

Supplementary Information

Hypoxic NK cells mediate a trade-off between wound healing and antibacterial defence in the skin

Michał Sobecki^{1,§}, Ewelina Krzywinska^{1, §}, Shunmugam Nagarajan¹, Annette Audigé¹, Khanh Huỳnh¹, Julian Zacharjasz¹, Julien Debbache¹, Yann Kerdiles², Dagmar Gotthardt³, Norihiko Takeda⁴, Joachim Fandrey⁵, Lukas Sommer¹, Veronika Sexl³ and Christian Stockmann^{1*}

Inventory of Supplemental Information

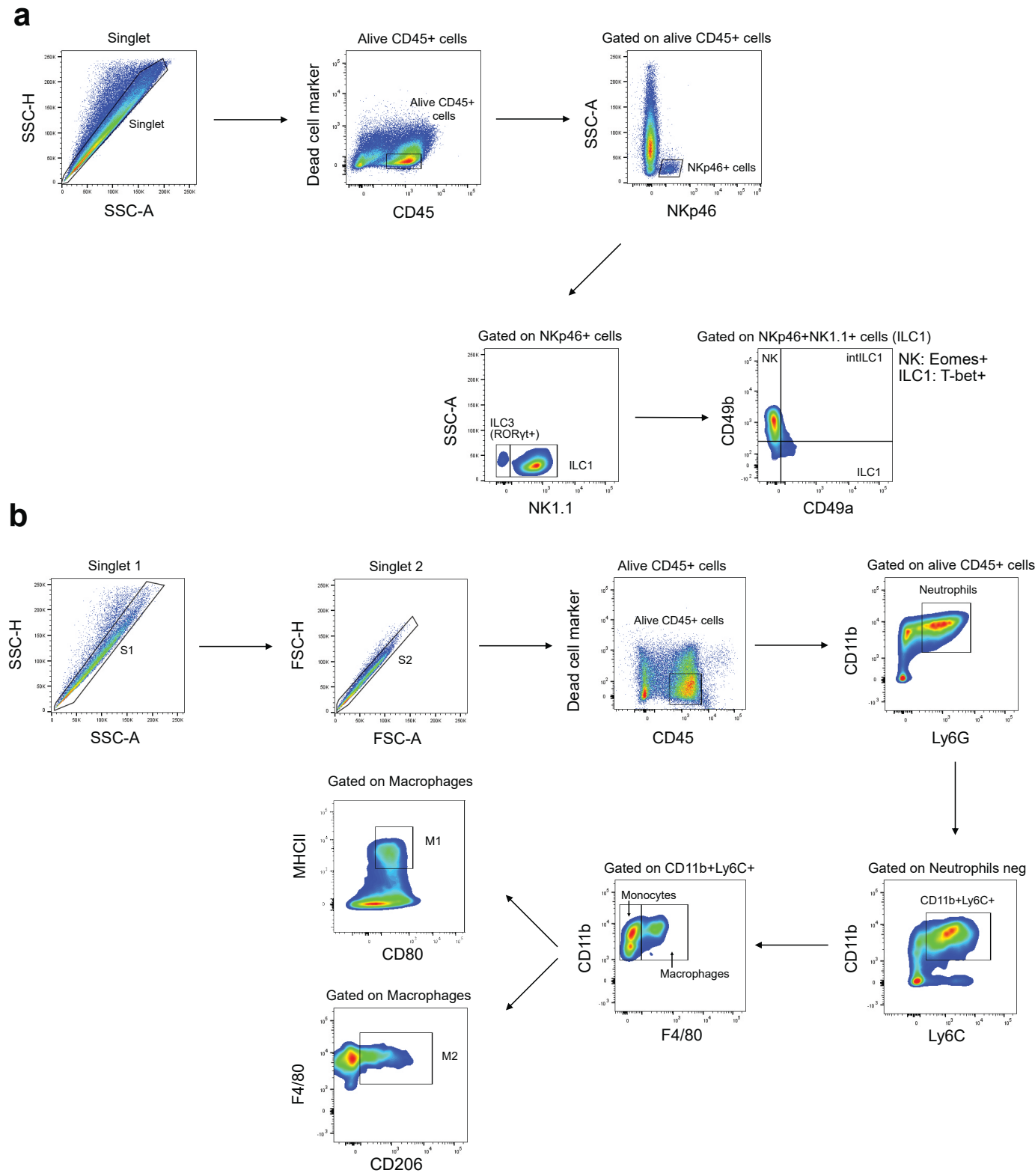
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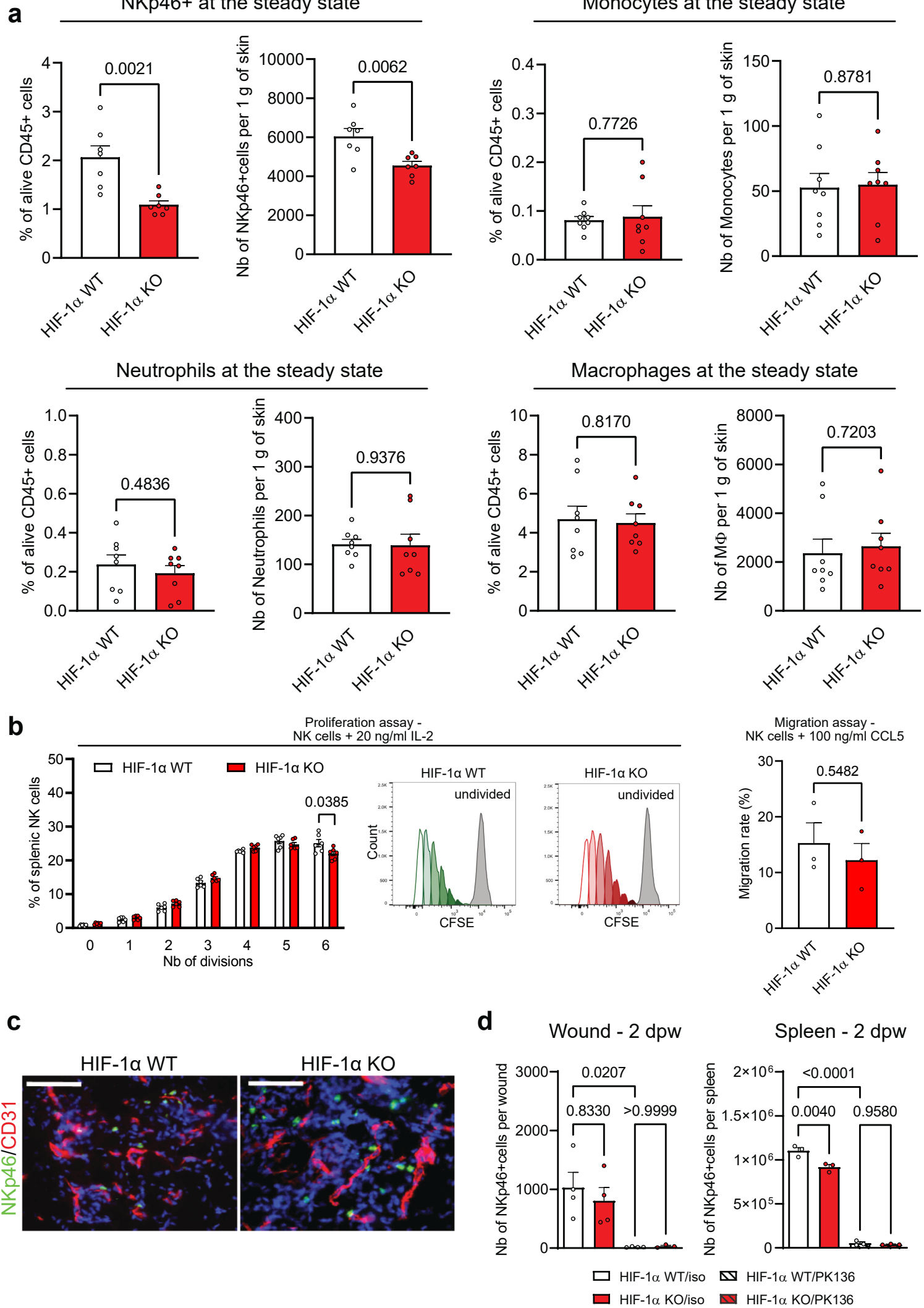
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Suppl. Fig. 1



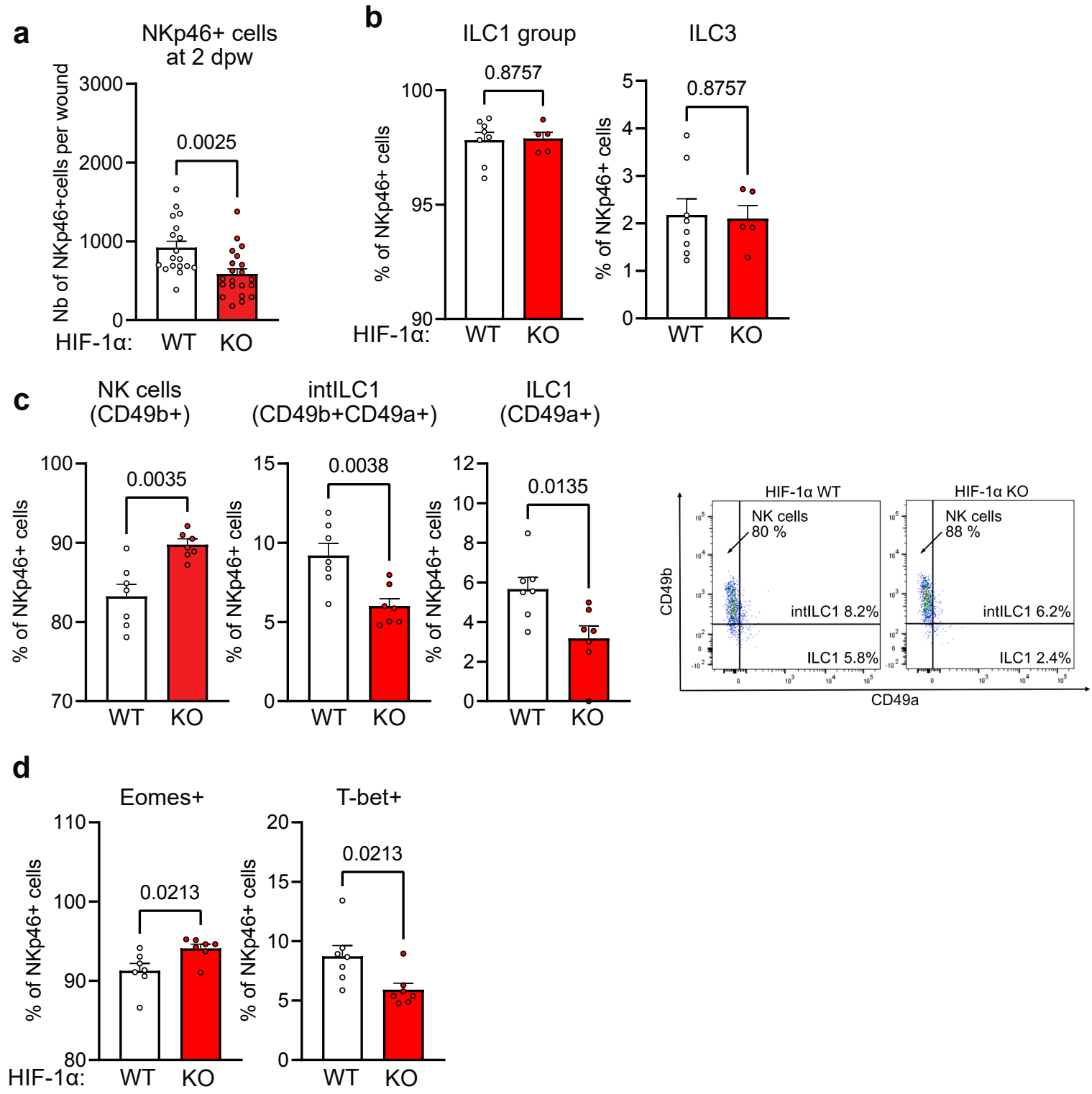
Supplementary figure 1. Gating strategy to detect immune cell subsets. **a** Gating strategy for NKp46⁺, ILC1 group cells (NKp46⁺, NK1.1⁺), ILC3 cells (NKp46⁺, NK1.1⁻, RORγt⁺), NK cells (NKp46⁺, NK1.1⁺, CD49b⁺, Eomes⁺), intermediate ILC1 cells (NKp46⁺, NK1.1⁺, CD49b⁺, CD49a⁺) and ILC1 cells (NKp46⁺, NK1.1⁺, CD49a⁺, CD49b⁻, T-bet⁺) cells population. **b** Gating strategy for neutrophils (CD11b⁺, Ly6G⁺), monocytes (CD11b⁺, Ly6C⁺), macrophages (CD11b⁺, Ly6C⁺, F4/80⁺), M1 macrophages (CD80⁺, MHCII⁺) and M2 macrophages (CD206⁺).

Suppl. Fig. 2



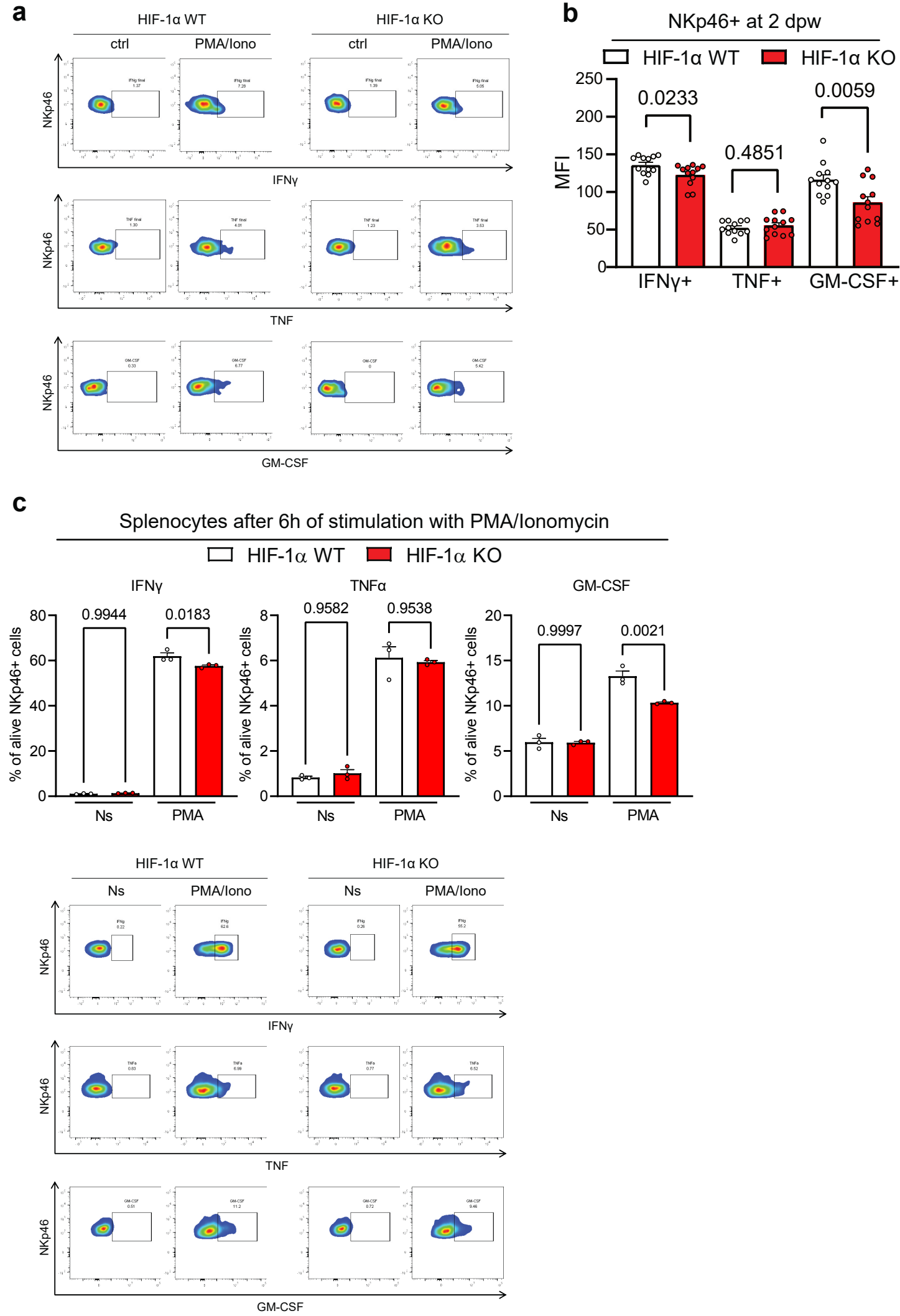
Supplementary figure 2. Loss of HIF-1 α in NKp46⁺ cells affects wound closure. **a** FACS analysis of NKp46⁺ cells, neutrophils (CD11b⁺, Ly6G⁺), monocytes (CD11b⁺, Ly6C⁺) and macrophages (CD11b⁺, Ly6C⁺, F4/80⁺), frequencies and absolute cell numbers per 1 gram of skin from WT and HIF-1 α KO mice, pooled data of 2 experiments, (for NKp46⁺ cells, n=7; for neutrophils, monocytes, macrophages, n=8), two-tailed Student's t test. **b** Left, analysis of purified splenic NK cells proliferation from HIF-1 α WT and HIF-1 α KO mice in the presence of IL-2 with corresponding FACS plots, (n= 6), two-tailed Student's t test. Right, analysis of purified splenic NK cell migration from WT and HIF-1 α KO mice in the presence of CCL5 (n=3), two-tailed Student's t test. **c** Representative images of CD31/NKp46 immunostaining on skin wounds from WT and HIF-1 α KO mice at day 6 post injury. **d** Left, flow cytometry analysis in skin wounds for NK cells (NKp46⁺, NK1.1⁺) absolute numbers from isotype control (iso) and PK136 antibody treated WT and HIF-1 α KO animals at day 2 post injury. Right, flow cytometry analysis of splenic NK cells (NKp46⁺, NK1.1⁺) absolute numbers from isotype control- (iso) and PK136 antibody-treated WT and HIF-1 α KO animals at day 2 post injury, (wounds n = 4; spleens, n=3), two-ways ANOVA test. Data are mean values $\pm$ SEM.

Supp. Fig. 3



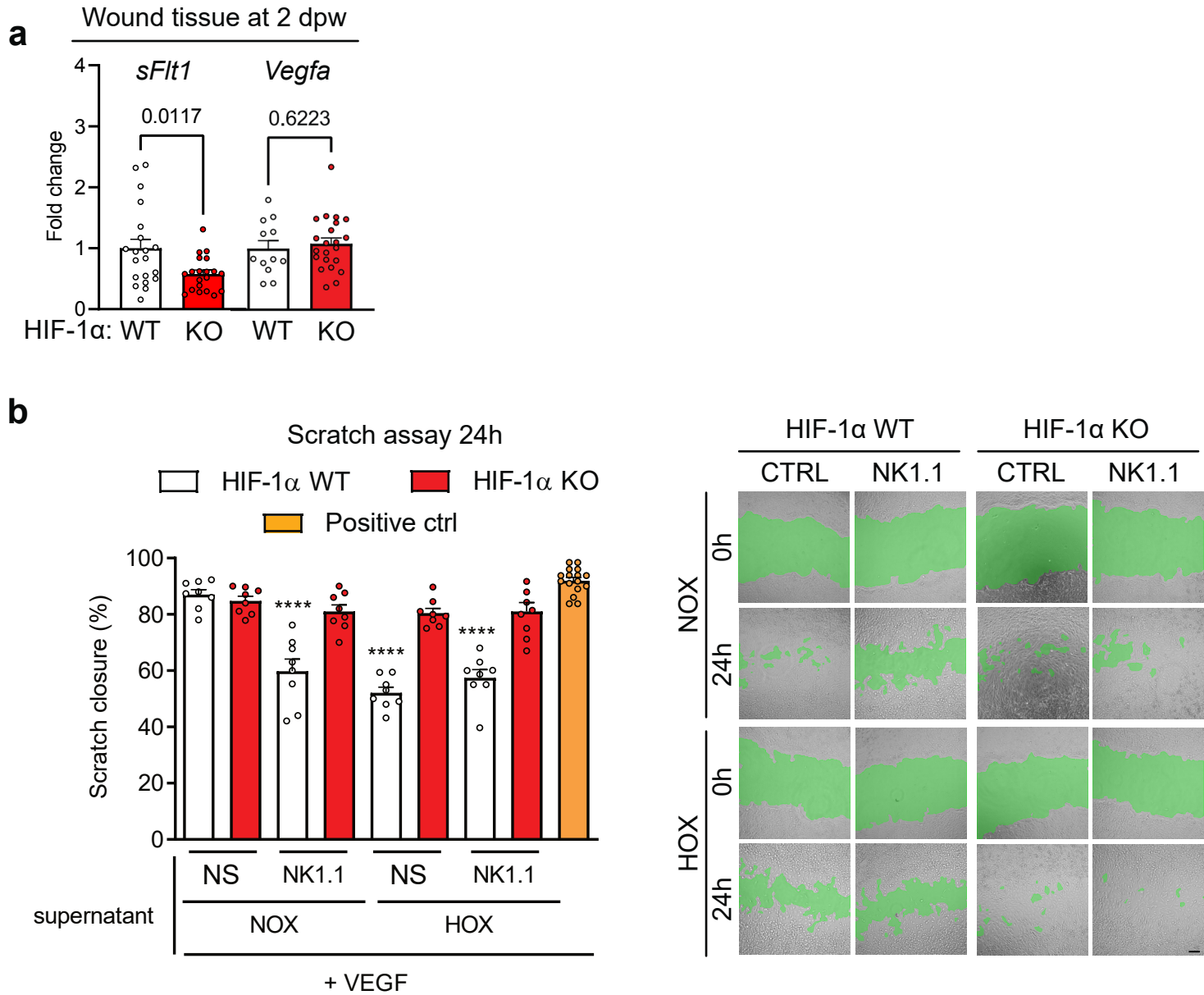
Supplementary figure 3. The role of HIF-1 α in NKp46⁺ cells for ILC composition in wounds. **a** Quantitative analysis by flow cytometry of NKp46⁺ cells, absolute numbers in skin wounds from WT and HIF-1 α KO mice at day 2 post injury, pooled data of 4 experiments (n=18 for WT and n=21 for HIF-1 α KO). **b** Flow cytometry analysis for ILC1 cells (NKp46⁺, NK1.1⁺), ILC3 cells (NKp46⁺, NK1.1⁻, ROR γ t⁺) in skin wounds from WT and HIF-1 α KO mice at day 2 post injury, pooled data of 2 experiments (n=8 for WT and n=5 for HIF-1 α KO). **c** Left, flow cytometry analysis for NK cells (NKp46⁺, CD49b⁺), intermediate ILC1 cells (NKp46⁺, CD49b⁺, CD49a⁺) and ILC1 cells (NKp46⁺, CD49a⁺, CD49b⁻) in skin wounds from WT and HIF-1 α KO mice at day 2 post injury, pooled data of 3 experiments (n=7). Right, corresponding representative FACS plots. **d** Flow cytometry analysis for NKp46⁺, NK1.1⁺, Eomes⁺ NK cells and NKp46⁺, NK1.1⁺, T-bet⁺ ILC1 cell populations in skin wounds from WT and HIF-1 α KO mice at day 2 post injury, pooled data of 3 experiments (n=7). Data are mean values $\pm$ SEM, statistical analysis: two-tailed Student's t test.

Supp. Fig. 4



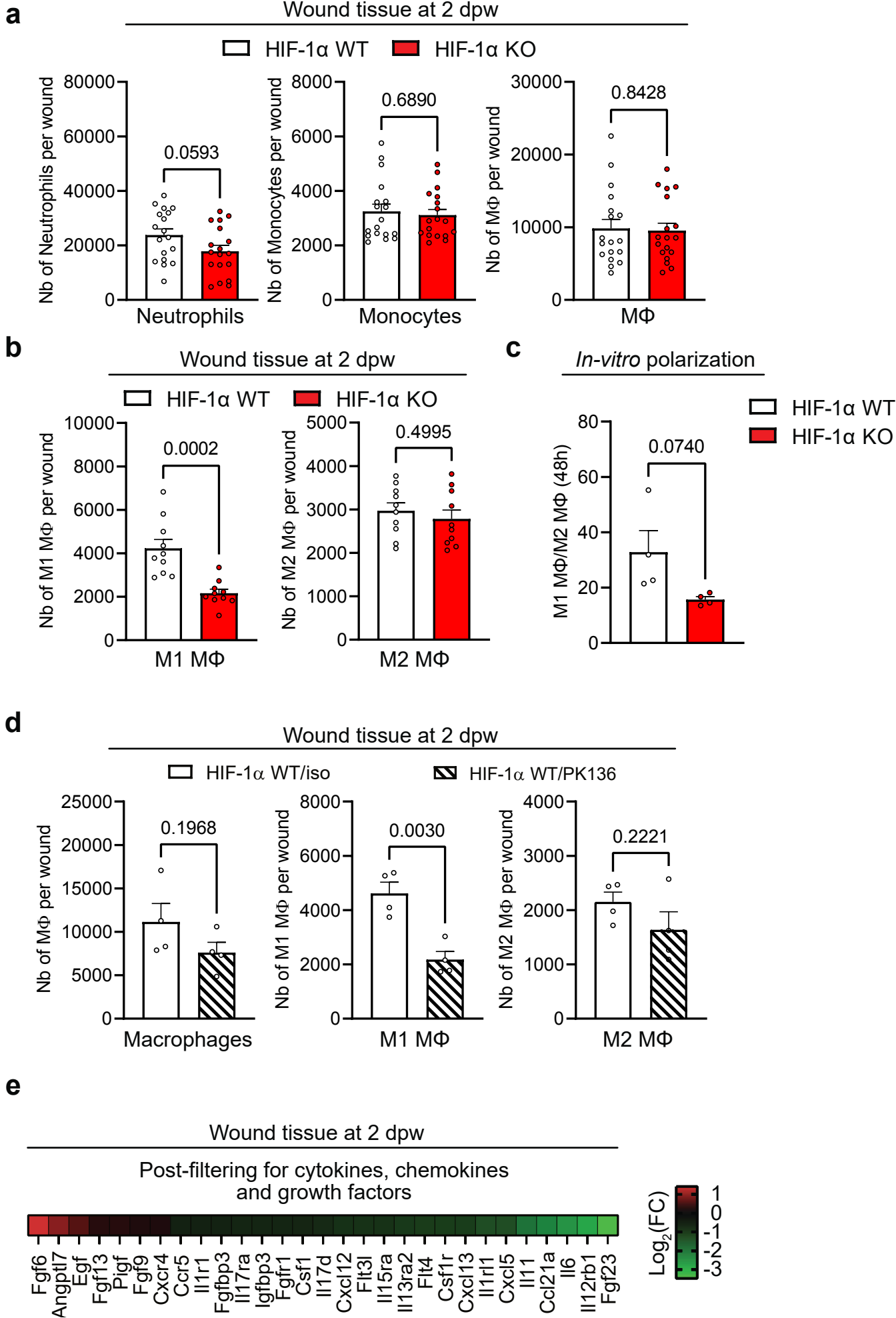
Supplementary figure 4. The effect of HIF-1 α on NKp46⁺ cell-derived cytokines. **a** Representative FACS plots showing the frequencies of IFN γ -, TNF- and GM-CSF-expressing NKp46⁺, NK1.1⁺ cells in skin wounds from WT and HIF-1 α KO mice at day 2 post injury after stimulation with PMA/Ionomycin (Iono) and corresponding unstimulated controls (ctrl). **b** Flow cytometry analysis of mean fluorescence intensity (MFI) of IFN γ , TNF α and GM-CSF in NKp46⁺, NK1.1⁺ cells, pooled data of 3 experiments (n=12), two-tailed Student's t test. **c** Top, flow cytometry analysis of IFN γ -, TNF- and GM-CSF-expressing splenic NKp46⁺, NK1.1⁺ cells upon stimulation with PMA/Ionomycin together with corresponding controls. Values are mean $\pm$ SEM (n = 3) with significant differences by two-ways ANOVA test. Bottom, representative FACS plots. Data are mean values $\pm$ SEM.

Supp. Fig. 5



Supplementary figure 5. Loss of HIF-1 α in NKp46⁺ cells facilitates angiogenesis. **a** Gene expression analysis of *sFflt1* (left) and *Vegfa* (right) in skin wounds of WT and HIF-1 α KO animals at day 2 post injury (n=20), two-tailed Student's t test. **b** Left, endothelial cell scratch assay, quantification of scratch closure relative to the initial scratch size at time point 0h, (n = 8, for positive control n=16), two-ways ANOVA test. *** P < 0.001, and **** P < 0.0001. Right, representative images of the scratch assay with the scratch area highlighted in green. Data are mean values $\pm$ SEM.

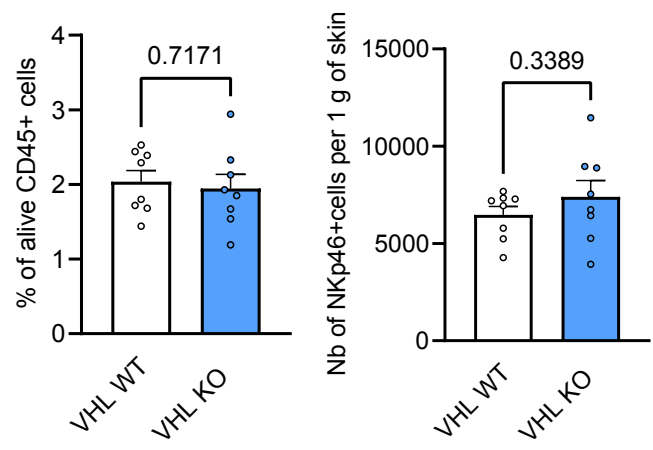
Supp. Fig. 6



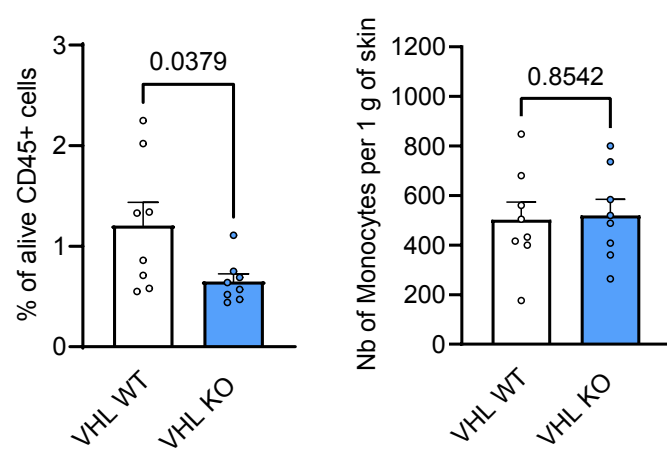
Supplementary figure 6. The role of HIF-1 α in NKp46⁺ cells for myeloid cell composition in wounds. **a** Flow cytometry analysis for neutrophils (CD11b⁺, Ly6G⁺), monocytes (CD11b⁺, Ly6C⁺) and macrophages (CD11b⁺, Ly6C⁺, F4/80⁺), absolute cell numbers in skin wounds from WT and HIF-1 α KO mice at day 2 post injury, pooled data of 4 experiments (n=18). **b** Flow cytometry analysis for M1 (CD80⁺, MHCII⁺) and M2 macrophages (CD206⁺), absolute numbers in skin wounds from WT and HIF-1 α KO mice at day 2 post injury, pooled data of 3 experiments, (n=10). **c** Flow cytometry analysis for M1 (CD80⁺, MHCII⁺) and M2 macrophages (CD206⁺) derived from splenocytes from WT and HIF1 α KO mice cocultured with pre-activated NK cells (PMA/ionomycin for 6 hours in normoxia) for 48 h (n=4). **d** Flow cytometry analysis in skin wounds for total macrophages (CD11b⁺, Ly6C⁺, F4/80⁺), M1 macrophages (CD80⁺, MHCII⁺) and M2 macrophages (CD206⁺), absolute numbers from isotype control (iso) and PK136 antibody treated HIF-1 α WT animals at day 2 post injury (n = 4). **e** Heat map of gene expression in skin wounds of HIF-1 α KO mice with a significantly differential expression to the skin wounds of WT mice from a post-filtered (cytokines, chemokines, growth factors and their respective receptors) pool of genes. Data are mean values $\pm$ SEM, statistical analysis: two-tailed Student's t test.

Suppl. Fig. 7

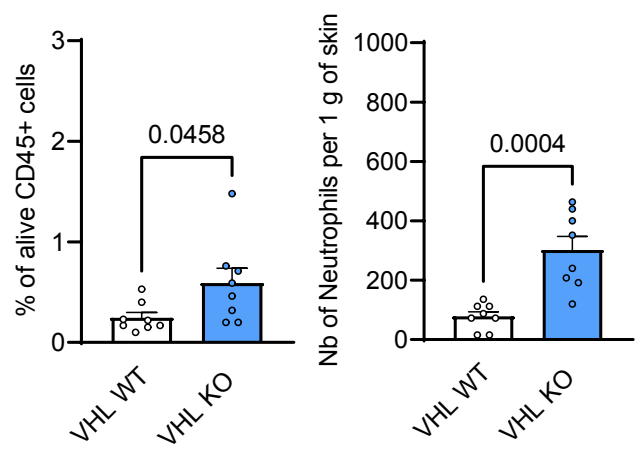
NKp46+ at the steady state



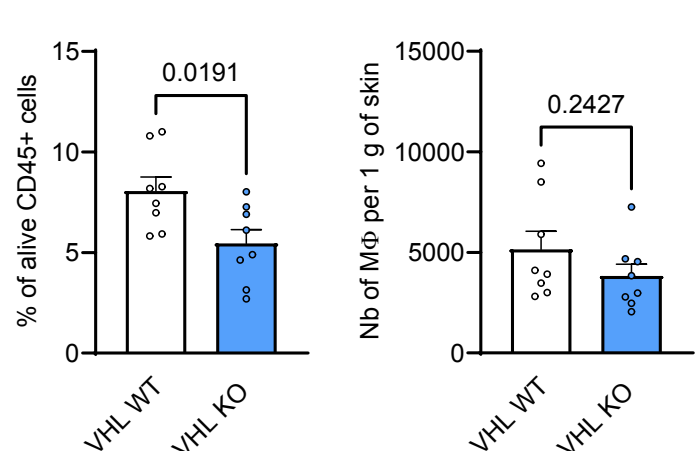
Monocytes at the steady state



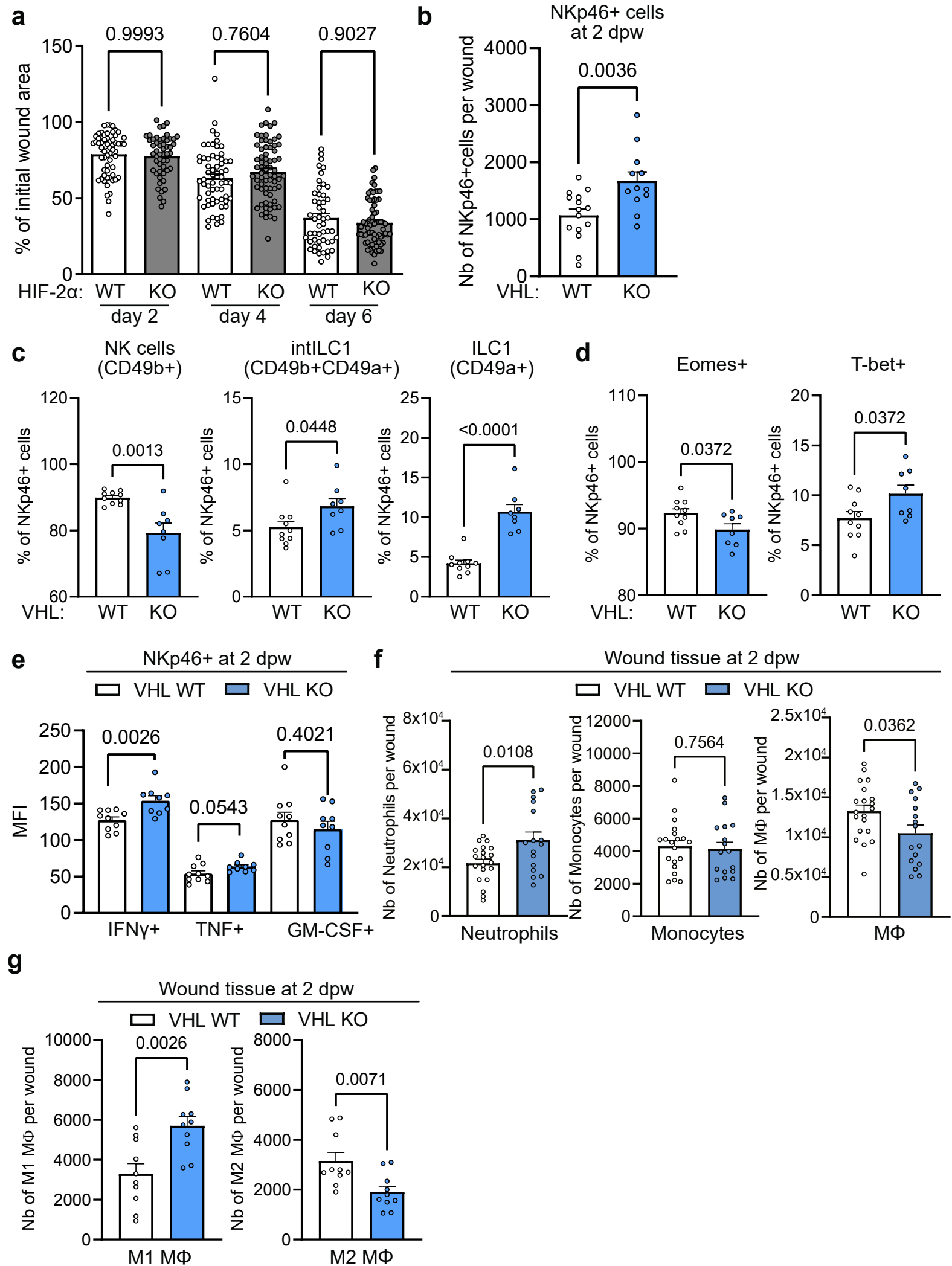
Neutrophils at the steady state



Macrophages at the steady state

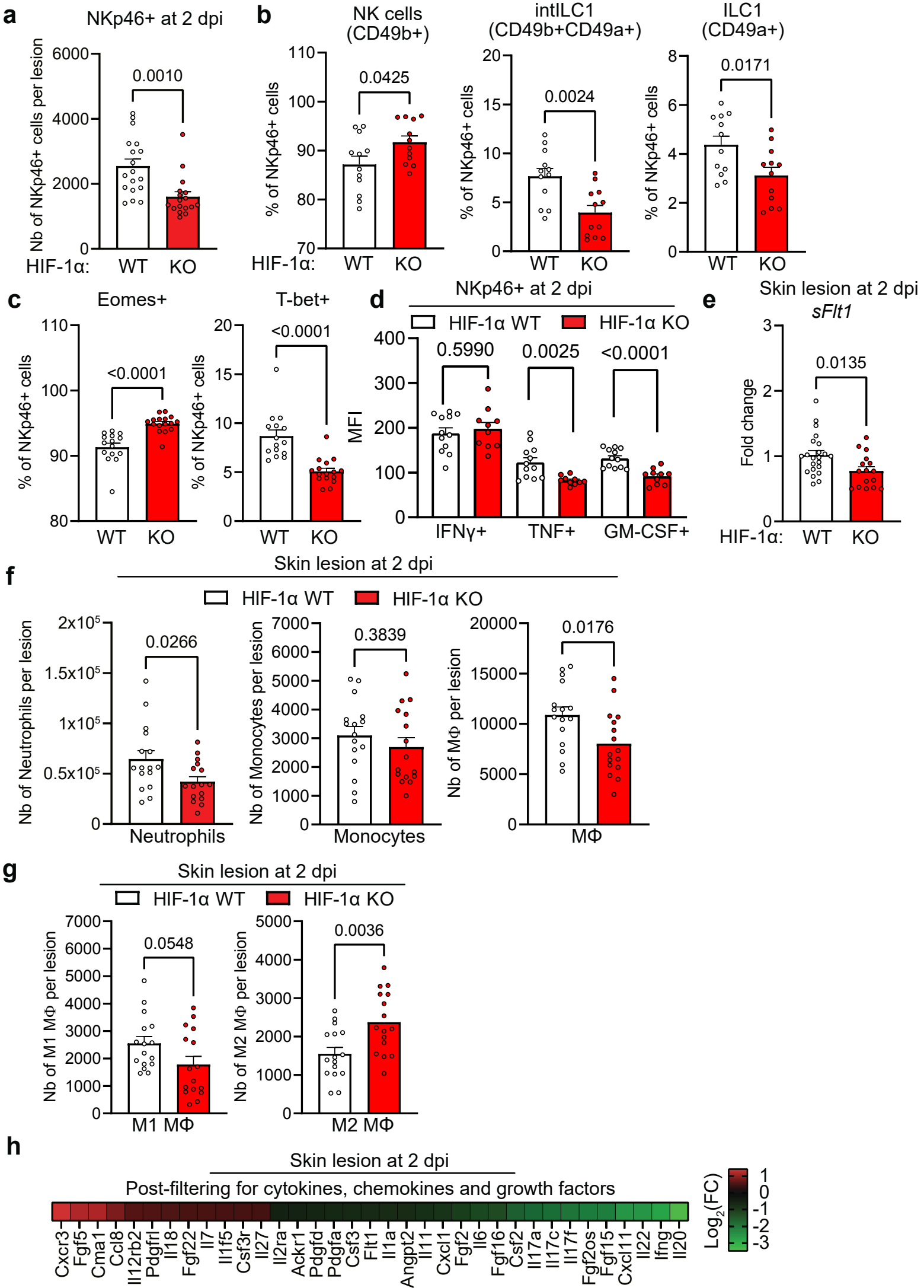


Supplementary figure 7. Constitutive activation of HIF-1 α in NKp46⁺ cells affects immune cell infiltration. Quantitative analysis by flow cytometry of NKp46⁺ cells, neutrophils (CD11b⁺, Ly6G⁺), monocytes (CD11b⁺, Ly6C⁺) and macrophages (CD11b⁺, Ly6C⁺, F4/80⁺), frequencies and absolute cell numbers per 1 gram of skin from WT and VHL KO mice, pooled data of 2 experiments (n=8). Data are mean values $\pm$ SEM, statistical analysis: two-tailed Student's t test.

Suppl. Fig. 8

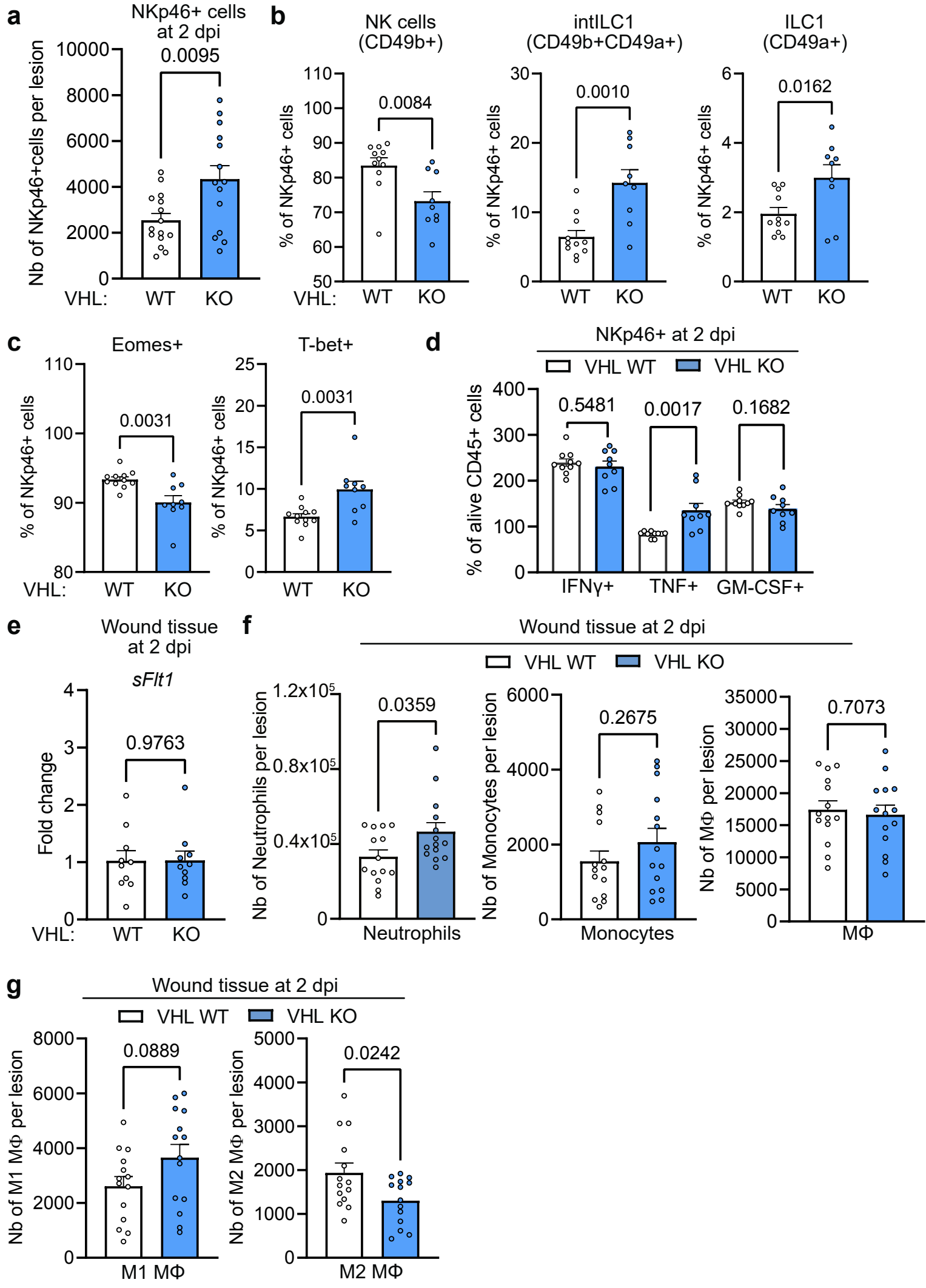
Supplementary figure 8. Loss of VHL in NKp46⁺ cells changes ILC and myeloid cell composition in wounds. **a** Quantification of individual wound areas at 2, 4 and 6 days post wounding (dpw) in WT and HIF-2 α KO animals relative to initial size at day 0, pooled data of 4 experiments, (n > 50), one-way ANOVA test. **b** Quantitative analysis of NKp46⁺ cells, absolute numbers in skin wounds at 2 dpw, pooled data of 4 experiments. (n=15 for WT and n=12 for VHL KO). **c** Flow cytometry analysis for NK cells (NKp46⁺, CD49b⁺), intermediate ILC1 cells (NKp46⁺, CD49b⁺, CD49a⁺) and ILC1 cells (NKp46⁺, CD49a⁺, CD49b⁻) in skin wounds at 2 dpw, pooled data of 3 experiments, (n=10 for WT and n=8 for VHL KO). **d** Flow cytometry analysis for NKp46⁺, NK1.1⁺, Eomes⁺ (NK cells) and NKp46⁺, NK1.1⁺, T-bet⁺ (ILC1) cell populations in skin wounds at 2 dpw, pooled data of 3 different experiments (n=10 for WT and n=8 for VHL KO). **e** Flow cytometry analysis of mean fluorescence intensity (MFI) of IFN γ , TNF α and GM-CSF in NKp46⁺, NK1.1⁺ cells in skin wounds at 2 dpw, pooled data of 3 experiments (n=10 for WT and n=9 for VHL KO). **f** Flow cytometry analysis for neutrophils (CD11b⁺, Ly6G⁺), monocytes (CD11b⁺, Ly6C⁺) and macrophages (CD11b⁺, Ly6C⁺, F4/80⁺), absolute numbers in skin wounds at 2 dpw, pooled data of 4 experiments. (n=20 for WT and n=16 for VHL KO). **g** Flow cytometry analysis for M1 (CD80⁺, MHCII⁺) and M2 macrophages (CD206⁺), absolute numbers in skin wounds at 2 dpw, pooled data of 3 experiments (n=10). Data are mean values $\pm$ SEM, statistical analysis: two-tailed Student's t test unless stated otherwise.

Suppl. Fig. 9



Supplementary figure 9. HIF-1 α in NKp46⁺ cells supports the antimicrobial defence in the skin. **a** FACS analysis of NKp46⁺ cells, absolute number in skin lesions at 2 days post infection (dpi), pooled data of 4 experiments, (n=18 for WT and n=17 for HIF-1 α KO). **b** Flow cytometry analysis for NK cells (NKp46⁺, NK1.1⁺, CD49b⁺), intermediate ILC1 cells (NKp46⁺, NK1.1⁺, CD49b⁺, CD49a⁺) and ILC1 cells (NKp46⁺, NK1.1⁺, CD49a⁺, CD49b⁻) in skin lesions at 2 dpi, pooled data of 3 experiments (n=12 for WT and HIF-1 α KO mice). **c** Flow cytometry analysis for NKp46⁺, NK1.1⁺, Eomes⁺ (NK cells) and NKp46⁺, NK1.1⁺, T-bet⁺ (ILC1) cell populations in skin lesions at 2 dpi, pooled data of 4 experiments (n=15 for WT and n=16 for HIF-1 α KO). **d** Flow cytometry analysis of mean fluorescence intensity (MFI) of IFN γ , TNF and GM-CSF in NKp46⁺, NK1.1⁺ cells in skin lesions at 2 dpi, pool data of 3 experiments (n=12 for WT and n=10 for HIF-1 α KO). **e** Gene expression analysis of *sFfl1* in skin lesions at 2 dpi, pooled of 4 experiments (n=22 for WT and n=16 for HIF-1 α KO). **f** Flow cytometry analysis for neutrophils (CD11b⁺, Ly6G⁺), monocytes (CD11b⁺, Ly6C⁺) and macrophages (CD11b⁺, Ly6C⁺, F4/80⁺), absolute numbers in skin lesions at 2 dpi, pooled data of 4 experiments (n=16 for WT and HIF-1 α KO mice). **g** Flow cytometry analysis for M1 (CD80⁺, MHCII⁺) and M2 macrophages (CD206⁺), absolute numbers in skin lesions at 2 dpi, pooled data of 4 experiments (n=16 for WT and HIF-1 α KO mice). **h** Heat map of gene expression in GAS skin lesions from HIF-1 α KO mice with a significantly differential expression relative to GAS skin lesions from WT mice from a post-filtered (cytokines, chemokines, growth factors and their respective receptors) pool of genes. Data are mean values $\pm$ SEM, statistical analysis: two-tailed Student's t test.

Supp. Fig. 10



Supplementary figure 10. Loss of VHL in NK cells protects against bacterial skin infections. **a** Quantitative analysis of NKp46⁺ cells, absolute numbers in skin lesions at 2 days post infection (dpi), pooled of 4 experiments (n=15 for WT and n=14 for VHL KO). **b** Flow cytometry analysis for NK cells (NKp46⁺, NK1.1⁺, CD49b⁺), intermediate ILC1 cells (NKp46⁺, NK1.1⁺, CD49b⁺, CD49a⁺) and ILC1 cells (NKp46⁺, NK1.1⁺, CD49a⁺, CD49b⁻) in skin lesions at 2 dpi, pooled data of 3 experiments (n=11 for WT and n=9 for VHL KO). **c** Flow cytometry analysis for NKp46⁺, NK1.1⁺, Eomes⁺ (NK cells) and NKp46⁺, NK1.1⁺, T-bet⁺ (ILC1) cell populations in skin lesions at 2 dpi, pooled data of 3 experiments (n=11 for WT and n=9 for VHL KO). **d** Flow cytometry analysis of mean fluorescence intensity (MFI) of IFN γ , TNF and GM-CSF in NKp46⁺, NK1.1⁺ cells in skin lesions at 2 dpi, pooled data of 3 experiments. (n=10 for WT and n=9 for VHL KO). **e** Gene expression analysis of *sFfl1* in skin lesions at 2 dpi, pooled data of 3 experiments (n=10 for WT and VHL KO mice). **f** Flow cytometry analysis for neutrophils (CD11b⁺, Ly6G⁺), monocytes (CD11b⁺, Ly6C⁺) and macrophages (CD11b⁺, Ly6C⁺, F4/80⁺), absolute numbers in skin lesions at 2 dpi, pooled data of 4 experiments (n=14 for WT and VHL KO mice). **g** Flow cytometry analysis for M1 (CD80⁺, MHCII⁺) and M2 macrophages (CD206⁺) absolute numbers in skin lesions at 2 dpi, pool data of 4 different experiments (n=14 for WT and VHL KO mice). Data are mean values $\pm$ SEM, statistical analysis: two-tailed Student's t test.

Supplementary Table 1. List of antibodies

	Antibody	Clone	Reference	Supplier	Dilution	Host Species
1	anti-F4/80	BM8	123107; 123131	BioLegend	1/100	Rat
2	anti-CD11c	N418	117310; 117306	BioLegend	1/100	Armenian Hamster
3	anti-CD64	X54-5/7.1	139307	BioLegend	1/100	Mouse
4	anti-CD8	53-6.7	100730	BioLegend	1/100	Rat
5	anti-CD206	C068C2	141732	BioLegend	1/100	Rat
6	anti-CD19	6D5	115530; 152404	BioLegend	1/100	Rat
7	anti-MHCII	M5/114.15.2	48-5321; 107616	eBioscience, BioLegend	1/100	Rat
8	anti-Ly6G	1A8	746448; 127618	BD, BioLegend	1/100	Rat
9	anti-Ly6C	HK1.4	128035	BioLegend	1/100	Rat
10	anti-CD80	16-10A1	104707	BioLegend	1/100	Armenian Hamster
11	anti-CD45	30-F11	564225; 103128	BD, BioLegend	1/100	Rat
12	anti-CD4	GK1.5	565974; 564667	BD	1/100	Rat
13	anti-B220	RA3-6B2	564662	BD	1/100	Rat
14	anti-CD11b	M1/70	564443; 101206	BD, BioLegend	1/100	Rat
15	anti-NK1.1	PK136	553165; 563220; 564667	BD	1/50	Mouse
16	anti-SiglecF	E50-2440	562757	BD	1/100	Rat
17	anti-TCR β	H57-597	109210; 109206	BioLegend	1/100	Armenian Hamster
18	anti-TCR $\gamma\delta$	GL3	118106	BioLegend	1/100	Armenian Hamster
19	anti-NKp46	29A1.4	25-3351	eBioscience	1/50	Rat
20	anti-TER119/Erythroid cells	TER-119	116206	BioLegend	1/100	Rat
21	anti-CD127	A7R34	135027	BioLegend	1/100	Rat
22	anti-CCR6	140706	747831	BD	1/100	Rat
23	anti-CD49b	DX5	741752	BD	1/100	Armenian Hamster
24	anti-CD49a	Ha31/8	741976	BD	1/100	Armenian Hamster
25	anti-ICOS	C398.4A	15-9949-82	eBioscience	1/100	Armenian Hamster
26	anti-IFN- γ	XMG1.2	566151	BD	1/100	Rat
27	anti-TNF	MP6-XT22	506333	BD	1/100	Rat
28	anti-GM-CSF	MP1-22E9	554406	BD	1/100	Rat
29	anti-ROR γ t	Q31-378	562682	BD	1/100	Mouse
30	anti-T-bet	4b10	644835	BD	1/100	Mouse
31	anti-GATA3	TWAJ	12-9966-42	eBioscience	1/100	Rat
32	anti-Eomes	Dan11mag	61-4875-82	eBioscience	1/100	Rat

Supplementary Table 2. qRT-PCR Primer sequences (mouse)

Name of gene		Sequence
16s	forward primer	5'-AGATGATCGAGCCGCGC -3'
	reverse primer	5'-GCTACCAGGGCCTTTGAGATGGA-3'
Ifng	forward primer	5'- TCAAGTGGCATAGATGTGGAAGAA -3'
	reverse primer	5'- TGGCTCTGCAGGATTTTCATG -3'
Tnfa	forward primer	5'- GCCTCTTCTCATTCTGCTTG -3'
	reverse primer	5'- CTGATGAGAGGGAGGCCATT -3'
Nos2	forward primer	5'- GCTTGGGTCTTGTTCACTCC -3'
	reverse primer	5'- GCAAGTGAAATCCGATGTGGC -3'
Arg1	forward primer	5'- AATCTGCATGGGCAACCTGT -3'
	reverse primer	5'- AGGGTCTACGTCTCGCAAG -3'
sFlt1	forward primer	5'- GTCACAGATGTGCCGAATGG -3'
	reverse primer	5'- TGACTTTGTGTGGTACAATC -3'
Il10	forward primer	5'- CCAGTTTTACCTGGTAGAGGTGATG -3'
	reverse primer	5'- TGTCTAGGTCCTGGAGTCCAGCAGACTC -3'
Csf2	forward primer	5'- TGGGCATTGTGGTCTACAGC -3'
	reverse primer	5'- GCGGGTCTGCACACATGTTA -3'