Supplemental tables

Table S1: Murine gene specific primers used in quantitative real-time PCR.

Primer name	Sequences (3`- 5`)
NRF2	GAG TCG CTT GCC CTG GAT ATC TCA TGG CTG CCT CCA GAG AA
HMOX1	TGA AGC AGG CAT CTG AGG G CGA AGG TGG AAG AGT GGG AG
NQO1	GGC ATC CAG TCC TCC ATC AA GTT AGT CCC TCG GCC ATT GTT
CAT	CAG AGA GCG GAT TCC TGA GAG A CTT TGC CTT GGA GTA TCT GGT GAT
SOD1	GAA ACA AGA TGA CTT GGG CAA AG TTA CTG CGC AAT CCC AAT CA
GPX2	GTG GCG TCA CTC TGA GGA ACA CAG TTC TCC TGA TGT CCG AAC TG
TRX	GCT AGA GAA GAT GGT CGC CAA GCA GCA TCC TCG TCC TTG ATC CCC ACA AAC TTG
GSR	TCG GAA TTC ATG CAC GAT CA GGC TCA CAT AGG CAT CCC TTT
iNOS	CCT GGT ACG GGC ATT GCT GCT CAT GCG GCC TCC TTT
eNOS	TCA GCC ATC ACA GTG TTC CC ATA GCC CGC ATA GCG TATC AG
CD31	CTG CCA GTC CGA AAA TGG AAC CTT CAT CCA CCG GGG CTA TC
KGF (FGF7)	ACC TGA GGA TTG ACA AAC GAG G CCA CGG TCC TGA TTT CCA TGA
bFGF (FGF2)	TCC AGT TGG TAT GTG GCA CTG A CAG TAT GGC CTT CTG TCC AGG TC
COX2	TGC CTG GTC TGA TGA TGT ATG CCA AGT AGT CGC ACA CTC TGT TGT GCT
Artn1	CCC TAG CTG TTC TAG CCC TG AGG GTT CTT TCG CTG CAC AA
Edn1	TTT CCC GTG ATC TTC TCT CTG C CTG AGT TCG GCT CCC AAG AC
CTNNB1	CCC AGT CCT TCA CGC AAG AG CAT CTA GCG TCT CAG GGA ACA
CDH5	CCA CTG CTT TGG GAG CCT T GGC AGG TAG CAT GTT GGG G
IL-1b	GCA ACT GTT CCT GAA CTC AAC T ATC TTT TGG GGT CCG TCA ACT
IL-4	GGT CTC AAC CCC CAG CTA GT GCC GAT GAT CTC TCT CAA GTG AT
IL-6	ATC CAG TTG CCT TCT TGG GAC TGA TAA GCC TCC GAC TTG TGA AGT GGT

MCP-1	TGA TCC CAA TGA GTA GGC TGG AG ATG TCT GGA CCC ATT CCT TCT TG
TNFα	TCT CAT GCA CCA CCA TCA AGG ACT ACC ACT CTC CCT TTG CAG AAC TCA
TGFβ	TTT GGA GCC TGG ACA CAC AGT ACA TGT GTT GGT TGT AGA GGG CAA GGA
p53	AAA GGA TGC CCA TGC TAC AGA GGA AGG ATT GTG TCT CAG CCC TGA AGT
BAX	ACA GCA ATA TGGA GCT GCA GAG GA TGT CCA GCC CAT GAT GGT TCT GAT
CDKN1A	GGA ATT GGA GTC AGG CGC AGA T GAA GAG ACA ACG GCA CAC TTT GCT
GADD45α	TCA GCG CAC GAT CAC TGT C CCA GCA GGC ACA ACA CCA C
GAPDH	CAT GGC CTC CAA GGA GTA AG TGT GAG GGA GAT GCT CAG TG

Table S2: Cold plasma promoted wound closure of dermal full-thickness wounds (**p*<0.05; ***p*<0.01).

	Groups/days	**d3**	**d6**	**d9**	**d12**
♂	ctrl	19+2.1	47+3.0	70+2.7	88+1.8
	3 s	22+4.0	61+3.7**	81+2.7*	92+2.4
	20 s	20+2.9	49+5.1	80+2.9*	90+3.9
	H_2O_2	17+3.8	45+3.2	78+2.5	85+1.6
♀	ctrl	28+3.8	48+3.5	75+3.5	94+1.3
	3 s	48+4.6**	67+4.9**	92+2.2*	97+1.2
	20 s	38+6	61+5.4	86+3.2*	95+2.5
	H_2O_2	33+5.2	57+3.7	87+3.1	97+1.9

Supplemental figures and figure legends

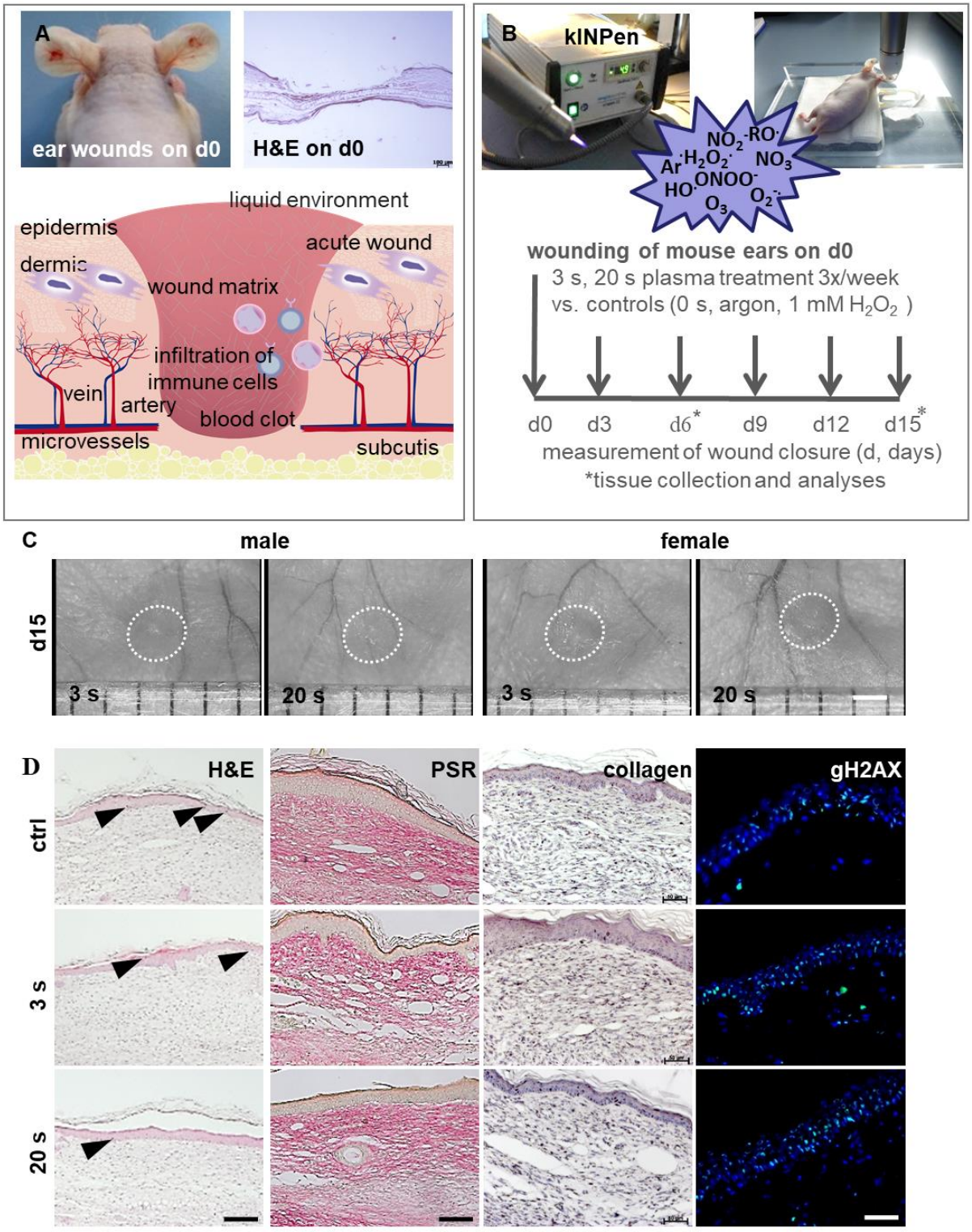

Figure S1. Schematic visualization of skin wound and study design for plasma treatment. (**A**) To analyze the molecular and cellular mechanisms of wound healing, we used an immunocompetent SKH1 mouse model. On both ears, full-thickness circular wounds were created using a microscissor Hematoxylin and eosin (H&E) staining of ear wounds on day 0. Schema of wounds on day 0 (lower figure). (**B**) After wounding, wounds were plasma-treated every third day with a kINPen jet generating

a plethora of reactive species (specified in the star) depending on the treatment time (3 s or 20 s) and compared to placebo (argon gas), H_2O_2 (1 mM), or untreated controls. At days 6 or 15, tissue was removed (dashed line region) for further cellular and molecular biological analyses. (**C**) No scarring was obtained in plasma-treated animals. (**D**) Visualization of sunburn cells (arrow heads) in H&E staining, collagen fibers in picrosirius red and collagen staining, and γH2AX immune fluorescence. Scale bars 1 cm (**C**), 100 µm (**D**); n≥8.

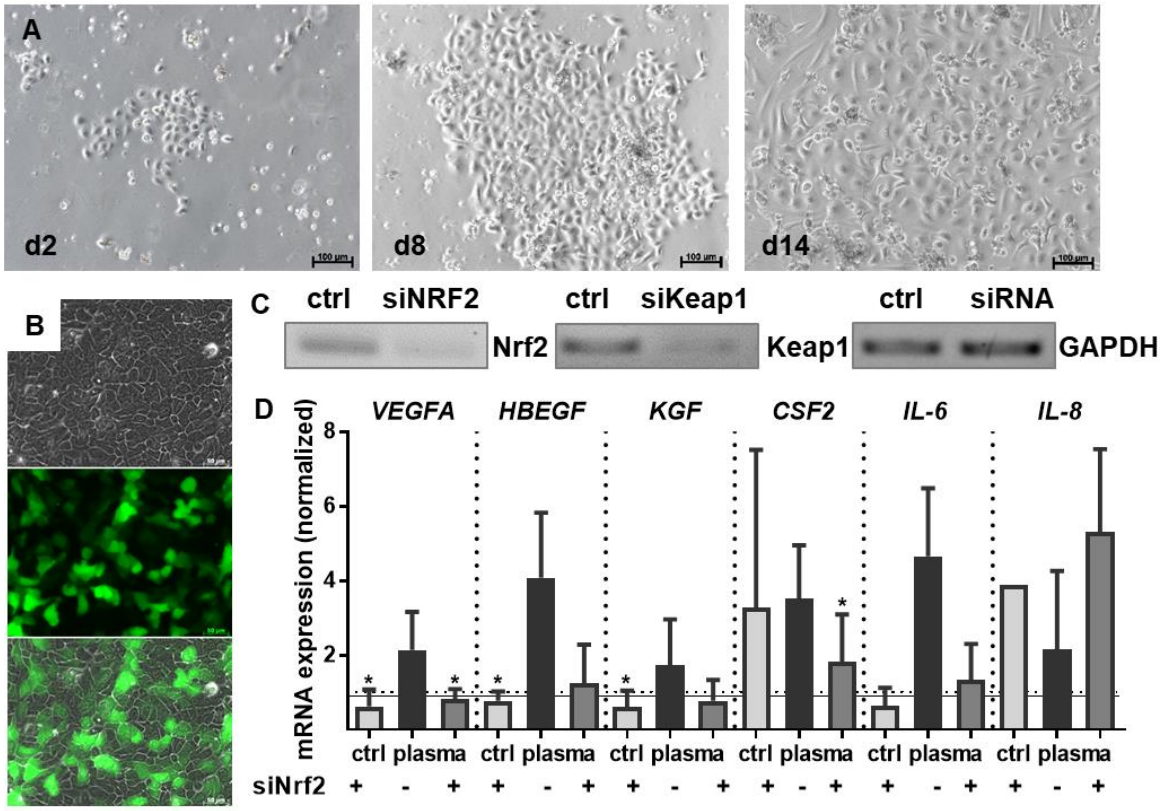

Figure S2. Changes in mRNA expression following siRNA knockdown targeting NRF2 in keratinocytes. (**A**) One representative picture of primary keratinocytes two, eight, or 14 days after isolation from SKH1 mouse skin (n=6). (**B**) Transfection of GFP plasmid into keratinocytes after 72 h. (**C**) NRF2 and KEAP1 expression after siRNA knockdown targeting Nrf2 and Keap1, respectively. (**D**) Cells were transfected with siNRF2 and evaluated *for VEGFA*, *HBEGF*, *KGF*, *CSF2*, and *IL-6/8* mRNA expression by qPCR without (-) and with (+) plasma treatment. The mRNA level of scrambled siRNA (black line) were set to 1.14 and the mock control without siRNA was 1 (dashed line). At least three independent experiments were performed and statistically compared to the scrambled siRNA (*$p < 0.05$). Scale bar 100 µm (**A**), 50 µm (**B**).

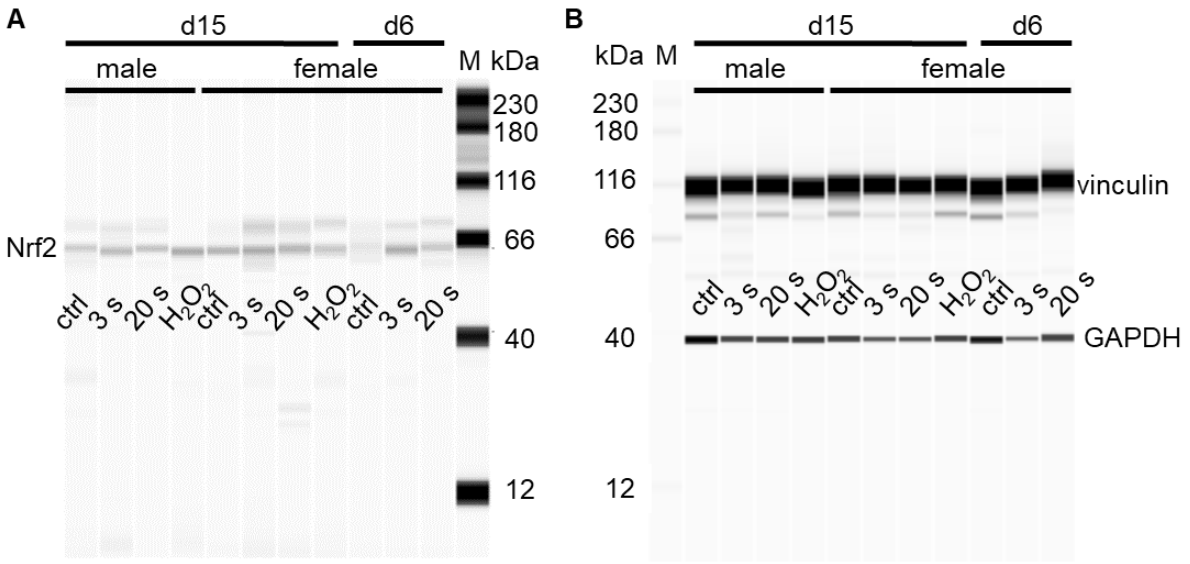

Figure S3. Nrf2 protein expression analysis using Western blot. One representative Western blot is shown for Nrf2 (**A**) and GAPDH/vinculin (**B**) expression ($n \geq 3$).