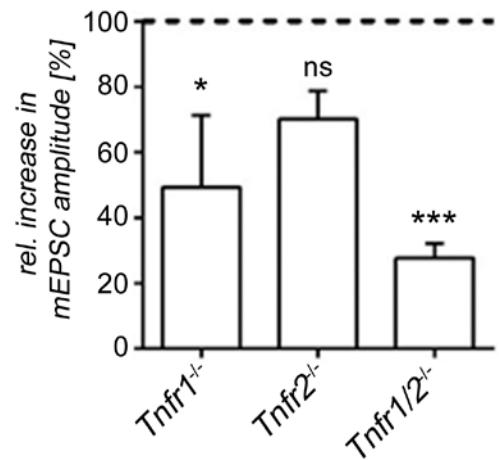


## SUPPLEMENTARY INFORMATION:

### Tumor necrosis factor (TNF)-receptor 1 and 2 mediate homeostatic synaptic plasticity of denervated mouse dentate granule cells by Denise Becker, Thomas Deller, Andreas Vlachos



**Figure S1:** Relative increase in mEPSC amplitudes of denervated dentate granule cells from TNFR deficient preparations (3 - 4 days post lesion; dpl) compared/normalized to the denervation-induced homeostatic synaptic strengthening seen in wild type preparations at 3 - 4 dpl (wild type data taken from Becker et al., 2013; wildtype:  $100 \pm 15\%$ ; *Tnfr1<sup>-/-</sup>*:  $49 \pm 21\%$ ; *Tnfr2<sup>-/-</sup>*:  $70 \pm 8\%$ ; *Tnfr1/2<sup>-/-</sup>*:  $27 \pm 4\%$ , n = 10-41 cells; at least 4 cultures per group; Kruskal-Wallis-test followed by Dunn's post-hoc-test; \* p <0.05; \*\*\* p <0.001; ns, not significant).

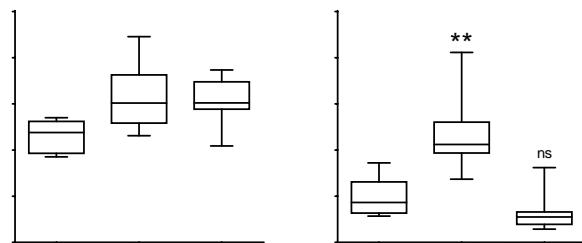
#### Reference:

Becker, D., Zahn, N., Deller, T. & Vlachos, A. Tumor necrosis factor alpha maintains denervation-induced homeostatic synaptic plasticity of mouse dentate granule cells. *Front Cell Neurosci* 7, 257, doi:10.3389/fncel.2013.00257 (2013).

**Figure S2: Wildtype slice cultures treated with TNFR-activating antibodies for 3 days**

GROUP	mEPSC amplitude [pA]			mEPSC frequency [Hz]		
	control	TNFR1-AB treated	TNFR2-AB treated	control	TNFR1-AB treated	TNFR2-AB treated
wild type	11.6 ± 0.5 (10)	15.6 ± 1.0 (12); **	15.2 ± 0.6 (15); **	1.9 ± 0.3 (10)	4.7 ± 0.4 (12); **	1.2 ± 0.2 (15); ns

All values expressed as mean ± standard error of the mean; number of neurons recorded per group indicated in brackets; Kruskal-Wallis-test followed by Dunn's post-hoc correction; \*\* p < 0.01. ns, not significant

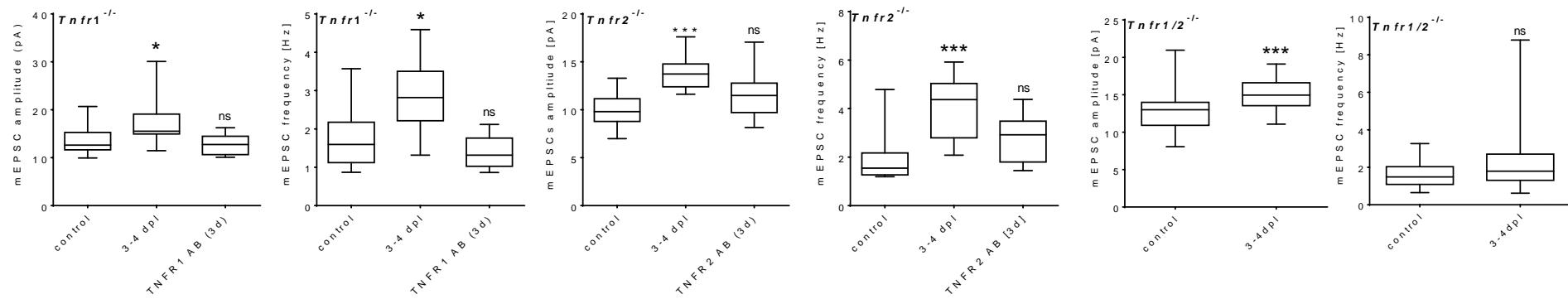


Box-Whisker-Plot of data from Table S1. \*\* p < 0.01; ns, not significant.

**Figure S3: Slice cultures prepared from TNFR-deficient mice**

GROUP	mEPSC amplitude [pA]			mEPSC frequency [Hz]		
	control	3 - 4 days post lesion	TNFR-AB treated	control	3 - 4 days post lesion	TNFR-AB treated
<i>Tnfr1</i> <sup>-/-</sup>	13.6 ± 0.7 (16)	17.3 ± 1.6 (10); *	12.9 ± 0.5 (15); ns	1.7 ± 0.2 (16)	2.8 ± 0.3 (10); *	1.4 ± 0.1 (15); ns
<i>Tnfr2</i> <sup>-/-</sup>	9.9 ± 0.5 (12)	13.8 ± 0.5 (13); ***	12.3 ± 0.6 (15); ns	2.0 ± 0.3 (12)	4.0 ± 0.3 (13); ***	2.9 ± 0.2 (15); ns
<i>Tnfr1/2</i> <sup>-/-</sup>	13.0 ± 0.5 (36)	15.0 ± 0.3 (41); ***	-----	1.6 ± 0.1 (36)	2.2 ± 0.2 (41); ns	-----

*Tnfr1*<sup>-/-</sup> treated with TNFR1-AB for 3d; *Tnfr2*<sup>-/-</sup> treated with TNFR2-AB for 3d; all values expressed as mean ± standard error of the mean; number of neurons recorded per group indicated in brackets: Kruskal-Wallis-test followed by Dunn's post-hoc correction for *Tnfr1*<sup>-/-</sup> and *Tnfr2*<sup>-/-</sup>; Mann-Whitney-test for *Tnfr1/2*<sup>-/-</sup>; \* p < 0.05; \*\*\* p < 0.001. ns, not significant

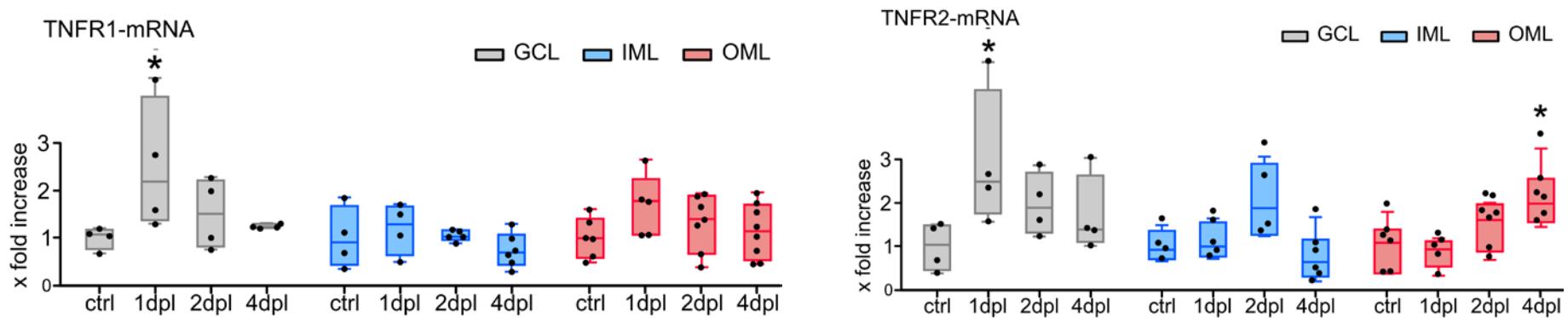


Box-Whisker-Plot of data from Table S2. days post lesion (dpl). \* p < 0.05; \*\*\* p < 0.001; ns, not significant.

**Figure S4: qPCR analysis of TNFR-mRNA levels**

TNFR1-mRNA (x fold change)				TNFR2-mRNA (x fold change)				
GROUP	control	1 dpl	2 dpl	4 dpl	control	1 dpl	2 dpl	4 dpl
GCL	1.0 ± 0.1 (4)	2.5 ± 0.7 (4); *	1.5 ± 0.4 (4); ns	1.2 ± 0.02 (4); ns	1.0 ± 0.3 (4)	3.0 ± 0.8 (4); *	2.0 ± 0.4 (4); ns	1.7 ± 0.5 (4); ns
IML	1.0 ± 0.3 (4)	1.2 ± 0.3 (4); ns	1.0 ± 0.1 (5); ns	0.7 ± 0.1 (6); ns	1.0 ± 0.2 (4)	1.1 ± 0.2 (5); ns	2.0 ± 0.4 (4); ns	0.8 ± 0.2 (6); ns
OML	1.0 ± 0.2 (6)	1.7 ± 0.3 (5); ns	1.3 ± 0.2 (7); ns	1.1 ± 0.2 (8); ns	1.0 ± 0.2 (6)	0.9 ± 0.1 (5); ns	1.5 ± 0.2 (7); ns	2.1 ± 0.3 (6); *

All values expressed as mean ± standard error of the mean; number of probes per group indicated in brackets: Kruskal-Wallis-test followed by Dunn's post-hoc correction; \* p < 0.05; \*\*\* p < 0.001. ns, not significant



Box-Whisker-Plot of data shown in Table S3. Days post lesion (dpl). \* p < 0.05.