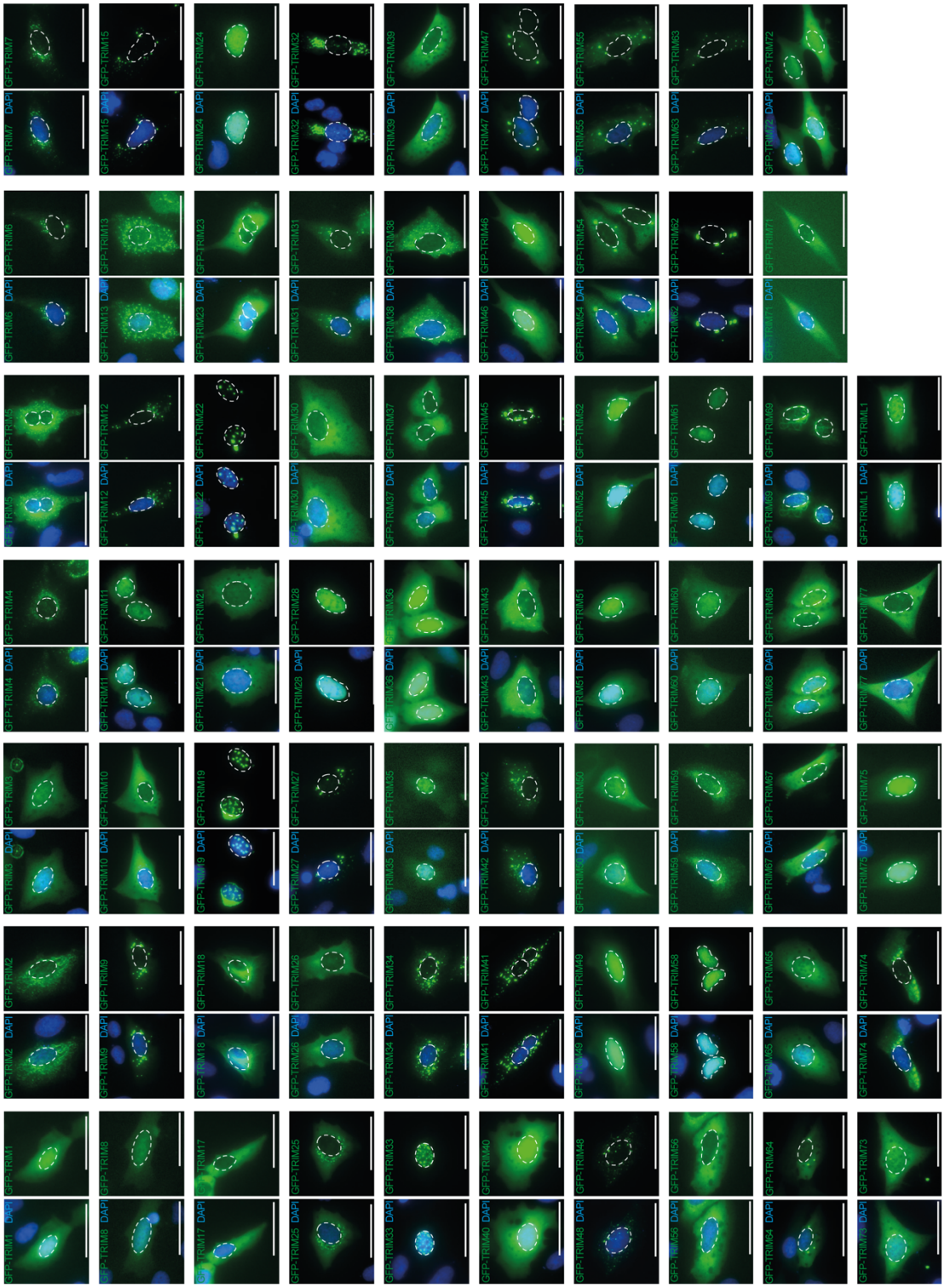
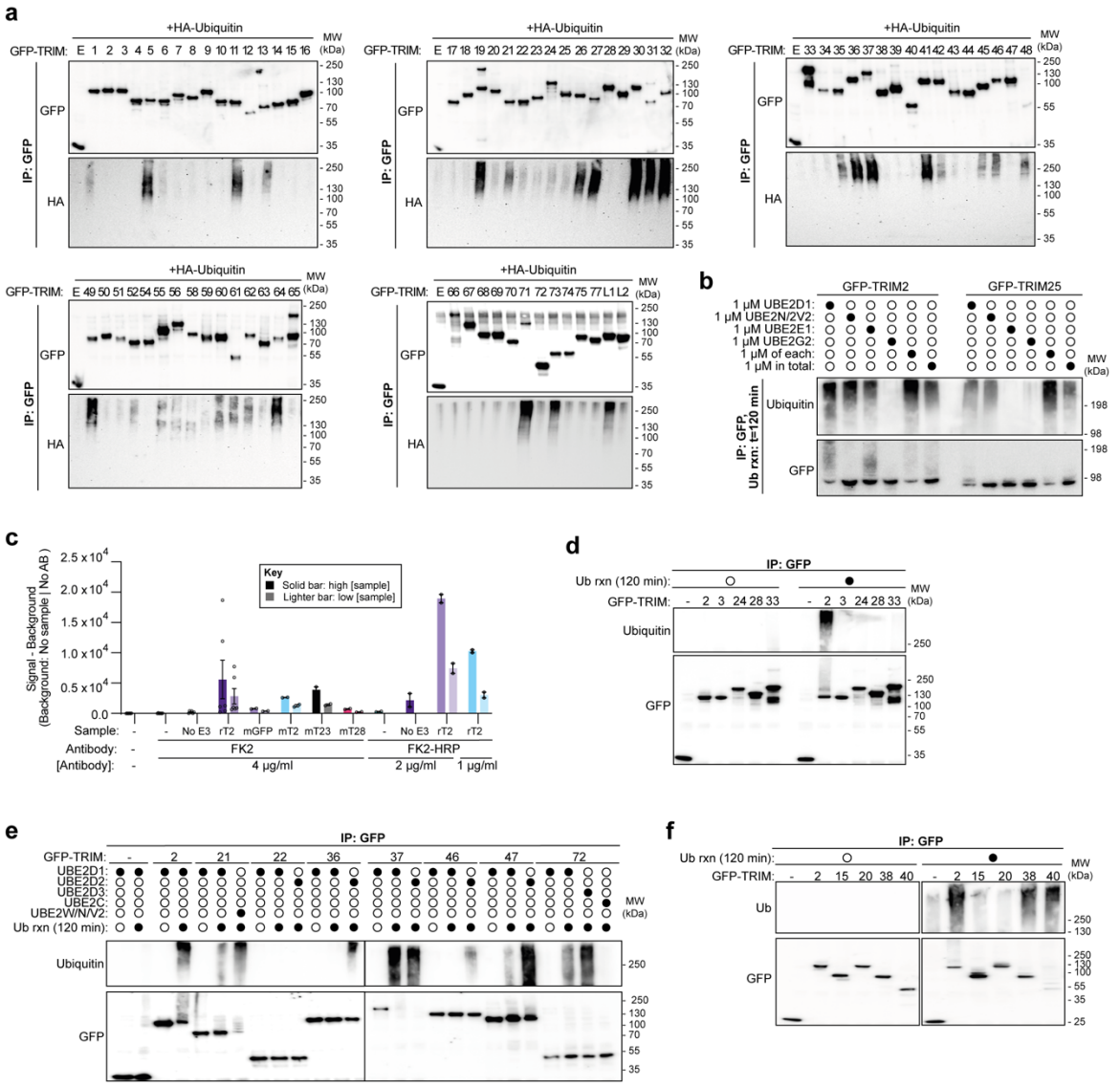


Supplementary Figure 1 – Localisation of RING-containing TRIM proteins

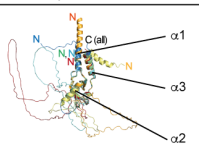
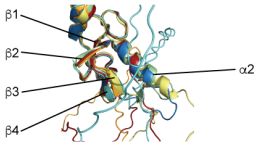
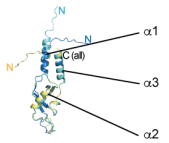
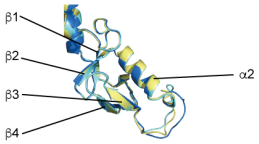
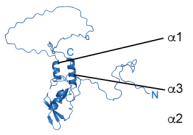
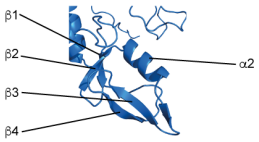
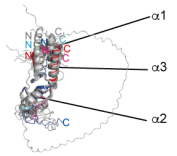
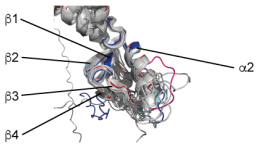
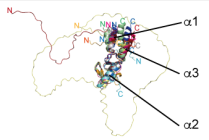
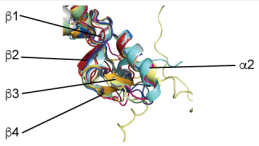
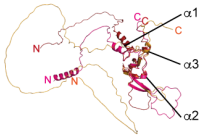
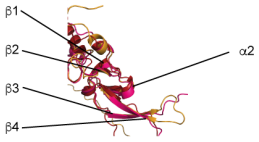
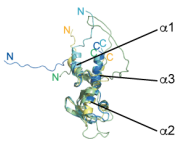
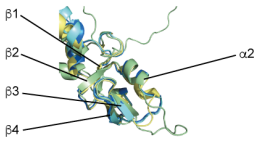
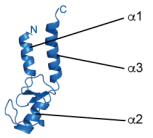
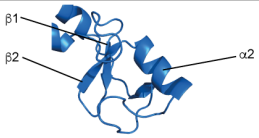
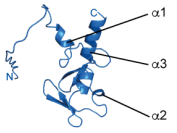
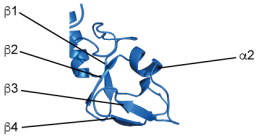
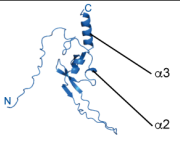
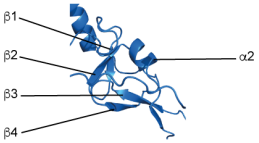
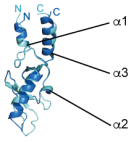
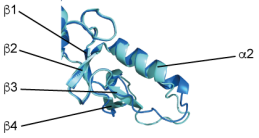
Representative images U2OS cells transiently over-expressing GFP-tagged RING-containing TRIM proteins 1 through to L1 (green), which were fixed and stained with DAPI (blue). Dashed lines denote the nucleus and the scale bars represent 50 μm. Images represent n=3.



Supplementary Figure 2 – Data supporting screening TRIM family for in-cell and in vitro auto-ubiquitination activities

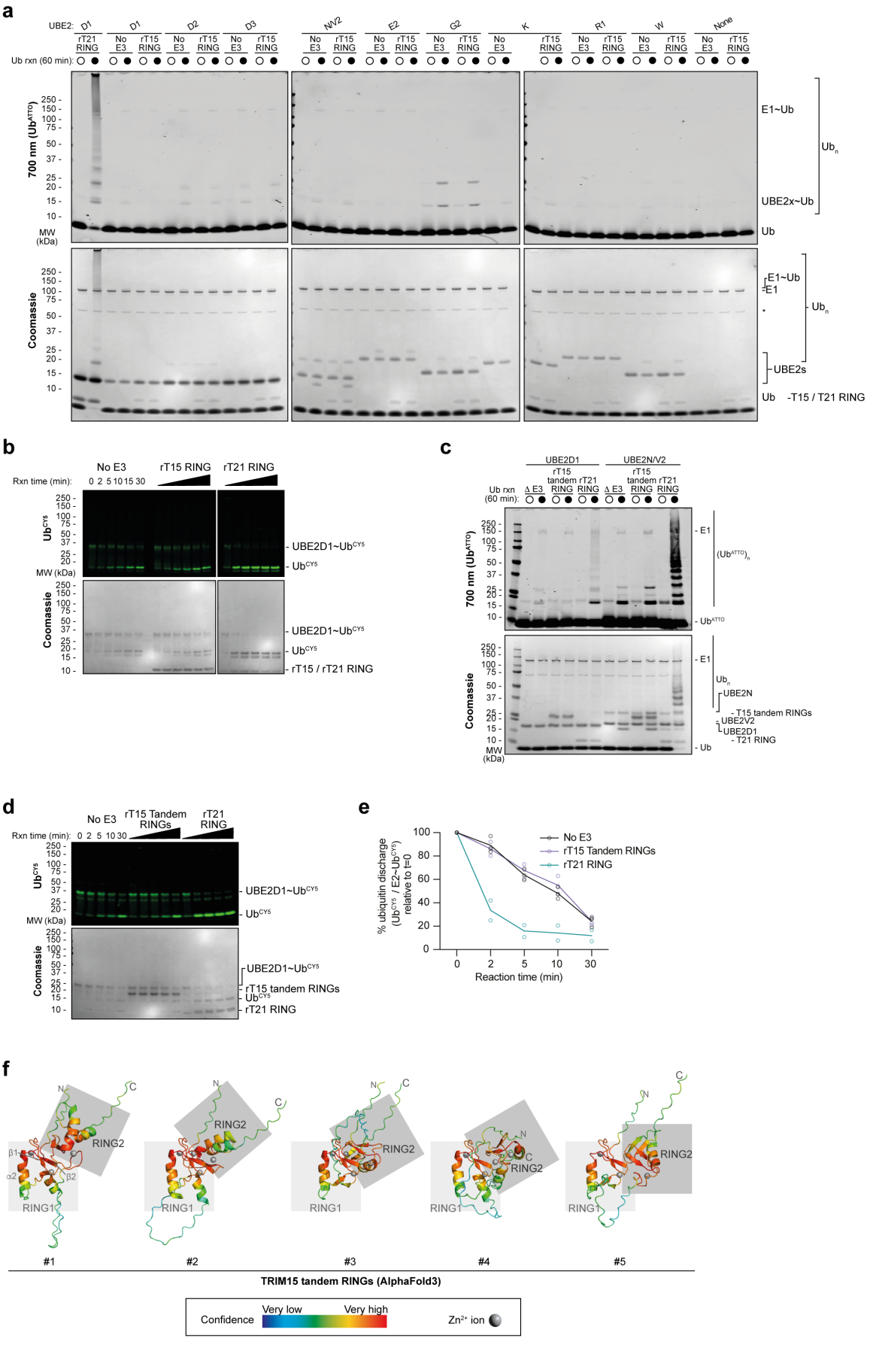
a, Relating to **Fig. 1f**, representative western blots using the indicated antibodies to detect in-cell TRIM ubiquitination using immunoprecipitated GFP-TRIMs transiently co-overexpressed with HA-Ubiquitin in HEK293T cells, treated with 10 µM PR619 and 10 µM MG132 4 h before lysis (n=3). **b**, Western blots using the indicated antibodies, demonstrating the efficacy of mixing E2 enzymes for in vitro auto-ubiquitination assays with GFP-tagged TRIM2 and TRIM25 isolated from HEK293T cells (n=2). **c,** Graph representing the validation of an ELISA assay specific to conjugated ubiquitin for assessment of in vitro auto-ubiquitination, using reaction mix without E3 or GFP only (negative controls), recombinant

TRIM2 RING domain (rT2: positive control) and full-length mammalian cell-derived TRIMs (mT2, mT23, or mT28) at high or low dilutions in the assay. FK2 antibody followed by anti-mouse-HRP was used to trial an indirect ELISA, whilst FK2-HRP was able to demonstrate the enhanced sensitivity of a direct ELISA (n=2). Error bars: mean ± SEM. **d**, Western blot using the indicated antibodies against immunoprecipitated GFP-tagged TRIM proteins from HEK293T cells and then used in an in vitro ubiquitination assay for 0 or 120 min with a mix of E2 enzymes as in **Fig. 1f** (n=3). **e**, Western blot using the indicated antibodies against immunoprecipitated GFP-tagged TRIM proteins purified from HEK293T cells, which were then used in an in vitro ubiquitination assay for 0 or 120 min with different E2 enzymes (UBE2C, UBE2D1, UBE2D2, UBE2D3, or a mix of UBE2N/UBE2V2/UBE2W) (n=3). **f**, Western blot using the indicated antibodies against immunoprecipitated GFP-tagged TRIM proteins purified from HEK293T cells, which were then used in an in vitro ubiquitination assay for 0 or 120 min with the mix of E2s as specified in **Fig. 1f** (n=3). Source data are provided as a Source Data file.

TRIM class	Class members	RING overview AlphaFold2	Core RING AlphaFold2	Notable predicted features
Class I	TRIM1 TRIM9 TRIM18 TRIM36 TRIM46 TRIM67			TRIM9, TRIM36, TRIM46, TRIM67 Long loop between α2 and β3
Class II	TRIM54 TRIM55 TRIM63			
Class III	TRIM42			TRIM42 Long N-terminus preceding RING domain
Class IV	TRIM4 TRIM5* TRIM6 TRIM7 TRIM10 TRIM11 Trim12 TRIM15 TRIM17 TRIM21* TRIM22 TRIM25* TRIM26 TRIM27 Trim30 TRIM34 TRIM35 TRIM38 TRIM39 TRIM41 TRIM43 TRIM47 TRIM48 TRIM49 TRIM50 TRIM51 TRIM58 TRIM60 TRIM62 TRIM64 TRIM65 TRIM68 TRIM69* TRIM72 TRIM75 TRIM77 TRIML1			TRIM6 Unfolded α2 TRIM15 Unfolded α1, 2, 3 and β3, 4 TRIM51 Unfolded β3, 4 TRIM41 Long loop between α2 and β3 See Fig. 2
Class V	TRIM8 TRIM19* TRIM31 TRIM40 TRIM52 TRIM56* TRIM61 TRIM73 TRIM74			TRIM8, TRIM19, TRIM40 Unfolded β3, 4 TRIM52 Long loop between α2 and β3 TRIM19 Long N-terminus preceding RING domain
Class VI	TRIM24 TRIM28* TRIM33			TRIM24, TRIM28 Largely unfolded α1, 2, 3 TRIM33 Unfolded α1, largely unfolded α2, 3 All Long N-terminus preceding RING domain
Class VII	TRIM2* TRIM3 TRIM32* TRIM71			TRIM3 Unfolded α1
Class VIII	TRIM37*			TRIM37 Unfolded β3, 4
Class IX	TRIM23*			
Class X	TRIM45			TRIM45 Unfolded α1, long loop between α2 and β3
Class XI	TRIM13 TRIM59			TRIM59 Unfolded β3, 4

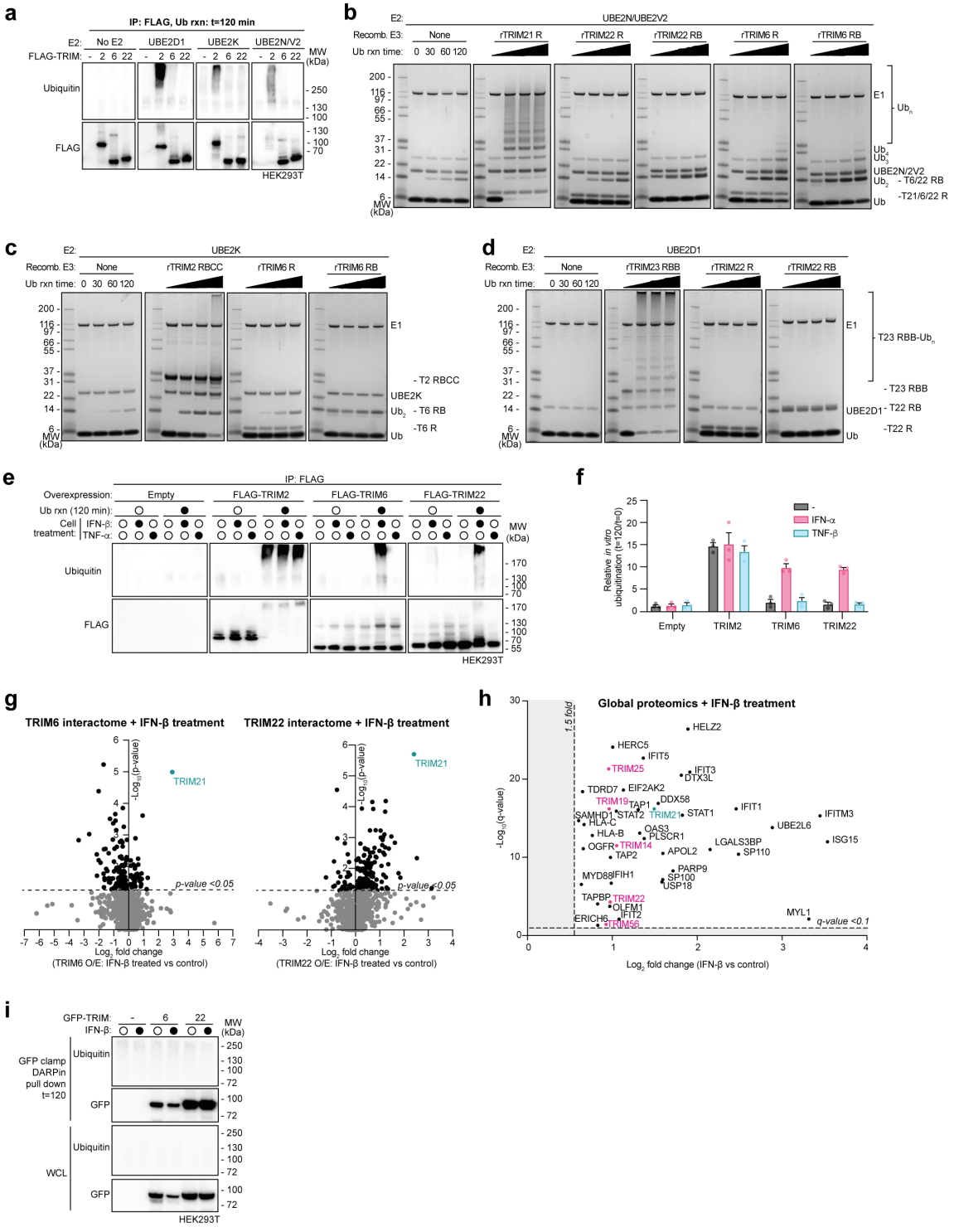
Supplementary Figure 3 – AlphaFold2 *in silico* analyses of TRIM family proteins highlights notable structural differences, including in TRIMs identified as inactive

Table of AlphaFold2 structural predictions of TRIM RING domains (N-terminal Met to end of α3 helix, or with a sequence of corresponding length where no α3 helix is predicted), aligned and arranged according to class designation, with descriptions of notably divergent structural features given for some TRIMs. * indicates TRIMs with a RING domain structure available in the PDB (TRIM2: 7ZJ3; TRIM5: 4TKP; TRIM19: 5YUF; TRIM21: 5OLM, 6FGA, 7BBD, 6S53; TRIM23: 5CZV; TRIM25: 5EYA, 5FER; TRIM28: 6QAJ, 6I9H; TRIM32: 5FEY; TRIM37: 3LRQ; TRIM56: 5JW7; TRIM69: 6YXE).


a
UBE2: D1 D1 D2 D3 Nv2 E2 G2 K R1 W None
rT21 RING
No E3
rT15 RING
Ub rxn (60 min):
700 nm (Ub^ATTO)
Coomassie
MW (kDa)
250 - 150 - 100 - 75 - 50 - 37 - 25 - 20 - 15 - 10 -
E1~Ub
UBE2x~Ub
Ub
Ub_n
E1
UBE2s
Ub -T15 / T21 RING
b
No E3
rT15 RING
rT21 RING
Rxn time (min): 0 2 5 10 15 30
Ub^CY5
UBE2D1~Ub^CY5
Ub^CY5
rT15 / rT21 RING
c
UBE2D1
UBE2N/V2
rT15 tandem rT21 RING
Δ E3
Ub rxn (60 min):
700 nm (Ub^ATTO)
Coomassie
E1
(Ub^ATTO)_n
Ub^ATTO
Ub_n
UBE2N
- T15 tandem RINGs
UBE2V2
UBE2D1
- T21 RING
Ub
d
No E3
rT15 Tandem RINGs
rT21 RING
Rxn time (min): 0 2 5 10 30
Ub^CY5
UBE2D1~Ub^CY5
Ub^CY5
rT15 tandem RINGs
rT21 RING
e
% ubiquitin discharge (Ub^CY5 / E2~Ub^CY5) relative to t=0
100 80 60 40 20 0
No E3
rT15 Tandem RINGs
rT21 RING
0 2 5 10 30
Reaction time (min)
f
RING1
RING2
β1
β2
α2
N
C
#1 #2 #3 #4 #5
TRIM15 tandem RINGs (AlphaFold3)
Confidence
Very low
Very high
Zn2+ ion

Supplementary Figure 4 – Data supporting TRIM15 has a monomeric RING domain that does not demonstrate ubiquitin ligase activity in isolation

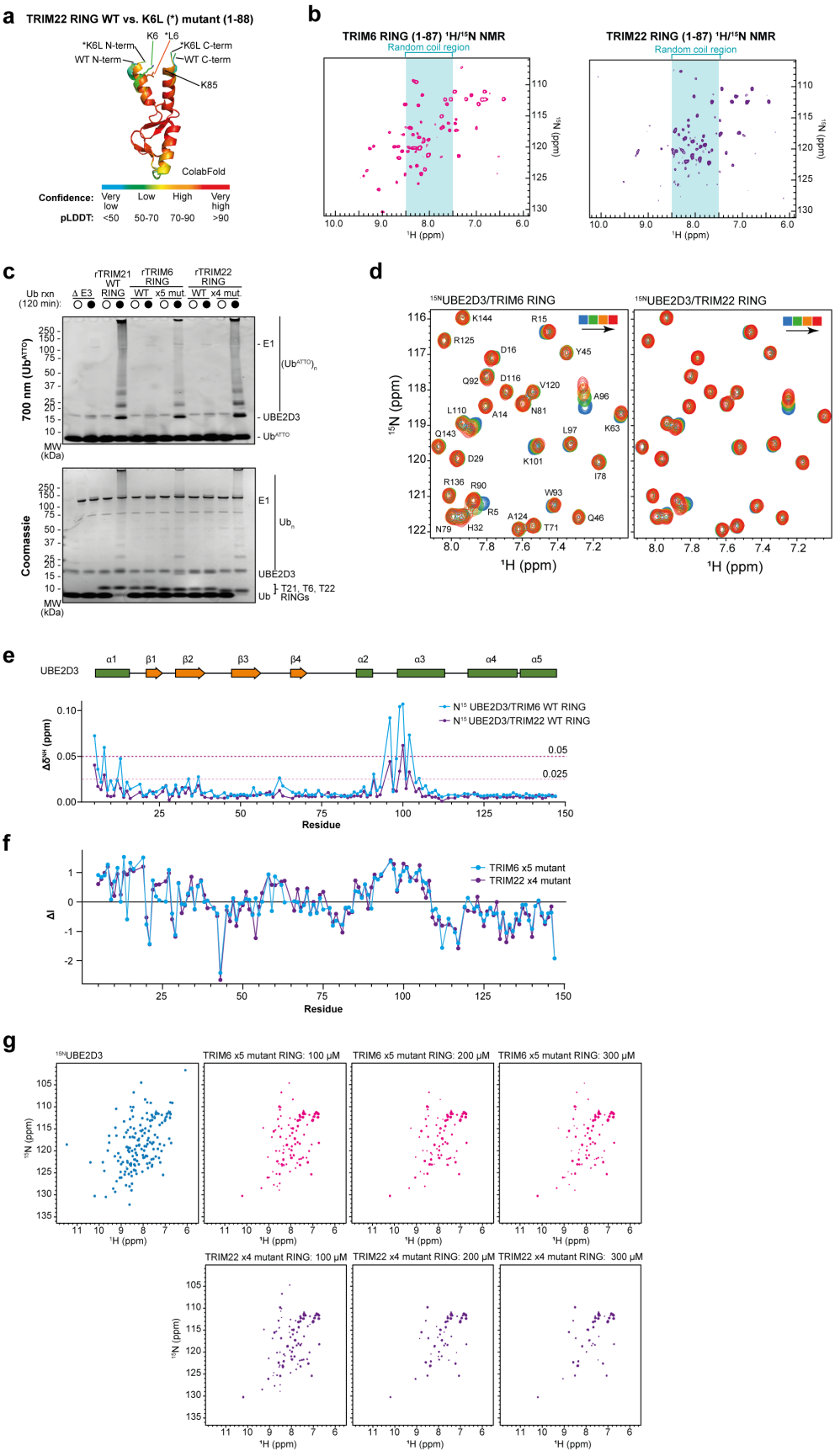
a, Fluorescent and Coomassie gel scans of auto-ubiquitination reaction carried out at 30 °C 60 min using 1 μM of each of the indicated E2 enzymes (UBE2R1, D1, D2, D3, N/V2, W, G2, K, or E2) with 1 μM UBA1, 50 μM ubiquitin, 1 μM UbATTO, and 3 mM ATP, using no E3 or 4 μM of recombinant TRIM23 RBCC or TRIM15 RING (n=2). **b**, Fluorescent and Coomassie gel scans showing the discharge of Ub^{CY5} from pre-charged UBE2D1 onto free lysine in solution, with 4 μM recombinant TRIM21 RING domain or recombinant TRIM15 RING domain, or with no E3 (see **Fig. 3b**, n=3). **c,** Fluorescent and Coomassie gel scans of auto-ubiquitination reaction carried out at 30 °C 60 min using 1 μM of UBE2D1 or UBE2N/V2 with 1 μM UBA1, 50 μM ubiquitin, 1 μM UbATTO, and 3 mM ATP, using no E3 or 4 μM of recombinant TRIM21 RING or TRIM15 tandem RING domains (n=3). **d**, Fluorescent and Coomassie gel scans showing the discharge of Ub^{CY5} from pre-charged UBE2D1 onto free lysine in solution, with 4 μM recombinant TRIM21 RING domain or recombinant TRIM15 tandem RING domains, or with no E3 (n=3). **e**, Quantification of n=3 repeats of the experiment in part **d**. **f**, Top 5 AlphaFold3 models of TRIM15 tandem RING construct (with 4 x Zn^{2+}, grey), aligned according to α2 of the first RING domain, with the second RING domain demonstrating 5 distinct conformations, as highlighted by the grey boxes (light grey: RING1 orientation, dark grey: RING2 orientation). Source data are provided as a Source Data file.



Supplementary Figure 5 – Analysis of TRIM6 and TRIM22 activity in response to interferon signalling

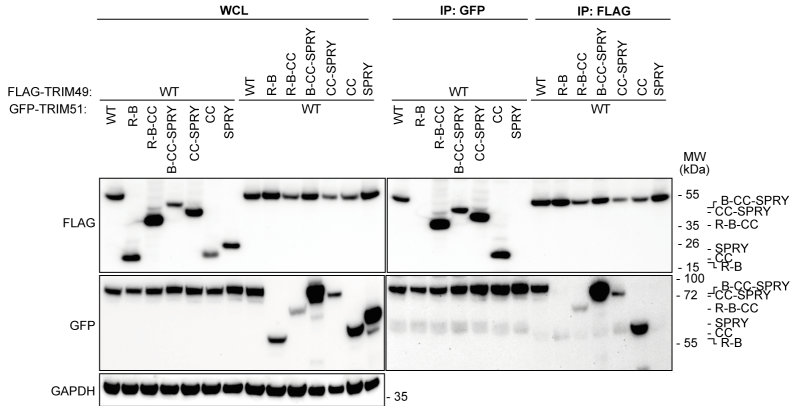
a, Western blots using the indicated antibodies against immunoprecipitated FLAG-tagged TRIM proteins purified from HEK293T cells, which were then used in an in vitro ubiquitination assay for 120 min with 1 μM of specified E2 enzymes (or no E2 control) with 1 μM UBA1, 50

μM ubiquitin, and 3 mM ATP (n=3). **b-d**, Coomassie gels of in vitro auto-ubiquitination assays for the indicated times as described in part a, excepting that 2 μM UBE2N/UBE2V2 (**b**), UBE2K (**c**), or UBE2D1 (**d**) was used, with recombinant TRIM21 RING (R), TRIM2 RBCC, or TRIM23 RBB as positive controls alongside either TRIM6 or TRIM22 R or RB (n=3). **e**, Western blots of auto-ubiquitination reaction carried out at 30 °C 120 min using 1 μM UBE2D1, 1 μM UBA1, 50 μM ubiquitin, and 3 mM ATP, using FLAG pull downs from either untransfected, FLAG-TRIM2, 6, or 22 transfected HEK293T cells that were either untreated or treated 18 h with 5,000 units/ml IFN-β or 20 ng/ml TNF-α (n=3). **f**, Quantification of n=3 independent experiments as described in part e, with individual values plotted as circles, error bars represent mean ± SEM. **g**, Volcano plots indicating the IFN-β-responsive interactomes of FLAG-TRIM6 (left) and FLAG-TRIM22 (right) (n=3), as determined by timsTOF mass spectrometry of anti-FLAG immunoprecipitated complexes from transfected HEK293T cells (5,000 units/ml IFN-β 18 h vs. untreated), with TRIM21 identified as a hit in both cases (teal). **h**, Volcano plot of global proteomic changes in HEK293T cells following treatment with 5,000 units/ml IFN-β 18 h (n=3). **i**, Pull down using 'GFP clamp' DARPin pull down against GFP-tagged TRIM6 and TRIM22 expressed in HEK293T cells, with or without pre-treatment with 5,000 units/ml IFN-β 18 h, before use in a ubiquitination reaction as described in part **e**. Source data are provided as a Source Data file.



Supplementary Figure 6 – Data supporting key interfaces with E2~ubiquitin are mutated in TRIM6 and TRIM22, leading to lack of ubiquitin ligase activity in vitro

a, Alignments of ColabFold70 predictions of wild-type (WT) and K6L mutant TRIM22 (residues 1-88), demonstrating increased confidence in well-folded and closer a1 and a3 helices. **b**, ^{1}H-^{15}N HSQC spectra of TRIM6 (left, pink) and TRIM22 (right, purple) RING domains, with the spectral regions corresponding to resonances characteristic of residues in random coil conformation indicated in teal. **c**, 700 nm fluorescent imaging and Coomassie stains of auto-ubiquitination reactions carried out at 30 °C 120 min using 2 μM UBE2D3 with 1 μM UBA1, 50 μM ubiquitin, 1 μM UbATTO and 3 mM ATP, with recombinantly purified RING wild-type (WT) or active mutants (TRIM6 P41A/N42V/G43I/R54S/Q60R 'x5 mutant'; TRIM22 K6L/K42V/Q60R/K85V 'x4 mutant') TRIM6 or TRIM22 (n=3). **d**, Details of the ^{1}H-^{15}N HSQC spectra of UBE2D3 titrated with the RING domain of TRIM6 and TRIM22 WT. Spectra from blue to red at different ligand concentrations (0, 100, 200, 300 μM) are plotted at the same contour level. **e**, Chemical shift perturbations (ΔδNH) versus residue number in the NMR spectra of ^{15}N-labelled UBE2D3 in the presence of two molar equivalents (300 μM) of the RING domains of TRIM6 (blue) and TRIM22 (purple). Secondary structure of UBE2D3 is reported as a function of residue number. **f**, Residue-specific values of differential line broadening (DI) of a 150 μM sample of ^{15}Nlabelled UBE2D3 induced by x5 mutant TRIM6 (blue) and x4 mutant TRIM22 (purple) at 100 μM concentration of RING domains. Residues with positive values above DI were mapped on the surface of UBE2D3 (**Fig. 4h**). **g**, Side-by-side comparison of the ^{1}H-^{15}N HSQC spectra of ^{15}N-labelled UBE2D3 in the absence (blue) or presence of the RING domain of x5 mutant TRIM6 (pink) and x4 mutant TRIM22 (purple) at increasing concentrations. Source data is provided as a Source Data file. Source data are provided as a Source Data file.



Supplementary Figure 7 – Data supporting TRIM49 and TRIM51 form an active:inactive pair that cross-regulate, with conflicting effects on autophagy

Western blot analysing the domains of FLAG-TRIM49 and GFP-TRIM51 that interact using co-immunoprecipitation of the indicated truncation mutant proteins from HEK293T cells (n=3, see **Fig. 5h**). Source data are provided as a Source Data file.

Supplementary Tables

Supplementary Table 1 – Comparative analysis of TRIM localisation identified in this study compared to that found previously in the literature, with any discrepancies highlighted in grey and the likely cause suggested

TRIM	Localisation		
	Literature	**This study**	**Cause of discrepancy** (listed respective to literature references)
1	Cytoskeleton[1-4]	Diffuse, nuclear	Different cell types (HeLa, H1299, Cos7, COS-1 cells)
2	Cytoskeleton[1,5]	Cytoskeleton	-
3	Diffuse[1,6]	Diffuse	-
4	Puncta[1,7], mitochondria[7]	Puncta	-
5	Puncta[1,8,9]	Puncta	-
6	Puncta[1,10]	Puncta	-
7	Diffuse[1,11], puncta[12], nuclear[1]	Puncta	-
8	Diffuse[13], puncta[1], nuclear[1,13]	Diffuse, nuclear	-
9	Puncta[1,14]	Puncta, aggregates	-
10	Diffuse[15], aggregates[1]	Diffuse	-
11	Diffuse[1], nuclear[1]	Diffuse, nuclear	-
12	Diffuse[1], puncta[1,16,17]	Puncta	-
13	Endoplasmic reticulum[1,18]	Puncta	Different cell type (HeLa) or endogenous staining
15	Puncta[19], cytoskeleton[20]	Puncta, aggregates	-
17	Diffuse[21]	Diffuse	-
18	Diffuse[14], cytoskeleton[1,22]	Cytoskeleton	-
19	Nuclear[1,23]	Nuclear	-
21	Diffuse[1], puncta[1,24]	Diffuse, puncta	-
22	Diffuse[1], puncta[1,25], nuclear[25,26]	Nuclear	-
23	Diffuse[27], puncta[1,27], nuclear[1]	Diffuse	-
24	Puncta[1], nuclear[28,29]	Nuclear	-
25	Diffuse[1], puncta[30], aggregates[1]	Puncta	-
26	Diffuse[1,31,32], puncta[33], nuclear[32]	Diffuse	-
27	Puncta[1,34], nuclear[34,35]	Puncta	-
28	Nuclear[1,36,37]	Nuclear	-
30	Diffuse[17], puncta[1,38], aggregates[17,38]	Diffuse	-
31	Diffuse[1], puncta[39-41]	Puncta	-
32	Puncta[1,14,42-45], nuclear[46]	Puncta, aggregates	-
33	Diffuse[47], nuclear[47-49]	Nuclear	-
34	Puncta[50]	Puncta	-
35	Diffuse[51]	Diffuse, nuclear	-
36	Cytoskeleton[52,53]	Diffuse, nuclear	Different cell type (HeLa)
37	Diffuse[54-57], puncta[55], aggregates[58], nuclear[56]	Diffuse	-
38	Puncta[59]	Puncta	-
39	Diffuse[60]	Diffuse	-
40	Diffuse[61], nuclear[61]	Diffuse, nuclear	-
41	Diffuse[62-64], nuclear[62]	Aggregates	Different cell type (SH-SY5Y, A549) with endogenous staining, or different cell type (RAW264.7)
42	Untested	Puncta	-
43	Puncta[65]	Diffuse	Different cell type (HFF) stimulated with HSV-1
45	Diffuse[66,67]	Diffuse, aggregates	-
46	Cytoskeleton[52,68,69]	Diffuse, nuclear	Different cell type (HeLa) or endogenous protein in hippocampal neurones
47	Diffuse[70]	Diffuse, aggregates	-
48	Untested	Puncta	-
49	Untested	Diffuse, nuclear	-
50	Diffuse[71,72], puncta[73-76]	Diffuse	-

51	Untested	Diffuse, nuclear	-
52	Nuclear[77]	Nuclear	-
54	Untested	Diffuse, aggregates	-
55	Diffuse[78-80], puncta[78]	Puncta	-
56	Diffuse[81,82]	Diffuse	-
58	Diffuse[83,84]	Nuclear	Different cell types (A549, HCC827, or HeLa) and tag (FLAG or mCherry)
59	Diffuse[85]	Diffuse	-
60	Aggregates[86]	Diffuse, nuclear	Different cell type (CHO-K1)
61	Untested	Nuclear	-
62	Diffuse[87], aggregates[88]	Diffuse, aggregates	-
63	Puncta[89-91], mitochondria[92]	Puncta	-
64	Untested	Diffuse, aggregates	-
65	Diffuse[93-95]	Diffuse, nuclear	-
67	Diffuse[96,97], puncta[96,97]	Diffuse	-
68	Diffuse[98]	Diffuse	-
69	Diffuse[99], aggregates[100,101]	Cytoskeleton	Different cell type (HeLa) and tags (FLAG or Myc)
71	Puncta[102,103]	Diffuse	Different cell types (KH2, embryocarcinoma, or HeLa cells) with endogenous staining
72	Diffuse[104,105], nuclear[104]	Diffuse	-
73	Untested	Diffuse	-
74	Untested	Diffuse, aggregates	-
75	Nuclear[106]	Nuclear	-
77	Untested	Diffuse	-
L1	Untested	Diffuse, nuclear	-

Supplementary Table 2 – Comparative analysis of TRIM ubiquitin ligase activity identified in this study compared to that found previously in the literature, with any discrepancies highlighted in grey and the likely cause suggested

TRIM	***in vitro* auto-ubiquitination activity**			**In cell auto-ubiquitination activity**		
	Literature	**This study**	**Likely cause of discrepancy** (listed respective to literature references)	**Literature**	**This study**	**Likely cause of discrepancy** (listed respective to literature references)
1	Yes[14]	Yes	-	Yes[2,14]	Yes	-
2	Yes[107]	Yes	-	Yes[107]	No	Different cell type (HeLa) and IP (His-Ub IP)
3	Yes[108]	No	Lacks key RING dimerisation residues	Yes[6,109,110]	No	Lacks key RING dimerisation residues
4	Yes[111]	Yes	-	Yes[7]	No	Substrate ubiquitination rather than auto-ubiquitination
5	Yes[8]	Yes	-	Yes[8,9]	Yes	-
6	Yes[10]	No	Substrate ubiquitination rather than auto-ubiquitination	Yes[10,112]	Yes	-
7	Yes[11,113,114]	Yes	-	Yes[11,12,113,114]	No	Substrate ubiquitination rather than auto-ubiquitination
8	Yes[13]	Yes	-	Yes[13,115]	No	Substrate ubiquitination rather than auto-ubiquitination
9	Yes[14]	Yes	-	Yes[116]	No	Unknown
10	Untested	Yes	-	Yes[15,117,118]	No	Substrate ubiquitination rather than auto-ubiquitination
11	Yes[14]	Yes	-	Yes[14]	Yes	-
12	Untested	Yes	-	Yes[16]	No	Different isoform (Trim12c rather than Trim12a)
13	Yes[18]	Yes	-	Yes[18]	Yes	-
15	Yes[119]	No	Substrate ubiquitination rather than auto-ubiquitination	Yes[120]	No	Substrate ubiquitination rather than auto-ubiquitination
17	Yes[121]	Yes	-	Yes[21,121]	No	Different cell type (COS7)
18	Yes[122]	Yes	-	Yes[22]	No	Substrate ubiquitination rather than auto-ubiquitination
19	Untested	Yes	-	No[23,123]	Yes	Different cell type (HeLa)
21	Yes[124]	Yes	-	Yes[24,125]	Yes	-
22	Yes[126]	No	Different E2 (activity shown with Ube2D2)	Yes[26,126]	Yes	-
23	Yes[127,128]	Yes	-	Yes[27,128-130]	Yes	-
24	Yes[28] / No[131]	No	-	Yes[28,132,133]	Yes	-
25	Yes[30,134-136]	Yes	-	Yes[134,135,137]	Yes	-
26	Yes[138-140]	Yes	-	Yes[31,33,138-141]	Yes	-
27	Yes[14,35,142,143]	Yes	-	Yes[14,34,142-146]	Yes	-
28	Yes[147] / No[131]	No	-	Yes[148]	No	Ubiquitin E3 ligase activity under debate
30	Untested	Yes	-	Yes[149]	Yes	-
31	Yes[40,41,150-152]	Yes	-	Yes[39,40,150-155]	Yes	-
32	Yes[14,45,136,156-158]	Yes	-	Yes[14,45,46,156,159,160]	Yes	-
33	Yes[161] / No[131]	No	-	Yes[161,162]	No	Ubiquitin E3 ligase activity under debate
34	Yes[163]	Yes	-	Yes[163]	No	Substrate ubiquitination rather than auto-ubiquitination
35	Yes[164]	Yes	-	Yes[164-167]	Yes	-
36	Yes[53]	No	Different E2 (activity shown with Ube2D2)	Yes[53,168]	Yes	-
37	Yes[57,58,169]	No	Different E2 (activity shown with Ube2D2)	Yes[54,55,58,169,170]	Yes	-
38	Untested	No	-	Yes[171-174]	No	Unknown
39	Yes[175]	Yes	-	Yes[176-178]	No	Substrate ubiquitination rather than auto-ubiquitination
40	Yes[179]	No	Substrate ubiquitination rather than auto-ubiquitination	Yes[179-181]	No	Substrate ubiquitination rather than auto-ubiquitination
41	Yes[63,64]	Yes	-	Yes[62-64,182]	Yes	-
42	Untested	Yes	-	Untested	Yes	-

43	Untested	Yes	-	Yes[65]	No	Substrate ubiquitination rather than auto-ubiquitination
45	Yes[66,183]	Yes	-	Yes[67,184]	Yes	-
46	Yes[183]	No	Substrate ubiquitination rather than auto-ubiquitination	Yes[183,185-187]	Yes	-
47	Yes[188]	No	Different E2 (activity shown with Ube2D2)	Yes[70,188-191]	No	Substrate ubiquitination rather than auto-ubiquitination
48	Yes[192]	Yes	-	Yes[192]	Yes	-
49	No[193]	Yes	Mammalian expression untested (purified from bacteria)	Yes[193]	Yes	-
50	Yes[76]	Yes	-	Yes[71-75,194]	No	Substrate ubiquitination rather than auto-ubiquitination
51	Untested	No	-	Untested	No	-
52	Yes[195]	Yes	-	Yes[196-198]	Yes	-
54	Yes[199,200]	Yes	-	Yes[201,202]	No	Substrate ubiquitination rather than auto-ubiquitination
55	Yes[203]	Yes	-	Yes[204]	Yes	-
56	Yes[205,206]	Yes	-	Yes[81,205]	Yes	-
58	Yes[83]	Yes	-	Yes[83,84,207-210]	Yes	-
59	Yes[211]	Yes	-	Yes[211-214]	Yes	-
60	Untested	Yes	-	Untested	Yes	-
61	Untested	Yes	-	Untested	Yes	-
62	Yes[88]	Yes	-	Yes[88,215,216]	Yes	-
63	Yes[90]	Yes	-	Yes[89,90]	Yes	-
64	Untested	Yes	-	Yes[217]	Yes	-
65	Yes[93,218]	Yes	-	Yes[93-95,218-220]	Yes	-
67	Untested	Yes	-	Yes[96,97,221]	No	Substrate ubiquitination rather than auto-ubiquitination
68	Yes[222]	Yes	-	Yes[98]	No	Substrate ubiquitination rather than auto-ubiquitination
69	Yes[100,223]	Yes	-	Yes[100,101,224]	No	Unknown
71	Yes[103]	Yes	-	Yes[103,225,226]	Yes	-
72	Yes[227,228]	No	Different E2 (activity shown with Ube2D3 or 2C)	Yes[228]	No	Substrate ubiquitination rather than auto-ubiquitination
73	Untested	Yes	-	Untested	Yes	-
74	Untested	Yes	-	Untested	Yes	-
75	Untested	Yes	-	Untested	Yes	-
77	Untested	Yes	-	Untested	No	-
L1	Untested	Yes	-	Untested	Yes	-

Supplementary Table 3 – TRIM RING sequences and AlphaFold2 references

TRIM	RING sequence	AlphaFold2 PDB
TRIM1	MGESPASVVLNASGGLFSLKMETLESELTCPICLELFEDPLLLPCAHSLCFSCAHRILVSSCSSGESIEPITAFQCPTCRYVISLNHRGLDGLKRNVTLQNIIDRFQKASVSGP	AF-Q9UJV3-F1-model_v4
TRIM2	MASEGTNIPSPVVRQIDKQFLICSICLERYKNPKVLPCLHTFCERCLQNYIPAHSLTLSCPVCRQTSILPEKGVAALQNNFFITNLMDVLQRTP	AF-Q9C040-F1-model_v4
TRIM3	MAKREDSPGPEVQPMDKQFLVCSICLDRYQCPKVLPCLHTFCERCLQNYIPAQSLTLSCPVCRQTSILPEQGVSALQNNFFISSLMEAMQQAP	AF-O75382-F1-model_v4
TRIM4	MEAEDIQEELTCPICLDYFQDPVSIECGHNFCRGCLHRNWAPGGGPFPCPECRHPSAPAALRPNWALARLTEKTQRRRLGPVP	AF-Q9C037-F1-model_v4
TRIM5	MASGILVNVKEEVTCPICLELLTQPLSLDCGHSFCQACLTANHKKSMLDKGESSCPVCRISYQPENIRPNRHVANIVEKLREVKLSP	AF-Q9C035-F1-model_v4
TRIM6	MTSPVLVDIREEVTCPICLELLTEPLSIDCGHSFCQACITPNGRESVIGQEGERSCPVCQTSYQPGNLRPNRHLANIVRRLREVVLGP	AF-Q9C030-F1-model_v4
TRIM7	MAAVGPRTGPGTGAEALALAAELQGEATCSICLELFREPVSVECGHSFCRACIGRCWERPGAGSVGAATRAPPFPLPCPQCREPARPSQLRPNRQLAAVATLLRRFSLP	AF-Q9C029-F1-model_v4
TRIM8	MAENWKNCFEEELICPICLHVFVEPVQLPCKHNFCRGCIGEAWAKDSGLVRCPECNQAYNQKPGLEKNLKLTNIVEKFNALHVEKP	AF-Q9BZR9-F1-model_v4
TRIM9	MEEMEEELKCPVCGSFYREPIILPCSHNLCQACARNILVQTPESESPQSHRAAGSGVSDYDYLDLDKMSLYSEADSGYGSYGGFASAPTTPCQKSPNGVRVFPPAMPPPATHLSPALAPVPRNSCITCPQCHRSLILDDRGLRGFPKNRVLEGVIDRYQQSKA	AF-Q9C026-F1-model_v4
TRIM10	MASAASVTSLADEVNCPICQGTLREPVTIDCGHNFCRACLTRYCEIPGPDLEESPTCPLCKEPFRPGSFRPNWQLANVVENIERLQLVSTLGLGE	AF-Q9UDY6-F1-model_v4
TRIM11	MAAPDLSTNLQEEATCAICLDYFTDPVMTDCGHNFCRECIRRCWGQPEGPYACPECRELSPQRNLRPNRPLAKMAEMARRLHP	AF-Q96F44-F1-model_v4
Trim12	MASQFMKNLKEEVTCPVCLNLMVKPVSADCGHTFCQGCITLYFESIKCDKKVFICPVCRISYQFSNLRPNRNVANIVERLKMFKPSP	AF-Q99PQ1-F1-model_v4
TRIM13	MELLEEDLTCPICCSLFDDPRVLPCSHNFCKKCLEGILEGSVRNSLWRPAPFKCPTCRKETSATGINSLQVNYSLKGIVEKYNKIKISP	AF-O60858-F1-model_v4
TRIM15	MPATPSLKVVHELPACTLCAGPLEDAVTIPCGHTFCRLCLPALSQMGAQSSGKILLCPLCQEEEQAETPMAPVPLGPLGE	AF-Q9C019-F1-model_v4
TRIM17	MEAVELARKLQEEATCSICLDYFTDPVMTTCGHNFCRACIQLSWEKARGKKGRRKRKGSFPCPECREMSPQRNLLPNRLLTKVAEMAQQHP	AF-Q9Y577-F1-model_v4
TRIM18	METLESELTCPICLELFEDPLLLPCAHSLCFNCAHRILVSHCATNESVESITAFQCPTCRHVITLSQRGLDGLKRNVTLQNIIDRFQKASVSGP	AF-O15344-F1-model_v4
TRIM19	MEPAPARSPRPQQDPARPQEPTMPPPETPSEGRQPSPSPSPTERAPASEEEFQFLRCQQCQAEAKCPKLLPCLHTLCSGCLEASGMQCPICQAPWPLGADTPALDNVFFESLQRRLSVYRQIVDAQ	AF-P29590-F1-model_v4
TRIM21	MASAARLTMMWEEVTCPICLDPFVEPVSIECGHSFCQECISQVGKGGGSVCPVCRQRFLLKNLRPNRQLANMVNNLKEISQEARE	AF-P19474-F1-model_v4
TRIM22	MDFSVKVDIEKEVTCPICLELLTEPLSLDCGHSFCQACITAKIKESVIISRGESSCPVCQTRFQPGNLRPNRHLANIVERVKEVKMSP	AF-Q8IYM9-F1-model_v4
TRIM23	MATLVVNKLGAGVDSGRQGSRGTAVVKVLECGVCEDVFSLQGDKVPRLLLCGHTVCHDCLTRLPLHGRAIRCPFDRQVTDLGDSGVWGLKKNFALLELLERLQNGP	AF-P36406-F1-model_v4
TRIM24	MEVAVEKAVAAAAAASAAASGGPSAAPSGENEAESRQGPDSERGGEAARLNLLDTCAVCHQNIQSRAPKLLPCLHSFCQRCLPAPQRYLMLPAPMLGSAETPPPVPAPGSPVSGSSPFATQVGVIRCPVCSQECAERHIIDNFFVKDTTEVP	AF-O15164-F1-model_v4
TRIM25	MAELCPLAEELSCSICLEPFKEPVTTPCGHNFCGSCLNETWAVQGSPYLCPQCRAVYQARPQLHKNTVLCNVVEQFLQADLAREP	AF-Q14258-F1-model_v4
TRIM26	MATSAPLRSLEEEVTCSICLDYLRDPVTIDCGHVFCRSCTTDVRPISGSRPVCPLCKKPFKKENIRPVWQLASLVENIERLKVDKGRQP	AF-Q12899-F1-model_v4
TRIM27	MASGSVAECLQQETTCPVCLQYFAEPMMLDCGHNICCACLARCWGTAETNVSCPQCRETFPQRHMRPNRHLANVTQLVKQLRTERP	AF-P14373-F1-model_v4
TRIM28	MAASAAAASAAAASAASGSPGPGEGSAGGEKRSTAPSAAASASASAAASSPAGGGAEALELLEHCGVCRERLRPEREPRLLPCLHSACSACLGPAAPAAANSSGDGGAAGDGTVVDCPVCKQQCFSKDIVENYFMRDSGSKAATDA	AF-Q13263-F1-model_v4
Trim30	MASSVLEMIKEEVTCPICLELLKEPVSADCNHSFCRACITLNYESNRNTDGKGNCPVCRVPYPFGNLRPNLHVANIVERLKGFKSIP	AF-P15533-F1-model_v4
TRIM31	MASGQFVNKLQEEVICPICLDILQKPVTIDCGHNFCLKCITQIGETSCGFFKCPLCKTSVRKNAIRFNSLLRNLVEKIQALQASEVQSKRKE	AF-Q9BZY9-F1-model_v4
TRIM32	MAAAAASHLNLDALREVLECPICMESFTEEQLRPKLLHCGHTICRQCLEKLLASSINGVRCPFCSKITRITSLTQLTDNLTVLKIIDTAGLSEAVGLLMCRSCGRRLP	AF-Q13049-F1-model_v4
TRIM33	MAENKGGGEAESGGGGSGSAPVTAGAAGPAAQEAEPPLTAVLVEEEEEEGGRAGAEGGAAGPDDGGVAAASSGSAQAASSPAASVGTGVAGGAVSTPAPAPASAPAPGPSAGPPPGPPASLLDTCAVCQQSLQSRREAEPKLLPCLHSFCLRCLPEPERQLSVPIPGGSNGDIQQVGVIRCPVCRQECRQIDLVDNYFVKDTSEAP	AF-Q9UPN9-F1-model_v4
TRIM34	MASKILLNVQEEVTCPICLELLTEPLSLDCGHSLCRACITVSNKEAVTSMGGKSSCPVCGISYSFEHLQANQHLANIVERLKEVKLSP	AF-Q9BYJ4-F1-model_v4
TRIM35	MERSPDVSPGPSRSFKEELLCAVCYDPFRDAVTLRCGHNFCRGCVSRCWEVQVSPTCPVCKDRASPADLRTNHTLNNLVEKLLREEAEGARWTSYR	AF-Q9UPQ4-F1-model_v4
TRIM36	MSESGEMSEFGYIMELIAKGKVTIKNIERELICPACKELFTHPLILPCQHSICHKCVKELLLTLDDSFNDVGSDNSNQSSPRLRLPSPSMDKIDRINRPGWKRNSLTPRTTVFPCPGCEHDVDLGERGINGLFRNFTLETIVERYRQAARA	AF-Q9NQ86-F1-model_v4
TRIM37	MDEQSVESIAEVFRCFICMEKLRDARLCPHCSKLCCFSCIRRWLTEQRAQCPHCRAPLQLRELVNCRWAEEVTQQLDTLQLCSLTKHE	AF-O94972-F1-model_v4
TRIM38	MASTTSTKKMMEEATCSICLSLMTNPVSINCGHSYCHLCITDFFKNPSQKQLRQETFCCPQCRAPFHMDSLRPNKQLGSLIEALKETDQE	AF-O00635-F1-model_v4
TRIM39	MAETSLLEAGASAASTAAALENLQVEASCSVCLEYLKEPVIIECGHNFCKACITRWWEDLERDFPCPVCRKTSRYRSLRPNRQLGSMVEIAKQLQAVKRKIRDE	AF-Q9HCM9-F1-model_v4
TRIM40	MIPLQKDNQEEGVCPICQESLKEAVSTNCGHLFCRVCLTQHVEKASASGVFCCPLCRKPCSEEVLG	AF-Q6P9F5-F1-model_v4
TRIM41	MAAVAMTPNPVQTLQEEAVCAICLDYFTDPVSIGCGHNFCRVCVTQLWGGEDEEDRDELDREEEEEDGEEEEVEAVGAGAGWDTPMRDEDYEGDMEEEVEEEEEGVFWTSGMSRSSWDNMDYVWEEEDEEEDLDYYLGDMEEEDLRGEDEEDEEEVLEEVEEEDLDPVTPLPPPPAPRRCFTCPQCRKSFPRRSFRPNLQLANMVQVIRQMHP	AF-Q8WV44-F1-model_v4
TRIM42	METAMCVCCPCCTWQRCCPQLCSCLCCKFIFTSERNCTCFPCPYKDERNCQFCHCTCSESPNCHWCCCSWANDPNCKCCCTASSNLNCYYYESRCCRNTIITFHKGRLRSIHTSSKTALRTGSSDTQVDEVKSIPANSHLVNHLNCPMCSRLRLHSFMLPCNHSLCEKCLRQLQKHAEVTENFFILICPVCDRSHCMPYSNKMQLPENYLHGRLTKRYMQEHGYLKWRFDRSSGP	AF-Q8IWZ5-F1-model_v4

TRIM43	MDSDFSHAFQKELTCVICLNYLVDPVTICCGHSFCRPCLCLSWEEAQSPANCP ACREPSPKMDFKTNILLKNLVTIARKASLWQFLSSE	AF-Q96BQ3-F1-model_v4
TRIM45	MSENRKPLLGFVSKLTSGTALGNSGKTHCPLCLGLFKAPRLLPCLHTVCTTCLE QLEPFSVVDIRGGDSDTSSEGSIFQELKPRSLQSQIGILCPVCDAQVDLPMGGV KALTIDHLAVNDVMLESLRGE	AF-Q9H8W5-F1-model_v4
TRIM46	MAEGEDMQTFTSIMDALVRISTSMKNMEKELLCPVCQEMYKQPLVLPCTHNVC QACAREVLGQQGYIGHGGDPSSEPTSPASTPSTRSPRLSRRTLPKPDRLDRLL KSGFGTYPGRKRGALHPQVIMFPCPACQGDVELGERGLAGLFRNLTLERVVER YRQSVSVG	AF-Q7Z4K8-F1-model_v4
TRIM47	MDGSGPFSCPICLEPLREPVTLPCGHNFCLACLGALWPHRGASGAGGPGGAA RCPLCQEPFPDGLQLRKNHTLSELLQLRQGSGP	AF-Q96LD4-F1-model_v4
TRIM48	MSRRIIVGTLQRTQRNMNSGISQVFQRELTCPICMNYFIDPVTIDCGHSFCRPCF YLNWQDIPILTQCFECIKTIQQRNLKTNIRLKKMASLARKASLWLFLSSE	AF-Q8IWZ4-F1-model_v4
TRIM49	MNSGILQVFQGELICPLCMNYFIDPVTIDCGHSFCRPCFYLNWQDIPFLVQCSE CTKSTEQINLKTNIHLKKMASLARKVSLWLFLSSE	AF-P0CI25-F1-model_v4
TRIM50	MAWQVSLPELEDRLQCPICLEVFKEPLMLQCGHSYCKGCLVSLSCHLDAELRC PVCRQAVDGSSSLPNVSLARVIEALRLP	AF-Q86XT4-F1-model_v4
TRIM51	MNSGILQVFQRALTCPICMNYFLDPVTIDCGHSFCRPCLYLNWQDTAVLAQCSE CKKTTRQRNLNTDICLKNMAFIARKASLRQFLSSE	AF-Q9BSJ1-F1-model_v4
TRIM52	MAGYATTPSPMQTLQEEAVCAICLDYFKDPVSISCGHNFCRGCVTQLWSKEDE EDQNEEEDEWEEEEDEEAVGAMDGWDGSIREVLYRGNADEELFQDQDDDEL WLGDSGITNWDNVDYMWDEEEEEEEEDQDYYLGGLRPDLRIDVYREEEILEAY DEDEDEELYPDIHPPPSLPLPGQFTCPQCRKSFTRRSFRPNLQLANMVQIIRQM CP	AF-Q96A61-F1-model_v4
TRIM54	MNFTVGFKPLLGDAHSMDNLEKQLICPICLEMFSKPVVILPCQHNLCRKCANDV FQASNPLWQSRGSTTVSSGGRFRCPSCRHEVVLDRHGVYGLQRNLLVENIIDI YKQESSRP	AF-Q9BYV2-F1-model_v4
TRIM55	MSASLNYKSFSKEQQTMDNLEKQLICPICLEMFTKPVVILPCQHNLCRKCASDIF QASNPYLPTRGGTTMASGGRFRCPSCRHEVVLDRHGVYGLQRNLLVENIIDIYK QESTRP	AF-Q9BYV6-F1-model_v4
TRIM56	MVSHGSSPSLLEALSSDFLACKICLEQLRAPKTLPCLHTYCQDCLAQLADGGRV RCPECRETVPVPPEGVASFKTNFFVNGLLDLVKARACGDLRAG	AF-Q9BRZ2-F1-model_v4
TRIM58	MAWAPPGERLREDARCPVCLDFLQEPVSVDCGHSFCLRCISEFCEKSDGAQG GVYACPQCRGPFRPSGFRPNRQLAGLVESVRRLGLG	AF-Q8NG06-F1-model_v4
TRIM59	MHNFEEELTCPICYSIFEDPRVLPCSHTFCRNCLENILQASGNFYIWRPLRIPLK CPNCRSITEIAPTGIESLPVNFALRAIIEKYQQEDHP	AF-Q8IWR1-F1-model_v4
TRIM60	MEFVTALVNLQEESSCPICLEYLKDPVTINCGHNFCRSCLSVSWKDLDDTFPCP VCRFCFPYKSFRRNPQLRNLTEIAKQLQIRRSKRKRQKE	AF-Q495X7-F1-model_v4
TRIM61	MEFVTALADLRAEASCPICLDYLKDPVTISCGHNFCLSCIIMSWKDLHDSFPCPF CHFCCPERKFISNPQLGSLTEIAKQLQIRSKKRKRQE	AF-Q5EBN2-F1-model_v4
TRIM62	MACSLKDELLCSICLSIYQDPVSLGCEHYFCRRCITEHWVRQEAQGARDCPEC RRTFAEPALAPSLKLANIVERYSSFP	AF-Q9BVG3-F1-model_v4
TRIM63	MDYKSSLIQDGNPMENLEKQLICPICLEMFTKPVVILPCQHNLCRKCANDIFQAA NPYWTSRGSSVSMSGGRFRCPTCRHEVIMDRHGVYGLQRNLLVENIIDIYKQE CSSRP	AF-Q969Q1-F1-model_v4
TRIM64	MDSDDLQVFQNELICCICVNYFIDPVTIDCGHSFCRPCLCLCSEEGRAPMRCPS CRKISEKPNFNTNVVLKKLSSLARQTRP	AF-A6NGJ6-F1-model_v4
TRIM65	MAAQLLEEKLTCAICLGLYQDPVTLPCGHNFCGACIRDWWDRCGKACPECRE PFPDGAELRRNVALSGVLEVVRAGP	AF-Q6PJ69-F1-model_v4
TRIM67	MEEELKCPVCGSLFREPIILPCSHNVCLPCARTIAVQTPDGEQHLPQPLLLSRGS GLQAGAAAAASLEHDAAAGPACGGAGGSAAGGLGGGAGGGGDHADKLSLYS ETDSGYGSYTPSLKSPNGVRVLPMVPAPPGSSAAAARGAACSSLSSSSSSITC PQCHRSASLDHRGLRGFQRNRLLEAIVQRYQQGRGAVP	AF-Q6ZTA4-F1-model_v4
TRIM68	MDPTALVEAIVEEVACPICMTFLREPMSIDCGHSFCHSCLSGLWEIPGESQNW GYTCPLCRAPVQPRNLRPNWQLANVVEKVRLLRLHP	AF-Q6AZZ1-F1-model_v4
TRIM69	MEVSTNPSSNIDPGDYVEMNDSITHLPSKVVIQDITMELHCPLCNDWFRDPLML SCGHNFCEACIQDFWRLQAKETFCPECKMLCQYNNCTFNPVLDKLVEKIKKLP	AF-Q86WT6-F1-model_v4
TRIM71	MASFPETDFQICLLCKEMCGSPAPLSSNSSASSSSSQTSTSSGGGGGGPGAA ARRLHVLPCLHAFCRPCLEAHRLPAAGGGAAGEPLKLRCPVCDQKVVLAEAAG MDALPSSAFLLSNLLDAVVATADEP	AF-Q2Q1W2-F1-model_v4
TRIM72	MSAAPGLLHQELSCPLCLQLFDAPVTAECGHSFCRACLGRVAGEPAADGTVLC PCCQAPTRPQALSTNLQLARLVEGLAQVP	AF-Q6ZMU5-F1-model_v4
TRIM73	MAWQVSLLELEDRLQCPICLEVFKESLMLQCGHSYCKGCLVSLSYHLDTKVRC PMCWQVVDGSSSLPNVSLAWVIEALRLP	AF-Q86UV7-F1-model_v4
TRIM74	MAWQVSLLELEDWLQCPICLEVFKESLMLQCGHSYCKGCLVSLSYHLDTKVRC PMCWQVVDGSSSLPNVSLAWVIEALRLP	AF-Q86UV6-F1-model_v4
TRIM75	MAVAAALTGLQAEAKCSICLDYLSDPVTIECGHNFCRSCIQQSWLDLQELFPCP VCRHQCQEGHFRSNTQLGRMIEIAKLLQSTKSNKRKQE	AF-A6NK02-F1-model_v4
TRIM77	MASAITQCSTSELTCSICTDYLTDPVTICCGHRFCSPCLCLLWEDTLTPNCCPVC REISQQMYFKRIIFAEKQVIPTRESVP	AF-I1YAP6-F1-model_v4
TRIML1	MSTADLMENLREELTCFICLDYFSSPVTTECGHSFCLVCLLRSWEEHNTPLSCP ECWRTLEGPHFQSNERLGRLASIARQLRSQVLQSEDEQGSYGRMP	AF-Q8N9V2-F1-model_v4

Supplementary Table 4 – Plasmid and antibody reagents used in this study

Antibody Database				
Antibody	**Use**	**Manufacturer**	**Catalogue Ref**	**Clone**
αGFP	Western, IP	Roche	11814460001	7.1 and 13.1
αUbiquitin (FK2: conjugated ubiquitin-specific)	Western	Sigma	ST1200	FK2
αUbiquitin-HRP (FK2: conjugated ubiquitin-specific)	ELISA	Generon	SMC-214D-HRP	FK2
αFLAG-HRP	Western	Merck	A8592	Clone M2
αFLAG	IF and IP	Merck	F1804	Clone M2
αUbiquitin (Ubi: pan-ubiquitin)	Western	Invitrogen	13-1600	Ubi-1
αTRIM6	Western, IF	Protein Tech	11953-1-AP	Polyclonal
αTRIM22	Western, IF	Atlas Antibodies	HPA003575	Polyclonal
αGAPDH	Western	Millipore	MAB374	Clone 6C5
αHA-HRP	Western	Merck	12013819001	Clone 3F10
αLC3B	Western, IF	Sigma	L7543	Polyclonal
αRabbit-HRP	Western	Cell Signaling	7074	Polyclonal
αMouse-HRP	Western	Cell Signaling	7076	Polyclonal
αMouse-HRP	Western	Dako	P0447	Polyclonal
αMouse-Alexa594	IF	ThermoFisher	A11032	Polyclonal
αRabbit-Alexa488	IF	ThermoFisher	A11008	Polyclonal
Plasmid Database				
Plasmid	**NCBI Protein Isoform Ref.**	**~Mol. Weight** (untagged kDa)	**Species**	**Derivation (and source)**
Bacterial expression				
pET28-His_6-UBA1	NP_003325.2	118	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[229])
pET52-His_6-UBE2C	NP_008950.1	20	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[229])
pGEX-6P1-GST-UBE2D1	NP_003329.1	17	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[229])
pET49b-GST-UBE2D2	NP_862821.1	17	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[131])
pET49b-His_6-UBE2D3	NP_003331.1	17	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[136])
pET49b-His_6-UBE2E1	NP_003332.1	21	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[131])
pET49b-GST-UBE2G2	NP_003334.2	19	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[229])
pET49b-His_6-UBE2K	NP_005330.1	22	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[131])
pNH-CTH-His_6-UBE2N	NP_003339.1	17	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[229])
pGEX-6P1-GST-UBE2V2	NP_003341.1	16	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[229])
pET22b-His_6-UBE2W	NP_001001481.3	17	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[229])
pET49b-His_6-TRIM6 RING	NP_477514.1	10	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[229])
pET49b-His_6-TRIM6 RING P41A/N42V/G43I/R54S/Q60R	N/A (mutant)	10	N/A (mutant)	This study (see Methods)
pET49b-His_6-TRIM6 RB	NP_477514.1	15	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[229])
pET49b-His_6-TRIM6 BCC	NP_477514.1	12	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[229])
pET49b-His_6-Trx-TRIM6 RING	NP_477514.1	10	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[229])
pET49b-His_6-TRIM22 RING	NP_006065.2	10	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[229])
pET49b-His_6-TRIM22 RING K6L/K42V/Q60R/K85V	N/A (mutant)	10	N/A (mutant)	This study (see Methods)
pET49b-His_6-TRIM22 RB	NP_006065.2	15	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[229])
pET49b-His_6-TRIM22 BCC	NP_006065.2	13	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[229])
pET49b-His_6-SUMO-TRIM22 RING	NP_477514.1	10	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[229])
pET49b-His_6-TRIM21 RING	NP_003132.2	10	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[229])

pET49b-His_6-TRIM15 tandem RINGs	NP_150232.2		*Homo sapiens*	This study (see Methods)
pET49b-His_6-TRIM23 RBB	NP_001647.1	23	*Homo sapiens*	N/A (Rittinger Lab, Francis Crick Institute[229])
pET49b-His_6-TRIM15 R	NP_150232.2		*Homo sapiens*	This study (see Methods)
pCMV-HA-ubiquitin	NP_001029102.1	9	*Homo sapiens*	N/A (Dundee PPU , #DU48359)
pcDNA3.1-FLAG-TRIM15	NP_150232.2	52	*Homo sapiens*	Sub-cloned from ptCMV-EGFP-TRIM15 (see below)
pcDNA3.1-FLAG-TRIM49	NP_065091.1	53	*Homo sapiens*	Sub-cloned from ptCMV EGFP-TRIM49 (see below)
pcDNA3.1-FLAG-TRIM51	NP_116070.2	53	*Homo sapiens*	Sub-cloned from ptCMV-GFP-TRIM49 (see below)
pcDNA3.1-FLAG-TRIM49 RB (1-128)	NP_065091.1	15	*Homo sapiens*	Sub-cloned from ptCMV-EGFP-TRIM49 (see below)
pcDNA3.1-FLAG-TRIM49 RBCC (1-259)	NP_065091.1	31	*Homo sapiens*	Sub-cloned from ptCMV-EGFP-TRIM49 (see below)
pcDNA3.1-FLAG-TRIM49 BCCSPRY (88-450)	NP_065091.1	43	*Homo sapiens*	Sub-cloned from ptCMV-EGFP-TRIM49 (see below)
pcDNA3.1-FLAG-TRIM 9 CC (129-259)	NP_065091.1	16	*Homo sapiens*	Sub-cloned from ptCMV-EGFP-TRIM49 (see below)
pcDNA3.1-FLAG-TRIM49 CCSPRY (129-450)	NP_065091.1	37	*Homo sapiens*	Sub-cloned from ptCMV-EGFP-TRIM49 (see below)
pcDNA3.1-FLAG-TRIM49 SPRY (260-450)	NP_065091.1	22	*Homo sapiens*	Sub-cloned from ptCMV-EGFP-TRIM49 (see below)
ptCMV-EGFP-TRIM51 RB (1-128)	NP_116070.2	15	*Homo sapiens*	Sub-cloned from ptCMV-EGFP-TRIM51 (see below)
ptCMV-EGFP-TRIM51 RBCC (1-259)	NP_116070.2	31	*Homo sapiens*	Sub-cloned from ptCMV-EGFP-TRIM51 (see below)
ptCMV-EGFP-TRIM5 BCCSPRY (88-450)	NP_116070.2	43	*Homo sapiens*	Sub-cloned from ptCMV-EGFP-TRIM51 (see below)
ptCMV-EGFP-TRIM51 CC (129-259)	NP_116070.2	16	*Homo sapiens*	Sub-cloned from ptCMV-EGFP-TRIM51 (see below)
ptCMV-EGFP-TRIM51 CCSPRY (129-450)	NP_116070.2	37	*Homo sapiens*	Sub-cloned from ptCMV-EGFP-TRIM51 (see below)
ptCMV-EGFP-TRIM51 SPRY (260-450)	NP_116070.2	22	*Homo sapiens*	Sub-cloned from ptCMV-EGFP-TRIM51 (see below)
pcDNA3.1-FLAG-TRIM49 β3-β4 TRIM51 swap	N/A (mutant)	53	*Homo sapiens*	gBlock (IDT) of TRIM51 β3-β4 inserted by Gibson Assembly into WT TRIM49 vector, opened by PCR primers flanking the relevant region
pcDNA3.1-FLAG-TRIM51 β3-β4 TRIM49 swap	N/A (mutant)	53	*Homo sapiens*	gBlock (IDT) of TRIM49 β3-β4 inserted by Gibson Assembly into WT TRIM51 vector, opened by PCR primers flanking the relevant region
ptCMV-EGFP-empty	N/A	N/A	N/A	N/A (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM1	NP_036348.2	55	*Homo sapiens*	PCR from 293ET human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM2	NP_001123539.1	82	*Homo sapiens*	PCR from 293ET human cDNA , ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM3	NP_001234935.1	82	*Homo sapiens*	Subcloned from pcDNA3.1-FLAG-TRIM3 (Rittinger Lab, Francis Crick Institute[229]), ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston

				Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM4	NP_148977.2	57	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM5	NP_149023.2	55	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM6	NP_001003818.1	56	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM7	NP_976038.1	57	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM8	NP_112174.2	62	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM9	NP_055978.4	80	*Homo sapiens*	PCR from 293ET human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM10	NP_006769.2	55	*Homo sapiens*	Subcloned from M6P-EGFP vector generated by PCR of mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM11	NP_660215.1	53	*Homo sapiens*	Subcloned from M6P-EGFP vector generated by PCR of mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM12	NP_001355683.1	53	*Mus musculus*	PCR from iBMDM murine cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM13	NP_005789.2	47	*Homo sapiens*	PCR from THP1 human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])

ptCMV-EGFP-TRIM14	NP_055603.2	50	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM15	NP_150232.2	52	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM16	NP_001335048.1	64	*Homo sapiens*	PCR from mixed human cDNA , ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM17	NP_001020111.1	54	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM18	NP_000372.1	72	*Homo sapiens*	PCR from Caco2 human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM19	NP_150241.2	98	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM20	NP_000234.1	86	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM21	NP_003132.2	54	*Homo sapiens*	PCR from U937 human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM22	NP_006065.2	57	*Homo sapiens*	Subcloned from M6P-EGFP vector generated by PCR of U937 human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM23	NP_001647.1	64	*Homo sapiens*	Subcloned from plasmid gifted from Michaela Gack[27] (T. Thurston Laboratory, Imperial College London)
ptCMV-EGFP-TRIM24	NP_056989.2	117	*Homo sapiens*	PCR from plasmid synthesised by Open Biosystems, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston

				Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM25	NP_005073.2	71	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM26	NP_001229712.1	62	*Homo sapiens*	PCR from U937 human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM27	NP_006501.1	58	*Homo sapiens*	PCR from 293ET human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM28	NP_005753.1	100	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM29	NP_036233.2	66	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM30	NP_001344396.1	105	*Mus musculus*	Subcloned from M6P-EGFP vector generated by PCR of iBMDM murine cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM31	NP_008959.3	48	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM32	NP_001093149.1	72	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM33	NP_056990.3	150	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM34	NP_001003827.1	36	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM35	NP_741983.2	55	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP

				plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM36	NP_061170.2	83	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM37	NP_001005207.1	130	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM38	NP_006346.1	53	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM39	NP_067076.2	60	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM40	NP_001273562.1	29	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM41	NP_291027.3	72	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM42	NP_689829.3	80	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM43	NP_620155.1	52	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM44	NP_060053.2	38	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM45	NP_079464.2	62	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])

ptCMV-EGFP-TRIM46	NP_079334.3	83	*Homo sapiens*	Subcloned from M6P-EGFP vector generated by PCR of mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM47	NP_258411.2	70	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM48	NP_077019.2	24	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM49	NP_065091.1	53	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM50	NP_001268380.1	55	*Homo sapiens*	Subcloned from plasmid gifted from Michaela Gack[27], ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM51	NP_116070.2	53	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM52	NP_116154.1	33	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM54	NP_115935.3	40	*Homo sapiens*	PCR from plasmid synthesised by Open Biosystems, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM55	NP_908973.1	60	*Homo sapiens*	PCR from plasmid synthesised by Open Biosystems, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM56	NP_112223.1	81	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])

ptCMV-EGFP-TRIM58	NP_056246.3	55	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM59	NP_775107.1	47	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM60	NP_001244954.1	55	*Homo sapiens*	Subcloned from M6P-EGFP vector generated by subcloning from plasmid synthesised by Open Biosystems, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM61	NP_001401833.1	24	*Homo sapiens*	PCR from plasmid synthesised by Open Biosystems, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM62	NP_060677.2	54	*Homo sapiens*	PCR from plasmid synthesised by Open Biosystems, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM63	NP_115977.2	40	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM64	NP_001129958.1	52	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM65	NP_775818.2	57	*Homo sapiens*	Subcloned from GenScript synthesised pcDNA-GFP vector, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM66	NP_001374951.1	135	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM67	NP_001004342.3	84	*Homo sapiens*	Subcloned from GenScript synthesised pcDNA-GFP vector, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston

				Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM68	NP_060543.5	56	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM69	NP_892030.3	57	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM70	NP_001340153.1	40	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM71	NP_001034200.1	93	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM72	NP_001008275.2	53	*Homo sapiens*	Subcloned from M6P-EGFP plasmid synthesised by Adolfo García-Sastre, , ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM73	NP_944606.2	29	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM74	NP_001304744.1	29	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM75	NP_001382999.1	54	*Homo sapiens*	Subcloned from M6P-EGFP vector generated by PCR of mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIM77	NP_001139634.1	52	*Homo sapiens*	Subcloned from M6P-EGFP vector generated by PCR of mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIML1	NP_848651.2	53	*Homo sapiens*	Subcloned from M6P-EGFP vector generated by PCR of mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T.

				Thurston Laboratory, Imperial College London[230])
ptCMV-EGFP-TRIML2	NP_001290348.1	44	*Homo sapiens*	PCR from mixed human cDNA, ptCMV-EGFP plasmid derived from pEGFP-N1 plasmid (Clontech) (T. Thurston Laboratory, Imperial College London[230])

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