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3 **Mechanisms of innate events during skin reaction following intradermal injection of seasonal**
4 **influenza vaccine**

5

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36

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50 **Abstract**

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52 The skin plays a crucial role in host defences against microbial attack and the innate cells must provide
53 the immune system with sufficient information to organize these defences. This unique feature makes
54 the skin a promising site for vaccine administration. Although cellular innate immune events during
55 vaccination have been widely studied, initial events remain poorly understood. Our aim is to determine
56 molecular biomarkers of skin innate reaction after intradermal (i.d.) immunization. Using an *ex vivo*
57 human explant model from healthy donors, we investigated by NanoLC-MS/MS analysis and
58 MALDI-MSI imaging, to detect innate molecular events (lipids, metabolites, proteins) few hours after
59 i.d. administration of seasonal trivalent influenza vaccine (TIV). This multimodel approach allowed to
60 identify early molecules differentially expressed in dermal and epidermal layers at 4 and 18 h after
61 TIV immunization compared with control PBS. In the dermis, the most relevant network of proteins
62 upregulated were related to cell-to-cell signalling and cell trafficking. The molecular signatures
63 detected were associated with chemokines such as CXCL8, a chemoattractant of neutrophils. In the
64 epidermis, the most relevant networks were associated with activation of antigen-presenting cells and
65 related to CXCL10. Our study proposes a novel step-forward approach to identify biomarkers of skin
66 innate reaction.

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78 **Abbreviations**

79 APC: antigen-presenting cells

80 Dermal DCs: Dendritic cells

81 FTICR: Fourier-transform ion cyclotron resonance

82 i.d.: Intradermal

83 IPA: Ingenuity pathway analysis

84 KCs: Keratinocytes

85 LCs: Langerhans cells

86 LFQ: Label-free quantification

87 MALDI: Matrix assisted laser desorption ionization

88 MS: Mass spectrometry

89 MSI: Mass spectrometry imaging

90 PCA: Principal component analysis

91 TIV: Trivalent influenza vaccine

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105 **Introduction**

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107 The skin's outer surface acts like a suit, forming a physicochemical shield with specialized cells that
108 scan and detect external molecules and danger signals. During barrier disruption (e.g., injuries,
109 vaccination, drug injection), external stimuli reach the epidermal and dermal layer cells. Epidermal
110 cells play a fundamental role in cutaneous innate immunity, providing both a physical barrier via tight
111 junction formation of CD45^{neg} keratinocytes (KCs), which constitute up to 90% of the epidermal cell
112 population, alongside the scarcer Langerhans cells (LCs) (1-5% of epidermal cells) [1,2]. Other
113 populations of antigen-presenting cells (APCs), such as dermal dendritic cells (dermal DCs), reside
114 beneath the epidermal layer. Skin epithelial and resident APC subsets take part in antigen uptake and
115 presentation to promote adaptive immunity in human and mouse models [2,3]. Skin barrier disruption
116 provokes the local production of proinflammatory cytokines and chemokines by local skin cells
117 including KCs, LCs, and dermal DCs. How these local resident cells are activated after barrier
118 disruption, starting with the recruitment of inflammatory cells, determines the immunological
119 outcome. However, the early *in situ* molecular biomarkers of skin reaction to this intrusion remain to
120 be studied.

121 Our recent work has demonstrated that KCs respond to innate sensors and release IL-32, which allows
122 LCs to detach from the epidermal layer, migrate to the dermis [4], and secrete proinflammatory
123 chemokines and cytokines. These mediators promote inflammatory cell recruitment and APC
124 activation [5–8]. This tissue reaction could reflect inflammatory processes necessary to bridge innate
125 to adaptive immunity. In murine models, intradermal (i.d.) vaccination induces the attraction of
126 neutrophils and monocytes to the immunization site [9,10]. However, initial molecular reaction at the
127 site of immunization needs to be studied. In homeostatic and inflammatory skin tissues [2], several
128 molecules such as mTORC1, the NLRP3 inflammasome, NF- κ B signalling, and the MAPK/ERK
129 pathway including EIF4/EIF2 factor transcription have been shown to regulate KCs proliferation and
130 differentiation [11], maturation of skin APCs [12]. Here, we propose to use differential proteomic,
131 lipidomic and metabolomic analysis using NanoLC-mass spectrometry/mass spectrometry (MS/MS)
132 analysis and matrix assisted laser desorption ionization imaging (MALDI)-mass spectrometry imaging

133 (-MSI) to dissect the early molecular events following dermal immunization in a human skin explant
134 model. Seasonal trivalent influenza vaccine (TIV) by i.d. route induces a potent local skin reaction and
135 has been shown to be efficient in the induction of both humoral and T cell responses [13–16]. We thus
136 planned to use TIV injection as a model antigen. We used an *ex vivo* human skin explant model,
137 which has the advantage of conserving whole tissue architecture. The originality of this work is based
138 on its spatio-temporal proteomic analysis of the epidermis and dermis at different time points after the
139 inoculation. To our knowledge, this study is the first to use an *ex vivo* human skin explant model for a
140 multiparametric analysis of proteins, lipids, metabolites, and mRNA to explore early cutaneous innate
141 immune events before an inflammatory reaction to a vaccine at the inoculation site.

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162 **Material and methods**

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164 **Human skin explants**

165 Human skin samples were obtained from healthy volunteers (women aged 21-63 years) undergoing
166 plastic surgery for breast, abdomen, or face lifts (Service de chirurgie plastique, reconstructrice et
167 esthétique - Centre de traitement des brûlés, Saint-Louis Hospital, Paris, France). All skin samples
168 were taken after informed consent in accordance with the local Institutional Ethics Committee
169 guidelines (IRB 00003835) and the ethics rules stated in the Declaration of Helsinki. Skin samples
170 were conserved in NaCl immediately after surgical excision and then processed within 4-6 hours post-
171 surgery. They were examined macroscopically for tissue damage. Either PBS or Intanza® [TIV
172 A/Michigan/45/2015 (H1N1)pdm09, A/Hong Kong/4801/2014 (H3N2), B/Brisbane/60/2008 -15 ug of
173 haemagglutinin (HA)] (Sanofi-Pasteur, Lyon, France) was administered according to the Mantoux
174 method by i.d. injection. In all, 45 µg of total HA protein/cm² of skin (volume: 25 µl of Intanza® and
175 15 µg of HA for each influenza strain) was injected in the dermis. Intanza formulation (100µL) was
176 diluted to a quarter to be injected in each of the 1 cm² pieces of skin. Influenza vaccine and PBS
177 control injected skin were incubated 4 and 18 h, draining in RPMI 1640 medium (Gibco® Thermo
178 Fisher Scientific, Waltham, MA, U.S.A.). As Figure 1 shows, skin donors (n=6) were used both for
179 cryosection for analysis by MALDI-Fourier-transform ion cyclotron resonance (-FTICR) and for
180 epidermal and dermal cell suspensions for high throughput proteomic analysis. Skin samples were also
181 used to validate cytokine and chemokine expression by qPCR (supplemental materials).

182

183 **Skin epidermal and dermal layers**

184 After the injections into fresh skin samples (1 cm²), the tissue was cut into small pieces and incubated
185 in RPMI 1640 medium with 2.4 IU/ml of dispase II (Sigma-Aldrich, St. Louis, MO, U.S.A.) overnight
186 at 4°C with agitation to separate epidermal sheets from the dermis. Epidermal sheets were then
187 removed from the dermis with mechanical tweezers. Epidermal cell suspensions were obtained after

188 10 minutes incubation at 37°C in RPMI 1640 and trypsin-EDTA 0.2% (Sigma-Aldrich), supplemented
189 with DNase I (10 µg/mL, Roche, Boulogne Billancourt, France). Fetal calf serum (FCS, Dominique
190 Dutscher, Brumath, France) was then added. Cell suspensions were washed in RPMI 1640 +20% FCS
191 medium, processed through a 70-µm filter (Falcon BD™, San Jose, CA, U.S.A.), and then washed in
192 PBS. Cell pellets were dried, then frozen and conserved at -80°C.

193

194 **Protein detection and identification**

195 See the supplementary information for the detailed protocol. Briefly, dermal and epidermal cells (the
196 equivalent of 2 million cells for each condition) were lysed and proteins extracted with a
197 Radioimmunoprecipitation assay (RIPA) buffer. Extracted proteins were digested with filter-aided
198 sample preparation (FASP), and the peptides retrieved were analysed with a nanoUPLC system
199 coupled with a high-resolution mass spectrometer for MS and MS/MS analysis. The detailed methods
200 are described in the supplemental materials and methods section.

201 All MS data were processed with MaxQuant (version 1.5.6.5) by using the Andromeda search engine.
202 The proteins were identified by searching MS and MS/MS data against the reviewed proteome for
203 Homo sapiens in the UniProt database (Release February 2017, 20 172 entries) and 262 commonly
204 detected contaminants. Trypsin specificity was used for digestion mode. N-terminal acetylation and
205 methionine oxidation were selected as variable modifications and carbamidomethylation of cysteines
206 as fixed. Up to two missed cleavages were allowed. An initial mass accuracy of 6 ppm was selected
207 for MS spectra. The MS/MS tolerance was set to 20 ppm for the HCD data (higher-energy-collisional-
208 dissociation). False discovery rates for peptide spectrum matches and for protein identifications were
209 estimated by using a decoy version of the previously defined databases (reverse construction) and set
210 at 1%. Relative label-free quantification (LFQ) of the proteins was conducted with MaxQuant, by
211 applying the MaxLFQ algorithm with default parameters. Analysis of the identified proteins was
212 performed with Perseus software (<http://www.perseus-framework.org>) (version 1.5.6.0). The file
213 containing the information from the identification was used. Hits from the reverse database and
214 proteins with only modified peptides were removed. Hits from potential contaminants were marked,
215 and proteins originating from culture medium (e.g., serum albumin from *Bos taurus*) or sample

216 preparation (e.g., trypsin from *Sus scrofa*) were manually removed to ensure that only proteins that are
217 part of the human skin structure were retained. LFQ intensities were transformed by base 2 logarithm
218 before statistical analysis.

219 **Statistical analysis**

220 Protein expression data were analysed using R software. Analysis of the difference between TIV and
221 PBS conditions at each time point was based on a paired nonparametric *t*-test (Wilcoxon signed-rank
222 test), with a two-tailed test (*p*-value <0.05) considered a statistically significant. Unsupervised
223 multivariate analysis was performed using Principal Component Analysis (PCA) using R software.
224 Heatmaps and hierarchical clusters were generated with R software based on the Pearson coefficient of
225 correlation with the complete linkage method.

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227 **Data availability statement.** The normalized proteomic data that support the findings of this study
228 have been deposited in ArrayExpress with the accession code XXXXX.

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Results and Discussion

A multimodal approach of early innate events during skin reaction following intradermal injection of seasonal influenza vaccine

Using an *ex vivo* human skin explant model, we examined the cutaneous early innate molecular events induced at early time points (4 and 18 h) after TIV administration. Of note, skin explants is an *ex vivo* model that allows the investigation of early tissue reaction without inflammatory cells recruitment (absence of blood flow). We have previously showed that 3-4 hours after intradermal injection in the skin explants allows the detection of KC and LC activation to several intradermal stimuli (nanoparticle vaccine, modified vaccinia Ankara and Toll-like receptor ligands) [4,17]. We also showed LC renewal in the epidermis at 18 hours post i.d. injection of MVA [17] while inflammatory cells continue to migrate to the dermis [18]. We thus have chosen these time points for the further omics analysis. Figure 1a presents the experimental plan. Skin explants from 6 healthy donors were injected by i.d. route with either TIV or PBS. For each donor, we divided skin samples in two parts: 1) dermal and epidermal cell suspensions were prepared for protein identification with MS-based proteomics at 4 and 18 h after treatment; 2) skin tissue sections were cryopreserved for *in situ* analysis by MALDI-MSI of metabolite and lipid alteration (Figure 1a, flow chart, left branch). Results of LFQ proteomics were analysed to identify the significant proteins (that is, those with significantly differential expression) detected after TIV and PBS administration (Figure 1a, flow chart, right). Finally, we used the IPA program to explore networks and pathways (Figure 1a).

First, NanoLC-MS/MS analyses of dermal and epidermal cell suspensions allowed the identification of 2.375 common proteins. Principal Component Analysis (PCA) of all samples, restricted to this list of 2.375 proteins, separated the dermal and epidermal samples (Figure 1b). Accordingly, the dermal and epidermal samples differed significantly in their protein detection levels and were therefore studied separately. In addition, control skin incubated for 4 or 18 h after PBS

272 injection did not differ in protein detection levels at either time point, as PCA showed (Figure 1c).
273 Additional analysis of the impact of age on protein distribution showed no difference between those
274 individuals <35 years and >35 years (data not shown).

275 In the epidermis, we found 73 significant proteins detected at 4 h and 35 proteins at 18 h that
276 were differentially expressed after TIV compared with PBS injection (Wilcoxon signed-rank test, P -
277 value<0.05) (Figure 1d, Supplemental Table 1). In the dermis, we found 32 proteins at 4 h and 45
278 proteins at 18 h detected with significantly differential expression after TIV injection compared with
279 PBS (Wilcoxon signed rank test, P -value<0.05) (Figure 1d, Supplemental Table 3). The Venn diagram
280 in Figure 1d showed significant proteins, exclusive to the treatment condition and tissue layer with
281 only few shared molecules, suggesting specific molecular events in each skin layer.

282

283 **Identification of early inflammatory proteins and metabolites induced in the epidermis in** 284 **response to i.d. TIV administration.**

285 Heat-maps represent the detection levels of significant proteins (73 and 35 proteins differentially
286 detected at 4 h and 18 h after treatment, respectively) in the epidermis of TIV-treated compared with
287 PBS control skin at 4 and 18 h (Figures 2a and 2b, Supplemental Table 1). The PCA of all samples
288 based on these proteins, separated TIV-treated from PBS control skin at both time points (Figure 2c,
289 d).

290 We performed a functional enrichment analysis using Ingenuity Pathway Analysis (IPA), in order to
291 understand the involvement of these proteins in immune functions. Supplemental Table 2 summarizes
292 the top upregulated and downregulated proteins and their contributions to immune responses in the
293 epidermis at, respectively, 4 h and 18 h. The Top IPA biological functions are cell-to-cell signalling
294 and interaction (IPA: P -value = 1.53×10^{-3} - 4.75×10^{-2}), cellular assembly and organization (IPA: P -
295 value = 3.39×10^{-4} - 4.31×10^{-2}), and immune cell trafficking (IPA: P -value = 2.41×10^{-3} - 4.05×10^{-2}).
296 Among major proteins, IFITM3, STAT1, and IFI35 are involved in interferon signalling (IPA: P -value
297 = 3.09×10^{-4}), while ICAM3 participates in cross-talk between cells (IPA: P -value = 3.2×10^{-4}) and
298 PLCD1 with STAT1 in DC maturation (IPA: P -value = 4.75×10^{-3}) (Supplemental Table 2). STAT 1 is
299 involved as well in the TH17 pathway, which is also a proposed outcome of skin immunization [4,17].

300 At 4 h after i.d. TIV administration, we detected the upregulation of ILK, LGALS1, SERPINB2, and
301 IRF6, which are reported to contribute respectively to cutaneous wound contraction, wound healing,
302 defects of the stratum corneum, and KC differentiation [19–22]. We also found the following proteins
303 to be upregulated: IFI35, an inflammatory marker observed in skin lesions from atopic dermatitis [23],
304 IFITM3, the expression of which increases on T cells after viral infection [24], and IRF6, which,
305 driven by TLR3 activation, plays a role in KC cytokine expression [25]. Also notably upregulated
306 were ICAM3 [26], HLA-B, and HLA-DRB5 [27] — all proteins allowing antigen presentation (IPA:
307 P -value = 8.54×10^{-3}).

308 Supplemental Table 2 describes the proteins making major contributions to immune responses
309 at 18 h. We found 9/35 proteins in the major IPA biological functions (Figure 2f). Most of these
310 molecules were downregulated in the skin at 18 h (in green) and are involved in inflammatory
311 responses (IPA: P -value = 1.73×10^{-3} - 2.10×10^{-2}), cell-to-cell signalling and interaction (IPA: P -value
312 = 1.73×10^{-3} - 1.20×10^{-2}), cell movement (IPA: P -value = 1.73×10^{-3} - 1.89×10^{-2}), or macrophage
313 functions (e.g., S100A10, HTT, MAPK13, PTPN6, GNG2, and MCAM) (IPA: P -value = 4.46×10^{-3} -
314 1.13×10^{-2}).

315 The protein networks significantly detected in the epidermis after TIV injection were
316 connected to proinflammatory cytokines and chemokines, which we measured by qPCR analysis in
317 epidermal cells before and after treatment. Figure 2g shows the mean gene expression in epidermal
318 cell suspensions for 5 healthy donors. We observed significant increased expression of CX3CL1,
319 CCL22, CXCL10, CXCL8, and TNF α genes at 4 h and 18 h after i.d. TIV injection.

320

321 **Identification of early inflammatory proteins and metabolites induced in the dermis in response** 322 **to i.d. TIV administration.**

323 Significant detected proteins that are differentially expressed in the dermis for TIV-treated
324 skin compared with PBS controls at 4 h and 18 h are represented in the heat maps (Figure 3a, 3b,
325 respectively). In the dermis, we found 32 significant proteins detected differentially at 4 h and 45
326 proteins at 18 h after TIV compared with PBS injection (Supplemental Table 3). The PCA of all
327 samples was based on the detection profiles of these genes, and the score plots showed that the

328 projections of PC1 (44.89% of the total variance for dermis 4 h and 48.10% for 18 h) and of PC2
329 (10.51 % for epidermis 4 h and 10.31% for 18 h) separated TIV-treated from PBS control skin for the
330 dermal layer at both time points (Figure 3c, 3d). We performed a functional enrichment analysis using
331 IPA for identification of top immunological pathways. Supplemental Table 4 summarizes the proteins
332 that were upregulated and downregulated in the dermis in TIV-treated skin compared to PBS controls.
333 These are mostly involved in cell-to-cell signalling and interaction (IPA: P -value = 6.29×10^{-3} -
334 2.19×10^{-2}) and interaction markers associated with skin inflammation (IPA Inflammatory Response:
335 P -value = 4.72×10^{-3} - 2.34×10^{-2}). TRAF6 is one of them; its involvement in DC maturation (IPA: P -
336 value = 3.43×10^{-2}) makes it an interesting biomarker of innate immunity for adaptive responses. Other
337 downregulated molecules include EIF4B, which has been linked to mTOR signalling (IPA: P -value =
338 3.63×10^{-3}) and identified as an essential regulator in skin morphogenesis [28]. Interestingly, MYLK, a
339 protein involved in cell morphology (IPA: P -value = 7.86×10^{-3} - 3.41×10^{-2}), was upregulated, and
340 changes in the morphology of LCs but also DCs upon activation or danger signals are among the main
341 features of skin APCs [17,2,12,4]. In the dermis, the production of some inflammatory markers was
342 modified, including the well-known NF κ B subunit and TRAF6 [29], as well as markers such as
343 ITGB5 and HLA-A, which have been observed in particular in inflammatory skin disorders and
344 cutaneous adverse reactions [30,31]. We also noted the upregulation of CD1a and the downregulation
345 of CD207, markers that might account for the migration of LCs and CD207+ dermal DCs after their
346 activation, respectively to the dermis and draining lymph nodes during cell trafficking [3,17]. Finally,
347 PSMB4 and PSMD13, both proteins involved in the proteasome complex, which is crucial for antigen
348 presentation, were also deregulated [32,33].

349 At 18 h, 11/45 molecules, all upregulated in TIV-treated skin, were involved in multiple
350 mechanisms (Supplemental Table 4), such as cell signalling and interaction (IPA: P -value = 2.29×10^{-3}
351 - 4.09×10^{-2}), cell repair (IPA: P -value = 2.29×10^{-3} - 4.92×10^{-2}), cell movement (IPA: P -value =
352 4.57×10^{-3} - 4.70×10^{-2}), injury (IPA: P -value = 2.29×10^{-3} - 4.72×10^{-2}), metabolism (IPA: P -value =
353 2.29×10^{-3} - 4.92×10^{-2}), molecular transport (IPA: P -value = 2.29×10^{-3} - 4.04×10^{-2}), and the cell cycle
354 (IPA: P -value = 9.13×10^{-3} - 3.38×10^{-2}). These activities suggest massive reorganization and repair in
355 the dermis — the site of injection of the vaccine compounds.

356 Because most of these molecules are also associated with inflammatory mediators, we
357 measured the expression of the genes for these proinflammatory cytokines and chemokines, in
358 connection with the protein network significantly detected by qPCR analysis of epidermal cells after
359 TIV injection in the dermis. Figure 3g shows the mean gene expression in the dermal cell suspension
360 in 5 healthy donors. We observed an increase in gene expression of CXCL10 at the early time points
361 and of CCL22 and CXCL8 at 18 h after i.d. TIV administration.

362

363 **Identification of major metabolites induced in the skin in response to i.d. TIV administration**

364 As shown in figures 2 and 3, IPA pathways highlighted several metabolites and lipids potentially
365 involved in top networks and may indicate changes in epidermal and dermal cellular processes.
366 MALDI-FTICR has proved its efficacy in detection drug compounds and small molecules on skin
367 explant tissue section imaging [34,35]. Using MALDI-FTICR, we performed *in situ* analyses on skin
368 cryosections treated for 4 h compared with PBS controls (Supplemental Figure 1). The vaccine
369 injection area was detected in the skin of 6 donors by a vaccine excipient, i.e. Octoxinol 10
370 (Supplemental Figure 1, left images). No detection of the vaccine excipient was found on PBS skin
371 tissue section (right images). Based on IPA data base, metabolites and lipids potentially involved in
372 top networks were analysed on tissue sections. As Figure 4a shows fold-changes of mean intensity of
373 8 metabolites and lipids (highlighted in IPA analysis), including phosphatidylcholine (PC) (32:0) and
374 (36:1), phosphatidylinositol (PI) (34:1), diacylglycerol (DG) (34:1), adenosine diphosphate (ADP),
375 linoleic acid (LA) (FA 18:2), phosphatidic acid (PA) (18:1), and sphingomyelin (SM) (d34:1),
376 observed in TIV-treated skin compared to PBS controls, for each skin layer (Figure 4a). PA (18:1) (*P*-
377 value = 0.049) and ADP or dGDP (*P*-value = 0.006) were overexpressed in the TIV condition and
378 localized in the epidermis. Whereas LA (*P*-value = 0.05) was overexpressed in the TIV condition and
379 localized in the dermis. PA (18:1) was overexpressed in the TIV condition and localized in the
380 epidermis. Figure 4b shows the molecular distribution of PA (18:1) on skin and underlines that it was
381 principally overexpressed in epidermis and at the top of the dermis. The molecular distribution of this
382 lipid was homogenous inside the epidermis tissue. Figure 4c shows the molecular distribution of LA
383 on each tissue. Mass spectrometry imaging (MSI) enabled the visualization of this compound's

384 overexpression in the dermis and epidermis. It is now well established that lipids and metabolites
385 affect cutaneous innate immunity [36,37]. The mass spectrometric analyses showed the *in situ*
386 modulation of metabolites and lipids related to proteins previously detected, such as MAPK3 and
387 phospholipase D3 involved in immune signalling. Indeed, SM molecules detected in the dermis, are
388 known to be related to such antimicrobial peptides as cathepsin B. Changes in SM and ceramide
389 content have also been reported to affect membrane physiology directly, thus modifying signal
390 transmission and interfering with diverse aspects of T cell activity [38]. For example, long-chain
391 polyunsaturated fatty acids, such as LA (FA (18:2), have immunoregulatory functions via several
392 mechanisms [39]. Some long-chain polyunsaturated fatty acids are precursors of lipid mediators [40],
393 which participate in inflammatory processes and also affect acquired immune cells.

394 DG and PA, observed in the epidermis, have demonstrated links to signalling kinase proteins
395 MAPK3. Moreover, DG can act as a second messenger to activate many downstream signalling
396 cascades. DG has been an established ligand for protein kinase C isoforms that can influence
397 inflammation [41,42]. We found additional dermal and epidermal molecules, detected by MALDI-
398 MSI, such as LA, PC, ADP, and inositol phosphate detected *in situ*, thus demonstrating their effect in
399 cutaneous immunity. Furthermore, PC in the form of several lipids, such as lysophosphatidic acid
400 (LPA) (lysoPA), lysophosphatidylcholine (lysoPC), PI, and PA, has been observed to be expressed
401 differentially in psoriasis patients compared with healthy volunteers [43]. Extracellular nucleotides
402 such as ADP have also demonstrated their role in the regulation of DCs and of other immune cell
403 functions, through their activation of some G-protein coupled receptors called P2 receptors or via ADP
404 ribosylation, which increases the cAMP concentration [44]. Finally, inositol phosphate is reported to
405 modulate the secretion of cytokines derived from both T and myeloid cells (IL-1 β , IL-6, and IL-22)
406 and TNF- α [45]. Accordingly, these mediators promote the recruitment of inflammatory cells such as
407 neutrophils but also monocytes, which also play a role in the transport of antigens from the skin to the
408 lymph nodes during inflammation; they also participate in CD8 T cell priming in the bone marrow and
409 inflammatory signals in the lymph nodes [9,10,18,46] . LC activation in the epidermis and dermis
410 consists of multiple events including CXCL10 production, morphological changes and down-
411 regulation of cellular adhesion molecules, which are necessary for induction of adaptive immunity

412 both in human and murin models [4,18,47]. In humans, TIV vaccination by the i.d. route induced
413 systemic production of CXCL10, correlated with adaptive immune responses [15]. These
414 inflammatory mediators also promote APCs activation as well as T cell activation and polarization [5–
415 8].

416 In conclusion, to our knowledge, this study is the first to use an ex vivo human skin explant
417 model for a multiparametric analysis, combining several approaches to determine
418 modifications of metabolites, lipids, mRNA and proteins in response to cutaneous TIV
419 administration. We explored early local cutaneous innate immune events, in the different skin
420 layers, before any inflammatory reaction induced at the inoculation site. We found major
421 modifications in protein profiles that differentiated vaccine-injected skin from control
422 skin. These results add more insight into the molecular reaction in the skin that could be
423 involved in changes in the behavior of cells following i.d. injection. Indeed, we previously
424 showed that 4 hours after MVA i.d. injection, LCs migrate to the dermis as shown by decrease
425 in LC numbers, LC morphological changes (round shape LC) and CXCL10 production [17].
426 We also demonstrated these modifications are due to the release of IL-32 by keratinocyte
427 which down regulates KC-LC adhesion [4]. In addition, in murine models, we showed that
428 innate cell migration (neutrophils, inflammatory monocytes are detected in the skin between 4
429 and 8 hours following i.d. injection of MVA or nanoparticles [10,18]. In our work protein
430 networks are related to several cytokines/chemokines detected in the epidermis and dermis.
431 These inflammatory molecules could be related to DCs/LCs activation status (such as
432 CXCL10) which could orientate IFN γ -type responses or participates to CD4 T cell activation
433 (such as CXCL10 and CCL22). This later chemokine is the ligand of CCR4 and help in
434 positioning of T cell memory in the skin [48]. Neutrophils are attracted to the skin via
435 CXCL8, however we observed a significant increase in CXCL10 mRNA at 18 hours post-
436 injection and not at early time points (<4 hours). This could be either due to dichotomy

437 between either CXCL8 mRNA and protein secretion or the involvement of additional
438 chemokines/chemokine receptors axis in early neutrophil trafficking [49]. We have also
439 detected CX3CL1 mRNA suggesting initiation of monocyte trafficking to the skin. Finally,
440 TNF- α could be involved in LC activation [50]. This study has demonstrated that proteomic
441 analyses might enable the identification of potential early biomarkers of activated skin after
442 vaccine administration by a cutaneous route.

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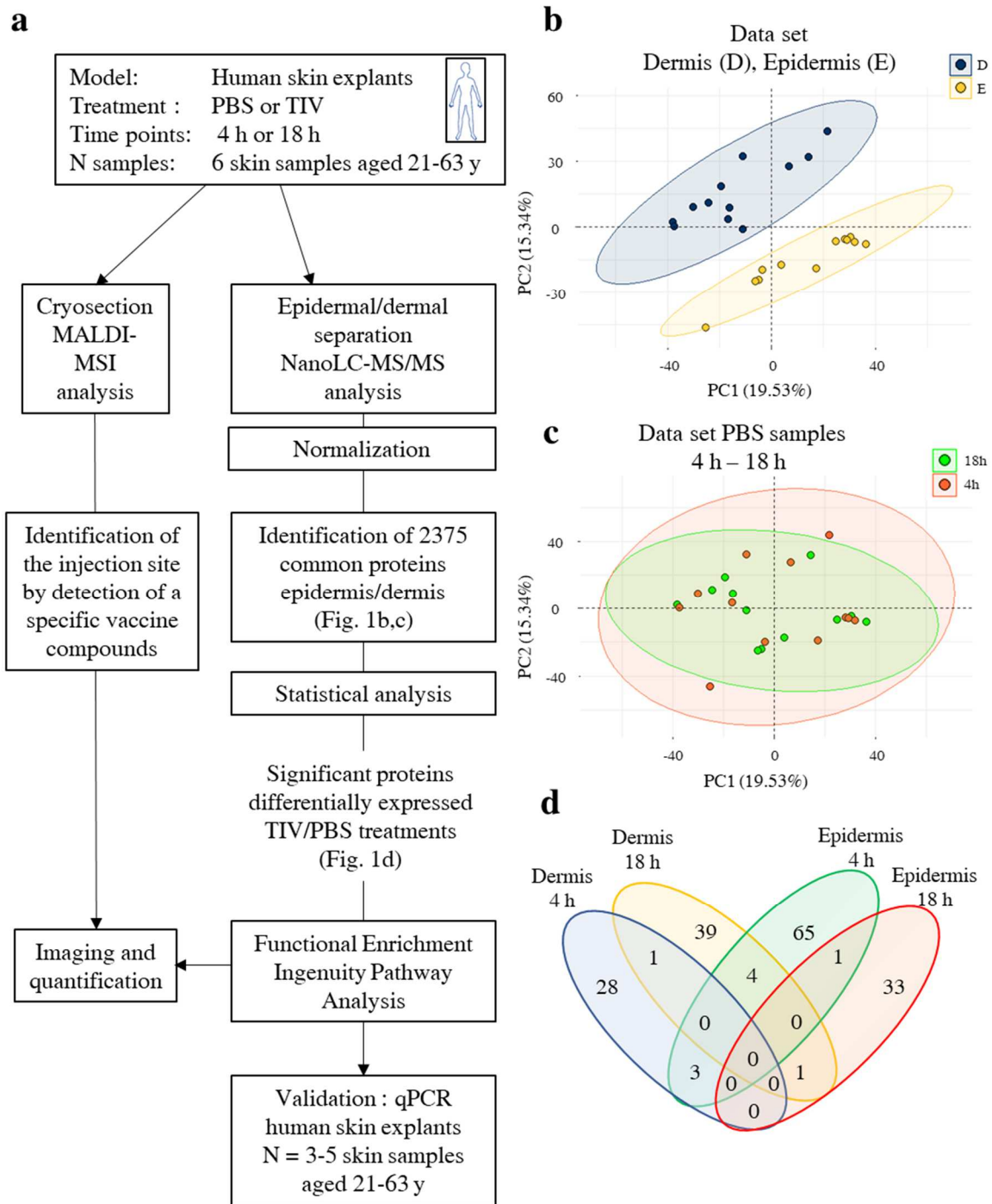


Figure 1: A multimodal approach of early innate events during skin reaction following intradermal injection of seasonal influenza vaccine

(a) **Flow Chart** : Human skin samples from six healthy donors (women aged 21-63 years), were cut into 1-cm² pieces after injection by TIV (Intanza®, microneedle device) or PBS by the i.d. route. Samples either underwent enzymatic digestion (flow chart, right) or cryopreservation (flow chart, left) for *in situ* investigation by MALDI-MSI of modifications in lipids and metabolites. Epidermal and dermal cell suspensions were used for proteomic analyses: the protein lysate was analysed by NanoLC-MS/MS; the peptide sequence analyses were processed by Maxquant software, and contaminants removed; and common proteins (n=2375) were identified in the epidermis and dermis after TIV and PBS administration. Following statistical analysis using Wilcoxon signed rank test, P -value<0.05. Statistical analyses were performed with R software (Wilcoxon matched-pairs signed rank test, with a two-sided P -value of <0.05). The Ingenuity Pathway Analysis (IPA) program was applied on significant proteins, to identify top gene networks and biological function. Gene expression was measured on mRNA samples extracted from the same donors (n=3-5 donors) by RT-qPCR. (b,c) Score plot from the PCA of all PBS samples based on the detection profiles of the 2375 proteins detected. (b) Projections of PC1 (19.53% of the total variance) and of PC2 (15.34%) separate the dermal (blue dots) and epidermal (yellow dots) samples defined by two concentration ellipses, (c) but do not separate 4 h (red dots) from 18 h (green dots) samples. (d) Venn diagram representing number of proteins significantly differentially detected in TIV compared to PBS in epidermis and dermis at 4 h and 18 h.

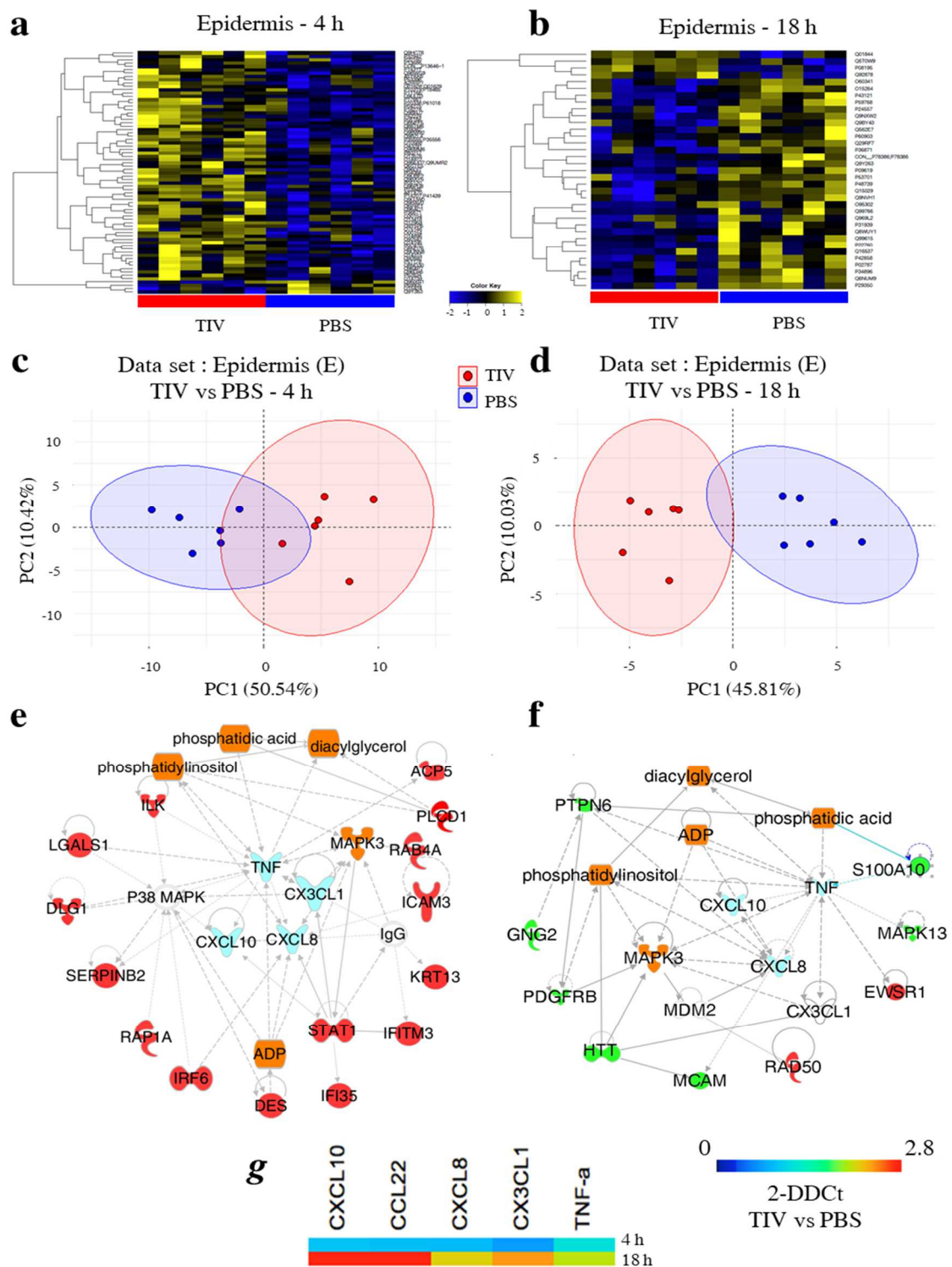


Figure 2: Identification of early inflammatory proteins and metabolites induced in the epidermis in response to i.d. TIV administration.

(a, b) Data set of significant proteins in the epidermis are represented in a heat-maps with the level of detection in TIV-treated compared to PBS-control skin at 4 h (a) and 18 h (b) (Wilcoxon matched-pairs signed rank test, P -value < 0.05). (c, d) Score plots from the PCA are represented based on detection profiles of the 73 and 35 significant proteins differentially expressed between treated (red dots) and control (blue dots) samples at the 4 h condition (c) and 18 h (d) respectively. (e, f) Top networks from IPA highlighting major proteins from comparison of TIV and control conditions at 4 h (e) and 18 h (f). Overexpression after trivalent influenza vaccine (TIV) administration is represented in red, overexpression for the PBS condition in green. In orange the metabolites and lipids and in blue the proinflammatory cytokines found linked to the proteins of interest. In white, the proteins added by IPA, to complete the top network but not identified in our study. solid lines = direct relations, dashed lines = indirect relations. (g) mRNA expression analysis in epidermal cells injected with either TIV or PBS. Gene expression was normalized to the mean of actin and GAPDH expression and presented as relative fold gene expression levels compared to PBS controls, after calculating the 2^{-ddCt} values.

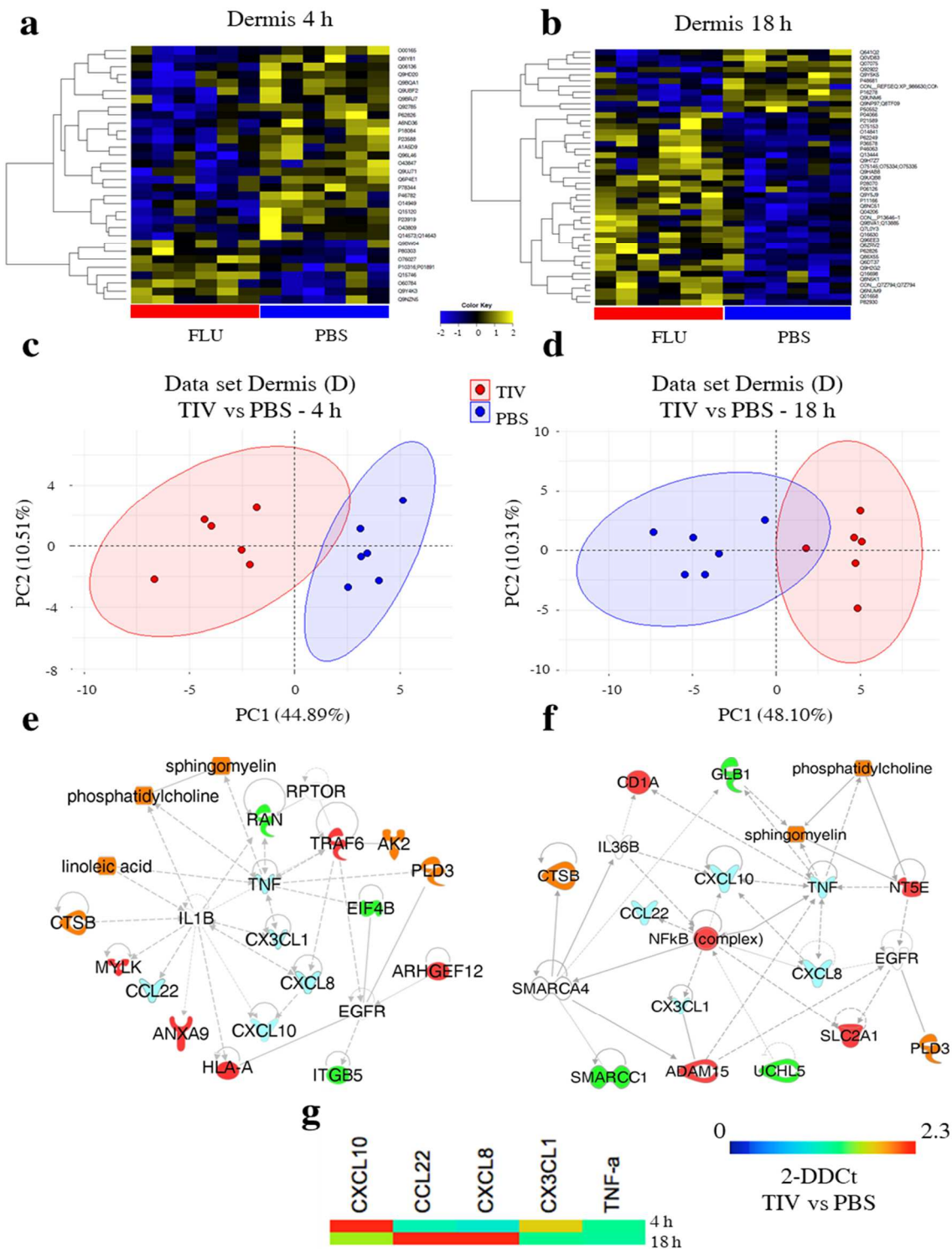


Figure 3: Identification of early inflammatory proteins and metabolites induced in the dermis in response to i.d. TIV administration.

(a, b) Data set of significant proteins in the dermis are represented in a heat-maps with the level of detection in TIV-treated compared to PBS-control skin at 4 h (a) and 18 h (b) (Wilcoxon matched-pairs signed rank test, P -value <0.05). (c, d) Score plots from the PCA are represented based on detection profiles of the 32 and 45 significant proteins differentially expressed between treated (red dots) and control (blue dots) samples at the 4 h condition (c) and 18 h (d) respectively. (e, f) Top networks from IPA highlighting major proteins from comparison of TIV and control conditions at 4 h (e) and 18 h (f). Overexpression after trivalent influenza vaccine (TIV) administration is represented in red, overexpression for the PBS condition in green. In orange the metabolites and lipids and in blue the proinflammatory cytokines found linked to the proteins of interest. In white, the proteins added by IPA, to complete the top network but not identified in our study. solid lines = direct relations, dashed lines = indirect relations. (g) mRNA expression analysis in epidermal cells injected with either TIV or PBS. Gene expression was normalized to the mean of actin and GAPDH expression and presented as relative fold gene expression levels compared to PBS controls, after calculating the 2^{-ddCt} values ($n=3-5$).

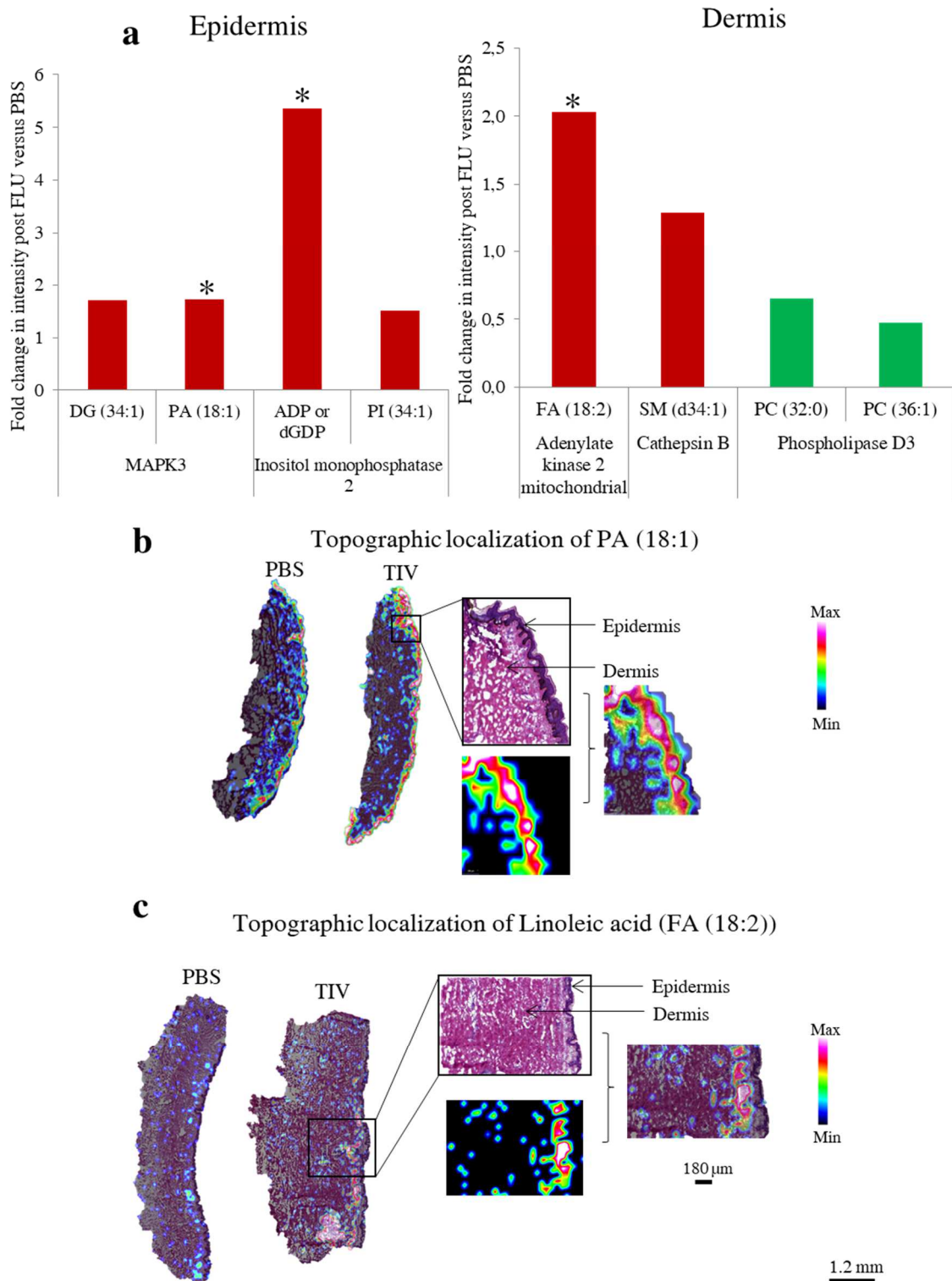


Figure 4: Identification of major metabolites induced in the skin in response to i.d. TIV administration

(a) Metabolites and lipids expression level in the epidermis (left) and in the dermis (right), according to IPA analysis. The fold changes of intensity were calculated comparing the TIV and PBS conditions. Overexpression after trivalent influenza vaccine (TIV) administration is represented in red, overexpression for the PBS condition in green. (b) Representative MALDI-MS imaging of PA (18:1) measured at m/z 435.2517 in TIV and PBS treated skins (c) Representative MALDI-MS imaging of Linoleic acid (FA 18:2) measured at m/z 279 in TIV and PBS treated skin. DG: diacylglycerol; ADP: adenosine 5'-diphosphate; dGDP: 2'-deoxyguanosine 5'-diphosphate; PI: phosphatidylinositol; LA: linoleic acid, FA: fatty acid; SM: sphingomyelin; PC: phosphatidylcholine.

