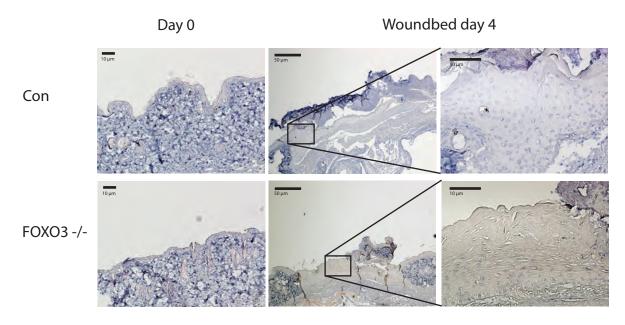
Α



Day 0 Woundbed day 4

Con

FOXO3 -/-

Supplementary figure 1

for murine neutrophils.

Samples of non-wounded and *in vivo* - wounded murine skin from FOXO3 knockout and wildtype mice were immunostained for markers of macrophages and neutrophils. Non-wounded skin was obtained by punch biopsy. New biopsies of the wound samples were taken on day 4 around the edges of the initial biopsy. Color was developed with Vulcan Fast Red Chromogen, and Harris Hematoxylin was used for counterstaining.

A) Immunohistochemistry was performed on non-wounded murine skin and in vivo wounded skin 4 days post wounding using antibodies against F4/80, a marker for mono-

cytes and macrophages B) Immnuohistochemistry using antibodies against Gr1, a marker

List of the 100 most differentially expressed genes between *in vivo* wounded and non-wounded human skin at day 4 in the E-MEXP-3305 data set. Please see the methods section for further details on selection criteria.

Affymetrix Probe I.D.	Gene Symbol	Description	Log2-fold change	Q-value (%)	Definition	Function
41469_at	MMP1	matrix metallopeptidase 1	9.9	0	Matrix metalloprotease	Keratinocyte migration
232170_at	DEFB4A	defensin, beta 4	9.8	0	Antimicrobial peptide	Antimicrobial activity, Induced in wounded skin
207356_at	SPP1	secreted phosphoprotein 1 (osteopontin)	8.2	0	Cytokine	Cytokine that upregulates expression of interferon-gamma and interleukin-12
211906_s_at	S100A7A	S100 calcium binding protein A7-like 1	7.7	0	S100 protein	Involved in epidermal differentiation
209720_s_at	SERPINB4	serpin peptidase inhibitor, clade B, member 4	7.2	0	Peptidase inhibitor	Inhibits granzyme M-induced cell death
204351_at	PI3	peptidase inhibitor 3, skin-derived (SKALP)	7.2	0	Peptidase inhibitor, antimicrobial	Elastase-specific inhibitor antimicrobial peptide against Gram+ and Gram- bacteria
232082_x_at	IL8	interleukin 8	6.5	1.4E-01	Interleukin	Attracts neutrophils to the wound bed
209800_at	S100A9	S100 calcium binding protein A9 (calgranulin B)	6.3	0	S100 protein, Antimicrobial	Antimicrobial activity towards bacteria and fungi
206561_s_at	IL24	interleukin 24	5.9	0	Interleukin	Terminal cell differentiation, overexpression leads to elevated expression of GADD family genes
223278_at	TCN1	transcobalamin I (vitamin B12 binding protein)	5.8	5.6E-02	Antimicrobial peptide	Antimicrobial activity, facilitates the transport of cobalamin into cells
209773_s_at	IL20	interleukin 20	5.7	0	Interleukin	Cytokine that may be involved in epidermal function and psoriasis. Acts through STAT3
224910_at	SPRR3	small proline-rich protein 3	5.3	0	Small proline rich protein	Cross-linked envelope protein of keratinocytes, important for barrier formation
208539_x_at	KRT16	keratin 16	5.0	0	Cytokeratin	Paired with keratin 6, forms intracellular intermediate filaments
204268_at	GZMB	granzyme B	5.0	0	Enzyme	Proapoptotic, target cell lysis in cell-mediated immune responses, cleaves caspase-3, -7, -9 and 10
206172_at	MMP10	matrix metallopeptidase 10	4.8	0	Matrix metalloprotease	Involved in keratinocyte migration
209875_s_at	PRSS27	protease, serine 27	4.8	0	Serine protease	Tryptic serine peptidase that cleaves peptides after an arginine residue
235075_at	IGFL1	IGF-like family member 1	4.6	0	Growth factor	Induced during inflammatory skin conditions
226817_at	SERPINE1	serpin peptidase inhibitor, clade E, member 1	4.6	0	Peptidase inhibitor	Inhibits plasminogen activator, urokinase, protein C and matriptase-3/TMPRSS7
232074_at	SERPINB3	serpin peptidase inhibitor, clade B, member 3	4.5	0	Peptidase inhibitor	May act as a protease inhibitor to modulate the host immune response
203535_at	IL6	interleukin 6	4.5	0	Interleukin	Produced at sites of acute and chronic inflammation, Cytokine with a wide variety of biological functions

214091_s_at	FPR1	formyl peptide receptor 1	4.3	0	Pro-inflammatory receptor	Chemotactic receptor
206211_at	MME	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	4.3	8.6E-02	Membrane metalloprotease	Can cleave angiotensin 1-9
216950_s_at	S100A7	S100 calcium binding protein A7 (psoriasin 1)	4.3	0	S100 protein	Overexpressed during psoriasis
227736_at	S100A12	S100 calcium binding protein A12 (calgranulin C)	4.2	0	S100 protein, Antimicrobial	Possesses antifungal activity against <i>C. albicans</i> and is also active against <i>E. coli</i> and <i>P. aeruginosa</i>
205916_at	AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)	4.1	0	Dual specificity phosphatase	Induced during oxidative stress
226218_at	SPRR2B	small proline-rich protein 2B	4.0	0	Small proline rich protein	Cross-linked envelope protein of keratinocytes
224917_at	APOBEC3A	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A	3.9	0	anti-viral activity	Destroys foreign DNA through extensive deamination of cytosine
206569_at	FOSL1	FOS-like antigen 1	3.9	0	Transcription factor	Part of transcription factor complex AP-1
210119_at	S100A8	S100 calcium binding protein A8 (Calgranulin A)	3.9	0	S100, Antimicrobial peptide	Has antimicrobial activity towards bacteria and fungi
203234_at	IL13RA2	interleukin 13 receptor, alpha 2	3.9	0	Decoy receptor	Lacks intracellular domain
222162_s_at	TMPRSS11 D	transmembrane protease, serine 11D	3.8	5.9E-02	Transmembrane protease	Involved in host defense systems on the mucous membrane
205863_at	CXCL2	chemokine (C-X-C motif) ligand 2	3.8	0	Chemokine	Chemotactic for polymorphonuclear leukocytes and hematopoietic stem cells
219554_at	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)	3.8	0	Fc-gamma receptor	High affinity receptor for the Fc region of immunoglobulins gamma
210873 x at	KRT6A	keratin 6A	3.8	0	Keratin	Forms intracellular intermediate filaments
210164_at	TDO2	tryptophan 2,3-dioxygenase	3.7	2.2E-01	Enzyme	Has antimicrobial, antiparasitic and antiviral effects
202672_s_at	AREG	amphiregulin	3.7	0	Growth factor	EGF receptor ligand
204475_at	TMPRSS4	transmembrane protease, serine 4	3.7	0	Transmembrane protease	Detaches keratinocytes from basement membrane
224071_at	HBEGF	heparin-binding EGF-like growth factor	3.6	5.6E-02	Growth factor	EGF receptor ligand
205207_at	SOCS3	suppressor of cytokine signaling 3	3.6	0	STAT-induced STAT inhibitor	Supresses cytokine signaling
218960_at	UPP1	uridine phosphorylase 1	3.5	0	Phosporylase	Metabolism, nucleotide synthesis
203936_s_at	KLK6	kallikrein 6	3.5	0	Serine protease	Sheds E-cadherin on keratinocytes
214370_at	GPX3	glutathione peroxidase 3 (plasma)	3.4	0	Peroxidase	Functions in the detoxification of hydrogen peroxide
204733_at	CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	3.3	1.3E-01	Chemokine	Associated with atopic dermatitis
205680_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	3.3	0	Peptidase inhibitor	Inhibits elastase etc
209125_at	MMP9	matrix metallopeptidase 9	3.2	0	Matrix metalloprotease	Keratinocyte migration
227697_at	MIR21	microRNA 21	3.2	0	Micro RNA	Involved in cell cycle regulation
202779_s_at	RHCG	Rh family, C glycoprotein	3.2	0	Ammonium transporter	May regulate transepithelial ammonia secretion
216248_s_at	NR4A1	nuclear receptor subfamily 4, group A	3.2	1.1E-01	Nuclear receptor	Transcription factor, Orphan nuclear receptor
203764_at	PI15	peptidase inhibitor 15	3.2	0	Peptidase inhibitor	Trypsin inhibitor
202628_s_at	S100P	S100 calcium binding protein P	3.1	0	S100 protein	Expressed in suprabasal layers of epithelial cells
217497_at	SELL	selectin L (lymphocyte adhesion molecule 1)	3.1	0	Selectin	Cell-surface glycoprotein having a role in immunoadhesion

239430_at	G0S2	G0/G1switch 2	3.1	7.4E-02	Cell cycle protein	Differentiation, Promotes apoptosis by binding to BCL2, upregulated in epidermolysis bullosa
211429_s_at	IL7R	Interleukin 7 receptor	3.1	0	Receptor	Interleukin receptor
228726_at	BCL2A1	BCL2-related protein A1	3.1	1.4E-01	BCL-2 family	Anti-apoptotic, reduces release of cytochrome c from mitochondria, blocks caspase activation
229947_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	3.0	0	Nuclear receptor	Transcription factor, Orphan nuclear receptor
215049_x_at	GJB2	gap junction protein, beta 2, 26kDa (connexin 26)	3.0	0	gap junction protein	Part of connexons
1569003_at	CXCR4	chemokine (C-X-C motif) receptor 4	3.0	0	chemokine receptor	Important for lung epithelial migration in response to wounding
205119_s_at	GPRC5A	G protein-coupled receptor, family C, group 5, member A	3.0	7.4E-02	type 3 G protein- coupling receptor	GPCR could modulate differentiation and maintaining homeostasis of epithelial cells.
228729_at	DSC2	desmocollin 2	2.9	0	desmosomal family protein	Component of intercellular desmosome junctions
204420_at	RGS1	regulator of G-protein signaling 1	2.9	0	Regulator of G- protein signalling	Inhibits signal transduction by increasing the GTPase activity of G protein alpha subunits
205239_at	SERPINB1	serpin peptidase inhibitor, clade B, member 1	2.9	0	Peptidase inhibitor	Inhibigts neutrophil elastase, cathepsin G, and proteinase-3 and thus protects tissues from damage
209774_x_at	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	2.9	0	potassium channel	Allows potassium to flow into a cell rather than out of a cell
217028_at	CTLA4	cytotoxic T-lymphocyte-associated protein 4	2.9	0	Inhibitory receptor	Inhibitory receptor acting as a major negative regulator of T-cell responses
227458_at	DLGAP5	discs, large homolog 7 (Drosophila)	2.8	0	Mitotic phosphoprotein	Key regulator of adherens junction integrity and differentiation
226535_at	ATF3	activating transcription factor 3	2.8	0	Transcription factor (CREB family)	Represses transcription from promoters with ATF sites, involved in cellular stress responses
236341_at	CHI3L2	chitinase 3-like 2	2.8	1.3E-01	Non-functional chitinase	Similar to bacterial chitinases but lacks chitinase activity, involved in cartilage biogenesis
204563_at	RRM2	ribonucleotide reductase M2 polypeptide	2.8	0	Ribonucleotide reductase	Catalyzes the biosynthesis of deoxyribonucleotides from the corresponding ribonucleotides.
216834_at	TFPI2	tissue factor pathway inhibitor 2	2.8	1.2E-01	Proteinase inhibitor	May regulated plasmin-mediated matrix remodeling. Inhibits trypsin, plasmin, factor VIIa/tissue factor
207602_at	C10orf99	chromosome 10 open reading frame 99	2.7	0	uncharacterized protein	Unknown function
205513_at	GPR183	Epstein-Barr virus induced gene 2 (lymphocyte- specific G protein-coupled receptor)	2.7	9.5E-02	Receptor	Unknown function
221601_s_at	CARHSP1	calcium regulated heat stable protein 1, 24kDa	2.6	0	Heat stable protein	Binds mRNA and regulates the stability of target mRNA.
38037_at	FAIM3	Fas apoptotic inhibitory molecule 3	2.6	5.6E-02	Receptor	Antiapoptotic, Protects cells from FAS-, TNF alpha- and FADD-induced apoptosis, Fc receptor for IgM
202340_x_at	CD274	CD274 molecule (programmed cell death 1 ligand 1)	2.6	0	Receptor ligand	Ligand for PD-1 receptor on CD8+ T cells. Transmits inhibitory signal to reduces proliferation of T-cells
216615_s_at	MMP12	matrix metallopeptidase 12 (macrophage elastase)	2.6	7.7E-02	Matrix metalloprotease	Degrades soluble and insoluble elastin, involved in tissue injury and remodeling
205419_at	VMP1	vacuole membrane protein 1 (TMEM49)	2.6	0	Stress-induced protein	Formation of cell junctions, involved in autophagy, contains MIR21 within the gene sequence
205428_s_at	HTR3A	5-hydroxytryptamine (serotonin) receptor 3A	2.6	1.0E-01	ligand-gated ion channel receptor	Receptor for serotonin
203434_s_at	UBE2S	ubiquitin-conjugating enzyme E2S	2.5	0	ubiquitin-conjugating enzyme	Ubiquitination and subsequent degradation of VHL, resulting in an accumulation of HIF1A.

204580_at	ITGB6	integrin, beta 6	2.5	0	Integrin	receptor for fibronectin and cytotactin, highly expressed in poorly healing human wounds
203108_at	TYMP	endothelial cell growth factor 1 (platelet-derived)	2.5	0	angiogenic factor	Angiogenic activity and chemotactic activity Catalyzes reversible phosphorolysis of thymidine.
213524_s_at	CALB2	2 calbindin 2, 29kDa (calretinin)		9.2E-02	intracellular calcium- binding protein	Intracellular calcium buffering
211506_s_at	SELE	selectin E (endothelial adhesion molecule 1)	2.5	0	Selectin	Cell-surface glycoprotein having a role in immunoadhesion
205681_at	DSG3	desmoglein 3 (pemphigus vulgaris antigen)	2.4	0	Desmoglein family member	Component of desmosomes, expressed in proliferating basal layers of epidermis
209924_at	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	2.4	0	ADAMTS protein family member	Cleaves aggrecan, may be involved in keratinocyte differentiation and migration during wound healing
213060_s_at	CCNB1	cyclin B1	2.4	0	Regulatory protein involved in mitosis	Essential for the control of the cell cycle at the G2/M (mitosis) transition
209278_s_at	S100A2	S100 calcium binding protein A2	2.4	0	S100 protein,	Toumor supressor, involved in keratinocyte differentiation
205943_at	CD163	CD163 molecule	2.4	0	Scavenger receptor	Recognizes gram positive and gram negative bacteria
218876 at	ELN	D elastin	ownregulated	9.8E-02	Extracellular matrix	Inhibits terminal differentiation of keratinocytes
218870_at	ELN	Clastiii	-4.3	9.6E-02	protein	minions terminal differentiation of keratinocytes
239183_at	WIF1	WNT inhibitory factor 1	-3.5	1.6E-01	Signal inhibitor	Inhibits WNT proteins and WNT signalling. Tumor supressor
203824_at	OMD	osteomodulin	-3.2	8.1E-02	Proteoglycan, Extracellular matrix protein	May be involved in mineralization process
228241_at	ANGPTL1	angiopoietin-like 1	-3.1	0	VEGF family member	Unknown function
212670_at	TNN	tenascin N	-3.0	2.0E-01	Extracellular matrix glycoprotein	May inhibit neuronal outgrowth
239349_at	BTC	betacellulin	-2.8	7.7E-02	Growth factor, member of the EGF family	Ligand for the EGF receptor
205907_s_at	AGR3	breast cancer membrane protein 11	-2.6	0	Membrane protein	Highly upregulated in ovarian tumors
241412_at	TSPAN8	tetraspanin 8	-2.5	0	Cell surface glycoprotein	Is known to complex with integrins, may mediate signal transduction events that play a role in the regulation of cell development, activation, growth and motility
205200_at	CLEC3B	C-type lectin domain family 3, member B (tetranectin)	-2.4	1.6E-01	C-type lectin	Binds to plasminogen and enhances plasminogen activation. Wound healing is delayed in tetranectin-null mice
204712_at	TNXA	tenascin XA	-2.4	2.5E-01	Pseudogene	
215271_at	C1QTNF7	C1q and tumor necrosis factor related protein 7	-2.4	8.6E-02	Receptor ligand	Unknown function
216333_x_at	TPPP3	tubulin polymerization-promoting protein family member 3	-2.4	0	Tubulin polymerization- promoting protein	Binds tubulin and has microtubule bundling activity. May play a role in cell proliferation and mitosis

List of the 100 most enriched transcription factor binding sites in the promoter regions of the 100 most differentially expressed genes between wounded and non-wounded skin during the proliferative phase of wound healing. The list of 100 genes used for analysis was acquired by a complete re-analysis of the data set previously published by Roupé et al 2009 (see Materials and Methods).

Transcription	No. of	Significant	% of motif presence in no. of
factor	hits	Enrichment (PE)	promoters
FOXO4	720	1.00E-05	100
FOXO1	728	1.00E-05	100
BCL6	1382	1.00E-05	100
STAT5A	1774	1.00E-05	100
SRY	959	1.00E-05	100
STAT6	1375	1.00E-05	100
AP1	2450	1.00E-05	98.97959
STAT4	599	1.00E-05	96.938774
HNF3	777	1.00E-05	96.938774
CEBPA	160	1.00E-05	74.4898
ZTA	92	1.00E-05	59.183674
GEN	1877	2.00E-05	100
ELF1	307	2.00E-05	94.89796
HMGIY	944	3.00E-05	100
FAC1	80	1.00E-04	55.10204
IPF1	348	1.50E-04	84.69388
AIRE	27	1.50E-04	20.408163
HNF3B	250	4.90E-04	80.61224
HFH3	172	5.80E-04	75.5102
HNF3ALPHA	200	6.40E-04	81.63265
CDXA	1200	6.60E-04	97.95918
GFI1	602	7.10E-04	94.89796
NFAT	1465	7.50E-04	100
LEF1	850	9.50E-04	100
CEBP	800	9.70E-04	100
BRN2	181	0.00108	74.4898
BACH2	45	0.00127	37.7551
FOXJ2	161	0.00148	73.46939
SOX17	344	0.00153	87.755104
IRF	163	0.00157	50
TBP	1039	0.0016	94.89796
CIZ	870	0.0021	95.918365
MTATA	65	0.00226	47.959183
TATA	378	0.00238	86.734695
GR	745	0.00246	94.89796
ETS	1281	0.00248	100
XVENT1	120	0.00251	62.2449

CEBPGAMMA	27	0.00321	23.469387
TCF11	265	0.00334	91.83673
IRF1	60	0.0039	40.816326
MEIS1	383	0.00395	98.97959
SOX9	202	0.00404	81.63265
LPOLYA	275	0.0041	84.69388
FREAC2	102	0.00416	50
_DSPOLYA	83	0.00454	57.142857
RBPJK	274	0.00476	87.755104
TEF	19	0.005	14.285714
PEA3	668	0.00567	100
ETS1	197	0.00608	82.65306
CEBPDELTA	88	0.00694	56.122448
DBP	467	0.00718	96.938774
MAF	84	0.00718	60.204082
CAP	406	0.00723	98.97959
PAX2	509	0.00793	97.95918
XFD1	52	0.00823	43.877552
TFE			
	117 265	0.00957	64.28571
PU1	365	0.01076	90.81633
FREAC7	224	0.01089	76.53061
NKX25	723	0.01109	96.938774
POU6F1	7	0.01283	7.142857
GATA1	1919	0.0144	100
BLIMP1	22	0.01546	22.44898
SOX5	107	0.01585	65.30612
AR	497	0.01696	98.97959
TAL1ALPHAE47	53	0.01791	37.7551
STAT	164	0.01909	74.4898
NKX61	29	0.01987	23.469387
AREB6	1745	0.02012	100
FOXO3	188	0.02122	75.5102
E4BP4	14	0.02214	12.244898
PR	480	0.02277	94.89796
RUSH1A	235	0.02335	79.591835
NFE2	17	0.02377	15.306123
DTYPEPA	9	0.02398	9.183674
LMO2COM	522	0.02436	100
LEF1TCF1	204	0.02441	87.755104
TEF1	122	0.02584	72.44898
OG2	472	0.02619	88.77551
S8	454	0.02687	88.77551
	20	0.02692	18.367348
BACH1	_0		
BACH1 NKX62	446	0.03088	88.77551
		0.03088 0.03199	88.77551 100

SOX10	597	0.03297	96.938774
TAL1BETAE47	55	0.03396	39.795918
HNF1	47	0.03425	22.44898
NKX3A	64	0.03475	37.7551
GFI1B	37	0.03478	30.612246
TFIIA	25	0.03559	21.428572
HLF	16	0.0371	15.306123
XFD2	73	0.03779	52.040817
GATA3	465	0.03784	95.918365
NKX32	492	0.03789	98.97959
HNF6	49	0.03795	40.816326
CHOP	58	0.03806	45.918365
CDX	34	0.03974	28.571428
HFH1	48	0.04116	32.65306
TGIF	179	0.04254	83.67347
XPF1	51	0.04265	41.836735

The list of genes is adapted from the list published by Kennedy-Crispin et al 2011. Since it originally contained several duplicates and 2 genes also were excluded from analysis the resulting list used for analysis contained the 88 genes listed below. Genes with increased expression are colored red and genes with decreased expression are colored blue. The 46 genes containing co-occurring FOXO1, FOXO4 and FOXO3 transcription factor binding sites are marked with *.

Gene symbol	Description
DSC2	desmocollin 2
LIPG*	lipase, endothelial
ZBTB10*	zinc finger and BTB domain containing 10
GABPB1*	GA binding protein transcription factor, beta subunit 1
SOX9	SRY-box 9
IQCG*	IQ motif containing G
UPP1	uridine phosphorylase 1
CAMK2N1*	calcium/calmodulin-dependent protein kinase II inhibitor 1
GADD45B	growth arrest and DNA-damage-inducible, beta
CXCL3*	chemokine (C-X-C motif) ligand 3
DUSP10	dual specificity phosphatase 10
PTP4A1	Protein tyrosine phosphatase type IVA, member 1
CXCL2*	chemokine (C-X-C motif) ligand 2
SOD2*	Superoxide dismutase 2, mitochondrial
SERPINB4*	serpin peptidase inhibitor, clade B (ovalbumin), member 4
BHLHE40	basic helix-loop-helix family, member e40
HS3ST1*	heparan sulfate (glucosamine) 3-O-sulfotransferase 1
ARL14*	ADP-ribosylation factor-like 14
EGR4	early growth response 4
INHBA	inhibin, beta A (activin A, activin AB alpha polypeptide)
TGFB2*	Transforming growth factor, beta 2
CXCR4	chemokine (C-X-C motif) receptor 4
FOSL1	FOS-like antigen 1
GPRC5A*	G protein-coupled receptor, family C, group 5, member A
IL13RA2	interleukin 13 receptor, alpha 2
PLAUR*	plasminogen activator, urokinase receptor
RHCG*	Rh family, C glycoprotein
NEDD4L*	Neural precursor cell expressed, developmentally down-regulated 4-like
ALDH1A3	aldehyde dehydrogenase 1 family, member A3
IL1RL1	interleukin 1 receptor-like 1
MMP1*	matrix metallopeptidase 1 (interstitial collagenase)
IL8*	interleukin 8
CCL20*	chemokine (C-C motif) ligand 20
MMP3*	matrix metallopeptidase 3 (stromelysin 1, progelatinase)
APOBEC3A	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A
PHLDA1*	pleckstrin homology-like domain, family A, member 1
KRT6B*	keratin 6B

ISG20* interferon stimulated exonuclease gene 20kDa

PPP1R15A protein phosphatase 1, regulatory (inhibitor) subunit 15A

ZNF165* zinc finger protein 165

PDE4B* phosphodiesterase 4B, cAMP-specific

AREG Amphiregulin (schwannoma-derived growth factor)

HBEGF heparin-binding EGF-like growth factor HSPA6 heat shock 70kDa protein 6 (HSP70B')

DHRS9* dehydrogenase/reductase (SDR family) member 9

KRT6A* Keratin 6A

S100A9 S100 calcium binding protein A9 (calgranulin B)
PMAIP1* phorbol-12-myristate-13-acetate-induced protein 1

ATF3 activating transcription factor 3

JUN*v-jun sarcoma virus 17 oncogene homolog (avian)TNFAIP3tumor necrosis factor, alpha-induced protein 3

APOBEC3B apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B

TM4SF1* transmembrane 4 L six family member 1

\$100A8* \$100 calcium binding protein A8 (calgranulin A)

FCGBP Fc fragment of IgG binding protein arachidonate 5-lipoxygenase

CMAH cytidine monophosphate-N-acetylneuraminic acid hydroxylase

CD1A* CD1a molecule

CD207 molecule, langerin

FCER1A* Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide

NHLH2* nescient helix loop helix 2

GPLD1* glycosylphosphatidylinositol specific phospholipase D1

ANK3* ankyrin 3, node of Ranvier (ankyrin G)

collagen, type XXI, alpha 1 /// collagen, type XXI, alpha 1

C14orf132 chromosome 14 open reading frame 132

FRY furry homolog (Drosophila) ZNF652 zinc finger protein 652

EF-hand domain (C-terminal) containing 2

UNC93A* unc-93 homolog A (C. elegans)

ANXA9 annexin A9

C1orf68* chromosome 1 open reading frame 68
SLURP1 secreted LY6/PLAUR domain containing 1

LAMB4* laminin, beta 4
ASPN asporin (LRR class 1)

B-cell CLL/lymphoma 11A (zinc finger protein)

EXPH5* Exophilin 5

SLC16A7* solute carrier family 16, member 7 (monocarboxylic acid transporter 2)

HLA-DPB1 major histocompatibility complex, class II, DP beta 1

CTSH cathepsin H

MXRA5 matrix-remodelling associated 5
AZGP1 alpha-2-glycoprotein 1, zinc
LCE2B* late cornified envelope 2B

HLA-DPA1* major histocompatibility complex, class II, DP alpha 1

ARG1 arginase, liver

HOXA9 homeobox A9

CDHR1 cadherin-related family member 1

FLG* filaggrin

LOR* loricrin

List of the 100 most enriched transcription factor binding sites in the promoter regions of the most differentially expressed genes between wounded and non-wounded epidermis published by Kennedy-Crispin et al 2011.

AP1 1927 1.00E-04 97.53086 FOXO4 566 1.90E-04 97.53086 FOXO1 566 2.10E-04 97.53086 FAC1 67 2.90E-04 54.320988 SRY 748 3.10E-04 100 ZTA 68 5.20E-04 55.555557 XPF1 53 6.10E-04 69.1358 HNF3ALPHA 169 8.40E-04 100 CDXA 1000 0.0012 98.765434 GR 633 0.00145 96.296295 HNF3 1327 0.00246 100 MAF 74 0.00305 61.728394 HFH3 138 0.00377 69.1358 TBP 850 0.00382 96.296295 P53 162 0.00426 77.77778 PR 421 0.00426 77.77778 PR 421 0.00426 96.296295 STAT4 441 0.0044 97.53086 XVENT1 99 0.00481 56.790123 HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	Transcription	No. of	Significant	% of motif presence in no. of
FOXO4 566 1.90E-04 97.53086 FOXO1 566 2.10E-04 97.53086 FAC1 67 2.90E-04 54.320988 SRY 748 3.10E-04 100 ZTA 68 5.20E-04 55.555557 XPF1 53 6.10E-04 69.1358 HNF3ALPHA 169 8.40E-04 75.30864 BCL6 1056 8.60E-04 100 CDXA 1000 0.0012 98.765434 GR 633 0.00145 96.296295 HNF3 595 0.00164 90.12346 STAT5A 1327 0.00246 100 MAF 74 0.00305 61.728394 HFH3 138 0.00377 69.1358 TBP 850 0.00382 96.296295 P53 162 0.00426 77.77778 PR 421 0.00426 96.296295 STAT4 441 0.0044 97.53086 XVENT1 99 0.00481 56.790123 HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	factor	hits	Enrichment (PE)	promoters
FOXO1 566 2.10E-04 97.53086 FAC1 67 2.90E-04 54.320988 SRY 748 3.10E-04 100 ZTA 68 5.20E-04 55.555557 XPF1 53 6.10E-04 69.1358 HNF3ALPHA 169 8.40E-04 75.30864 BCL6 1056 8.60E-04 100 CDXA 1000 0.0012 98.765434 GR 633 0.00145 96.296295 HNF3 595 0.00164 90.12346 STAT5A 1327 0.00246 100 MAF 74 0.00305 61.728394 HFH3 138 0.00377 69.1358 TBP 850 0.00382 96.296295 P53 162 0.00426 77.77778 PR 421 0.00426 96.296295 STAT4 441 0.0044 97.53086 XVENT1 99 0.00481 56.790123 HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259				
FAC1 67 2.90E-04 54.320988 SRY 748 3.10E-04 100 ZTA 68 5.20E-04 55.555557 XPF1 53 6.10E-04 50.617283 AP3 122 7.30E-04 69.1358 HNF3ALPHA 169 8.40E-04 75.30864 BCL6 1056 8.60E-04 100 CDXA 1000 0.0012 98.765434 GR 633 0.00145 96.296295 HNF3 595 0.00164 90.12346 STAT5A 1327 0.00246 100 MAF 74 0.00305 61.728394 HFH3 138 0.00377 69.1358 TBP 850 0.00382 96.296295 P53 162 0.00426 77.77778 PR 421 0.00426 96.296295 STAT4 441 0.0044 97.53086 XVENT1 99 0.00483 19.753086				
SRY 748 3.10E-04 100 ZTA 68 5.20E-04 55.555557 XPF1 53 6.10E-04 50.617283 AP3 122 7.30E-04 69.1358 HNF3ALPHA 169 8.40E-04 75.30864 BCL6 1056 8.60E-04 100 CDXA 1000 0.0012 98.765434 GR 633 0.00145 96.296295 HNF3 595 0.00164 90.12346 STAT5A 1327 0.00246 100 MAF 74 0.00305 61.728394 HFH3 138 0.00377 69.1358 TBP 850 0.00382 96.296295 P53 162 0.00426 77.77778 PR 421 0.00426 96.296295 STAT4 441 0.0044 97.53086 XVENT1 99 0.00481 56.790123 HLF 17 0.00485 85.18519 <				
ZTA 68 5.20E-04 55.55557 XPF1 53 6.10E-04 50.617283 AP3 122 7.30E-04 69.1358 HNF3ALPHA 169 8.40E-04 75.30864 BCL6 1056 8.60E-04 100 CDXA 1000 0.0012 98.765434 GR 633 0.00145 96.296295 HNF3 595 0.00164 90.12346 STAT5A 1327 0.00246 100 MAF 74 0.00305 61.728394 HFH3 138 0.00377 69.1358 TBP 850 0.00382 96.296295 P53 162 0.00426 77.77778 PR 421 0.00426 77.77778 PR 421 0.00446 97.53086 XVENT1 99 0.00481 56.790123 HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197	FAC1	67	2.90E-04	
XPF1 53 6.10E-04 50.617283 AP3 122 7.30E-04 69.1358 HNF3ALPHA 169 8.40E-04 75.30864 BCL6 1056 8.60E-04 100 CDXA 1000 0.0012 98.765434 GR 633 0.00145 96.296295 HNF3 595 0.00164 90.12346 STAT5A 1327 0.00246 100 MAF 74 0.00305 61.728394 HFH3 138 0.00377 69.1358 TBP 850 0.00382 96.296295 P53 162 0.00426 77.77778 PR 421 0.00426 77.77778 PR 421 0.00446 97.53086 XVENT1 99 0.00481 56.790123 HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447	SRY			100
AP3 122 7.30E-04 69.1358 HNF3ALPHA 169 8.40E-04 75.30864 BCL6 1056 8.60E-04 100 CDXA 1000 0.0012 98.765434 GR 633 0.00145 96.296295 HNF3 595 0.00164 90.12346 STAT5A 1327 0.00246 100 MAF 74 0.00305 61.728394 HFH3 138 0.00377 69.1358 TBP 850 0.00382 96.296295 P53 162 0.00426 77.77778 PR 421 0.00426 96.296295 STAT4 441 0.0044 97.53086 XVENT1 99 0.00481 56.790123 HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	ZTA	68	5.20E-04	55.55557
HNF3ALPHA 169 8.40E-04 75.30864 BCL6 1056 8.60E-04 100 CDXA 1000 0.0012 98.765434 GR 633 0.00145 96.296295 HNF3 595 0.00164 90.12346 STAT5A 1327 0.00246 100 MAF 74 0.00305 61.728394 HFH3 138 0.00377 69.1358 TBP 850 0.00382 96.296295 P53 162 0.00426 77.77778 PR 421 0.00426 96.296295 STAT4 441 0.0044 97.53086 XVENT1 99 0.00481 56.790123 HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	XPF1	53	6.10E-04	50.617283
BCL6 1056 8.60E-04 100 CDXA 1000 0.0012 98.765434 GR 633 0.00145 96.296295 HNF3 595 0.00164 90.12346 STAT5A 1327 0.00246 100 MAF 74 0.00305 61.728394 HFH3 138 0.00377 69.1358 TBP 850 0.00382 96.296295 P53 162 0.00426 77.77778 PR 421 0.00426 96.296295 STAT4 441 0.0044 97.53086 XVENT1 99 0.00481 56.790123 HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	AP3	122	7.30E-04	69.1358
CDXA 1000 0.0012 98.765434 GR 633 0.00145 96.296295 HNF3 595 0.00164 90.12346 STAT5A 1327 0.00246 100 MAF 74 0.00305 61.728394 HFH3 138 0.00377 69.1358 TBP 850 0.00382 96.296295 P53 162 0.00426 77.77778 PR 421 0.00426 96.296295 STAT4 441 0.0044 97.53086 XVENT1 99 0.00481 56.790123 HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	HNF3ALPHA	169	8.40E-04	75.30864
GR 633 0.00145 96.296295 HNF3 595 0.00164 90.12346 STAT5A 1327 0.00246 100 MAF 74 0.00305 61.728394 HFH3 138 0.00377 69.1358 TBP 850 0.00382 96.296295 P53 162 0.00426 77.77778 PR 421 0.00426 96.296295 STAT4 441 0.0044 97.53086 XVENT1 99 0.00481 56.790123 HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	BCL6	1056	8.60E-04	100
HNF3 595 0.00164 90.12346 STAT5A 1327 0.00246 100 MAF 74 0.00305 61.728394 HFH3 138 0.00377 69.1358 TBP 850 0.00382 96.296295 P53 162 0.00426 77.77778 PR 421 0.00426 96.296295 STAT4 441 0.0044 97.53086 XVENT1 99 0.00481 56.790123 HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	CDXA	1000	0.0012	98.765434
STAT5A 1327 0.00246 100 MAF 74 0.00305 61.728394 HFH3 138 0.00377 69.1358 TBP 850 0.00382 96.296295 P53 162 0.00426 77.77778 PR 421 0.00426 96.296295 STAT4 441 0.0044 97.53086 XVENT1 99 0.00481 56.790123 HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	GR	633	0.00145	96.296295
MAF 74 0.00305 61.728394 HFH3 138 0.00377 69.1358 TBP 850 0.00382 96.296295 P53 162 0.00426 77.77778 PR 421 0.00426 96.296295 STAT4 441 0.0044 97.53086 XVENT1 99 0.00481 56.790123 HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	HNF3	595	0.00164	90.12346
HFH3 138 0.00377 69.1358 TBP 850 0.00382 96.296295 P53 162 0.00426 77.77778 PR 421 0.00426 96.296295 STAT4 441 0.0044 97.53086 XVENT1 99 0.00481 56.790123 HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	STAT5A	1327	0.00246	100
TBP 850 0.00382 96.296295 P53 162 0.00426 77.77778 PR 421 0.00426 96.296295 STAT4 441 0.0044 97.53086 XVENT1 99 0.00481 56.790123 HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	MAF	74	0.00305	61.728394
P53 162 0.00426 77.77778 PR 421 0.00426 96.296295 STAT4 441 0.0044 97.53086 XVENT1 99 0.00481 56.790123 HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	HFH3	138	0.00377	69.1358
PR 421 0.00426 96.296295 STAT4 441 0.0044 97.53086 XVENT1 99 0.00481 56.790123 HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	TBP	850	0.00382	96.296295
STAT4 441 0.0044 97.53086 XVENT1 99 0.00481 56.790123 HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	P53	162	0.00426	77.77778
XVENT1 99 0.00481 56.790123 HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	PR	421	0.00426	96.296295
HLF 17 0.00483 19.753086 SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	STAT4	441	0.0044	97.53086
SOX9 170 0.00485 85.18519 FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	XVENT1	99	0.00481	56.790123
FREAC2 86 0.00516 61.728394 HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	HLF	17	0.00483	19.753086
HNF3B 197 0.0052 77.77778 GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	SOX9	170	0.00485	85.18519
GEN 1447 0.00537 100 HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	FREAC2	86	0.00516	61.728394
HFH4 23 0.00736 24.691359 GATA 461 0.00812 92.59259	HNF3B	197	0.0052	77.77778
GATA 461 0.00812 92.59259	GEN	1447	0.00537	100
	HFH4	23	0.00736	24.691359
GATA6 230 0.00848 92.59259	GATA	461	0.00812	92.59259
57.11.10 250 0.000-10 JE.3JE3J	GATA6	230	0.00848	92.59259
RUSH1A 204 0.00957 83.950615	RUSH1A	204	0.00957	83.950615
POU1F1 52 0.00969 49.382717	POU1F1	52	0.00969	49.382717
BACH2 33 0.01003 33.333332	BACH2	33	0.01003	33.333332
NKX22 32 0.01103 27.160494	NKX22	32	0.01103	27.160494
AIRE 18 0.01276 18.518518	AIRE	18	0.01276	18.518518
HFH8 84 0.01289 56.790123	HFH8	84	0.01289	56.790123
SOX17 273 0.01335 95.06173	SOX17	273	0.01335	95.06173
TFE 96 0.01384 59.25926	TFE	96	0.01384	59.25926
CART1 21 0.01465 22.222221	CART1	21	0.01465	22.22221
DBP 385 0.01494 98.765434	DBP	385	0.01494	98.765434

LPOLYA	222	0.01567	83.950615
STAT6	1048	0.01604	100
BRCA	341	0.01605	96.296295
HNF6	44	0.01622	38.271606
LDSPOLYA	65	0.0176	54.320988
FREAC7	184	0.01825	80.24691
LEF1TCF1	173	0.01844	83.950615
XFD3	23	0.02062	24.691359
ROAZ	2	0.02113	2.4691358
GCNF	3	0.02138	3.7037036
FREAC4	11	0.02341	12.345679
MTATA	49	0.02457	45.679012
XFD1	42	0.02471	43.209877
LEF1	672	0.0248	100
NKX25	593	0.02617	97.53086
ETS1	158	0.02889	88.888885
BACH1	17	0.02984	18.518518
GATA1	1577	0.03079	100
CDPCR3	3	0.03233	3.7037036
SOX5	87	0.03406	64.19753
FOXJ2	122	0.03414	66.666664
HFH1	41	0.03792	41.975307
IPF1	251	0.03837	83.950615
CEBPB	131	0.03994	72.83951
MMEF2	57	0.03994	46.91358
TEF1	100	0.04279	69.1358
FOXM1	72	0.04327	49.382717
TFIIA	21	0.04358	22.222221
MSX1	31	0.04961	29.62963
CEBP	623	0.05385	100
GATA2	425	0.0549	96.296295
POU6F1	5	0.05509	6.1728396
NFAT	1139	0.05558	100
OG2	384	0.05624	88.888885
PXRRXR	271	0.05635	83.950615
MEIS1	300	0.0566	97.53086
PAX2	405	0.0571	93.82716
TAL1BETAE47	45	0.05752	44.44443
TATA	263	0.05755	81.48148
S8	369	0.05909	88.888885
KAISO	102	0.06064	69.1358
SMAD	742	0.06077	100
GRE	4	0.06097	4.9382715
RBPJK	211	0.06103	87.65432
SOX10	489	0.06179	96.296295
NKX62	363	0.06234	88.888885

GFI1B	30	0.06291	29.62963
CHX10	33	0.06365	29.62963
XFD2	59	0.06499	51.851852
HMGIY	706	0.06794	100
CEBPA	105	0.07179	66.666664
TAL1ALPHAE47	41	0.07331	39.506172
IRF	114	0.07431	49.382717
FOXD3	50	0.08827	40.74074
ELF1	204	0.0897	87.65432
MYB	974	0.09114	97.53086
TCF4	99	0.09133	72.83951
FOXO3	148	0.09215	81.48148
TST1	38	0.09462	30.864197