Supplemental Information

Supplemental Information encompasses 5 figures (figures S1-S5), associated figure legends and two tables (tables S1 and S2).

Supplemental Figure Legends

Figure S1 related to figure 1: In response to TNF the proteolytic turnover of p105 (NF-κ**B1) and I**κ**B**ε **but not p100 (NF-**κ**B2) is regulated in a phosphorylation- and CRL-dependent manner in the cytosol and the nucleus.** After pre-treatment with MLN4924 (3 µM) 10 min prior to TNF (10 ng/ml) stimulation, cells were harvested by subcellular fractionation at indicated times. Leptomycin B (LMB, 10 ng/ml) was added 15 min after TNF stimulation to prevent Crm1 dependent nuclear export. Samples, as indicated, were analyzed by IB. Detection of either Tubulin (cytosol) or HDAC1 and Lamin B2 (total nuclear fractions, N_t) was performed for control of fractionation success and equal protein load.

Figure S2 related to figure 2: Classical IKKs (the IKK complex) but not IKK-related kinases (IKKε **and TBK1) regulate the UPS-dependent degradation of I**κ**B**α **and the liberation of RelA in response to TNF.** A) The IKK complex but not phosphoinositol-3-kinase (PI3K) promotes phosphorylation and UPS-dependent turnover of $\text{lkB}\alpha$ in response to TNF. B) IKKrelated kinases are dispensable for the TNF-induced phosphorylation of $I_{\kappa}B_{\alpha}$ and ReIA as well as the UPS-dependent degradation of $\text{IkB}\alpha$ in the cytosol, but appear to contribute to the limitation of either the nuclear accumulation or the residence/turnover of (phosphorylated) RelA. A, B) Subcellular fractions of cells treated with either the $IKK\alpha/\beta$ -selective inhibitor TPCA-1 (10 µM), the IKKα/β-selective inhibitor BMS-345541 (25 µM), the PI3K inhibitor wortmannin (10 µM) or the selective IKKε/TBK1 inhibitor MRT67307 (10 µM), as indicated, 20 min prior to TNF stimulation (10 ng/ml) were prepared at indicated times. Cells were not treated with Leptomycin B. Samples, as indicated, were analyzed by IB. Detection of Tubulin (cytosol), Nucleolin (soluble nuclear fraction, N1) or HDAC1 and Lamin B2 (insoluble nuclear fraction, N2) was performed for control of fractionation success and equal protein load.

Figure S3 related to figure 3: p97/VCP promotes cell proliferation and protects from apoptosis induction. RNAi-mediated depletion of p97/VCP (transiently) decelerates cell proliferation and initiates apoptosis. Cells (6.000/well) were seeded in two triplicates 1 day after siRNA treatment. Every 24h cell numbers (mean, $n = 6$, left panel) were determined by use of Cell Titer-Glo® Luminescent Cell Viability Assay. p97/VCP knockdown efficiency and induction of apoptosis were analyzed by IB analysis of RIPA cell lysates the third day after siRNA transfection (insert). Differences between control and knockdown cells at selected times after siRNA transfection are additionally presented in a bar chart diagram (mean cell numbers +/- s.d., $n = 6$, right panel). All data derive from one representative experiment. (*, $p \le 0.01$).

Figure S4 related to figure 4: Functional inactivation of p97/VCP does not affect cell viability upon TNF stimulation. Cells (20.000/well) were seeded in triplicate one day prior to serum starvation overnight. Serum-starved cells were then exposed to either p97/VCP inhibitor NMS-873 (2,5 µM, 20 min) or CHX (30 µg/ml, 5 min) prior to TNF stimulation (10 ng/ml in perpetuated presence of the inhibitors) for the indicated times. Afterwards, Cell Titer-Glo[®] Luminescent Cell Viability Assay, calibrated to determine cell numbers, was performed. Data (mean cells numbers $[%]$ +/- s.d. $[CV\%]$; n = 3) obtained from one representative experiment are presented. $(*, p \le 0.01)$.

Figure S5 related to figures 3-5: Structural organization and sites of functional relevance in human p97/VCP. The structural organization of human p97/VCP (P55072.4) is illustrated.

Borders of domains and motifs, as well as well as the location of relevant functional sites were retrieved from the NCBI Protein Database. N1 and N2, subdomains of the p97/VCP N-domain; D1 and D2, p97/VCP ATPase domains; D1 α and D2 α , C-terminal α -helical subdomains of the ATPase domains; C, C-terminal oligomerization domain; WA and WB, Walker A (aa 245-252 and aa 518-525) and Walker B motifs (aa 300-305 and aa 573-578) of the ATPase domains, involved in nucleotide binding (WA) and ATP hydrolysis (WB) respectively [Wang et al., 2005]; Rfinger, arginine finger, being part of the second region of homology (SRH), situated in the ATPase domains, which is involved in interprotomer communication and wiring of conformational changes within the p97/VCP hexamer during ATP hydrolysis [Wang et al., 2005]. The SRH of the D1 domain additionally contributes to poly-Ub-substrate binding of the N-domain and cofactor communications with the chaperone [Wang et al., 2005]. Under physiologic conditions, the D2 domain is responsible for the majority of p97/VCP ATPase activity, whereas (stable) nucleotide binding in the D1 domain [DeLaBarre and Brunger, 2003] primarily contributes to hexamer formation and binding of ubiquitinated client proteins with the help of adapter proteins [Wang et al., 2005], e.g. the UFD1L-NPL4 heterodimer involved in the association of p97/VCP with lk_α -Ub [Li et al., 2014]. The Following information is additionally provided: (I) Binding sites for p97/VCP adapter proteins, being recruited to the p97/VCP N-domain or C-terminus via the indicated domains or motifs present in the adapter proteins [Meyer and Weihl, 2014]. Association of the UFD1L-NPL4 heterodimer with the p97/VCP N-domain is accomplished via a UBX-L domain and a SHP motif located in NPL4 and UFD1L respectively [Meyer and Weihl, 2014]. (II) The epitopes recognized by different p97/VCP-specific antibodies available from *Santa Cruz Biotechnology* (sc-catalogue number) and *Abcam* respectively (ab catalogue number). The antibodies from *Abcam* are functional according to our experience, but were not applied in the present study. (III) The target sites of p97/VCP inhibitors, including their mechanism of action, according to published reports [Chou et al., 2011; Chou and Deshaies, 2011; Magnaghi et al., 2013]. NMS-859 [Magnaghi et al., 2013] shares the mechanism of action with MDBN, but was not used in the present study. The binding site for allosteric p97/VCP inhibitor NMS-873 was determined [Magnaghi et al., 2013].

Supplemental References

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Supplemental Tables

Table S2: Secondary antibodies used in the study

Fig S2 IKK complex, but not IkKε **mediates the degradation of I**κ**B**α **and the release of RelA**

Fig S3 p97/VCP promotes cell proliferation and protects from apoptosis induction

Fig S5 Structural organization and sites of functional relevance of human p97/VCP