

Figure S-1. The novel NF- κ B activation/TRAF2 binding site is highly conserved. Multiple sequence alignment of TNFR2 intracellular region from different species: *Homo sapiens*, *Pan troglodytes*, *Macaca mulata*, *Mus musculus*, *Rattus norvegicus*, *Ailurupoda melanoleuca*, *Bos Taurus*, *Sus scrofa*, *Equus caballus* and *Canis familiaris*. The residues with 100% identity are shaded in black and those with 80% identity are shaded in grey. Numbers indicate the aminoacid position in the full-length human sequence. The alignment was generated using ClustalW and edited with GENEDOC. The Roman numerals I, II and III refer to the conserved modules found in TNFR2.

Figure S-2. The region comprising aminoacids 343-349 of TNFR2 is responsible of TRAF2 depletion induced by the receptor. A) Schematic representation of deletions and mutations of the region 343-379 of TNFR2. Diagrammatic representation of TNFR2 deletions and mutants is as in figure 2. The ability to induce degradation of TRAF2 is also indicated on the right. B) Analysis of TRAF2 degradation by different TNFR2 variants affecting the region 343-349. HEK 293 cells were transiently transfected with 0.3 μ g de pRK-Myc-TRAF2 and increasing amounts of pR2-BKO- Δ 365-378, pR2-BKO- Δ 344-356 or pR2-BKO- Δ 350-378 (all FLAG tagged) as indicated. 36 h after transfection cells were harvested and lysed. Equal aliquots of the lysates were resolved by SDS-PAGE and Western blotted with anti-TRAF2, anti-FLAG (receptors) or anti- β -actin antibodies.

FIGURE S1

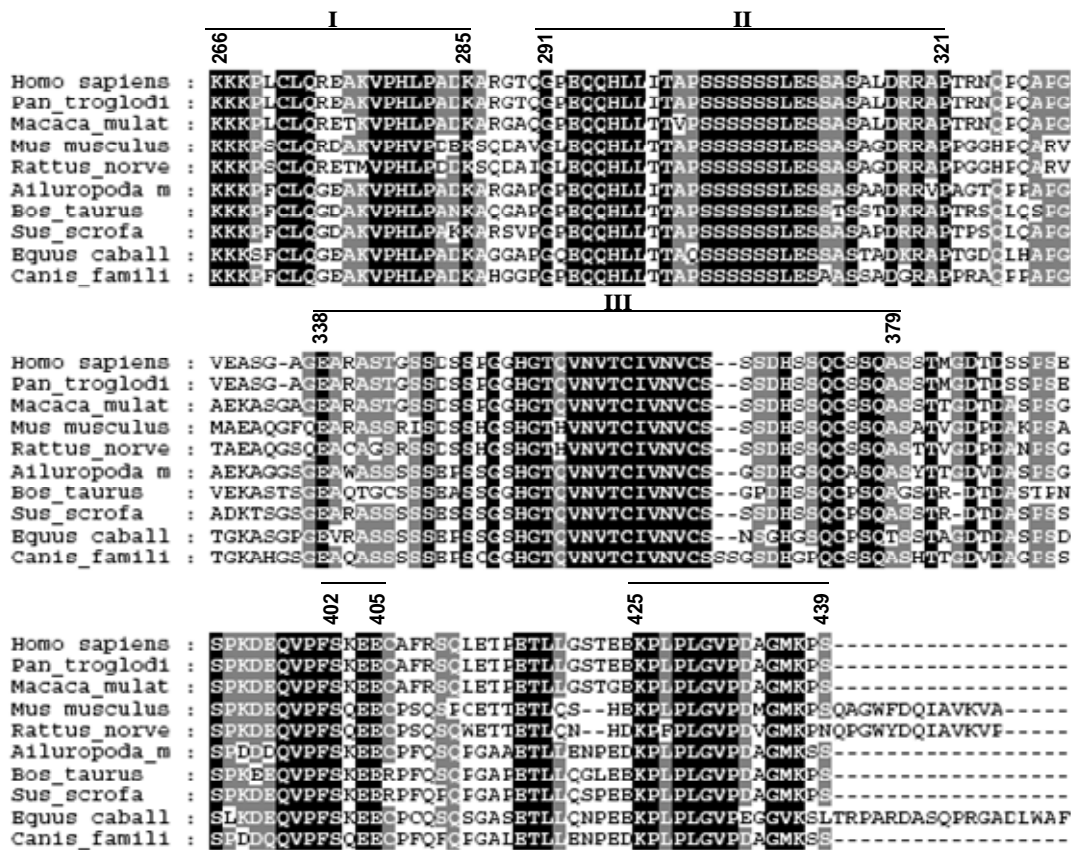


FIGURE S2

