Keloid-Specific Gene Expression Profiling for Accurate Diagnostic and Therapeutic Applications

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Abstract

Scars are a heterogeneous disease including normotrophic scars, hypertrophic scars, and keloids. Of these lesions, keloids are a distinct subtype from any other type of scar. Clinically, it causes pain, itching, or tenderness, causing life discomfort and characteristically irreversible.

Despite various treatment modalities, restoring keloids to normal tissues is difficult, and frequent recurrences have been reported. Therefore, it is essential to identify keloid-specific genes for accurate diagnosis and treatment of keloids. In an effort to find out keloid-specific genes, several studies compared keloids with scar-free normal skin, which leading general scar-related genes to be chosen rather than keloid-specific genes. To select for highly accurate keloid-specific genes and pathways, we compared the transcriptome profile of keloids with those of normotrophic scars and hypertrophic scars, which acquired from formalin-fixed paraffin-embedded human skin samples using high-throughput RNA-sequencing techniques. Differential expression analyses and over-representation analyses revealed that genes related to nervous system process were upregulated in keloids, whereas genes related with immune responses were downregulated in keloids. Additionally, the extracellular matrix related processes were highlighted in both hypertrophic scars and keloids. Finally, we highlight potential keloid-specific biomarkers and expression changes that can be employed for future therapeutics of keloids.

Introduction

A scar is an area of fibrous tissue that replaces normal skin after an injury. Scarring is a biological process of wound healing. Despite tremendous progress in unravelling the science behind wound healing, the mechanisms for elucidating scar formation caused by abnormal wound healing are still unknown[1]. Deep injury to the reticular dermis sometimes results in pathological abnormal fibrous scars such as hypertrophic scars and keloids, which are thought to be caused by abnormal wound healing due to altered gene expression in the wound healing tissue. Hypertrophic scars and keloids consist of numerous inflammatory cells, proliferating fibroblasts, progressive collagen deposition and enhanced angiogenesis[4] and they present distinct clinical, histological, and developmental features. Clinically, hypertrophic scars are confined within the wound boundary, while keloids extend growth beyond the wound borders[5,6]. Histologically, hypertrophic scars have fewer thick collagen fibers than keloids[7,8]. Furthermore, hypertrophic scar tissues are composed of low-density dermatan sulfate (DS) proteoglycans, while keloid scar tissues are composed of both low-density DS and chondroitin sulfate (CS) proteoglycans, with CS proteoglycans in higher proportion[9,10]. Hypertrophic scars usually develop within two months from injury and tend to regress over time. In contrast, keloids develop and progress after 3 months or more, grow irreversibly for years[11], and cause medical problems as well as life problems such as itchiness and unusual appearance for patients. Hypertrophic scars tend to respond well to treatment. On the other hand, once formed, keloids are very difficult to restore to normal tissues, and frequent recurrences and exacerbations over a long period of time become another obstacle to treatment[12]. It has not been reported yet what kind of scars would be occurred when the skin is damaged. Therefore, it is essential to

understand the pathological factors behind the various scar types and gene expression profiles of pathological scars caused by abnormal wound healing, for the development of efficient treatment strategies for the treatment of abnormal scars.

To date, there have been five reports comparing gene expression patterns in keloid and related scar lesions using whole transcriptome analysis such as cDNA microarray or RNA-seq. Onoufriadis, A. *et al.*[13] and Wu, J. *et al.*[14] performed RNA-seq on keloids and normal skin tissue. Hahn, J.M. *et al.*[15], Chao-Kai, Hsu *et al.*[16], and Matsumoto, N.M *et al.*[17] compared mRNA expression patterns between keloids and normal skin tissue using cDNA microarrays. Although these studies have provided new insights into keloids, there are limitations in that the selected keloid-specific gene expression profile could not be distinguished from a scar-related genes expression profile, since they compared keloids to scar-free normal skin tissue not to reversible scars. Considering different responses of irreversible keloids and reversible hypertrophic scars to the treatment, it is crucial to compare the overall gene expression patterns of irreversible scars such as keloids and reversible scars. In this study, we aimed to compare the overall gene expression patterns of reversible and irreversible scars and provide insight into the molecular and cellular mechanisms behind these lesions. Toward this goal, high-throughput RNA-sequencing techniques using next-generation sequencing technology were employed. By elucidating highly specific genes and related signaling pathways for abnormal fibroproliferative scar lesions, this study can contribute to the development of effective and targeted therapeutic strategies for these lesions.

Results

Expression analysis of keloids and related lesions through RNA-seq

To reveal the gene expression characteristics of keloids and related lesions, we collected 4 keloid tissues, 5 hypertrophic scars, and 3 normotrophic scars. The three types of lesions were categorized by characteristic appearance, histological morphology and clinical features[19]. From normotrophic scars and hypertrophic scars to keloids, the epidermal cell layer becomes thicker and the collagen fibers become thicker and denser. Consistent with previous reports, keloids and hypertrophic scars showed abundant vasculature, high mesenchymal cell density, inflammatory cell infiltration, and thickened epidermal cell layer compared to normotrophic scars (Fig. 1A)[20,21]. In particular, thick collagen fibers composed of numerous tightly packed fibrils were observed in keloids, while hypertrophic scars exhibit a nodular structure composed of fibroblasts, small blood vessels, and randomly organized collagen fibers[22] (Fig. 1A, B).

To confirm the histopathologic classification of the samples, the expression profiles of these collected tissue samples were analyzed by unsupervised clustering using a machine learning-based dimensionality reduction algorithm such as MDS (Multi-Dimensional Scaling) and tSNE (t-Distributed Stochastic Neighbor Embedding). The results showed that these lesions were separated into three clusters, relatively

consistent with their diagnoses (Fig. 1C). The differential genes of these normotrophic scar (S), hypertrophic scar (HS), and keloid (K) were grouped into 8 classes depending on expression pattern: UU (Up-Up, S<HS<K), UF (Up-Flat, S<HS~K), FD (Flat-Down, S~HS>K), UD (Up-Down, S<HS>K), DD (Down-Down, S>HS>K), DF (Down-Flat, S>HS~K), FU (Flat-Up, S~HS<K), and DU (Down-Up, S>HS<K). The genes were separated as upregulated (U), downregulated (D), or not differentially expressed (F). Expression pattern of grouped genes over scar types were also separated in patterns as expected (Fig. 1D).

Derivation of keloid-specific genes and signaling pathways by comparing gene expression profiles of keloids and reversible scars

Once keloids were developed, they grow irreversibly for years, compared to normoptophic and hypertrophic scars which regress over time. In an attempt to discover genes specifically regulated in keloids as irreversible scars, we classified normotrophic and hypertrophic scars as one group-reversible scars and compared their gene expression profiles with that of keloids. To identify genes specifically up or downregulated in keloids, we performed mRNA sequencing and differential expression analysis on RNA-Seq data from normotrophic scars, hypertrophic scars, and keloids with following statistical methods. For differential expression analysis, we implemented Ensemble approaches as three widely used methods (Limma-voom, edgeR and DESeq2) to achieve lower false positive DEGs. In this approach, genes were flagged as DEG on at least two different analysis were used for further analysis (Fig. 2A, C). Overall, 195 genes were downregulated in keloids compared with reversible scars, whereas 306 genes were upregulated in keloids. Of these genes, golgin A6 family genes and ERICH6B (Glutamate-Rich 6B) genes were identified as the most significantly changed genes as described in volcano plots (Fig. 2B). It should be noted that the levels of golgin A6 family genes and ERICH6B genes were not only significantly changed, but also exhibited the highest magnitude of fold change among the genes in keloids compared with reversible scars. Golgins are a family of predominantly coiled-coil proteins that are localized to the Golgi apparatus[23]. Anchored to the Golgi membrane, they are predicted to project into the surrounding cytoplasm and are involved in various functions of the Golgi apparatus, such as vesicular traffic through golgin-mediated tethering. Second, golgins are involved in maintenance and positioning of the Golgi apparatus within cells. In addition to acting as tethers, some golgins can sequester various factors at the Golgi membrane, allowing spatiotemporal regulation of downstream cellular functions. However, the specific functions and clinical relevance of the Golgin A6 family has not been elucidated yet. In the case of ERICH6B, there is little information on the structure, function and clinical relevance of the gene, except for its predominant expression in the testis.

Next, up and downregulated 501 DEGs (up: 306, down: 195) was classified as expression changes on normotrophic scars – hypertrophic scars – keloids. Specifically, most of the downregulated DEGs in keloids belonged to the FD (Flat-Down, 64.6%) subgroup, in contrast to very few belonged to DD (Down-Down, 0%) or DF (Down-Flat, 5.6%) subgroup. On the other hand, most of upregulated DEGs in keloids belonged to the FU (Flat-Up, 67.3%) subgroup, while very few belonged to UU (Up-Up, 1.0%) or UF (Up-Flat, 1.0%) subgroup. These results indicate that most of the DEGs exhibited small differences between normotrophic and hypertrophic scars but were higher or lower in keloids (Fig. 2D, E).

For better understanding of biological function of genes that exhibited specifically high or low expression in keloids. DEGs are enriched to Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway (Fig. 2F). Over-representation analysis on GO Biological Process showed that the genes involved in ‘activation of immune response’, ‘antigen processing and presentation of peptide antigen’ and ‘immunoglobulin mediated immune response’ are significantly downregulated in keloids (Supplementary Table. I). These findings suggest that immune regulation and inflammatory mechanisms play important roles in keloid formation. On the other hand, DEGs upregulated in keloids were over-represented in roles of ‘sensory perception’, ‘neuron development’, and ‘muscle filament sliding’ (Supplementary Table. III). Over-representation analysis on KEGG pathway demonstrated that downregulated DEGs in keloids were enriched in ‘systemic lupus erythematosus’ and ‘antigen processing and presentation’, (Supplementary Table. II) whereas upregulated DEGs in keloids were enriched in ‘protein digestion and absorption’ and ‘insulin secretion’. Overall, downregulated DEGs in keloids were associated with immune functions, (Supplementary Table. IV) whereas upregulated DEGs in keloids were associated with neuron development and muscle contraction.

Keloids and hypertrophic specific upregulated DEGs are predominantly associated with remodeling of extracellular matrix structural tissue

Hypertrophic scars and keloids have a commonality in that they are present in abnormally high levels in fibroproliferative lesions. To gain insight into the mechanisms behind this abnormality, we attempted to identify DEGs that are specifically upregulated in hypertrophic scars and keloids. Our study revealed 88 upregulated genes in these exaggerated scars compared to normotrophic scars, including RYR2 (ryanodine receptor 2), ARMC3 (armadillo repeat including 3), and SMCO2 (single-pass membrane protein with coiled-coil domains 2) as representative genes with larger fold changes (Fig. 3A). Particularly, these 88 DEGs were highly over-represented on ‘extracellular structure/matrix organization’ among GO Biological Process terms (Fig. 3B, Supplementary Table. V). Overall, these results are in consistently implies that the clinical observation of excessive ECM depositions are represented in both hypertrophic scars and keloids (Supplementary Table. VI).

Keloids and hypertrophic scar specific downregulated DEGs are associated with keratinization, epidermal development, and the estrogen signaling pathway

Compared to upregulated genes, we identified 809 downregulated genes in exaggerated scars such as hypertrophic scars and keloids (Fig. 3C). Over representation analysis on GO Biological Process terms found most represented terms as ‘keratinization’ and ‘epidermal development’ (Supplementary Table VII). Also, in KEGG pathways, ‘estrogen signaling pathway’ was the most represented term (Fig. 3D, Supplementary Table VIII).

Hypertrophic scar specific genes are associated with epidermal cell differentiation and the lipid catabolic process

Although hypertrophic scars are reversible, the degree of fibrosis is more severe and prolonged compared to that of normotrophic scars. Therefore, we attempted to find hypertrophic scar-specific genes to distinguish them from both keloids and normotrophic scars. Only four DEGs specifically were upregulated in hypertrophic scars, including TUBB2B (tubulin, beta 2B class 2 B), TNFSF4 (tumor necrosis factor superfamily, member 4), TNC (tenascin C), and TNN (tenascin N) (Fig. 4A). In contrast, a total of 237 DEGs was specifically downregulated in hypertrophic scars (Fig. 4B). Among the mostly changed genes in fold changes, KRTAP5-1 (keratin associated protein 5-1), KRT9 (keratin9), and KRTAP10-6 (keratin associated protein 10-6) are commonly related to keratin. Over-representation analysis results on GO Biological processes revealed that these hypertrophic scar specific expressions were associated with ‘epidermal cell differentiation’, ‘epidermal development’, and ‘water homeostasis’ (Fig. 4C, Supplementary Table. IX). Conversely, over-represented KEGG pathway terms were ‘arachidonic acid metabolism’, ‘linoleic acid metabolism’ (Supplementary Table X).

Scar-free normal skin is not a proper control group for determining keloid-specific genes

Previous studies have used scar-free normal skin as a control for comparison with keloids. Since keloids are a possible outcome of wound healing, it is uncertain if it is appropriate to compare keloids with unwounded skin tissue. This limitation suggests that documented studies comparing keloids with scar-free normal skin as a control group are including expression profiles of overall scars rather than keloid-specific chracteristics. To overcome this issue, we hypothesized that comparing expression profiles between types of scar tissues would find scar subtype specific features better than comparison between keloid and scar-free normal tissue. For scar-free normal comparisons, we imported publicly available normal skin tissue data from GEO (ID : GSE113619). We implemted the same Ensemble approaches on differential expression analysis and identified DEGs (Fig. 5A). According to over representation analyses with those DEGs, expression profile changes of keloids, hypertrophic scars, and normotrophic scars than normal skin present very similar shared results expeacially in GO Biological Processes (Fig. 5B). Specifically, the genes for ‘extracellular matrix/structure organization’ and ‘extracellular matrix assembly’ were upregulated in all three types of scars compared to normal skin (Supplementary Table. XI, XIII, XV). In addition, the genes for ‘keratinization’, ‘epidermal development’, and ‘epithelial cell differentiation’ were downregulated in all three types of scars (Supplementary Table. XII, XIV, XVI). These results implies previous studies that directly compared keloids with scar-free normal skin were more likely to discover general scar-specific features rather than keloid-specific features (Fig. 5C). Therefore, keloid-specific features can be found better by comparing keloids with other reversible scars instead of with scar free normal skin. From these scar tissue type based comparisons, The keloid-specific genes obtained from this improved comparison were related to sensory perception, neuron development, activation of the immune response, and the lipid biosynthetic process (Fig. 2F).

Discussion

In this study, to identify keloid-specific gene expression profiles, keloid tissues were compared with reversible scar tissues using whole transcriptome analysis. In addition, hypertrophic scar-specific genes

were determined. Our present study suggests that peripheral development- and immune regulation-related genes are involved in the pathogenesis of keloids. To the best of our knowledge, no such results have been reported previously.

The wound repair process has several phases: the (1) inflammatory phase, (2) proliferative phase, and (3) remodeling phase[24,25,26]. In the first step, activation of platelets and the clotting cascade cause blood clotting and immobilization of platelets at the wound site. Then inflammatory cells are recruited to the wound site. During the proliferation phase, fibroblasts are activated and differentiated into myofibroblast-producing and -organizing ECM molecules, activating the process of re-epithelialization. Finally, during the remodeling (maturation) phase, collagen fibers are remodeled, and excessive fibroblasts are removed by apoptosis.

We confirmed that the expression of genes related to extracellular matrix organization and disassembly was highly expressed in hypertrophic scars and keloids compared to scar free normal skin tissue based on the analysis of GO biological process and KEGG pathway, as well as elevated expression of genes related to regulation of neuron differentiation and expression. It should be noted that the high expression of genes related to muscle filament sliding and actin-myosin filament sliding was observed only in keloids.

When comparing scars that have undergone such a wound healing process with healthy normal skin tissue, wound healing-related genes were discovered preferentially as DEGs rather than genes unique to each scar. Indeed, our present study revealed that scar-free normal skin is an inappropriate control group for determining a unique gene-set for any type of scar (Fig. 5C). Therefore, we compared keloids, as an irreversible scar, with reversible scars that had undergone the same wound healing process as keloids.

Of the keloid-specific genes discovered by comparison with reversible scars, the Golgin A6 family and ERICH6B were prominent in terms of both fold-change and p-value (Fig. 2B). The Golgin A6 family is a type of coiled-coil protein located in the Golgi apparatus, called golgin[23]. Although the function of the Golgin A6 family is not known, the major functions of related golgins have been determined. Golgin protein maintains the Golgi architecture, is responsible for vesicular traffic, and plays a role in intracellular signal modulation. Since one of the distinguishing characteristics of keloids is the formation of collagen bundles through hypersecretion of collagen, the golgin family which is involved in the intracellular transport of collagen, is highly likely to be a keloid-specific marker. These results are supported other studies comparing keloids and scar-free normal skin (Supplement Fig. 1,2). Although little is known about ERICH6B, it is highly expressed in hypersecretory fibroblasts found in various lesions of the skin[27]. This result also is supported by other studies that have discovered keloid-specific genes.

To further dissect the pathogenesis of keloids, we conducted ORA to identify keloid specifically activated or inactivated pathways. By comparing keloids with reversible scars, we discovered that ‘visual/sensory perception’ and ‘response to corticosteroids’ were highly specific and upregulated pathways for keloids. Interestingly, common symptoms of keloids are itching and pain, both of which are associated directly or

indirectly with ‘visual/sensory perception.’ In addition, corticosteroid injections or ointments have been determined to be effective treatments for keloids[28], which is highly consistent with our findings.

Another finding of our present study is that genes related to ‘activation of immune response,’ ‘antigen processing and presentation of peptide antigen,’ ‘B cell mediated immunity,’ and the ‘regulation of T cell activation’ were downregulated specifically in keloids. In line with these findings, several studies have underscored the role of the immune cell population in keloids. Jaclyn, B. A. *et al*. reported that CD20+ and CD19+ B cells were significantly increased in keloid tissue compared to normal skin[29]. Murao, N. *et al*. reported that coculture of keloid fibroblasts with T cell populations enhanced collagen synthesis within fibroblasts[30]. Chen, Y. *et al*. reported that Treg-associated gene expression was significantly higher in keloids compared to normal skin, which is in agreement with our results[31]. These findings suggest a connection between immune cells and keloids. However, further research is required to validate this suggestion.

Although hypertrophic scars are milder than keloids, they are frequently accompanied by a number of esthetics, functional, and social impairments that can lead to decreased quality of life[32]. Therefore, it is valuable to discover hypertrophic scar-specific gene sets to help in understanding the etiology of hypertrophic scars. As illustrated in Fig. 4, a total of 241 HS-specific genes was discovered and is involved in lipid metabolism and water homeostasis. Interestingly, the significance of lipid metabolism in scar formation and wound healing was highlighted in several studies by Louw[33,34,35,36]. Proper epidermal hydration is essential for homeostasis of the skin based on the differentiation of epidermal keratinocytes and dermal fibroblasts and modulation of the inflammatory phase[37,38]. Interestingly, in dermatologic treatment, hydration is a recommended method for patients with hypertrophic scars.

In this study, using more accurate controls of hypertrophic and normotrophic scars, we discovered keloid-specific pathways and genes. The results of our present study strongly suggest that immune cell immunity and sensory perception are involved in the pathogenesis of keloids. Furthermore, our present study contributed to the understanding of keloid pathogenesis by providing potential biomarkers of keloids such as the golgin A6 family and ERICH6B.

Methods

Patients and tissue samples

Tissue samples were obtained from the biobanks at the Samsung medical center, Seoul, Republic of Korea. All patients provided informed consent and the study was performed according to internal ethics review board approvals at Samsung medical center. Four keloid tissue samples, five hypertrophic scars tissue samples and three mature scar tissue samples were obtained after a thorough histopathological examination and clinical manifestations of patients. All experiments involving humans were performed in adherence to the Helsinki Guidelines. These samples were fixed in formalin, embedded in paraffin, and stained with hematoxylin and eosin.

RNA isolation

Consecutive 10 µm sections were generated from each of the FFPE cell blocks using a standard microtome blade. Deparaffinization of FFPE samples was performed using xylene at room temperature for 30 min followed by two washes with 100% ethanol. Then lesion of each slide was manually dissected. The manual isolation of RNA was performed using RNeasy Mini Kit (Qiagen GmbH, Hilden, Germany) according to manufacturers' instructions. RNA concentration was measured using the NanoDrop 1000 spectrophotometer (Thermo Fisher Scientific) and RNA quality was evaluated with RNA 6000 Pico LabChip kit by using BioAnalyzer 2100 microcapillary electrophoresis system (Agilent Technologies, Inc., Santa Clara, CA USA). Reverse transcription was performed using Transcriptor First Strand cDNA Synthesis Kit (Roche Applied Science) from 250 ng of total RNA and the combination of anchored-oligo(dT) and random hexamer primers.

Next-generation sequencing

For library preparation, the Illumina TruSeq RNA Access Library Prep Kit (Cat. No. 20020189, Illumina, San Diego, CA, USA) was used with 40 ng of FFPE RNA. The libraries were prepared according to the manufacturer's protocol with the following change for the FFPE samples: the hybridization/capture was performed individually instead of as pooled samples after the first PCR step. Library concentrations were adjusted to 1nM and pooled for multiplex sequencing. Pooled libraries were denatured and diluted to 7.5 pM and were sequenced on the Illumina HiSeq 2500 Platform to 101bp paired-end reads.

Data processing and quantification

Adaptor sequences were trimmed out with Cutadapt (version 2.3)[39] and reads shorter than 50 base pair after trimming were filtered out. All reads were aligned to the human reference genome and corresponding gene annotation (Gencode V22) with STAR aligner 2-pass mode (version 2.4.2a)[40]. Aligned reads were quantified in gene level, by HTSeq (version 0.12.4)[41] with "intersection-nonempty" mode. Multidimensional scaling analysis were processed via clustermap function of python seaborn package (version 0.11.1) with log2(FPKM+1) values using genes with mean FPKM >1 among the samples. tSNE plots were visualized with Rtsne packages[42].

Differential Expression with Ensemble approaches

We implemented an ensemble approach for differential gene expression analysis. From all quantified counts of HTSeq, we performed 3 independent differential gene expression analysis with the most commonly used methods, Limma-voom[43], edgeR[44], and DESeq2[45], for Hypertrophic Scar VS Scar and Keloid VS Hypertrophic Scar comparisons. We discarded low read count genes below 3 for all samples within tissue types. We applied cut-off on limma-voom and Deseq2, log2 fold change > 1 & adjusted P-Value < 0.1, and on edgeR, abs (log2 fold change) > 1 & FDR < 0.1, for enlisting differentially expressed genes. After getting 3 differentially expressed gene lists of Hypertrophic Scar vs Scar, we overlapped 3

lists and genes with 2 or more than 2 methods regarded as differentially expressed genes for ensemble approaches.

Over-Representation Analysis

Over-representation analyses were performed with Enrichr[46] via GSEAPY (version 0.9.19) user predefined GO_Biological_Process_2015 and KEGG_Human_2019 gene sets enrichment analyses. Adjusted P-value < 0.1 was applied

Public high-throughput normal data collection and processing

For comparison over Keloid and normal tissue, we downloaded raw sequenced reads from GEO via accession number GSE113619. Among sequenced samples, Day 0 of the normal cases (13 samples) were regarded as normal tissue samples. Analysis over Keloid VS Normal tissue was processed with the same ensemble approaches implemented. Since Keloid and normal tissue comparison have more biases because of using two different experimental procedures, we applied higher cutoff as log2 fold change > 3 & adjusted P-Value < 0.0001 on DEGs. Over-representation analyses were processed in the same methods as previously described.

Declarations

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Author Information

All authors helped conceive and design the study and develop the hypothesis. Y.O. and E.L. conducted the laboratory experiment. J.L. conducted the data analysis. J.L, K.M. and M.C. analyzed and interpreted the data and wrote the manuscript. J.H.L and S.H.K. designed experiments, supervised the study.

Data availability

RNA-seq data that support the findings of this study have been deposited in the GEO under accession number GSE188952. All other relevant data supporting the main findings of this study are available from the corresponding authors upon reasonable request.

Competing interests

The authors declare no competing interests.

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Figures

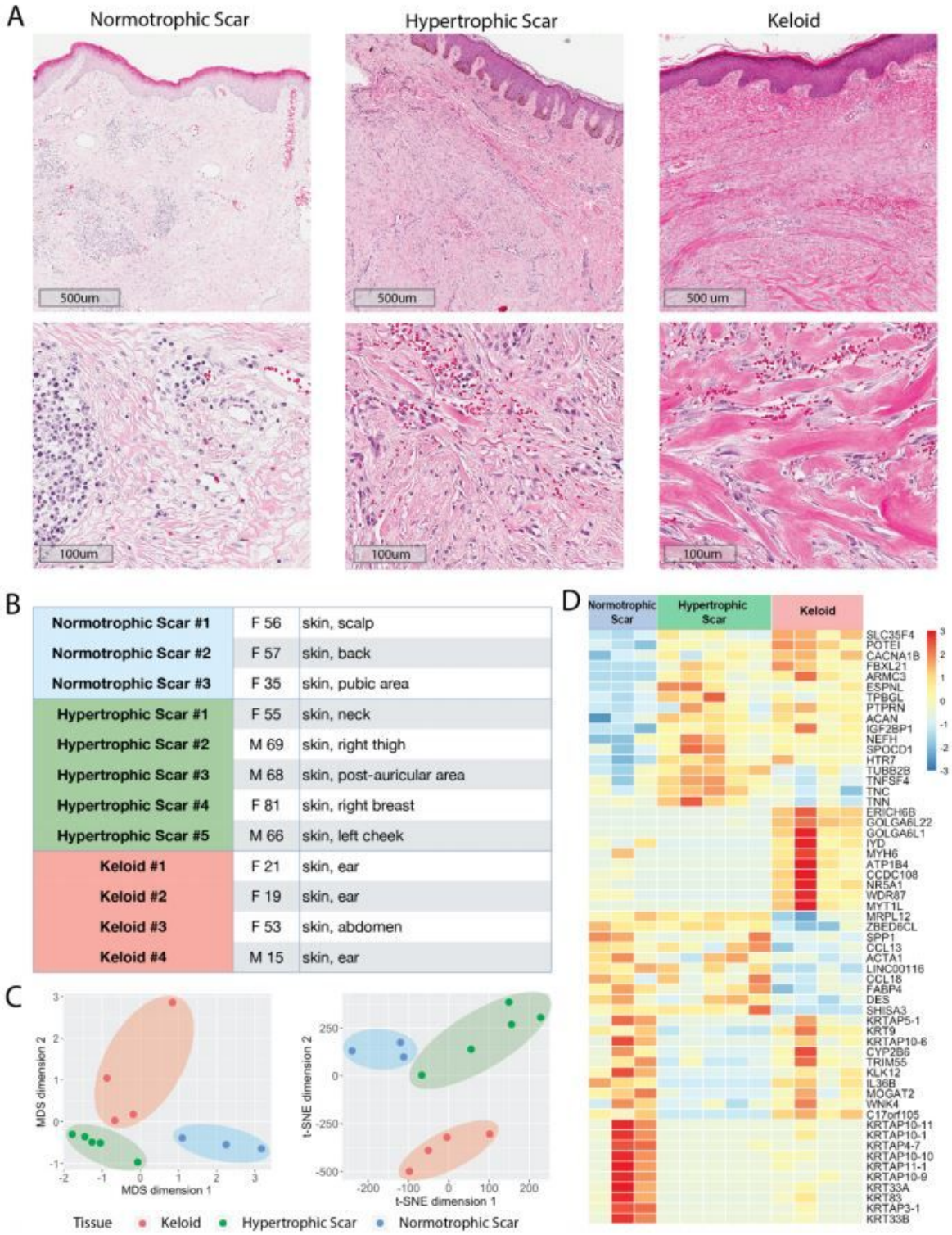


Figure 1

Differences in the pathology and gene expression patterns of normotrophic scars, hypertrophic scars, and keloids. A Representative photomicrograph of Hematoxyl in & Eosin-stained sections of tissues. B Summary of information on scar tissues used in this study. C MDS and tSNE clustering of 12 skin tissues. Tissues are color coded by an algorithm for determining expression clusters and tissue types. D Heatmap of gene expression grouped under different expression pattern across the three types of scars.

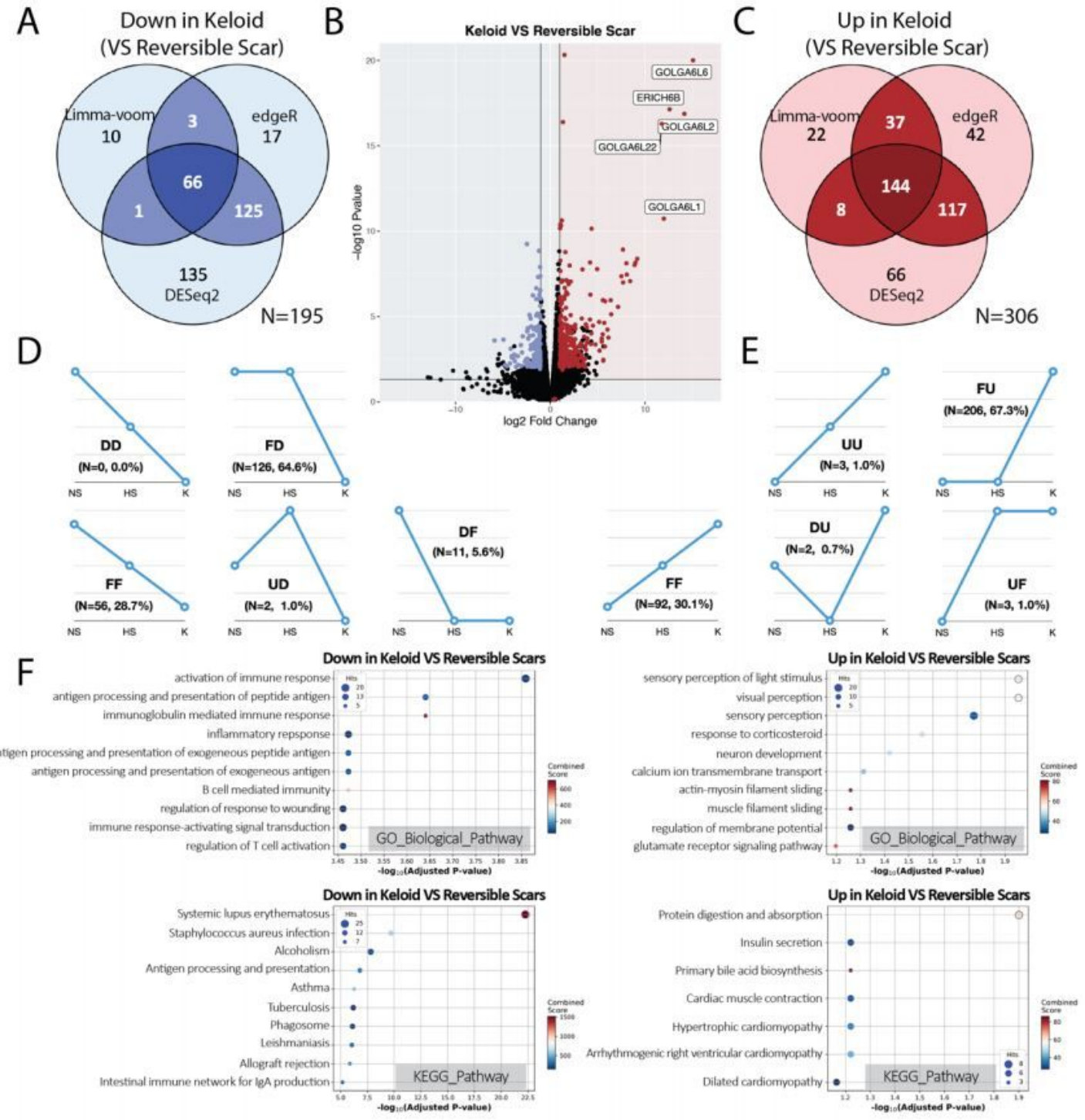


Figure 2

Differentially expressed genes (DEGs) specifically upregulated and downregulated in keloids compared to reversible scars. A Venn diagrams of up and C down regulated DEG counts among 3 different methods (Limma-voom, edgeR and DESeq2) between keloid and reversible scars. B Volcano plot of DEGs of log2 fold change of the standardized mean and the p-value for the all genes. Five genes with the largest fold changes among upregulated in keloids were annotated. D Downregulated DEGs in keloids compared to

reversible scars categorized in five patterns: DD (Down-Down), FD (Flat-Down), DF (Down-Flat), UD (Up-Down), FF (Flat-Flat). E Upregulated DEGs in five categorized patterns: UU (Up-Up), FU (Flat Up), UF (Up-Flat), DU (Down-Up), FF (Flat-Flat). F Over-represented GO Biological Process and KEGG Pathway terms of keloids specific DEGs.

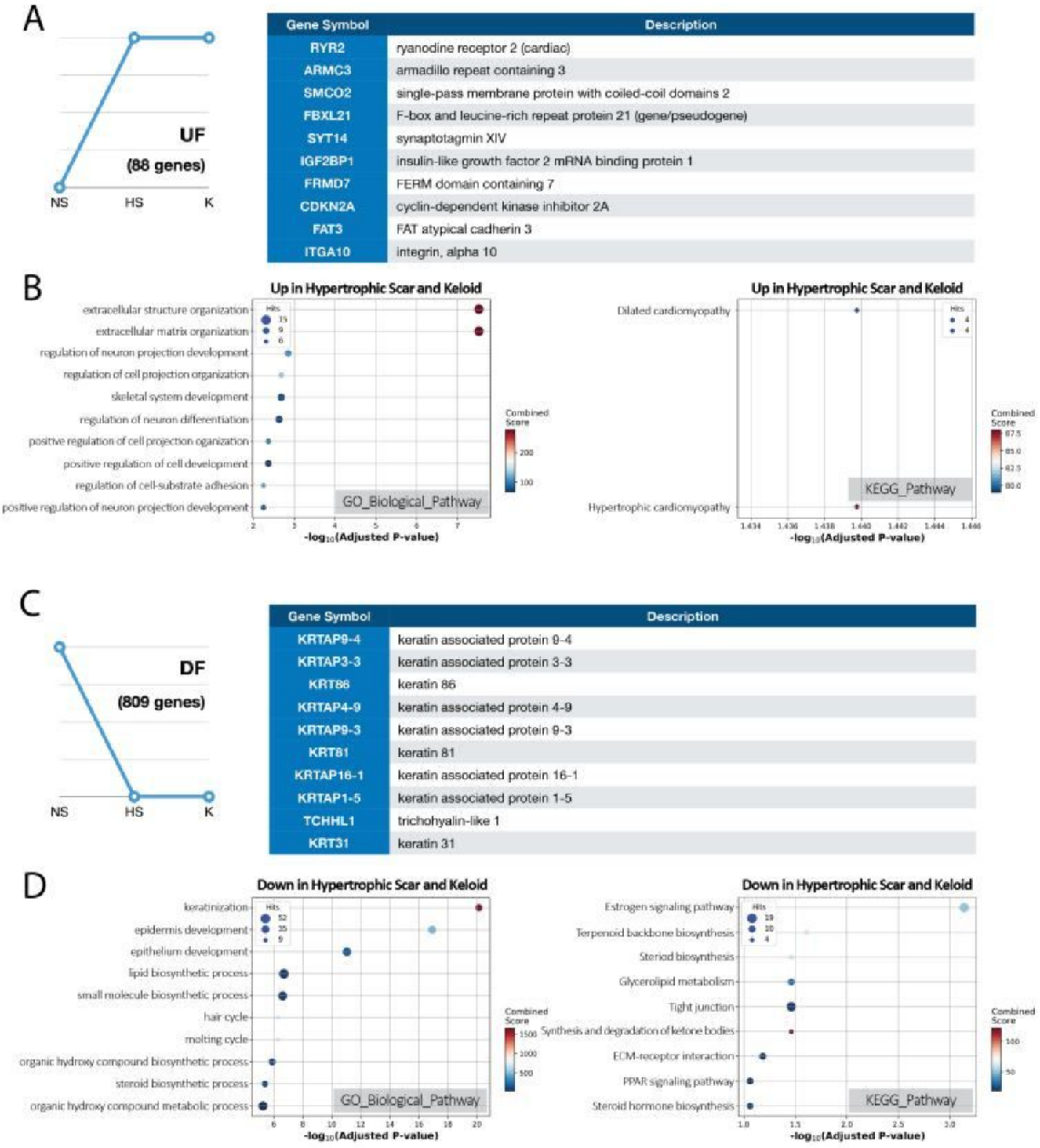
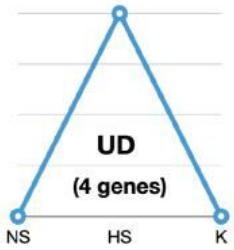


Figure 3

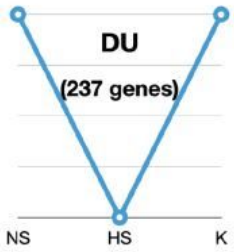
Hypertrophic Scars and Keloids specific DEGs and over-represented terms compared to Normotrophic Scars. A Upregulated DEGs and B over-representated GO Biological Process and KEGG pathway of dowpregulated DEGs in hypertrophic scars and keloids. C Downregulated DEGs and D over-representated GO Biological Process and KEGG pathways.

A



Gene Symbol	Description
TUBB2B	tubulin, beta 2B class IIb
TNFSF4	tumor necrosis factor (ligand) superfamily, member 4
TNC	tenascin C
TNN	tenascin N

B



Gene Symbol	Description
KRTAP5-1	keratin associated protein 5-1
KRT9	keratin 9
KRTAP10-6	keratin associated protein 10-6
CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6
KLK12	kallikrein-related peptidase 12
IL36B	interleukin 36, beta
TRIM55	tripartite motif containing 55
KREMEN2	kringle containing transmembrane protein 2
C17orf105	chromosome 17 open reading frame 105
WNK4	WNK lysine deficient protein kinase 4

C

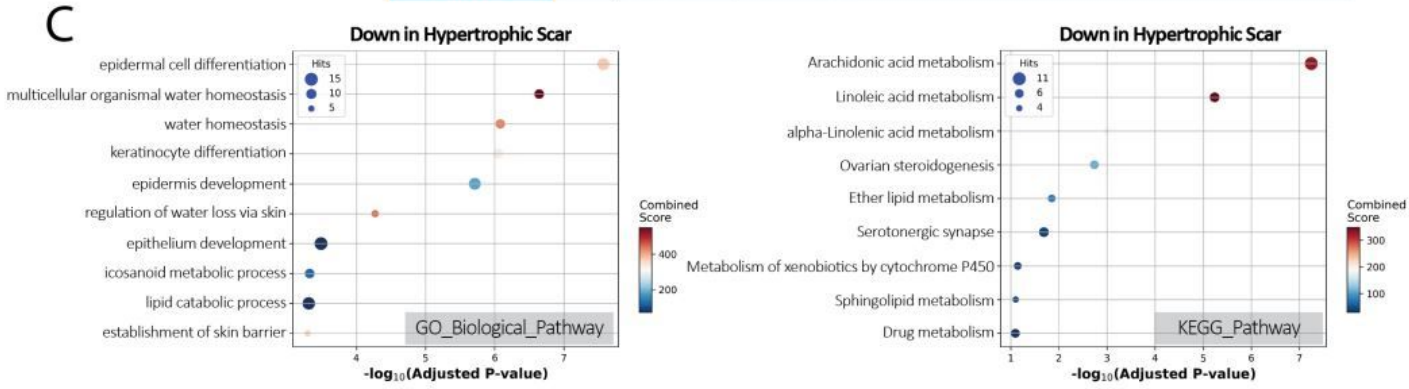


Figure 4

Hypertrophic scar specific expression signatures. Among hypertrophic scar specific changes, A only 4 genes are upregulated and B most genes were downregulated (N=237). C Over-representation analysis result over GO Biological Process and KEGG pathways.

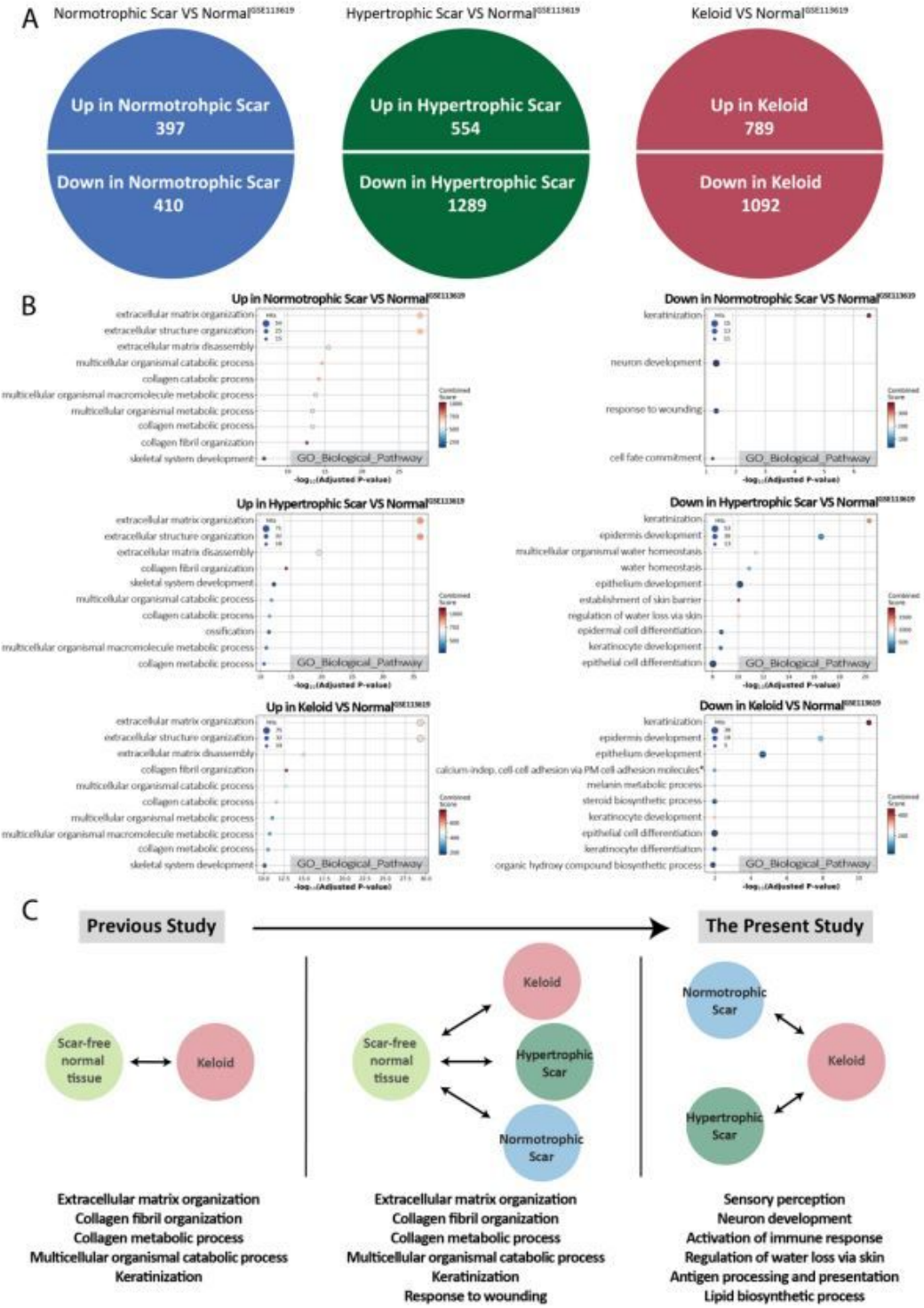


Figure 5

Normotrophic scar, rather than scar free normal skin is ideal for the identification of scar subtype specific DEGs. A Expression profiles of normotrophic scars, hypertrophic scars and keloids from the current study against scar free normal skin sample obtained from public GEO data (GSE113619). B Over-represented GO Biological Process terms in each scar types and normal skin comparisons. C A schematic experimental design comparison between previous and present study.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- SupplementaryFigure1.pdf
- SupplementaryFigure2.pdf
- SupplementaryTable.116.docx