1 Title:

- 2 Genipin Crosslinks the Extracellular Matrix to Rescue Developmental and Degenerative
- 3 Defects, and Accelerates Regeneration of Peripheral Neurons
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31 Abstract:

32 The peripheral nervous system (PNS) is essential for proper body function. A high percentage of the population suffer nerve degeneration or peripheral damage. For 33 34 example, over 40% of patients with diabetes or undergoing chemotherapy develop 35 peripheral neuropathies. Despite this, there are major gaps in the knowledge of human 36 PNS development and therefore, there are no available treatments. Familial 37 Dysautonomia (FD) is a devastating disorder that specifically affects the PNS making it 38 an ideal model to study PNS dysfunction. FD is caused by a homozygous point mutation 39 in *ELP1* leading to developmental and degenerative defects in the sensory and autonomic 40 lineages. We previously employed human pluripotent stem cells (hPSCs) to show that 41 peripheral sensory neurons (SNs) are not generated efficiently and degenerate over time 42 in FD. Here, we conducted a chemical screen to identify compounds able to rescue this 43 SN differentiation inefficiency. We identified that genipin, a compound prescribed in Traditional Chinese Medicine for neurodegenerative disorders, restores neural crest and 44 45 SN development in FD, both in the hPSC model and in a FD mouse model. Additionally, 46 genipin prevented FD neuronal degeneration, suggesting that it could be offered to

47 patients suffering from PNS neurodegenerative disorders. We found that genipin crosslinks the extracellular matrix, increases the stiffness of the ECM, reorganizes the 48 actin cytoskeleton, and promotes transcription of YAP-dependent genes. Finally, we show 49 50 that genipin enhances axon regeneration in an *in vitro* axotomy model in healthy sensory 51 and sympathetic neurons (part of the PNS) and in prefrontal cortical neurons (part of the 52 central nervous system, CNS). Our results suggest genipin can be used as a promising drug candidate for treatment of neurodevelopmental and neurodegenerative diseases, 53 54 and as a enhancer of neuronal regeneration. 55 56 One sentence summary:

57 Genipin rescues the developmental and degenerative phenotypes of the peripheral 58 neuropathy familial dysautonomia and enhances neuron regeneration after injury.

60 Main text:

61 Introduction

The peripheral nervous system (PNS) consists of sensory, sympathetic, 62 63 parasympathetic, and enteric neurons, all of which develop from the neural crest (NC). 64 The PNS innervates all organs of the body and is essential for its homeostasis. Loss, as 65 well as hyper-function of the PNS lead to an array of human disorders caused by genetic 66 mutations, metabolic problems, traumatic injury, inflammation, toxins, and infections. While lots of research is invested in finding treatments¹, to date, there is no FDA approved 67 68 treatment available. For example, peripheral nerve degeneration (peripheral neuropathy) 69 and peripheral nerve damage are common, i.e. 20 million people and 20-30% of the population, respectively are sufferers. Together, they cause a large impact on life and are 70 71 a major healthcare cost burden^{2,3}.

To improve our general understanding of PNS function and missregulation, it is 72 73 useful to study a model disease; ideally one that is well defined, specific and causes a 74 strong phenotype⁴. The autosomal recessive childhood disorder Familial Dysautonomia 75 (FD) serves as such a model disorder. FD is caused by a homozygous point mutation in 76 the gene ELP1 (formerly IKBKAP), the scaffolding component of the transcriptional 77 elongator complex⁵. The mutation leads to aberrant splicing and tissue-specific reduction of functional ELP1 protein⁶. This reduction is particularly prominent in the neural crest 78 79 (NC) progenitor lineage and its progeny: the peripheral nervous system (PNS), especially in sensory and autonomic neurons⁶. These neurons develop at a reduced rate and they 80 degenerate rapidly over time⁷. As a result, patients experience loss of pain perception, 81 82 ataxic gait, trouble regulating heart rate and blood pressure and debilitating dysautonomic

83 crisis, characterized by tachycardia, blood pressure spikes and extensive vomiting^{2,8}. Although FD mouse models show the same phenotypes: reduced size and neuron 84 numbers in the dorsal root ganglia (DRG)⁹, the mechanism of how SNs fail to develop 85 86 and quickly degenerate remains elusive. Thus, none of the interventions available to FD patients target SN symptoms¹⁰. However, this problem is not limited to FD: other patients 87 88 with SN loss or defects stemming, for example from peripheral neuropathies or cancer chemotherapy treatment have limited pharmacological options as well¹¹. Thus, a drug 89 that targets SNs is necessary to treat a wide range of diseases. 90

Human pluripotent stem cell (hPSC) technology¹² is ideal to gain cellular and 91 92 mechanistic insight into genetic, early-onset human disorders; as it allows the retrieval of 93 patient specific cells, their reprogramming into hPSCs, followed by their differentiation 94 into SNs¹³, and parallel comparison between healthy control and disease cells for disease 95 mechanistic studies¹⁴. Additionally, it provides the possibility to generate large numbers 96 of neurons that can be employed for high-throughput drug screening approaches. In fact, 97 FD was one of the first diseases that was modeled using the hPSCs technology¹⁵ and provided one of the first proof-of-principle drug screens employing hPSCs¹⁶. We 98 99 previously showed that this disease modeling technique is highly sensitive in that it allows 100 the recapitulation of specific phenotypes accounting for patient's varying severity of 101 symptoms¹⁷. We showed that in FD, both NC cells and SNs are not developing efficiently 102 and that the SNs degenerate/die over time in vitro. These findings are consistent with 103 patients being born with less SNs in the DRG⁷, equivalent findings in the FD mouse DRG⁹ and the fact that patient's pain/temperature perception decreases with age¹⁸. 104

105 Here, we conducted a high-throughput chemical screen and identified genipin as 106 a hit compound that targets SN defects in FD. Genipin is derived from the fruit of Gardenia 107 Jasminoides and is the active ingredient of the Traditional Chinese Medicine (TCM) Zhi Zi¹⁹, which is being prescribed for neurodegenerative disorders, including Alzheimer's^{20,21} 108 109 and Parkinson's disease^{22,23}. In this context genipin has shown a safe profile in humans. Genipin has been implicated as an inhibitor of UCP2, preventing UCP2-mediated proton 110 leak in mitochondria and increasing mitochondrial membrane potential²⁴. Furthermore, 111 112 genipin has been shown to have anti-inflammatory effects by inhibiting nitric oxide synthesis *in vitro* and *in vivo*²⁵. Lastly, genipin is being used by bioengineers to crosslink 113 extracellular matrices (ECM), due to its low toxicity^{26,27}. We show that genipin reverses 114 the differentiation inefficiency observed in FD NC and SNs and prevent degeneration of 115 116 SNs in vitro. We also demonstrate that genipin can be fed to pregnant FD mice to rescue 117 the neurodevelopmental phenotypes in embryos. We provide evidence that genipin acts via ECM crosslinking and reverses FD phenotypes by activating the transcription of YAP-118 119 dependent genes. Lastly, we show that genipin promotes rapid regeneration of neurons 120 from the peripheral (sensory and sympathetic) and central (prefrontal cortex) nervous 121 systems. Together, our data provides support that genipin is a novel drug candidate to 122 treat neurodevelopmental diseases, prevent neurodegeneration, and promote neuronal 123 regeneration upon injury. Thus, genipin has the potential to be used as a treatment for a 124 broad range of neurological diseases.

125

126 **Results**

127 <u>Chemical screen to rescue sensory neuron phenotypes in Familial Dysautonomia</u>

128 We first reproduced our previous findings that hPSC-derived SNs from FD patients 129 cannot be generated efficiently in vitro¹⁷. The differentiation protocol defined by 130 Chambers et al.²⁸ (Fig. 1A) was employed to differentiate hPSCs, derived from healthy 131 control embryonic stem cells (H9/WA09, hPSC-ctr-H9), healthy control iPSCs (iPSC-ctr-C1) and two iPSC lines from FD patients (iPSC-FD-S2 and iPSC-FD-S3)¹⁷. While the 132 133 undifferentiated colonies looked normal in all four lines, once SNs were generated by 134 day 13 of the differentiation protocol, the efficiency/number of neurons dropped 135 dramatically in the FD lines compared to the control lines (**Fig. 1B**). Based on this 136 phenotype, we set out to conduct a chemical drug screen to identify compounds that 137 could reverse this phenotype and allow FD-iPSCs to efficiently generate SNs. We first 138 adapted the SN differentiation protocol to high-throughput screening conditions. We 139 tested the following adaptation parameters: 96 and 384 well plate formats, feeding 140 frequency of twice (day 2, 5) or three times (day 2, 5, 8; normal, non-screening feeding 141 is done every other day), shortening the protocol to 10 days total and thus removing the 142 replating step at day 12, and replacing the media gradient with a 1:1 mixture of the KSR 143 and N2 media, respectively instead of the gradual change of media (Fig. 1C). The 144 simplifications of the protocol lead to an overall decrease in SN numbers from ~60% (in 145 the regular protocol²⁸ to ~30% (in our screening protocol) in hPSC-ctr-H9 cells. Within 146 these conditions, the 96-well format and 3 times feeding produced the most robust SNs 147 in the healthy control (Fig. 1D) and the largest difference between control and FD (Sup. 148 **Fig. 1A, B**). We used these conditions to conduct a pilot screening using only positive (149 hPSC-ctr-H9) and negative (iPSC-FD-S2) controls. In these conditions, the calculated Z' 150 factor for the screen was 0.14, which denotes a marginal assay. However, thanks to the

151 design and read-out of our screening, positive and negative controls were clearly 152 distinguishable. We planned for a relatively small screen and thus proceeded with 153 confidence. We reasoned that treatment starting on differentiation day 2 would allow 154 initial specification into ectoderm but influence differentiation into NC and SN fates. We 155 then screened 640 compounds, i.e. half of the LOPAC chemical library of 156 pharmacological active compounds from Sigma, that contains a mixture of compounds 157 from the fields of cell signaling and neuroscience (Fig. 1E). Each compound was 158 screened at 1 mM and 10 mM in DMSO. All wells were then stained for the pan-SN 159 marker BRN3A and DAPI and hit compounds were called if the fold change (FC) over 160 the average of all DMSO wells was above the average of all compounds plus 3 SDs 161 (Fig. 1F, Sup. Table 1, 2). Our screen resulted in 3 hits: Fluphenazine dihydrochloride 162 (Flu, at 10 mM, a dopamine receptor antagonist), AC-93253 iodide (AC, at 1 mM, a retinoic acid receptor agonist) and genipin (at 1 mM and 10 mM, Sup. Fig. 1C). The 163 164 controls on the screen were: Healthy hPSC-ctr-H9 and iPSC-FD-S2, both in DMSO, and 165 DMSO alone. The Z-score for genipin was 15 at 1 mM and 17 at 10 mM.

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167 <u>Hit validation</u>

Next, we performed several validation assays to further assess the hit compounds. The 3 hit compounds were tested in a repeat of the same conditions as performed in the screen itself (**Sup. Fig. 1D**) and then repeated in a different well format (48-wells) using the non-screening differentiation protocol (**Sup. Fig. 1E**). This analysis revealed that indeed genipin rescues the SN defect in FD (**Sup. Fig. 1E**, red rectangle), whereas Flu did not have much of a rescue effect and was auto-fluorescent (**Sup. Fig. 1E**, blue

174 rectangle), and AC did not rescue the FD phenotype and showed high cytotoxicity (DAPI staining, Sup. Fig. 1E, green rectangle). We also tested the three hits on 175 176 additional cell lines, including healthy iPSC-ctr-C1 and a FD line from patients with 177 milder symptoms (iPSC-FD-M2)¹⁷. We observed the same phenotypes in iPSC-ctr-C1 and iPSC-FD-M2 cells (Sup. Fig. 1F). Thus, we focused on genipin. We titrated the 178 179 genipin concentration (Fig. 2A, B) and found that, while genipin increased the number of SNs in a dose dependent manner in control hPSC-ctr-H9 and iPSC-ctr-C1cells (about 180 181 7-fold), the increase of SNs in genipin treated iPSC-FD-S2 cells was dramatically larger 182 (over 30-fold). To further confirm genipin's effect, we tested it in our newer SN differentiation protocol that is fully chemically defined (E8/E6)¹³ (Sup. Fig. 1G). Indeed, 183 184 we found that genipin robustly rescued both the NC and the SN defect in iPSC-FD-S2 185 cells (Fig. 2C). However, in this protocol the cells were more sensitive, showing mild cytotoxic effects at 20 µM (likely due to the lack of the buffering KSR), thus the ideal 186 concentration of genipin was lower (10 µM) (Fig. 2C-E). All data from here on was done 187 188 in the chemically defined SN protocol¹³. Lastly, we tested genipin from different 189 commercial sources (Sigma and Biomaterials) and found that, while both compounds 190 worked, genipin from Biomaterials showed a more robust phenotype at 10 μ M. Further 191 experiments were done using genipin from this source (Fig. 2F). Together, we show 192 that our small molecule screen resulted in the identification of genipin as a rescue 193 compound in our FD model.

194

Effects of genipin on neurodevelopment of neural crest cells and sensory neurons in FD
 <u>iPSCs</u>

197 We sought to carefully characterize genipin's effects throughout development. In human embryonic development, NC cells (marked by SOX10) give rise to SN-specified 198 199 NC cells (marked by NGN1/2), followed by BRN3A⁺ SNs that also express ISL1, PRPH, 200 TRKA, TRKB, and TRKC. Thus, we first assessed the effects of genipin on NC formation. 201 We found an increase of typical dark NC ridges that correlate with SOX10 expression (on 202 mRNA and protein level) in all the cell lines tested (Fig. 3A-C, arrows and Sup. Fig. 2A). 203 Additional NC genes (FOXS1 and P75NTR) were restored by genipin (Sup. Fig. 2B). We 204 found that genipin increased TFAP2A, however non-significant, probably because 205 TFAP2A is also expressed in non-neural ectoderm (Sup. Fig. 2B). We then confirmed 206 that genipin further is capable of rescuing SN development by increasing the number of 207 SNs in FD via staining for BRN3A, TUJ1, ISL1, and PRPH (Fig. 3D, Sup. Fig 2C) and 208 guantification of the number of BRN3A⁺ positive neurons via intracellular FACS analysis 209 (Fig. 3E, Sup. Fig. 2D). Furthermore, the expression of various SN genes (BRN3A, ISL1, PRPH, TRKA, TRKB, and TRKC) was rescued in FD by genipin, shown by RT-gPCR 210 211 (Fig. 3F, Sup. Fig. 2E) and immunoblotting (Fig. 3G). Finally, we show that the firing rate 212 in FD SNs also increases upon treatment with genipin compared to DMSO (Fig. 3H), 213 likely because of the increased number of differentiated SNs. From here on forward, we 214 pooled iPSC-FD-S2 and iPSC-FD-S3 data, also indicated in the figure legends. In sum, 215 our results show that genipin rescues FD neurodevelopmental defects at the NC and SN 216 stage.

217

218 Genipin rescues sensory deficits in FD mice

219 We next assessed whether genipin can also rescue the FD neurodevelopmental 220 defects *in vivo*. Since FD mutant mouse embryos (*Elp1*^{Δ 20/flox}) have significant deficits 221 already at late gestation⁹, we assessed whether genipin has the potential to rescue their 222 developmental defects. Pregnant dams were treated with genipin-supplemented chow 223 from mid-gestation. At E18.5 embryos were harvested and analyzed (Fig. 4A). Genipin 224 was well tolerated during gestation and no significant effect was observed in female 225 gestational weight gain, litter size, or embryonic development (Sup. Fig. 2F and Sup. 226 Table 3).

227 At E18.5, FD embryos treated with genipin did not differ significantly in weight and 228 size compared to untreated FD embryos (779.33 mg \pm 94.00 versus 783.6 mg \pm 137.62, respectively) but remained significantly smaller than control embryos⁹. On the other hand, 229 230 genipin treatment during gestation significantly rescued FD DRG volume and neuronal 231 cell numbers (Fig. 4B-D). Since sensory nociceptive neurons are particularly depleted in FD at late gestation^{9,29,30}, we assessed the paucity of nociceptive neurons by 232 233 immunohistochemistry for calcitonin gene related protein (CGRP), a specific marker for 234 nociceptive neurons³¹. As shown in Fig. 4E and F, while in FD embryos CGRP-positive 235 neurons are reduced to 20% of total lumbar L1 DRG neurons, in genipin-treated FD 236 embryos the number of CGRP-positive neurons increased significantly to about 40% of 237 total neurons. Interestingly, we found that genipin treatment also rescued sensory skin 238 innervation in FD mouse embryos (Fig. 4G), which is severely compromised in FD patients and FD mouse models^{29,32}. Unexpectedly, we found that genipin also rescued 239 240 neurodevelopmental phenotypes in sympathetic neurons, assessed by an increase in the 241 size of the stellate ganglion (Fig. 4H, I).

These results suggest that genipin is well tolerated and rescues FD sensory and sympathetic phenotypes *in vivo*. Furthermore, they confirm the results we obtained in the hPSC-based system and strengthen our hypothesis that genipin is a suitable candidate for as a therapeutic to treat neurodevelopmental diseases such as FD.

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247 Effects of genipin on neurodegeneration in sensory neurons in FD

248 We have previously shown that SNs in FD degenerate and die over time *in vitro* in 249 our PSC model¹⁷. This correlates with reports in FD patients of deteriorating symptoms with age, including pain perception and autonomic regulation¹⁸. Since FD is both a 250 251 neurodevelopmental and a neurodegenerative disorder and thus patients are born with 252 reduced numbers of SNs, it would be imperative for patient care to develop a novel drug 253 that halts or slows degeneration of existing SNs. Therefore, we set out to assess genipin's 254 capability to halt SN degeneration. We first had to adapt our *in vitro* degeneration assay¹⁷ to the new SN differentiation protocol¹³. Titration of NGF revealed that 1 ng/ml of NGF 255 256 leads to degeneration of iPSC-FD-S2 SNs over 20 days while being able to maintain 257 healthy SNs alive (Sup. Fig. 3A, red rectangles). Also, exclusion experiments showed 258 that LM, but not FN or PO could be omitted in the surface coating for SNs (**Sup. Fig. 3B**). 259 Thus, survival assays were done in 1 ng/ml NGF on dishes coated with PO and FN. SNs 260 were differentiated from hPSC lines without genipin until day 12, when they were replated 261 and treatment with genipin began (Fig. 5A). We found that, healthy control SNs survive 262 well in vitro until day 34 and beyond, and they show the classical clustering/ganglia-like 263 structure formation over time (Fig. 5B, arrows). Severe FD SNs, however, die starting 264 from day 13 (Fig. 5B, C). When the SNs are treated with genipin from day 13, this

265 degeneration is prevented (Fig. 5B, C). We confirmed this effect in the KSR-based protocol (Fig. 1A, Sup. Fig. 3C). Furthermore, we show that neurite length from FD SNs 266 267 increases compared to untreated SNs (Fig. 5D, E). We also found that genipin increased 268 the number of dendrites of FD SNs and renders a distribution more similar to healthy SNs 269 (**Sup. Fig. 3D**). It is of note that in a 2D *in vitro* system SNs show more neurites compared 270 to *in vivo*³³. To make sure that there are not substantial numbers of NC cells remaining at 271 day 13, that could be induced by genipin to make more SNs, we stained day 13 and day 272 34 cultures for SOX10, showing the largely absence of NC cells (Sup. Fig. 3E). Thus, 273 genipin truly supports survival of SNs in FD. Together, these results suggest that genipin 274 is a promising candidate drug to halt the progressive SNs degeneration in FD and further 275 might become an interesting candidate drug for the treatment of other peripheral 276 neuropathies.

277

278 ELP1 targets ECM gene expression

279 We next addressed the mode of action through which genipin exerts these rescue 280 effects. FD is caused by a homozygous mutation in *ELP1*, leading to a splicing defect and 281 eventually causing patients to have reduced levels of wild type ELP1 protein, with 282 particularly low levels in PNS tissues, including SNs⁶. Several reports have shown compounds that reverse this splicing defect^{34–37}, thus we first assessed if genipin directly 283 284 affects ELP1. We found that genipin does not change splicing of *ELP1*, assessed on the 285 mRNA and on the protein level (Sup. Fig. 4A, B). Thus, in FD at the SN level genipin 286 must exert its action in a different way.

287 Genipin has been implicated in several contexts, including inhibition of mitochondrial protein UCP2, activation of neuronal nitric oxide synthetase (NOS)²⁰ and 288 its ability to crosslink ECM proteins³⁸. Our previous work ¹⁷ has shown that severe FD 289 290 patients have a modifier mutation in LAMB4, which is an ECM protein. Furthermore, 291 proper composition and availability of ECM proteins have been shown to be essential for SN development^{39–41}. Additionally, Goffena et al. showed that loss of Elp1 particularly 292 293 affects long transcripts and AA- and AG-ending transcripts⁴². We analyzed their 294 sequencing data and found that ECM proteins fall within this highly affected group (Sup. 295 Fig. 4C, D). Furthermore, we conducted RNA sequencing analysis comparing SNs from 296 healthy control and iPSC-FD-S2 cells. Gene ontology analysis revealed that ECM 297 proteins significantly downregulated in FD SNs (Sup. Fig. 4E). Further analysis of gene 298 differential expression showed that the ECM-related proteins FBLN1, COL1A2, HAPLN1, 299 TNC, and HSPG2, among others are downregulated (Sup. Fig. 4F). Thus, loss of ELP1 300 is predicted to lead to ECM defects and we hypothesized that genipin's ability to crosslink 301 ECM proteins might alleviate these issues in FD.

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303 <u>Genipin acts via crosslinking of extracellular matrix proteins in Familial Dysautonomia</u>

304 Genipin forms inter- and intramolecular crosslinks (**Fig. 6A**), which cause the cells 305 to be stained blue due to formation of genipin-methylamine monomers during crosslinking 306 reactions (**Fig. 6B**). Thus, we reasoned that if the rescue in FD functions via ECM 307 crosslinking, then other crosslinking agents should have the same rescue effect as 308 genipin in our FD model. We first tried dimethyl pimelimidate (DMP), a membrane-309 permeable compound that crosslinks crosslink primary amines of proteins (due to

310 imidoester groups present on each end of the molecule) both within the ECM and inside 311 the cell (Sup. Fig. 5A). We found that DMP rescued both the NC deficit (Sup. Fig. 5B, top) as well as the SN deficit (Sup. Fig. 5B, bottom) in FD cells in a dose dependent 312 313 manner (Sup. Fig. 5C). This result suggests that protein crosslinking is sufficient to 314 rescue the neurodevelopmental FD phenotype. However, it remains unclear whether 315 crosslinking of extracellular or intracellular proteins or both rescue the FD phenotype. 316 Thus, we used bis-(sulfosuccinimidyl) suberate (BS3), a membrane-impermeable 317 crosslinker which only crosslinks proteins in the ECM (Fig. 6C). We found that BS3 318 rescues both the NC (Fig. 6D, top) as well as the SN phenotypes (Fig. 6D, bottom) in a 319 dependent manner (**Sup. Fig. 5D**). Additionally, when we used dose N-320 hydroxysulfosuccinimide (Sulfo-NHS), a form of BS3 with no crosslinking capabilities, the 321 rescue effect was abolished in both the NC and SN phenotypes (Sup. Fig. 5E). Together, 322 our data suggests that crosslinking of only extracellular proteins (i.e. the ECM) is 323 necessary and sufficient to rescue the developmental phenotype in FD. Moreover, these 324 results strongly support a model where genipin exerts its action in FD via crosslinking 325 proteins in the ECM. To confirm that the FD phenotype is rescued only by genipin's 326 crosslinking activity and not its other predicted function (i.e. UCP2 inhibition), we used 327 1,10-anydrogenipin (AG, Fig. 6E). AG has been shown to specifically remove genipin's 328 ability to crosslink proteins, while keeping its other actions intact²⁴. Confirming that AG 329 does not have crosslink activity, we found that AG did not stain the FD cells blue (Fig. 330 6F). Furthermore, in contrast to genipin, AG was not able to rescue the NC (Sup. Fig. 5F, 331 G) nor the SN phenotype in FD cells (Fig. 6G,H, Sup. Fig. 5H, I). Together, our results 332 show that genipin's crosslinking action is responsible for the FD phenotype rescue.

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334 Genipin increases stiffens of the ECM of FD SNs

335 Atomic force microscopy (AFM) can be used to study how the morphology and 336 mechanical properties of live or fixed cells are affected under different conditions (for 337 example, changes in the ECM)^{43–45}. In AFM, a tip is roughly aligned on the surface of the 338 cell using an optical microscope, then contact AFM mode is applied where the tip scans 339 the surface (**Fig. 6I**). A laser beam, aimed at the cantilever holding the tip, is detected by 340 a photodetector. Vertical changes in the position of the tip (due to different height in the 341 surface) are measured, resulting in high-resolution topographic images of the samples 342 (Fig. 6I, Sup. Fig. 6A). Interestingly, we found that genipin re-orientates the ECM as shown by the presence of ordered "strips" (possibly due to the presence of crosslinking 343 344 bundles), in stark contrast to DMSO controls where the ordered "strips" are missing (**Sup.** 345 Fig 6A). Also, the height of the samples increased with genipin (from to 2.09 µm to 3.5 346 μm for SNs, from 0.8 μm to 1.2 μm for ECM) (Sup. Fig 6A) due to formation of crosslinked 347 bundles. From these acquired cell images, we selected different points on the surface 348 (Fig. 6I, black crosses) and measured their force spectroscopy. The deflection of the 349 cantilever tip was recorded and converted to force-distance curves (Sup. Fig. 6B, solid 350 lines). Force-distance curves were further fitted with the Hertz model (suitable for fitting under small deformation in nanoindentation measurements⁴⁶) to calculate the Young's 351 352 modulus (a measurement of stiffness) of individual cells (Sup. Fig. 6B, dotted lines). We 353 found that FD SNs treated with genipin have a higher Young's modulus (~8,000 Pa) 354 compared to DMSO control (~2,000 Pa) (Fig. 6J, Sup. Fig 6B, C), agreeing with previous 355 reports^{45,47,48}. Furthermore, genipin-treated SNs show narrower distributions, suggesting 356 a stiffer and more uniform surface due to ECM crosslinking (Sup. Fig 6D). To confirm our 357 results, we removed the SNs and measured only the remaining ECM. Agreeing with our 358 previous results, we found that the ECM deposited by genipin-treated SNs has a Young's 359 Modulus ten times higher compared to untreated controls (~13,300 Pa vs ~1,300 Pa) (Fig. 6J, Sup. Fig 6B, C). These changes could only be attributed to the direct 360 361 crosslinking of genipin with ECM, further strengthening our hypothesis that ECM crosslinking by genipin is necessary to rescue the FD neurodevelopmental and 362 neurodegenerative phenotypes. 363

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365 ECM crosslinking causes actin reorganization and transcription of YAP-dependent genes

Based on our previous results, we asked whether a stiffer ECM (due to genipin-366 367 dependent crosslinking) has any intracellular effects. The ECM is necessary for proper 368 development and distribution of the cytoskeleton⁴⁹, and previous reports showed that the actin cytoskeleton is missregulated in FD⁵⁰. Thus, we first assessed whether the actin 369 370 expression pattern is different between healthy and FD SNs. We measured the signal 371 from the cell bodies (Sup. Fig. 6E, black line) or the axons (Sup. Fig. 6E, blue lines). We 372 found that the actin signal in healthy SNs is the highest in the cell body, whereas FD SNs 373 show stronger actin signal in the axon (Fig. 6K, Sup. Fig. 6F, G). Treatment with genipin 374 was able to partially restore the actin expression pattern in FD SNs (Fig. 6K). Changes in actin cytoskeleton organization due to ECM stiffness activate the Hippo pathway⁵¹. In 375 376 a stiff ECM, the transcriptional coactivator YAP (the most downstream effector of the 377 Hippo pathway), translocates from the cytoplasm to the nucleus to activate a transcriptional program⁵¹. We sought to assess YAP localization in SNs by 378

379 immunofluorescence. We found that in both healthy and FD SNs, YAP is present in the cytoplasm as assessed by the presence of YAP signal outside of the nucleus (stained 380 381 with DAPI) (Fig. 6L, M, black arrows). However, upon genipin treatment, YAP is 382 transported to the nucleus as shown by detection of YAP fluorescent signal only within 383 the boundaries of the nucleus (stained with DAPI) (Fig. 6L, M). This suggests that the 384 increase in ECM stiffness due to genipin-mediated crosslinking activates the Hippo pathway in SNs. We next assessed whether YAP nuclear translocation results in 385 386 transcription of YAP-dependent genes. Indeed, we found that YAP1 and CYR61 387 expression is significantly higher in FD SNs treated with genipin (Fig. 6N). RUNX1 is a 388 transcription factor necessary for maturation of nociceptors (a subtype of SNs). Interestingly, in cancer YAP interacts with RUNX1 to regulate transcription^{52,53}, thus we 389 390 asked whether these genes are also activated in FD SNs in the presence of genipin. We 391 found that genipin increased the expression of all the tested genes that are dependent on 392 YAP-RUNX1 interaction: SULF1, S100A8, S100A14, COL12A1, and TMEM2 (Fig. 6M). 393 Together, our data suggest that genipin-dependent ECM crosslinking causes actin 394 reorganization and activation of the Hippo pathway in SNs, which rescue development 395 and survival in FD phenotypes.

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397 <u>Genipin enhances axon regeneration of neurons from the peripheral and central nervous</u> 398 <u>system.</u>

Our results show that genipin rescues both developmental and degenerative FD phenotypes in SNs, suggesting its beneficial support of neurons in this disease. We wondered whether genipin might be beneficial in more common disorders of the PNS. To

402 test this hypothesis, we inquired if genipin is beneficial for axon regeneration. We first 403 assessed whether we can use our in vitro system as an axotomy model. We have 404 previously shown that in our system, hPSC-ctr-H9-derived SNs can be replated at late 405 stage¹³, which is known to enzymatically cut neurites and thus serving as an axotomy 406 model (Fig. 7A). Employing this approach, in combination with genipin treatment during 407 the regeneration phase, we found that this process causes expression of ATF3 and SPRR1A, two critical genes involved in neuron regeneration⁵⁴, in DMSO treated SNs 408 409 differentiated from hPSC-ctr-H9 cells (Fig. 7B). Interestingly, we found that SNs replated 410 in the presence of genipin express higher levels of both genes (Fig. 7B). Furthermore, 411 high ATF3 expression is maintained for a longer period of time. We next assessed whether genipin affects the speed of axon regeneration. We found that SNs treated with 412 413 genipin showed longer axons 18 hours and 6 days post replating (Fig. 7C, D). To expand 414 genipin's application in the PNS further, we tested peripheral sympathetic neuron 415 regeneration. To do so, we employed a microfluidic device, which maintains cell bodies 416 and axons in two different compartments, allowing us to break the axons without 417 disturbing the cell bodies (Fig. 7E). An NGF gradient guides the direction of axonal growth 418 and neurites can be cut and removed with a pipet tip from the left chamber without hurting 419 the cell bodies in the right chamber (Fig. 7E). We found that genipin increases the number 420 and length of regenerated axons from hPSC-ctr-H9-derived sympathetic neurons 2 days 421 post injury, measured by an increase in PRPH staining by immunofluorescence (Fig. 7F, 422 **G**). These results suggest that our system can be used to model axonal injury in the PNS 423 and that genipin increases the regeneration speed in peripheral neurons. Finally, we 424 asked if genipin might be beneficial for neurite regeneration in CNS neurons, possibly

extending its usefulness further to spinal cord injury in a broader context. To do that, we tested prefrontal cortical (PFC) neurons differentiated from hPSC-ctr-H9 cells⁵⁵. Using our replating method (**Fig. 7H**), we found that PFC neurons treated with genipin regenerate their axons faster than DMSO-treated neurons by IF, measured by the increase in the number of pixels positive for TUJ1 (**Fig. 7I-J**). Taken together, our results suggest that genipin can be used to promote neuronal regeneration in both PNS and CNS neurons applicable to a broad range of degenerative diseases.

432

433 Discussion

434 Here, we discovered that genipin rescues both neurodevelopmental and 435 neurodegenerative phenotypes in a hPSC-based disease model of FD. We further 436 showed that genipin rescues sensory ganglia phenotypes in vivo. Additionally, we 437 demonstrate that these phenotypes are due to crosslinking of ECM proteins causing 438 rearrangement of the cytoskeleton and activates transcription of YAP-dependent genes. 439 Finally, we showed that genipin promotes regeneration of neurons from the peripheral 440 and central nervous system after injury. Thus, genipin has a broad application potential 441 in a wide range of neurological disorders.

To date there is a lack of treatments that specifically target either the neurodevelopmental or the neurodegenerative aspects of FD. This void leads to patient's symptoms being managed both surgically and pharmacologically^{2,10} without clearly targeting the molecular cause of the disease. Over the past 20 years, multiple compounds have been identified that target the ELP1 splicing defect in FD have been identified, however they have failed in clinical trials or there is no evidence that they target the PNS.

448 These include the plant hormone kinetin, which, despite its promising results in FD 449 animals³⁴, worsened the nausea and vomiting episodes in patients². Phosphatydilserine (PS) which increased ELP1 expression in patient-derived fibroblasts⁵⁶ and animal 450 models⁵⁷ but has not successfully undergone clinical trials². Finally, tocotrienol (vitamin 451 452 E) and the antioxidant epigallocatechin gallate (ECGC) were increase *ELP1* expression in cells lines^{58,59} but did not increase *ELP1* expression in patients, nor improved clinical 453 outcomes^{16,60,61}. A recent study showed that the small molecule RECTAS restores normal 454 455 ELP1 splicing in SNs differentiated from FD iPSCs and in vivo, however it is unclear whether it rescues any FD phenotype³⁷. Finally, gene therapy approaches, such as 456 antisense oligonucleotides (ASO), have been shown to restore ELP1 expression in 457 patient fibroblasts and FD animals^{62–64}. Importantly, however, they did not show a rescue 458 459 in PNS tissues and human clinical trials are note initiated yet. In sum, the field lacks 460 specific drugs to treat FD and the available candidates have not been tested or are not 461 effective in human tissues affected in patients, such as PNS neurons.

462 Similar to FD, more common neurodegenerative disorders affecting the PNS 463 experience a dramatic absence of available treatments. These include diabetes (in up to 464 50% of patients) or chemotherapy-induced (in up to 40% of patients) peripheral 465 neuropathy, as well as neuropathies caused by injury, infections, medications, 466 alcoholism, and even vitamin deficiencies. In fact, there are very few FDA-approved drugs 467 available for peripheral neuropathy and PNS injury and the ones available mainly focus on managing symptoms^{11,65}. Furthermore, although there is extensive research aimed to 468 469 identify treatment that regenerate peripheral neurons after injury, very few of them are or 470 have been in clinical trials. They include gene therapy, electrical stimulation, and nerve

transfer of an expendable, uninjured donor nerve⁶⁶. Due to these difficulties, genipin could be a cost-effective treatment for nerve regeneration. Our results show that genipin is a highly promising compound with potential to be further developed as a treatment option for neurodevelopmental and neurodegenerative diseases (including peripheral neuropathies). Additionally, its lack of toxicity on cells²⁶ and *in vivo*^{24,25}, and the fact that it can transverse through the placenta, makes genipin a safe drug. Further studies will be needed to address this.

Our results showing genipin's ability to rescue neurodevelopmental defects in 478 479 hPSC-derived FD SNs and in SNs in mice highlight the importance of ECM proteins 480 during development. This data lays the groundwork to further investigate the ECM 481 composition necessary for normal PNS development, as well as how defects in ECM 482 proteins, such as laminin¹⁷, contribute to PNS disorders⁶⁷. The rescue on 483 neurodevelopment that we see in FD mice is interesting and urges the investigation of the effects of genipin on neurodegeneration further. As we report, genipin reverses the 484 485 progressive loss of SNs in the FD hPSC-based disease model and it enhances neurite 486 growth and density (Fig. 5B-E, Sup. Fig. 3D). This is consistent with the literature, where 487 it has been shown that the extracellular environment (presence of growth factors, ECM composition, and 2D vs 3D cultures) affect neurite length and arborization^{33,40,68,69}. This 488 489 is in agreement with the role of genipin as an ECM crosslinker. It will be crucial to assess 490 this finding further, as this may provide real promise for patients with neurodegenerative 491 diseases. For instance, in chemotherapy-derived neuropathies, patients who are more susceptible to axonal degeneration are affected by paclitaxel-induced neuropathy⁷⁴. 492 493 Genipin could be used as a supplement to prevent neuronal degeneration.

494 Most research on the molecular implications of FD focus primarily on ELP1. We show that genipin exerts it effects via crosslinking of ECM proteins and that its rescue 495 496 effect is removed upon removal of its crosslinking activity (Fig. 6E-H, Sup. Fig. 5F-I). 497 Agreeing with this, we show that genipin increases surface stiffness of SNs and isolated, deposited ECM proteins (Fig. 6J, Sup. Fig. 6B-D). Previous reports, showed that loss of 498 499 ELP1 results in defective actin and microtubule organization in fibroblasts or brain 500 tissues^{50,70}. Here, we report that these phenotypes are conserved in SNs differentiated 501 from human FD iPSCs (Fig. 6K, Sup. Fig. 6F, G). Furthermore, we found that increasing 502 stiffness of the ECM by crosslinking rescues this phenotype, agreeing with studies 503 showing that biomechanical cues (such as stiffness of the ECM) affect actin cytoskeleton 504 organization⁷¹. Our RNAseq results show that upon loss of *ELP1* a myriad of ECM-related 505 proteins are downregulated causing an aberrant cellular environment. Therefore, 506 signaling multiple pathways are missregulated. One of them is the Hippo pathway, which 507 translates external mechanical cues into biochemical signals that affect gene 508 expression⁵¹. Interestingly, we show that YAP (the most downstream effector of the Hippo 509 pathway) is mainly present in the cytoplasm of SNs, suggesting that it is inactive, agreeing with previous reports⁷². However, upon genipin treatment, YAP translocates to the 510 511 nucleus and promotes transcription of genes associated with cell proliferation (CYR61, 512 S100A14), cell cycle progression (S100A8), ECM remodeling (SULF1, COL12A2, 513 *TMEM2*) (Fig. 6L-N). We hypothesized that YAP activation initiates a transcriptional 514 program that allows the proliferation of progenitor cells, thus increasing the number and survival of SNs. Very little is known of the role of the Hippo pathway and YAP function in 515 516 the PNS, although mechanotransduction (including ECM-cell interaction) is important in

517 NC migration and differentiation⁶⁷. Furthermore, it has been proposed that mechanical 518 modulation of the Hippo pathway could potentially be used as a treatment for peripheral 519 neuropathies⁷³. Genipin, by its ECM-crosslinking activity, fit in this category. Our results 520 show that potential treatment options for FD lay beyond ELP1 splicing correction and that 521 modifying the ECM may be key. Furthermore, our findings suggest that looking at basic 522 cellular mechanisms is necessary to identify new potential therapeutic targets.

In sum, genipin shows great promise as a future treatment option for FD as well as other more common neuropathies. Its action via ECM crosslinking and our exciting results about its ability to increase axon regeneration make it an interesting compound for the future application to nerve regeneration in the PNS and possibly prevention of peripheral neuropathies.

528

529 Materials and methods

530 Chemical screen

531 For the chemical screen hPSC-ctr-H9 control and iPSC-FD-S2 cells were cultured in KSR 532 conditions (see below). 96-well plates were coated with Matrigel. hPSCs were detached 533 from MEF cultures using Trypsin (52) and cells were seeded at 80,000 cells/well for iPSC-534 FD-S2 and 40,000 cells/well for hPSC-ctr-H9 in order to start the differentiation at equal 535 cell numbers the following day (=day 0). The SN differentiation was performed as 536 described in Fig. 1c. The compounds of the LOPAC chemical library (Sigma) were added 537 on differentiation days 2, 5 and 8 and the plates were fixed and stained for BRN3A and 538 DAPI on day 10. 16 tiles/well were imaged using the MetaXPress software: Cell Scoring 539 by Molecular Devices. The percentage of BRN3A+ cells over DAPI of all DMSO control

wells was averaged. Each compound-treated well number was divided by this DMSO average to calculate the fold change/fold increase of compound-treated wells over controls. To call a hit the average + 3 SD was used. The Z' score (53) (Z'=0.25) was calculated before conducting the screen, using a pilot screen with only hPSC-ctr-H9 and iPSC-FD-S2 lines in a small format, but in the final screening conditions. The Z-score for genipin at 1 mM was 15 and at 10mM it was 17.

546

547 hPSC maintenance

In KSR conditions, hPSCs were maintained on MEFs as described¹⁷. In E8 conditions, 548 549 human embryonic stem cells (WA-09, WiCell) and all iPSC lines were grown on dishes 550 coated with vitronectin (5µg/mL, 1h at RT) at 37°C with 5% CO2 and fed daily with 551 Essential 8 Medium + Supplement. For splitting, hPSC-ctr-H9 colonies were washed with PBS and incubated with 0.5mM EDTA, 3.08M NaCl in PBS with for 2 min at 37°C. Cells 552 were then resuspended in E8 + Supplement and split at a ratio of 1:10. iPSC-ctr-C1. 553 554 iPSC-FD-M2, iPSC-FD-S2, and iPSC-FD-S3 cells were previously characterized ¹⁷ and maintained under the same conditions. 555

556

557 <u>Neural crest and sensory neuron differentiation</u>

In KSR conditions: hPSCs were differentiated into SNs as described previously¹⁷. In E8/6 conditions: Differentiations were done as previously described¹³. Briefly, prior to differentiation, plates were coated with vitronectin (5 μg/mL) and incubated for 1h at RT. hPSCs were harvested using 0.5 mM EDTA, 3.08 M NaCl in PBS for 20 min and plated at a density of 200,000 cells/cm². On day of plating (day 0) and day 1, cells were fed with NC differentiation media (day 0-1) containing: Essential 6 Medium, 10 μM SB431542, 1 ng/mL BMP4, 300 nM CHIR99021, and 10 μM Y-27632. BMP4 concentration is very sensitive at this stage and was titrated for each line. Accordingly, BMP4 was not used with iPSC-FD-S3 cells. From day 2 to 12, cells were fed every other day with NC differentiation media (day 2-12): Essential 6 Medium, 10 μM SB431542 0.75 μM CHIR99021, 2.5 μM SU5402, and 2.5 μM DAPT.

569 On day 12, cells were replated at a density of 250,000 cells/cm² onto plates coated with 570 15 µg/ml poly-L-ornithine, 2 µg/ml laminin-1, and 2 µg/ml human fibronectin (PO/LM/FN). 571 Cells were incubated with Accutase for 20 min, washed with PBS, and resuspended in 572 SN Media: Neurobasal media containing N2, B-27, 2 mM L-glutamine, 20 ng/ml GDNF, 573 20 ng/ml BDNF, 25 ng/ml NGF, 600 ng/ml of laminin-1, 600 ng/ml fibronectin, 1 µM DAPT 574 and 0.125 µM retinoic acid. Cells were fed every 2-3 days until day 20. On day 20, DAPT 575 was removed. Differentiation progress was followed using a brightfield microscope 576 (Leica). Genipin (Sigma or Biomaterials), 1,10 anhydrogenipin (AG), dimethyl 577 pimelimidate (DMP, ThermoFisher), bis-(Sulfosuccinimidyl) suberate (BS3, CovaChem), N-hydroxysulfosuccinimide (Sulfo-NHS, ThermoFisher) were added on day 2 of the 578 579 differentiation and included every media change. Genipin and AG were resuspended in 580 DMSO and aliquoted. DMP, BS3, and sulfo-NHS were resuspended in DMSO (DMP and 581 BS3) or PBS (sulfo-NHS) immediately prior to use.

582

583 Sympathetic neuron (symN) differentiation

584 The detailed differentiation protocol was described in previous publications^{17,75}. Briefly, 585 hPSCs were dissociated using EDTA and replated on Geltrex (Invitrogen, A1413202)-

586 coated plates at 125x10³/cm² density in Essential 6 medium+0.4 ng/ml BMP4 (PeproTech, 314-BP)+10 µM SB431542 (R&D Systems, 1614)+300 nM CHIR99021 587 588 (R&D Systems, 4423). On day two, cells were fed with Essential 6 medium+10 µM 589 SB431542+0.75 µM CHIR99021 every two days until day 10 for neural crest induction. 590 Day 10 neural crests were dissociated using Accutase and replated on ultra-low 591 attachment plates (Corning, 07 200) in Neurobasal medium+B27+L-Glutamine+3 µM 592 CHIR99021+ 10 ng/ml FGF2 to induce sympathoblast spheroids. On day 14, spheroids were dissociated using Accutase and replated on PO/LM/FN-coated plates at 1x10⁵/cm² 593 594 density in Neurobasal medium+B27+L-Glutamine+25 ng/ml GDNF+25 ng/ml BDNF+25 595 ng/ml NGF+200 µM ascorbic acid (Sigma, A8960)+0.2 mM dbcAMP (Sigma, 596 D0627)+0.125 µM retinoic acid. Medium was changed every three days from day 14 to 597 20. After day 20, neurons were fed weekly until desired timepoints.

598

599 Prefrontal cortical neuron (PFC) differentiation

600 The detailed differentiation protocol was described in previous publications^{55,76}. Briefly, 601 hPSCs were dissociated using EDTA and replated on Matrigel (Corning, 356234)-coated plates at 260,000 cells/cm² density in Essential 8 medium supplied with Y-27632. Next 602 603 day (defined as day 0), cells were fed with E6+100nM LDN193189 (Selleck Chemicals, 604 S2618)+10 µM SB431542 +2 µM XAV939 (TOCRIS, 3748). On day 2, cells were fed with 605 E6 + 100 nM LDN193189 + 10 µM SB every two days until day 8. On day 8, cells were 606 dissociated using Accutase and replated as droplets on PO/LM/FN-coated plates (cells 607 from each well of the 6-well plate were replated into 10 droplets, 10 µl per droplet) in 608 Neurobasal+N2+B27 (1:1000)+FGF8 (50 ng/mL, R&D)+SHH (25 ng/mL, R&D). On day

16, droplets were dissociated using Accutase and replated on PO/LM/FN-coated plates
at 1x10⁶ cells/cm² density in Neurobasal+N2+B27 (1:1000)+FGF8 (50 ng/mL). On day
22, neurons were dissociated using Accutase and replated on PO/LM/FN-coated plates
at 100,000 cells/cm² density in Neurobasal+N2+B27 (1:50)+FGF8 (50 ng/mL). Neurons
were fed without FGF8 after day 40.

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615

616 <u>Electrophysiology</u>

Experiments were performed using a Maestro Pro (Axion Biosystems) MEA system. BioCircuit MEA 96 plates containing 8 embedded electrodes/well were coated with Poly-L-ornithine/laminin/fibronectin (as previously described), seeded with day 12 NCCs (250,000 cell/cm²) and allowed to continue differentiating. Repeated recordings were made every 2-3 days at 37°C with a sampling frequency of 12.5 kHz for 5 min. Recordings from at least 6 wells per reading were averaged. Firing frequency was normalized to the number of active electrodes.

624

625 Survival and neurite growth assays

Day 12 NCCs, cells were replated on 4-well plates, at 250,000 cells/cm² (for survival assay) or 25,000 cells/cm² (neurite growth assay), coated with PO/FN in SN media with 1 ng/ml NGF. Media was changed every 2-3 days. DAPT was removed after day 20. Cells were fixed on day 13, 20, 27, and 34 and stained for BRN3A and TUJ1 (survival assay) or on day 25 (neurite growth assay) and stained for TUJ1.

632 Axotomy models

For SN regeneration, day 25 SNs were dissociated with Accutase for 45min. Cells were then collected in a conical tube and filled 1X with PBS. Cells were then centrifuged and resuspended in SN media with DMSO or genipin (10 μ M). SNs were seed in PO/LM/FNcoated plates at 250,000 cells/cm² and incubated for 6 days. RNA was collected on the indicated days. Alternatively, SNs were fixed as previously described at the indicated times.

639 *For PFC regeneration*, day 40 PFCs were dissociated using Accutase and replated on 640 PO/LM/FN-coated plates at 25×10^3 /cm² density with DMSO or genipin (10 μ M). Replated 641 neurons were fed every two days until day 45 and fixed for evaluation.

642 For symN regeneration, day 14 sympathoblasts were replated on the PO/LM/FN-coated 643 microfluidic culture devices (eNUVIO, OMEGA4) on one side at 100,000 cells/cm² 644 density. The replating side was defined as the cell body chamber, while another was 645 defined as the axon chamber. NGF containing medium was given to both chambers. On 646 day 20, NGF was given only to the axon chamber to induce axon outgrowth for 10 days. 647 On day 30, axons in the axon chamber were removed using the suction, and DMSO or 648 genipin containing media were added to both chambers for 48 hours. On day 32, 649 regenerating axons were fixed for evaluation.

650

651 <u>Antibodies</u>

The following primary antibodies were used: SOX10 (Santa Cruz, cat# sc-365692),
TFAP2A (Abcam, cat# ab108311), BRN3A (Millipore, cat# MAB1585), TUJ1 (Biolegend,
cat# 801201), ISL1 (DSHB, cat# 39.4D5-c), PRPH (Santa Cruz, cat# sc-377093), Actin

(BD Biosciences, cat# 612656), YAP1 (Proteintech, cat# 13584-1-AP), Phalloidin-iFluor
488 (abcam, cat# ab176753). The following secondary antibodies were used: From
ThermoFisher: goat anti-mouse IgG1 AF488 (cat# A21121), goat anti-mouse IgG2a (cat#
A-21131), goat anti-mouse IgG2b (cat# A21242), donkey anti-rabbit AF647 (cat#
A31573), donkey anti-mouse AF488 (cat# A21202), goat anti-mouse HRP (cat# 626520), and goat anti-rabbit HRP (cat# 65-6120). The dilutions used are indicated in each
section.

662

663 Flow cytometry

Cells were dissociated with Accutase for 30 min and then washed in Flow buffer (DMEM, 664 2% FBS, and 1mM L-glutamine). Cells were centrifuged at 200 g for 4 min, resuspended 665 666 in cold PBS, counted, and diluted to a concentration of 1x10⁶ cells/100µL. Cells were then centrifuged and resuspended in 300 µL BD Cytofix/Cytoperm (BD Biosciences) buffer 667 and incubated on ice for 30 min. Cells were centrifuged for 4 min at 2,000 RPM and 668 669 resuspended in 600 µL of cold BD Permeabilization/Wash buffer (BD Biosciences). 30 µL 670 goat serum was added followed by incubation on ice for 30 min. Cells were divided in 3: 671 unstained control, secondary antibody control, and sample to stain (200 µL each). All 672 tubes were centrifuged for 4 min at 2,000 RPM and the cells were resuspended in 200 µL 673 of Antibody buffer: BD perm/wash buffer + 10 µL goat serum with or without BRN3A 674 antibody (1:100). Cells were incubated o/n at 4°C. Cells were then washed twice with 300 675 µL BD Permeabilization/Wash buffer, resuspended in Antibody buffer with or without 676 AF488 goat-anti-mouse (1:500), and incubated on ice for 30 min. Cells were then washed

677 3X with BD perm/wash buffer. Cells were filtered and analyzed using a Cytoflex S 678 (Beckman). Analysis was done using FlowJo.

679

680 Immunoblotting

Whole cell lysates were obtained from day 12 NCCs or day 20 SNs. Cells were washed 681 682 once with PBS and incubated with RIPA buffer (ThermoFisher) with 1 mM PMSF and Phospho-STOP (Roche) for 15min on ice. Cells were then vortexed for 10 s and 683 684 centrifuged at 12,000 RPM for 10 min at 4°C. Protein concentration from supernatants 685 was measured and ran in 7.5% polyacrylamide gels using MOPS buffer (GenScript) at 686 130 V. Proteins were transferred to a nitrocellulose membrane and blocked for 30 min in 687 5% non-fat dry milk in 0.1% Tween-20 in TBS (TBS-T, 50 mM Tris-HCl, 150 mM NaCl, 688 pH7.6). Primary antibodies were added to blocking buffer (SOX10 - 1:1000, BRN3A -689 1:1000, and Actin - 1:5000) and membranes were incubated overnight at 4°C. Blots were 690 then washed 3X with 0.1% TBS-T and incubated with goat anti-mouse HRP antibody 691 (1:5000) for 1 h at room temperature. Blots were washed 3X with 0.1% TBS-T followed 692 by incubation with Clarity Western ECL Substrate (BioRad). Chemiluminescence signal 693 was detected using UVP ChemStudio (Analytic Jena).

694

695 <u>Immunofluorescence</u>

NCCs and SNs (day 12 and day 20, respectively, unless indicated otherwise) from either
24- or 4-well plates were fixed with 4% paraformaldehyde for 20 min at RT. Cells were
washed with PBS and incubated for 20 min with Permeabilization buffer containing 1%
BSA, 0.3% Triton-X, 3% goat or donkey serum and 0.01% sodium azide in PBS. Cells

700 were then incubated with the indicated primary antibodies (SOX10 – 1:100, TFAP2A – 701 1:500, BRN3A – 1:100, TUJ1 – 1:1500, ISL1 – 1:200, PRPH – 1:100) in Antibody buffer 702 containing 1% BSA, 3% goat or donkey serum and 0.01% sodium azide overnight at 4°C. 703 The cells were washed 3X in PBS and incubated for 1h with Secondary antibodies in 704 Antibody buffer. Cells were washed with PBS and incubated with DAPI (1:1,000) for 5min, 705 washed with PBS and stored at 4°C. All imaging was done using a Lionheart FX 706 fluorescence microscope (BioTek). All image analysis and guantifications were done in 707 Fiji. For quantifications, 5 different fields were imaged and quantified. To measure the 708 area of NCCs, day 12 NCCs images were analyzed using Gen5. A mask measuring DAPI 709 signal intensity was used. Threshold was established as the 25% signal intensity from the 710 average signal of each field. The areas of objects between 100 µm to 1000 µm where 711 DAPI signal above background were measured. To measure neurite length, images were 712 transformed to 8 bit grayscale images and neurites were measured using NeuronJ⁷⁷. For 713 confocal microscopy, on day 12, 50,000 NCCs were seeded in iBidi dishes (cat# 80426) 714 in the presence or absence of genipin. On day 20, SNs were fixed and steined as 715 previously described. Primary antibodies used: TUJ1 – 1:1500, YAP1 – 1:100. Phalloidin-716 iFluor 488 (1:1000) was incubated with secondary antibodies for 1 h. Imaging was done 717 in an Olympus FV1200 Confocal Laser Scanning Microscope using Argon and Helium-718 Neon lasers. Images were taken as Z-stacks of 3 µm of height. ImageJ was used to obtain 719 maximum intensity projections and to measure the signal intensity profiles.

720

721 <u>RT-qPCR</u>

722 RNA was isolated using Trizol (ambion) according to manufacturer's conditions, resuspended in 20 µL RNase-free water and concentration was measured using 723 724 NanoDrop One (Thermo Scientific). 1 µg of RNA was converted to cDNA using iScript 725 cDNA Synthesis kit (BioRad) according to manufacturer's instructions and diluted 1:100 726 in water. RT-qPCR reactions were run with 1 ul of cDNA and SYBR Green Supermix 727 (BioRad) according to the manufacturer's conditions. Reactions were run in a C1000 Touch Thermal Cycler CFX96 (BioRad) using the following cycling parameters: 95°C for 728 729 5 min, 40 cycles of 95°C for 5s and 60°C for 10 s. Results were analyzed using the 730 comparative CT method. GAPDH was used as a housekeeping gene.

731

732 Primers

The following primers were used in this study:

734 SOX10f-5'CCAGGCCCACTACAAGAGC, SOX10r-5'CTCTGGCCTGAGGGGTGC, 735 TFAP2Af-5'GACCTCTCGATCCACTCCTTAC, TFAP2Ar-736 5'GAGACGGCATTGCTGTTGGACT, FOXS1f-5'ATCCGCCACAACCTGTCACTCA, FOXS1r-5'GTAGGAAGCTGCCGTGCTCAAA, P75f-737 738 5'CCTCATCCCTGTCTATTGCTCC, P75r-5'GTTGGCTCCTTGCTTGTTCTGC, NGN1f-5'GCCTCCGAAGACTTCACCTACC, NGN1r-5'GGAAAGTAACAGTGTCTACAAAGG 739 NGN2f-5'CAAGCTCACCAAGATCGAGACC, 740 NGN2r 741 5'AGCAACACTGCCTCGGAGAAGA, BRN3Af-5'AGTACCCGTCGCTGCACTCCA, 742 BRN3Ar-5'TTGCCCTGGGACACGGCGATG, ISL1f-743 5'GCAGAGTGACATAGATCAGCCTG, ISL1r-5'GCCTCAATAGGACTGGCTACCA, 744 PRPHf-5'GTGCCCGTCCATTCTTTGC, PRPHr-5'GTGCCCGTCCATTCTTTGC,

745	TRKAf-5'CACTAACAGCACATCTGGAGACC,				TRKAr-
746	5'TGAGCACAAGGAGC	AGCGTAGA	, TRKBf	-5'ACAGTCAG	CTCAAGCCAGACAC,
747	TRKBr-5'GTCCTGCTCAGGACAGAGGTTA,				TRKCf-
748	5'CCGACACTGTGGTC/	ATTGGCAT,	TRKC	r-5'CAGTTCTC	GCTTCAGCACGATG,
749	YAP1f-5'	TGTCCCA	GATGAACG	TCACAGC,	YAP1r-5'
750	TGGTGGCTGTTTCACT	GGAGCA,	CYR61f-5'	GGAAAAGG	CAGCTCACTGAAGC,
751	CYR61r-5'	GGAGATA	ACCAGTTCC	ACAGGTC,	SULF1f-5'
752	GGTCCAAGTGTAGAAG	CCAGGATC,	SULF1r-5'	GACAGACT	TGCCGTCCACATCA,
753	S100A8f-5'	ATGCCGT	CTACAGGG	ATGACCT,	S100A8r-5'
754	AGAATGAGGAACTCCT	GGAAGTTA	Α,		S100A14f-5'
755	CCTCATCAAGAACTTT	CACCAGTA	, S100A14r-5	5' GGTTGGCA	ATTTTCTCTTCCAGG,
756	COL12A1f-5'	CAGTGCC	TGTAGTCA	GCCTGAA,	COL12A1r-5'
757	GGTCTTGTTGGCTCTG	STGTCCT,	TMEM2f-5'	GGAATAGGA	CTGACCTTTGCCAG,
758	TMEM2r-5'	TTCTGA	CCACCCTGA	AAAGCCGT,	ATF3f-5'
759	CGCTGGAATCAGTCAC	CTGTCAG,	ATF3r-5'	CTTGTTTCG	GCACTTTGCAGCTG,
760	SPRR1Af-5'	GTGAAAC	AACCTTGC	CAGCCTC,	SPRR1Ar-5'
761	TGGCAGGGCTCTGGA	ACCTTG			

- 762
- 763 <u>RNAseq</u>

Global gene clustering. For the first round, paired-end RNA sequencing was performed
 on hPSC-ctr-H9, iPSC-ctr-C1, and iPSC-FD-S2 day 15 SNs (differentiated as previously
 described ¹⁷) with no replicates. Reads were mapped to the human genome build hg19
 using TopHat software ⁷⁸. Reads that aligned with no more than 2-bp mismatches were

768 accepted for downstream analysis. After mapping, we computed the expression count 769 matrix from the mapped reads using HTSeq (https://htseq.readthedocs.io/en/master/) 770 and one of several possible gene model databases. The generated count matrix was then 771 processed R Bioconductor using the package DESeq 772 (http://www.huber.embl.de/users/anders/DESeg/) to normalize the full data set and 773 analyze differential expression between samples.

GOterm analysis. Genes that showed significant downregulation in iPSC-FD-S2 SNs vs
 hPSC-ctr-H9 and iPSC-ctr-C1 SNs were subjected to GO term analysis using the DAVID
 functional annotation tool (https://david.ncifcrf.gov/tools.jsp). The occurrence of GO terms

- with a FDR score <0.05 were graphed.
- 778

779 Synthesis of 1,10-anhydrogenipin

780 Genipin (1.52 g, 6.7 mmol) and triphenylphosphine (1.85 g, 7.1 mmol) were dissolved in 781 33.5 mL of distilled methylene chloride, brought to 0°C, and stirred for 15 minutes. To this 782 solution was added diisopropyl azodicarboxylate (DIAD, 1.38 ml, 7.1 mmol) dropwise over 783 10 min and the mixture was stirred on ice for one hour. The reaction was removed from 784 the ice bath and allowed to be stirred overnight at room temperature. TLC (Rf=0.55 in 5:1 785 hexane/EtOAc) analysis revealed the presence of the product which was purified by flash 786 chromatography (5:1 hexane/EtOAc) to yield a white solid (0.45g, 33%). Mass spectrometry and NMR analysis matched previously published data ²⁴. 787

789 Atomic Force Microscopy measurements

790 To prepare the samples for AFM imaging and Young's Modulus measurements, Day 25 sensory neurons (SNs) were differentiated in the presence of DMSO or genipin in 791 792 Nunclon Delta surface dishes (ThermoFisher, cat# 150460 vendor). Cells were washed 793 with PBS and fixed with 4% paraformaldehyde for 20 min at room temperature, followed 794 by 3X washes with PBS. Alternatively, SN-derived extracellular matrix (ECM) was isolated 795 as previously described⁷⁹. SNs were washed with PBS and stripped by incubation with 796 20mM Ammonium Hydroxide with agitation for 5min. The dishes were then washed 5X 797 with water and the ECM was fixed with 4% paraformaldehyde for 20 min at room 798 temperature followed by 3 washes with PBS. AFM measurements were done using an 799 Agilent 5500 SPM system. Before the AFM experiments, the spring constant of the 800 conical AFM tip on a rectangular cantilever (NANOSENSORS gp-BioAC) was calibrated 801 to be 6pN/nm. The sensitivity of the cantilever was obtained using a very hard glass 802 substrate to be 34.15nm/V. The AFM tip was roughly aligned on the surface of the cell by 803 using an optical microscope, then contact AFM mode was applied to obtain the high-804 resolution topographic images of the samples. Large area (\sim 80µm²) AFM images were 805 obtained . For each sample, we chose multiple spots on the sample to measure the force-806 distance curves and calculate the YMs so that a reliable YM can be statically determined. Force-distance curves were further fitted with Hertz model ⁴⁶ (suitable for fitting under 807 808 small deformation in nanoindentation measurements) and calculate the YM of individual cell by a commercial software PUNIAS 80,81. We carefully control the applied force 809 810 (setpoint) of 60pN to minimize the deformation. ECM was isolated as previousy described 811 ⁷⁹. Briefly, on day 20, SNs were washed with PBS and incubated for 5 min with 20 mM
Ammonium Hydroxide (Sigma, cat# 221228-100ML-A) with constant shaking. Dishes were washed with 5 mL of de-ionized H₂O and fixed with 4% PFA for 20 min. Cells were then washed 3 times with PBS prior to processing for AFM.

815

816 Animal experiments

817 *Mice.* $Elp1^{flox/+}$ and $Elp1^{\Delta 20/+}$ mice (previously named lkbkap⁹) were housed and bred at the 818 University of Tennessee Health Science Center Comparative Medicine Department 819 animal core facility.

Timed-pregnancies and Genipin treatment. Female $Elp1^{flox/+}$ mice were crossed with Elp1^{Δ 20/+} males ⁹ for timed-pregnancies. At E10.5 a fresh mouse cage was provided to pregnant female mice for acclimatization and shortly after breeder mouse chow was replaced with genipin-containing moist breeder chow (500 mg/Kg of chow), corresponding to daily consumption of 75 mg of genipin per Kg of body weight. Genipin-containing moist chow was supplied fresh daily. Females were weighed daily and sacrificed at late gestation (E18.5).

827 *Genotyping of embryos.* Genomic DNA was prepared from embryo tail biopsies, and 828 embryos were genotyped by PCR amplification as described previously ⁹.

Histological analyses. Embryos were fixed in 4% paraformaldehyde in phosphatebuffered saline (PBS) for at least one week. Embryos and placentas were weighed and then incubated for 24 hours at 4°C in PBS containing 0.25 M sucrose, 0.2 M glycine; dehydrated; cleared with toluene; and embedded in paraffin. Paraffin blocks were serially

sectioned at 7 μm, mounted in superfrost slides (Fisher) and stained with haematoxylin
and eosin (H&E).

Volumetric determination and neuronal counts. Volumes of sensory ganglia were 835 determined as described previously^{9,29}. In brief, H&E-stained serial paraffin sections (7) 836 μm) spanning the whole ganglia were analyzed under a Zeiss stereomicroscope, and 837 width and length were measured every 5th section. Volumetric measurements were 838 839 performed by calculating and adding the volumes between every section analyzed. For 840 neuronal counts, neurons with clearly visible nucleoli were counted from photomicrographs of H&E-stained paraffin sections. Total neuronal numbers were 841 estimated based on the total volume of the ganglia. 842

Immunohistochemistry on paraffin sections. For immunohistochemistry on paraffin 843 844 sections (IHC-P), slides were deparaffinized, rehydrated, and incubated with 0.3% H₂0₂ 845 in methanol for 20 min, to guench endogenous peroxidase. Sections were then washed with PBS, blocked for 1 hr with 4% BSA, 0.2% Triton X-100 in PBS, and incubated at 4°C 846 847 for 24hrs with primary rabbit monoclonal anti-CGRP antibody (Calbiochem PC205) diluted 1:200 in 0.4% BSA; 0.2% Triton X-100 in PBS. After several washes in PBS, 848 849 primary antibody detection was carried out using the Vector ABC Elite kit according to 850 manufacturers' instructions, followed by incubation with DAB brown substrate (BD 851 Biosciences).

Quantification of CGRP+ sensory nociceptive neurons. Nociceptive neurons were quantified at E18.5 by counting CGRP-positive staining of neurons in cross sections of lumbar L1 DRG. For each embryo, four images per DRG from at least two independentlyimmunostained sections were captured at 20X and divided into quadrants. Total number

of cells and number of CGRP-positive cells per quadrant were determined using ImageJ.

857 Positive signal was established as 30% above background.

858

859 Statistical analysis

All analysis and graphs were done using PRISM (GraphPad). Number of independent 860 861 experiments (biological replicates, n) and statistical analysis are indicated on each figure 862 legends. Biological replicates are defined as independent differentiations started at least 863 3 days apart or from a freshly thawed vial of cells. Statistics for animal data, see below. 864 Data presented are shown as mean ± SD. For experiments in vivo: data were derived 865 from multiple independent experiments from distinct mice. Animal studies were performed 866 without blinding of the investigator. Histological analyses were performed in at least 3 867 embryos per genotype and treatment. No statistical method was used to predetermine sample size, but sample size was based on preliminary data and previous publications. 868 869 In all experiments the differences were considered significant when p<0.05. The 870 differences between groups were assessed using one-way ANOVA followed by Tuckey HSD post hoc test. 871

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873 <u>Study approval:</u>

Animal experiments were carried out in strict accordance with the Guide for the Care and Use of Laboratory Animals of the National Institutes of Health. The protocol was approved by the Animal Care and Use Committee of the University of Tennessee Health Science Center.

878

879 List of Supplementary Materials:

- 880 Sup Fig. 1 to Sup. Fig. 6
- 881 Sup. Table 1 to Sup. Table 3
- 882

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1175

1176 **Acknowledgements:** We thank Michael Tiemeyer and Yao Yao for critical discussions.

1177 Harold 'Skip' Ralph at the Weill Cornell Microscopy and Image Analysis Core facility for

1178 image analysis. Julie Nelson from the UGA Cytometry Shared Resource Laboratory for

1179 her help with flow cytometry experiments.

1180

Funding: This work was funded by faculty start-up funds from the University of Georgia
to N.Z. and NIH/NINDS 1R01NS114567-01A1 to N.Z., a core grant from the US National
Institutes of Health (P30CA08748), the New York State Stem Cell Science (NYSTEM)
(C026446 and C026447) and the Tri-institutional Stem Cell Initiative (Starr Foundation)
to L.S. Schematics were done using Biorender.com.

1186

Author Contributions. KS-D conceived, conducted and analyzed experiments, and wrote manuscript. PD and ID conducted animal experiments and tissue analysis. AJP conducted experiments. CW, ARP, and GB synthesized 1,10-anhydrogenipin, SC provided the chemical library, LS provided support, advice, and funds for the chemical screen. NZ conceived, designed, led the study, conducted experiments, wrote the manuscript and provided funds.

1193

1194 Competing interests: L.S. is a scientific co-founder and consultant and has received1195 research support from BlueRock Therapeutics.

1196

1197 Data and materials availability: All data needed to evaluate the conclusions in the paper

- are present in the paper or the Supplementary Materials. Requests for reagents should
- be directed to the corresponding author, Nadja Zeltner (nadja.zeltner@uga.edu)

1201 Figures:



Figure 1. Chemical screen on FD sensory neurons. **A)** Differentiation protocol adapted from Chambers et al., 2012. **B)** Bright filed imaging shows normal morphology of undifferentiated hPSCs in all lines (left column). SN differentiation is impaired in both FD lines, but normal in healthy control lines (right two columns). **C)** Differentiation protocol adapted to high-throughput screening conditions. **D)** The SN differentiation protocol is

1208 most efficient in 96 wells when the cells are fed three times. E) Cartoon of the screen set 1209 up. F) 640 compounds from the LOPAC chemical library (the first half) were screened. 1210 Controls included DMSO only wells, healthy hPSC-ctr-H9 with DMSO (blue dot = positive 1211 control), iPSC-FD-S2 iPSCs with DMSO (yellow dot=negative control). Hit compounds were called when the fold change (FC) over the average of all DMSO wells was above 1212 the average of all compounds plus 3 SDs (here 3.8, red dots). Every compound was 1213 screened at 1 mM and 10 mM. 16 images were taken for each well, all wells were imaged 1214 1215 for the ratio of BRN3A⁺/DAPI⁺ staining.



1217

Figure 2. Validation of the hit compound genipin. A) Titration of genipin during the SN
 differentiation in healthy hPSC-ctr-H9 and iPSC-FD-S2 iPSCs. Differentiation protocol

1220 depicted in Fig. 1a was used. B) Quantification of genipin titration based on IF of BRN3A⁺ SNs. n=3-4 biological replicates. C) Titration of genipin in iPSC-FD-S2 cells during 1221 1222 differentiation into SN-biased neural crest cells (top row) and SNs (bottom row). Cells 1223 were treated with indicated concentrations of genipin starting on day 2. Cells were then fixed on the indicated days and stained for SOX10 and TFAP2A (top) or BRN3A (bottom) 1224 1225 and DAPI. D and E) Quantification of size of NC ridges and number of SNs upon genipin treatment. **D)** Area of ridges in **c** marked by DAPI staining (n=4-7 biological replicates) 1226 and E) number of BRN3A⁺ SNs in c were quantified (n=3-5 biological replicates). F) 1227 1228 Genipin commercially obtained from both Sigma and Biomaterials rescues SN 1229 differentiation in iPSC-FD-S2. Cells were differentiated in the presence of genipin from 1230 either source starting on day 2. Cells were fixed on day 20 and stained for BRN3A and DAPI. n=3-7 biological replicates. All graphs show mean ± s.d. For **B**, **D**, **E**, and **F**, one-1231 way ANOVA, *p<0.05, **p<0.005. 1232







1244 S3 cells were treated with genipin (10 µM) and differentiated into SNs. RNA was isolated on day 20 or cells were fixed and stained using the indicated antibodies and analyzed by 1245 1246 D) IF (n=5 biological replicates). E) intracellular flow cytometry (n=3-4 biological 1247 replicates), and F) RT-qPCR (n=6 biological replicates). G) Western blot analysis confirms the increase in SN production upon genipin treatment. Cells differentiated with 1248 genipin (10 µM) were lysed on day 20 and immunoblotted with the indicated antibodies 1249 (left) and quantified (right). n=3-4 biological replicates. H) Genipin increases firing rate of 1250 FD SNs. Cells were differentiated in the presence of genipin (10 μ M) and firing rate was 1251 analyzed by MEA. n=4-6 biological replicates. In C, E, F, G, H, Two-tailed Student's t-1252 test. ns, non-significant, *p<0.05, **p<0.005. All graphs show mean ± s.d. Data from iPSC-1253 FD-S2 and iPSC-FD-S3 are pooled as FD in C and F. 1254



1256

1257 Figure 4. Genipin rescues FD peripheral deficits in vivo. A) Breeding and treatment schematic. B) Representative H&E-stained transverse sections through lumbar (L1) 1258 1259 dorsal root ganglia (DRG) of untreated control, genipin-treated control, untreated FD, and 1260 genipin-treated FD E18.5 embryos, at their largest dimensions. C) Volumes of lumbar (L1) DRGs of untreated (n=6) and genipin-treated (n=5) controls, and untreated (n=6) and 1261 genipin-treated (n=6) FD E18.5 embryos, displayed as percentage of control. D) Neuronal 1262 counts of lumbar (L1) DRGs of untreated (n=6) and genipin-treated (n=5) controls, and 1263 1264 untreated (n=6) and genipin-treated (n=6) FD E18.5 embryos, displayed as percentage 1265 of control. E) Percentage of CGRP-positive neurons in lumbar (L1) DRGs of control 1266 untreated (n=3), FD untreated (n=3), and genipin-treated FD (n=3). F) Representative 1267 images of transverse sections through lumbar (L1) DRGs of untreated FD and genipin-

1268 treated FD E18.5 embryos immunostained with CGRP. G) Representative images of transverse sections through dorso-lateral skin of untreated FD and genipin-treated FD 1269 1270 E18.5 embryos immunostained with CGRP. Arrows show positive signal. H) 1271 Representative H&E-stained sections of stellate ganglia (SG) of genipin-treated control, untreated FD, and genipin-treated FD E18.5 embryos. I) Volumes of SG of untreated 1272 (n=6) and genipin-treated (n=3) FD E18.5 embryos, plotted as percentage of control. All 1273 graphs show mean ± s.d.. For C, D, E, one-way ANOVA followed by Tuckey HSD post 1274 1275 hoc test. For I, two-tailed t-test. *p<0.05, **p<0.01, ***p<0.001





Figure 5. Genipin rescues sensory neuron degeneration in FD. A) Schematic of 1278 survival assay. B) Healthy or FD cells were treated with genipin from day 12 on (when 1279 neurons are born) and monitored for survival for 21 days. Cells were fixed on the indicated 1280 days and stained for BRN3A, TUJ1 and DAPI. Arrows indicate healthy, ganglia-like SN 1281 1282 clusters. C) Image quantification of B. n=8, Two-way ANOVA followed by Šídák multiple comparisons. **p<0.005, ***p<0.001, ****p<0.0001. **D,E**, Genipin increases neurite length 1283 and number in FD cells. D) Representative images of neurite length. E) Measurement of 1284 neurite length (number of pixels) of D. n=6-8 biological replicates, one-way ANOVA 1285

- 1286 followed by Tukey's multiple comparisons. ns, non-significant, ****p<0.0001. All graphs
- 1287 show mean ± s.d. Data from iPSC-FD-S2 and iPSC-FD-S3 are pooled as FD in **C**, and
- 1288 **E**.
- 1289



1291 Figure 6. Genipin rescues FD phenotypes via crosslinking of extracellular matrix proteins and activates. A) Genipin chemical structure and schematic of intermolecular 1292 1293 and intramolecular crosslinking. B) Treatment with genipin turns cells blue. C) Schematic 1294 of BS3 crosslinking action and its extracellular location. D) BS3 rescues the NC and SN 1295 differentiation defect in FD. FD cells were differentiated in the presence of DMP and fixed 1296 on day 12 (NC) and day 20 (SN). Following staining using the indicated antibodies. n=3-5 biological replicates. E-H) 1,10-anhydrogenipin (AG) does not rescue the SN defect in 1297 FD. E) AG chemical structure. F) AG does not turn cells blue. G, H) AG does not promote 1298 1299 FD SN differentiation. Cells were differentiated into SNs in the presence of genipin or AG. 1300 SNs were fixed on day 20 and stained for BRN3A for intracellular flow cytometry analysis 1301 (G, n=6-8 biological replicates), or stained for BRN3A, TUJ1, and DAPI for IF (H, n=6-8 biological replicates). I, J) Genipin-mediated crosslinking increases ECM stiffness. I) AFM 1302 Experiment schematics. J) Genipin increases the Young's modulus of SNs. iPSC-FD-S3 1303 SNs were fixed on day 25 and analyzed by AFM (n=3 biological replicates). K-M) Genipin 1304 1305 reorganizes the actin cytoskeleton and induces transcription of YAP-dependent genes. 1306 **K)** Genipin partially rescues the differences of actin expression pattern in healthy and FD 1307 SNs. Day 20 SNs were fixed and stained for the indicated antibodies. Images were 1308 obtained by confocal microscopy. Actin signal in the cell body (arrows) or the axons 1309 (arrowheads) are highlighted. L, M) YAP localization changes in the presence of genipin. 1310 Day 20 SNs were fixed and stained for the indicated antibodies. M) YAP and DAPI signal intensity from images on L) was measured and plotted n=6-7 biological replicates). 1311 1312 Arrows indicate YAP signal outside of the nucleus (stained with DAPI). N) Expression of 1313 YAP-dependent genes. RNA from FD SNs treated with DMSO or Genipin was extracted

- 1314 on day 20 and gene expression was analyzed by RT-qPCR (n=7-9 biological replicates).
- 1315 All graphs show mean ± s.d.. For **G**, one-way ANOVA followed by Tukey's multiple
- 1316 comparisons. For J, two-tailed t test with Welch's correction. For N, two-tailed t test. ns,
- 1317 non-significant, *p<0.05, **p<0.005, ***p<0.001. In **G**, **M**, and **L** data from iPSC-FD-S2
- 1318 and iPSC-FD-S3 are pooled as FD.





Figure 7. Genipin accelerates axon regeneration after injury in different neuronal types. **A-D)** Genipin enhances rengeneration of healthy SNs. **A)** Experiment schematics. **B)** Genipin increases expresison of injury-related genes. RNA from hPSC-ctr-H9 SNs was isolated at indicated times and gene expression was measured by RT-qPCR (n=4-7 biological replicates). **C,D)** Genipin increases axon length after injury. Day 25 SNs from hPSC-ctr-H9 cells were fixed at indicated times after replating in the presence of DMSO or Genipin, and stained for TUJ1. Axons were traced (magenta) and measurement were

1329 plotted in D (n>20 cells from 5 biological replicates). E-G) Genipin increases length and complexity of axons from sympathetic neurons. E) Experiment schematics. For details, 1330 see Methods. F,G) Axons from sympathetic neurons were removed. After 48 h treatment 1331 1332 with Genipin, neurons were fixed and stained for PRPH. Axons were measured 1333 (arrowheads indicate length of axons) and the pixels with high PRPH signal were 1334 measuered and graphed in J (n=4 biological replicates). H-J) Genipin promotes axon regeneration in prefrontal cortical (PFC) neurons. H) Experiment schematics. For details, 1335 see Methods. I,J) hPSC-ctr-H9 PFC neurons reaplted and incuabted with Genipin for 5 1336 1337 days. Neurons were then fixed and stained for TUJ1 as shown in I. Measurement of the 1338 pixels with high TUJ1 signal were normalized to DAPI and plotted in J (n=3 biological 1339 replicates). All graphs show mean \pm s.d. For **B**, two-way ANOVA followed by Sídák multiple comparisons. For **D**, **G**, and **H**, two-tailed t test. p<0.05, *p<0.005, **p<0.001, 1340 ****p<0.0001. 1341



Supplementary Figures

Supplementary Figure 1. Adaptation of the SN differentiation protocol to highthroughput screening conditions and hit validation. A) Quantification of the number of BRN3A⁺ SNs over total DAPI⁺ cells. Two-tailed Student's t-test, *p<0.01. B) Imaging of 30 fields per 96 well for each condition. C) Example wells are shown from the screen. D) Repeat of the SN differentiation in the presence of the hit compounds in 96 wells in screening conditions outlined in Fig. 1C. Whole wells are shown, imaged in 16 tiles. E) Repeat of SN differentiation in the presence of the hit compounds in a different well format, i.e. 48 wells and using non-screening conditions outlined in Fig. 1A. Whole wells are shown, imaged in 25 tiles. F) Effect of hit compounds tested on additional cell lines, i.e. healthy iPSCs and FD iPSCs from patients with mild FD symptoms (iPSC-FD-M2). Non-screening differentiation conditions were used in a 48 well format. All differentiations were performed in KSR conditions. G) Schematic representation of the SN differentiation in E8/E6 conditions (as previously reported¹).



Supplementary Figure 2. *in vitro* and *in vivo* developmental phenotypes in FD are rescued by genipin (related to Fig.3 and Fig. 4). A) Immunoblotting of SOX10 from day 12 NC cells. Representative blot is shown (left) and quantification (right, n=2-3 biological replicates). B) RT-qPCR-based gene expression analysis of SN-primed NC at day 8 (n=6-7 biological replicates). C) Genipin restores SN differentiation. Day 20 SNs were treated with genipin and fixed and stained using the indicated antibodies (n=5 biological replicates). D) Representative histogram of BRN3A signal measured by flow cytometry. E) RT-qPCR-based gene expression analysis of SNs at day 20 (n=6 biological replicates). F) Gestational female weight gain in genipin-treated (squares, n=6) and untreated (circles, n=3) dams. For A, B and D, Two-tailed Student's t-test. ns, non-significant, **p<0.005, ***p<0.001. All graphs show mean ± s.d. For B and D, iPSC-FD-S2 and iPSC-FD-S3 data are pooled as FD.



Supplementary Figure 3. SN survival assay adaptation and characterization

(related to Fig 5). A) NGF titration to assess SN survival over 21 days by IF in iPSC-

FD-S2 and healthy iPSC-ctr-C1 cells. **B)** Exclusion experiment to assess which of the surface coating proteins LM, PO, FN are required in iPSC-FD-S2 SNs. **C)** Survival assay performed in KSR conditions (Fig 1A). 16-tile images are shown of SNs at day 12 and day 27, with or without genipin treatment (bottom). Quantification of BRN3A signal intensity is plotted relative to day 12 (top). **D)** Number of neurites of hPSC-ctr-H9 and iPSC-FD-S2 SNs differentiated in the presence of genipin (10 μ M) were quantified. n=2-4 biological replicates. **E)** Few SOX10+ NC cells are present in the SN differentiation at day 13 and 20. All graphs show mean ± s.d.



Supplementary Figure 4. Effects of genipin in ELP1 and expression of ECMrelated genes in FD mouse and iPSC-derived FD SNs. A) Treatment with genipin of NC cells up to day 8 does not alter *ELP1* splicing inefficiency (RT-qPCR). n=3 biological replicates. one-way ANOVA followed by Tukey's multiple comparisons. ns, nonsignificant, **p<0.005. B) Genipin does not change ELP1 protein levels in FD (immunoblot). n=3 biological replicates. Representative blot is shown. C,D) Analysis of genes predicted to be controlled by Elp1 in FD mouse. C) Gene ontology of predicted genes that are regulated by Elp1. D) Percentage of genes predicted to be regulated by Elp1. E, F) RNA sequencing in hPSC-derived SNs comparing healthy (hPSC-ctr-H9 and iPSC-ctr-C1) versus FD (iPSC-FD-S2). E) Gene ontology analysis of significantly downregulated genes in FD vs healthy SNs. F) Differential gene expression of hPSCctr-H9 vs FD SNs (left) and iPSC-ctr-C1 vs FD SNs (right). ECM-related genes downregulated in FD are highlighted. Dotted line indicates significance threshold (p<0.05).


Supplementary Figure 5. Genipin's mode of action is through crosslinking of ECM proteins (related to Fig 6). A) Schematic of DMP crosslinking action and its intracellular/extracellular location. D) DMP rescues the NC and SN differentiation defect in FD. iPSC-FD-S2 cells were differentiated in the presence of DMP and fixed on day 12

(NC) and day 20 (SN). Following staining using the indicated antibodies. n=3-4 biological replicates.

C) DMP titration on iPSC-FD-S2-derived SNs on day 20. n=3-4 biological replicates. one-way ANOVA followed by Tukey's multiple comparisons. *p<0.05, **p<0.005. **D)** BS3 titration on iPSC-FD-S2-derived SNs on day 20. n=3-5 biological replicates. one-way ANOVA followed by Tukey's multiple comparisons. *p<0.05, **p<0.005. E) Sulfo-NHS (inactive BS3) does not rescue NC formation, nor SN formation in iPSC-FD-S2 cells. n=3-5 biological replicates. one-way ANOVA followed by Tukey's multiple comparisons. ns, non-significant, **p<0.005. F) Genipin that has been chemically altered to delete its crosslinking effects (1,10-anhydrogenipin) is not capable to rescue NC formation in FD cells. G-I) 1,10-anhydrogenipin does not properly restore NC cells (G) or SNs (H and I) compared to genipin. Assessed by RT-gPCR (G and I) and IF quantification (**H**, related to **Fig. 6H**). For **G**, n=7-8 biological replicates. Two-way ANOVA followed by Sídák multiple comparisons. For **H** and **I**, n=6-8 biological replicates. one-way ANOVA followed by Tukey's multiple comparisons. *p<0.05, **p<0.005, ***p<0.001, ****p<0.0001. All graphs show mean ± s.d. For F, G, H, and I, iPSC-FD-S2 and iPSC-FD-S3 data are pooled as FD.



Supplemental Figure 6. Effects of Genipin crosslinking of ECM (related to Fig 6).

A) AFM topographic images (Scale bar: 10µm). B) Force-distance curves (solid)

recorded by force spectroscopy, along with Hertz model fitted curves (dash) which was used to calculate the Young's Modulus. **C)** Comparison of Young's Modulus for four different samples from a representative experiment. **D)** Histogram of Young's Modulus for SNs in DMSO (green) and genipin (red) with Gaussian distribution. A Gaussian distribution fit curve is overlayed to highlight sample variability. **E)** Schematics for actin signal measurement in cell bodies (black) and axons (blue) in SNs with different *in vitro* morphology. **F, G)** Quantification of actin signal intensity from images in **Fig.6K** (n=7-10 cells from 3 biological replicates).

Supplementary tables

Category	Parameter	Description
Assay	Type of assay	IF staining
-	Target	Increase in sensory neuron
		differentiation
	Primary measurement	IF staining of BRN3A+ cells
	Key reagents	Differentiated sensory neurons
	Assay protocol	Adapted from Chambers et al., 2012
	Additional comments	
Library	Library size	640 compounds, i.e. half of the LOPAC library
	Library composition	Cell signaling and neuroscience
	Source	Sigma
	Additional comments	
Screen	Format	96 well plates
	Concentration(s) tested	1mM and 10mM
	Plate controls	DMSO treated wells, healthy hPSCs (+
		control) and disease cells without
		compounds (- control)
	Reagent/ compound dispensing system	Manual multi-pipettor
	Detection instrument and	MetaXPress software: Cell scoring
	software	Module from Molecular Devices
	Assay validation/QC	 + and – controls and DMSO only wells (see above)
	Correction factors	n/a
	Normalization	DAPI+ cells and DMSO only treated wells
	Additional comments	
Post-HTS analysis	Hit criteria	Phenotype reproducible in screening and non-screening format
	Hit rate	1
	Additional assay(s)	Phenotype reproducible in different well format
		Phenotype reproducible in additional control and disease bPSC lines
	Confirmation of hit purity and	n/a
	structure	
	Additional comments	

Supplementary Table 1. Small molecule screening data

Compound name	Screen [c]	Fold change over DMSO (average)
DMSO only	10µM	4.5
hPSC-ctr-H9 in DMSO	10µM	7.7
iPSC-FD in DMSO	10µM	1.6
Fluphenazine dihydrochloride	10µM	17.5
AC-93253 iodide	1µM	16.5
genipin	1µM	14.2
genipin	10µM	16.1

Supplementary Table 2. Hit compounds

	Total	Live embryos	Resorptions	Number of
	embryos			litters
No treatment	46	40	6	6
+ Genipin	44	41	3	6

Supplementary Table 3. Genipin does not affect normal embryonic development