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TITLE: Strain-Programmable Bioadhesive Patch for Accelerated Healing of Diabetic Ulcer

PRINCIPAL INVESTIGATOR: Xuanhe Zhao, PhD

CONTRACTING ORGANIZATION: Massachusetts Institute of Technology

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13. SUPPLEMENTARY NOTES

14. ABSTRACT

We accomplished all tasks that were proposed for months 13-24. More specifically, in collaboration with Veves team, my team prepared and optimized the strain-programmable patches for Veves team's biocompatibility tests (Subtask 1), carried out biomechanical characterization and finite-element modeling to systematically validate and optimize the patches (Subtask 2), and prepared the optimized patches for Veves team's animal tests (Subtask 3).

15. SUBJECT TERMS

NONE LISTED

16. SECURITY CLASSIFICATION OF:			**17. LIMITATION OF ABSTRACT**	**18. NUMBER OF PAGES**	**19a. NAME OF RESPONSIBLE PERSON**
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TABLE OF CONTENTS

Page No.

TABLE OF CONTENTS

Page

The objective of this proposal is to develop a novel strain-programmed bioadhesive patch as a potential therapeutic solution for enhanced wound healing in diabetic foot ulcers (DFU). Our proposed strain-programmed bioadhesive patch offers a unique and novel treatment for diabetic wound healing by synergistically combining 1) instant yet robust adhesion on wet wounded tissues and 2) fully programmable mechanical contraction of wounds, potentially offering an unprecedented platform that can fulfill the unmet clinical needs to improve impaired diabetic wound healing. We hypothesized that a tissue adhesive biomaterial capable of providing programmed mechanical contractions can facilitate healing of DFU by addressing this mechanical imbalance. The first aim focuses on the development of a strain-programmed bioadhesive patch to control mechanical contraction around wound and the second aim on the optimization of the strain-programmed bioadhesive patch for DFU treatment. The third aim involved the pre-clinical validation of the strain-programmed bioadhesive patch for DFU treatment via *in vivo* and *ex vivo* models.

Diabetes, impaired wound healing, strain-programmed patch, rapid robust adhesion, controlled mechanical contraction, theoretical and numerical models, *ex vivo* human skin culture, *in vivo* diabetic mice and porcine skin, and diabetic humanized mouse skin, wound healing models.

What were the major goals of the project?

The goal of this grant is to develop a novel strain-programmed bioadhesive patch to achieve improved diabetic wound healing by programming mechanical contractions of wounds. We envision that the proposed platform can serve as a promising therapeutic solution for diabetes patients with DFU and other chronic diabetic wounds.

What was accomplished under these goals?

The accomplished work is indicated in the SOW below.

Specific Aim 1: Development of a strain-programmed bioadhesive patch to control mechanical contraction around wound.	**Timeline**	**Site 1 (Zhao, MIT)**	**Site 2 (Veves, BIDMC)**
Major Task 1	Months		
Subtask 1: Validation of the strain-programmed bioadhesive patch design.	1-12	Material preparation & fabrication **(accomplished)**	Clinical input on patch design **(accomplished)**
Subtask 2: Theoretical analysis and experimental validation the bioadhesive patch.	1-12	Theoretical & experimental validation of patch **(accomplished)**	
Subtask 3: Characterization of strain-programmed bioadhesive patch.	1-12	Mechanical characterization of patch **(accomplished)**	
Subtask 4: *In vivo* biocompatibility evaluation.	6-24	Patch preparation **(accomplished)**	Animal study **(accomplished)**
Milestone(s) Achieved			
#1: Local IACUC Approval			IACUC approval from BIDMC and MIT
#2: ACURO Approval			ACURO approval from USAMRDC ORP
Specific Aim 2: Optimization of the strain-programmed bioadhesive patch for DFU.			
Major Task 2			
Subtask 1: Biomechanical characterization of diabetes skin.	12-18	Biomechanical characterization **(accomplished)**	Skin sample supply & data analysis **(accomplished)**
Subtask 2: Modeling and optimization of programming mechanical contraction of wound.	18-30	Finite-element modeling & optimization **(in progress)**	Biomechanical analysis & input **(in progress)**
Subtask 3: Validation and optimization of the strain-programmed bioadhesive patch based on the mechanical models.	18-30	Patch optimization & mechanical modeling **(in progress)**	Clinical input on validation & optimization **(in progress)**
Milestone(s) Achieved			

#1: Biomechanical characterization protocol establishment		Biomechanical characterization Protocol **(accomplished)**	Biomechanical characterization Protocol **(accomplished)**
#2: Finite-element modeling platform establishment		Finite-element modeling **(in progress)**	
Specific Aim 3: Pre-clinical validation of the strain-programmed bioadhesive patch for DFU treatment via in vivo and ex vivo models.			
Major Task 3			
Subtask 1: Assessment of patch in the *in vivo* diabetic mice model including the humanized skin-graft diabetic mice model.	18-36	Patch preparation **(In Progress)**	Animal study **(In Progress)**
Subtask 2: Assessment of patch in the *in vivo* diabetic pig model.	24-38	Patch preparation **(In Progress)**	Animal study **(In Progress)**
Subtask 3: Assessment of patch in *ex vivo* human skin model.	30-48	Patch preparation **(In Progress)**	Animal study **(In Progress)**
Milestone(s) Achieved			
#1: Local IACUC approval			IACUC approval from BIDMC and MIT
#2: ACURO Approval			ACURO approval from USAMRDC ORP
#3: USAMRDC HRPO Approval			USAMRDC HRPO approval from BIDMC

Major Task 1.

Subtask 1. Validation of the strain- programmed bioadhesive patch design (months 1-12).

Accomplished and reported in Year 1 report.

Subtask 2. Theoretical analysis and experimental validation the bioadhesive patch (months 1-12).

Accomplished and reported in Year 1 report.

Subtask 3: Characterization of strain-programmed bioadhesive patch (months 1-12).

Accomplished and reported in Year 1 report.

Subtask 4: *In vivo* biocompatibility evaluation (months 6-24).

Zhao Lab prepared a systematic set of the patches with different levels of pre-stretches. Zhao Lab and Veves Lab tested the in vitro and in vivo biocompatibility of patches with different levels of pre-stretches. We validated that the levels of pre-stretches do not affect the biocompatibility of the patches. The biocompatibility and inflammation level of the patches with different pre-stretches are similar to those of commercially available counterparts. The accomplishment of this subtask laid the foundation for optimization of the patches by tuning the pre-stretch level yet maintaining the biocompatibility.

Major Task 2.

Subtask 1: Biomechanical characterization of diabetes skin (12-18 months).

Zhao Lab and Veves Lab accomplished biomechanical characterization of diabetes skins. Based on the biomechanical properties of diabetes skin, Zhao Lab further optimized the pre-stretch level of the patch while maintaining its biocompatibility (based on Major Task 1, Subtask 4). We identified that a strain programmable patch with a pre-stretch over 1.2 can significantly shrink the size of the wound in the diabetes skin.

Subtask 2: Modeling and optimization of programming mechanical contraction of wound (18-30 months).

Zhao and Veves Labs successfully developed finite-element models of the strain programmable patch applied on the wound (**Fig 1**). From the model, we can confirm that the strain programmable patch indeed can shrink the wound area and reduce stress concentration around the wound edge (**Figure 1**). We are currently using the models to identify the optimized pre-stretch level and mechanical properties of the patch.

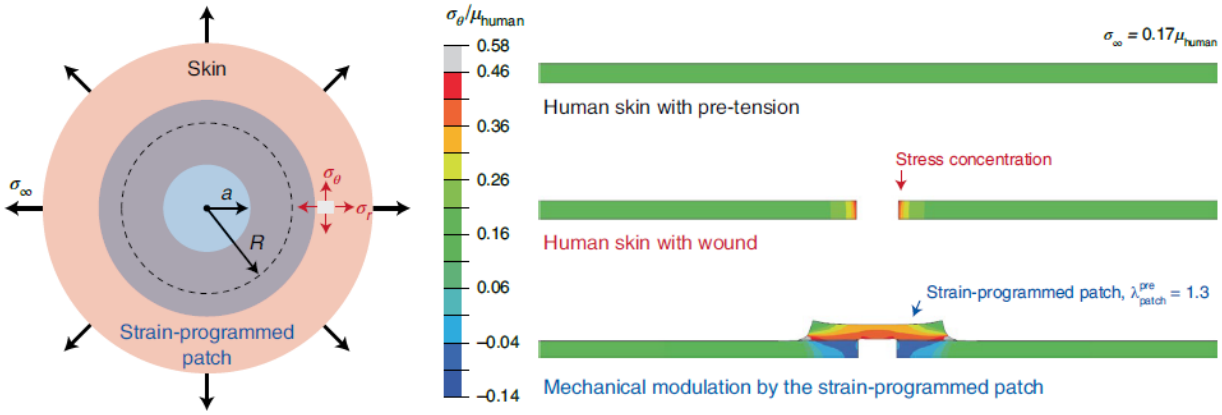

Fig 1. A representative finite-element model of the strain programmable patch applied on the wound.

Subtask 3: Validation and optimization of the strain-programmed bioadhesive patch based on the mechanical models (18-30 months).

Zhao and Veves Labs are further optimizing the strain-programmed bioadhesive patch based on the mechanical models we developed (**Fig 1**).

Major Task 3.

Subtask 1: Assessment of patch in the *in vivo* diabetic mice model including the humanized skin-graft diabetic mice (18-36 months).

The Veves lab continued the in depth characterization of diabetic mouse wounds treated with the strain patch. To evaluate the presence of adipocytes, an important cell type participating in wound repair, we stained for Perilipin 1 (Plin1) an established marker of adipose tissue that is abundantly expressed in mature adipocytes (**Fig 2**). We found no differences with the strain patch at any of the time points, but a trend for increased on Day 5 and statistically significant fewer adipocytes for the no strain group on Day 10 suggesting an interplay with the increased inflammatory response observed for this treatment.

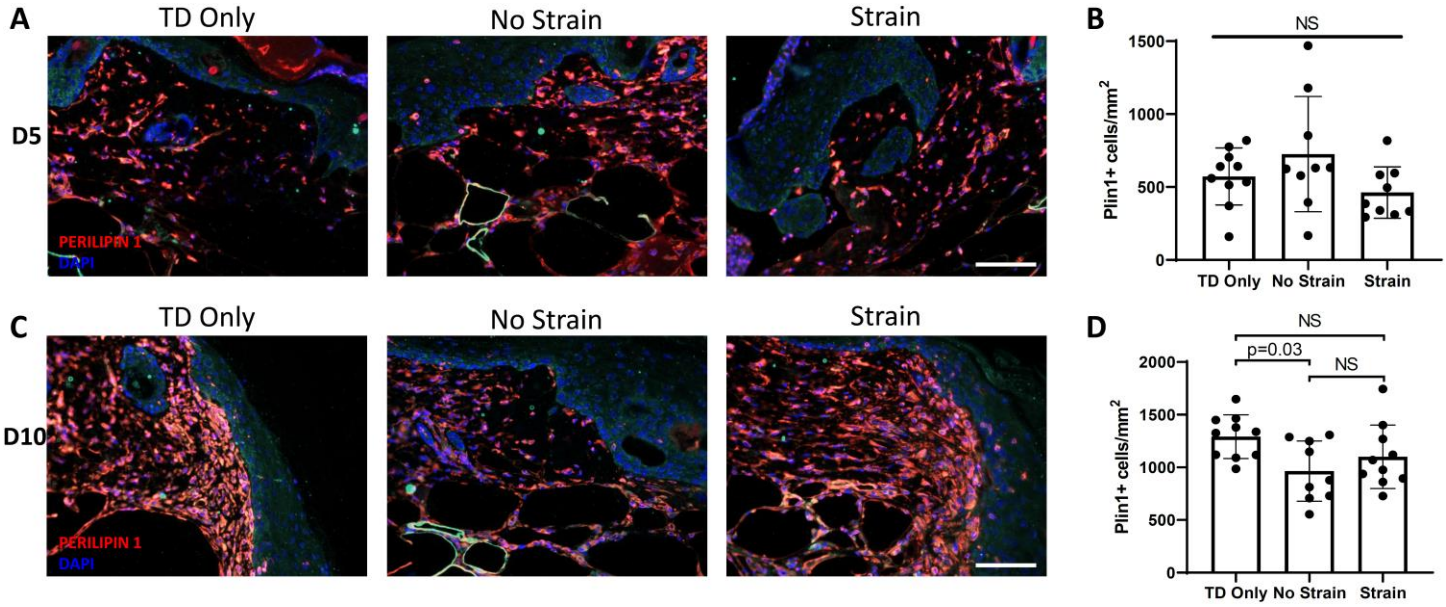

Fig 2. Adipocyte presence in db/db mouse wounds.

To further disentangle the immune cell complexities of treated diabetic mouse wounds, we employed RT-qPCR to measure markers for inflammatory associated (N1) neutrophils, as well as pro-growth associated (N2) neutrophils. We found that the no strain group displayed particularly enhanced expression of N1 neutrophil markers on D5, such as *Fas*, *Tnf* and *Cxcl10*, while the strain group was enhanced for N2 markers *Cxcl1* and *Cxcr2* (**Fig 3A**). This is in agreement with our previous findings indicating a generalized pro-reparative effect of the strain patch. Moreover, we analyzed the presence of a recently identified important cell type for wound healing: the type 2 innate lymphoid cells (ILC2). These cells are derived from the common lymphoid progenitor, but lack antigen specific B or T cell receptor. We found that the strain treated wounds exhibited high expression of markers *Il33* and *Gata3* on Day 10 post-injury (**Fig 3D**) suggesting that the applied mechanical stress also promotes the migration of ILC2 to the wound site.

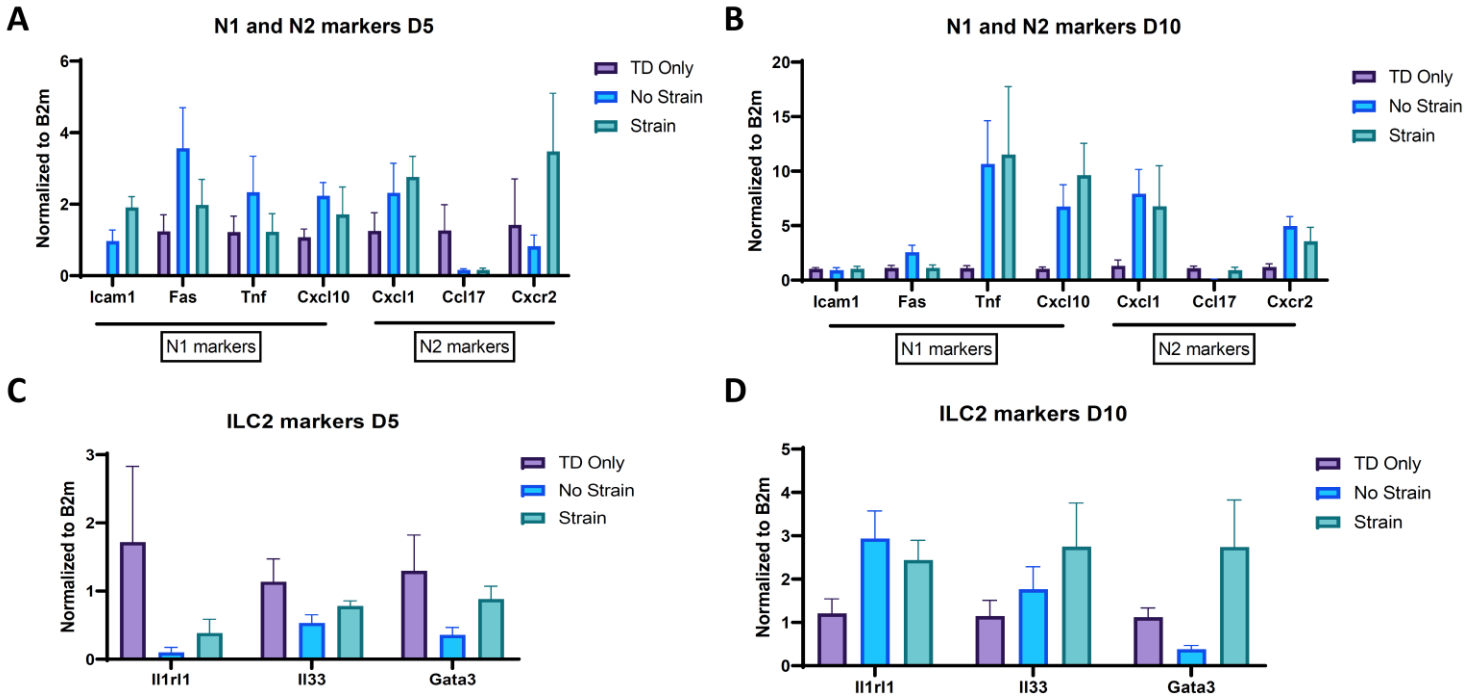

Fig 3. Gene expression of neutrophil subtype and type 2 innate lymphoid cells markers in db/db mouse wounds.

We also sought to establish similarities and discrepancies between human, mouse and pig samples for diabetic wound healing studies. For these inter-species comparisons, we utilized in house and published generated single-cell libraries from 27 human samples, 18 mouse, and 18 porcine samples, the initial phase of this study. After quality control, over 100k human cells, 230k mouse cells and 160k porcine cells were retained for downstream analysis. Normalization was applied for each dataset using SCTransform v2 and samples were integrated using Reciprocal PCA to factor our technical effects. Linear Dimensionality reduction on the corrected expression using PCA, followed by non-linear dimensionality reduction using UMAP was then performed. The shared nearest neighbor graph was then used to obtain clusters and the Wilcoxon test was utilized to obtain markers for each cluster. Expression was compared using depth-normalized counts. When comparisons were performed for genes between species, homologs were utilized using BiomaRt. Comparisons were also carried out on the pathway level.

To exhibit the clinical relevance of the porcine model, we compared single-cell libraries from porcine, murine, and human wound healing samples (**Fig 4A**). When exploring canonical cell marker expression for several cell types across the whole dataset, the porcine dataset resembles the human dataset more closely than the murine one (**Fig 4B**). Corroborating that, the correlation between homologous genes is higher for human and mouse (spearman-rho 0.47) than human and mouse (spearman-rho 0.21) (**Fig 4C** and **D**). However, once transitioning from the gene space to the pathway space, correlations become much closer, highlighting the usefulness of pathways to overcome species differences (**Fig 4E** and **F**). Finally, as a model for wound healing

specifically, it seems that the porcine samples more closely resemble the human samples across cell types as well, underlining their usefulness (**Fig 4G**).

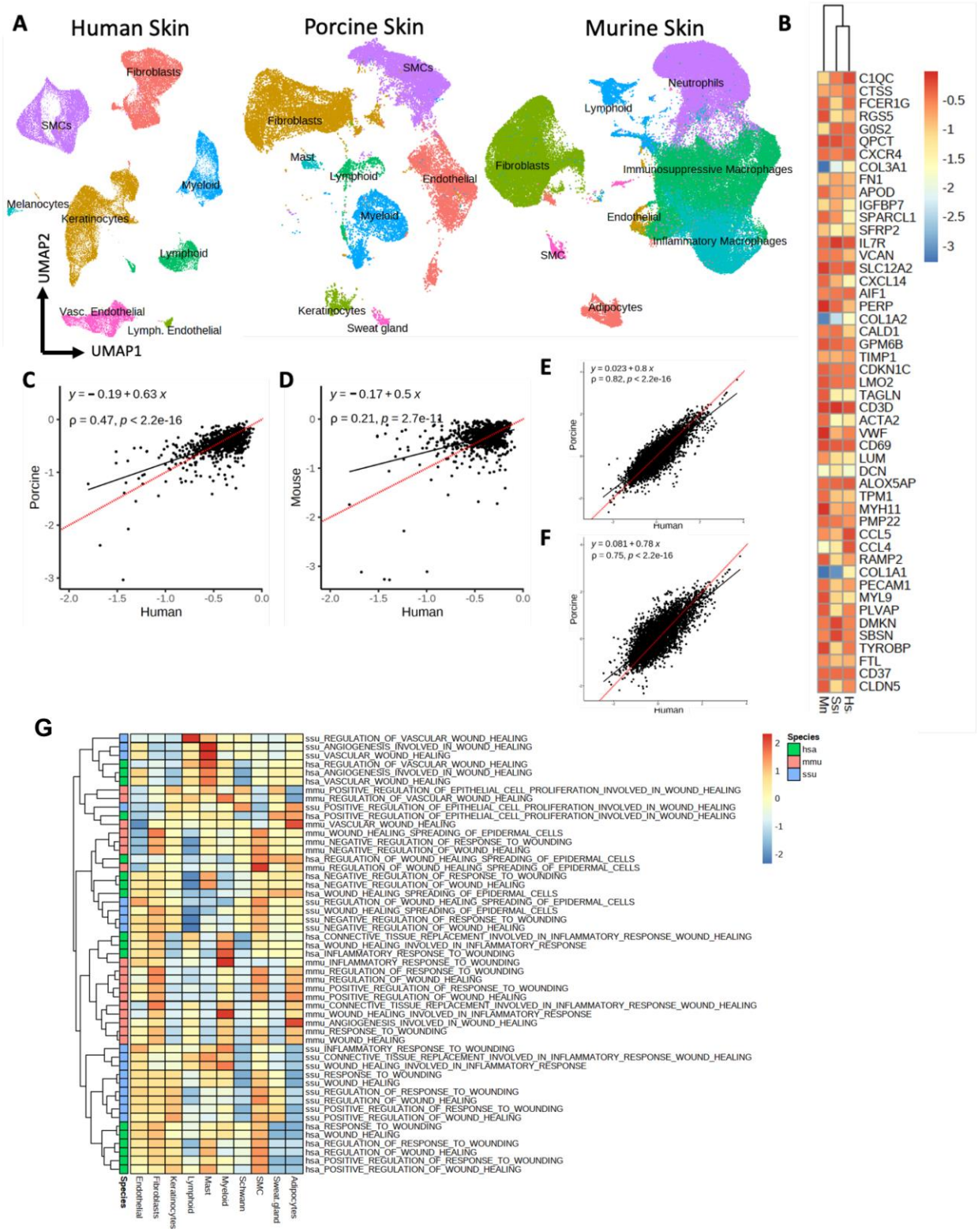

Fig 4. Inter-species comparison of wound healing models.

Zhao Lab provided the strain-programmable patches in the Subtask, participated in the study design and discussion, received feedback from the Veves Lab, and further optimized the patches.

Subtask 2: Assessment of patch in the *in vivo* diabetic pig model (24-38 months).

To elucidate the complex interplay between cell types in diabetic wound healing following treatment with the strain-programmable patch, the Veves lab sought to employ the porcine model, as pig skin matches more anatomically and biochemically to human, when compared to murine skin.

In this effort, we sequenced a total of 36 single cell libraries using 10X Genomics 3 prime sequencing. Porcine skin wound samples from Yucatan minipigs were harvested on different Days Post Wounding (DPW): Day 3, Day 7, Day 14, and Day 28 from 3 different treatments: the TegaDerm (TD) patch, a non-strain programmable patch (No-Strain), and a strain programmable patch (Strain) which was previously described. These time points were To our knowledge, this constitutes the biggest single-cell dataset on porcine skin to date.

Such datasets can prove instrumental in uncovering novel mechanisms involved in wound healing, as they allow for unparalleled resolution and can capture many rare cell types and states. Additionally, they help inform which of those are different between treatments and assist in the prioritization of compounds or mechanisms, as well as new experiments.

We endeavored to maximize the information we can gain from this dataset by utilizing several different, complementary methods of analyses that probe into different transcriptomic aspects of wound healing. After processing the initial sequencing data, we perform stringent quality control to exclude bad quality cells from downstream analyses. Several methodologies were assessed in order to ascertain that technical effects were minimized, ranging from the experimental design, where samples were allotted randomly between the sequencing runs to computational ones, evaluating different popular methods for integration of different samples.

We then annotate our cells in 3 layers of granularity, ranging from gross cell types (“Compartments”) to very fine-grained states of said cell types (“Clusters”) by utilizing both reference mapping to other datasets through gene homologs, as well as canonical markers found in the literature and used in previous seminal studies on wound healing, such as our diabetic foot ulcers atlas and cell states described in other publications.

We then proceed to investigate how the porcine skin transcriptome is affected between different treatments and days. We utilize three main workhorse methodologies:

- Differential gene and pathway expression to characterize which genes & pathways most differ between days of the same treatment or between treatments at same DPW.
- Trajectory Inference & Velocity, where cells are placed on a pseudotime axis to define transitions between closely related cell types, related to DPW or treatment.
- Gene Regulatory Network (GRN) Inference & Cell Cell Communication (CCC) analysis to illuminate the means by which cells are interacting with each other, as well as master regulators.

Initially, an optimized harvest & single-cell isolation protocol was devised to sequence the samples. After single-cell library generation and quality check using the Fragment Analyzer, samples were sequenced either on a NovaSeq 6000 or a Singular G4 sequencer in 9 total runs for the 36 libraries.

A new reference genome was constructed using the Sso11 genome and ENSEMBL release 105 annotation. Since there is no Yucatan minipig genome, we aligned against the most closely related phylogenetic neighbors to the Yucatan minipig[17625002], as well as the Sso11 genome. We found that there was very little difference in the alignment percentages between different genomes used; however, the richness of the annotation for the Sso11 genome led us to choose it. Samples were then aligned using CellRanger 7.

The alignments BAM files were used as input to velocyto to estimate RNA velocity, while the count matrices were imported into R using Seurat. Contamination was assessed using DecontX and SoupX for each sample separately and 2 samples were flagged as lower quality, though there were no samples that were removed. Doublets were then identified using both DoubletFinder and scDblFinder and fine-grained clusters high on both were flagged in downstream analysis. Cells that were damaged, as assessed by DropletQC, or had few total counts or total genes expressed, as well as very high mitochondrial or ribosomal content were removed from downstream analysis.

The initial dataset consisted of 285601 cells and 21303 genes. After examining sample level quality metrics such as cells per sample (**Fig 5A**) genes per cell (**Fig 5B**) and mapping percentages (**Fig 5C**), we utilized DropletQC to calculate the cell damage score, as well as the number of different genes expressed and the total number of counts per cell to pick thresholds for cell filtering. To annotate doublets, we used a combination of DoubletFinder v3 and scDblFinder (**Fig 5D**) and flagged cells as potential doublets. Those cells were kept in the dataset, but were excluded from downstream analysis. Additionally, we calculated the contamination percentage, compared to non-cell barcodes of each cell using DecontX (**Fig 5E**) and SoupX (**Fig 5F**). During that process, outlier samples were spotted, such as 3_CR7 (1L8, Day 7, No-Strain Patch), 14_CR7 (2L9, Day 14, Strain Patch) and 17_CR7 (1L3, Day 3, TegaDerm Patch). Those samples were also flagged to ensure that any downstream analysis interpretation is not driven by those outlier samples. After filtering, the dataset consisted of 225951 cells 17929 genes.

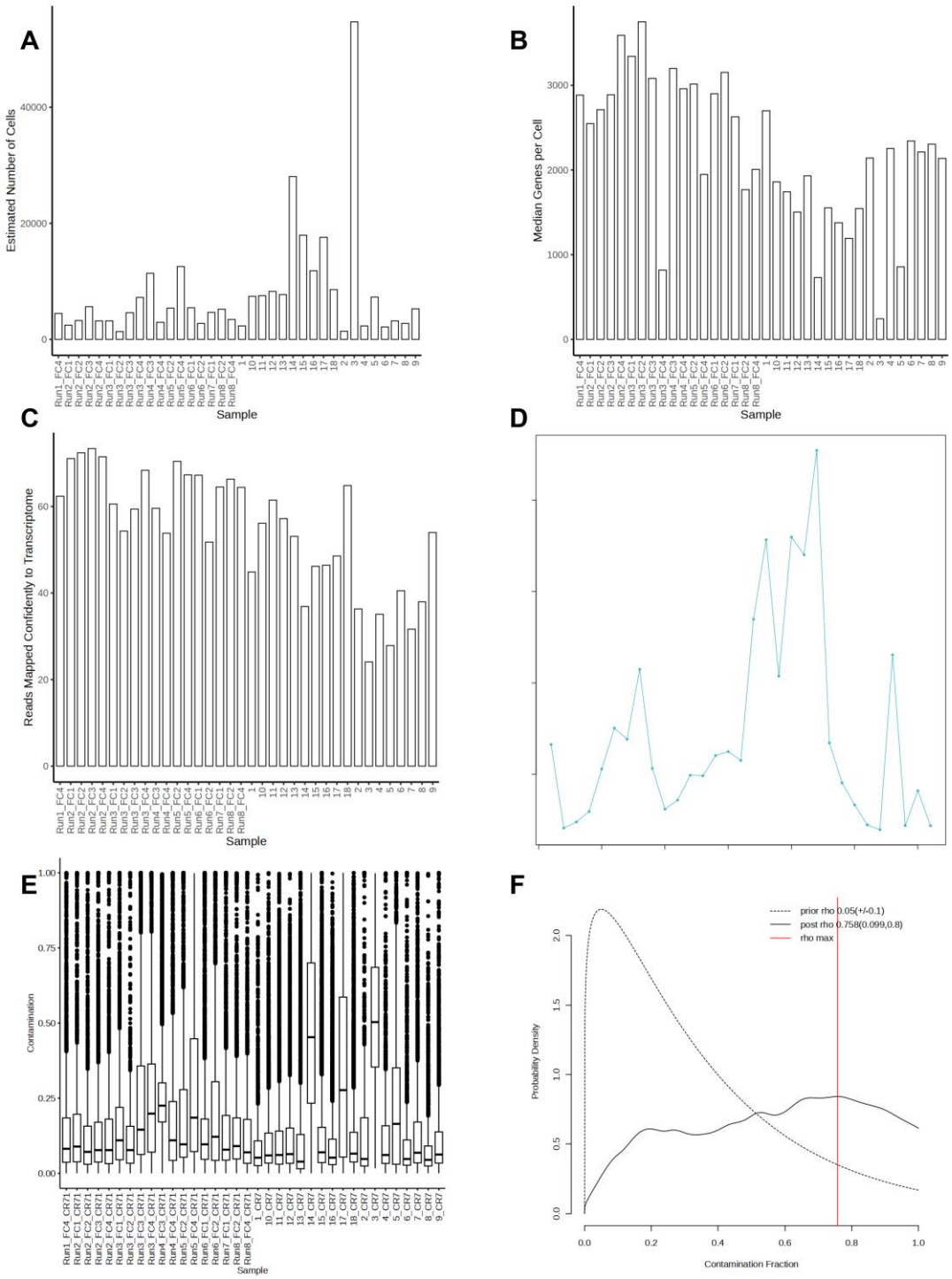

Fig 5. Quality control of the porcine single-cell RNA-seq study.

Samples were normalized using either Log Normalization or SCTransform. PCA was then performed and a shared nearest neighbor graph was constructed. Markers were identified by fitting a generalized linear model on raw counts using limma and by re-correcting depth corrected counts resulting from SCTransform v2 based on the median UMI counts in all libraries. Cluster identities were then curated by examining several markers. To establish finer levels of annotation, after annotating the initial cell type, the marker identification process was repeated by first subsetting the cell type in question then repeating the clustering process in an automated manner by leveraging cluster quality metrics - the Average Silhouette Width (ASW) and Local Inverse Samson

Index (LISI). For larger clusters, 10000 cells were subsampled for calculation of the resolution and then the whole cluster was sub-clustered. This was repeated two times to generate the 3 levels of annotation - Celltype (Coarse), Celltype (Fine),Celltype (State). After attempting to process the samples as raw counts, we noticed that a large percentage of the variance in the top Principal Components was explainable by the sample identity and batch run, rather than discovered clusters or biological covariates (**Fig 6A**, **Fig 6B**), as well as had a higher local inverse samson index coefficient (LISI) for batch, instead of the discovered clusters, implying that the current embeddings were driven by batch, rather than biological differences. Samples were then integrated using reciprocal PCA and new UMAP embeddings were calculated (**Fig 6C**, **Fig 6D**). Markers were then discovered using the Wilcoxon test by comparing each cluster to the average expression of all other clusters and cells were annotated according to the expression of canonical markers (**Fig 6E**). These steps were repeated for the finer levels of clustering. UNK clusters were populated predominantly with cells of samples with high contamination and mitochondrial content.

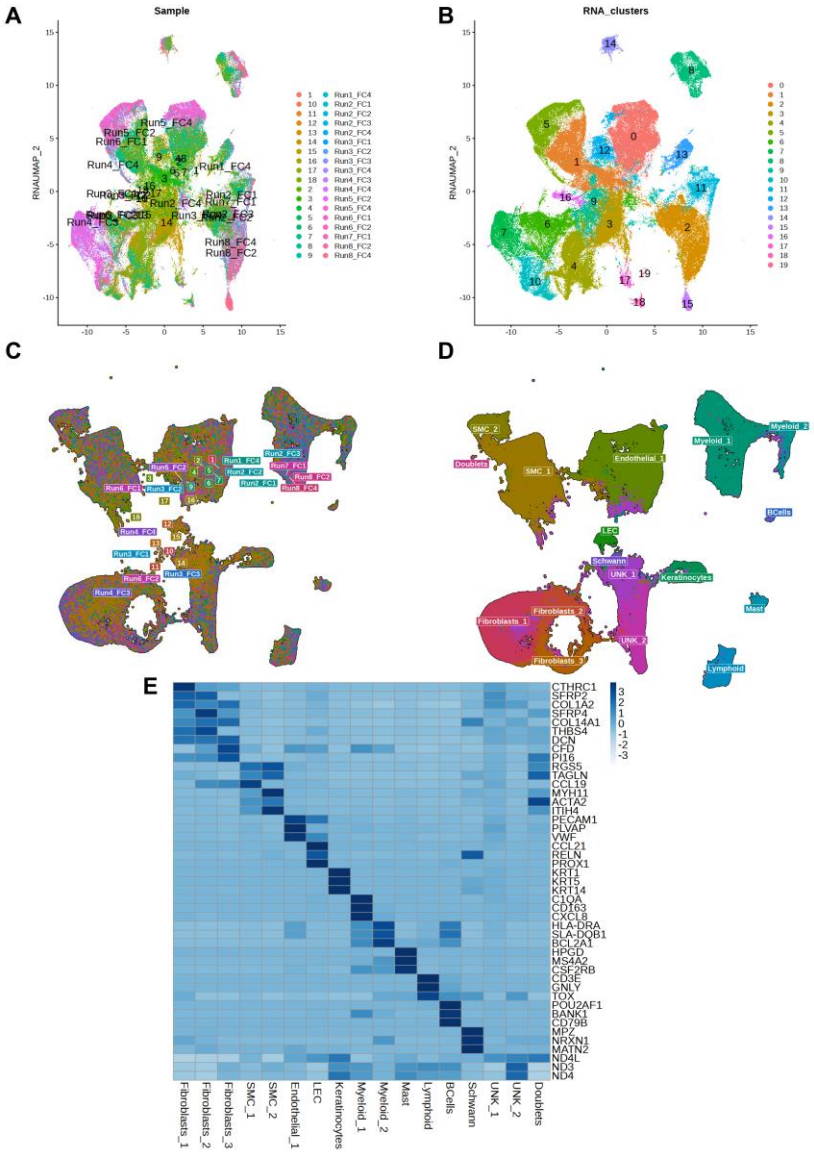

Fig 6. Integration and Annotation of samples.

To reduce the complexity of the dataset and ease implementation, we utilized Pathway Activity Score, a single-cell level method that can help summarize gene expression through pathways and can scale to very large datasets with hundreds of thousands of cells. Pathway Activity Scores were computed as the average rank of a geneset's genes for each cell in each dataset, divided by the square root of the number of genes for variance stabilization. Pathway Activity Scores then underwent Inverse Rank Normalization. Genesets were obtained from MSigDB for Sus scrofa. Subsequently, we proceeded to downstream analysis, carrying out each analysis both for the whole dataset and by subsetting each day.

To discover genes differentially expressed between treatments, we fit a negative binomial mixed model accounting for both day and treatment at the single-cell level using Presto, as well as utilize pseudobulking by treatment and day and use limma to conduct differential expression analysis. Differential abundance analysis was performed using miloR to highlight specific cell types or states that were affected by treatment. Cell Cell Communication analysis was carried out for the whole object and per-day using CellChat and the differential interactions were identified in order to serve as leads for specific compounds that can enhance wound healing. Finally, we utilized a scalable implementation of Weighted Gene Correlation Network Analysis (WGCNA), named hdWGCNA to identify co-varying modules of genes, discovering the driver genes from those modules and pathways they are involved in. Differential expression analysis revealed 837 genes differentially expressed between Strain and No-Strain, taking into account different cell types and DPW at an FDR level of 0.05 (**Fig 7A**), demonstrating large differences in wound healing. Focusing on Day 3, specific cell types have pathways that are associated with wound healing, such as vascularization pathways and complement activation activated, highlighting the involvement of fibroblasts in wound healing (**Fig 7B**). Additionally, in Day 3, the strain programmable patch seems to be promoting the inflammatory wound healing response to a large extent (**Fig 7C**, **Fig 7D**) suggesting that the patch application promotes the faster, scar wound healing pathway instead of the slower, regenerating wound healing pathway, which can be instrumental in the treatment of wounds that need immediate attention, including diabetic ulcers.

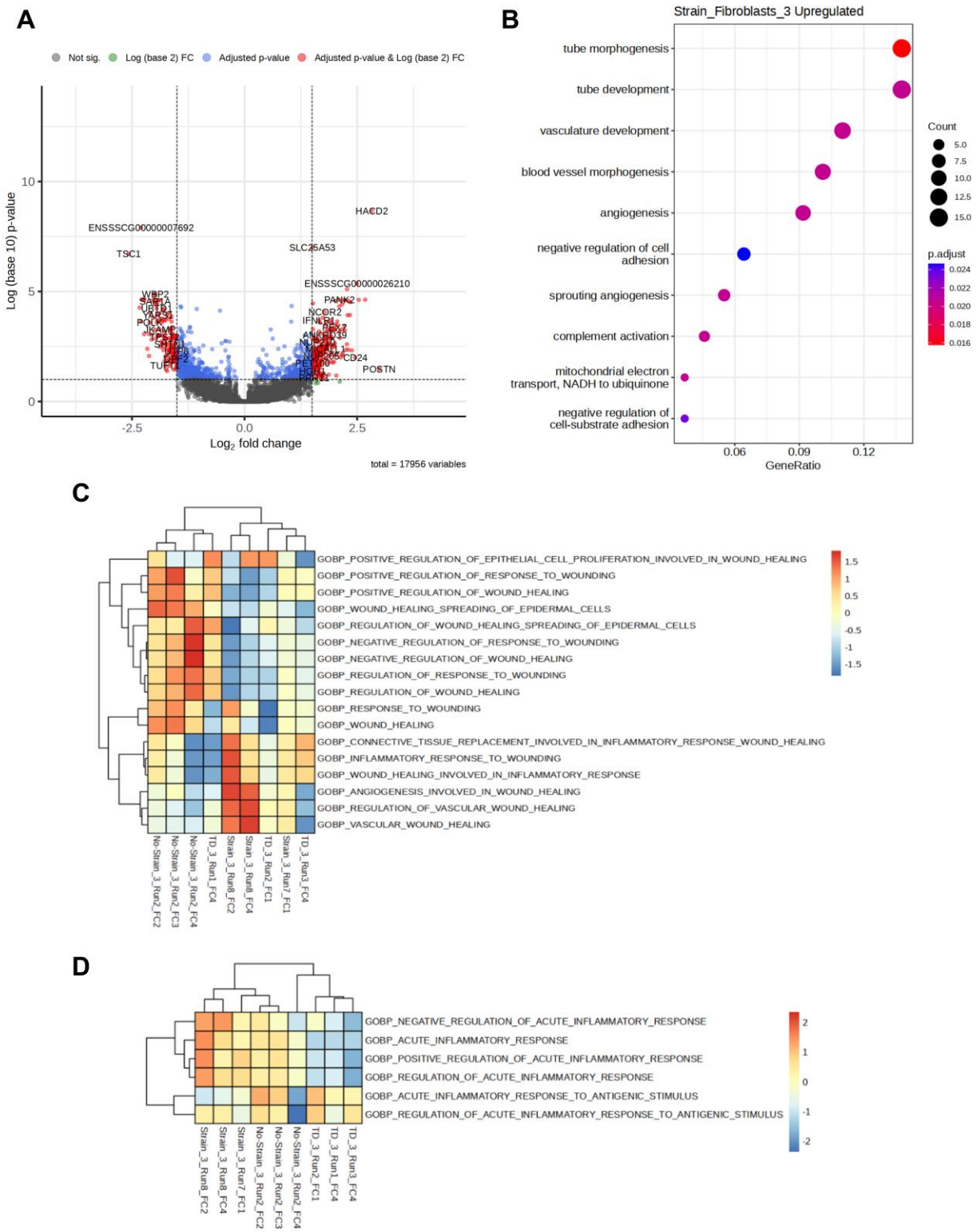

Fig 7. Widespread differences between treatments.

By combining the results obtained from these different, yet complementary methods, we are able to create a comprehensive layout of wound healing, establishing a first-of-its-kind rich resource that can be leveraged to explore the many different facets of the underlying processes. After the analysis of this dataset has been thoroughly completed and validated, we can take advantage of *in silico* perturbation models, as well as external data on response to compounds to further clarify which specific molecules are the key players in this process and design more optimized products. Finally, the study, even at its current stage, serves to underline

the usefulness of porcine samples as models for human wound healing, which can drastically shorten the time of establishing therapeutics in human patients.

Zhao Lab provided the strain-programmable patches in the Subtask, participated in the study design and discussion, received feedback from the Veves Lab, and further optimized the patches.

What opportunities for training and professional development has the project provided?

The project has been instrumental in the professional development of researchers working in my lab at MIT. More specifically, postdoctoral associates, Dr. Bolei Deng, Dr. Shucong Li, Dr. Gengxi Lu and Dr. Tao Zhou, gained considerable experience by participating in all activities, including planning of activities, study design, data collection, analysis and interpretation and participating in the writing the first draft of the paper. Notably, Dr. Tao Zhou joined Pennsylvania State University as an assistant professor in 2022. Dr. Bolei Deng obtained an assistant professor position at Georgia Institute of Technology in 2023.

How were the results disseminated to communities of interest?

We presented parts of our results at Materials Research Society Conference in 2022 Fall and 2023 Spring.

What do you plan to do during the next reporting period to accomplish the goals?

The next reporting period we plan to perform all tasks at all included in our SOW. More specifically:

Major Task 1: We have accomplished Subtasks 1-4 as planned.

Major Task 2: We have accomplished Subtask 1 as planned. Optimization of the patches will be the focus on in the next reporting period. In Subtask 2, Zhao Lab will further optimize the programming mechanical contraction of wound based on models we developed. In Subtask 3, Zhao Lab will further optimize the strain-programmed bioadhesive patch based on the mechanical models we developed. The Veves Lab will work closely with Dr. Zhao's team at MIT and provide all required input to complete all remaining elements in Subtasks 2 and 3.

Major Task 3: *Subtask 1.* The Veves Lab will investigate the mechanisms of action based on RNA seq and immunohistology studies that involve humanized mice. The Zhao Lab will provide the strain-programmable patches, participate in the study design and discussion, receive feedback from the Veves Lab, and further optimize the patches.

Subtask 2. The Veves Lab will further analyze the mechanism of the patch by performing complementary multiplex staining to corroborate the single-cell RNA-seq results at the protein level. We will also use in vitro models with porcine and/or human cells to corroborate the most striking findings.

The Zhao Lab will provide the strain-programmable patches, participate in the study design and discussion, receive feedback from the Veves Lab, and further optimize the patches.

Subtask 3. The Veves lab will investigate the effects of strain-programmable patches in wounds created in *ex vivo* skin. The lab will also investigate similarities and differences when compared to the effects of the patch in humanized mice and pig wounds. This will provide a full picture of the mechanisms of action of the patch.

4. IMPACT

What was the impact on the development of the principal discipline(s) of the project?

In agreement to our previous report last year, we believe that the obtained data so far has the potential to have a considerable impact in the field of impaired diabetic wound healing. More specifically, the project can provide alternative novel therapeutic approaches for the management of diabetic foot ulceration. In addition, it contains very innovative research design, which includes *ex vivo* human skin cultures, humanized mice and state-of-the-art transcriptomics that can be adapted by other researchers will conduct research that will investigate additional potential therapeutic approaches.

What was the impact on other disciplines?

We believe that the patch, or alterations of it, along with the research design we developed, can be employed for the management of other chronic or acute wounds.

What was the impact on technology transfer?

A patent titled '*Shape Memory Adhesive Materials for Diabetic Wound Healing'* has been already submitted and has been licensed to the start-up company SanaHeal.

What was the impact on society beyond science and technology?

Nothing to Report

5. CHANGES/PROBLEMS

Changes in approach and reasons for change

Nothing to report

6. PRODUCTS

Publications, conference papers, and presentations

There were no publication this past year but papers are in preparation for submission in the near future. We would like to remind that the following paper was published last year:

Theocharidis G[#], Hyunwoo Yuk H[#], Roh H, Wang L, Mezghani M, Wu J, Kafanas A, Contreras M, Sumpio B, Li Z, Wang E, Chen L, Fei Guo C, Jayaswal N, Katopodi XL, Kalavros N, Nabzdyk CS, Vlachos IS, Veves A*, Zhao X*. Strain-Programmed Patch for Diabetic Wound Healing. Nature Biomedical Engineering, https://doi.org/10.1038/s41551-022-00905-2. *[#]: These authors contributed equally, *:These authors jointly supervised this work*

Inventions, patent applications, and/or licenses

Shape Memory Adhesive Materials for Diabetic Wound Healing, U.S. Application No. 63/148,901.

7. PARTICIPANTS & OTHER COLLABORATING ORGANIZATIONS

What individuals have worked on the project?

Name:	Xuanhe Zhao
Project Role:	PI
Researcher Identifier (ORCID ID):	
Nearest person month worked:	1
Contribution to Project:	Supervise the project; Participate in all activities, including planning of activities, study design, data collection, analysis and interpretation and participating in writing the first draft of the paper.
Funding Support:	MIT

Name:	Chase Michael Hartquist
Project Role:	Graduate student
Researcher Identifier (ORCID ID):	
Nearest person month worked:	6
Contribution to Project:	Participate in patch design, fabrication, characterization, and validation.
Funding Support:	NSF graduate fellowship

Name:	Bolei Deng
Project Role:	Postdoc associate
Researcher Identifier (ORCID ID):	
Nearest person month worked:	7
Contribution to Project:	Participate in patch design, fabrication, characterization, and validation.
Funding Support:	MIT

Name:	Shucong Li
Project Role:	Postdoc associate
Researcher Identifier (ORCID ID):	
Nearest person month worked:	6
Contribution to Project:	Participate in patch design, fabrication, characterization, and validation.
Funding Support:	MIT

Name:	Gengxi Lu
Project Role:	Postdoc associate
Researcher Identifier (ORCID ID):	
Nearest person month worked:	4
Contribution to Project:	Participate in patch design, fabrication, characterization, and validation.
Funding Support:	MIT

Name:	Tao Zhou
Project Role:	Postdoc associate
Researcher Identifier (ORCID ID):	
Nearest person month worked:	2
Contribution to Project:	Participate in patch design, fabrication, characterization, and validation.
Funding Support:	MIT

Has there been a change in the active other support of the PD/PI (s) or senior/key personnel since the last reporting period?

Yes

What other organizations were involved as partners?

Nothing to Report

8. SPECIAL REPORTING REQUIREMENTS

Collaborative awards

Independent reports are provided

9. APPENDICES

No appendices