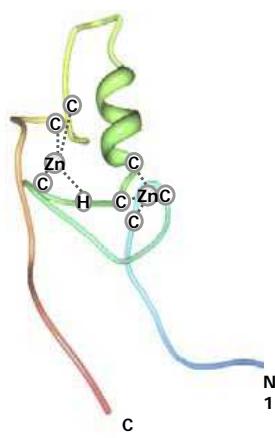
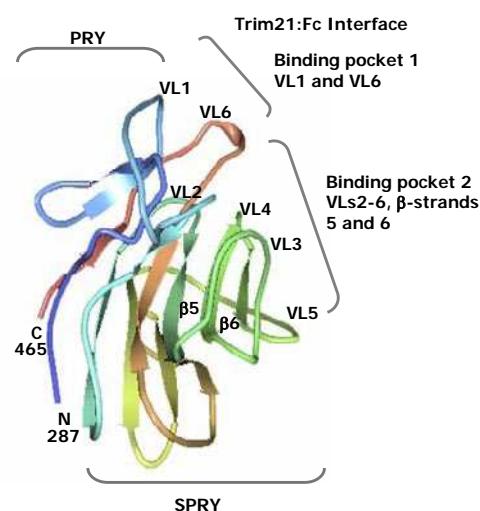
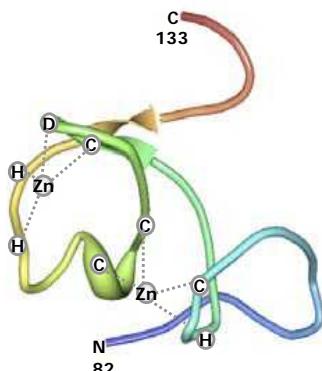


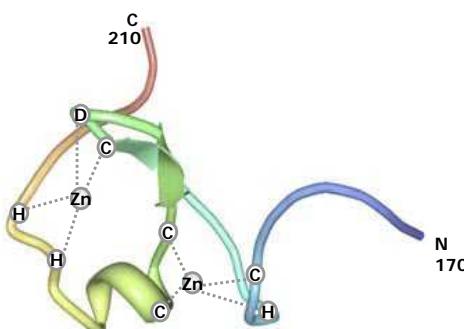
S2 Figure

A Human TRIM5 α RING

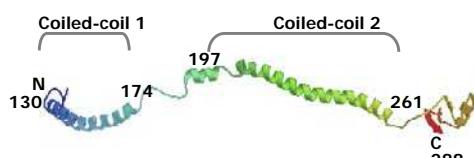
TRIM5 α 15 18 30 32 35 38 55 58
 huTRIM5 α (1) - MASGI LVNVKEEVTCPI CLELLTOPLSLDCGHSHFCOACITANHKSMLDKG- ESSCPVCRI SYOPENI RP NRHVANI VE (78)
 huTRIM21 (1) MASAARLTMMEEVTCPICLDPFVEPVSI ECCHSHFCOECISQVG-----KGG- GSVCPVCRI QRFLLKNLRPNRQLANMW(74)
 huTRIM34 (1) - MASKIL LNVQEETCPICLELLTEPLSLDCGHSHLCRACITVSNKEAVTSMGKSSCPVCGISYSFELQANOHLANI VE (79)
 Consensus MAS IL NV EEVTCPI CLELLTEPLSLDCGHSHFCOACIT K G SSCPVCRI SY ENLRPNRHLANI VE

D Human TRIM21 PRYSPRY**B Human TRIM5 α B-Box2**

TRIM5 α 95 98 106 109 114 117 123 126
 huTRIM5 α (86) SPE- GQKVDHCARGEKLLLFCQEKGKVI CW LCERSQE HRRHHITF (129)
 huTRIM21 (82) EAREGTGGERCAVHGERLHLF CEKDKALCW VCAOSRKHRDHAMV (126)
 huTRIM34 (87) SP DNGK KRDL CDHIGEKLLLFC KCEDRKVI CW LCERSQE HRRHHITV (131)
 Consensus SP G K D CA H GEKL LLL FC EDGKVI CW LCERSQE HRRHHITV

Human MID1 B-Box2

MID1 175 178 187 190 195 198 204 207
 huMID1 (170) I RGL MCLEHE DEKVNMYCVSDQOL CAL CKLV GRHRDHQVAAL (212)
 huMID2 (171) LRGIT CLDHE NEKVNNMYCVSDQOL CAL CKLV GRHRDHQVAL (213)
 Consensus I RGI CLDHE EKVNNMYCVSDQOL CAL CKLV GRHRDHQVAAL

C Human TRIM5 α coiled-coil

Coiled-coil 1
 huTRIM5 α (130) L TEEVARE YQVKL QAALEM LROKQEA EELADI REEKASWK TQI OYDKTNVL ADFEQL RDI L DWEESNE L ONL EKEEE (208)
 huTRIM21 (127) P LEEAAQEYQEKL QVALGEL RRKQEL AEKLEV EIAI KRADWKKT VETOKSR I HAEFVQOKNF L VEEEOQRL QEL EKDER (205)
 huTRIM34 (132) L TEEVF KECOEKL QAVLK RL KKEEEA EAKLEADI REEKASWK YQVOTERORI QT EFDQRLS I L NNEE OREL QRL EEEEK (210)
 Consensus LTEEVA EYQEKL QAAAL LR KQEA EAKLEADI REEKASWK QVOT K RI AEF QLR IL EEORELQ LEKEE

Coiled-coil 2
 huTRIM5 α (209) D I LKSL TNSET EMV QOT S LRE I S DLE HRL QGS VM ELL QGV DGV I KRTEN VTL KKPET FPKN ORRV F RAP DL KGM L E VF (288)
 huTRIM21 (206) EOLRI L GEKEA LKAQOS QAL QEL I SEL DLR CRHSS A L L QEV I V L ERS E WNL KDL DI TSPE L RSV CHV P GL KML RTC (285)
 huTRIM34 (211) K TLDKFA EAEDEL VQOKL VREL I SDV C R S QNS TME L L QDMG I MKWS E I WRL KKP KM VSK L KTV F HAP DLS RML QMF (290)
 Consensus L L E E ELVQ O L REL I S DLE R Q S M L L O V GV KRSE W L KKP SK LR VF HAP DL K M L F

SUPPLEMENTARY INFORMATION

3D structures of TRIM domains

(A) The RING domain. Nuclear magnetic resonance (NMR) analysis of tripartite motif-containing 5 α (TRIM5 α), deposited by Abe, H. *et al.* (PDB ID: [2ECD](#) in the RCSB Protein Data Bank). The RING-finger motif (from C15 to C58) coordinates two zinc atoms. Comparison of the RING domain amino-acid sequences in three TRIM members with the cysteine (C) and histidine (H) residues involved in zinc-binding are marked with asterisks (*). The grey blocks indicate the conserved regions that contain identical and related amino acids. The rainbow colour represents the N-terminal to C-terminal orientation.

(B) The B-Box domain (B-BOX 2 motif). NMR analysis of TRIM5 α , deposited by Qin, X. R., Hayashi, F. & Yokoyama, S. (PDB ID: [2YRG](#)). The MID1 B-Box is from Massiah, M. *et al.*¹ (PDB ID: [2DQ5](#)). This domain also has a zinc coordinating motif with cysteine (C) and aspartic acid (D) or histidine (H) marked by asterisks.

(C) The coiled-coil domain. Predictions by the (PS)²: protein structure prediction server for the indicated TRIM members. Grey blocks indicate predicted coiled-coil structures.

(D) The PRYSPRY (also known as B30.2) domain. Crystal structure analysis of TRIM21 is by James, L. C. *et al.*² (PDB ID: [2IWG](#)). These domains of TRIM21 interact with the Fc domain of IgG. The PRY and SPRY subdomains are indicated by lines.

1. Massiah, M. A. *et al.* Solution structure of the MID1 B-box2 CHC(D/C)C₂H₂ zinc-binding domain: insights into an evolutionarily conserved RING fold. *J. Mol. Biol.* **369**, 1–10 (2007).
2. James, L. C., Keeble, A. H., Khan, Z., Rhodes, D. A. & Trowsdale, J. Structural basis for PRYSPRY-mediated tripartite motif (TRIM) protein function. *Proc. Natl Acad. Sci. USA* **104**, 6200–6205 (2007).