Cell-type-specific execution of effector-triggered immunity

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Summary

Effector-triggered immunity (ETI) is a central component of host defense, but whether all cell types execute ETI similarly remains unknown. We combined chemically imposed immune activation with single-cell transcriptomics to profile ETI responses across all leaf cell types in Arabidopsis. Despite uniform ETI perception, we find striking divergence between transcriptional outputs: a core set of defense genes is broadly induced, while distinct cell types activate specialized immune modules. We infer that downstream immune execution is shaped not only by immune receptor activation, but also by cell identity and its associated transcriptional regulatory context, including local transcription factor availability and chromatin accessibility. We further demonstrate that transcriptional regulators preferentially induced in epidermal cells are required to restrict invasion by non-adapted pathogens. Their absence permits pathogen entry into deeper tissues despite intact recognition, revealing a spatial division of immune functions. Our findings uncover a layered immune architecture in plants, challenges the assumption of uniform immune execution, and provides a framework for exploring cell-type-specific resistance logic in multicellular hosts.

Key words

Effector-triggered immunity (ETI), cell-autonomous immunity, cell-type-specific immunity, single-cell RNA sequencing, transcriptional regulation

Introduction

In multicellular organisms lacking adaptive immunity, such as plants, immune responses are largely cell-autonomous: each cell must independently perceive and counter pathogenic threats in the absence of mobile immune cells[1]. While this principle has long shaped our understanding of plant defense, recent studies highlight the importance of intercellular communication in modulating local responses and coordinating systemic immunity[2–4]. Nevertheless, how immune execution at the resolution of individual cell types remains poorly understood. Specifically, it is unknown whether all plant cell types engage immune programs equivalently, or whether transcriptional responses are modulated by cell identity, developmental state, or physiological role.

Effector-triggered immunity (ETI), mediated by intracellular nucleotide-binding leucine-rich repeat (NB-LRR) receptors (NLRs), is a core component of plant innate immunity. Upon recognizing pathogen-derived effectors, ETI activates a robust transcriptional response that drives defense gene expression, cell wall fortification, immune metabolite production, and often culminates in a localized cell death[5]. While ETI is widely regarded as a canonical and system-wide immune program, most insights to date stem from bulk tissue measurements or natural infections, where immune activation is spatially heterogeneous and confounded by pathogen distribution and pattern-triggered immunity (PTI), mediated by cell-surface immune receptors. These limitations have obscured a fundamental question: Do all plant cell types execute ETI similarly when immune activation is synchronized?

Recent studies have begun to explore immune responses at single-cell resolution. For example, single-cell profiling of *Pseudomonas syringae*-infected Arabidopsis leaves revealed transcriptional shifts linked to pathogen proximity[6], and fungal infection studies have identified cell-type-specific defense signatures under biotic stress[7]. Most recently, the concept of a primary immune responder (PRIMER) cell state was proposed, based on single-cell RNA-seq analysis of ETI-inducing bacterial infections during which host cells experience PTI, ETI and also defense suppression via pathogen effectors[8]. While these studies have uncovered valuable spatial features of plant immunity, they are inherently confounded by pathogen load, PTI co-activation, and the spatial unpredictability of natural infections.

To overcome these limitations, we established a synthetic system for uniform and pathogen-free ETI induction using estradiol-triggered NLR activation in Arabidopsis[9]. Combining this with single-cell RNA sequencing, we constructed a high-resolution atlas of ETI-responsive transcriptional states across major leaf cell types. Our analysis uncovered a layered immune architecture: despite of a shared core transcriptional response activated across all cell types, ETI responses were shaped by local gene regulatory networks in cell-type-specific transcriptional modules, demonstrating a complementary mechanism between both. This suggests that immune execution

is not merely a product of perception but is also intrinsically constrained by cell identity and chromatin context.

To directly test whether cell-type-specific transcriptional modules are functionally required for immune execution, we focused on CAMODULIN-BINDING PROTEIN 60 G (CBP60g) and SYSTEMIC ACQUIRED RESISTANCE DEFICIENT 1 (SARD1), two closely related transcription factors known to act downstream of NLR signaling. Both have been established as central regulators of salicylic acid biosynthesis and systemic acquired resistance during ETI [10–13]. Strikingly, our single-cell data revealed their preferential induction in pavement cells, the epidermal layer that interfaces directly with the external environment. This was particularly intriguing in the context of enabling a non-adapted *Albugo candida*, isolate to invade Arabidopsis through stomata that would normally be resisted. While guard cells form the stomatal pore, it is the surrounding pavement cells that must constrain early pathogen entry. We hypothesized that CBP60g and SARD1 may act as key mediators of spatial immune execution in this vulnerable layer. Supporting this, we found that *cbp60g sard1* mutants permitted haustoria formation by *A. candida* specifically in the epidermal and sub-epidermal cells, despite intact immunity in internal tissues. This provides direct evidence that cell-type-specific transcriptional activation, rather than receptor activation alone, is required to restrict nonhost pathogen ingress.

Together, our findings redefine our understanding of immune coordination in plants, not as a uniform switch, but as a mosaic of modular, spatially distributed programs embedded within tissues. By decoupling immune activation from pathogen-associated variables and resolving transcriptional responses at cellular scale, this work has broad implications for how multicellular hosts orchestrate defense and opens avenues for engineering more precise and spatially tuned immune activation in multicellular systems, including crops.

Results

ETI activation defines distinct immune-responsive cell clusters

To profile the transcriptional landscape of effector-triggered immunity (ETI) at single-cell resolution, we developed a synthetic ETI activation system in *Arabidopsis thaliana* (Arabidopsis thereafter) leaves using estradiol (E2)-inducible expression of *AvrRps4*, a bacterial effector recognized by the nucleotide-binding leucine-rich repeat (NB-LRR) receptor (NLR) pairs, RESISTANT TO RALSTONIA SOLANACEARUM 1 (RRS1)/RESISTANT TO PSEUDOMONAS SYRINGAE 4 (RPS4) and RRS1B/RPS4B, referred to as the SUPER ETI (SETI) line[9,14]. Leaves of the SETI plants were infiltrated with mock or E2 solution, and protoplasts were isolated 4 hours post-infiltration (hpi) for single-cell analysis (Figure 1A). Real-time quantitative PCR confirmed robust induction of one of the ETI early responsive marker genes, *ISOCHORISMATE SYNTHASE 1* (*ICS1*) (Figure 1B)[15,16], validating effective immune activation.

We performed single-cell RNA sequencing (scRNA-seq) on protoplasts from mock and E2 treated samples using the 10X Genomics Chromium X platform and obtained approximately 300 million reads. After quality control, we recovered 7932 and 5739 high-quality cells in the mock- and E2-treated samples, respectively, with a median of 527 and 1134 genes and 776 and 2153 unique transcripts per cell, recovering approximately 70% of annotated protein-coding genes in the Arabidopsis genome. ETI activation led to notable changes in the relative abundance of specific cell types (Figure S2A), possibly reflecting global transcriptional reprogramming.

Unsupervised graph-based clustering identified 16 major cell clusters after integration of mock and E2 treated samples, visualized using uniform manifold approximation and projection (UMAP) (Figure 1C and 1D). Cells from both mock and E2 conditions were represented across clusters (Figure S1A and B). To assign cell identities, we leveraged a recently published single-cell atlas of Arabidopsis leaf tissue and the well-known canonical marker genes[17]. A violin plot of selected cell-type-specific genes (Figure S1C) confirmed robust classification of 16 clusters corresponding to nine distinct cell types, with a predominant mesophyll identity (clusters M1–M8) along with pavement cells (epidermal cells), bundle sheath, hydathode, phloem, and other known leaf cell types (Figure 1D).

Together, these data establish a comprehensive single-cell atlas of early ETI activation across Arabidopsis leaf tissue, in the absence of PTI, providing a foundation for dissecting immune responses at cellular resolution without confounding pathogen-derived heterogeneity or defense suppression.

Uniform immune activation elicits heterogeneous transcriptional responses

To dissect the spatial pattern of immune execution, we examined the expression of canonical immune and susceptibility genes across annotated cell types. Core components of the Toll/Interleukin-1 receptor/Resistance protein (TIR) NLR immune signaling cascades including *ENHANCED DISEASE SUSCEPTIBILITY 1* (*EDS1*), *PHYTOALEXIN DEFICIENT 4* (*PAD4*) and *SENESCENCE ASSOCIATED GENE 101* (*SAG101*) were broadly expressed, along with downstream helper NLR encoding genes, *ACTIVATED DISEASE RESISTANCE 1* (*ADR1*), *ADR1-L1, ADR1-L2*, *N REQUIREMENT GENE 1.1* (*NRG1.1*) and *NRG1.2* (Figure 2A)[18], with *ADR1* and *NRG1.2* exhibiting relatively sparse expression. This widespread expression suggests that the EDS1-dependent module is transcriptionally accessible across the entire leaf tissue, equipping most cell types to mount ETI responses upon intracellular effector recognition.

Consistently, the phytohormone salicylic acid (SA) biosynthesis pathway[19], downstream of EDS1 signaling, was also globally activated. Genes including *ICS1*, *EDS5* and *AVRPPHB*

153 *SUSCEPTIBLE 3* (*PBS3*) were robustly expressed across nearly all cell clusters (Figures 2A, S2B
154 and S2C)[19], in line with broad SA pathway activation previously observed in ETI[16,20]. The
155 widespread induction of *ETHYLENE INSENSITIVE 2* (*EIN2*) further supports the notion of a
156 tissue-wide immune readiness (Figure 2A). Notably, negative immune regulators such as Nudix
157 hydrolase encoding genes, *NUDTs*, and *CALMODULIN-BINDING TRANSCRIPTION*
158 *ACTIVATORs* (*CAMTAs*) were also broadly induced (Figure 2A), indicating that immune
159 repression mechanisms are similarly embedded across the tissue.
160
161 Moreover, key signaling components that mediate the mutual potentiation between PTI and ETI,
162 including shared protein kinases and transcriptional regulators[14], were also ubiquitously
163 expressed (Figure S3A). This suggests that all cells in Arabidopsis leaves harbor an immunity-
164 supporting infrastructure that is transcriptionally primed to interpret and integrate diverse immune
165 cues.
166
167 In contrast to these broadly distributed immune modules, we identified marked spatial restriction
168 in the expression of N-hydroxy pipecolic acid (NHP) biosynthesis genes. Specifically, *AGD2-LIKE*
169 *DEFENSE RESPONSE PROTEIN 1* (*ALD1*) and *FLAVIN-CONTAINING MONOOXYGENASE 1*
170 (*FMO1*), which encodes enzymes catalyzing the first and last steps in NHP production[21–23], were
171 almost exclusively expressed in companion cells (Figures 2A, and S2D and S2E), consistent with
172 recent findings[8]. Surprisingly, *SYSTEMIC ACQUIRED RESISTENCE DEFICIENT 4* (*SARD4*),
173 which encodes the oxidoreductase catalyzing the intermediate step of NHP biosynthesis[21,24],
174 exhibited widespread expression (Figure S2F), suggesting a division of labor wherein companion
175 cells complete NHP biosynthesis to support systemic signal propagation. These findings indicate
176 a spatial configuration of NHP biosynthesis and reinforce the role of companion cells as
177 specialized immune hubs for systemic acquired resistance (SAR)-related metabolites.
178
179 We also observed cell-type-restricted expression for genes in the jasmonic acid (JA) signaling
180 pathway and members of the E2F transcription factor family (Figure 2A), previously implicated in
181 cell cycle control and immune regulation[15,25,26]. These results suggest that hormone signaling, and
182 proliferation-linked regulators may modulate ETI output in a spatially restricted and context-
183 dependent manner. For instance, loss-of-function of *E2Fa/b/c* compromises ETI responses
184 mediated by both TIR and coiled-coil (CC) NLRs[26].
185
186 Importantly, because our system triggers ETI uniformly and in a pathogen-free manner[9], it offers
187 a unique opportunity to examine whether immune-enhanced cell states, such as primary immune
188 responder (PRIMER) and bystander cell states[8], can arise independently of pathogen spatial
189 distribution. We observed broad induction of the trihelix transcription factor encoding gene, *GT-*
190 *MOTIF BINDING FACTOR-3A* (*GT-3A*)[27], a canonical marker of the PRIMER cell state[8], across

all ETI-activated cell types (Figure 2A), consistent with its role as a general ETI-responsive gene. This confirms that *GT-3A* expression reflects the proximity to pathogens that can induce robust cell-autonomous ETI. In contrast, its close homologues *GT-3B* and *GT-4* were preferentially induced in hydathodes (Figure 2A), indicating cell-type-specific modulation of the transcriptional responses mediated by putatively redundant components. These findings refine the PRIMER cell state concept by suggesting that its transcriptional hallmarks can be broadly accessible to almost all plant cells but differentially tuned by cell identity. Rather than being exclusively driven by pathogen contact, PRIMER-like transcriptional cell states may emerge from intrinsic regulatory programs that govern immune execution across tissues.

Taken together, these results reveal that while the capacity to initiate immune signaling is broadly encoded in all leaf cells, the execution of immune programs is highly modular and spatially patterned. Even under synchronized and pathogen-free ETI activation, immune outputs such as NHP biosynthesis and PRIMER-like transcriptional states remain confined to specific cell types. This indicates that plant tissues harbor intrinsic immune compartmentalization, likely reflecting functional specializations that balance defense intensity, metabolic cost, and coordination of systemic immunity. These insights offer a new framework to explore how spatial immune signaling is uncoded in development and potentially exploited during natural infections.

Shared and cluster-specific gene programs structure immune execution

To map the cellular architecture of immune execution, we performed differential gene expression (DEG) analysis across all annotated cell clusters (Figure S3B), followed by gene ontology (GO) term enrichment. As anticipated, defense-related GO terms were predominantly enriched in epidermal and mesophyll cells (Figure 2B, Table S2), consistent with prior bulk RNA-seq findings[16]. Interestingly, GO terms related to photosynthesis, especially photosystem I components, were significantly enriched among downregulated genes in several mesophyll clusters (Figure S4A), indicating that ETI alone can suppress core metabolic programs in addition to activating defense.

To evaluate how cell-resolved responses relate to canonical ETI programs, we compared upregulated DEGs in each cluster with a previously defined list of EDS1-dependent immune-responsive genes (Table S3)[16]. Most clusters showed significant overlap, with pavement cells and mesophyll cells exhibiting the highest concordance (Figure 3A and S4B). This supports the presence of a broadly conserved core immune program across major cell types.

However, beyond this shared module, many cell clusters displayed distinct expression of immune-activation indicators or regulators, such as *CALMODULIN-BINDING PROTEIN 60 G* (*CBP60g*), *SARD1*, *ALD1*, *FMO1*, *SWEET4* and *E2F* family transcription factors etc., which may mediate

229 cell-autonomous immune amplification, niche-specific defense execution, or immune signal
230 propagation contributing to pathogen restriction and distal immune priming signal propagation.
231
232 To delineate these features systematically, we classified DEGs as shared (included in more than
233 2 different clusters; Table S7) or cluster-specific (uniquely induced; Table S8). Many cluster-
234 specific genes still overlapped with bulk-identified ETI targets, suggesting these are not artifacts
235 of cellular noise but reflect specialized, cell type-enriched immune indicators and putative
236 regulators. Additionally, these genes overlapped with known EDS1-dependent ETI-responsive
237 genes from bulk RNA-seq, supporting their role as specialized, cell type-enriched immune markers
238 or execution components. Together, these results define a layered transcriptional framework for
239 ETI in Arabidopsis: a core set of conserved immune genes is broadly deployed, while modular,
240 cell-specific programs likely tailor immune outputs in a spatially precise manner. This modular
241 immune architecture likely enables plants to coordinate tissue-scale defense while optimizing
242 energy use and in parallel restrict pathogen invasion.
243
244 **Gene regulatory networks orchestrate cell-type-specific immune outputs**
245 To elucidate how a uniform ETI activation translates into spatially heterogeneous immune
246 execution, we examined the underlying regulatory mechanisms at the transcriptional level. We
247 intersected upregulated DEGs from pavement and mesophyll 1 clusters with genes previously
248 shown to be both ETI-induced (bulk RNA-seq) and exhibit ETI-enhanced chromatin accessibility
249 (Table S4)[20]. This revealed a core set of chromatin-licensed immune genes (Figures 3B and 3C;
250 Table S5 and S6), likely under transcriptional control during early ETI, and broadly conserved
251 across both pavement and mesophyll 1 cell types.
252
253 To further dissect upstream regulatory control, we mapped cell-type specific DEGs to the
254 Arabidopsis transcription factor (TF) *cistrome* and *epicistrome* database[28]. The *cistrome* defines
255 the genome-wide landscape of transcription factor binding, while the *epicistrome* extends this by
256 incorporating epigenetic features, such as DNA methylation, that modulate TF-DNA interactions,
257 thereby shaping functional access to regulatory DNA. Together, they provide a comprehensive
258 view of how gene regulatory networks are both encoded and epigenetically tuned[28]. WRKY, NAC,
259 ERFs, MYB and bZIP TFs were prominently enriched in our analysis, consistent with established
260 roles in plant immunity and suggesting that shared TF modules are deployed in distinct
261 configurations across cell types to shape local defense outputs (Figure 4A)[29].
262
263 Notably, the enriched TFs exhibited varied responses across cell types, reflecting diverse
264 regulatory roles in immune activation. Pavement and mesophyll cells showed the highest number
265 of DEGs and the strongest GO enrichment for immune-related processes. We therefore compared
266 these two cell types to investigate transcriptional regulators underlying spatial specificity.

267 Strikingly, *WRKY8* and *SYSTEMIC ACQUIRED RESISTANCE DEFICIENT 1* (*SARD1*) were both
268 exclusively expressed in the epidermis (Figure 4A and 4B). Mapping to the *cistrome* and
269 *epicitrome* database, WRKY8 was enriched at the promoters of a large fraction of pavement-
270 specific ETI-induced DEGs (Figure 4C), consistent with its proposed role as an epidermal immune
271 amplifier (Figure 4B)[8]. SARD1, a master regulator known to act redundantly with CBP60g to
272 regulate plant immunity[10,11], was similarly epidermis-specific and targeted more than 80% of
273 upregulated DEGs in this cell type (Figure 4C). Together, these TFs accounted for the majority of
274 regulatory activity in the epidermal immune network, underscoring their importance in
275 orchestrating cell type–specific defense programs. Similar modular patterns were observed for
276 other TFs with respect to other cell-types (Figure 4A), reinforcing idea that different TF families
277 contribute to spatially specialized transcriptional circuits.
278
279 Collectively, these findings support a model in which ETI activation is interpreted through a
280 preconfigured, cell-intrinsic transcriptional framework, governed by chromatin accessibility and
281 transcription factor availability. This spatially modular regulatory architecture allows for the
282 diversification of immune outputs despite a common upstream signal, enabling plants to finely
283 tune defense intensity, coordinate intercellular signaling, and maintain metabolic balance under
284 immune stress or during pathogen attack.
285
286 **Epidermis-specific immune regulators restrict non-host pathogen entry at the leaf surface**
287 While many immune-related genes were broadly expressed across all leaf cell types upon ETI
288 induction, certain transcriptional regulator exhibited strikingly cell-type-specific induction patterns,
289 suggesting functional compartmentalization in immune execution. Among these, *CBP60g* and
290 *SARD1*, two well-established, partially redundant immune activators[10,11,13], were preferentially
291 more upregulated in pavement cells (Figure 2A). SARD1 is a DEG specific to only pavement cells
292 (Figure 4A), indicating a potential role in epidermis-localized defense mediated by ETI.
293
294 To assess whether this spatial enrichment reflects a functional requirement for immunity, we
295 challenged *cbp60g sard1* double mutants and wild-type (WT) Col-0 with *Albugo candida* isolate
296 AcEm2, a non-adapted oomycete pathogen that exhibits an incompatible interaction with Col-0
297 due to the NLR WHITE RUST RESISTANCE 4 (WRR4)-mediated recognition[30–32]. In contrast to
298 WT plants, *cbp60g sard1* mutants permitted haustorial formation specifically in the epidermal and
299 sub-epidermal cell layers, by not in deeper mesophyll tissues (Figure 5A and 5B). This indicates
300 that while CBP60g and SARD1 are not globally required for ETI, they play a cell-type-specific role
301 in restricting early pathogen entry at the leaf surface.
302
303 Despite their loss, ETI signaling in mesophyll cells appears intact, likely due to broad expression
304 of core components such as EDS1, PAD4, and other transcriptional regulators like WRKY33 or

305 E2Fs that may independently sustain immune competence in internal tissues. This reinforces the
306 concept that cell-type-specific TF modules mediate immune execution in distinct spatial zones,
307 with CBP60g and SARD1 acting as epidermis-enriched executors to enforce localized resistance
308 against non-adapted pathogens. While we did not perform pathogen-infected single-cell profiling,
309 our data provide a transcriptional reference framework for immune potential across cell types and
310 highlight testable hypotheses for future spatial challenge assays.
311
312 Furthermore, testing additional pathogens with alternative invasion routes, such as *Blumeria*
313 *graminis*, which penetrates directly through the epidermis[33], may clarify whether CBP60g- and
314 SARD1-dependent immunity represents a generalizable outer-layer defense strategy. Such
315 studies will further refine our understanding of how immune competence and execution are
316 partitioned across tissue layers to collectively enforce nonhost resistance.
317
318 **Discussion**
319 Our study presents a single-cell transcriptional atlas of ETI in Arabidopsis leaves, enabled by the
320 SETI system[9], which uncouples immune activation by pathogen-derived cues (*e.g.* Mechanical
321 perturbations, cell-wall integrity and apoplastic chemical matrix alternations, and cell-surface
322 receptor-mediated signaling upon elicitor recognition, etc.) from the effects of pathogen effectors.
323 This approach reveals how intracellular ETI is broadly perceived yet executed in a spatially
324 heterogeneous manner across different cell types, offering new insights into the modular logic of
325 plant immunity.
326
327 ETI activation via TIR-NLRs induces a widespread transcriptional competence across leaf cell
328 types. Genes encoding core components such as EDS1, PAD4, SAG101 and enzymes involved
329 in salicylic acid (SA) biosynthesis are broadly expressed, indicating that immune signal
330 transduction is not restricted to a specialized subset of cells within the leaf, but is accessible to
331 diverse cell types. Nonetheless, specific immune outputs, including the NHP and JA pathways,
332 are spatially restricted, suggesting compartmentalization of defense metabolism. These results
333 imply that metabolic branches of ETI may follow cell-type-specific coordination, raising the need
334 for future integration of single-cell metabolomics to map the immune metabolome with cellular
335 precision.
336
337 At the gene regulatory level, our data support a layered and modular tissue architecture of immune
338 control. While certain transcriptional modules are shared across cell types, others are distinctly
339 partitioned. WRKY25 and WRKY70 exhibit broad deployment, whereas WRKY8 appears to
340 function almost exclusively in pavement cells, regulating the majority of immune-induced genes in
341 that cellular layer. Such spatial exclusivity is consistent with proposed role of WRKY8 in the
342 PRIMER cell state. However, our results challenge the notion of the PRIMER state as a rare

343 phenomenon. Instead, we propose that it represents a manifestation of differential ETI execution
344 programs across cell types, embedded in their intrinsic components such as chromatin
345 landscapes and transcription factor availability. The observed spatial heterogeneity reflects not a
346 stochastic occurrence, but a structured immune regulatory mechanism encoded in tissue
347 architecture. Other TFs, including WRKY17, WRKY33, E2Fs, and trihelix factors, further reinforce
348 the diversity of transcriptional programs orchestrating immune output across spatial domains. This
349 emphasizes that transcriptional immune competence is not synonymous with uniform immune
350 execution. Despite shared upstream signaling through TIR-NLRs and EDS1, each cell type
351 interprets immune signals through its own transcriptional lens, shaped by chromatin accessibility,
352 TF availability, and cellular identity. This modular state likely allows plants to fine-tune defense
353 intensity, optimize resource allocation, and coordinate systemic signaling in a spatially controlled
354 manner.
355
356 Conventionally, nonhost resistance (NHR) represents a durable and broad-spectrum form of plant
357 immunity, in which an entire plant species is resistant to all strains of a non-adapted pathogen[34].
358 While traditionally attributed to preformed barriers and pattern-triggered immunity (PTI), recent
359 studies suggest that intracellular nucleotide-binding leucine-rich repeat (NLR) receptors can also
360 contribute to nonhost restriction, particularly through effector recognition and ETI-like responses
361 in specific pathosystems[35]. For instance, Arabidopsis NLR WRR4A mediates resistance to
362 multiple isolates of *Brassica*-infecting isolates of *Albugo candida* [36], by recognizing lineage-
363 specific effectors and triggering localized immune activation[30–32]. Our results extend this model by
364 demonstrating that spatially restricted transcriptional regulators such as CBP60g and SARD1 are
365 essential for enforcing cell-type-specific resistance against non-adapted *Albugo* isolates,
366 preventing pathogen ingress at the epidermal layer. In *cbp60g sard1* double mutants, *A. candida*
367 haustoria are formed in cell types at the outer layer of the leaf tissue, despite intact immunity in
368 underlying tissues. This provides direct evidence that immune competence alone is insufficient
369 without proper transcriptional execution at vulnerable interfaces. It also underscores a broader
370 principle: spatially localized immune regulators enforce layered defense barriers that guard
371 vulnerable tissue interfaces, a robust framework that could likely be conserved across diverse
372 plant-pathogen interactions. Building on this, future studies could extend similar analyses,
373 combined with spatial omics approaches, to identify additional spatially enriched immune
374 components and evaluate their cell type–specific functional relevance.
375
376 The hydathode, a specialized structure at the leaf margin that connects to the vasculature,
377 exemplifies this principle. Unlike the epidermis, which confronts external pathogens, hydathodes
378 represent potential internal entry points. Prior work has shown that hydathode immunity is
379 mediated by EDS1-PAD4-ADR1 signaling[37,38], and our findings extend this by identifying GT-
380 family transcription factors and GT-3A paralogs, GT-3B and GT-4, as selectively induced in

hydathodes during ETI. While GT-3A is expressed in almost all cell types during ETI activation, the restricted expression pattern of GT-3B and GT-4 suggests that these TFs constitute a hydathode immune regulatory module. This underscores how even uniformly activated ETI is interpreted through distinct local transcriptional regulation, shaped by structural vulnerability and functional necessity.

Our findings deliver several conceptual advances. First, we provide direct transcriptional evidence that innate immune competence is broadly encoded in all major cell types of the Arabidopsis leaf, supporting a model of fully distributed, cell-autonomous immunity. Second, we show that even under uniform activation of intracellular immunity, cell identity exerts a major constraint on the spectrum and strength of transcriptional output. This introduces the concept of cell-type-specific immune execution, highlighting new questions about how chromatin features, TF availability, and metabolic state shape these responses. Our dataset offers a valuable resource for future mechanistic studies into these layers of regulation. Third, our functional validation of the epidermis-enriched transcriptional regulators CBP60g and SARD1 establishes that NHR mediated by NLR-triggered ETI is not uniform across tissues but depends on precise execution in specific cell types. In *cbp60g sard1* double mutants, haustoria of resisted races of oomycete *A. candida* formed specifically in the epidermal and sub-epidermal cells, despite intact immunity in inner layers. This demonstrates that immune competence alone is insufficient without proper transcriptional execution at vulnerable tissue interfaces. These findings provide, to our knowledge, the first direct evidence that NLR-driven NHR displays cell-type specificity, with functional consequences for pathogen entry.

Altogether, our results define a spatially modular model of ETI, where uniformly initiated immune signaling is filtered through localized transcriptional programs. This allows for precise deployment of immunity, which is stronger in vulnerable cell types in Arabidopsis leaf tissue like the epidermis and hydathodes than elsewhere. These insights raise compelling research questions: What molecular features prime certain cells for heightened immune execution? Can spatial chromatin states predict immunocompetence? How do localized defenses coordinate with systemic signaling? Is infection spatially random, or shaped by host–pathogen combinations at the single-cell level? How do highly responsive cells compensate for neighboring cells with limited immune potential to maintain tissue-wide resilience?

In summary, this work provides a foundational framework for understanding cell-type-resolved immunity in plants. By demonstrating how immune signaling is broadly competent yet differentially executed, we reveal the principles of spatial immune execution. These insights offer a roadmap for engineering durable, precision immune responses in crops, tailored to the distinct roles and vulnerabilities of each cell type.

419

420 **Methods**

421 **Plant material and growth conditions**

422 *Arabidopsis thaliana* Col-0 ecotype was used as the wild-type background. The β-estradiol (E2)–
423 inducible SUPER-ETI line (SETI_WT) and the *cbp60g sard1* double mutant used in this study
424 have been previously described[9,10]**.** Plants were grown at 21°C under long-day conditions (16 h
425 light, 8 h dark), and at 50% humidity.

426

427 **Protoplast isolation**

428 Four-week-old leaves from SETI_WT plants were infiltrated with 50 μM estradiol (E2), and
429 protoplasts were isolated 4 hours post-infiltration (hpi) using the Tape-Arabidopsis Sandwich
430 method[39]. Peeled leaf tissue was incubated in enzyme digestion solution containing 0.4 M D-
431 sorbitol, 20 mM KCl, 20 mM MES, 10 mM $CaCl_2$, 0.1% (w/v) BSA, 1.5% (w/v) Cellulase R10
432 (Duchefa), 0.5% (w/v) Macerozyme R10 (Duchefa), 5% (v/v) Viscozyme® L (Sigma), and 3.56
433 mM 2-mercaptoethanol. The digestion was carried out for 2 hours at 40 rpm. The resulting
434 protoplast suspension was filtered through a 40 μm mesh and centrifuged at 200 × g for 5 minutes
435 at 4°C using a swinging bucket rotor with minimal deceleration.

436

437 Protoplasts were resuspended in 2 mL of washing buffer composed of 0.4 M D-mannitol, 20 mM
438 KCl, 20 mM MES, 1 mM $CaCl_2$, 0.1% (w/v) BSA, and 3.56 mM 2-mercaptoethanol. Purification of
439 intact protoplasts was achieved using a three-phase density gradient centrifugation with
440 OptiPrep™ (Stemcell Technologies). The OptiPrep working solution (WS) was prepared by
441 dissolving 0.06 g of KCl in 10 mL of OptiPrep. For the gradient, 2 mL of protoplast suspension
442 was mixed with 500 μL of OptiPrep WS (final density: 1.064 g/mL) and layered at the bottom of a
443 5 mL centrifuge tube. The middle layer consisted of 1 mL of a 2:0.4 (v/v) mix of resuspension
444 buffer and OptiPrep WS (final density: 1.053 g/mL), gently added atop the bottom layer. The top
445 layer comprised 200 μL of resuspension buffer carefully pipetted over the middle layer.

446

447 The gradient was centrifuged at 200 × g for 5 minutes at 4°C using a swinging bucket rotor.
448 Protoplasts were recovered from the topmost layer, resuspended in washing buffer, visualized
449 under microscope and adjusted to a final concentration of ~1,000 cells/μL. The purified protoplast
450 suspension was loaded into the 10x Genomics Chromium Controller for microfluidic droplet
451 generation. Single-cell libraries were prepared using the Chromium Single Cell 3' Reagent Kit v3.1
452 (10x Genomics), following the manufacturer's protocol. Libraries were sequenced on an Illumina
453 NovaSeq X Plus platform (paired-end 150 bp reads).

454

455 **Single cell data analysis**

456 Cellranger (10X Genomics) was used to map the reads to the Arabidopsis reference genome
457 (Araport11). Upon alignment, the 'force-cells' option was used to detect the top 10,000 cells based
458 on UMI counts. For each sample, low-quality cells were removed based on mitochondrial and
459 chloroplast read counts (5% mitochondrial and 20% chloroplast counts), which resulted in the
460 identification of 7932 and 5739 high-quality cells in the mock and induced samples, respectively.
461 The Seurat R package (reference) was used for the integration, dimensionality reduction, scaling,
462 clustering and DEG analysis. We used the canonical correlation analysis (CCA) integration option
463 for the integration of both datasets. Uniform manifold approximation and projection (UMAP) were
464 calculated using 32 principal component dimensions and cell-clusters were identified using the
465 Seurat 'FindClusters' function with the resolution parameter set to 0.8, which resulted in the
466 identification of 16 cell clusters. For each cluster, gene markers were identified using the
467 'FindAllMarkers' function with a threshold of adjusted P-value < 0.01, log2FC > 0.25, percentage
468 of cells within the cluster that expresses the gene greater than 10% and percentage difference to
469 other clusters greater than 20%. The identities of each cell cluster were determined based on the
470 expression of putative leaf cell-markers [17]. For the DEG analysis we first aggregate the expression
471 values of both datasets using the 'AggregateExpression' function followed by a pair-wise
472 comparison between from mock and treated sample in each individual cluster using the function
473 'FindMarkers', with a threshold of adjusted P-value <= 0.01, log2FC >= 1 for genes that are
474 expressed in at least 20% of the cells.
475
476 **Reverse transcription–quantitative PCR (RT–qPCR)**
477 For gene expression analysis, RNA was isolated from protoplast isolated from 4-week-old
478 Arabidopsis leaves 4hpi after E2 infiltration and used for subsequent RT–qPCR analysis. RNA
479 was extracted with a Quick-RNA Plant Kit (R2024; Zymo Research) and treated with RNase-free
480 DNase (4716728001; Merck-Roche). Reverse transcription was carried out using SuperScript IV
481 Reverse Transcriptase (18090050; ThermoFisher Scientific). qPCR was performed using a
482 CFX96 Touch™ Real-Time PCR Detection System. Primers for qPCR analysis
483 of *ISOCHORISMATE SYNTHASE1* (*ICS1*), *ELONGATION FACTOR 1 ALPHA* (*EF1α*) are as
484 follows: *ICS1* primers (*ICS1*_F: 5′-CAATTGGCAGGGAGACTTACG-3'; *ICS1*_R: 5′-
485 GAGCTGATCTGATCCCGACTG-3′). *EF1α* primers (*EF1α*_F: 5′-
486 CAGGCTGATTGTGCTGTTCTTA-3'; *EF1α*_R: 5′GTTGTATCCGACCTTCTTCAGG-3′) and Data
487 were analyzed using the double delta Ct method[40]. All results are plotted using ggplot2 in R[41], and
488 a detailed statistical summary can be found in Table S1.
489
490 ***Albugo candida* propagation and infection assay**
491 For testing the susceptibility in the A. thaliana genotypes in this study, an incompatible isolate of
492 A. candida AcEm2 was used[42]. Infection assays were performed as previously described[32]. Pre-
493 infected leaves with pustules bearing sporangiophores were suspended in water (c.

494 10^5 spores ml^{-1}). This suspension was incubated on ice for 30 min for release of the zoospores.
495 The inoculum of spore suspension was filtered through a double layered muslin cloth and then
496 sprayed on plants using a Humbrol® (Hornby Hobbies Ltd, Sandwich, UK) spray gun (c. 700 µl
497 per plant). Post spraying, plants were incubated at 4°C overnight in the dark, for promoting
498 zoospore germination. Infected plants were kept under 10 h light (20°C) and 14 h dark (16°C)
499 cycles. Susceptibility on the infected plants with an incompatible strain was scored at 6 days post
500 infection (dpi) by trypan blue imaging of the AcEm2 colonization and its establishment in the host.
501

502 **Trypan blue staining**

503 Infected leaves were boiled for 1 min in stain solution (10 ml lactic acid, 10 ml glycerol, 10 g
504 phenol, 10 mg trypan blue and water in a final volume of 10 ml, mixed in a 1 : 1 ratio with ethanol)
505 and then decolorized in chloral hydrate (2.5 gm chloral hydrate in water in a final volume of 1 ml).
506 The leaves were mounted in 60% glycerol and examined using a Leica M165 FC
507 stereomicroscope.
508

509 **Data availability**

510 All sequencing datasets generated in this study have been deposited in the European Nucleotide
511 Archive (ENA) under the accession number PRJEB91113. All custom scripts and analysis code
512 are publicly available at our GitHub repository: https://github.com/dinglab-plants/scETI.
513

514 **Author contributions**

515 PD conceptualized and oversaw the inception of the research project. The experimental work was
516 collaboratively conducted by HC, AR, and PD, and. Data analysis and figure generation were
517 performed by LJ, HC, AR, KK, and PD. JDGJ provides valuable discussions that significantly
518 shaped the research during this project. The initial manuscript draft was written by HC, LJ, and
519 PD. All co-authors contributed to subsequent revisions and editorial processes. The final
520 manuscript was prepared by HC and PD and was approved for submission by all authors.
521

522 **Declaration of interests**

523 The authors declare no competing interests.
524

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530

531 **Figures and figure legends**

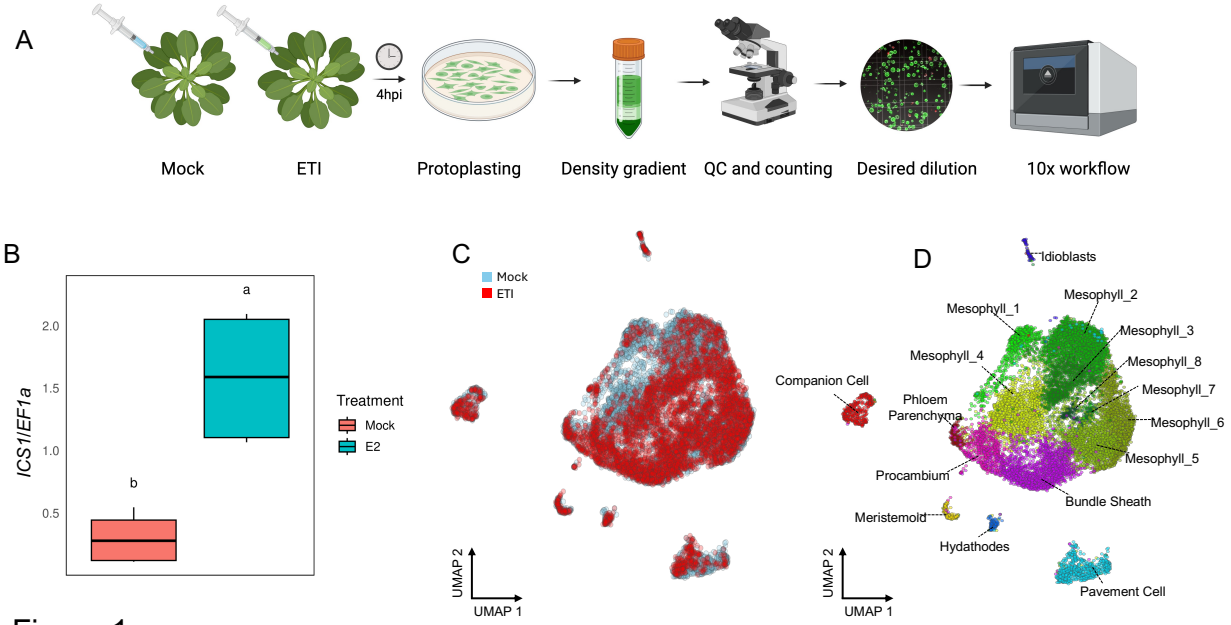

Figure 1

Figure 1. Single-cell transcriptomic landscape of immune activation in Arabidopsis leaf tissue.

(A) Experimental workflow. Arabidopsis leaves were treated with mock or estradiol to induce effector-triggered immunity (ETI), followed by protoplast isolation at 4 hours post-infiltration (hpi) and single-cell RNA sequencing (scRNA-seq).

(B) qPCR analysis of the immune marker gene *ISOCHORISMATE SYNTHASE 1* (*ICS1*). This confirms effective ETI induction in treated samples, validating immune activation prior to scRNA-seq library preparation.

(C) UMAP projection of integrated single-cell transcriptomes from mock and ETI-treated samples, colored by condition.

(D) UMAP showing unsupervised clustering of major Arabidopsis leaf cell types including pavement cells, mesophyll subtypes (Mesophyl_1 to Mesophyl_8), phloem parenchyma, companion cells, hydathodes, idioblasts, meristemoids, procambium, and bundle sheath cells.

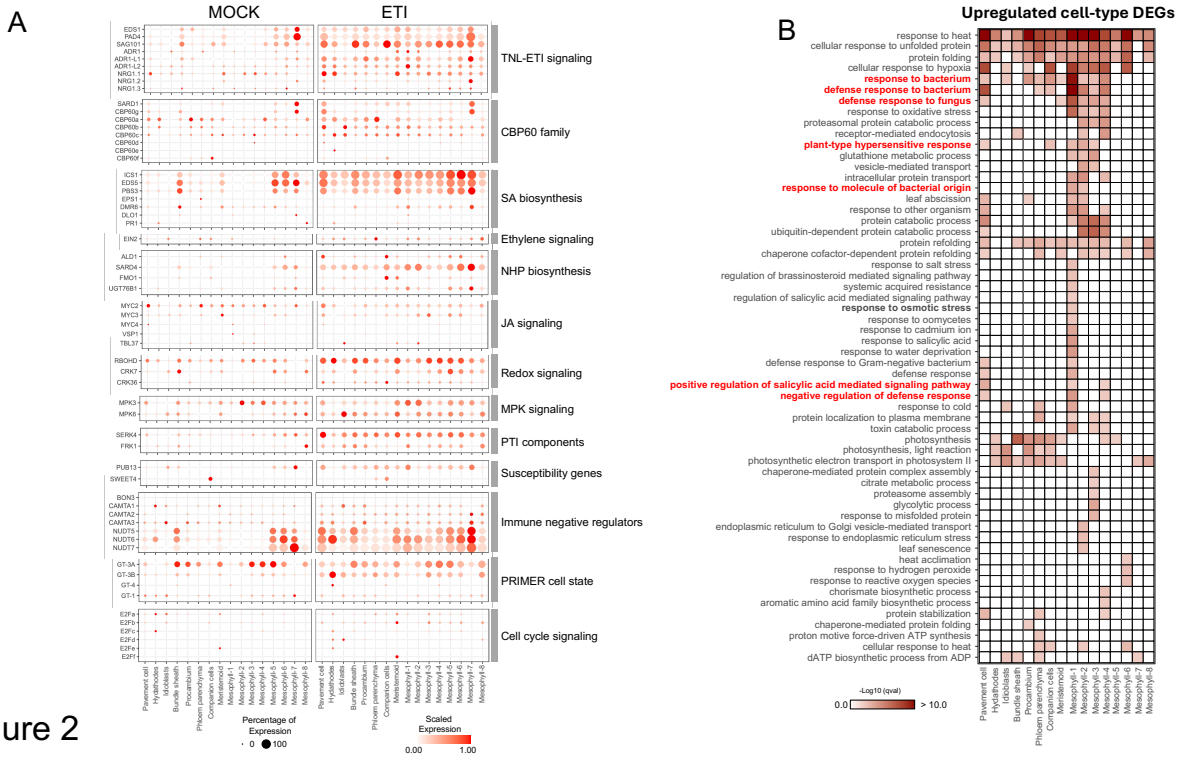

Figure 2

Figure 2. Cell-type-specific transcriptional responses to ETI in Arabidopsis leaf tissue. (A) Bubble plot showing expression of representative immune-related genes across annotated cell types under mock and E2 conditions. Categories include TNL-ETI signaling components, CBP60 family members, salicylic acid (SA), jasmonic acid (JA), ethylene, and NHP signaling, redox and MAP kinase pathways, PTI components, susceptibility factors, and immune repressors. (B) Gene Ontology (GO) enrichment of upregulated DEGs in ETI-treated cells. Functional categories include defense responses, hormone signaling, oxidative stress, protein folding, photosynthesis, and vesicle-mediated transport. Enrichment significance is shown as –log10(q-value), illustrating spatially resolved immune reprogramming during ETI.

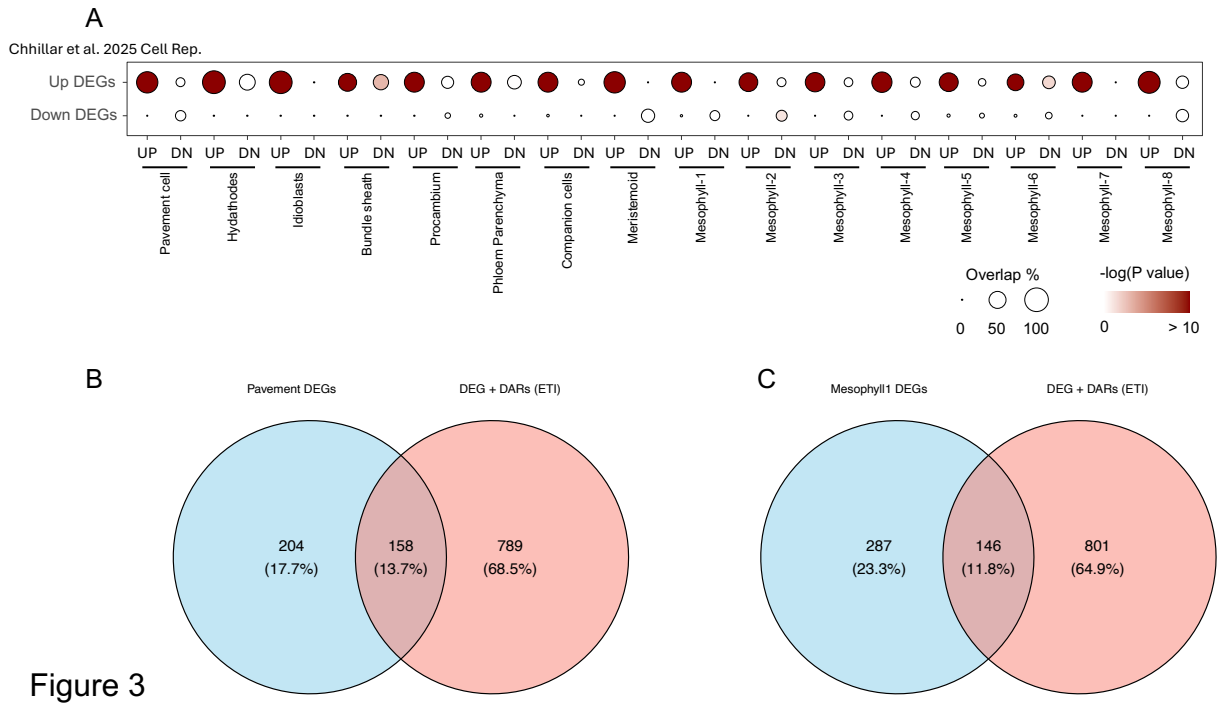

Figure 3

Figure 3. Integration of bulk RNA-seq and chromatin accessibility data with cell-type-specific ETI responses.

(A) Hypergeometric test showing the significance of overlap between bulk ETI-responsive genes (Chhillar et al. 2025, *Cell Rep.*) and DEGs identified in individual cell clusters from single cell RNA-seq.

(B–C) Venn diagrams showing overlap between DEGs and genes associated with differentially accessible regions (DARs) during ETI (from Ding et al. 2021, *JXB*) in pavement cells (B) and mesophyll-1 cells (C). A majority of cell-type-specific DEGs are also associated with DARs, suggesting coordinated transcriptional and chromatin-level regulation. Percentages reflect the proportion of DEGs overlapping with DARs in each cell type.

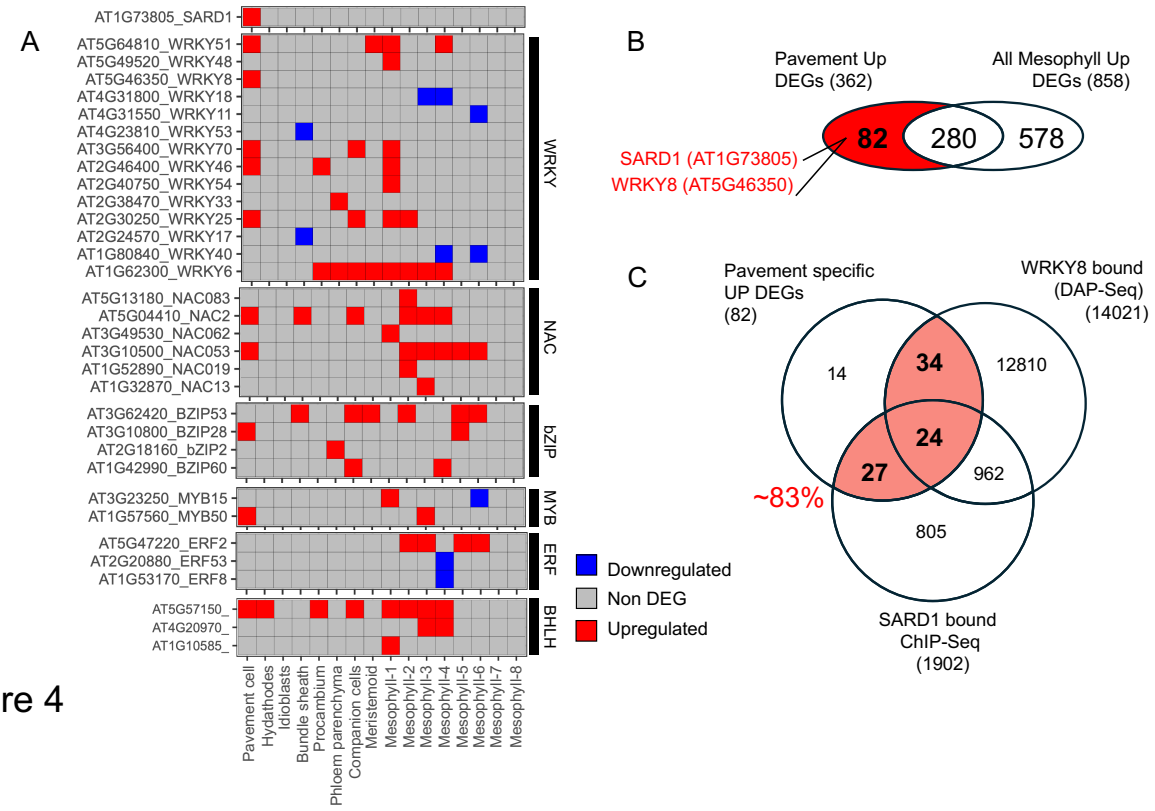

Figure 4

Figure 4. Cell-type-specific transcription factor activity underlies spatial immune regulation.

(A) Heatmap showing differential expression patterns of selected transcription factors (TFs) across annotated Arabidopsis leaf cell types. TFs are grouped by family (WRKY, NAC, bZIP, MYB, ERF, and bHLH). Red and blue indicate up- and downregulated expression, respectively, under ETI. Each column represents an individual cell type.

(B) Venn diagram comparing upregulated DEGs in pavement versus mesophyll cells. A subset of 82 genes is uniquely upregulated in pavement cells, including *SARD1* (*AT1g73805*) and *WRKY8* (*AT5g46350*).

(C) Overlap between pavement-specific upregulated DEGs and genomic targets of WRKY8 (DAP-seq) and SARD1 (ChIP-seq). Approximately 83% of pavement-specific DEGs are putative direct targets of WRKY8 and/or SARD1, indicating coordinated transcriptional control of epidermal immune programs.

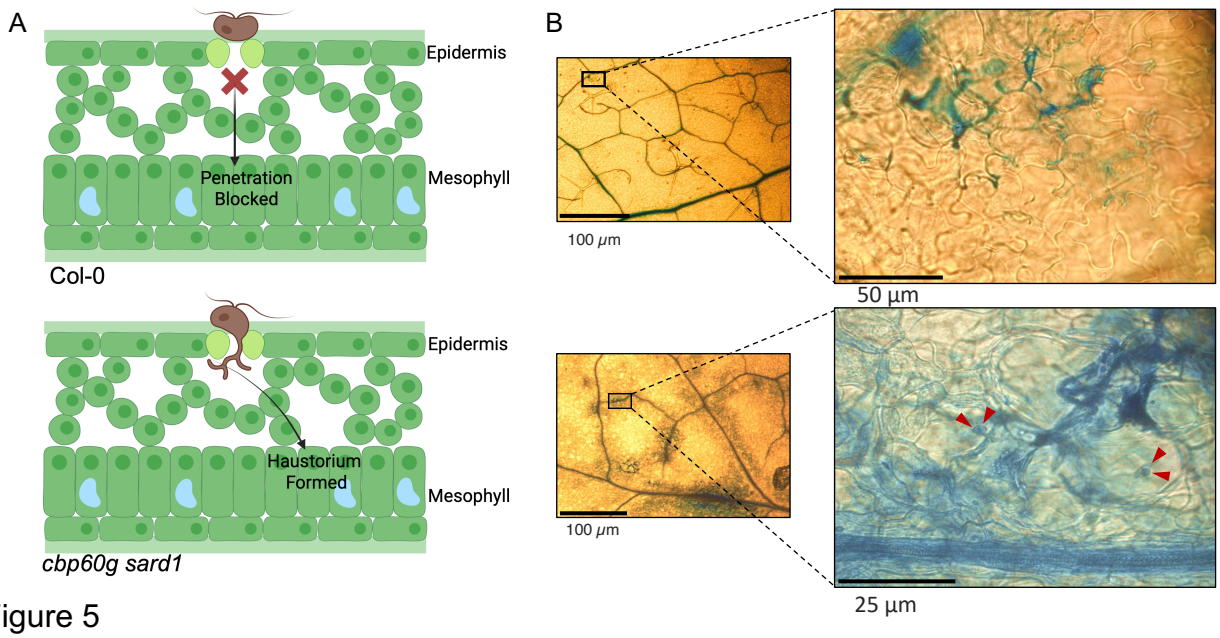

Figure 5

Figure 5. CBP60g and SARD1 mediate epidermis-specific immunity that *Albugo candida* entry.

(A) Schematic representation of infection outcomes in *Arabidopsis thaliana* Col-0 and the *cbp60g sard1* double mutant following inoculation with *Albugo candida* isolate AcEm2. In Col-0, pathogen entry is blocked at the epidermal layer, whereas *cbp60g sard1* mutants permit haustorium formation in underlying mesophyll cells, indicating compromised epidermal defense.

(B) Microscopic images of trypan blue-stained leaves infected with *A. candida* AcEm2. In Col-0, infection is restricted to the epidermis with no visible haustoria. In contrast, *cbp60g sard1* leaves show extensive hyphal growth and haustoria (red arrowheads) penetrating into mesophyll tissues, consistent with the model shown in (A).

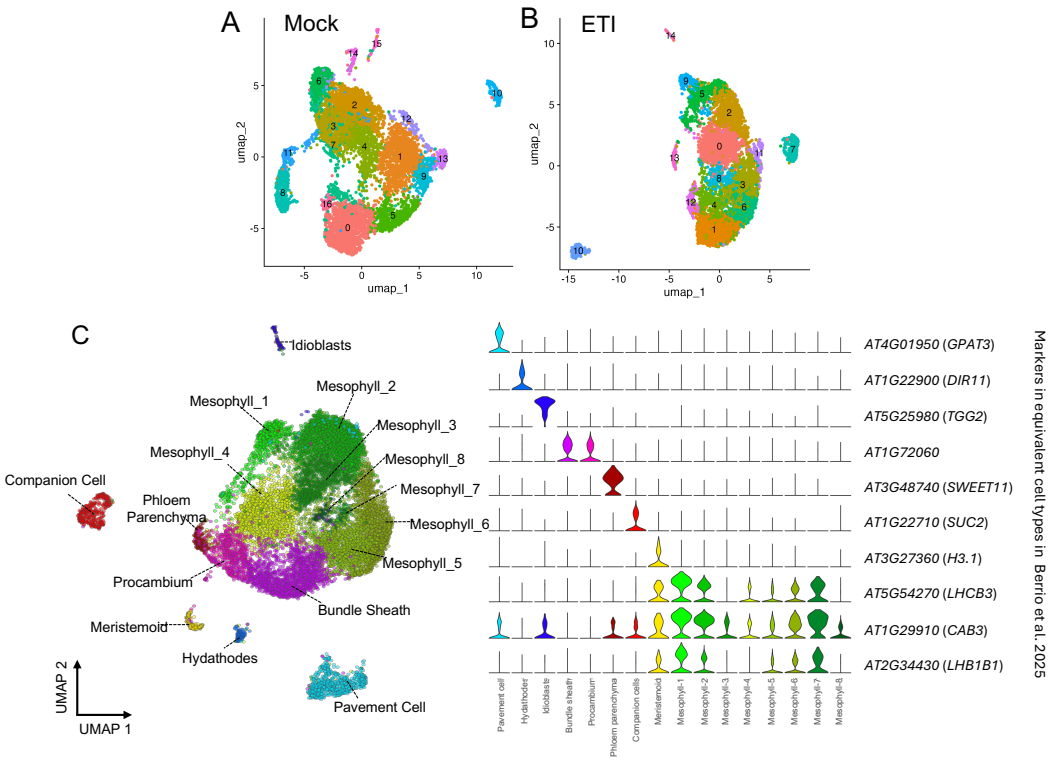

Figure S1

Figure S1. UMAP-based clustering and cell-type annotation of Arabidopsis leaf single-cell transcriptomes.

(A, B) UMAP projections of single-cell transcriptomes from mock-treated (A) and ETI-induced (B) Arabidopsis leaf tissues. Cells are colored by unsupervised clusters, corresponding to major and minor leaf cell types. Overall cluster architecture remains conserved upon ETI induction.

(C) Cell-type assignment based on the expression of canonical marker genes. Violin plots display representative marker expression across annotated clusters, supporting the identification of pavement, hydathode, idioblast, vascular, mesophyll, and meristem-like cell types. Marker gene identities are cross-referenced with equivalent annotations from Barrio et al., 2025.

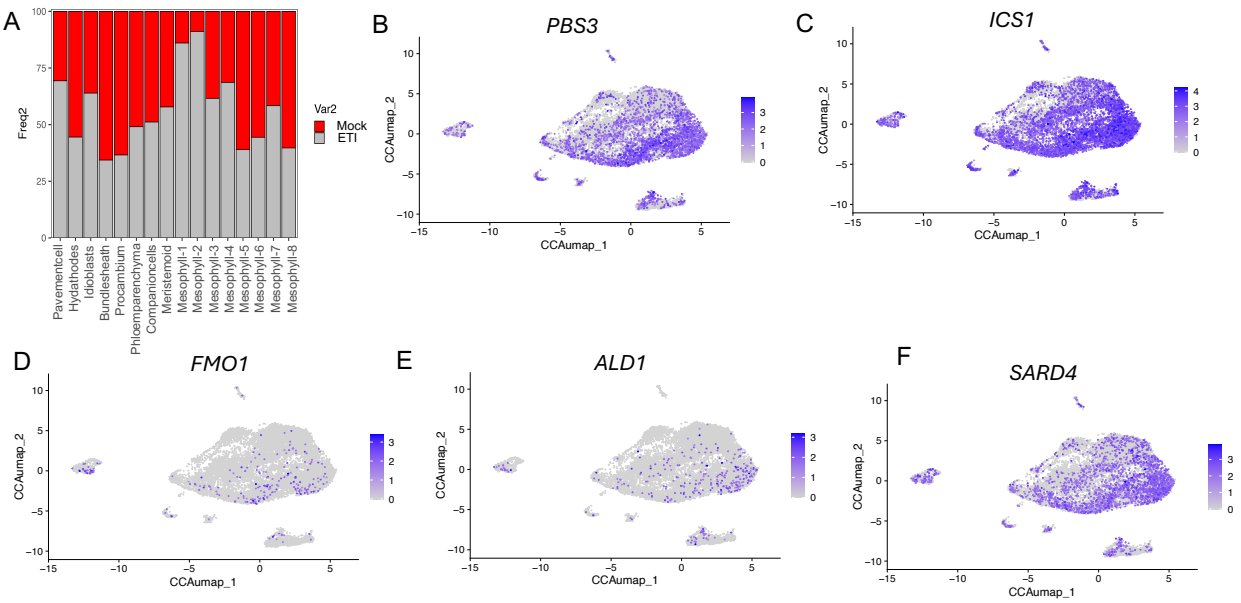

Figure S2

Figure S2. Cell-type compositional changes and activation of salicylic acid and NHP biosynthetic pathways during ETI.

(A) Stacked bar plot showing the relative abundance of annotated cell types under mock (gray) and ETI-induced (red) conditions. Increased representation of epidermal and multiple mesophyll subtypes is observed under ETI, indicating shifts in cellular transcriptional states.

(B–F) Single-cell feature plots depicting expression of genes involved in salicylic acid (SA) biosynthesis (*ICS1*, *PBS3*) and N-hydroxy pipecolic acid (NHP) biosynthesis (*ALD1*, *SARD4*, *FMO1*). Expression of *ICS1* and *SARD4* is broadly distributed across mesophyll and vascular cells, whereas *FMO1* and *ALD1* show more spatially restricted activation.

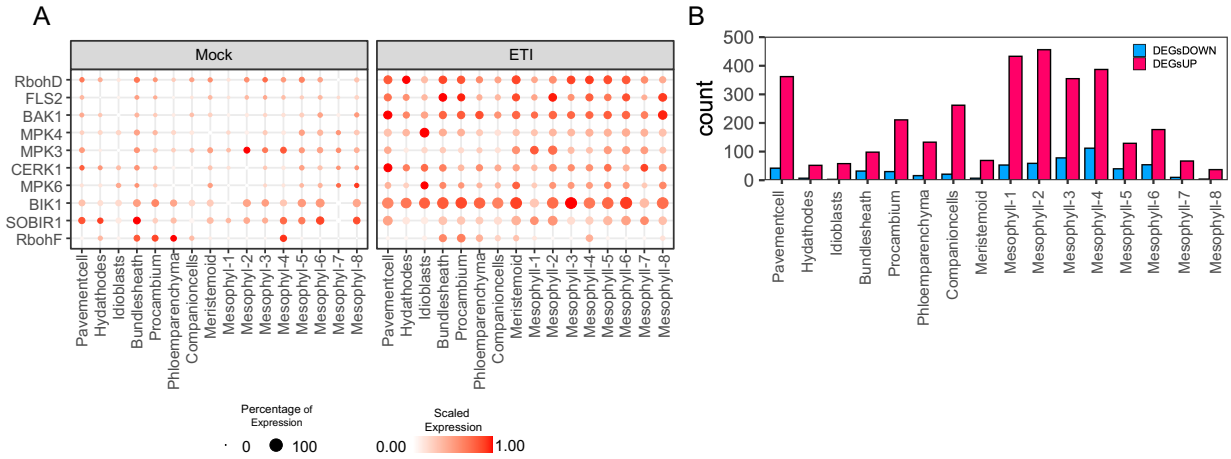

Figure S3

Figure S3. Cell-type-specific expression and transcriptional activation of immune signaling components during ETI.

(A) Dot plot illustrating the expression of key pattern-triggered immunity (PTI) and effector-triggered immunity (ETI) signaling genes across annotated leaf cell types under mock and ETI conditions. Dot size indicates the proportion of cells expressing each gene, and color intensity reflects scaled average expression. Genes include receptor kinases (*FLS2*, *BAK1*, *CERK1*), MAP kinases (*MPK3, MPK4, MPK6*), and signaling intermediates (*BIK1*, *SOBIR1*, *RbohD*, *RbohF*).
(B) Bar graph showing the number of upregulated (pink) and downregulated (blue) differentially expressed genes (DEGs) across each cell type upon ETI induction. Strong transcriptional activation is observed in mesophyll and pavement cells, consistent with their central role in immune responses.

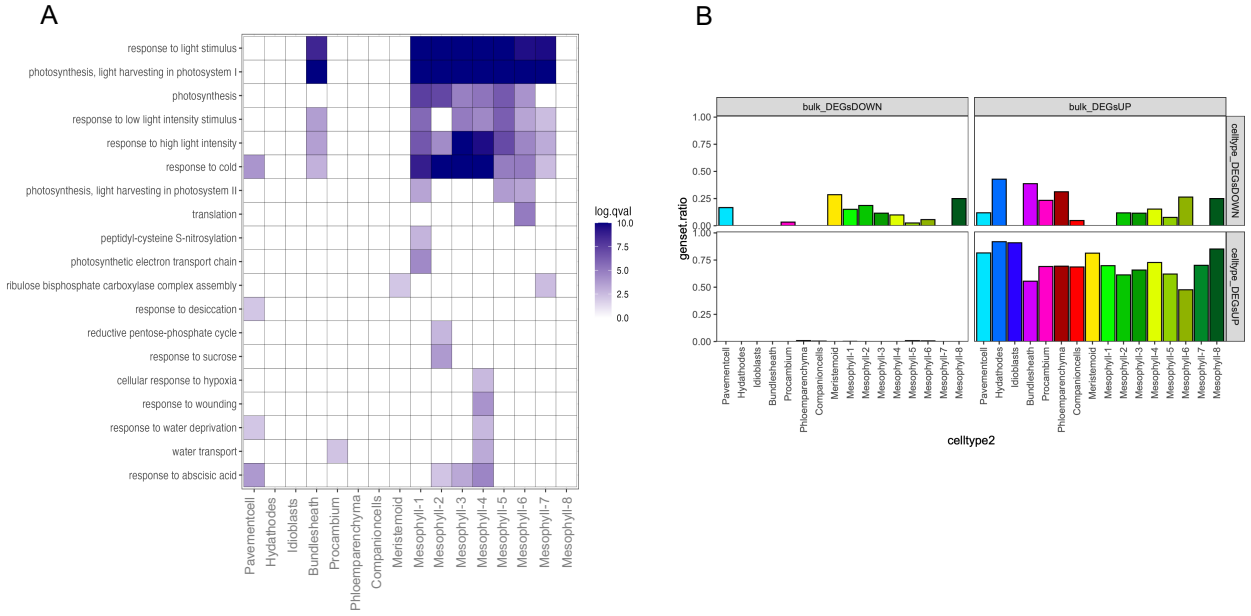

Figure S4

Figure S4. Functional enrichment analysis of bulk ETI-regulated genes across leaf cell types.
(A) Heatmap showing Gene Ontology (GO) biological process terms enriched among downregulated genes (DEGsDOWN) mapped to specific cell types using single-cell deconvolution. Color scale indicates statistical significance ($\log_{10}$- transformed adjusted *q*-value). Suppressed photosynthetic and light-responsive pathways are predominantly enriched in mesophyll cluster.
(B) Bar plots showing the cell-type distribution of upregulated (DEGsUP, bottom) and downregulated (DEGsDOWN, top) bulk DEGs, inferred by scRNA-seq expression patterns. ETI-upregulated genes are broadly represented across epidermal and mesophyll cells, while downregulated genes are more restricted to photosynthetically active mesophyll populations.

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