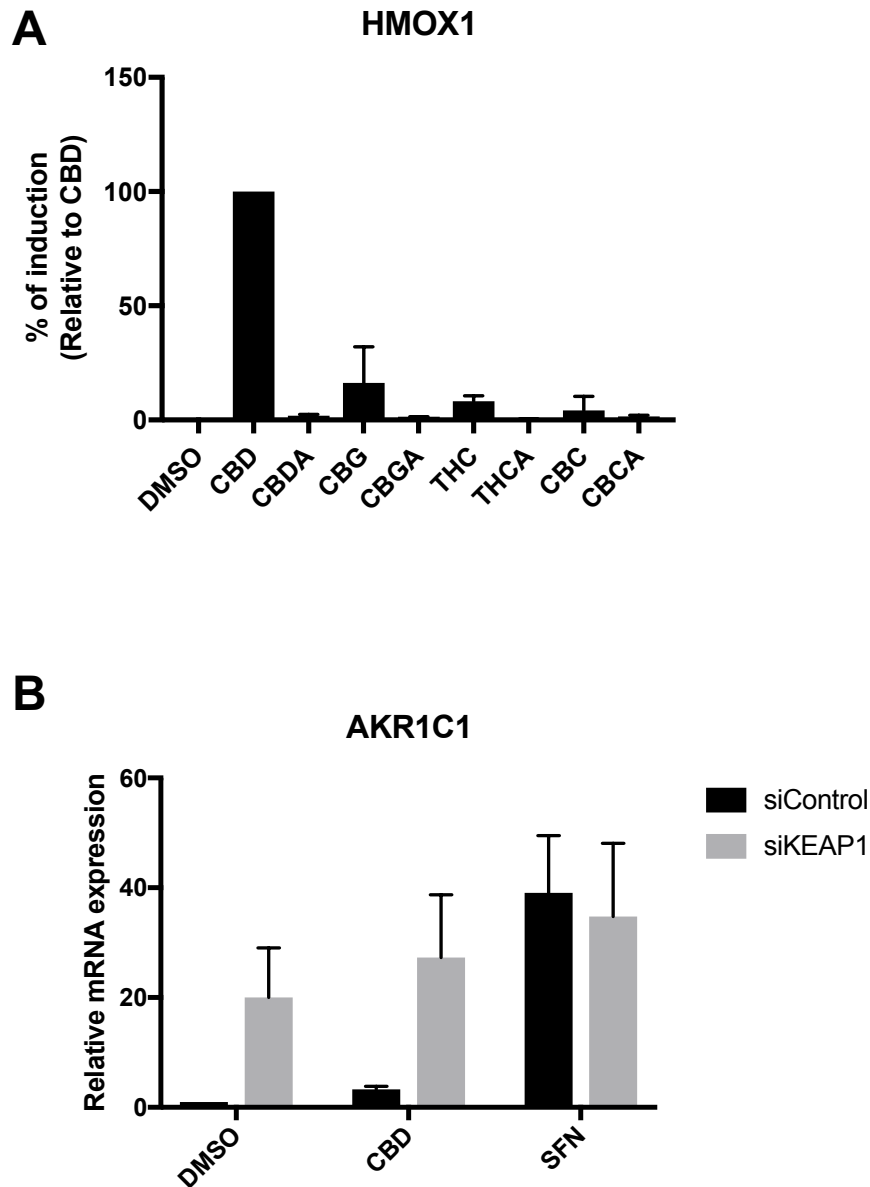


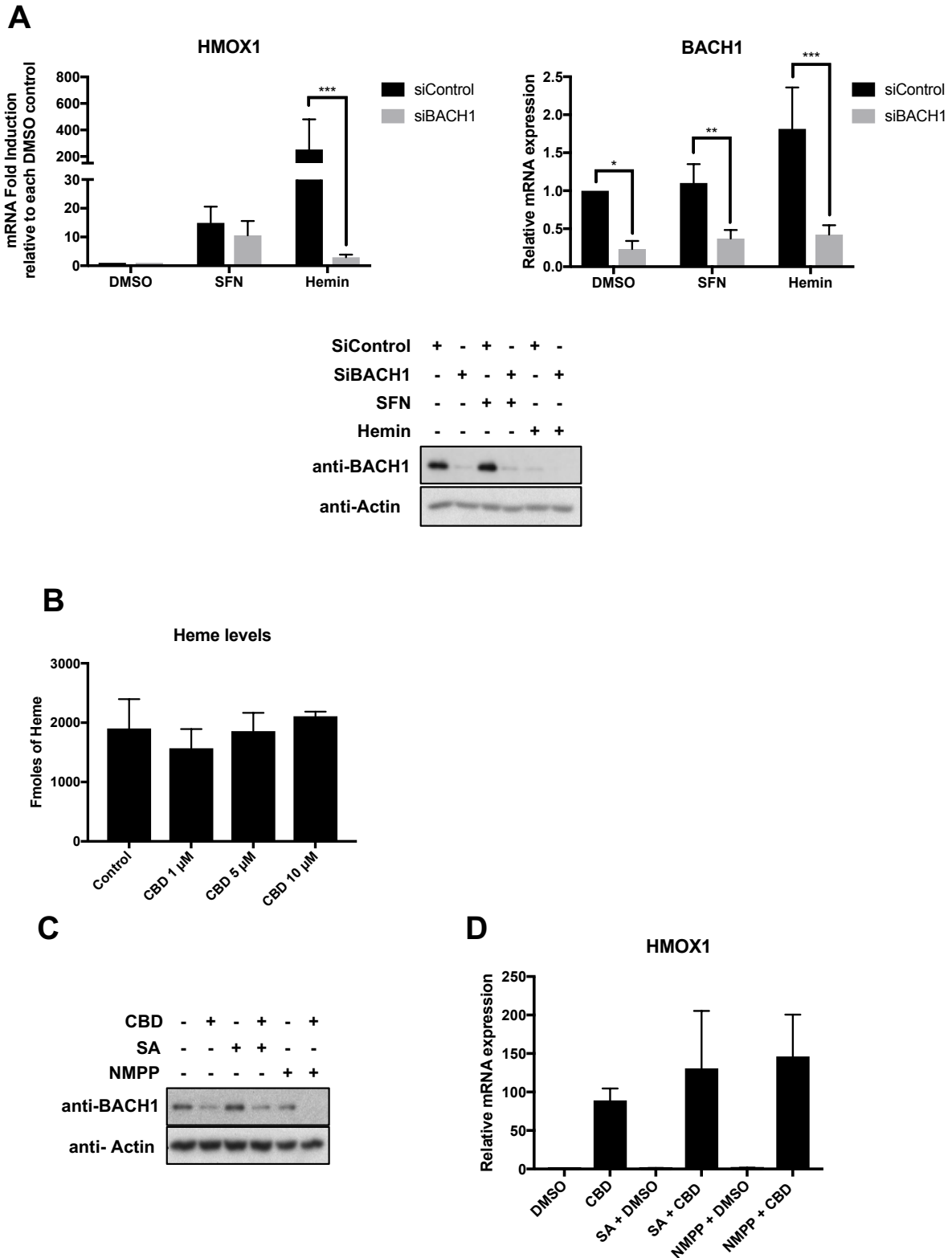
## SUPPLEMENTARY MATERIAL

**Supplementary Table 1: Primers used in this study:**

<b>H-HMOX1 f</b>	5'-CTCAAACCTCCAAAAGCC-3'
<b>H-HMOX1 r</b>	5'-TCAAAAACCACCCCAACCC-3'
<b>H-SQSTM1 f</b>	5'- CTGGGACTGAGAAGGCTCAC-3'
<b>H-SQSTM1 r</b>	5'-GCAGCTGATGGTTTGGAAAT-3'
<b>HPRT1</b>	Hs02800695_m1 HPRT1 TaqMan (s)
<b>HMOX1</b>	Hs01110250_m1 HMOX1 TaqMan (s)
<b>NQO1</b>	Hs01045993_g1 NQO1 TaqMan (m)
<b>AKR1C1</b>	Hs01061917_g1 SQSTM1 TaqMan (s)
<b>AKR1B10</b>	Hs00252524_m1 AKR1B10 TaqMan (s)
<b>SQSTM1</b>	Hs01061917_g1 SQSTM1 TaqMan (s)
<b>IL-1<math>\beta</math> f</b>	5'-CTCCACCTCAATGGACAGAA-3'
<b>IL-1<math>\beta</math> r</b>	5'-GCCGTC TTTCATTACACAGG-3'
<b>TNF<math>\alpha</math> f</b>	5'-CTACTCCCAGGTTCTCTTCAA-3'
<b>TNF<math>\alpha</math> r</b>	5'-GCAGAGAGGAGGTTGACTTTC-3'
<b>IL-6 f</b>	5'-GTATGAACAACGATGATGCACTTG-3'
<b>IL-6 r</b>	5'-ATGGTACTCCAGAAGACCAGAGGA-3'
<b>KRT17 f</b>	5'-GATGGAGCAGAACCAGGAGTAC-3'
<b>KRT 17 r</b>	5'-GGTCTCAAGCATAGGAATGCTGGGG-3'

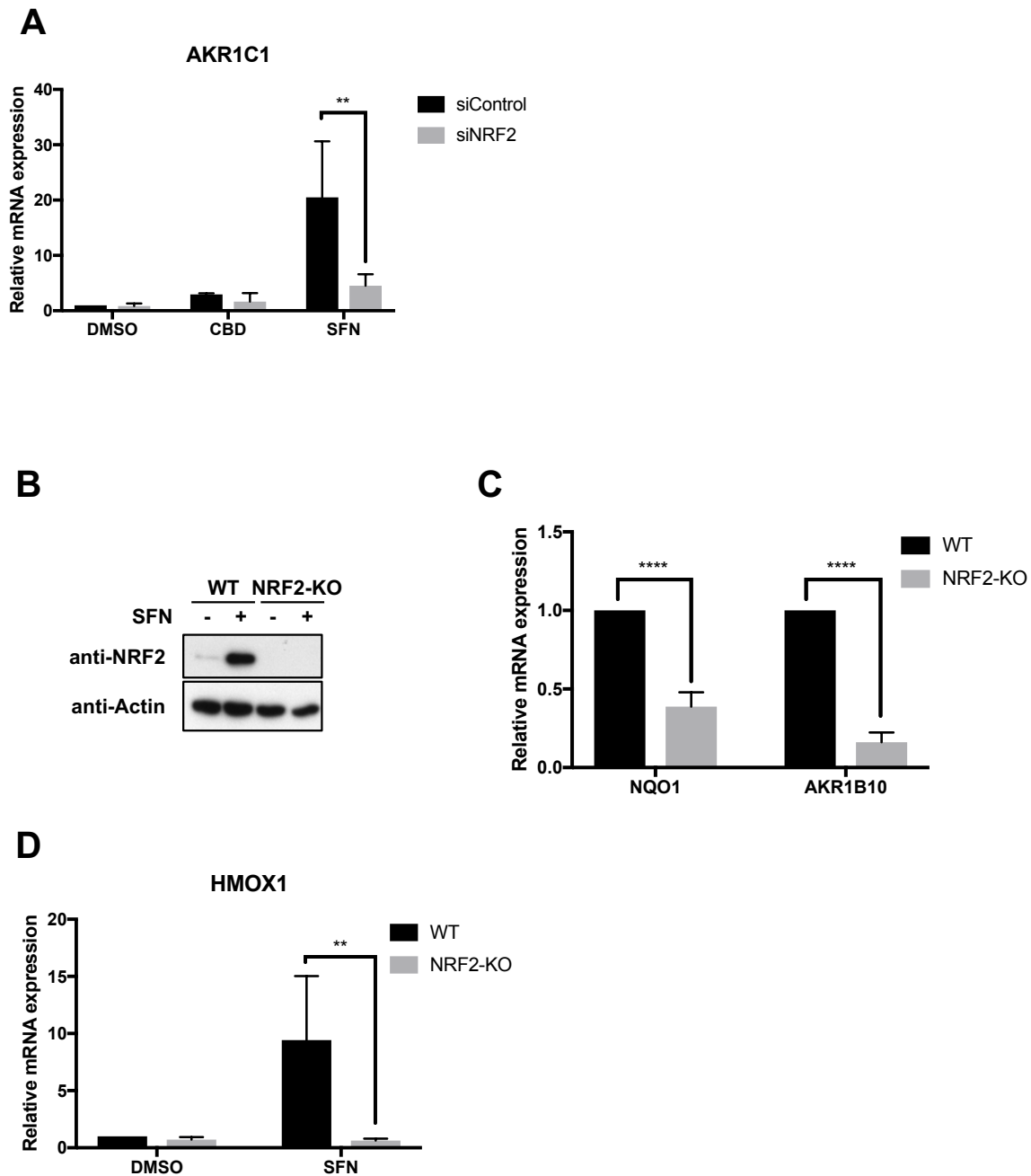


**Figure S1. A)** HaCaT cells were incubated with either DMSO, CBD (10  $\mu$ M) or the indicated cannabinoids (10  $\mu$ M). 16 hours later the mRNA levels for *HMOX1* were quantified as previously described (n=3). **B)** HaCaT cells were transfected with either siControl or siKEAP1. 36 hours later cells were incubated with either DMSO, SFN (5  $\mu$ M), or CBD (10  $\mu$ M) for another 16 hours. The mRNA levels for *AKR1C1* were quantified as previously described (n=3).

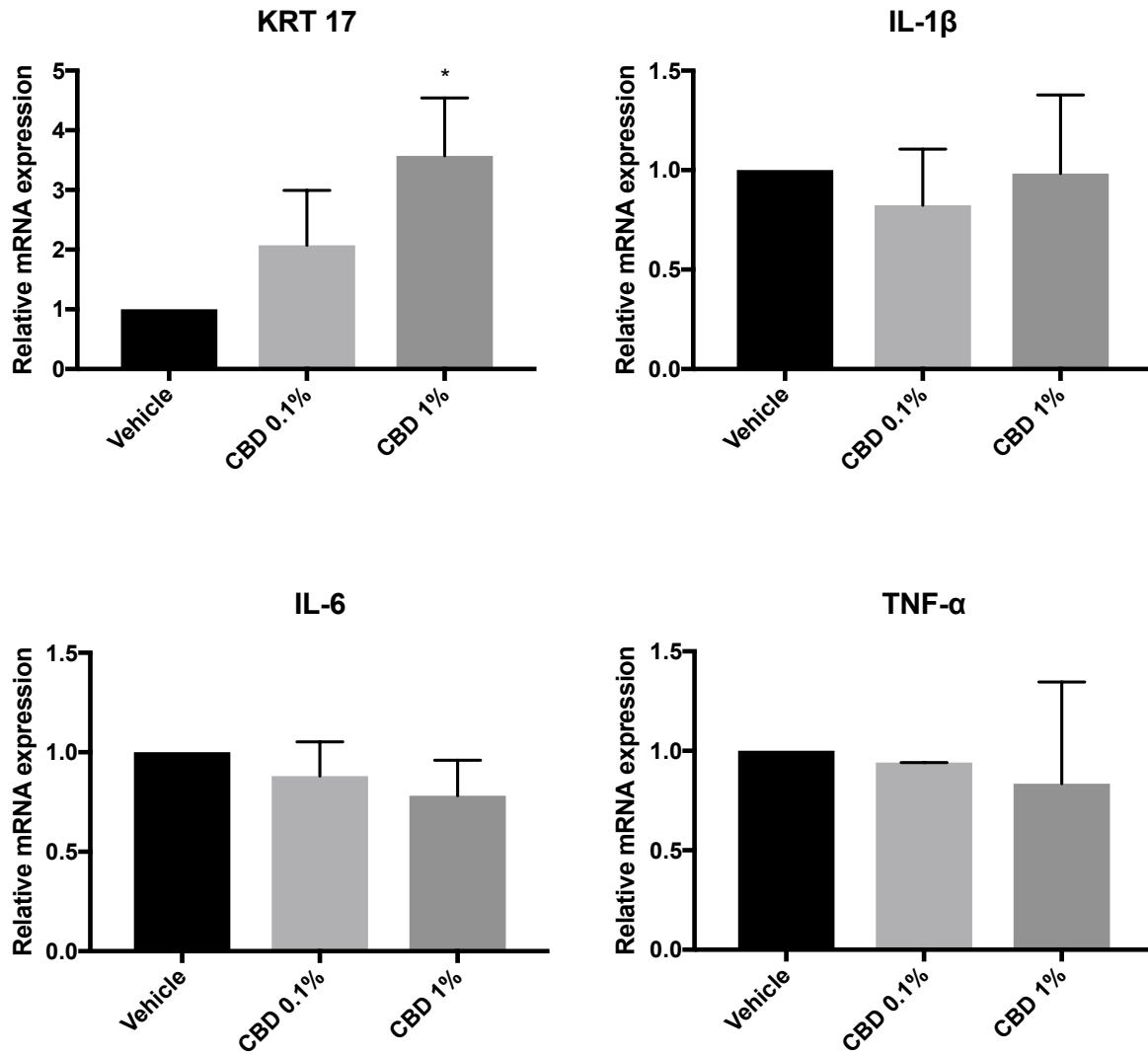


**Figure S2. A)** HaCaT cells were transfected with either siControl or siBACH1. 36 hours later cells were incubated with either DMSO, SFN (5  $\mu$ M) or Hemin (10  $\mu$ M) for another 8 hours. The mRNA levels for *HMOX1* were quantified by real-time PCR using *HPRT1* as an internal control. Data represent means  $\pm$  SD (n=3). To compare the *HMOX1* induction upon treatment in each cell line, the levels of *HMOX1* in each siRNA treated cell line (either siControl SFN/Hemin or siBACH1 SFN/Hemin) was compared against the levels of *HMOX1* in their

own DMSO control sample (set in both cases as 1) (i.e. either siControl DMSO or siBACH1 DMSO respectively) (*upper leftt panel*). To control for the efficiency of the knockdown, the mRNA levels (*upper right panel*) and protein levels (*lower panel*) of BACH1 were analyzed by real-time PCR and western blot respectively. \*P ≤ 0.05, \*\*P ≤ 0.01, \*\*\*P ≤ 0.001, \*\*\*\*P ≤ 0.0001. **B)** HaCaT cells were treated with increasing concentrations of CBD for 3 h and the levels of Heme detected in the supernatants. **C)** HaCaT cells were incubated with either DMSO, Succinylacetone (SA) (1 mM) or N-methyl Protoporphyrin IX (NMPP) (20 μM). 36 hours later CBD (10 μM) was added. Three hours later cells were lysed and levels of BACH1 were analysed by western blot. **D)** HaCaT cells were incubated with either DMSO, Succinylacetone (SA) (1 mM) or N-methyl Protoporphyrin IX (NMPP) (20 μM). 36 hours later CBD (10 μM) was added. 16 hours later the mRNA levels for *HMOX1* were quantified using real-time PCR as previously described (n=3).



**Figure S3.** **A)** HaCaT cells were transfected with either siControl or siNRF2. 36 hours later cells were incubated with either DMSO, SFN (5  $\mu$ M) or CBD (10  $\mu$ M) for another 16 hours. The mRNA levels for *AKR1C1* were quantified using real-time PCR. The data were normalized using HPRT1 as an internal control. Data represent means  $\pm$  SD (n=3) and are expressed relative to the siControl DMSO sample. \*\*P  $\leq$  0.01. **B)** Control (WT) and NRF2-KO HaCaT cells were incubated with either DMSO (-) or SFN (5  $\mu$ M). Three hours later, cells were lysed and the levels of NRF2 were analyzed by western blot. **C)** Control (WT) and NRF2-KO HaCaT cells were collected and the mRNA levels for *NQO1* and *AKR1B10* were quantified using real-time PCR as previously described (n=3). **D)** Control (WT) and NRF2-KO HaCaT cells were incubated with either DMSO (-) or SFN (5  $\mu$ M). Eight hours later, the mRNA levels for *HMOX1* were quantified using real-time PCR as previously indicated (n=3)



**Figure S4.** The mRNA levels for Keratin 17 (*KRT17*), *Interleukin 1 beta (IL1 $\beta$ )*, *Interleukin 16 (IL-6)* and *Tumour Necrosis Factor alpha (TNF $\alpha$ )* in mouse skin after 5 days of treatment with vehicle, CBD 0.1% or CBD 1% were quantified using real-time PCR. The data were normalized using HPRT1 as an internal control. Data represent means  $\pm$  SD (n=3) and are expressed relative to treatment with vehicle. \*P  $\leq$  0.05.