Tape strips in dermatology research*

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Summary

Tape strips have been used widely in dermatology research as a minimally invasive method to sample the epidermis, avoiding the need for skin biopsies. Most research has focused on epidermal pathology, such as atopic eczema, but there is increasing research into the use of tape strips in other dermatoses, such as skin cancer, and the microbiome. This review summarizes the technique of tape stripping, and discusses which dermatoses have been studied by tape stripping and alternative minimally invasive sampling methods. We review the number of tape strips needed from each patient and the components of the epidermis that can be obtained by tape stripping. With a focus on protein and RNA extraction, we address the techniques used to process tape strips. There is no optimal protocol to extract protein, as this depends on the abundance of the protein studied, its level of expression in the epidermis and its solubility. Many variables can alter the amount of protein obtained from tape strips, which must be standardized to ensure consistency between samples. No study has compared different RNA extraction techniques, but our own experience is that RNA yield is optimized by using 20 tape strips and the use of a cell scraper.

What is already known about this topic?

- Tape strips have been widely used in dermatology research as a minimally invasive method to collect epidermal samples.
- Tape strips can be used as an alternative to skin biopsies in certain circumstances.
- Tape strips can be used to determine protein, RNA, lipid and microbial expression.
- There is currently no standardized protocol used for collecting and processing tape strips.

What does this study add?

- This review summarizes the technique of tape stripping, what information can be obtained from tape stripping and which dermatoses have been studied by tape stripping.
- Evidence regarding different protocols for protein and RNA extraction from tape strips is reviewed.
- Maximal RNA yield is obtained from 20 tape strips using a cell scraper.

Background

Skin is an accessible organ that can be biopsied with minimal risk to the patient. However, biopsies are not feasible in young children, and the time, pain and inconvenience of biopsies can deter adults. Tape stripping is a less invasive method to obtain skin samples. Tape strips (TS) are plastic discs with an adhesive side. The adhesive sticks to the skin surface and components of the epidermis adhere to the plastic when removed. Sequential application allows deeper levels of the stratum corneum (SC) to be accessed with each strip. The technique causes only mild discomfort and leaves a temporary red mark. TS require no skin preparation and cause neither bleeding nor scarring.
Figure 1 Images of tape stripping (a) Photographs demonstrating the tape stripping procedure. (1) The TS is placed on the skin and marked with a pen to ensure the same site is used. (2–3) A pressure instrument is used to deliver a standardized pressure to the TS for a specific amount of time (5–10 s). (4) The TS is removed, ideally with forceps and a new TS can be placed on the same site. (b) Illustration showing how sequential layers of the stratum corneum (SC) are removed. (1) The SC is intact when the TS is placed. (2) Superficial components of the epidermis adhere to the first TS and are removed with it. TS 1–4 can be used to detect microbes on the skin surface, lipids/ceramides and superficially expressed proteins and peptides, such as natural moisturizing factor, proteases and some cytokines. (3) With increasing numbers of TS, deeper layers of the SC are accessed. TS 5–10 can detect structural proteins of the SC such as filaggrin and secreted soluble proteins such as cytokines. (4) After approximately 20 TS the SC has been stripped and the granular layer is accessed. TS 11–20 have the most abundant RNA, and lipids at this level are less likely to be oxidized. (c) A red shiny mark indicates that the SC has been completely stripped and the stratum granulosum accessed, after approximately 20 TS.
TS were developed to assess the morphology and number of keratinocytes using microscopy\textsuperscript{6,12,13} and also used to disrupt the skin barrier in order to study barrier function.\textsuperscript{6,14} TS were later used to determine the percutaneous penetration of topically applied drugs.\textsuperscript{15} TS have been used to quantify SC protein; initially by weighing individual strips, and then by spectroscopy, which allows more accurate quantification of total protein.\textsuperscript{16} Keratins were first detected from TS using sodium dodecyl sulfate (SDS)-polyacrylamide gel electrophoresis and Coomassie Blue staining.\textsuperscript{17} The advent of antibody-based immunofluorescence allowed the detection of many other proteins.\textsuperscript{18}

**Which dermatoses can be studied from tape strips?**

As TS sample the SC,\textsuperscript{3,19} most studies focus on upper epidermal pathologies such as atopic eczema (AE) (Table S1; see Supporting Information). However, upper epidermal pathology is not a prerequisite, as exemplified by the use of TS to detect skin cancers.\textsuperscript{20–22} The dermatoses studied using TS are listed in Table 1.

TS are well suited for childhood AE studies, providing a simple and noninvasive method to obtain samples from young children.\textsuperscript{2,3} Adult biopsies cannot be substituted, as childhood AE is a distinct disease endotype.\textsuperscript{23} TS could eventually be used to noninvasively diagnose or predict the onset of AE, but research is currently identifying and categorizing biomarkers.\textsuperscript{24} Seibold et al. used RNA-seq from TS to identify patients with AE with increased T helper (Th)2 gene expression in their nonlesional skin who could be targeted with precision biological therapy.\textsuperscript{25} Another potential use of TS is to assess emollient adherence, as artificial ceramides from emollients can be quantified and differentiated from naturally occurring ceramides using TS.\textsuperscript{26}

The hyperkeratotic SC in psoriasis is also accessible to TS sampling.\textsuperscript{18} However, there are fewer studies regarding the use of TS sampling in psoriasis than in AE (Table S1). This may be because TS have been used to induce and study the Koebner phenomenon.\textsuperscript{17} However, up to 20 TS have been used in nonlesional psoriasis studies without report of koebnerization.\textsuperscript{5} One study specifically reported that four TS did not induce the Koebner phenomenon in any patient.\textsuperscript{6} He et al. identified that nitric oxide synthase (NOS)2/inducible NOS (iNOS) expression was elevated in TS from lesional psoriasis and could differentiate psoriasis from AE with 100% accuracy.\textsuperscript{5} Berekmér et al. found TS interleukin (IL)-36 expression could differentiate psoriasis from AE with a sensitivity of 94% and specificity of 100%.\textsuperscript{24}

TS have been used to sample cutaneous microbes.\textsuperscript{28,29} Lange-Asschenfeldt et al. showed that bacteria were found on all 15 sequential TS and that 85% of bacteria resided in the first six TS.\textsuperscript{28} Unlike biopsies, differential tape stripping allows the identification of microorganisms within specific SC layers.\textsuperscript{28} Skin swabbing detects only surface bacteria.\textsuperscript{30} Ogai et al. found that, while microbiome bacterial composition was equivalent between TS and skin swabs using next-generation sequencing or anaerobic culture, there was greater bacterial diversity in TS samples using culture-based assays.\textsuperscript{29} Chng et al. compared the use of TS to swabs and cup scrubs in patients with AE and found a higher intrapatient concordance of microbial organisms detected using TS.\textsuperscript{31}

TS have been used to detect exposures to environmental chemicals that embed into the SC and can be removed with sequential TS, such as silver particles in patients with AE who used silver garments.\textsuperscript{32}

Although skin cancer extends beyond the epidermis, TS can detect epidermal transcriptomic changes from melanoma.\textsuperscript{10,33} The company DermTech Inc. (La Jolla, CA, USA) offers a noninvasive assay to differentiate pigmented lesions from melanoma.\textsuperscript{33} This uses quantitative real-time polymerase chain reaction (qPCR) from four TS to assess expression of two

| Dermatosis | Type of studies |
|-----------|-----------------|
| Atopic eczema | WB, ELISA, PA, IM, MS-P, MS-L, qPCR/M, RNA-seq, Chr, SM, 3DM, NGS/qPCR |
| Psoriasis | WB, ELISA, IM, MS-P, qPCR/M, Chr, SM, 3DM |
| Contact dermatitis | ELISA, qPCR/M, M, Chr |
| Photodamage | WB, ELISA, MS-P, Chr |
| Actinic keratosis | MS-P |
| Melanoma | IM, qPCR/M, SM |
| Basal cell carcinoma | qPCR/M |
| Squamous cell carcinoma | qPCR/M |
| Cutaneous T-cell lymphoma | MSP |
| Pityriasis versicolor | M/C |
| Seborrhoeic dermatitis | M/C, NGS/q-PCR |
| Dermatophytooses | M/C, NGS/q-PCR |
| Candida balanoposthitis | M/C |
| Scabies | M/C |
| Cutaneous leishmaniasis | NGS/q-PCR |
| Perioral dermatitis | M/C |
| Rosacea | PA, M/C |
| Acne vulgaris | ELISA |
| Lichen planus | IM |
| Genodermatoses (Netherton syndrome, ichthyosis | ELISA, IM |
| vulgaris, peeling skin syndrome type B, X-linked recessive ichthyosis) |

WB, Western blot; ELISA, enzyme-linked immunosorbent assay or multiplex; PA, protease assay; IM, immunostaining microscopy; MS-P, mass spectrometry protein; MS-L, mass spectrometry lipid; Chr, chromatography; qPCR, quantitative real-time polymerase chain reaction; qPCR/M, qPCR or microarray; RNA-seq, RNA-sequencing; SM, staining and microscopy (keratinocytes); 3DM, 3D microscopy; M/C, microscopy and/or culture of microbes; NGS, next-generation sequencing; NGS/q-PCR, q-PCR/NGS of microbes. References are provided in Table S1 (see Supporting Information).
genes, LINC and PRAME, as biomarkers for melanoma. Sensitivity is 91–95%, specificity is 69–91%, and 99–94% of negative samples avoided a surgical biopsy at 12 months. This company has also made progress in differentiating basal cell and squamous cell carcinomas from benign lesions. This is the first example where TS have been incorporated into clinical practice and we anticipate that this will grow in the future.

**What information can be obtained from tape strips?**

Many epidermal components can be extracted from TS (summarized in Table 2). Soluble proteins, such as ILs, are detectable in the TS from inflammatory dermatoses. Hulshof et al. detected 13 of 28 immunomodulatory mediators tested from six TS using an electrochemiluminescence immunoassay. One mediator, CXCL8, significantly correlated with Scoring Atopic Dermatitis (SCORAD) severity score in both lesional and nonlesional AE. Tape stripping facilitates serial sampling of biomarkers. Méhul et al. used TS before and after treatment to determine chemokines and cytokines, such as IL-12p40, that are upregulated in lesional psoriatic skin and normalize after topical calcipotriol-betamethasone treatment.

Structural proteins of the SC are highly cross-linked and hence difficult to solubilize. Egawa et al. could not detect

| Technique | Component detected | Description | Median number of TS used | Range |
|-----------|--------------------|-------------|--------------------------|-------|
| Western blotting | Protein | Semi-quantifies individual proteins by separating them by size followed by antibody-based chemiluminescence. Can only detect solubilized proteins | 2 | 1–30 |
| ELISA and bead-based multiplex assays | Protein | Semi-quantifies individual proteins by antibody fluorescence. Can only detect solubilized proteins | 5 | 1–35 |
| Protease assay | Proteases | Quantification of proteases using a standardized enzyme substrate that is fluorescence tagged | 7.5 | 3–15 |
| Immunostaining microscopy | Protein | Detects individual proteins directly on the TS surface using antibody fluorescence. Allows visualization of proteins in situ but is less effective at quantifying the protein | 1 | 1–9 |
| Mass spectrometry (proteins) | Protein | Quantification of large protein sets. Proteins are fragmented and charged, then separated by their mass-to-charge ratio | 15 | 8–30 |
| Mass spectrometry (lipids) | Lipids | Quantification of large lipid sets. The same principal of separation by mass-to-charge ratio is applied to lipids | 8 | 1–16 |
| Quantitative-PCR and microarrays | RNA | Quantifies the expression of key genes | 20 | 4–30 |
| RNA-seq | RNA | Quantifies gene expression of the whole transcriptome using next-generation sequencing | 20 | 16–20 |
| Chromatography | Lipids, peptides, amino acids | Semi-quantifies individual lipids, peptides or amino acids. Chromatography separates the molecule of interest, which is then detected by a method such as ultraviolet absorption | 4 | 1–16 |
| Staining and microscopy (keratinocytes) | Cellular morphology | 2D characterization of keratinocytes | 1 | 1–9 |
| 3D microscopy (scanning electron, laser and atomic force) | Cellular morphology | 3D characterization of keratinocytes | 3 | 1–23 |
| Microscopy and/or culture of microbes | Bacterial, fungal or parasitic organisms | Detects and quantifies microorganisms. TS are placed directly onto a culture medium or slide (with or without a stain or potassium hydroxide digestion) | 1 | 1–15 |
| q-PCR or NGS of microbial species | Bacterial, fungal or parasitic organisms | Detects and quantifies microorganisms from specific DNA sequences (NGS) or RNA expression (q-PCR) | 1 | 1–3 |

ELISA, enzyme-linked immunosorbent assay; q-PCR, quantitative real-time polymerase chain reaction; NGS, next-generation sequencing. The deepest TS is documented if more superficial TS were not used. Studies where TS were repeatedly pressed onto the skin are not included. References are provided in Table S1 (see Supporting Information).
filaggrin (FLG) from a single TS using Western blotting, but were able to do so following 12 h of pretreatment with salicyclic acid before taking the TS.\textsuperscript{38} Unfortunately, this resulted in erythema and pigmentation for a number of weeks.\textsuperscript{38} Son \textit{et al.} detected profilaggrin from five TS using Western blotting following solubilization in 2% SDS in Tris–HCl.\textsuperscript{39} Multiple SC barrier proteins, including FLG, can be detected from TS using mass spectrometry (MS).\textsuperscript{40} Many studies have also chosen to quantify FLG by measuring its breakdown products.\textsuperscript{36,41–44} FLG is broken down by proteases in the upper SC to natural moisturizing factors (NMFs).\textsuperscript{45} FLG breakdown products can be separated by chromatography and quantified by MS\textsuperscript{43} or ultraviolet spectroscopy.\textsuperscript{16,41} McAleer \textit{et al.} showed that NMFs are reduced in AE using TS, and this correlated with transepidermal water loss (TEWL), a measure of barrier function.\textsuperscript{44}

MS and RNA-seq enable vast sets of proteins and genes to be obtained from a single set of TS.\textsuperscript{2,5,15,43,46–48} Pavel \textit{et al.} identified 1829 differentially expressed genes in paediatric lesional AE relative to controls, including downregulated terminal differentiation genes, not previously identified in studies using paediatric biopsies.\textsuperscript{2} Functional analysis of datasets allows a deeper understanding of the immunopathomechanisms of disease.\textsuperscript{3,41,48} Goleva \textit{et al.} identified that three groups of proteins: keratin-intermediate filaments, inflammatory response proteins and glycolysis/antioxidant defense enzymes, were differentially expressed in AE with food allergy relative to AE without food allergy and that their expression correlated with TEWL, suggesting that AE associated with food allergy has a separate immunopathomechanism to other forms of AE.\textsuperscript{48}

Multiple techniques can be used on a single set of TS, allowing ‘multiomic’ analysis from individual patients.\textsuperscript{47} For example, one study used TS numbers 5–6 to measure proteins and lipids, and TS numbers 11–20 to measure RNA from each patient.\textsuperscript{47}

How many tape strips should be used for each patient?

The number of TS used varies widely between studies (Table 2). The mass of SC removed declines exponentially with each TS\textsuperscript{7} and SC thickness varies between individuals (16–30 0 cell layers on the forearm).\textsuperscript{16} For studies quantifying proteins it is not necessary to strip the SC completely.\textsuperscript{7} Breternitz \textit{et al.} found that less pressure (using a 2N stamp) and shorter pressure application (2 s), led to a more linear increase in protein mass.\textsuperscript{7} Less protein is collected per TS, but this is more likely to give comparable protein yield between patients.\textsuperscript{7} Many authors recommend 15 TS per patient,\textsuperscript{2,50} but this number depends on the component of the epidermis measured and the disease pathology.\textsuperscript{50} For example, proteins abundant in the SC can be detected from as few as one TS.\textsuperscript{34} Hyperkeratotic dermatoses tend to need fewer TS for protein analysis, for example, Desmoglein-1 can be detected from only one TS in lesional psoriasis.\textsuperscript{51}

Studies that assess gene expression need more TS in order to access the granular layer, where intact cells and mRNA reside.\textsuperscript{3} Although the number of TS needed to strip the SC varies between individuals,\textsuperscript{19} Kim \textit{et al.} demonstrated, through immunostaining of punch biopsies taken after sequential tape stripping, that 20 TS reaches the granular layer.\textsuperscript{3} Most studies assessing gene expression sample 20 consecutive TS and use TS numbers 11–20 for RNA extraction,\textsuperscript{3,43,47,51,52} although our own experience has found a higher yield of RNA when using all 20 TS (Figure 2).

The number of TS used for lipid analysis varies too. Chiba \textit{et al.} detected a difference in trihydroxy-linoleic acid levels from only one TS.\textsuperscript{53} Leung \textit{et al.} compared TS levels 5 and 6 with those from levels 15 and 16.\textsuperscript{51} This study found no difference in ceramide abundance at TS levels 5–6 between patient groups, but a substantial difference at levels 15–16.\textsuperscript{43}

![Figure 2](image-url) **Figure 2** Bar chart showing RNA yields from different quantities of tape strips. Tape strips from a single set were cut into quarters and quarters were pooled according to depth. RNA was extracted using the RNeasy Plus Micro Kit (Qiagen, Hilden, Germany) using a scraper. RNA was quantified using a one-step reverse-transcriptase polymerase chain reaction kit using 18S rRNA primers against a HeLa RNA standard (RNA Quantification Kit for SYBR Green I and ROX Passive Reference Dye, ThermoFisher Scientific). \( P < 0.05 \) using the Kruskal–Wallis nonparametric analysis. Three experimental replicates were performed. Ct, cycle threshold.
What is the expected yield per sample?

RNA and protein yield are higher when there is active disease, such as lesional AE relative to nonlesional AE. Lesional AE has increased intracorneocyte cohesion and a subsequent lower yield of protein from TS than nonlesional skin; however, the barrier defect in lesional AE leads to serum ‘leakiness’ and an increase in the proportion of soluble protein. Lesional psoriasis is hyperkeratotic and yields more protein than nonlesional skin. Some variables, such as skin hydration, cannot be standardized, so the data must be normalized. To do this, most studies quantified the total soluble protein per TS sample using an assay to ensure equal protein loading for each sample. For qPCR, a housekeeping gene is used to normalize gene expression.

Protein extraction regimens require mechanical disruption (mechanical shaker, cell scraper, sonication and/or chemical disruption, such as methanol) to remove proteins from the TS. Propylene glycol was added by one author to hydrate keratinocytes and prevent ice crystals forming during sonication. Hendrix et al. found that 60 min of sonication led to lower detection of certain biomarkers and recommended 30 min of sonication to avoid denaturing proteins. Clausen et al. found that 10 min of sonication with phosphate-buffered saline (PBS) led to a 50–90% reduction of protein remaining on TS, with no significant difference in protein yield between 10 and 15 min of sonication.

Mechanical/chemical disruption is sufficient to study soluble proteins, but if an insoluble protein is studied (and 85% of protein in the SC is insoluble), these must be solubilized first. Extraction buffers containing reducing agents [e.g., dithiothreitol (DTT)], surfactants (e.g., Tween-20) or bases (e.g., sodium

Table 3 A summary of the factors that can affect protein yield

| Factor                          | Comment |
|--------------------------------|---------|
| Anatomical site                | The same site should be used within a study. The volar forearm is commonly used. |
| Pressure of TS application     | Pressure application can be standardized by using a pressure instrument (e.g., D500 D-square® pressure instrument, 225 g cm⁻²). |
| Duration of pressure applied  | The time that pressure is applied to each TS should be standardized, usually between 2 s and 10 s. |
| Contaminants on the skin surface | TS number 1–2 TS are typically discarded, although bacteria have been shown to be present up to TS 15. |
| Stretching the skin during application | A decision must be made about whether to stretch the skin in the study design. |
| Speed of removal of TS         | Slow speed of TS removal was shown to increase transepidermal water loss, but protein yield was not directly studied. The speed of TS removal should be considered. |
| Brand of adhesive tape         | The same brand of TS must be used throughout the study. |
| Hydration of the skin          | There have been no attempts to standardize hydration. Emollients and occlusion have been shown to alter gene expression and could therefore confound attempts to standardize this variable. |
| Activity of skin disease       | Nonlesional atopic eczema (AE) has more protein per TS than lesional AE, but less soluble protein. Studies should distinguish between samples from lesional and nonlesional skin. |
| Season                         | Exposed sites should be avoided if studies are longer than one season. |

The authors hypothesized that environmental oxidation of lipids affects the results of TS levels 5–6 but not levels 15–16.

What is the best protocol?

Extraction protocols vary depending on the epidermal component studied, type of dermatosis and method of analysis. Many variables affect the cohesion of the SC and subsequent yield of protein from TS, which are summarized in Table 3. The type of dermatosis and activity of skin disease affect protein yield. Lesional AE has increased intracorneocyte cohesion and a subsequent lower yield of protein from TS than nonlesional skin; however, the barrier defect in lesional AE leads to serum ‘leakiness’ and an increase in the proportion of soluble protein. Lesional psoriasis is hyperkeratotic and yields more protein than nonlesional skin. Some variables, such as skin hydration, cannot be standardized, so the data must be normalized. To do this, most studies quantified the total soluble protein per TS sample using an assay to ensure equal protein loading for each sample. For qPCR, a housekeeping gene is used to normalize gene expression.

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Figure 3 Bar charts comparing the total RNA yield from different extraction techniques. A set of tape strips (number 11–20) was cut into quarters. Pooled sets of quarters were subject to different extraction techniques using the RNeasy Plus Micro Kit (Qiagen, Hilden, Germany). Vigorous shaking lasted for a duration of 150 s. Sonication took place for a total of 90 s on high with a 30-s interval every 30 s. RNA was quantified using a one-step RT-PCR kit using 18S rRNA primers against a HeLa RNA standard (RNA Quantification Kit for SYBR Green I and ROX Passive Reference Dye, ThermoFisher Scientific, Waltham, MA, USA). P < 0.05 was calculated using the Kruskal–Wallis nonparametric analysis. Three experimental replicates were performed. Ct, cycle threshold.

Figure 3

RNA yield ng per sample

Scraped
Sonicated
Shaken

0.0
0.5
1.0
1.5
2.0
2.5
3.0

Ct value
RNA yield

Alternatives to tape stripping

The gold standard will continue to be skin biopsies, as biopsies access more substantial tissue to a deeper level. TS are representative of biopsies; Kim et al. showed expression of five terminal differentiation genes (FLG, loricrin, keratin-1, involucrin and corneodesmosin) from 20 TS positively correlated with the gene expression from matching biopsies. TS have several advantages, as certain genes have more pronounced differential expression in TS than in biopsies, because biopsies dilute measured differences of genes expressed in the upper epidermis. Dyjack et al. compared RNA transcriptome expression in TS samples with matching biopsies that had been split into epidermal and dermal components. They found that terminal differentiation genes were most highly expressed in the TS samples and were least expressed in the dermis, suggesting that TS more accurately represent terminal differentiation gene expression. Both nonlesional AE and nonlesional psoriasis show greater differential gene expression for inflammatory markers (Th2 in AE, Th1 in psoriasis) using TS when compared with biopsies. He et al. identified a biomarker to differentiate AE from psoriasis from one gene (NOS2/iNOS) using TS, but required two genes from biopsies.

Suction cupping uses suction pressure to create a blister, where fluid can be aspirated and the epidermis removed. This is an alternative to TS, as proteins, lipids and RNA can be extracted from a single sample. Svboda et al. directly compared TS with suction cupping and found that suction cupping provided higher total protein and RNA yield, with more proteins and genes detectable on Western blotting and q-PCR, respectively. However, the formation of a blister and needle aspiration can deter patients. Furthermore, suction cupping is more time-intensive and requires specialist training.

Raman spectroscopy is a noninvasive method that uses the scattering of light to detect small molecules within the epidermis, including lipids and NMF. Koppes et al. compared TS with Raman spectroscopy. Although both methods measure different NMF components, there was a strong correlation of both total and depth-dependent NMF concentration. The group concluded that both methods had comparable performance.
Conclusions

TS offer a simple and minimally invasive method to access components of the epidermis. TS have been applied broadly in dermatology research, but their widespread adoption has been limited by variability between protocols and a lack of standardization. For RNA extraction, we recommend using 20 TS and a commercial guanidinium thiocyanate lysis buffer with a scraper, then purification using a spin column kit. For psoriasis and koebnerizing dermatoses we advise caution if taking over 10 TS from nonlesional skin. There is no optimum protocol to extract protein, and methodology should be designed based on the target studied. The number of TS should correspond to the depth of target expression and abundance. For soluble proteins, we recommend starting with 10 min of sonication in PBS. For insoluble proteins, we recommend 30 min of sonication with a buffer containing 0-2% SDS in PBS. The addition of DTT should be considered if the yield is suboptimal (note that compatibility with downstream analysis kits should be checked). If both protein and RNA extraction are required from the same set of TS, TS 2–10 can be used for protein extraction and TS 11–20 for RNA. Wider sharing of protocols and yield data will allow TS to be more widely used as an alternative to biopsies.

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Supporting Information

Additional Supporting Information may be found in the online version of this article at the publisher’s website:

Table S1 Full list of techniques used to extract components of the epidermis from tape strips, the number of tape strips utilized and the details of the dermatoses involved.