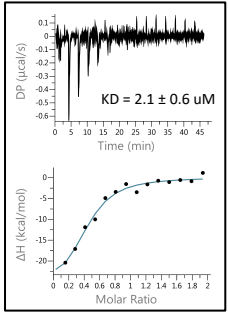


Figure S1. ITC traces for GYG protein and main peptides

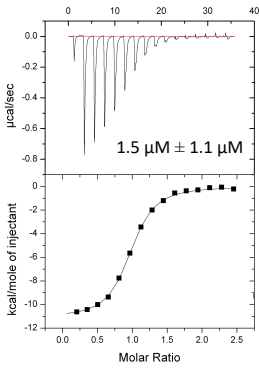
A

Human GYG1 vs
Human TRIM7



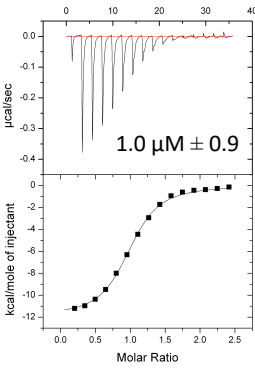
B

Rabbit Glycogenin
vs Mouse TRIM7



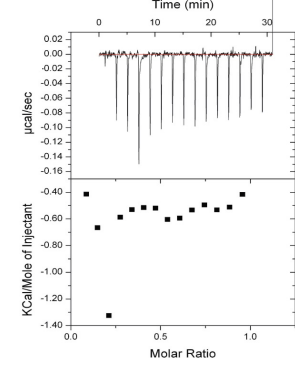
C

Mouse Glycogenin
vs Mouse TRIM7



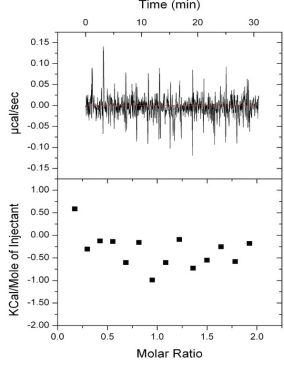
D

rGYG1₁₋₂₄₆ vs
Human TRIM7



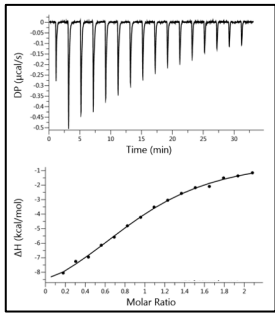
E

rGYG1₁₋₂₉₉ vs
Human TRIM7

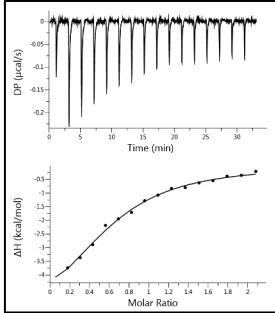


GYG1₃₂₂₋₃₃₃ **RACO-1₂₂₉₋₂₃₇** **2BC₁₄₃₄₋₁₄₄₀** **NS6₁₁₇₁₋₁₁₇₇**

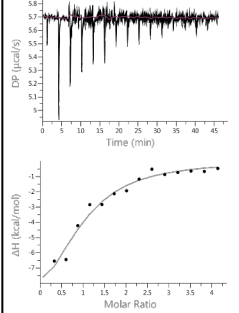
F



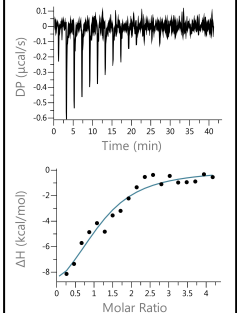
G



H

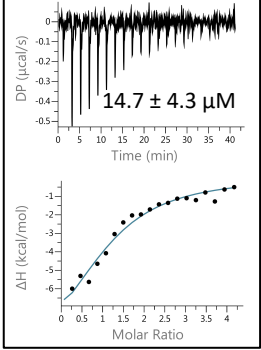


I



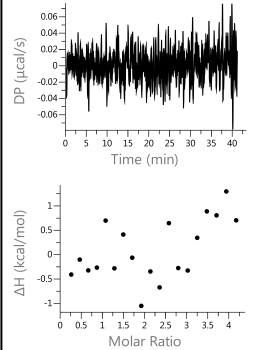
J

NS3 (HDDFGLQ) vs WT

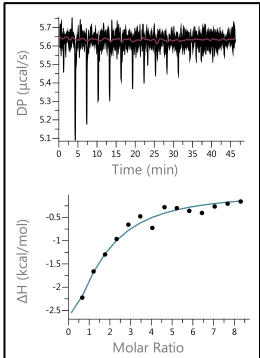


K

NS3 vs R385A

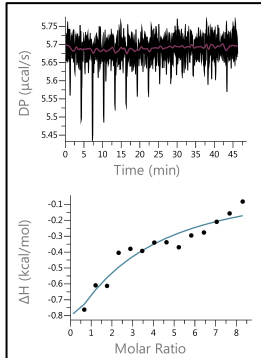


L



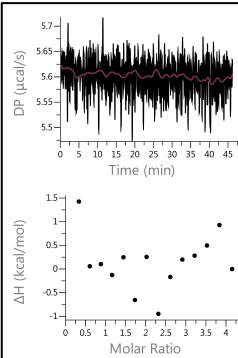
Ac-LLQ

M



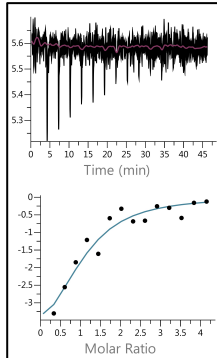
Ac-LQ

N



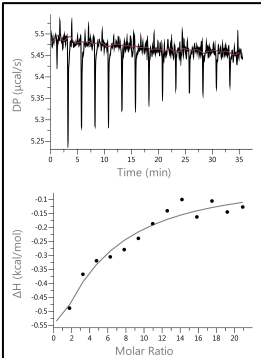
AAAAAA

O



AAAAALQ

P



LQ

Figure S2. Crystal structures of TRIM7-peptide complexes

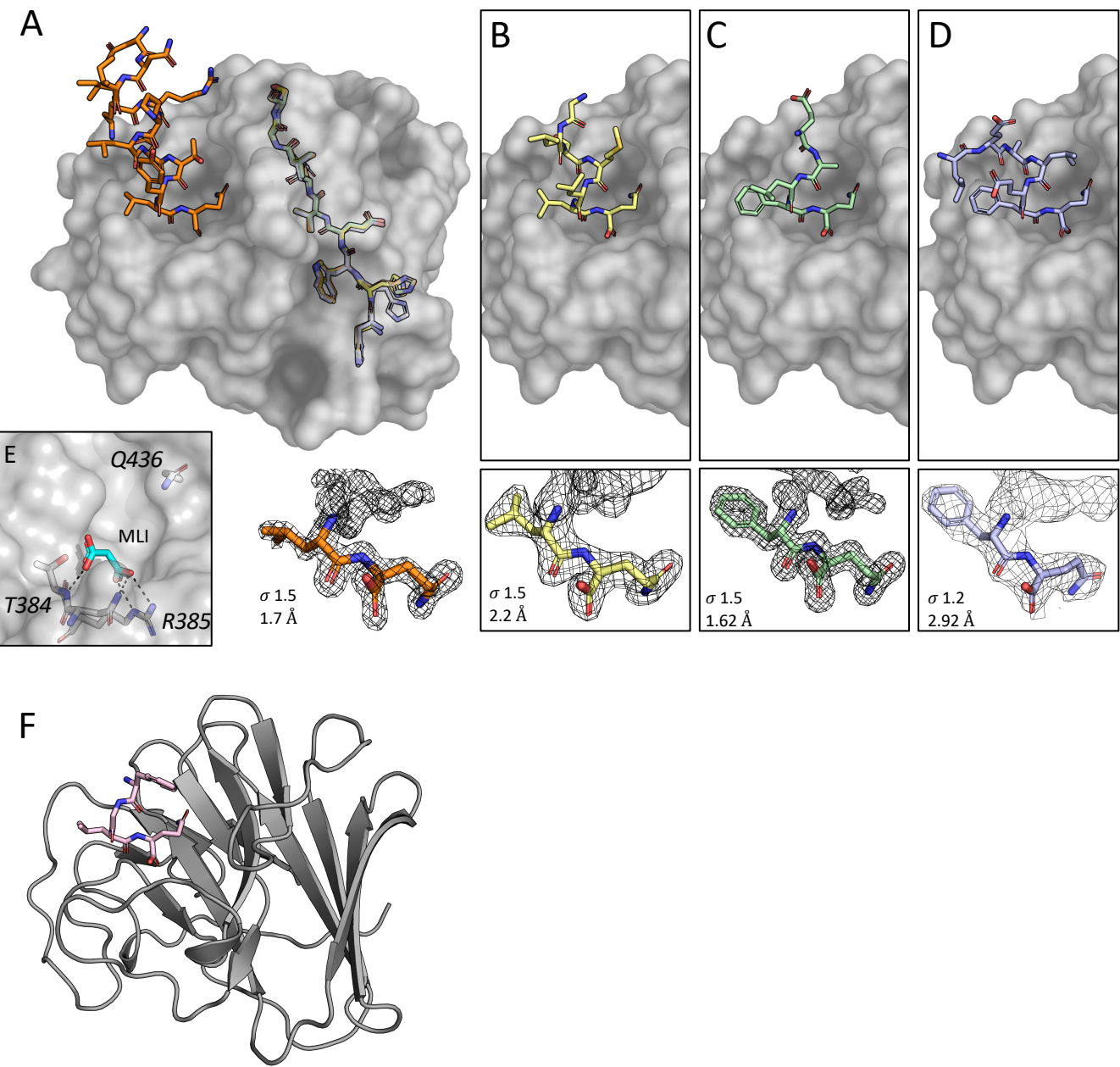
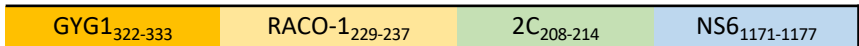


Figure S3 ITC traces for mutant TRIM7 proteins and peptides



N383A

T384A

R385A

L423A

F426A

Q436A

N438A

2BC_{T1423A}

2BC_{Q1429A}

Trim7	GYG1 ₃₂₂₋₃₃₃	RACO-1 ₂₂₉₋₂₃₇	2BC ₁₄₂₃₋₁₄₂₉	NS6 ₁₁₇₁₋₁₁₇₇
WT	8 ± 0.6 μM	7.9 ± 1.0 μM	11.2 ± 4.2 μM	8.7 ± 3.2 μM
N383A	No Binding	No Binding	No binding	NT
T384A	22.6 ± 6.6 μM	12.3 ± 2.0 μM	21.2 ± 5.84 μM	NT
R385A	No Binding	No Binding	No binding	No binding
L423A	No Binding*	No Binding*	No binding*	NT
F426A	No Binding	No Binding	No binding	NT
Q436A	No Binding	No Binding	No binding	NT
N438A	2.3 ± 0.3 μM	3.9 μM ± 1.8 μM	7.82 ± 1.18 μM	NT

Figure S4. GYG isoforms

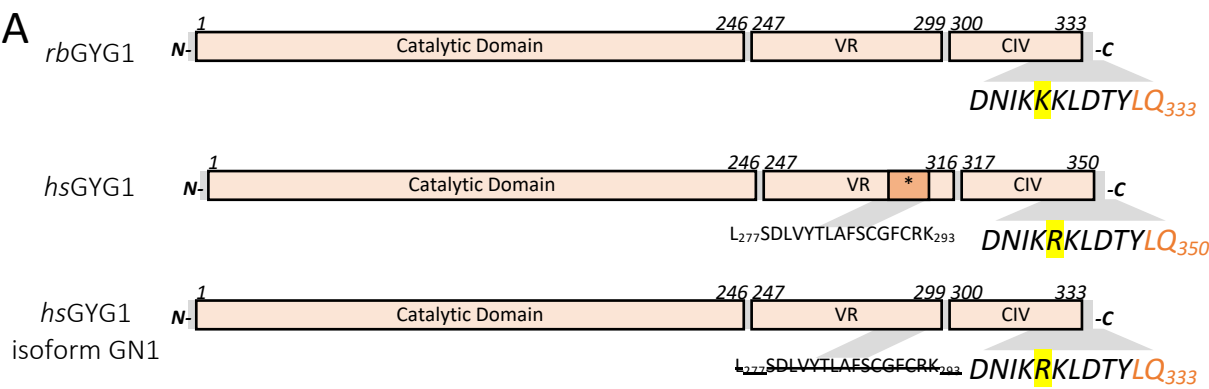


Figure S5. GYG1 colocalizes to TRIM7 cytoplasmic bodies

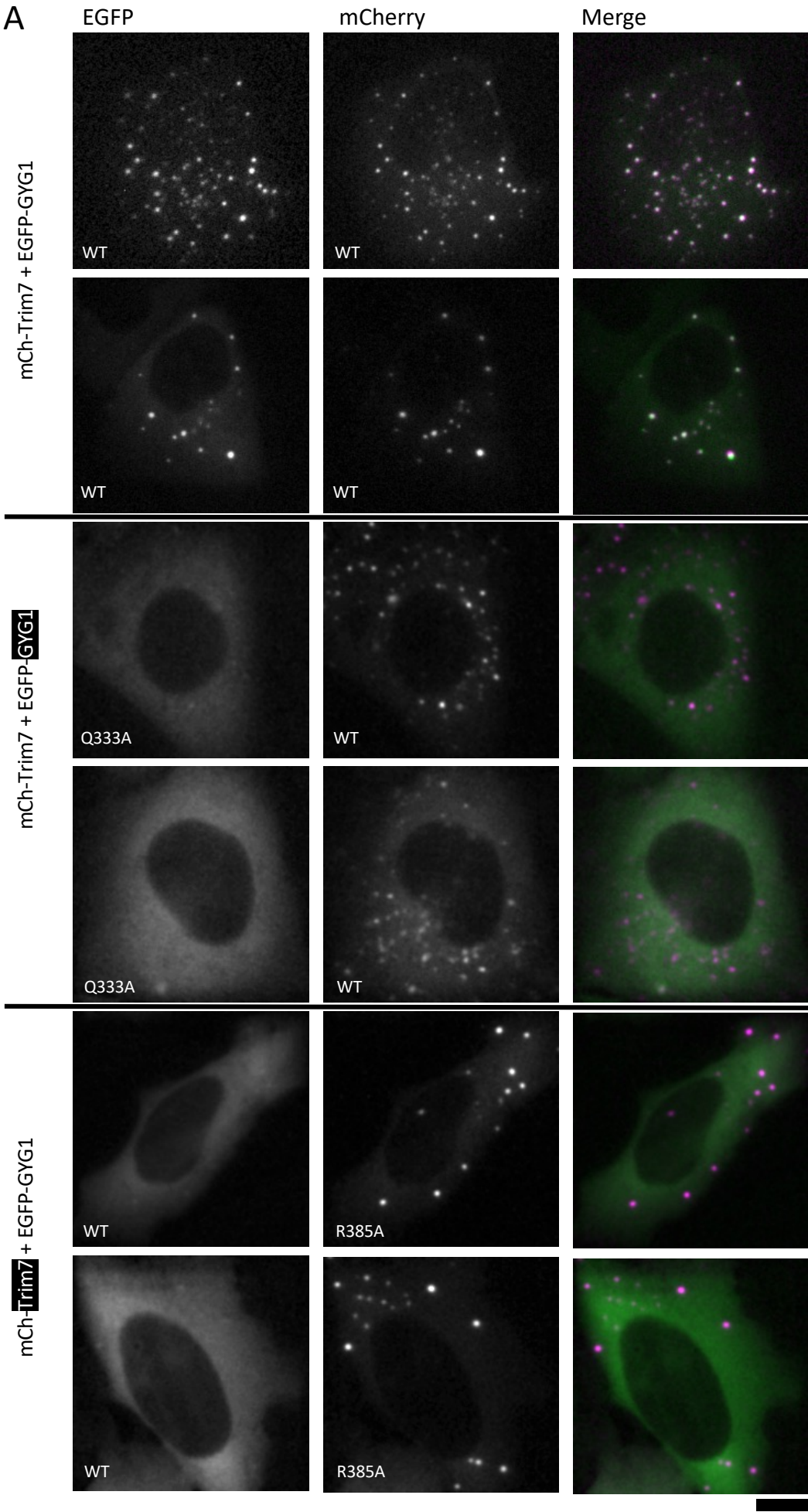


Figure S6. Stable cell line validation.

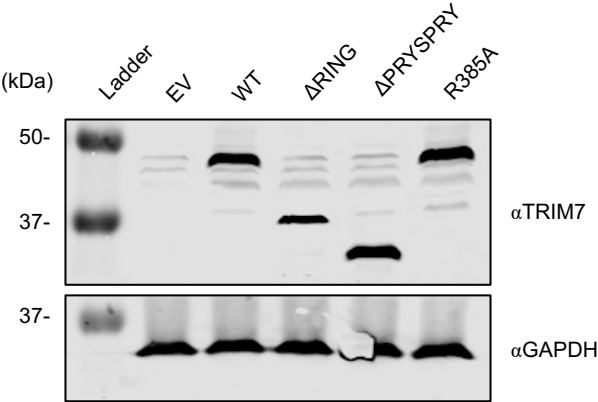
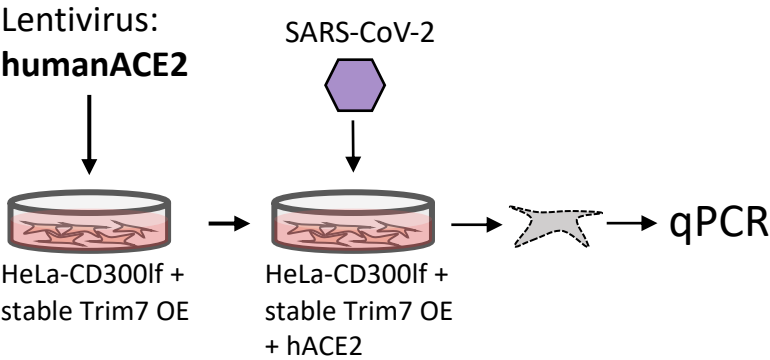


Figure S7. SARS-CoV-2 infection is not restricted by TRIM7

A

Protein	C-term
NSP4	'LQ'
NSP5	'FQ'
NSP6	'VQ'
NSP7	'LQ'
NSP8	'LQ'
NSP9	'LQ'
NSP10	'LQ'
NSP11	
NSP12	'LQ'
NSP13	'LQ'
NSP14	'LQ'
NSP15	'LQ'

B



C

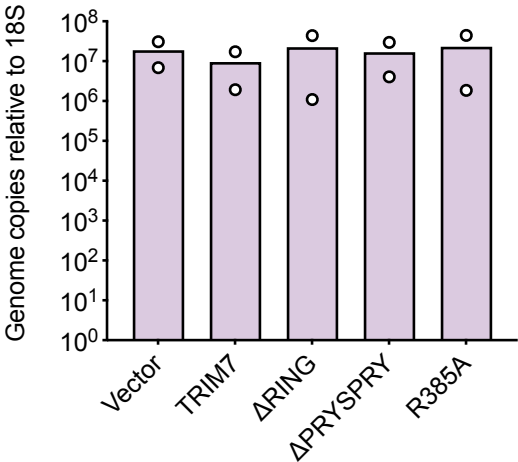


Figure S8. Phylogenetic trees for GYG1 and TRIM7

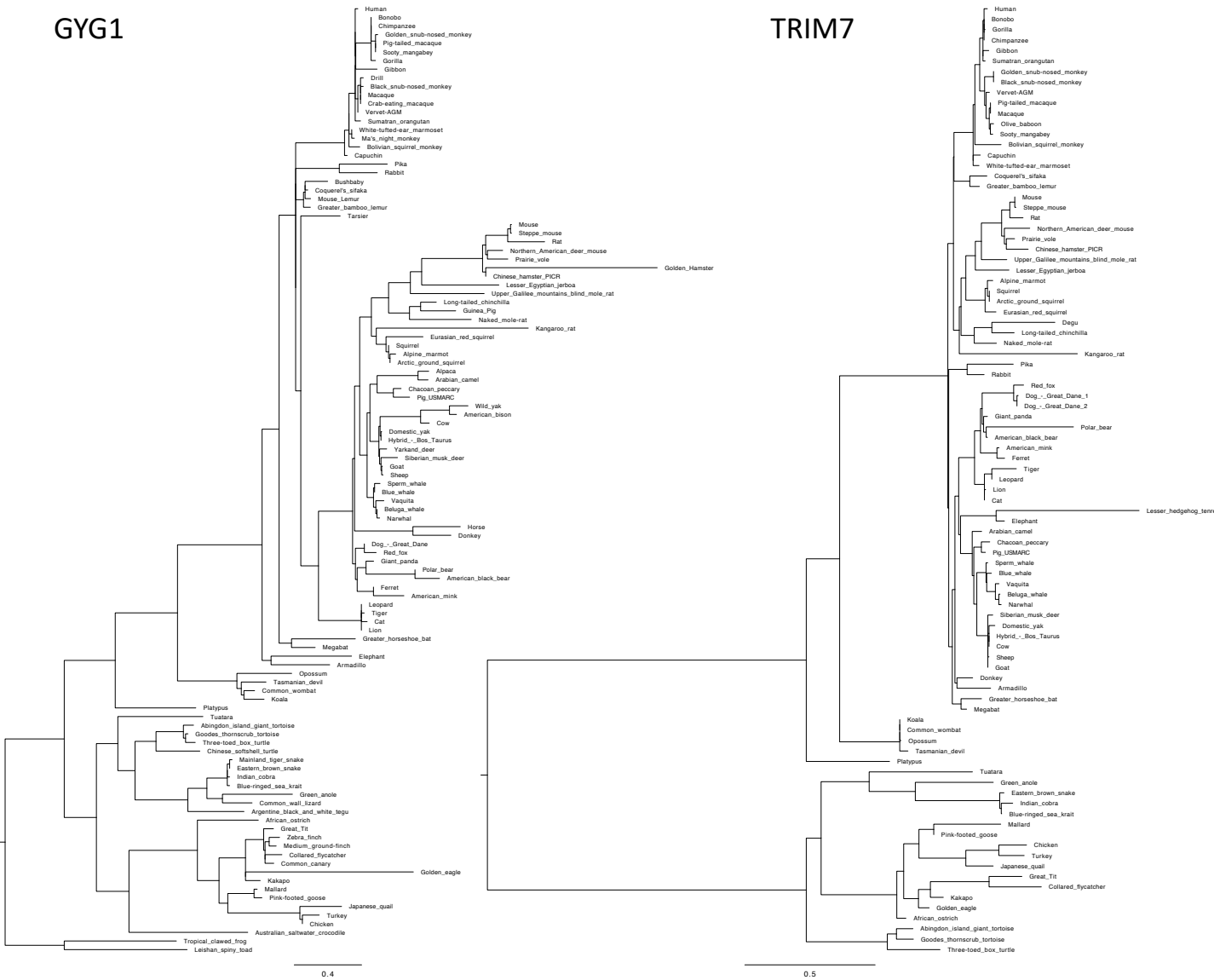


Figure S9. Tissue expression of TRIM7 and associated proteins

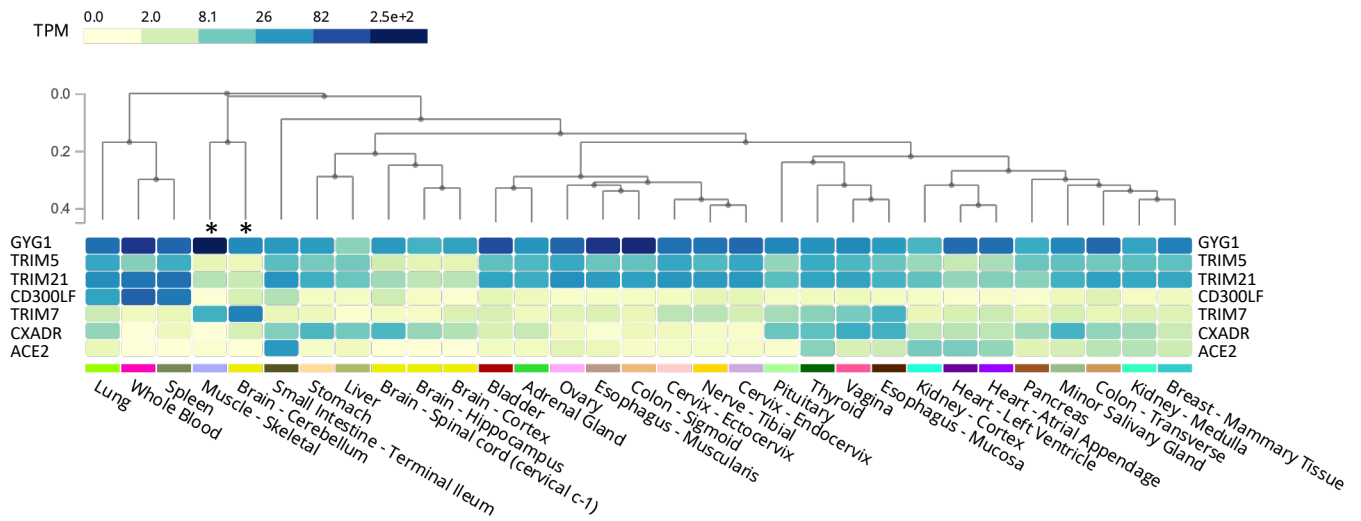


Table S1 Data collection and refinement statistics

	7OVX (TRIM7: GYG1 ₃₂₂₋₃₃₃)	7OW2 (TRIM7: RACO-1 ₂₂₉₋₂₃₅)	8A5L (TRIM7:2C ₂₀₈₋₂₁₄)	8A5M (TRIM7:MNV1- NS6 ₁₁₇₁₋₁₁₇₇)	8A8X (TRIM7:MNV1- NS3 ₆₉₉₋₇₀₅)
Data collection					
Space group	P212121	P61	P65	P1211	P1211
Cell dimensions <i>a</i> , <i>b</i> , <i>c</i> (Å)	37.63, 54.23, 81.40	108.12, 108.12, 137.14	79.89, 79.89, 53.2	40.92, 112.97, 53.04	51.25, 53.67, 73.60
α , β , γ (°)	90.0, 90.0, 90.0	90.0, 90.0, 120.0	90.0, 90.0, 120.0	90.0, 102.93, 90	90, 105.5, 90
Resolution (Å)	19.3-1.7 (1.78-1.70)	93.64-2.2 (2.29-2.20)	29-1.62 (1.62- 1.66)	112.97-2.92 (3.10-2.92)	70.91-2.37 (2.37-2.43)
<i>R</i> _{meas}	9.6 (30.1)	10.3 (48.1)	11.4 (92.5)	9.4 (N/A)	17.7 (96.1)
CC _{1/2} (%)	99.4 (91.2)	99.7 (96.3)	99.7 (59.9)	96.4(33.8)	100 (60)
<i>I</i> / σ <i>I</i>	8.9 (2.8)	12.6 (3.1)	11.1 (1.6)	24.4(1.4)	6.8 (1.2)
Completeness (%)	99.0 (98.8)	99.2 (98.5)	99.7 (95.6)	99.9 (98.8)	97.4 (74.4)
Redundancy	3.3 (3.1)	6.4 (5.6)	4.9 (3.7)	3.5 (3.4)	3.3 (2.4)
Resolution (Å)	1.7	2.2	1.62	2.92	2.37
No. reflections	17598	47982	24565	10246	15418
<i>R</i> _{work} / <i>R</i> _{free}	0.18/0.22	0.20/0.24	0.15/0.18	0.19/0.29	0.19/0.26
No. atoms	1657	5750	1619	2857	2875
Protein	1506	5614	1443	2815	2819
Ligand/ion	0	2	10	15	0
Water	151	135	152	24	56
B-factors					
Protein	21.81	41.62	17.99	57.69	30.68
Ligand/ion	0	46.39	33.52	92	N/A
Water	33.54	36.74	30.03	33.6	26.02
R.m.s. deviations					
Bond lengths (Å)	0.01	0.01	0.01	0.01	0.01
Bond angles (°)	1.60	1.40	1.7	1.9	1.7

*Values in parentheses are for highest-resolution shell.

Table S2 – ITC data. Concentration for proteins and peptides is given as monomer. * indicates where N was fixed in analysis. **Concentration of GYG1 (and MBP-T7-CC-PS) dimer was used in the analysis. NB = no binding.

TRIM7	CONC. [UM]	LIGAND	CONC. [UM]	SEQUENCE	N	K _D	ΔH (CAL/MOL)	TEMP[°C]
HTR7-PS WT	500	rbGYG1	100	see methods	1.07±0.014	2.2 μM±0.17	-7271±130	15
MTR7-PS WT	500	rbGYG1	100	see methods	0.93±0.005	1.5 μM±0.27	-1113±79	15
MTR7-PS WT	500	mGYG1	100	see methods	0.96±0.008	1.04 μM ±0.15	-1192±132	15
HTR7-PS WT	20	hGYG1-GN1	400	see methods	0.42±0.03 **	2.16 μM±0.06	-27000±3300	25
HTR7-PS WT	500	rbGYG1 _{VR-ClV}	100	see methods	1.05±0.011	2.6 μM ±0.33	-6433±95	15
HTR7-PS WT	500	rbGYG1 _{ClV}	100	see methods	0.70±0.034	4.8μM ±4.0	-9191±615	15
HTR7-PS WT	500	rbGYG322-333	50	DNIKKKLDTYLQ	0.70±0.03	21 ± 1.8 μM	-9191±615	15
HTR7-PS WT	25	hGYG1322-333	250	DNIKRKLDTYLQ	0.97±0.02	8 ± 0.64 μM	-11200±383	20
HTR7-PS WT	25	RACO-1 ₂₂₇₋₂₃₅	250	NLGLSMLQ	0.61±0.04	7.9 ± 1.06 μM	-6360±561	20
HTR7-PS WT	20	CVB-2C ₂₀₈₋₂₁₄	400	TIEALFQ	0.90±0.2	11.2 ± 4.2 μM	-12600±3580	25
HTR7-PS WT	20	MNV1-NS6 ₁₁₇₂₋₁₁₇₈	400	LEALEFQ	1.13±1.62	8.7 ± 3.2 μM	-11700±2250	25
HTR7-PS WT	20	MNV1-NS3 ₇₀₀₋₇₀₆	400	HDDFGLQ	1.18±0.19	14.3 ± 4.3 μM	-10900±2280	25
HTR7-PS WT	20	polyA	400	AAAAAAA	NB	NB	NB	25
HTR7-PS WT	20	polyA-LQ	400	AAAAALQ	1*	8.92 ± 3.03 μM	-4870±513	25
HTR7-PS WT	20	LQ	2000	LQ	1*	201 ± 30 μM	-5720±507	25
HTR7-PS WT	20	Ac-LQ	800	Ac-LQ	1*	144 ± 26 μM	-6600±760	25
HTR7-PS WT	20	Ac-LLQ	800	Ac-LLQ	1*	38.7 ± 5.16 μM	-7720±484	25
HTR7-PS WT	20	TIEALFA	400	TIEALFA	NB	NB	NB	25
HTR7-PS WT	20	AIEALFQ	400	AIEALFQ	0.80±0.19	17.0 ± 4.3 μM	-15500±4410	25
HTR7-PS N383A	25	hGYG1322-333	250	DNIKRKLDTYLQ	NB	NB	NB	20
HTR7-PS T384A	25	hGYG1322-333	250	DNIKRKLDTYLQ	0.71±0.18	22.6 ± 6.6 μM	-7280±2410	20
HTR7-PS R385A	25	hGYG1322-333	250	DNIKRKLDTYLQ	NB	NB	NB	20
HTR7-PS L423A	25	hGYG1322-333	250	DNIKRKLDTYLQ	NB	NB	NB	20
HTR7-PS F426A	25	hGYG1322-333	250	DNIKRKLDTYLQ	NB	NB	NB	20
HTR7-PS Q436A	25	hGYG1322-333	250	DNIKRKLDTYLQ	NB	NB	NB	20
HTR7-PS N438A	25	hGYG1322-333	250	DNIKRKLDTYLQ	0.64±0.02	2.32 ± 0.26 μM	-9830±318	20
HTR7-PS N383A	25	RACO-1 ₂₂₇₋₂₃₅	250	NLGLSMLQ	NB	NB	NB	20
HTR7-PS T384A	25	RACO-1 ₂₂₇₋₂₃₅	250	NLGLSMLQ	0.99±0.05	12.3 ± 2.00 μM	-2870±253	20
HTR7-PS R385A	25	RACO-1 ₂₂₇₋₂₃₅	250	NLGLSMLQ	NB	NB	NB	20
HTR7-PS L423A	25	RACO-1 ₂₂₇₋₂₃₅	250	NLGLSMLQ	NB	NB	NB	20
HTR7-PS F426A	25	RACO-1 ₂₂₇₋₂₃₅	250	NLGLSMLQ	NB	NB	NB	20
HTR7-PS Q436A	25	RACO-1 ₂₂₇₋₂₃₅	250	NLGLSMLQ	NB	NB	NB	20
HTR7-PS N438A	25	RACO-1 ₂₂₇₋₂₃₅	250	NLGLSMLQ	0.67±0.08	3.93 ± 1.75 μM	-4930±852	20
HTR7-PS N383A	20	CVB-2C ₂₀₈₋₂₁₄	400	TIEALFQ	NB	NB	NB	25
HTR7-PS T384A	20	CVB-2C ₂₀₈₋₂₁₄	400	TIEALFQ	1 *	21.2 ± 5.84 μM	-6120±704	25
HTR7-PS R385A	20	CVB-2C ₂₀₈₋₂₁₄	400	TIEALFQ	NB	NB	NB	25
HTR7-PS L423A	20	CVB-2C ₂₀₈₋₂₁₄	400	TIEALFQ	NB	NB	NB	25
HTR7-PS F426A	20	CVB-2C ₂₀₈₋₂₁₄	400	TIEALFQ	NB	NB	NB	25
HTR7-PS Q436A	20	CVB-2C ₂₀₈₋₂₁₄	400	TIEALFQ	NB	NB	NB	25
HTR7-PS N438A	20	CVB-2C ₂₀₈₋₂₁₄	400	TIEALFQ	0.92±0.06	7.82 ± 1.18 μM	-10400±910	25
HTR7-PS R385A	20	MNV1-NS6 ₁₁₇₂₋₁₁₇₈	400	LEALEFQ	NB	NB	NB	25
HTR7-PS R385A	20	MNV1-NS3 ₇₀₀₋₇₀₆	400	HDDFGLQ	NB	NB	NB	25
HTR7-CC-PS WT	12	hGYG322-333	300	DNIKRKLDTYLQ	1.7 ± 0.8	15 ± 6 μM	-9680±5770	25
HTR7-CC-PS WT	12	hGYG1-GN1	150	see methods	0.8 ± 0.02	0.16 ± 0.05 μM	-23800±991	25