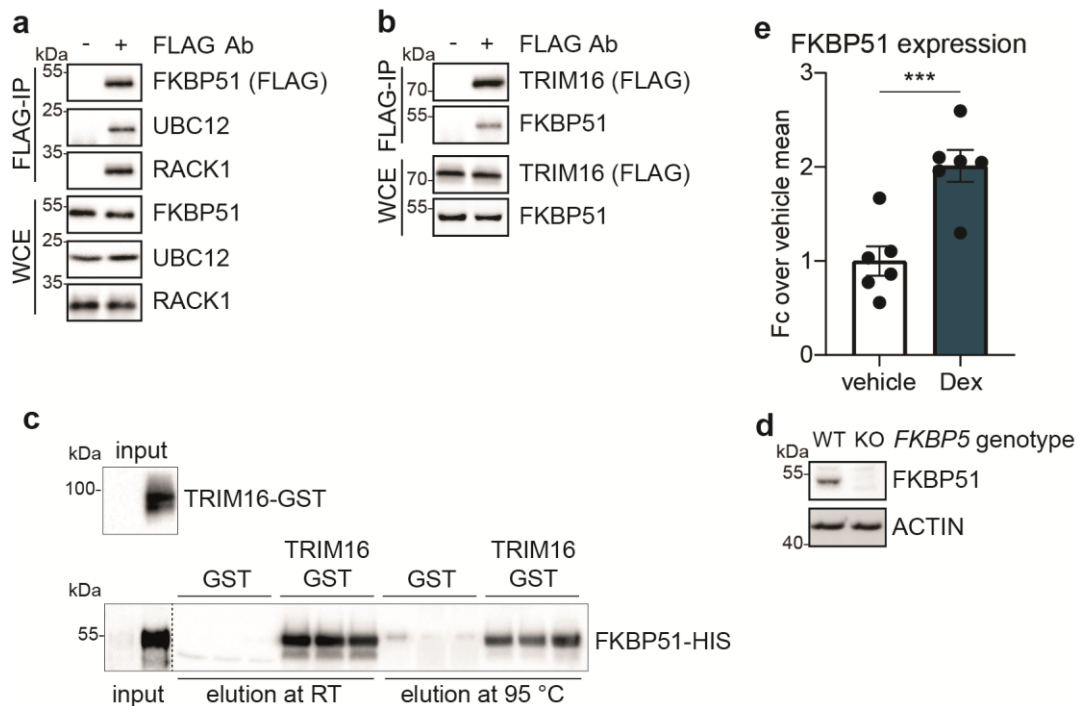
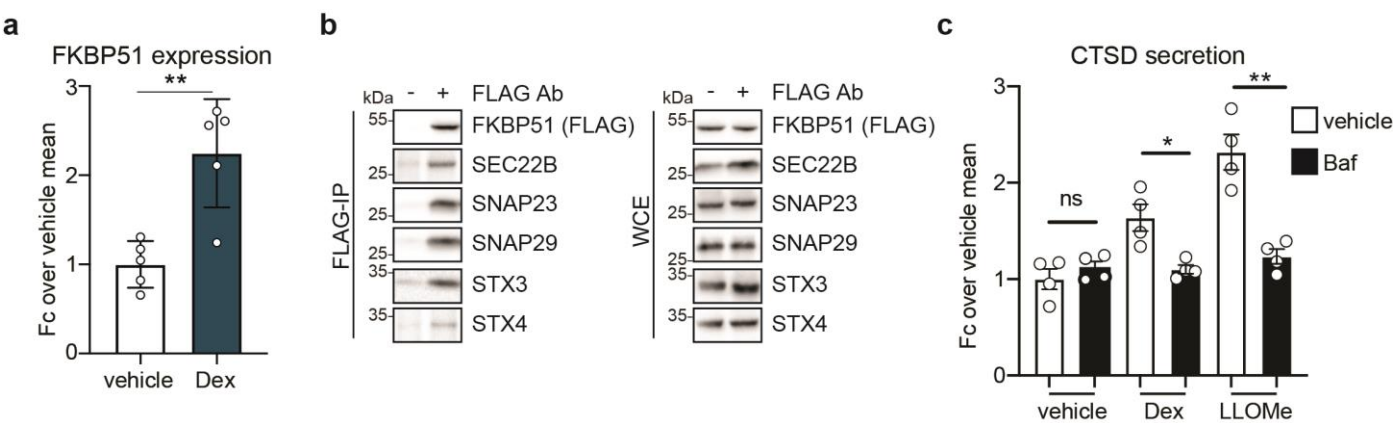


1 Supplementary Figures



3 Figure S1

a) Western blotting for FKBP51, UBC12 and RACK1 in FLAG-tagged FKBP51 co-IP (FLAG-IP) and whole cell extract (WCE) as control. **b)** Western blotting for TRIM16 and FKBP51 in FLAG-tagged TRIM16 co-IP (FLAG-IP) and whole cell extract (WCE) as control. **c)** GST pull down assay. HIS-tagged FKBP51 was incubated with purified magnetic beads-GST-tagged TRIM16 or magnetic beads-GST protein alone. After incubation, bead bound proteins were eluted at room temperature (RT) or at 95 °C and subjected to western blot analysis using antibodies against GST and HIS. Input lane contains GST alone (left) or GST-tagged TRIM16 (right). The dotted line separates the blot shown into two parts according to blot exposition time. Due to the high amount of recombinant FKBP51-HIS of the input a shorter exposition time was selected for imaging. **d)** Western blotting for FKBP51 in WT and *FKBP5* KO SH-SY5Y cells. **e)** Quantifications of western blots for FKBP51 in SH-SY5Y cells treated with vehicle or 100 nM dexamethasone (Dex) for 4 hours. Data shown as mean $\pm$ s.e.m. of $n=6$ biologically independent samples. Unpaired one-tailed t-test was performed; *** $P < 0.001$. Ab, antibody; Fc, fold change.

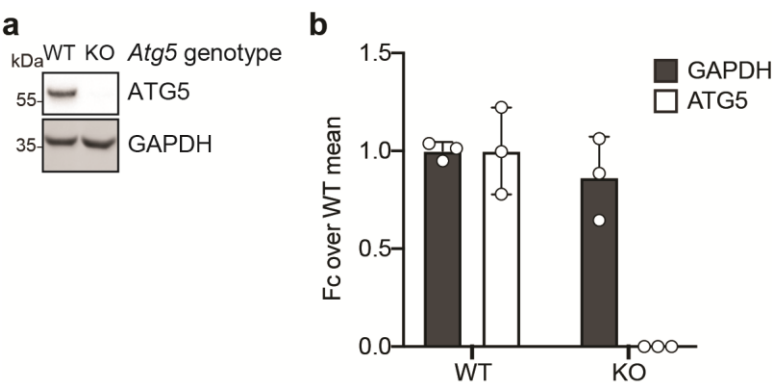


19

20 **Figure S2**

21 **a)** Quantifications of western blots for FKBP51 in SIMA-9 cells treated with vehicle or 300 nM
22 dexamethasone (Dex) for 4 hours. Data shown as mean $\pm$ s.e.m. of n=5 biologically
23 independent samples. Unpaired one-tailed t-test was performed; **p < 0.01. Fc, fold change.
24 **b)** Western blotting for FKBP51, SEC22B, SNAP23, SNAP29, STX3 and STX4 in FLAG-
25 tagged FKBP51 co-IP (FLAG-IP) performed in SIMA-9 cells and whole cell extract (WCE) as
26 control. Ab, antibody. **c)** ProteinSimple quantifications of secreted CTSD in vehicle, 300 nM
27 Dex or 50 nM LLOMe treated SIMA-9 cells, co-treated with vehicle or Baf for 4 hours. Data
28 shown as mean $\pm$ s.e.m. of n=4 biologically independent samples. Unpaired, two-tailed t-test
29 was performed; *p < 0.05, **p < 0.01. Fc, fold change.

30



31

32 **Figure S3**

33 **a)** Western blotting for ATG5 and GAPDH in WT and *Atg5* KO SIM-A9 cells and **b)** relative
 34 quantifications. Data shown as mean $\pm$ s.e.m. of n=3 biologically independent samples.

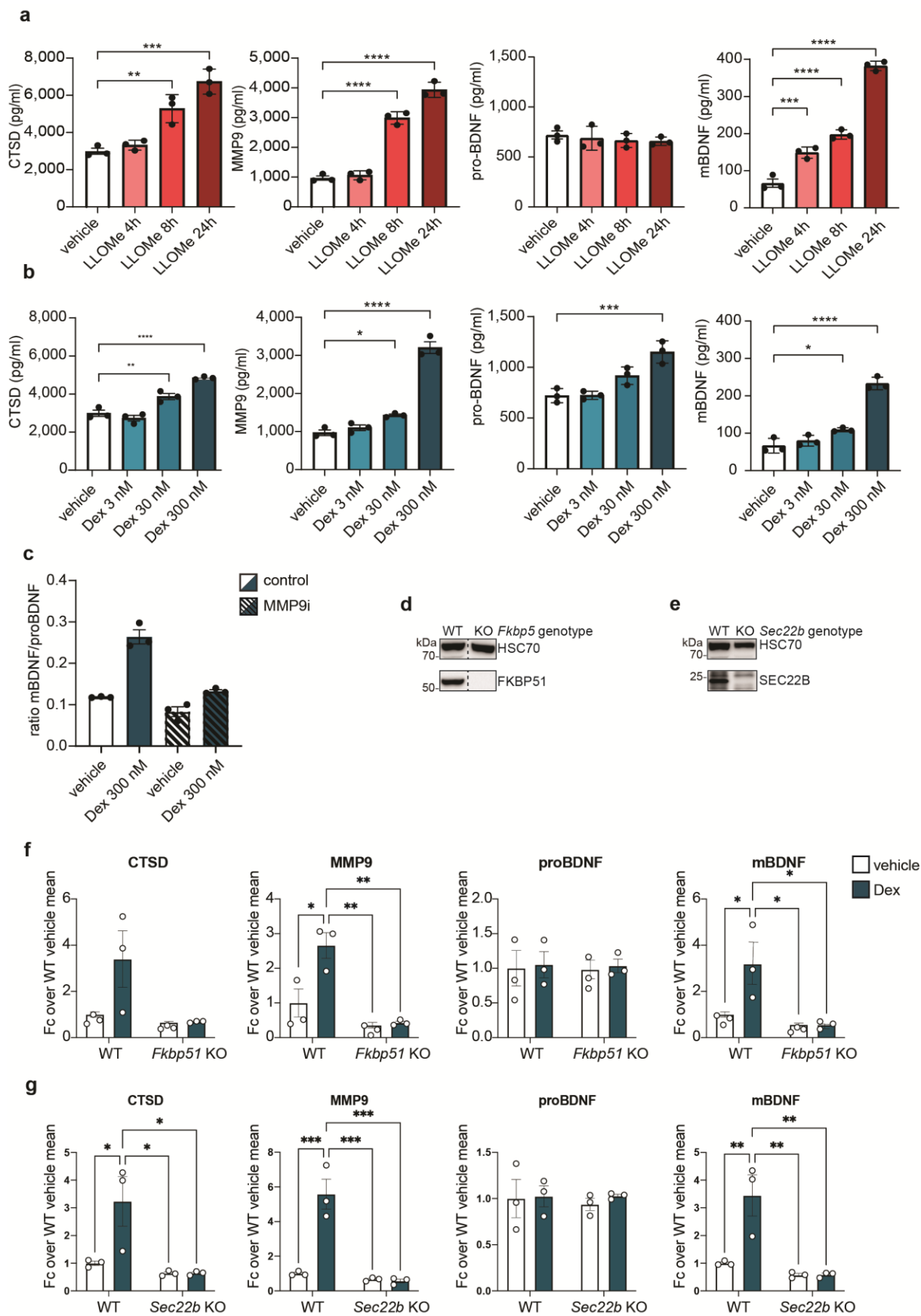


Figure S4

a) CTSD, MMP9, proBDNF, mBDNF levels from supernatants measured via ELISA after WT SIM-A9 cells were treated with 1 mM LLOMe for 4, 8 or 24 hours or vehicle or 24 hours; **b)** CTSD, MMP9, proBDNF, mBDNF levels from supernatants measured via ELISA after WT SIM-A9 cells were treated with 3 nM, 30 nM or 300 nM dexamethasone (Dex) or vehicle for 4 hours; **c)** mBDNF/proBDNF ratio from supernatants measured via ELISA after WT SIM-A9 cells were treated with 300 nM Dex, Dex + Mmp9 inhibitor I (MMP9i), or vehicle for 4 hours. a)-c) Data shown as mean $\pm$ s.e.m. of n=3 biologically independent samples. **d)** Western blotting for FKBP51 and Vinculin in WT and *Fkbp5* KO SIM-A9 cells. **e)** Western blotting for FKBP51 and Vinculin in WT and *Sec22b* KO SIM-A9 cells. The dotted line indicates a cut in the blot in order to close samples of interest that were separate on the blot. **f)** ProteinSimple quantifications of secreted CTSD, MMP9, proBDNF, mBDNF of WT and *Fkbp5* KO SIMA-9 cells treated with vehicle or 300 nM Dex for 4 hours. **g)** ProteinSimple quantifications of secreted CTSD, MMP9, proBDNF, mBDNF of WT and *Sec22b* KO SIMA-9 cells treated with vehicle or 300 nM Dex for 4 hours. f) and g) Data shown as mean $\pm$ s.e.m. of n=3 biologically independent samples. Tukey's multiple comparison tests were performed; only significant comparisons are shown. *p < 0.05; **p < 0.01; ***p < 0.001; ****p < 0.0001.

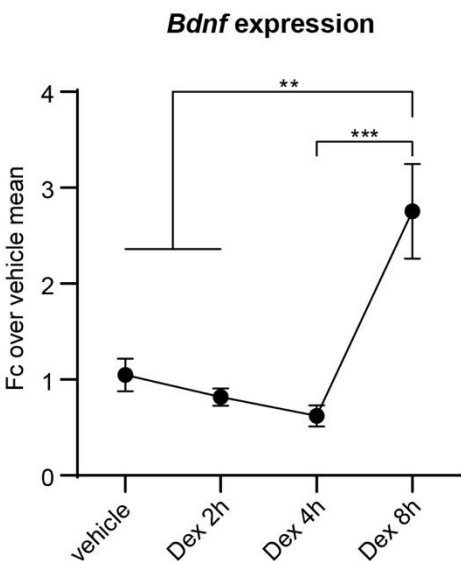


Figure S5

Quantitative polymerase chain reaction (qPCR) of *Bdnf* expressed in SIM-A9 cells treated with vehicle or 100 nM Dex for 2, 4 and 8 hours. Data shown as mean $\pm$ s.e.m. of n=3 biologically independent samples. Tukey's multiple comparison test was performed; **P < 0.01; ***P < 0.001.

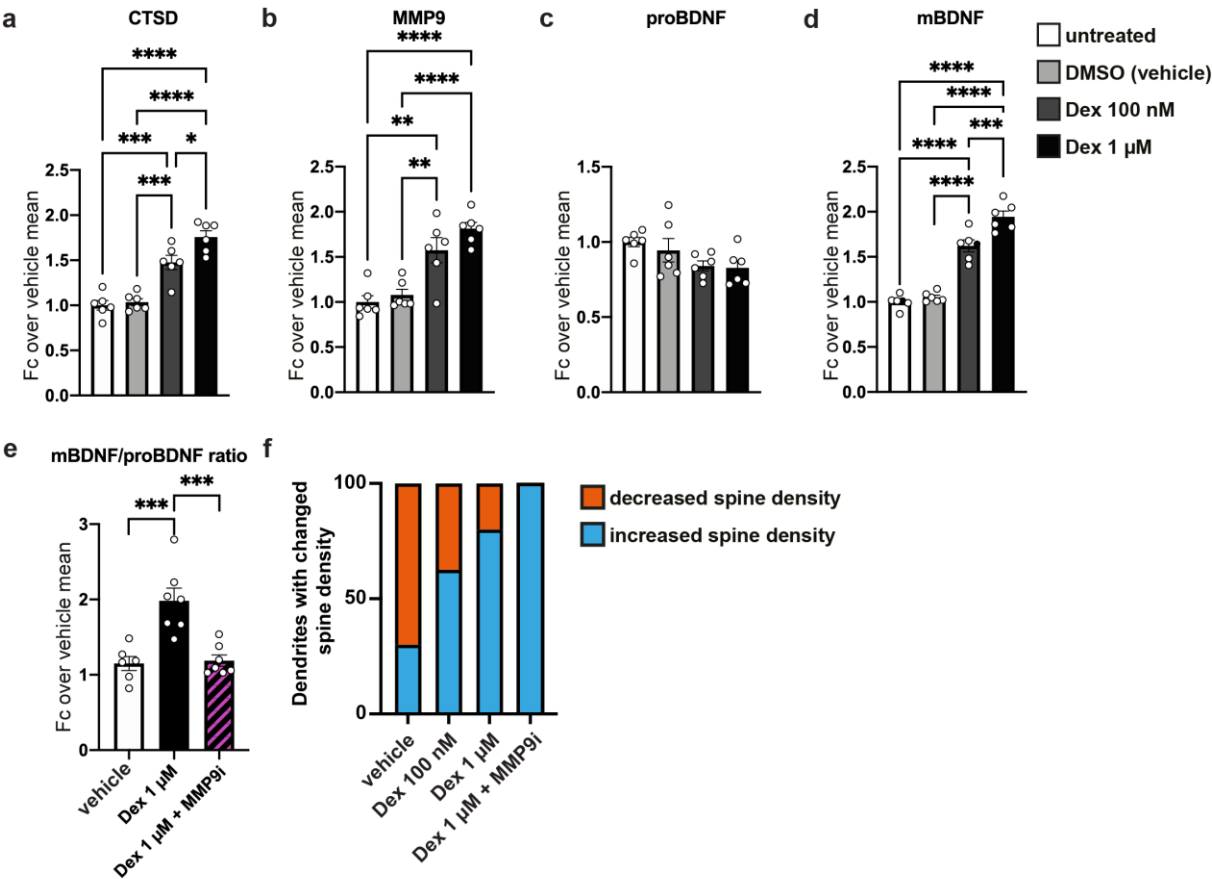


Figure S6

a-d) Quantifications of western blotting for CTSD, MMP9, proBDNF, mBDNF from culture media of OHSC treated with vehicle (DMSO), 100 nM Dex, 1 μ M Dex or nothing (untreated) for 4-6 hours; Data shown as mean $\pm$ s.e.m. of n=6 biologically independent samples. **e)** Ratio of mBDNF over proBDNF relative to Fig. 6 d and e. Data shown as mean $\pm$ s.e.m. of n=7 biologically independent samples. Tukey's multiple comparison tests were performed; only significant comparisons are shown. *p < 0.05; **p < 0.01; ***p < 0.001; ****p < 0.0001. **f)** Quantification of imaged spine densities of OHSC treated with vehicle (DMSO), 100 nM Dex,

69 1 μ M Dex and 1 μ M Dex + MMP9i expressed as percentage of dendrites with changed spine
70 densities over the 30 min imaging span, and subdivided into increased and decreased spine
71 densities.

List of references to neuroplasticity-related proteins listed in Table 1

Protein	Reference
APP	1–3
JUN	4,5
VIM	6,7
CDC42	8,9
MMP9	10–12
CCL2	13,14
EEF2	15–17
HMGB1	18
IGF1	19–21
KDR	22,23
LRP1	24–27
PAK1	28,29
PAK3	30,31
STMN2	32,33
TF	34
TGFB1	35–37
CAT	38,39
HMOX1	40
JUNB	41

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