

# Understanding Chronic Pain at Its Source: How Small Molecular Changes Drive Pain in Schwannomatosis

**Presented by:** Chrissa Baldy

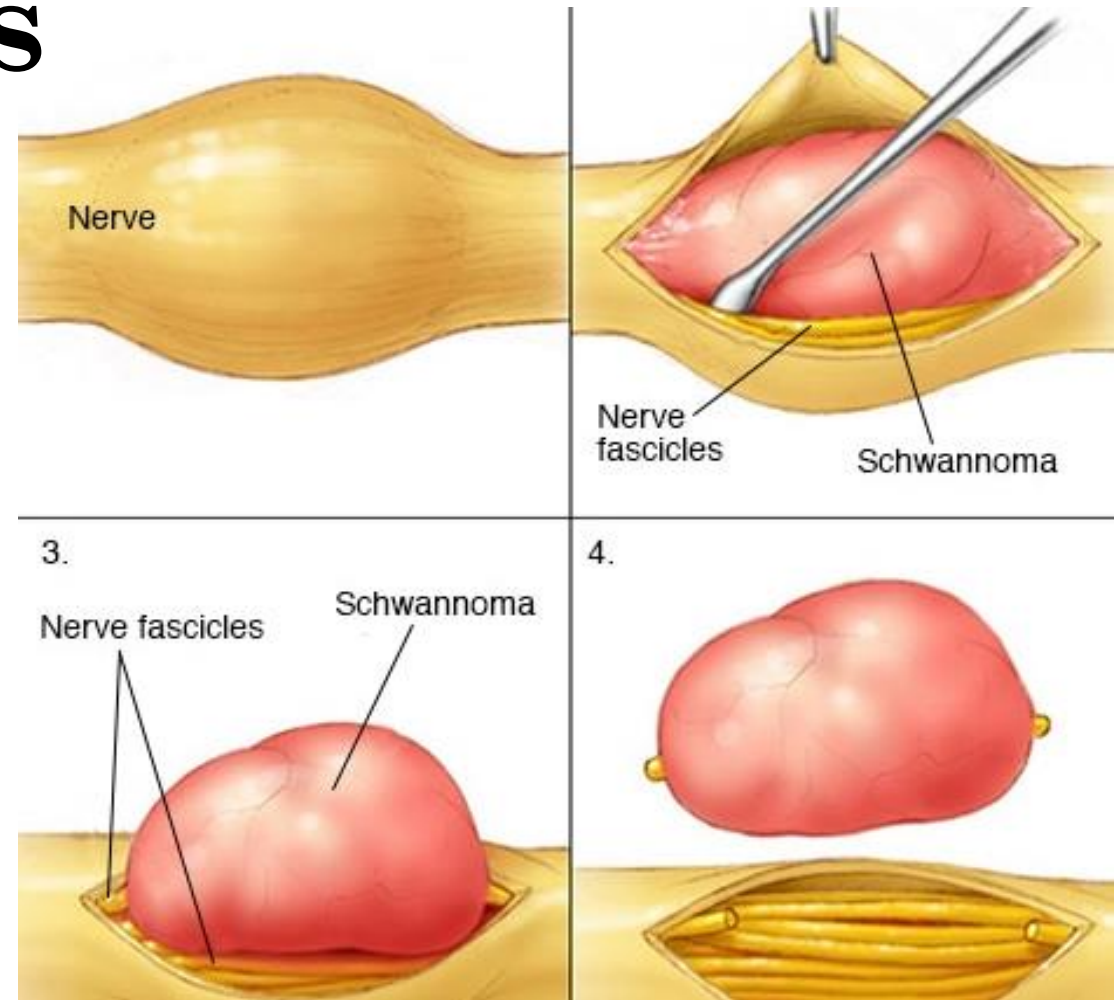
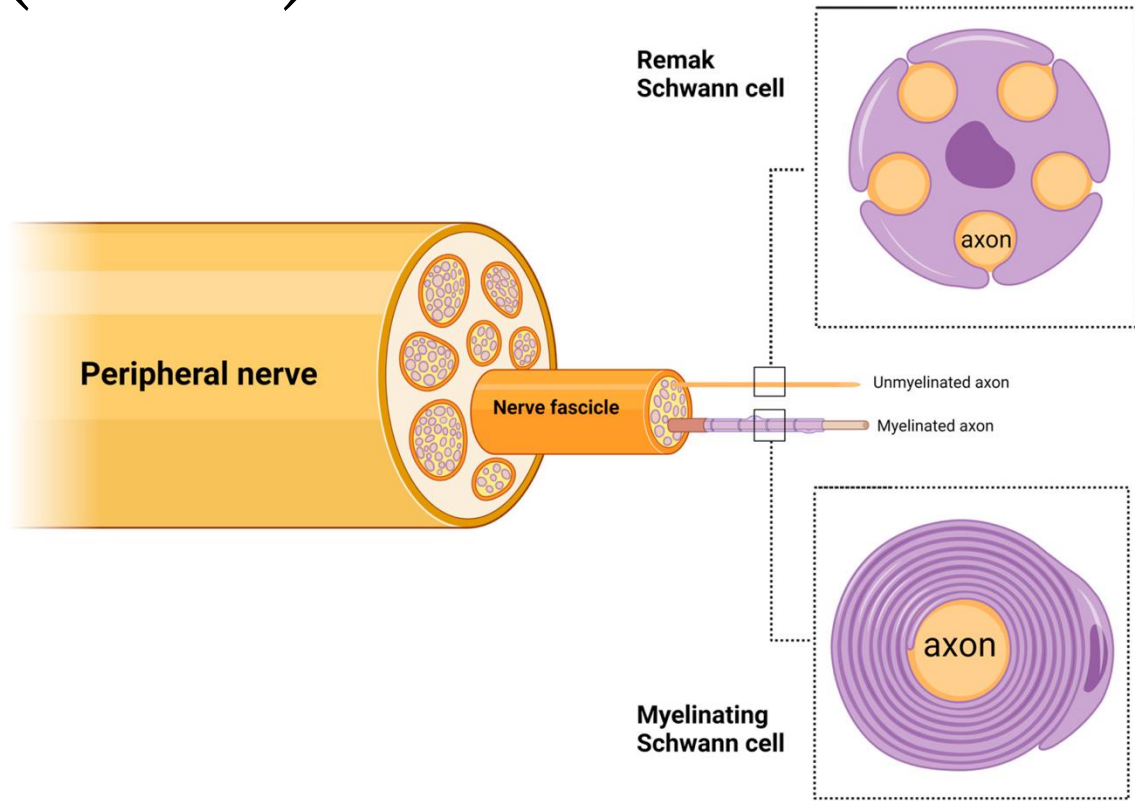
**Supervised by:** Dr. Claudia Thompson<sup>1</sup>, Kimberly Ostrow<sup>2</sup>, and DMV Petri Dish<sup>3</sup>

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**Pain.**



# Schwannamatosi (SWN)



Schwannomatosis (SWN) is a rare genetic disease characterized by the development of multiple benign tumors (known as **schwannomas**) along nerves throughout the body.

To treat pain effectively, we need to understand *why* it persists

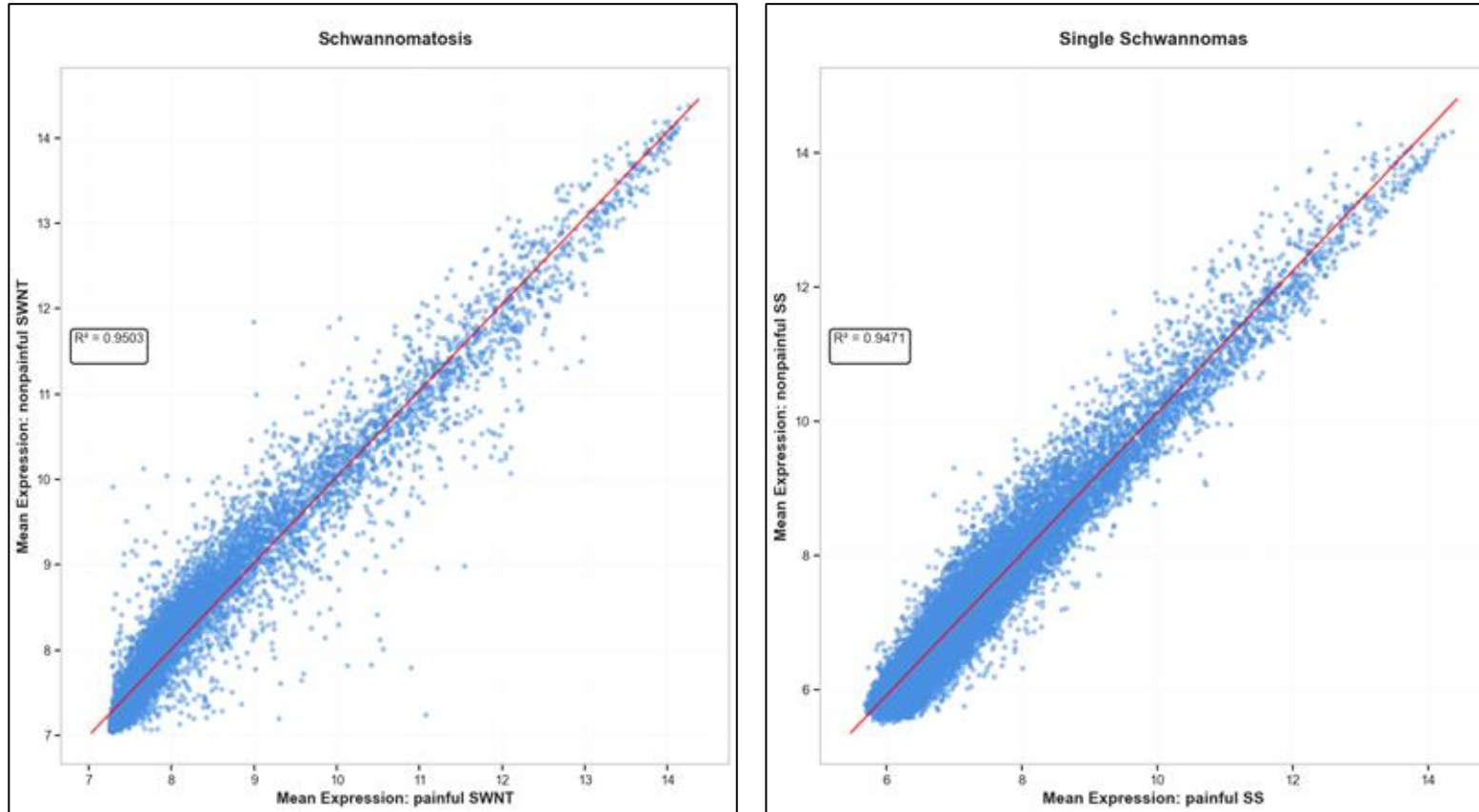
# The Question Guiding My Research: What is going wrong?

## Examined:

- (1) Schwannomatosis (SWN) samples: painful vs. nonpainful
- (2) Painful schwannomatosis vs painful solitary schwannomas (SS)

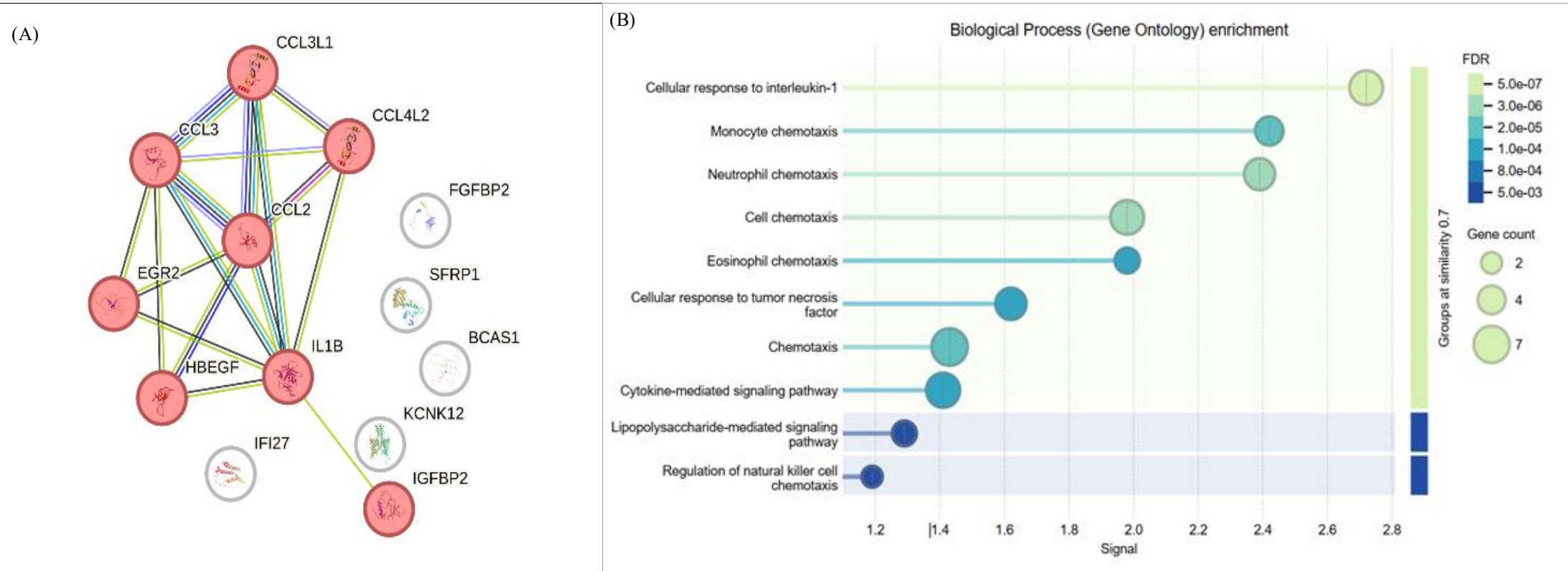
# Painful and Nonpainful Tumors

*Painful and Nonpainful Samples are Highly Similar in Both Schwannomatosis and Solitary Schwannoma Tumors*

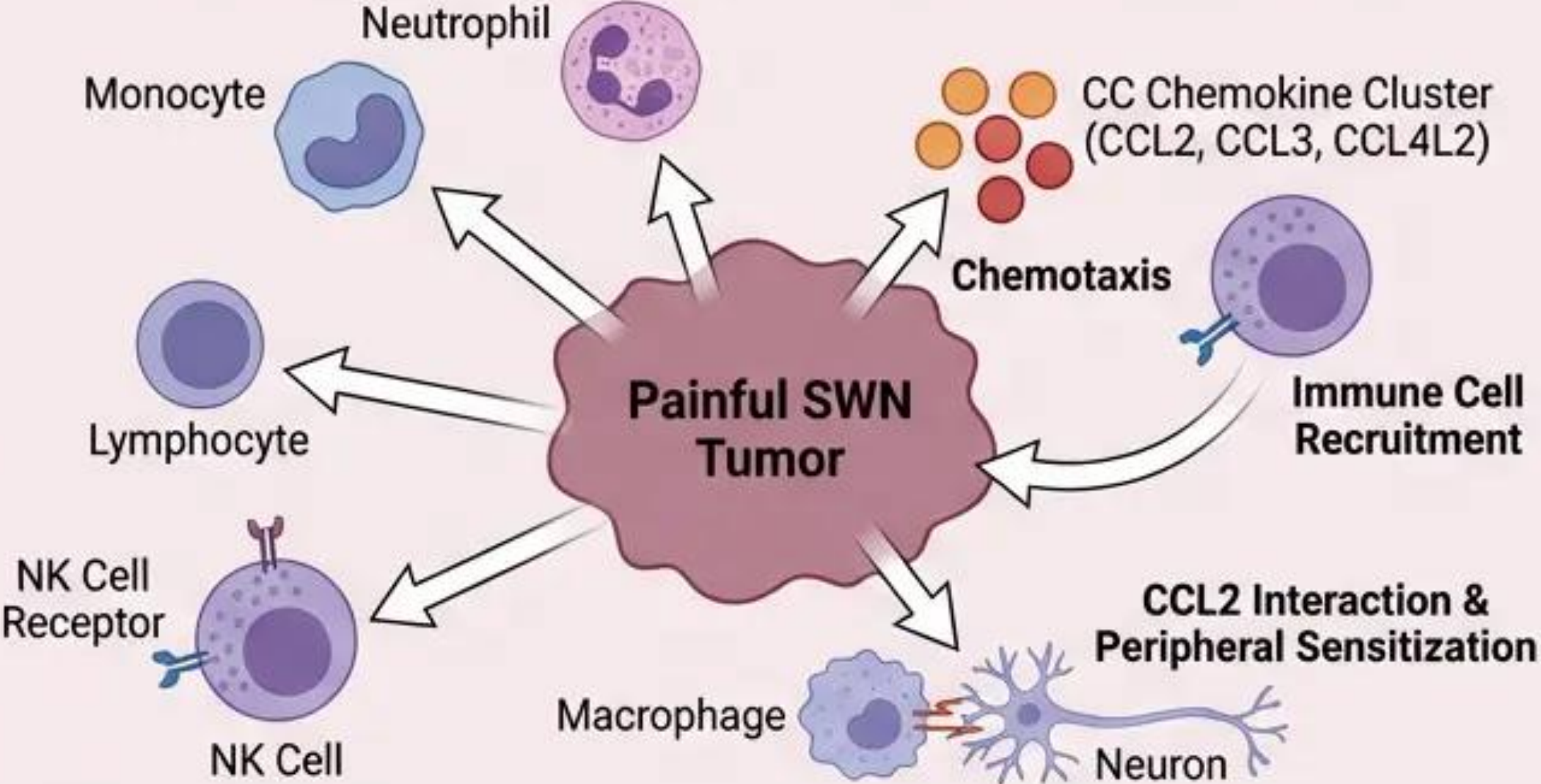


*Note.* The average gene expression of painful samples (x-axis) plotted against the average gene expression nonpainful samples (y-axis) in (A) schwannomatosis tumors (N = 7) ( $R^2 = 0.9503$ ) and (B) single schwannoma samples (N = 21) ( $R^2 = 0.9471$ ) for 14,656 common genes.

# SWN Highest Expressing Pain-Upregulate Genes

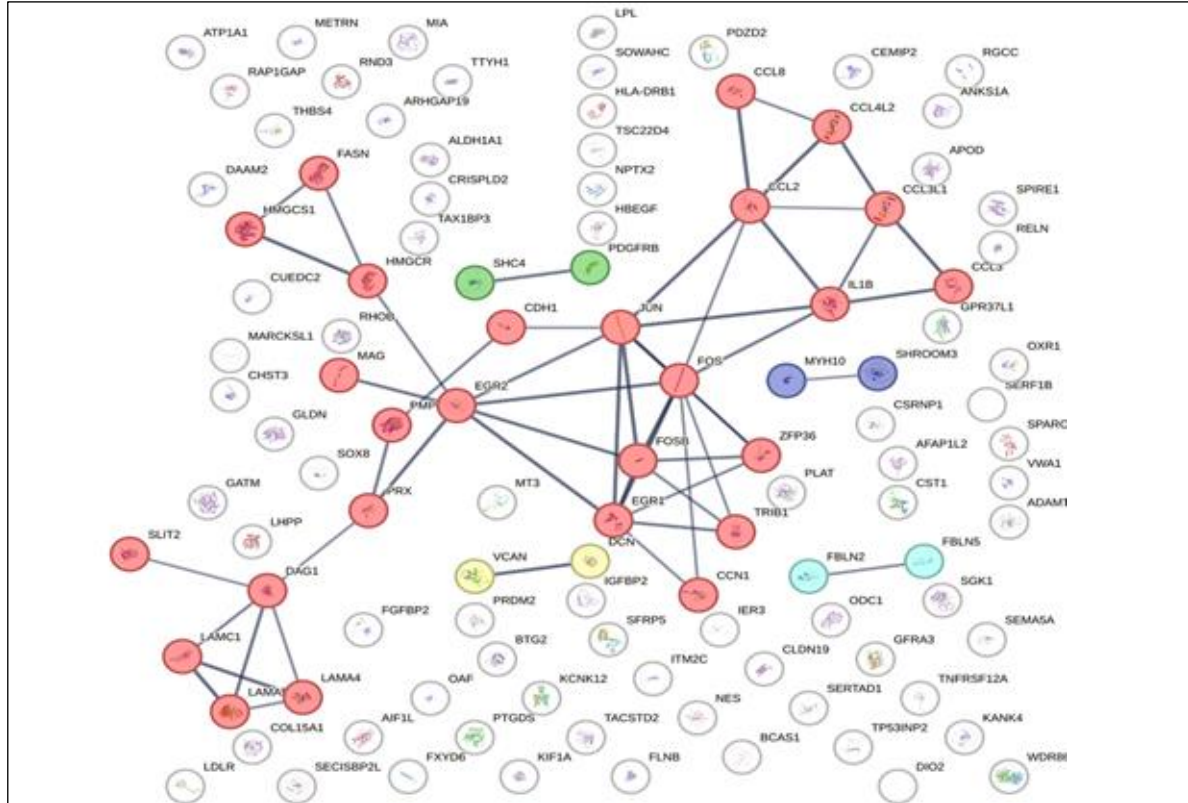


# Immune Cell Recruitment and Chemokine Activity



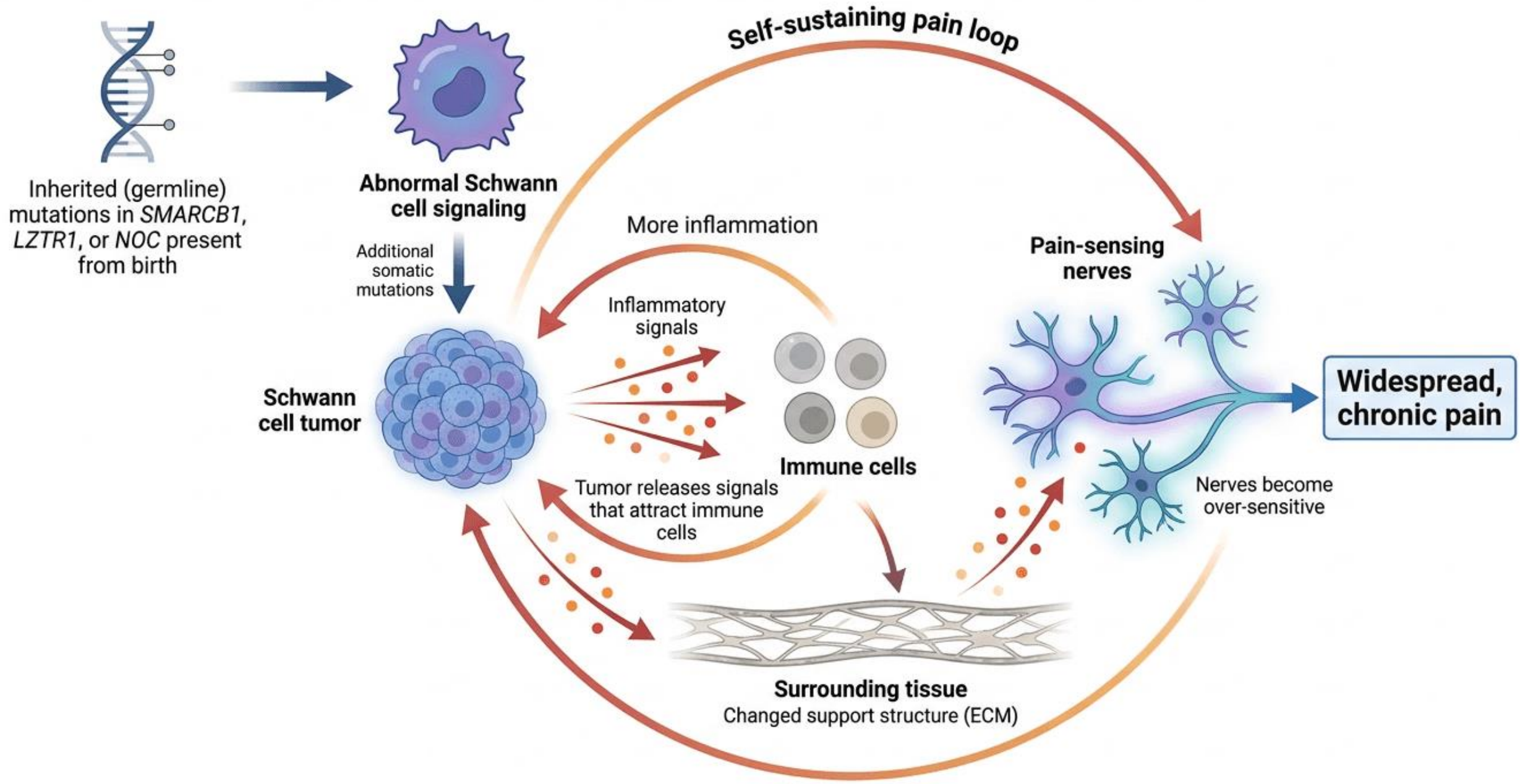
# Painful SWN vs Painful SS

*Upregulated Painful Schwannomatosis versus Painful Single Schwannomas PPI Networks*

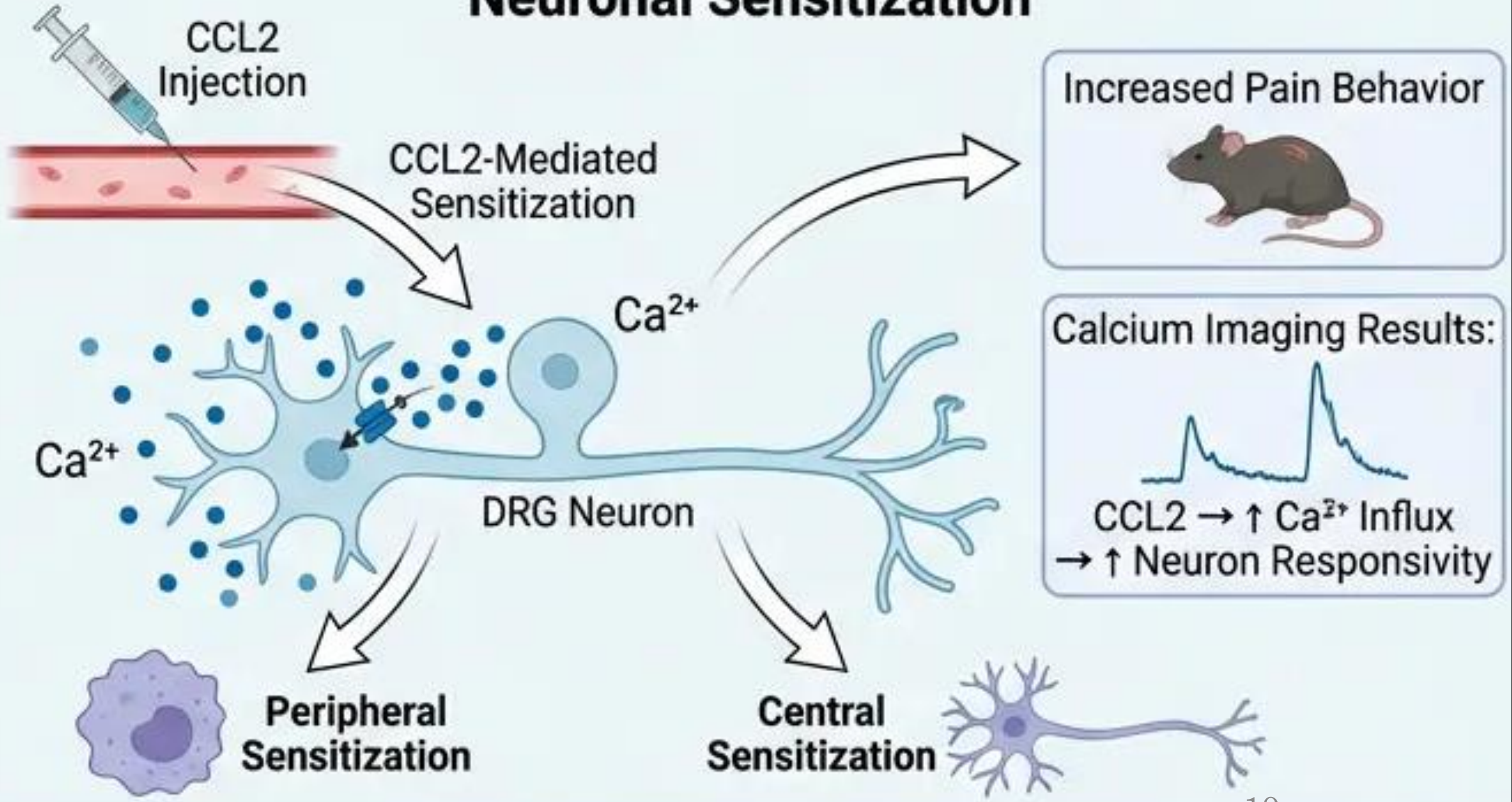


Functionally enriched pathways aligned with the following categories:

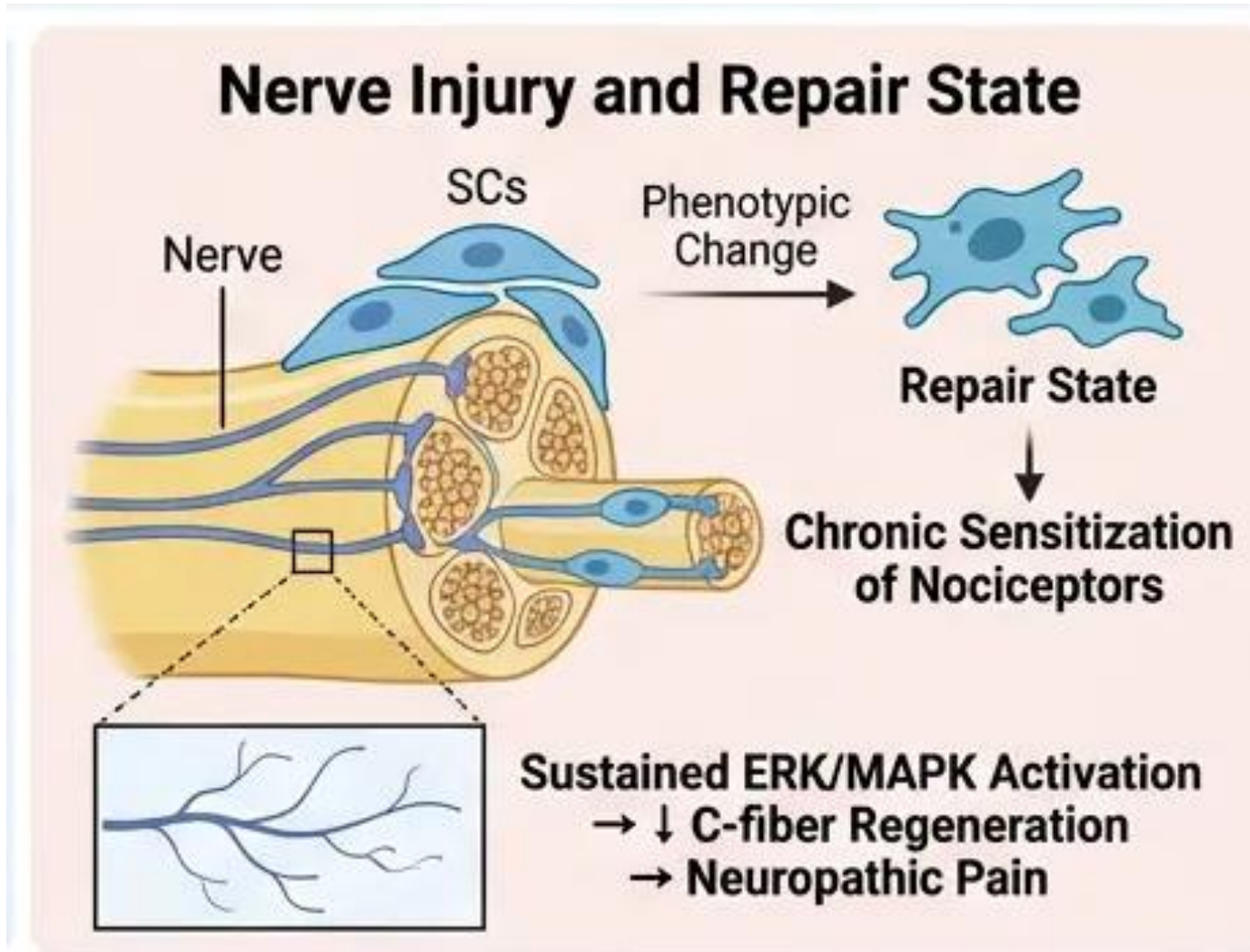
1. **immune-inflammatory** pathways and ERK/MAPK signaling
2. extracellular matrix (**ECM remodeling**) and adhesion
3. glial and **Schwann cell** facilitated **repair**
4. neural injury and repair context



# Neuronal Sensitization



# RAS/MAPK Signaling



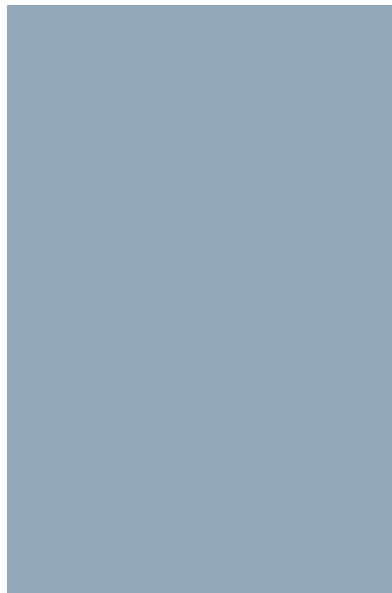
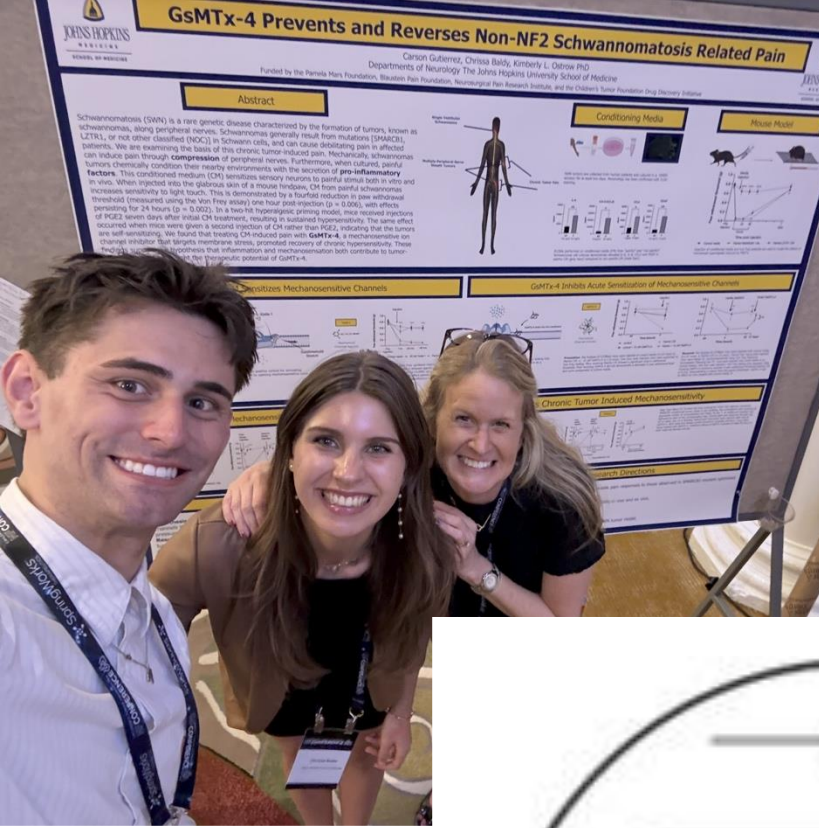
# Understanding Chronic Pain at Its Source

## **Study Findings:**

- Painful tumors show heightened inflammatory signaling
- Repair pathways meant to heal nerves can become chronically activated

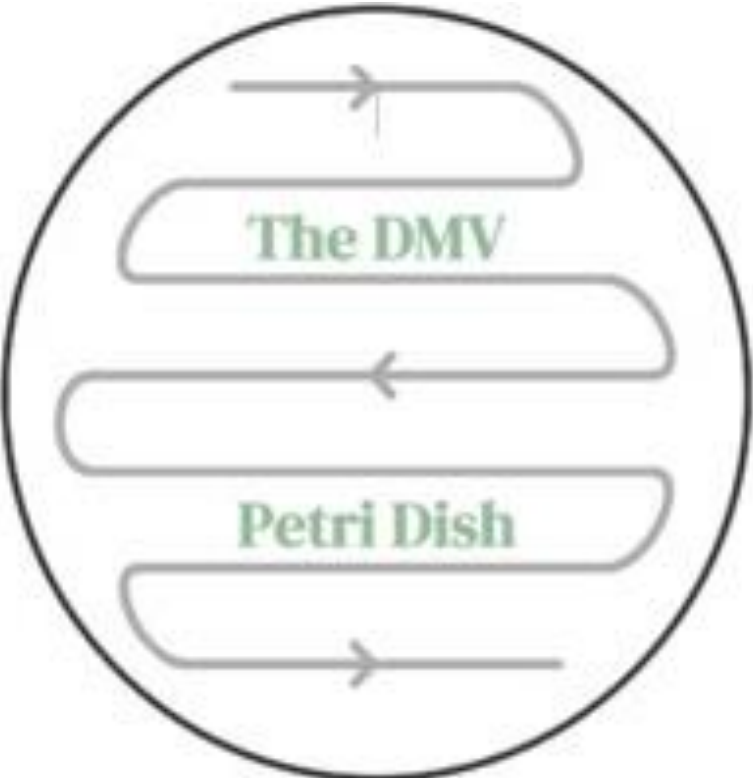
This mechanistic insight reveals new therapeutic targets, such as CCL2 and RAS/MAPK Signaling

**Take-Home Message:** By understanding how pain begins at the molecular level, we move closer to treating its cause, not just its symptoms.



# Acknowledgements

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DMV PetriDish  
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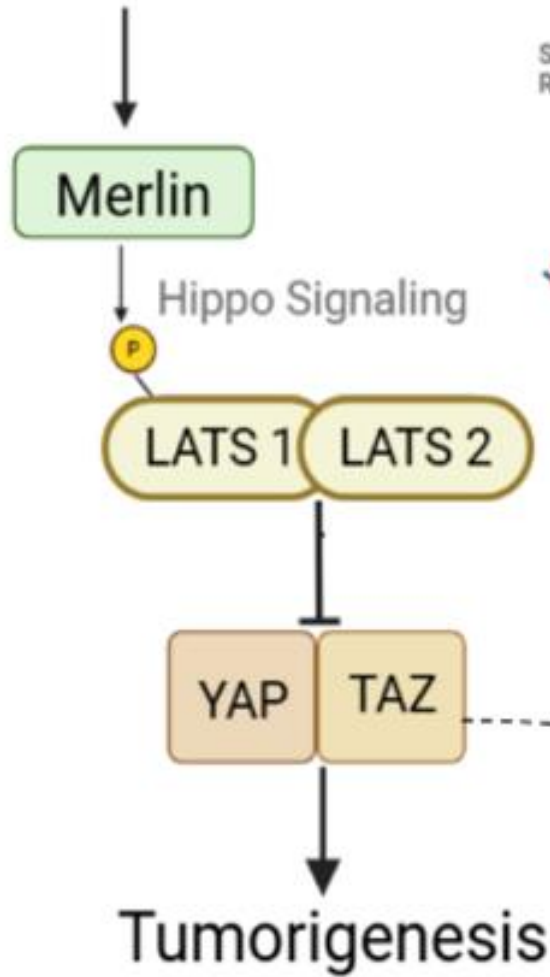
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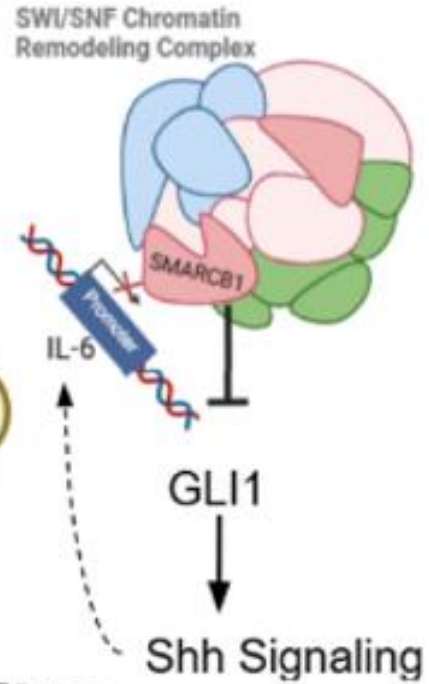
Thank  
You!

# Bonus Slides!

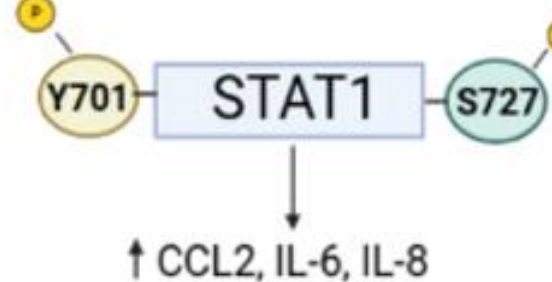
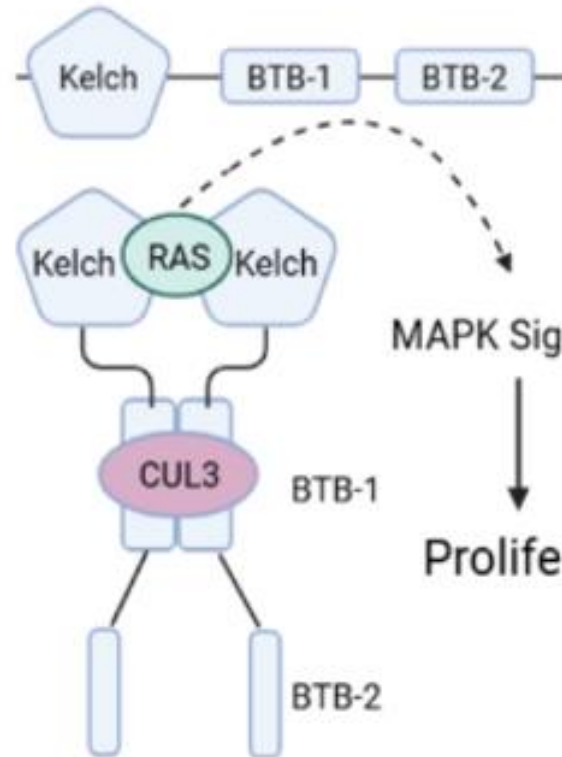
# NF2



# SMARCB1



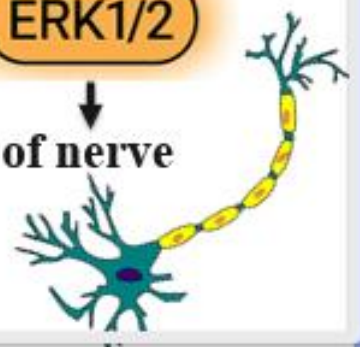
# LZTR1



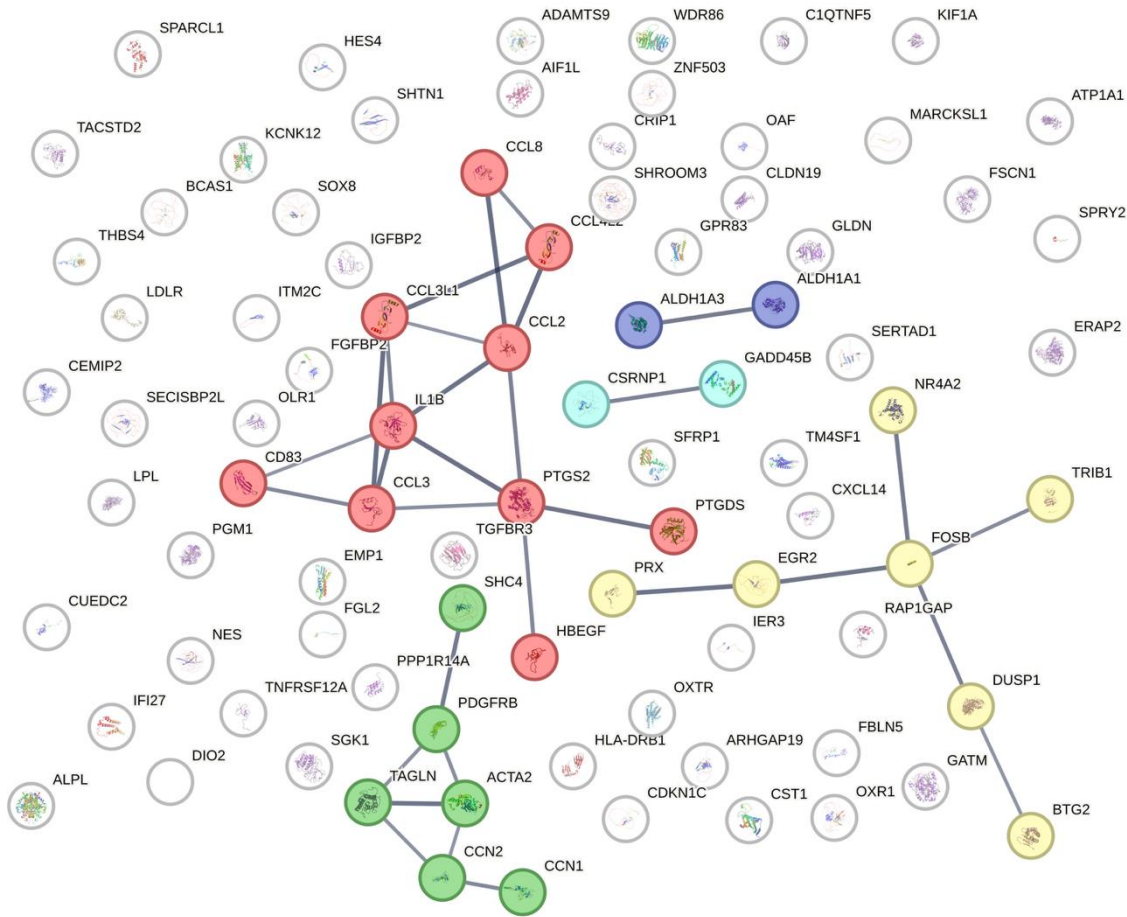
MAPK Signaling

Proliferation ↑

Dysregulation of nerve repair



# SWN Pain-Upregulate Genes

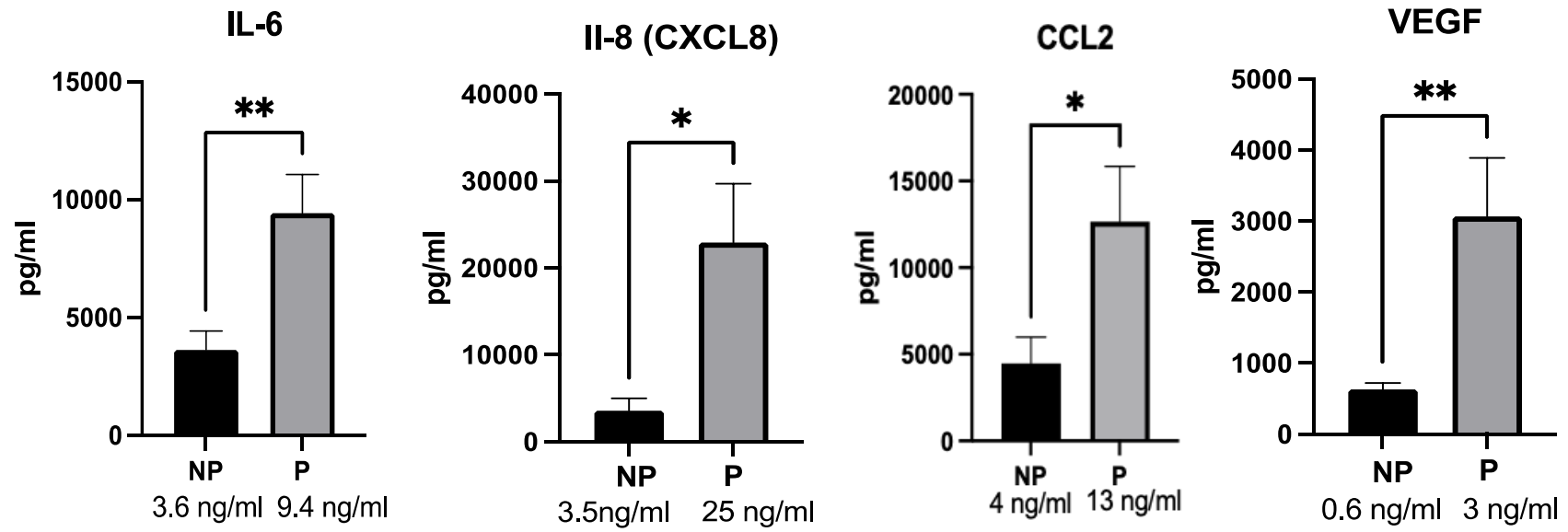
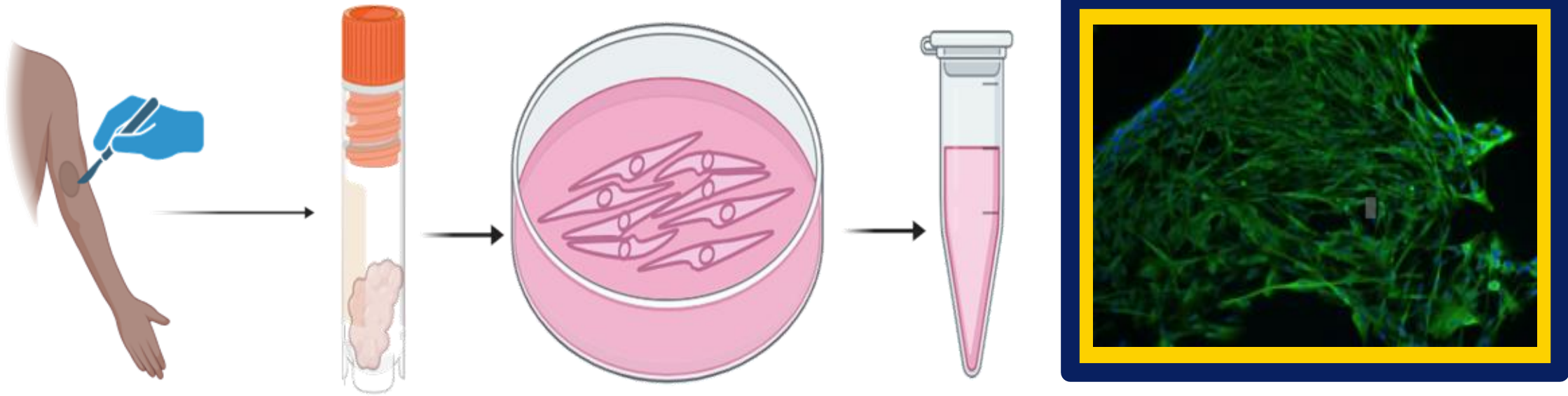


*SWN Pain-Upregulated Gene Ontology Functional Enrichment*

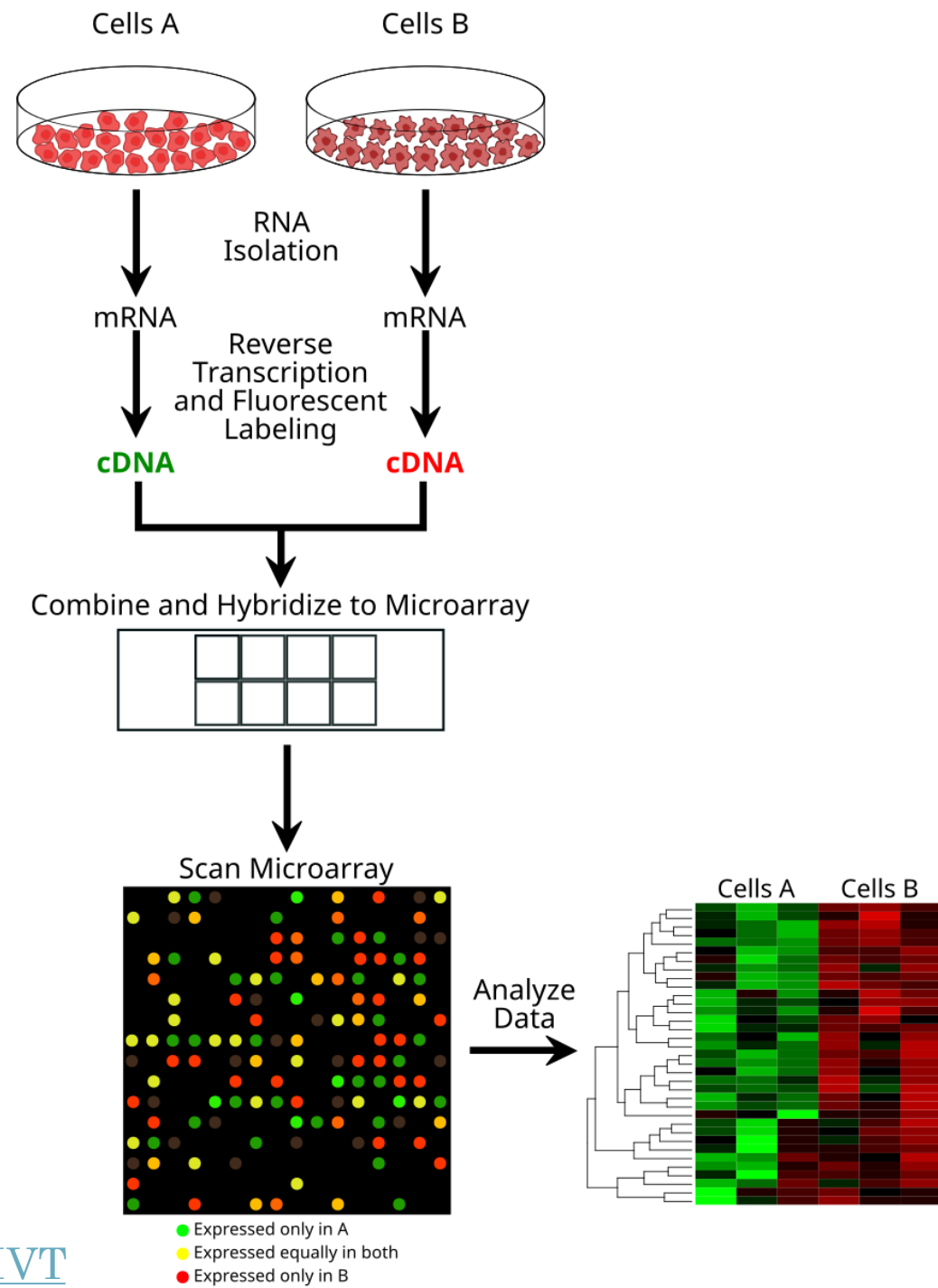
Biological Process (Gene Ontology)					
GO-term	description	count in network	strength	signal	false discovery rate
GO:0002548	Monocyte chemotaxis	5 of 21	1.55	0.99	0.00038
GO:0070372	Regulation of ERK1 and ERK2 cascade	12 of 209	0.93	0.94	6.25e-05
GO:0071347	Cellular response to interleukin-1	7 of 68	1.19	0.91	0.00037
GO:0060326	Cell chemotaxis	9 of 143	0.97	0.82	0.00039
GO:2000501	Regulation of natural killer cell chemotaxis	3 of 5	1.95	0.75	0.0034
GO:0048545	Response to steroid hormone	10 of 211	0.85	0.72	0.00071
GO:0150077	Regulation of neuroinflammatory response	4 of 25	1.38	0.63	0.0068
GO:0032355	Response to estradiol	6 of 82	1.04	0.61	0.0051
GO:0090280	Positive regulation of calcium ion import	3 of 11	1.61	0.57	0.0127
GO:0045933	Positive regulation of muscle contraction	4 of 32	1.27	0.55	0.0120
GO:0051384	Response to glucocorticoid	6 of 103	0.94	0.51	0.0116

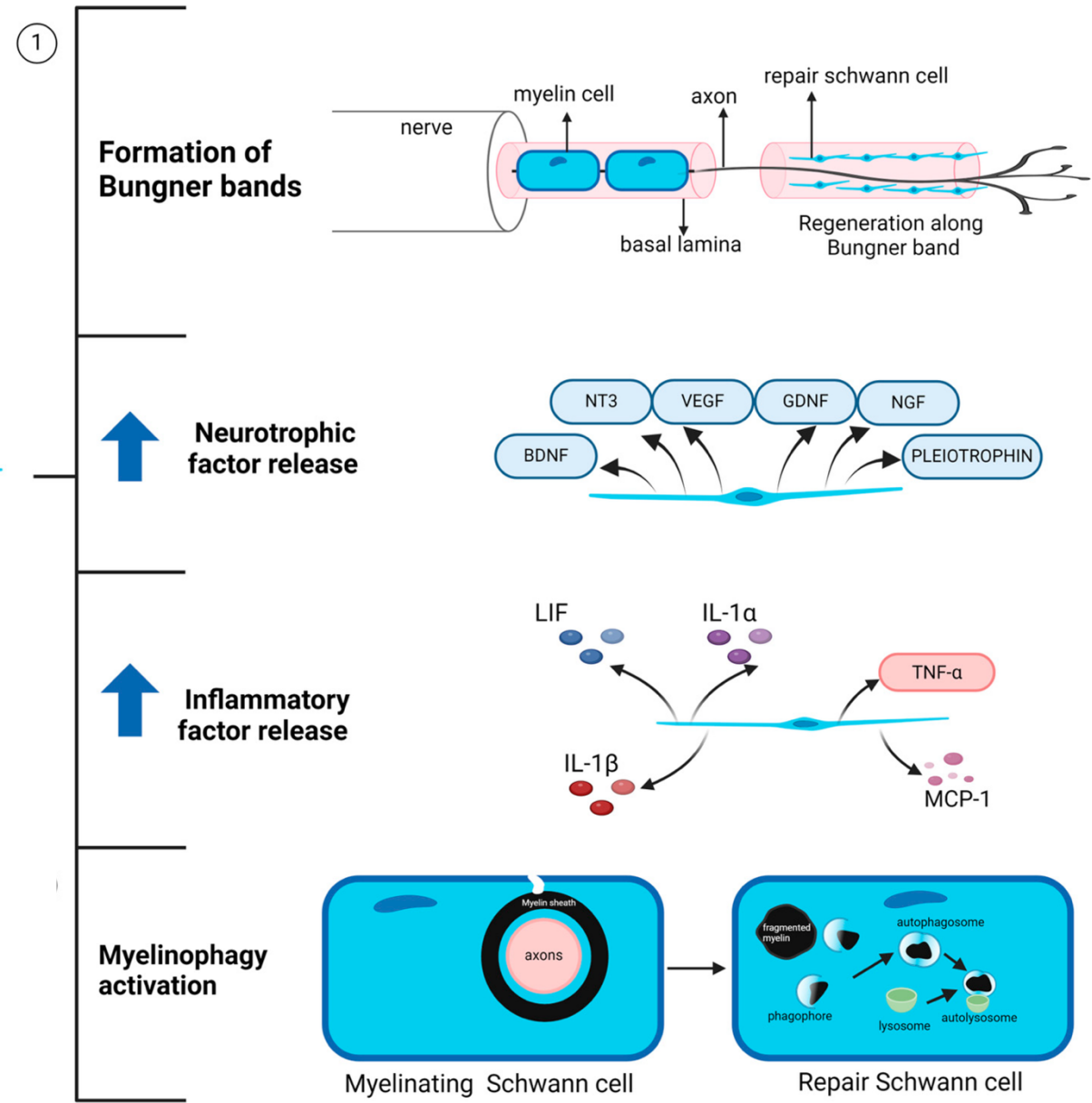
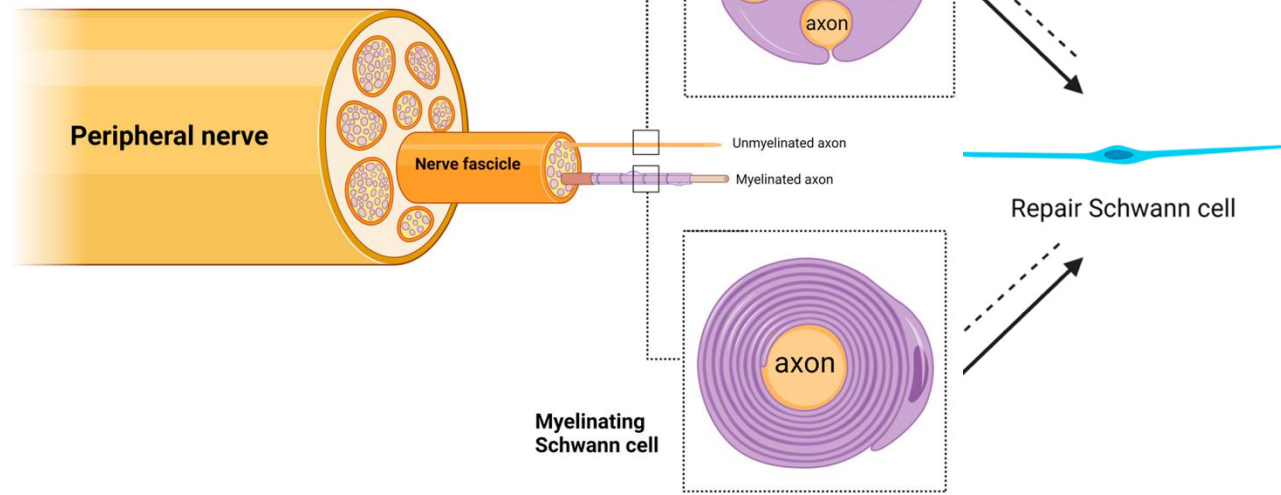
  

Molecular Function (Gene Ontology)					
GO-term	description	count in network	strength	signal	false discovery rate
GO:0042379	Chemokine receptor binding	7 of 39	1.43	1.17	5.83e-05
GO:0008201	Heparin binding	8 of 114	1.02	0.77	0.00086
GO:0005126	Cytokine receptor binding	9 of 161	0.92	0.73	0.00092
GO:0005125	Cytokine activity	7 of 107	0.99	0.64	0.0034
GO:0048018	Receptor ligand activity	10 of 232	0.81	0.63	0.0019

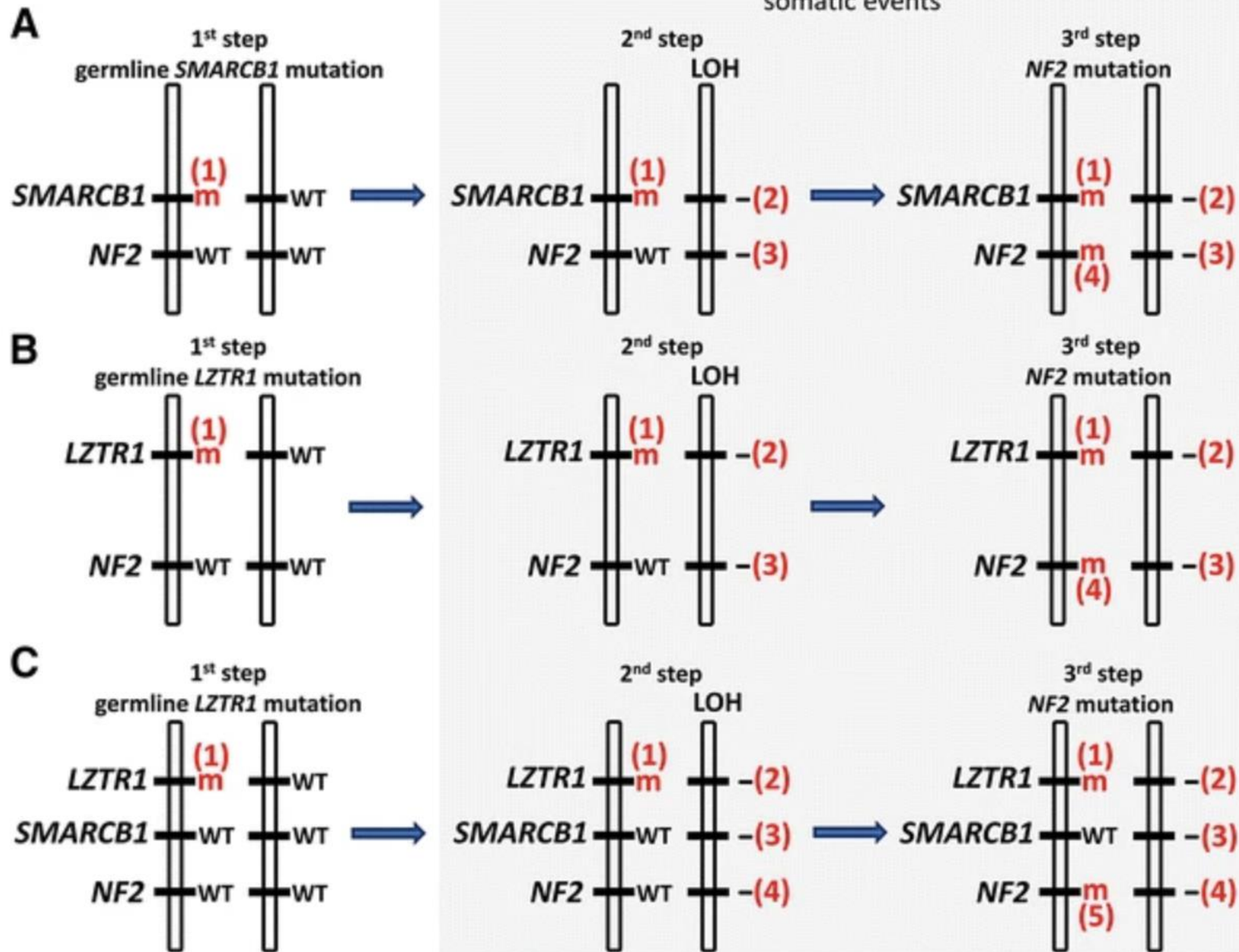


ELISAs performed on conditioned media (CM) from "painful" and "non-painful" Schwannoma cell cultures demonstrate elevated IL-6, IL-8, CCL2 and VEGF in painful CM (grey bars) compared to non-painful CM (black bars).

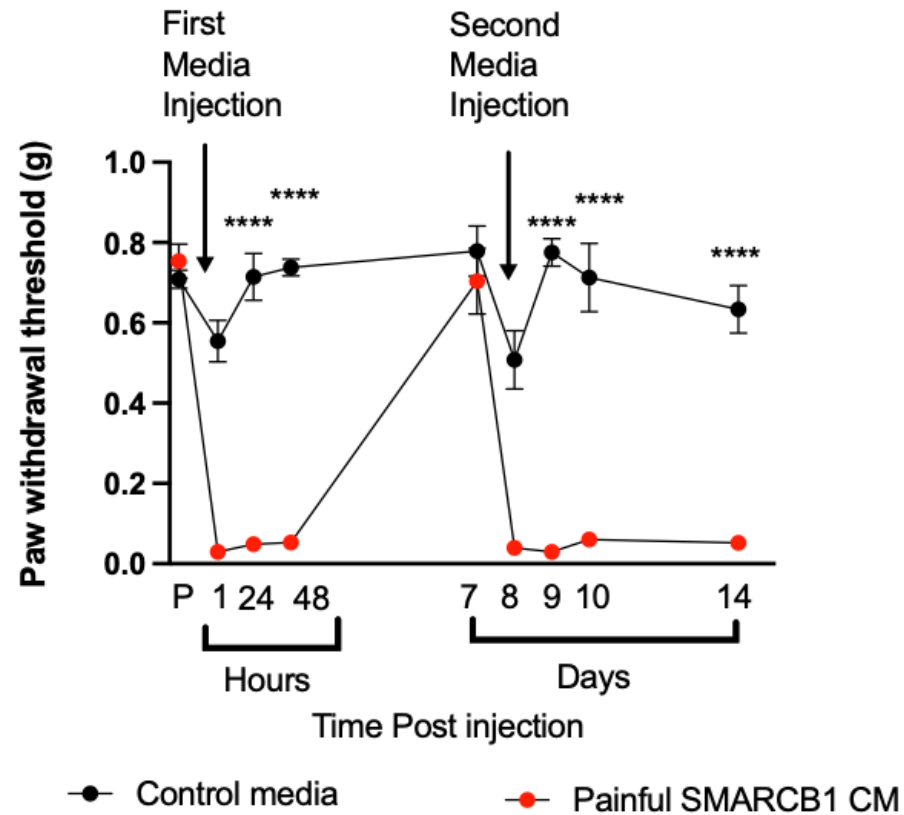
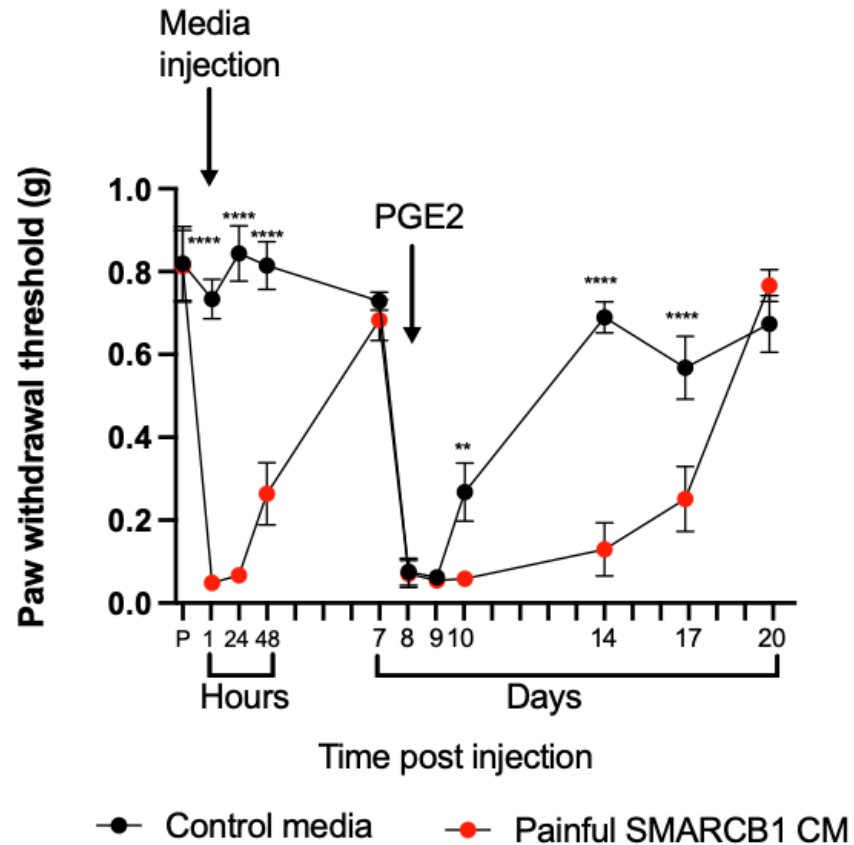




# Bonus Slide:



# Bonus Slide:



Wild Type Black C57 8-week-old mice received an initial 10ul injection of painful SMARCB1 conditioned tumor media in one hindfoot, the contralateral side received an equivalent volume of unconditioned cell media. One week post injection, both hind paws received a 10ul dose of PGE2 at 100nM. Sustained hyperalgesia in the foot treated with painful CM confirmed that a chronic pain model of SWN was established. Painful phenotypes resolved by day 20 and no significant differences were found in either the male or female versions of the chronic pain model. When the second hit was replaced with an additional CM injection, chronic pain states were still observed regardless of sex.

# BIOLOGY OF PAIN: MECHANISMS & TYPES

## NOCICEPTIVE PAIN



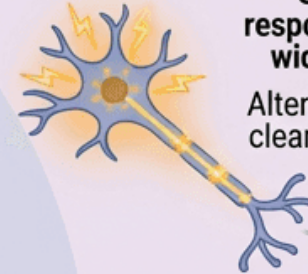
Throbbing, aching, pressure-like  
Forces threatening tissue integrity  
(thermal, chemical, mechanical).

## NEUROPATHIC PAIN



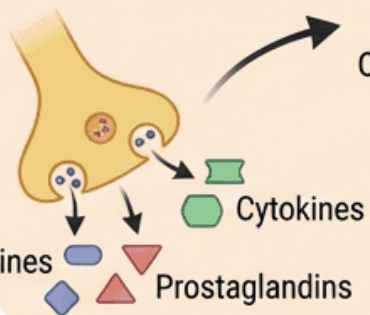
Sharp, shooting, burning, tingling,  
electric shock-like  
Damage to CNS or PNS (trauma,  
neurodegeneration, autoimmune, nerve  
compression, metabolic, viral, chemo)

## NOCIPLASTIC PAIN

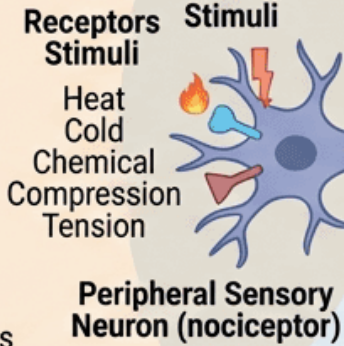


Globally enhanced  
responsivity, visceral pain,  
widespread sensitivity  
Altered CNS processing (no  
clear tissue/nerve damage)

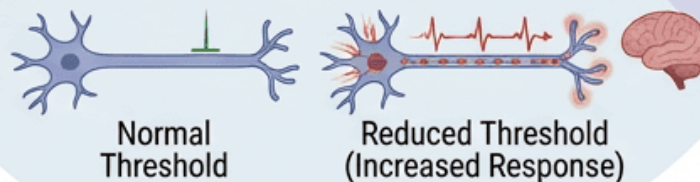
## INFLAMMATORY PAIN



Prolonged pain, sensitization  
of nearby nociceptors.



## SENSITIZATION



## MIXED-PAIN STATES & MECHANISTIC OVERLAP

Pain is a continuum of inter-related mechanisms. Patients may experience mixed-pain states.

