day, between 50-100 colonies across each plate were harvested and combined, and the pooled plasmid DNA was isolated using the Classic Miniprep Kit (Zymo Research). Amplicon sequencing was used to determine the barcodes in the FP library (see *Amplicon Sequencing* & *Data Processing*).

Arabidopsis thaliana Open Reading Frame (ORF) library: ORFs from *At* genes of interest were obtained from The Arabidopsis Information Resource (TAIR). Twist Bioscience synthesized gene fragments with the following syntax for each ORF: [5' primer binding site]-[ORF]-[adapter sequence]-[10-nt unique barcode]-[3' primer binding site]. (See Supplementary Table 2 for sequence information.) ORFs were cloned into a linearized, intron-containing pTRBO backbone using HiFi DNA assembly mix (New England Biolabs). Each pTRBO-*At*ORF construct was individually transformed into DH10-beta competent *E. coli* cells (New England Biolabs) and plated on an LB-agar plates with 50 ug/mL kanamycin for overnight growth. A single colony was picked for outgrowth, and the following day, plasmid DNA was isolated using the Classic Miniprep Kit (Zymo Research). Plasmids were sequence-verified with whole-plasmid sequencing (Plasmidsaurus). Equal concentrations of each pTRBO-*At*ORF construct were combined to generate a pooled *At*ORF plasmid library. For the PIVOT screen, plasmid from the pooled *At*ORF library was combined with intron-containing, barcoded pTRBO-GFP library plasmid (for construction, see *Barcoded fluorescent protein (FP) libraries*

above) for pooled *Agro* transformation (see *Agrobacterium Transformation and Growth Conditions* below).

*Systemic-moving AtORF constructs: At*ORFs were inserted into coat protein-containing viral vectors (pTRBOcp) via restriction cloning. *At*ORFs were PCR-amplified from parent pTRBO-ORF constructs appended with restriction sites compatible with a pTRBOcp vector. *At*ORFs and the pTRBOcp vector were cut with restriction enzymes (New England Biolabs) and ligated with T4 ligase (New England Biolabs), both according to manufacturer's specifications. *E. coli* transformation, plasmid miniprep, and sequencing procedures were performed in the same manner as described above for the *At*ORF library.

***Agrobacterium* Transformation and Growth Conditions**

Individual constructs or pooled plasmids purified from *E. coli* were transformed into *Agrobacterium tumefaciens* (strain GV3101) using either electroporation (preset *Agrobacterium* protocol on BioRad GenePulser Xcell) or the freeze-thaw method. Transformed cell suspension in medium 523 was shaken at ~200 rpm at 30 °C for 2 hours, and the post-outgrowth solution was plated on medium 523-agar plates with 50 µg/mL kanamycin and 30 µg/mL gentamicin at 30 °C for 2 days. For individual constructs, a single colony per construct was picked for overnight clonal outgrowth, while for pooled plasmid libraries, 10^2-10^3 colonies across multiple plates were harvested and combined to ensure full library coverage. The *GV3101* colonies underwent outgrowth in medium 523 with 50 µg/mL kanamycin and 30 µg/mL gentamicin at 30 °C and 200 rpm for ~2 days before *Agro*infiltration preparation. Frozen stocks were prepared for each construct by adding glycerol to the culture to a final concentration of 50%.

***Agro*infiltration**

GV3101 cultures in medium 523 were centrifuged for ~10 minutes at 4,000 x g and resuspended in an infiltration buffer (0.1M MES buffer, pH 5.6, 1M $MgCl_2$). Suspensions were vortexed, measured for Optical Density at 600 nm (OD_{600}), and delivered to the abaxial side of a 4-5 week-old *Nicotiana benthamiana* leaf using a needleless syringe. Figure captions and experiment-specific methods sections specify OD_{600} values used.

Plant Growth Conditions

Nicotiana benthamiana plants were grown indoors at room temperature for ~4-5 weeks before infiltration. Briefly, *N. benthamiana* seeds were sown into fertilized soil and covered for two weeks. Two-week-old seedlings were thinned and covered with a humidity dome for an additional week before acclimating to open-air conditions. Following infiltration, plants were incubated in a growth chamber at 22 °C with 50% humidity under a 16/8 day/light cycle until tissue harvesting.

Confocal Microscopy

N. benthamiana tissue samples were prepared and imaged according to previously reported methods (see ref. 14, Carlson et al., 2023).

Widefield Stereoscope Microscopy for Whole-Leaf Imaging
Fluorescent protein (FP) expression in whole leaves was visualized using Leica THUNDER Imager Model Organism paired with LAS-X software (Leica Microsystems). Clear plastic wrap was used to secure leaves mounted on the microscope stage. Leaves were scanned at 1.25x magnification in "Tilescan" mode in the respective FP channel: CFP (Ex. 436/20 nm; Em. 480/40 nm); YFP (Ex. 510/20 nm; Em. 535/30 nm); mCherry (Ex. 540/40 nm; Em. 593/60 nm); GFP (Ex. 470/40 nm; Em. 525/50 nm). Following mosaic merge, the multichannel image stack was processed using Image J for brightness/contrast adjustments and false coloring.

Protoplasting of *N. benthamiana* Tissue
Cell wall digestion buffer (DB) was prepared fresh on the day of protoplasting: MES buffer (20mM, pH 5.7), mannitol (400mM), and KCl (20 mM) were combined with cellulase R-10 (1%) and macerozyme R-10 (0.4%) and heated for 10 minutes at 55 °C. The solution was cooled to room temperature before adding $CaCl_2$ (10mM) and BSA (1%). *N. benthamiana* leaf tissue was sliced into 0.5-1mm strips using a razor blade, transferred into a 6-well plate, and submerged in DB. A desiccator was used to vacuum infiltrate the DB into leaf strips for 30 minutes. Tissue underwent digestion in the dark for 3-4 hours on a plate shaker at 30 °C and 50 rpm. Digested cells were passed through a 100 µm filter, washed in an enzyme-free cell wash buffer (CWB: 20 mM MES buffer, pH 5.7; 20 mM KCl, 10mM $CaCl_2$, and 0.5% BSA), and pelleted by centrifugation at 100 x g. A small aliquot of protoplasts resuspended in CWB was stained with Fluorescein Diacetate (FDA) to count live cells using a BioTek Cytation 5 Cell Imaging Multimode Reader (see *Cell Counting and Fluorescence Microscopy of Protoplasts*). Biological replicates were normalized to the desired protoplast concentration (typically between 150-300k cells/mL).

Magnetic-activated Protoplast Sorting (MAPS)
Immediately following harvesting (see *Protoplasting of N. benthamiana Tissue*), *N. benthamiana* protoplasts were incubated with Promega HaloTag® PEG-Biotin Ligand (2 µL per 2 mL protoplasts) with end-to-end rotation for 1 hour. Protoplasts were then pelletted at 100 x g and washed multiple times with cell wash buffer (CWB) to remove excess ligand. Ligand-bound protoplasts were incubated with CWB-washed, magnetic Dynabeads MyOne T1 Streptavidin beads (ThermoFisher, 20 µL per 100k protoplasts) with end-to-end rotation for 1 hour. An aliquot of bead-bound protoplasts before magnetic sorting was saved as the "Input" fraction. The remainder of the protoplast population was subject to sorting using a StemCell Technologies magnet. Protoplasts bound to the magnet were washed with CWB three times. The first two washes were kept as the "Unbound" fraction, the final wash was discarded, and the remaining protoplasts were resuspended in CWB ("Bound" fraction). Aliquots of "Input","Unbound", and "Bound" populations were imaged using a BioTek Cytation 5 Cell Imaging Multimode Reader when applicable, and the remaining cell pellets were frozen for RNA extraction.

Cell Counting and Fluorescence Microscopy of Protoplasts

Protoplasts were visualized and counted using a BioTek Cytation 5 Cell Imaging Multimode Reader paired with BioTek Gen5 Imaging software (Agilent Technologies).

Protoplast counting: a 50 µL aliquot of protoplasts diluted to 1 mL in cell wash buffer (CWB) was incubated with Fluorescein Diacetate (FDA, ThermoFisher) (2 µL per 1 mL diluted protoplasts) for 5-10 minutes in the dark. Protoplasts were then pelleted by centrifugation at 100 x g and washed with CWB to remove excess FDA stain. Triplicate 200 µL aliquots of FDA-stained protoplasts were loaded in a 96-well black-sided, clear bottom plate (Corning) and imaged using a 4x objective in the GFP channel (Ex. BP 469/35 nm; Em. BP 525/39 nm). Live protoplast counts were gated based on the following post-image processing parameters (Size: 15-100 µm; Circularity: >0.5; Fluorescence: >5000).

Protoplast fluorescence microscopy: Following cell sorting, 200 µL aliquots of MAPS Input, Unbound, and Bound fractions were loaded in a 96-well black-sided, clear bottom plate and imaged using a 4x objective in GFP (Ex. BP 469/35 nm; Em. BP 525/39 nm) and RFP (Ex. BP 531/40 nm; Em. BP 593/40 nm) channels. For each fluorescence channel, protoplast counts were gated based on the following post-image processing parameters (Size: 15-100 µm; Circularity: >0.5; Fluorescence: >5000). ImageJ was used for brightness/contrast adjustments and false coloring.

RNA Extraction and Preparation of complementary DNA (cDNA)

N. benthamiana tissue was flash-frozen and ground by hand in 2-mL Eppendorf tubes using plastic pestles. RNA was extracted using a RNeasy Plant Mini Kit (Qiagen) and purified using a RNase-free DNase set (Qiagen). RNA concentration was measured using Nanodrop and normalized across samples (typically to 1000 ng). cDNA was prepared using the SuperScript IV First-Strand Synthesis System (ThermoFisher); random hexamers were used to amplify virus-encoded, barcoded ORF RNAs in library representation experiments (Figure 3 and Supplementary Figure 4) and the PIVOT screen (Figure 5C), while oligo dT primers were used to amplify TCSn transcript (Figure 5F) and endogenous *N. benthamiana* RNAs (Figure 5H), respectively, before qPCR analysis.

Amplicon Sequencing & Data Processing

When applicable, first-strand cDNA was amplified by PCR using library-specific primers (see Supplementary Table 4) with Platinum SuperFi II PCR Master Mix (ThermoFisher) and purified using a DNA Clean & Concentrator kit (Zymo Research). Plasmid or amplified cDNA (25 µL of 20 ng/uL) was sent to Azenta Life Sciences for Amplicon-EZ Next Generation Sequencing. Paired-end sequencing reads were processed and separated by barcode using Geneious Prime Bioinformatics software. Raw read counts were normalized to between 1-3 x 10^5 total reads per replicate depending on the experiment before graphical analysis (see figure captions in Supplementary Tables 5-7 for details). A single sample was sequenced for *E. coli* and *Agro* plasmid samples, and figure and table captions indicate the number of sequenced replicates (3 or 4) for leaf cDNA reads.

Calculation of MAPS Enrichment Ratios
For the proof-of-concept protoplast sorting experiment (Figure 4), MAPS enrichment ratio was calculated by dividing the Cytation 5-derived cell counts (see *Cell Counting and Fluorescence Microscopy of Protoplasts*) for the Bound fraction by the Unbound fraction for each replicate. For the PIVOT screen (Figure 5), Bound and Unbound reads were normalized (see *Amplicon Sequencing & Data Processing*), and for each replicate, the number of Bound reads was divided by Unbound reads. For the PIVOT screen p-values (Figure 5C, Supplementary Tables 3 and 8), a one-sample, two-tailed *t*-test was performed comparing the MAPS enrichment ratios for each *At*ORF and GFP ORF (four replicates) to the mean MAPS enrichment ratio for the GFP population (n = 52, theoretical mean = 0.8980).

Leaf Spot Assays for Validating PIVOT Screen Hits
*At*ORFs chosen for further inquiry following the PIVOT screen were individually transformed into *Agro* GV3101. Each pTRBO-encoded ORF *Agro* strain was mixed with an *Agro* strain harboring the TCSn-mCherry reporter construct at *Agro* OD_{600} values of 0.1 and 0.5, respectively, and infiltrated in a ~15mm diameter spot on a 4-6-week-old *N. benthamiana* leaf. At four DPI, the abaxial side was imaged using an Invitrogen iBright FL1500 Imager (ThermoFisher). ImageJ was used for brightness/contrast adjustments, false coloring, and fluorescence quantification. After imaging, three 0.7 cm leaf punches for each construct were harvested for ensuing RNA extraction and qPCR analysis.

Systemic Overexpression of CRFs in *Nicotiana benthamiana*
Select CRFs and ARR controls were cloned into coat protein-containing virus vectors (pTRBOcp) that enabled systemic movement of the virus-encoded constructs. pTRBOcp-*At*ORFs were agroinfiltrated (OD_{600} = 0.5) into the third youngest leaf (deemed L0) of individual 4-week-old *N. benthamiana* plants. The ORF-containing virus spread throughout the plant for 13 days, at which point the fourth leaf above L0 (deemed L4) was harvested for endogenous transcript (qPCR) analysis.

Quantitative PCR (qPCR) for Synthetic Reporter and Endogenous Transcript Analysis
Primer design for detecting endogenous N. benthamiana transcripts: Sol Genomics Network nucleotide BLAST tool was used to query coding sequences of *Arabidopsis thaliana* type-A response regulators (RRs) for *N. benthamiana* homologs. Within the region of greatest homology in the top *N. benthamiana* candidate, primers (~20nt in length; annealing temp: 59-60 °C) were designed to amplify an ~120-150nt region. The NCBI primer design tool (https://www.ncbi.nlm.nih.gov/tools/primer-blast/) was used to avoid off-target binding and primer pair self-complementarity. See Supplementary Table 4 for qPCR primers used.

qPCR: First-strand cDNA (~50 ng/µL) was diluted 1:5 to ensure the sample concentration was in the linear range of the primer set efficiency[49]. Diluted cDNA mixed with the appropriate primers (final concentration: 0.25 mM) and SensiMix™ SYBR® Hi-ROX was PCR-amplified using an Applied Biosystems™ QuantStudio™ 6 Pro (ThermoFisher). *N. benthamiana* Protein Phosphatase 2A (PP2A) was used as a

housekeeping gene[50], and the $2^{-\Delta\Delta CT}$ method[51] was used to calculate transcript fold change values.

Statistical Tests

Statistical tests were performed as described in figure captions using GraphPad Prism Version 10.4.2 (534). For unpaired, two-way *t*-tests, F test was used to ensure equal variances, except for Figure 5C, where discrepancy is reported instead. For ANOVA, Brown-Forsythe test was used to ensure there was no statistically significant differences in standard deviations amongst the tested groups. If variances were deemed equal, with Tukey's multiple comparisons test was used. If variances were unequal, Welch's ANOVA with Dunnett's T3 multiple comparisons test was used. Additional parameters for all null hypothesis testing can be found in Supplementary Table 8.

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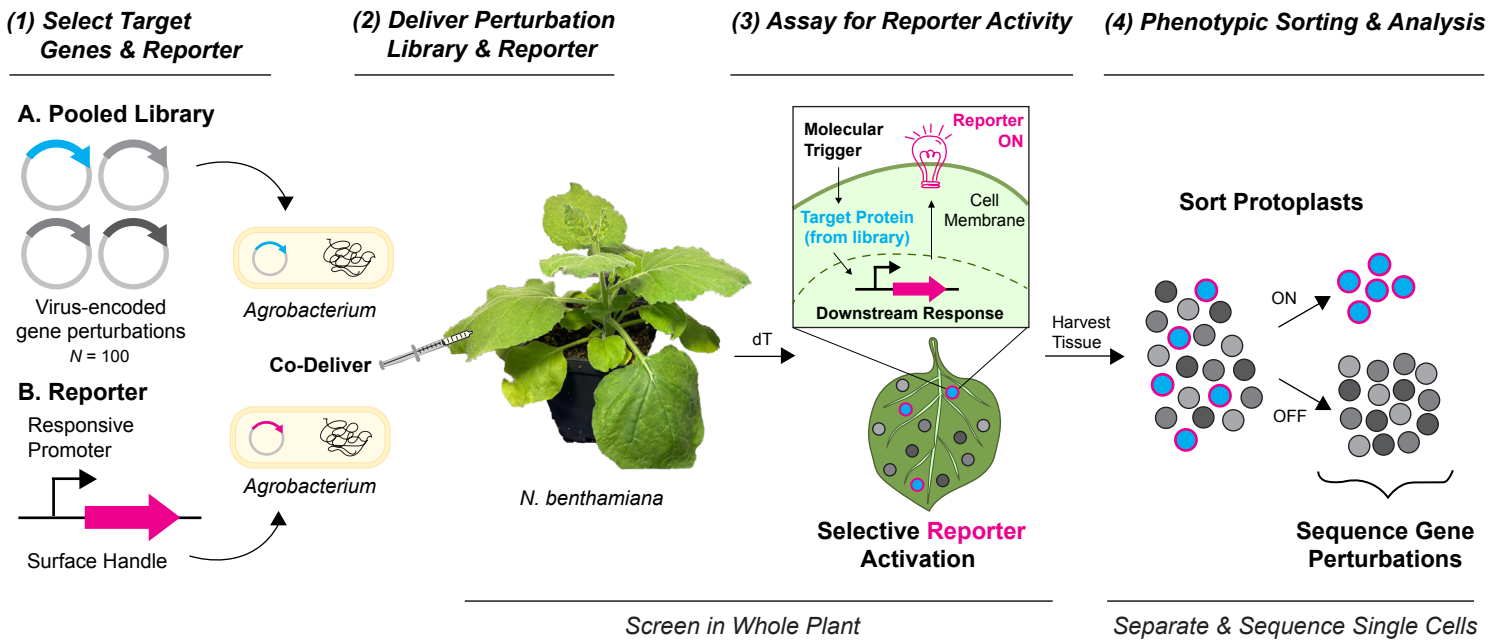

Figure 1. PIVOT Workflow for Pooled Genetic Screens in *Nicotiana Benthamiana*. (Steps 1 & 2) *Agrobacterium* strains harboring virus-encoded gene perturbations or a selectively responsive reporter are co-delivered into a mature *N. benthamiana* leaf. (Step 3) Following a molecular trigger and incubation period, some gene perturbations cause reporter activation. (Step 4) Single cells (protoplasts) are harvested from leaf tissue, sorted by reporter activity, and sequenced to link phenotype to gene perturbation.

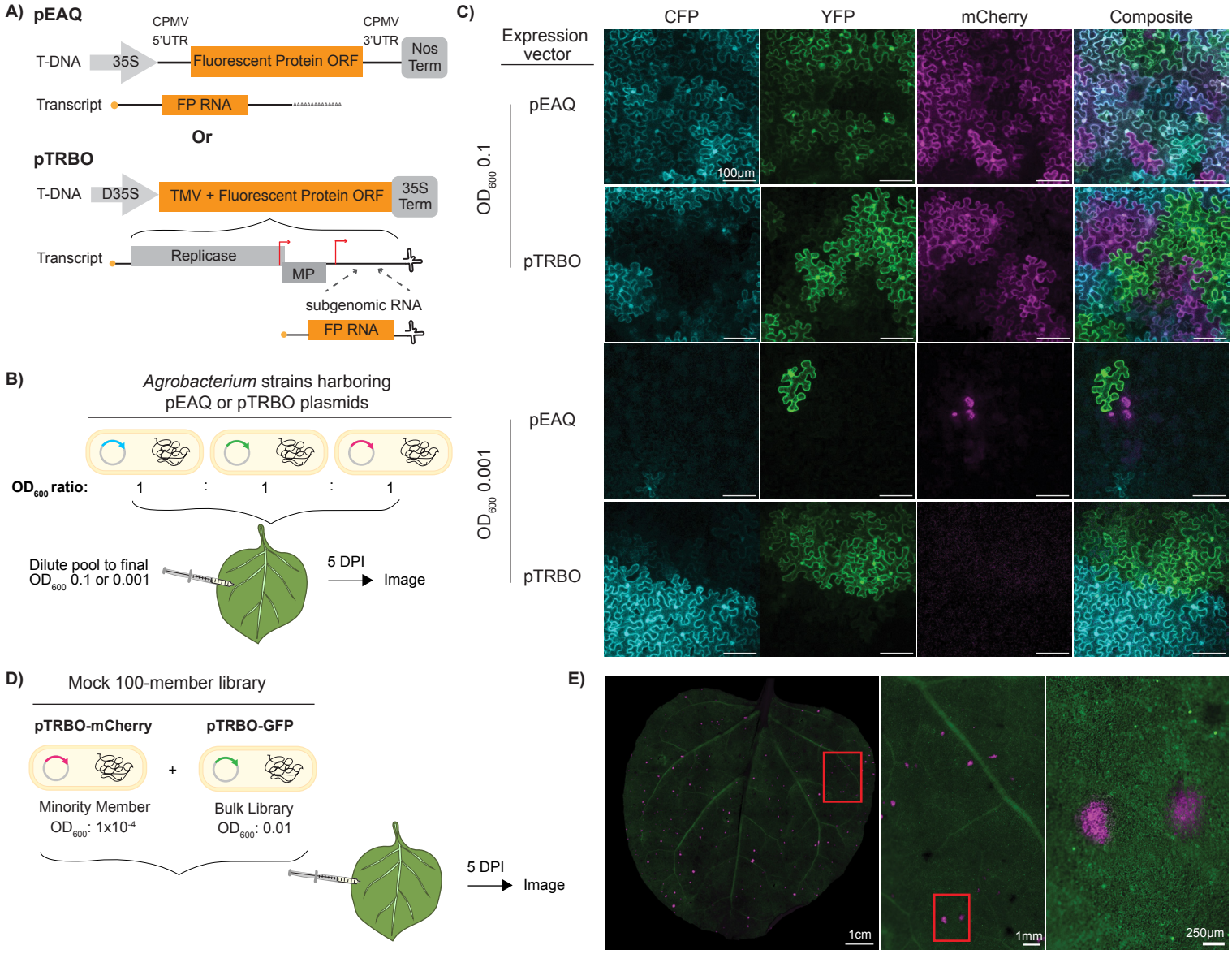

Figure 2. Virus-based open reading frame (ORF) expression enables pooled library delivery *in planta* while limiting the expression of multiple ORFs per cell. (A) Abbreviated plasmid maps showing *Agro*-delivered Transfer DNA (T-DNA) and in-leaf produced transcript from pEAQ and pTRBO vectors. pEAQ T-DNA directly encodes a fluorescent protein (FP) ORF flanked by cowpea mosaic virus (CPMV)-derived untranslated regions (UTRs), while pTRBO T-DNA encodes tobacco mosaic virus (TMV) with a FP ORF inserted after an engineered 3' subgenomic promoter (red); MP = movement protein. (B) Workflow for pooled fluorescent protein (FP) delivery using either pEAQ or pTRBO vectors: individual FP *Agro* strains were combined at equal 600 nm optical densities (OD_{600}), and the mixture was diluted to high (0.1) or low (0.001) final OD_{600} for delivery into *N. benthamiana* leaves. (C) Confocal microscopy of *N. benthamiana* tissue five days post infiltration (DPI) of pooled FP delivery. (D) Workflow for pooled delivery of a mock 100-member library: *Agro* strains harboring pTRBO-mCherry (minority member; OD_{600}: $1x10^{-4}$) and pTRBO-GFP (bulk library; OD_{600}: 0.01) were mixed for pooled delivery into *N. benthamiana* tissue. (E) Widefield stereoscope images at increasing magnification of *N. benthamiana* leaf five DPI with mock 100-member FP library.

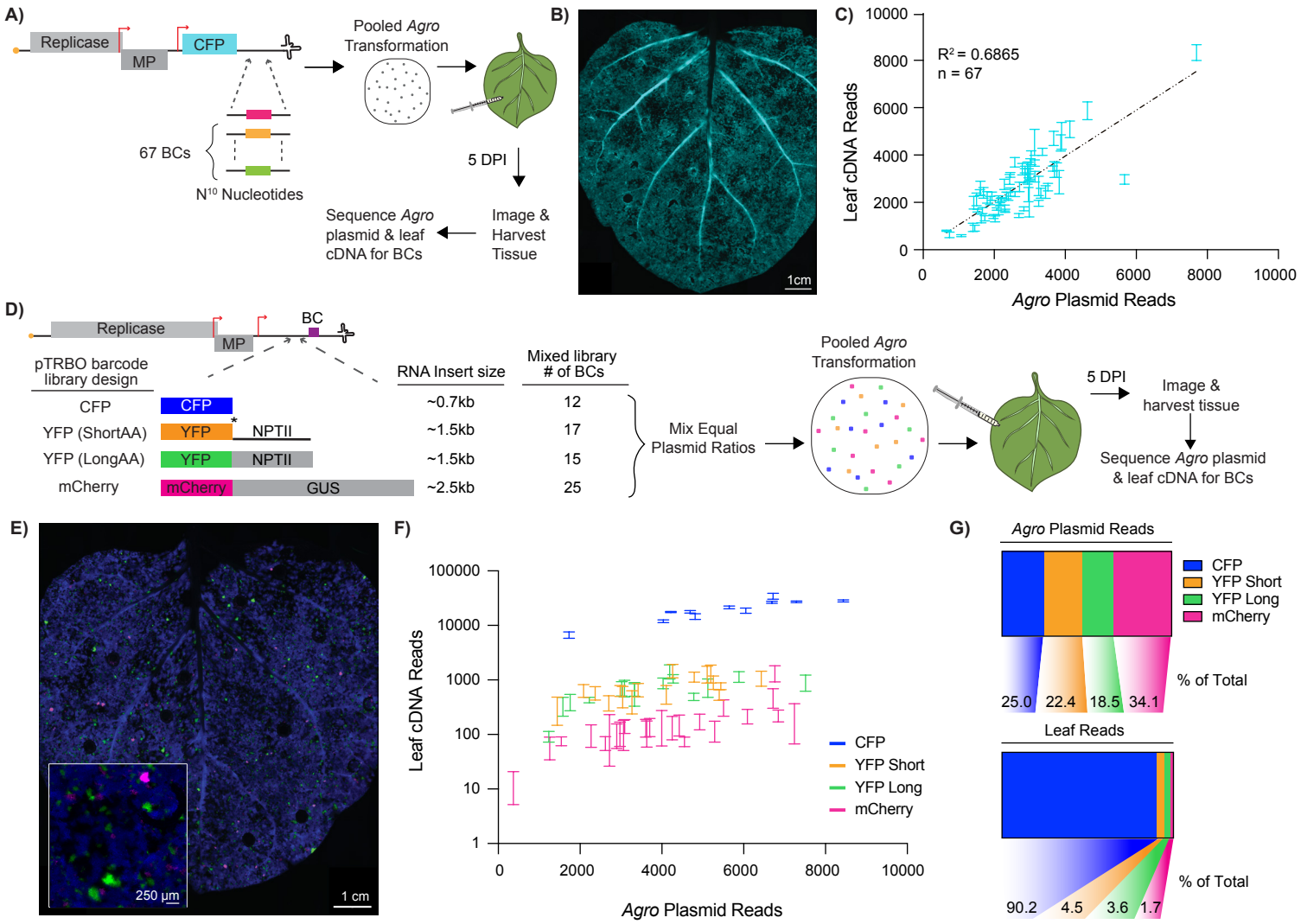

Figure 3. Quantification of representation dynamics for virus-delivered ORF library members. (A) Workflow for quantification of in-leaf barcodes for viral-delivered, equal ORF length library: 67-individually barcoded pTRBO-CFP plasmids were pooled for transformation into *Agro* and infiltrated into *N. benthamiana* (OD_{600} = 0.01). Leaf RNA was extracted five DPI. Plasmid DNA and leaf-derived cDNA were sequenced for barcode quantification. (B) Widefield stereoscope image of pTRBO-CFP-infiltrated *N. benthamiana* leaf at five DPI. (C) Plot of barcode reads before infiltration (*Agro* Plasmid) and five DPI (Leaf cDNA). Each mark represents the standard deviation of 3 replicate reads for an individual pTRBO-CFP barcode, n = 67. Dotted line indicates linear regression, R^2 = 0.6865. (D) Workflow for quantification of in-leaf barcodes for viral-delivered, mixed size library: pools of barcoded fluorescent proteins (FPs) appended with additional RNA cargo were cloned into the pTRBO-vector. An equal plasmid ratio of each pTRBO-FP sub-library was combined for pooled *Agro* transformation and subsequent delivery into *N. benthamiana* (total OD_{600} = 0.01). (E) Widefield stereoscope, merged channel image of *N. benthamiana* leaf five DPI with mixed size pTRBO-FP pooled library. Increased magnification insert in bottom left corner. (F) Plot comparing barcode representation before infiltration (*Agro* Plasmid Reads) and five DPI (Leaf cDNA Reads). Each mark represents the standard deviation of 3 replicate leaf reads for an individual pTRBO-FP barcode. See (D) for sample size of each pTRBO-FP library. (G) Part-of-whole charts demonstrating input (*Agro*, top) and output (Leaf, bottom) representation of each pTRBO-FP sub-library.

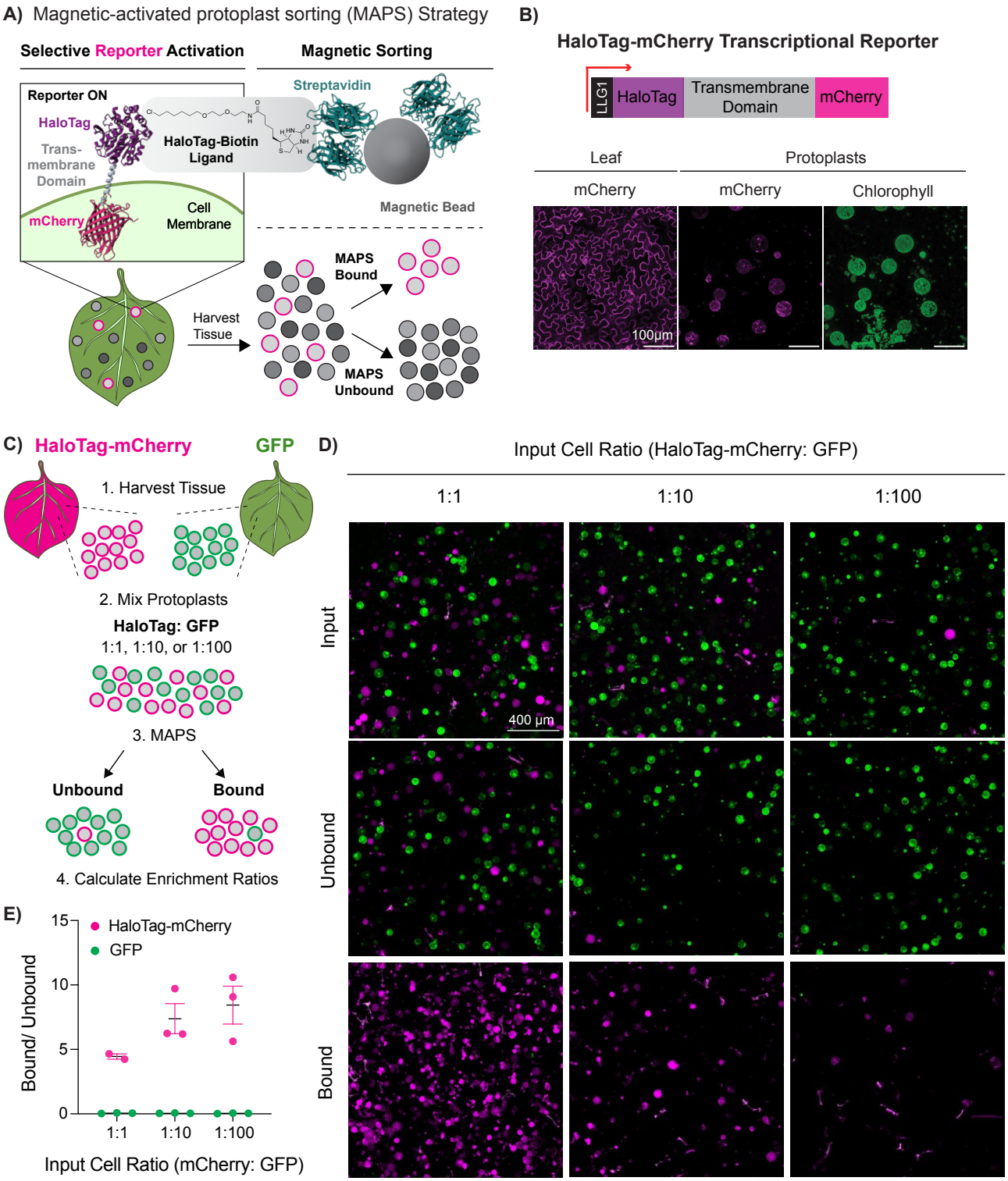

Figure 4. A surface-expressed engineered receptor enables Magnetically-activated protoplast sorting (MAPS) of target cells in mixed protoplast populations. (A) MAPS strategy: exogenously added ligand and magnetic beads are used to isolate cells of interest (pink) harboring a selectively expressed cell surface receptor. (B) Abbreviated vector map of a MAPS-capable transcriptional reporter: a promoter of interest (red) drives transcription of HaloTag, which is fused to mCherry for visualization; the signal peptide, LLG1, directs HaloTag to the cell surface, where it is stabilized by a transmembrane domain. Confocal microscope images of infiltrated tissue and protoplasts demonstrating the surface localization of the transcriptionally-encoded HaloTag receptor. (C) Workflow for MAPS selectivity experiments: protoplasts harvested from HaloTag-mCherry (receptor-positive, pink) or GFP (receptor-negative, green)-infiltrated *N. benthamiana* leaves (OD_{600}: 0.5) were combined in HaloTag:GFP ratios of 1:1, 1:10, or 1:100, respectively, and then separated using MAPS. (D) Representative fluorescence microscopy images of mixed protoplast populations before (Input) and after (Unbound, Bound) MAPS. See Supplementary Figure 3 for source whole-well images. (E) Enrichment ratios (Bound/Unbound) for GFP versus HaloTag-harboring cells following MAPS. Mean and standard error of the mean enrichment ratios plotted are based on cell counts from 2 or 3 replicates.

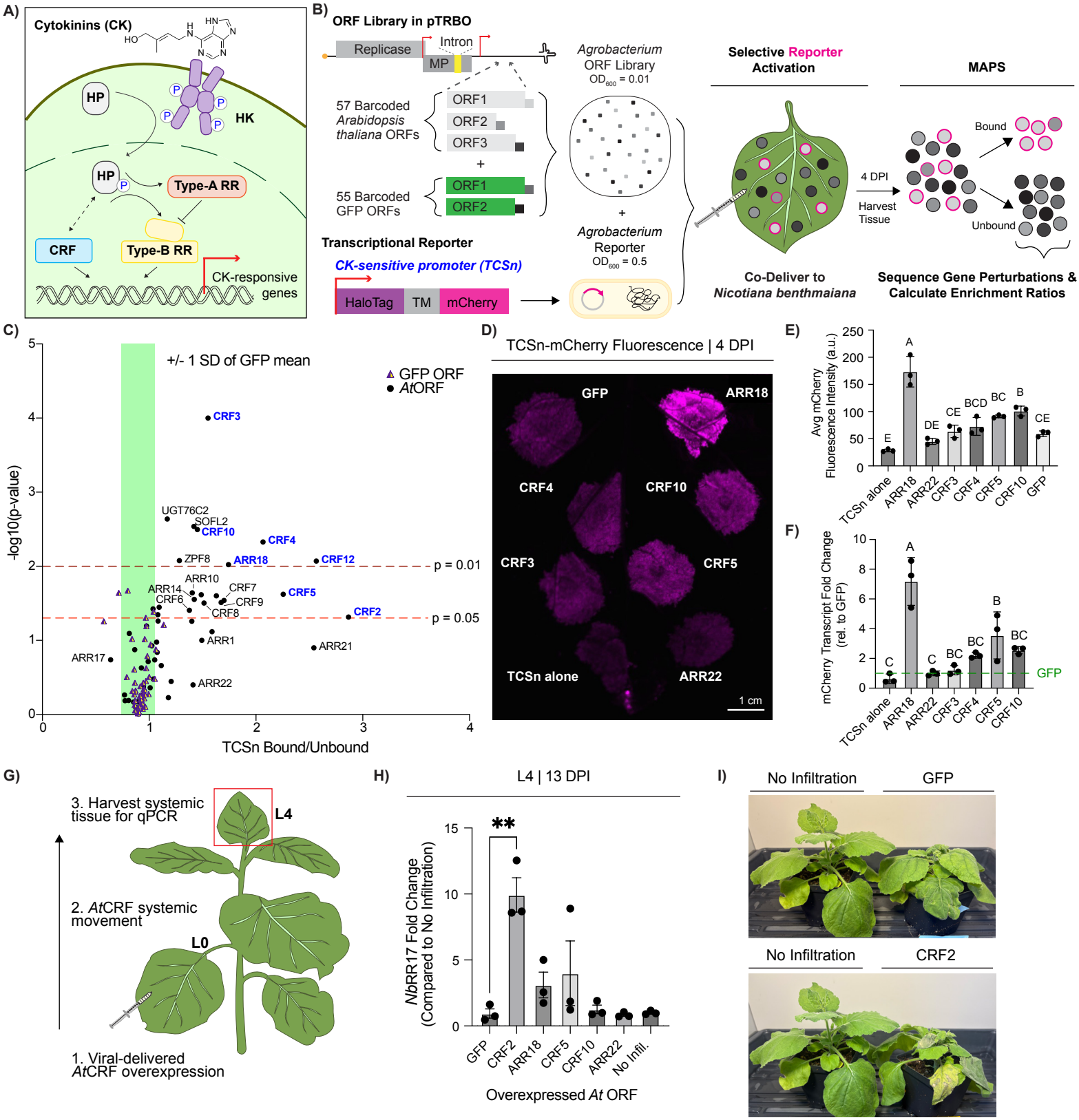

Figure 5. Proof-of-concept PIVOT screen recapitulates CRFs as positive modulators of cytokinin signaling. (A) Abbreviated cytokinin signaling cascade: upon sensing cytokinins (CK), activated histidine kinase (HK) receptors transfer a phosphate group to histidine phosphotransfer (HP) proteins, causing nuclear translocation of HPs. Nuclear HPs can phosphorylate positive (type-B) or negative (type-A) response regulators (RRs). HPs interact with cytokinin response factors (CRFs), but direct phosphorylation has not been shown. CRFs and type-B RRs share some downstream cytokinin-responsive transcriptional targets. (B) Workflow for pooled ORF overexpression screen in *Nicotiana benthamiana*: 57 barcoded *Arabidopsis thaliana* ORFs and 55 barcoded GFP ORFs individually cloned into intron-containing pTRBO vectors were combined for pooled *Agro* transformation and co-delivered into a *N. benthamiana* leaf with a MAPS-capable transcriptional reporter driven by the established cytokinin-sensitive TCSn promoter. Individual *At*ORF activity yields differential reporter activation (pink), generating a marker upon which to sort protoplasts by MAPS. MAPS Bound and Unbound populations are sequenced for barcodes to calculate enrichment ratios for each library

member. (C) Volcano plot demonstrating the average of four replicate MAPS enrichment ratios (TCSn Bound/Unbound) for each barcoded GFP (purple triangles, n = 52) or *At*ORF (black circles, n = 52) in the PIVOT screen described in (B). Statistical significance (p-value) derived from independent one-sample, two-tailed *t*-tests comparing the GFP mean MAPS enrichment ratio to that of each barcoded query (See “Calculation of MAPS Enrichment Ratios” in *Methods* for details). Green bar represents +/- 1 standard deviation of the GFP mean enrichment ratio (0.8980 +/- 0.1553), and the light and dark red lines denote p = 0.05 and p = 0.01 significance, respectively. (D) Representative whole-leaf fluorescent image of post-screen leaf spot assay where *At*ORF candidates were individually assessed for activation of the TCSn reporter. (E) Mean and standard deviation of three repeat measure fluorescence values derived from the leaf image in panel D. Letters signify statistically significant ANOVA groups from a Tukey’s multiple comparisons test. (F) Quantification of mCherry reporter transcript in tissue harvested from leaf spots shown in (D). Transcript quantifications were normalized to a GFP control. Each dot represents the mean of 3 replicates from an independent experiment. Letters signify statistically significant ANOVA groups from a Tukey’s multiple comparisons test. (G) Workflow for assessing CRF-upregulated genes: ORFs of *At*CRFs were cloned into pTRBO vectors capable of systemic movement and delivered to a *N. benthamiana* leaf. At 13 days post infiltration (DPI) in L0, L4 tissue was harvested for qPCR-based transcript analysis. (H) Mean and standard error of the mean fold change of *N. benthamiana* Response Regulator 17 (*Nb*RR17) for three replicates following systemic overexpression of an *At*ORF. Asterisk indicates significance for two-tailed, unpaired t-test between individual query and GFP, ** $p < 0.01$. (I) Representative images of *N. benthamiana* plants 13 DPI with a virus control (pTRBO-GFP) or pTRBO-CRF2 compared to a non-infiltrated plants.