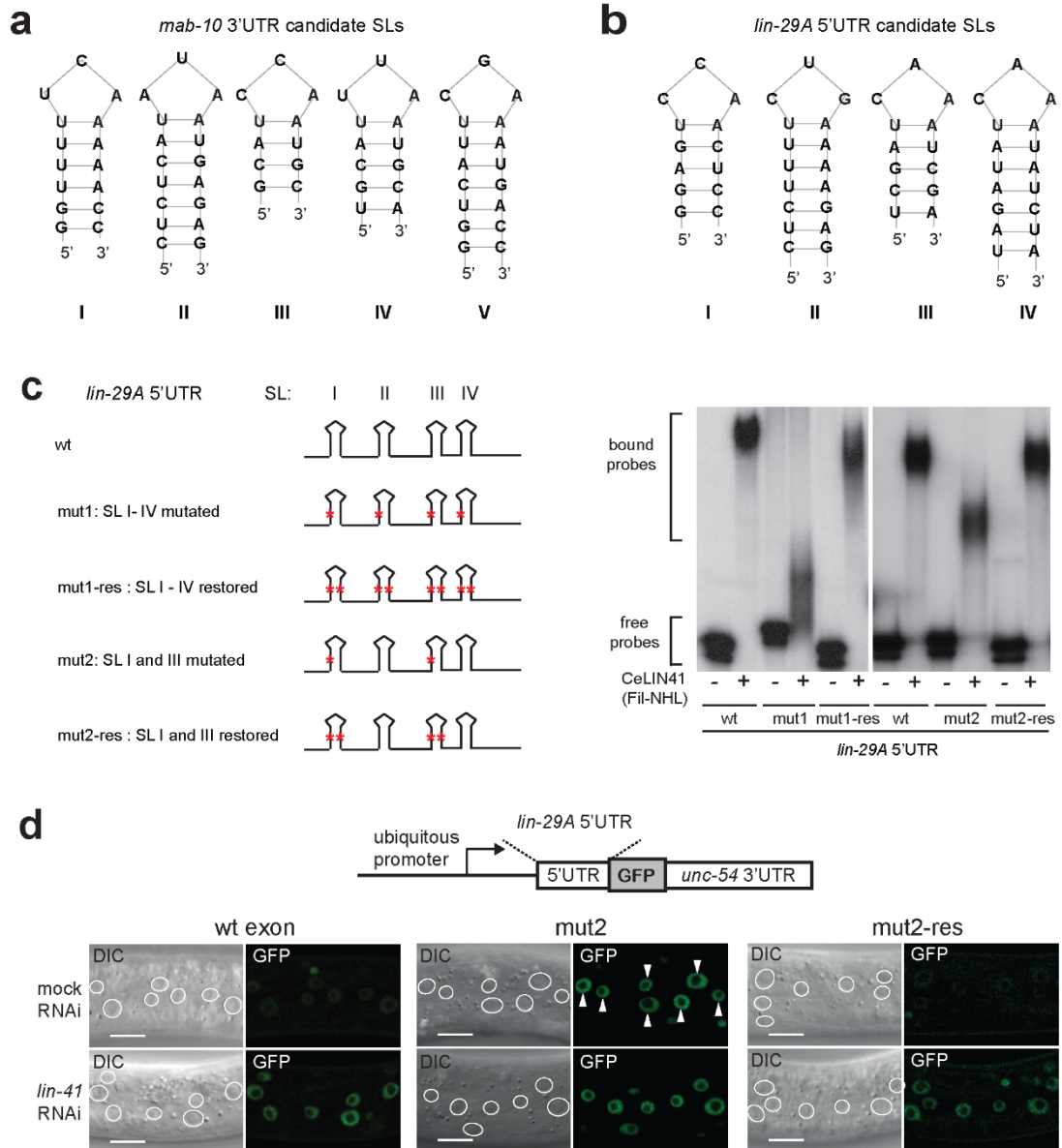


Supplementary Information

**Evolutionary plasticity of the NHL domain underlies distinct solutions to
RNA recognition**

Kumari et al.



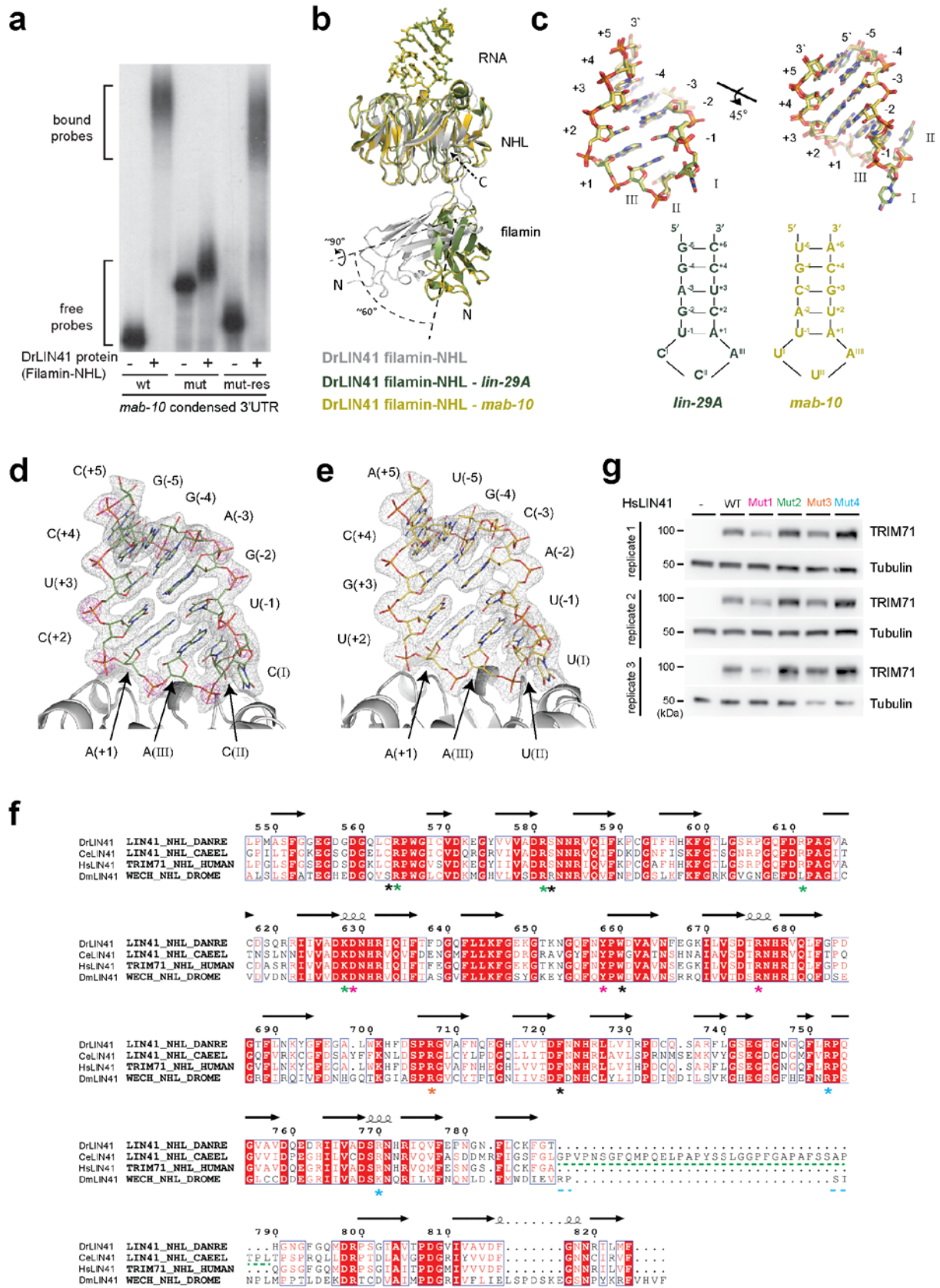
Supplementary Figure 1: CeLIN41 binds to SL motifs of *mab-10* 3'UTR and *lin-29A* 5'UTR. Related to Fig. 2

(a) Sequences of candidate CeLIN41 binding SLs in the *mab-10* 3'UTR.

(b) Sequences of candidate CeLIN41 binding SLs in the *lin-29A* 5'UTR exon-1.

(c) CeLIN41 binding to *lin-29A* 5'UTR. Left: Schematics representing wild-type and modified *lin-29A* RNA probes. Respective sequences are listed in [Supplementary Table 1](#). Right: Gel-shift experiments showing binding of CeLIN41 to the *lin-29A* RNA probes described in the schematics on the left. Whereas CeLIN41 bound to the *lin-29A* 5'UTR, mutations disrupting all the four SLs (mut1) significantly reduced the binding to CeLIN41. Mutations disrupting SL I and III (mut2) led to the formation of a smaller protein-RNA complex as compared to the wild-type. Compensatory mutations in the stem (mut1-res and mut2-res) restored the protein-RNA complex to wild-type levels.

(d) Micrographs of early L3-stage *C. elegans* larvae, treated with either *lin-41* or mock RNAi expressing nuclear-localized GFP (to concentrate the signal; white circles demarcate nuclei) from the *dpy-30* promoter and under an unregulated 3'UTR, *unc-54*. The 5'UTR corresponds to the constructs in c. GFP was imaged under identical microscope settings for all animals. The wild-type but not the mutant (mut2) *lin-29A* 5'UTR imposed CeLIN41-mediated repression on the GFP (white arrowheads point to GFP-expressing nuclei). The restored 5'UTR (mut2-res) reinstated CeLIN41-mediated regulation comparable to the wild-type levels. Scale bars - 10 μ m.



Supplementary Figure 2: Crystal structures of DrLIN41 filamin-NHL domain and conformation of RNA stem loops. Related to Fig. 4 and 5

(a) Gel-shift experiment showing the binding of DrLIN41 to the *mab-10* condensed 3'UTR probes described in the schematics in Fig. 2c. Whereas DrLIN41 bound the *mab-10* condensed 3'UTR, mutations disrupting the stem (mut) abolished the binding, whereas compensatory mutations (mut-res) restored the binding.

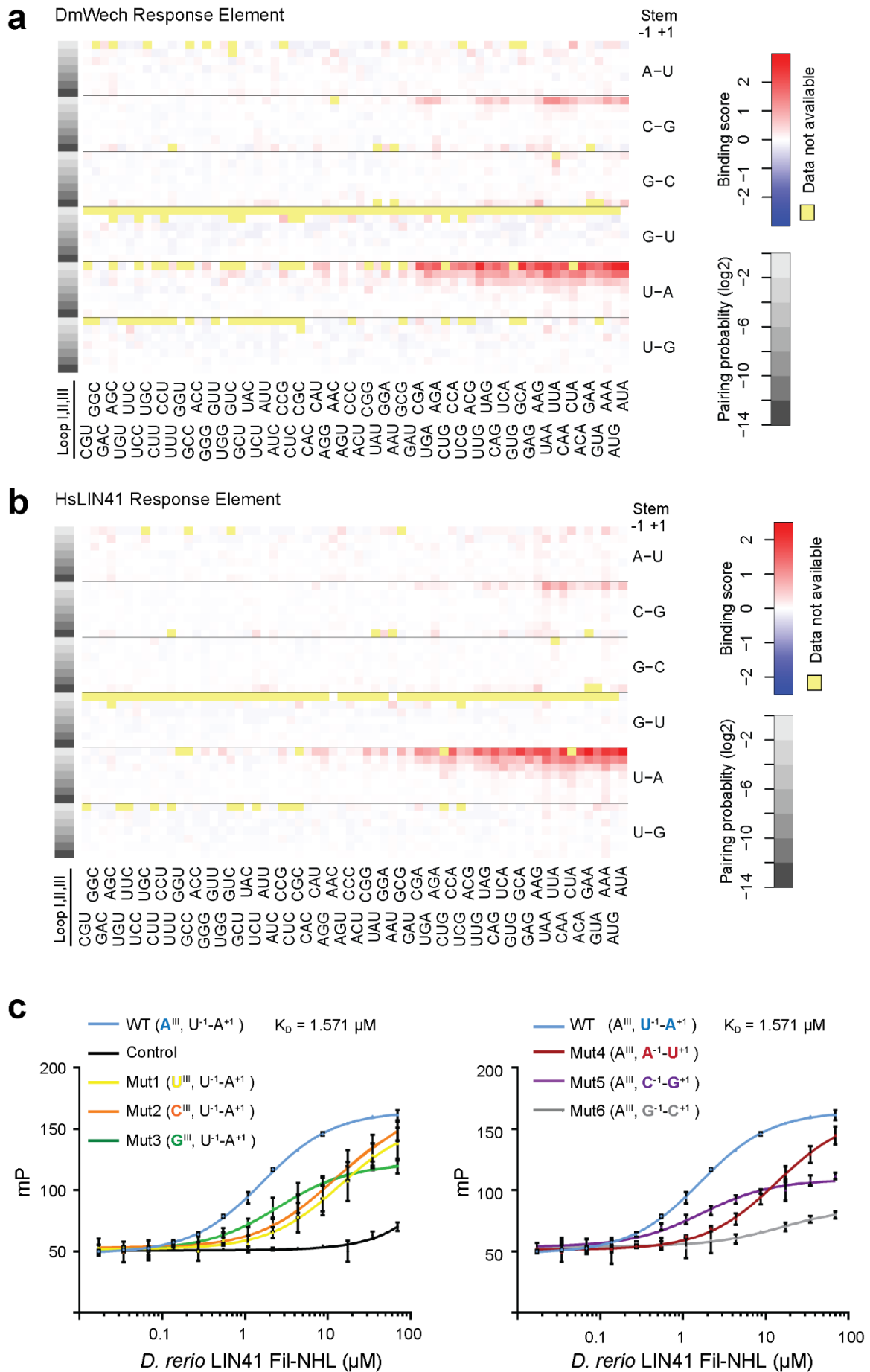
(b) Superposition of DrLIN41 filamin-NHL crystal structures (unbound: grey, LIN41-*lin-29A* complex: olive, LIN41-*mab-10* complex: gold). The protein is displayed as cartoon model and RNA is shown as sticks. Differences in the position of the filamin domain between unbound and complex structures are highlighted; protein domains and RNA are labeled.

(c) Detailed presentation of superimposed *lin-29A* (olive, sticks in atom colors) and *mab-10* (gold, sticks in atom colors) stem loop RNAs as present in the LIN41 RNA complex structures. Two views are shown where the RNA is rotated by ~45 degrees along the indicated axis. RNA positions in the stem loop are labeled and schematic diagrams depicting RNA sequences are inserted below.

(d, e) Electron density maps for *lin-29A* and *mab-10* stem loop RNAs as present in the corresponding crystal structures of the DrLIN41 complexes. RNA molecules are displayed as in b, while the protein is shown as cartoon in grey. 2mF_o-DF_c simulated annealing composite omit maps are shown in grey (1σ). An anomalous difference Fourier electron density map featuring peaks at phosphorus positions of the RNA backbone for *lin29-A* is displayed in magenta (5 σ) in d. Nucleotide sequences are labeled.

(f) A ClustalO multiple sequence alignment between LIN41 NHL domains from *D. rerio* (LIN41_NHL_DANRE, Uniprot E7FAM5), *C. elegans* (LIN41_NHL_CAEEL, Uniprot Q9U489) *H. sapiens* (TRIM71_NHL_HUMAN, Uniprot Q2Q1W2), and *D. melanogaster* (WECH_NHL_DROME, Uniprot Q9V4M2), showing a high degree of sequence conservation. Secondary structure elements present in the DrLIN41 filamin-NHL crystal structure are displayed as arrows (β-strands) and spirals (3.10 helices) above the alignment. The *C. elegans* protein contains a 37 amino acid-long insert in the loop connecting propeller blades V and VI, which is highlighted with a dotted line in green. Shorter inserts are also found in the *Drosophila* protein and are highlighted by dotted lines in cyan. Residues involved in RNA SL binding in the DrLIN41-RNA complex crystal structures are marked with an asterisk under the alignment. Residues that were mutated to investigate their contribution to SL binding are colored as in Fig. 5c.

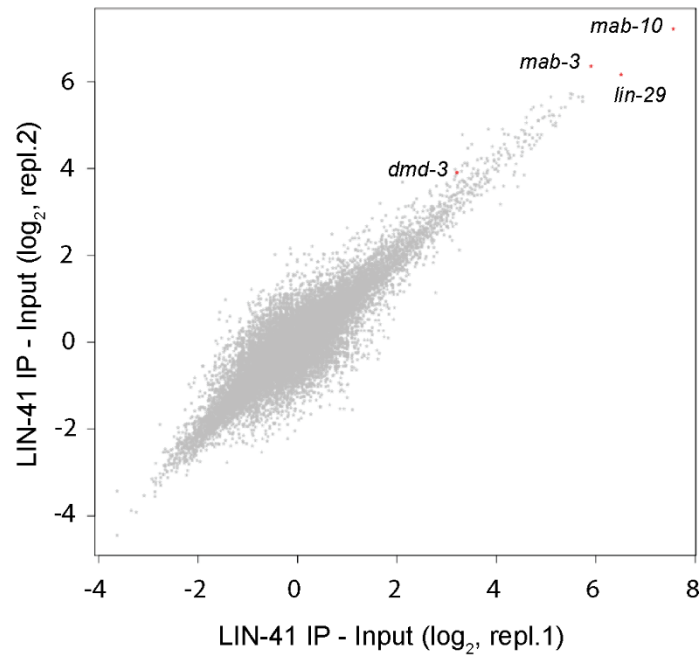
(g) Western blot showing expression levels of mutant HsLIN41 proteins used in Fig. 5d. Uncropped gels with markers are shown in Supplementary Fig. 8.



Supplementary Figure 3: LIN41 Response Element - LRE. Related to Fig. 6-7

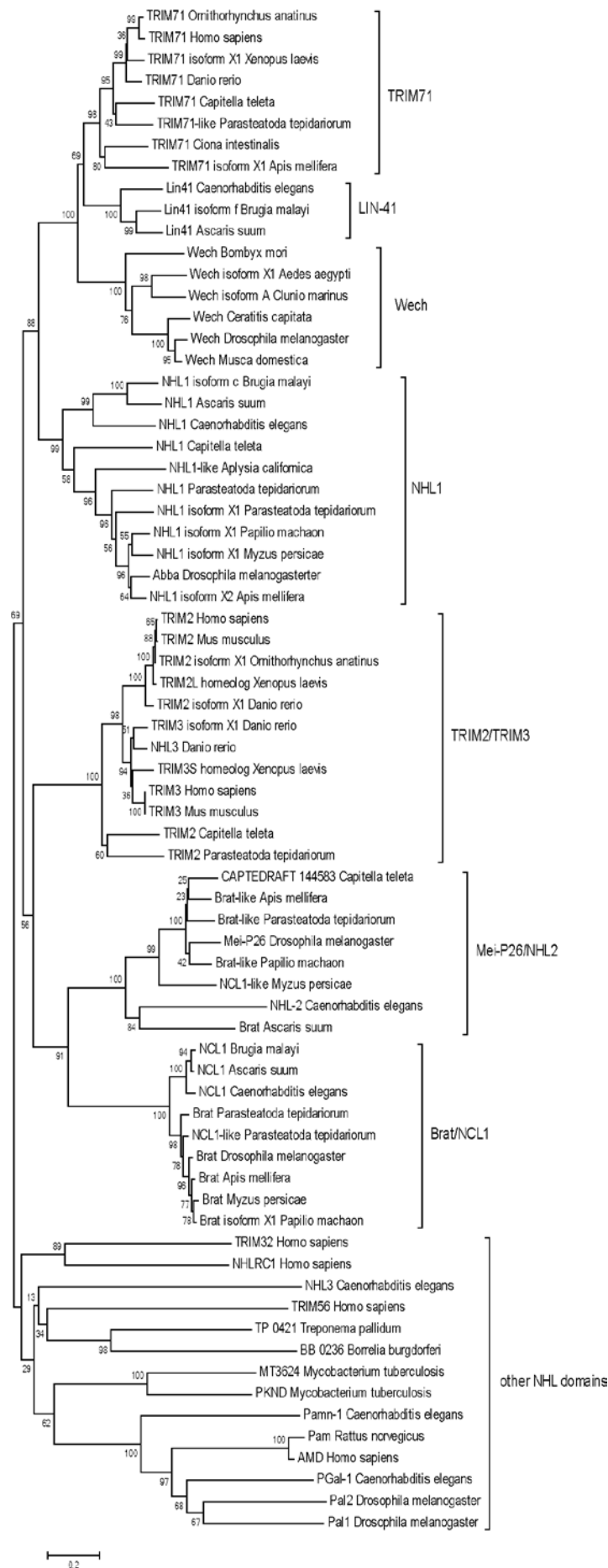
(a, b) A heat map showing the average DmWech and HsLIN41 binding scores from the RNAcompete experiment for all RNAs containing any particular motif variant as described in [Fig. 6a](#). The data was clustered based on the CeLIN41 binding score. Yellow: data not available (RNA motif variants supported by less than 20 oligonucleotide sequences).

(c) The FP assay to determine binding constants - Raw FP data of DrLIN41 interacting with a WT LRE (SL I in [Supplementary Fig. 1b](#)), a control stem-loop RNA with five nucleotides in the loop and mutant LREs are shown in units of millipolarization (mP). The equilibrium dissociation constant (K_D) is shown for the WT LRE. Each data point is a mean of three experiments and the error bars represent the standard deviation. The WT LRE data plotted in both graphs is the same.



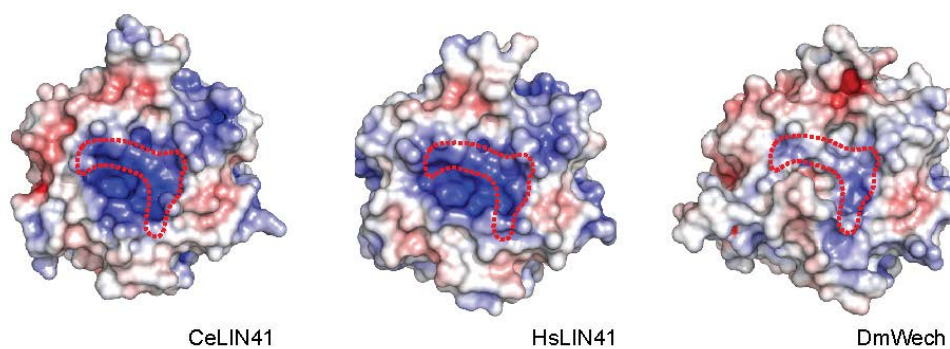
Supplementary Figure 4: CeLIN41 associated RNAs. Related to Fig. 7

The plot shows enrichment of transcripts in CeLIN41 immunoprecipitates (IP) versus inputs in two biologically independent experiments. Known somatic mRNA targets of CeLIN41 are marked in red and labeled.



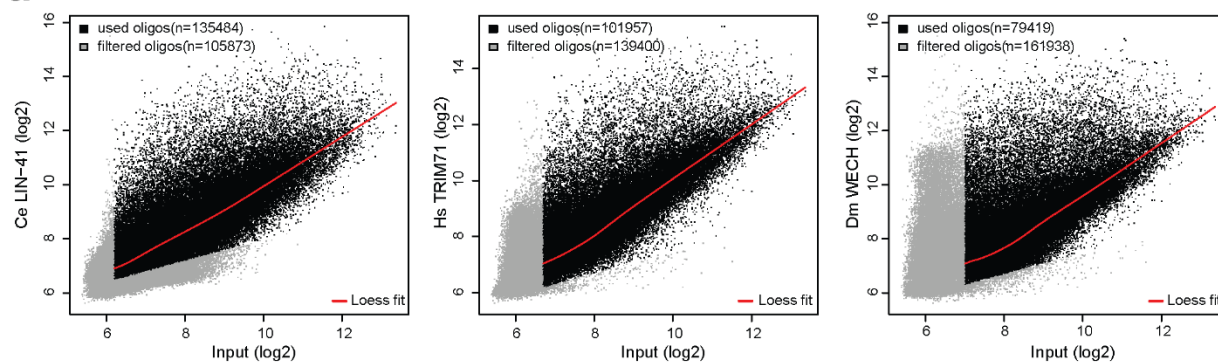
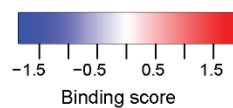
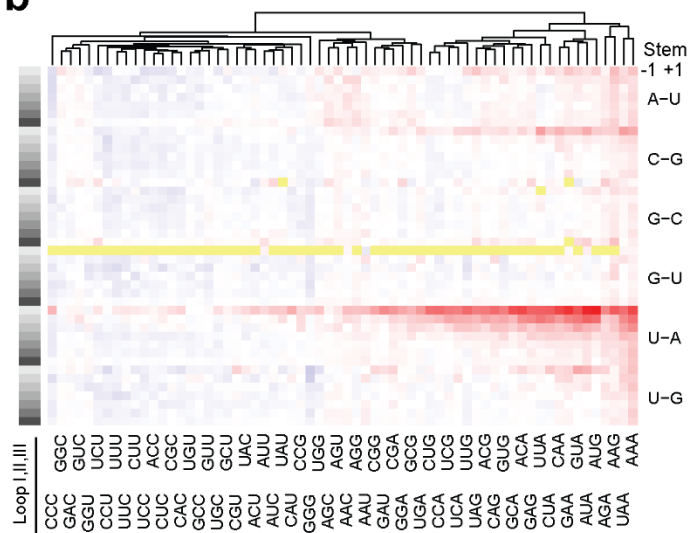
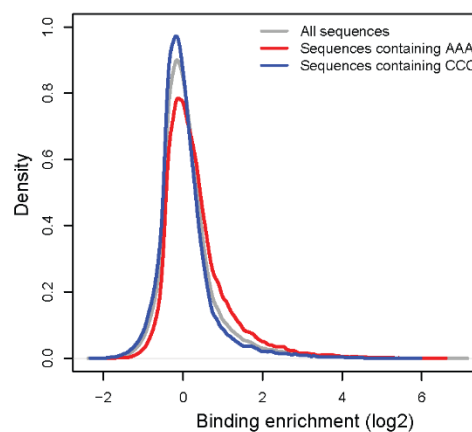
Supplementary Figure 5: Molecular phylogeny analysis of NHL domains of various NHL domain-containing proteins. Related to Fig. 9

The evolutionary history was inferred using the Minimum Evolution method and the optimal tree is shown in [Fig. 9](#). The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as evolutionary distances used to build the phylogenetic tree. The evolutionary distances were computed using the Poisson correction method and are in the units of the number of amino acid substitutions per site. Each subgroup has been named as shown in the compressed tree in [Fig. 9](#).



Supplementary Figure 6: Structural basis of RNA recognition by LIN41 orthologs. Related to Fig. 9

Homology models of CeLIN41, HsLIN41, and DmWech are shown in a surface mode, with their respective electrostatic surface potentials (scale as in Fig. 8). The approximate footprint of the RNA stem loop on the protein surface is shown as a dotted red line.

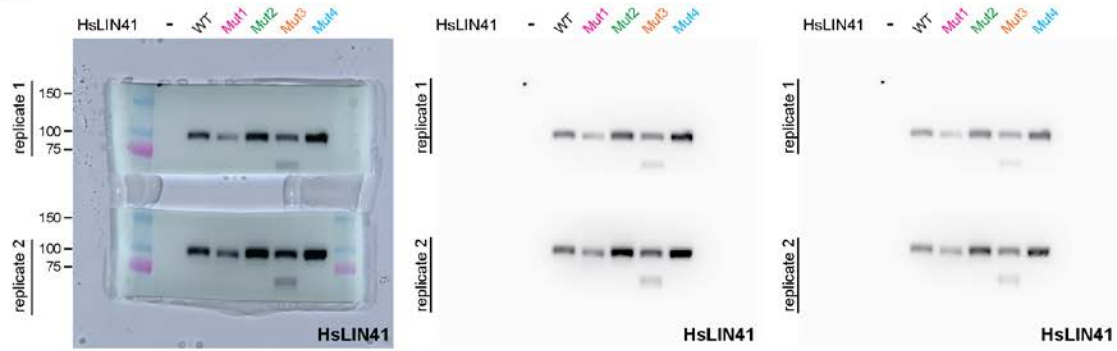
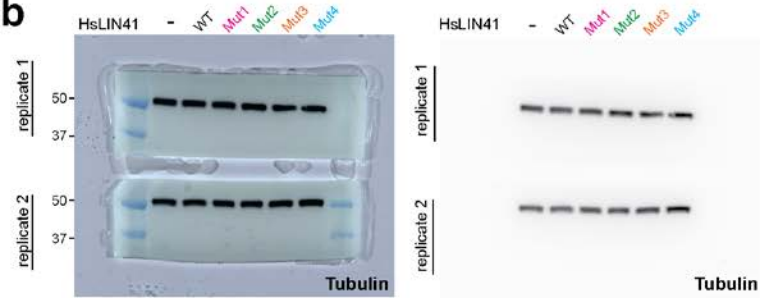
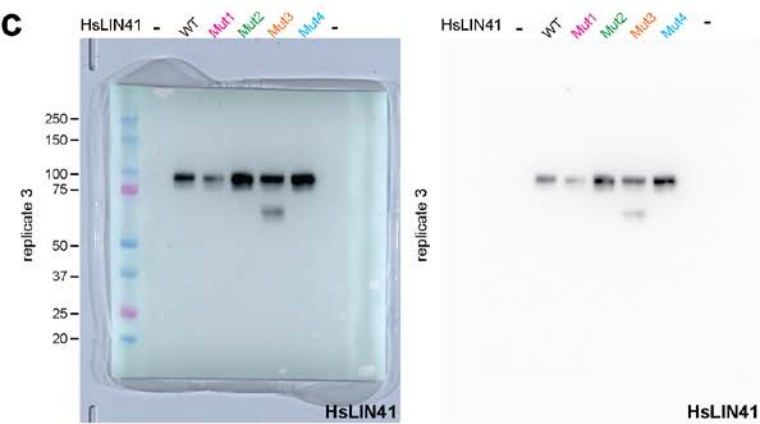
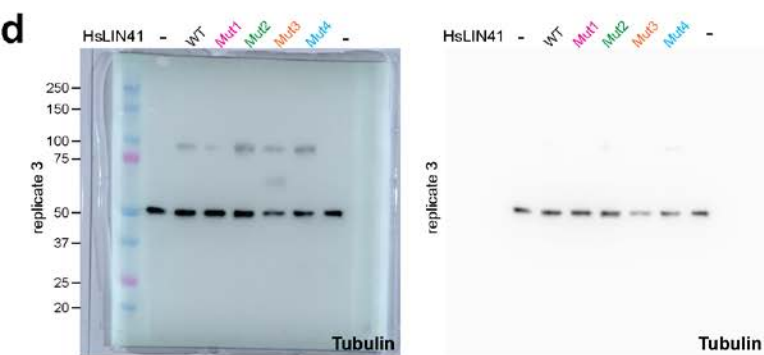
a**b****c**

Supplementary Figure 7: Analysis of RNAcompete data for CeLIN41, HsLIN41 and DmWech.
Related to methods.

(a) Grey dots indicate the oligonucleotide sequences that were removed from the analysis due to possible technical artifacts. These include: 1. The oligonucleotide sequences that showed a median intensity lower than 6 (log2 space) over the full set of 244 experiments (hugheslab.ccbr.utoronto.ca/supplementary-data/RNAcompete_eukarya/raw_data.txt.gz) as their intensity is less reliable. 2. The oligonucleotide sequences that were depleted in input. 3. For HsLIN41 and DmWech, oligonucleotides that were enriched in pull-down but showed very low intensity in input.

(b) CeLIN41 response element before setting a cut-off for enrichment values.

(c) RNAcompete enrichments for all sequences and sequences containing an AAA or a CCC. Sequences containing an AAA showed a slight shift in the distribution present at even low enrichment values (<1). CCC showed the opposite trend.

a**b****c****d**

Supplementary Figure 8: Uncropped western blots with markers. Related to Supplementary Fig. 2g.

(a) Left: Two gels showing HsLIN41 levels, from independent experiments (replicates 1 and 2), with different exposures to the right. The middle exposure is shown for replicate 1, and the right exposure for replicate 2 in Supplementary Fig. 2g.

(b) Tubulin levels from replicates 1 and 2, corresponding to **a**, shown in Supplementary Fig. 2g.

(c) Left: The gel from replicate 3, showing HsLIN41 levels. The exposure on the right is shown in Supplementary Fig. 2g.

(d) Tubulin levels from replicate 3, corresponding to **c**, shown in Supplementary Fig. 2g.

Supplementary Table 1: Probes for gel-shifts. Related to Fig. 2 and Supplementary Fig. 1.

mab-10 part 2
uaaaaucccgccccuucgcucggagucuaauaaauuuccuucucuccuaucauuuuuugucuaguuuucaaaaaacccc ccauuuuuuccggcgguuuuucaaaaaaccaaugccaagcucucuaauaaugggagucuaaacacaguucgguuccaaaacca acgccacggccccgcccccauuagauauuuuaaua
mab-10 part 2 mut
uaaaaucccgccccuucgcucggagucuaauaaauuuccuucucuccuaucauuuuuugucuaguuuucaaaaaacccc ccauuuuuuccggcgCuuuuucaaaaaaccaaugccaagcucuGauauaaugggagucuaaacacaguucgguuccaaaacca acgccacggccccgcccccauuagauauuuuaaua
mab-10 part 2 mut-res
uaaaaucccgccccuucgcucggagucuaauaaauuuccuucucuccuaucauuuuuugucuaguuuucaaaaaacccc ccauuuuuuccggcgCuuuuucaaaaaGcaaugccaagcucuGauauaaCggagucuaaacacaguucgguuccaaaacca acgccacggccccgcccccauuagauauuuuaaua
mab-10 part 4
Ucgcauccaauugcauugcaaguugauugcuuuuuauaaaauuuugggucucgaagcgaaaagcccauaggauuuucacaaaa auuuugcauuuaugcagugaaaaaucaaaaaauucaagauuuuucugaaugaucauuuuucaaauuuuccggucuu cgaaugggccuaauuugcuccaaaaauugaauaaucc
mab-10 part 4 mut
ucgGauccaauugcauugcaaguugauugcuuuuuauaaaauuuugggucucgaagcgaaaagcccauaggauuuucacaaaa auuuugGauuuuaugcagugaaaaaucaaaaaauucaagauuuuucugaaugaucauuuuucaaauuuuccggGauu cgaaugggccuaauuugcuccaaaaauugaauaaucc
mab-10 part 4 mut-res
ucgGauccaauCcauugcaaguugauugcuuuuuauaaaauuuugggucucgaagcgaaaagcccauaggauuuucacaaaa auuuugGauuuauuCcagugaaaaaucaaaaaauucaagauuuuucugaaugaucauuuuucaaauuuuccggGauu cgaaauCgccuaauuugcuccaaaaauugaauaaucc
mab-10 condensed 3'UTR
ucuaguuuucaaaaaaccccccauuuuuccggcgguuuuucaaaaaaccaaugccaagcucucuaauaaugggagucuaaac acaguucgguuccaaaacugaaaaacucauuuucgcauccaauugcauugcaaguugauugcuuuucacaaaaauuuugca uuuaaagcagugaaaaauuuccggucuuuugcaaauggccuaauuugcuccaaaaa
mab-10 condensed 3'UTR mut
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mab-10 condensed 3'UTR mut-res
ucuaguuuucaaaaaaccccccauuuuuccggcgCuuuuucaaaaaGcaaugccaagcucuGauauaaCggagucuaaac acaguucgguuccaaaacugaaaaacucauuuucgGauccaauCcauugcaaguugauugcuuuucacaaaaauuuugGa uuuaaCcagugaaaaauuuccggGauucgaaaCgccuaauuugcuccaaaaa
lin-29A
guuccgaaccaauucgcuagcgaaccuuggaguccaacuccguuuuuacucuuuucugaaaagagccuacuaaaauauugg aacuaauaaucaaaacuauucgaucacacaccuacuaugauaaucaauaauacuggaaccaagguuugggaaac cugaaacugugcgaaauuggagcagaaauauu
lin-29A mut2
guuccgaaccaauucgcuagcgaaccuuggaCuccaacuccguuuuuacucuuuucugaaaagagccuacuaaaauauugg aacuaauaaucaaaacuauucCaucaaaucgacacaccuacuaugauaaucaauaauacuggaaccaagguuugggaaac cugaaacugugcgaaauuggagcagaaauauu
lin-29A mut2-res
guuccgaaccaauucgcuagcgaaccuuggaCuccaaGuccguuuuuacucuuuucugaaaagagccuacuaaaauauugg aacuaauaaucaaaacuauucCaucaaaUGacacaccuacuaugauaaucaauaauacuggaaccaagguuugggaaac cugaaacugugcgaaauuggagcagaaauauu
lin-29A mut1
guuccgaaccaauucgcuagcgaaccuuggaCuccaacuccguuuuuacuGuuuucugaaaagagccuacuaaaauauugg aacuaauaaucaaaacuauuGGaucaaaucgacacaccuacuaCauaaucaauaauacuggaaccaagguuugggaaac cugaaacugugcgaaauuggagcagaaauauu
lin-29A mut1-res
guuccgaaccaauucgcuagcgaaccuuggaCuccaaGuccguuuuuacuGuuuucugaaaaCagccuacuaaaauauugg aacuaauaaucaaaacuauuGGaucaaaCcacacaccuacuaCauaaucaauaauGuaauacuggaaccaagguuugggaaac cugaaacugugcgaaauuggagcagaaauauu

Mutations are marked in red.

Supplementary Table 2: Crystallographic data collection and refinement statistics.
Related to Fig. 4-5 and Supplementary Fig. 2

	<i>D. rerio</i> LIN41 filamin-NHL unbound ^a	<i>D. rerio</i> LIN41 filamin-NHL <i>lin-29A</i> complex	<i>D. rerio</i> LIN41 filamin-NHL <i>mab-10</i> complex
Data collection			
Space group	P2 ₁ 2 ₁ 2 ₁	P3 ₁ 21	P3 ₁ 21
Unit cell dimensions			
<i>a</i> , <i>b</i> , <i>c</i> (Å)	65.80, 90.59, 131.05	101.85, 101.85, 109.89	101.49, 101.49, 108.94
α , β , γ (°)	90.0, 90.0, 90.0	90.0, 90.0, 120.0	90.0, 90.0, 120.0
Resolution range (Å) ^b	50.00-2.60 (2.67-2.60)	50.00-1.90 (1.95-1.90)	50.00-2.35 (2.41-2.35)
Wavelength (Å)	1.260	1.000	1.000
Completeness (%) ^b	91.6 (86.8)	99.4 (92.1)	99.4 (92.2)
Redundancy ^b	1.9 (1.8)	7.7 (7.7)	16.5 (15.4)
<i>R</i> _{sym} ^b	0.124 (0.491)	0.042 (2.172)	0.124 (2.468)
<i>I</i> / σ (<i>I</i>) ^b	5.28 (1.48)	20.24 (0.81)	16.02 (0.99)
CC (1/2) (%) ^b	98.7 (77.9)	99.9 (38.1)	99.9 (42.9)
Unique reflections	42647	51941	27367
Refinement			
<i>R</i> _{work}	0.182	0.158	0.172
<i>R</i> _{free}	0.244	0.180	0.211
Resolution range (Å)	46.43 - 2.60	46.64 – 1.90	46.30 – 2.35
Reflections (all)	23630	51933	27359
Reflections (test set)	1182 (5%)	2596 (5%)	1368 (5%)
Number of atoms			
Overall	6217	3541	3384
Protein	6002	3024	3013
RNA	-	272	271
Solvent	215	245	100
B-Factors (Å²)			
Overall	30.6	61.4	67.1
Protein	31.0	61.3	67.1
RNA	-	58.9	68.3
Solvent	19.2	63.7	66.7
RMS Deviations			
Bond lengths (Å)	0.01	0.007	0.007
Bond angles (°)	1.20	0.792	0.842
Ramachandran plot			
Allowed (%)	98.3	100	100
Outliers (%)	1.7	0	0

^aData collection statistics is reported for unmerged Friedel pairs

^bValues in parentheses refer to the highest resolution shell

Supplementary Table 3: LRE categories. Related to Fig. 7.

RNA motif Variant	1/-1	I,II,III	Pairing Probability Bin	Score	Level
UAUGA:7	U-A	AUG	7	1.84441	Strong
UAUAA:7	U-A	AUA	7	1.63461	Strong
UGAAA:7	U-A	GAA	7	1.45818	Strong
UCAAA:7	U-A	CAA	7	1.2545	Strong
UACAA:7	U-A	ACA	7	1.22135	Strong
UAAAA:7	U-A	AAA	7	1.16811	Strong
UGCAA:7	U-A	GCA	7	1.11358	Strong
UGUAA:7	U-A	GUA	7	1.06096	Strong
UCUAA:7	U-A	CUA	7	1.05241	Strong
UAAGA:7	U-A	AAG	7	0.9707	Strong
UUUAA:7	U-A	UUA	7	0.96786	Strong
UCAGA:7	U-A	CAG	7	0.94788	Strong
UAUAA:6	U-A	AUA	6	0.9321	Strong
UGUGA:7	U-A	GUG	7	0.8991	Medium
UUUGA:7	U-A	UUG	7	0.89742	Medium
UUAGA:7	U-A	UAG	7	0.87829	Medium
UGAGA:7	U-A	GAG	7	0.86413	Medium
UGUAA:6	U-A	GUA	6	0.83564	Medium
UUAAA:7	U-A	UAA	7	0.83551	Medium
UUCAA:7	U-A	UCA	7	0.83404	Medium
UAUGA:6	U-A	AUG	6	0.81587	Medium
UACGA:7	U-A	ACG	7	0.80056	Medium
UCCAA:7	U-A	CCA	7	0.77021	Medium
UAAAA:6	U-A	AAA	6	0.76223	Medium
UCUGA:7	U-A	CUG	7	0.74896	Medium
UAGAA:7	U-A	AGA	7	0.73576	Medium
UUCGA:7	U-A	UCG	7	0.73005	Medium
UUUAA:6	U-A	UUA	6	0.72904	Medium
UGAGA:6	U-A	GAG	6	0.71494	Medium
UCUAA:6	U-A	CUA	6	0.68443	Medium
UGAUA:7	U-A	GAU	7	0.6844	Medium
UACAA:6	U-A	ACA	6	0.67449	Medium
UUAAA:6	U-A	UAA	6	0.61226	Medium
UUGAA:7	U-A	UGA	7	0.60406	Medium
UCGAA:7	U-A	CGA	7	0.5824	Medium
UCGGA:7	U-A	CGG	7	0.57692	Medium
UGAAA:6	U-A	GAA	6	0.56925	Medium
UAAAA:5	U-A	AAA	5	0.54223	Medium
UCAAA:6	U-A	CAA	6	0.52941	Medium
CUUAG:7	C-G	UUA	7	0.49976	Medium
UGCGA:7	U-A	GCG	7	0.4898	Medium
UGUAA:5	U-A	GUA	5	0.45918	Medium

UGUGA:6	U-A	GUG	6	0.45877	Medium
UCCCA:7	U-A	CCC	7	0.44002	Weak
UUCAA:6	U-A	UCA	6	0.43203	Weak
CUAAG:7	C-G	UAA	7	0.42949	Weak
UUCGA:6	U-A	UCG	6	0.4135	Weak
CAUAG:7	C-G	AUA	7	0.39446	Weak
UACUA:7	U-A	ACU	7	0.39307	Weak
UUAAA:5	U-A	UAA	5	0.39234	Weak
UCAGA:6	U-A	CAG	6	0.36546	Weak
UUAGA:6	U-A	UAG	6	0.35639	Weak
UUUA:7	U-A	UAU	7	0.35141	Weak
UACGA:6	U-A	ACG	6	0.35003	Weak
CAAAG:7	C-G	AAA	7	0.34865	Weak
UGGAA:7	U-A	GGA	7	0.34131	Weak
UCCAA:6	U-A	CCA	6	0.32522	Weak
UAUAA:5	U-A	AUA	5	0.32497	Weak
UUUGA:6	U-A	UUG	6	0.3208	Weak
UACAA:5	U-A	ACA	5	0.3126	Weak
UUCAA:5	U-A	UCA	5	0.31073	Weak
CCAAG:7	C-G	CAA	7	0.30293	Weak
UAAUA:7	U-A	AAU	7	0.29526	Weak
UUUAA:5	U-A	UUA	5	0.28141	Weak
UGAAA:5	U-A	GAA	5	0.27765	Weak
UCUAA:5	U-A	CUA	5	0.27139	Weak
UGCGA:6	U-A	GCG	6	0.26833	Weak
UUAAA:4	U-A	UAA	4	0.25887	Weak
CGUAG:7	C-G	GUA	7	0.25801	Weak
UCAUA:7	U-A	CAU	7	0.25633	Weak
UUUGA:5	U-A	UUG	5	0.2535	Weak
UUGAA:6	U-A	UGA	6	0.25261	Weak
CCUAG:7	C-G	CUA	7	0.24647	Weak
UCAAA:5	U-A	CAA	5	0.24372	Weak
UAACA:6	U-A	AAC	6	0.2429	Weak
UUCUA:7	U-A	UCU	7	0.241	Weak
UCUGA:6	U-A	CUG	6	0.23796	Weak
UCGCA:7	U-A	CGC	7	0.23787	Weak
UUAGA:5	U-A	UAG	5	0.23348	Weak
CGAAG:7	C-G	GAA	7	0.23094	Weak
UGUGA:5	U-A	GUG	5	0.23041	Weak
UAAGA:6	U-A	AAG	6	0.22696	Weak
CAUGG:7	C-G	AUG	7	0.2242	Minimal
UAAGA:5	U-A	AAG	5	0.22194	Minimal
UGCAA:6	U-A	GCA	6	0.2187	Minimal
UAGAA:6	U-A	AGA	6	0.2184	Minimal

UAUGA:5	U-A	AUG	5	0.213	Minimal
UCUCA:7	U-A	CUC	7	0.20311	Minimal
UGCAA:5	U-A	GCA	5	0.20054	Minimal
UAACA:7	U-A	AAC	7	0.19932	Minimal
UCCGA:7	U-A	CCG	7	0.19771	Minimal
UAUCA:7	U-A	AUC	7	0.19687	Minimal
UCUAA:4	U-A	CUA	4	0.19199	Minimal
UAUUA:7	U-A	AUU	7	0.18267	Minimal
UAUAA:4	U-A	AUA	4	0.17849	Minimal
UAGUA:7	U-A	AGU	7	0.17612	Minimal
UCAGA:5	U-A	CAG	5	0.17534	Minimal
CUAGG:7	C-G	UAG	7	0.17524	Minimal
UGUAA:4	U-A	GUA	4	0.17498	Minimal
UCUGA:5	U-A	CUG	5	0.17405	Minimal
UAGUA:5	U-A	AGU	5	0.16971	Minimal
UCACA:7	U-A	CAC	7	0.16886	Minimal
UAGUA:6	U-A	AGU	6	0.16481	Minimal
UGUGA:4	U-A	GUG	4	0.16412	Minimal
UAGGA:7	U-A	AGG	7	0.16237	Minimal
CUUGG:7	C-G	UUG	7	0.1543	Minimal
UCGAA:6	U-A	CGA	6	0.1542	Minimal
UGAGA:5	U-A	GAG	5	0.14935	Minimal
CACAG:7	C-G	ACA	7	0.14653	Minimal
UUGAA:5	U-A	UGA	5	0.14441	Minimal
UGCGA:5	U-A	GCG	5	0.1441	Minimal
UGGGA:7	U-A	GGG	7	0.14338	Minimal
UAGGA:6	U-A	AGG	6	0.13911	Minimal
UGGAA:6	U-A	GGA	6	0.13808	Minimal
CAAGG:7	C-G	AAG	7	0.13713	Minimal
CAGAG:7	C-G	AGA	7	0.13602	Minimal
CGUGG:7	C-G	GUG	7	0.12768	Minimal
UGAGA:4	U-A	GAG	4	0.12282	Minimal
CUCAG:7	C-G	UCA	7	0.11913	Minimal
UCUCA:6	U-A	CUC	6	0.1165	Minimal
CCGAG:7	C-G	CGA	7	0.11584	Minimal
UCACA:5	U-A	CAC	5	0.11195	Minimal
UACCA:7	U-A	ACC	7	0.10635	Minimal
UAAAA:4	U-A	AAA	4	0.10354	Minimal
UACAA:4	U-A	ACA	4	0.10163	Minimal
UUCGA:5	U-A	UCG	5	0.10112	Minimal
UGAUA:6	U-A	GAU	6	0.10001	Minimal

Supplementary Table 4: *C. elegans* strains. Related to Methods

Experimental Models: <i>C. elegans</i> Strains		
Strain	Source	Identifier
Wild-type	CGC	N2
EG6699, <i>xeSi147</i> [<i>Pdpy-30::lin-29A 5'UTR exon 1::gfp(pest)/h2b::unc-54 3'UTR, unc-119(+)</i>] II	Aeschimann et al., 2017 ¹	HW1619
EG6699, <i>xeSi313</i> [<i>Pdpy-30::lin-29A 5'UTR exon 1 mut2::gfp(pest)/h2b::unc-54 3'UTR, unc-119(+)</i>] II	This study	HW1994
EG6699, <i>xeSi314</i> [<i>Pdpy-30::lin-29A 5'UTR exon 1 mut2-res::gfp(pest)/h2b::unc-54 3'UTR, unc-119(+)</i>] II	This study	HW1995
EG6699, <i>xeSi318</i> [<i>Plin-29A(act-1 5'UTR exon)::gfp(pest)/h2b::unc-54 3'UTR(mab-10 condensed 3'UTR), unc-119(+)</i>] II	This study	HW1999
EG6699, <i>rrrSi473</i> [<i>Plin-29A(act-1 5'UTR exon)::gfp(pest)/h2b::unc-54 3'UTR(mab-10 condensed 3'UTR mut), unc-119(+)</i>] II	This study	RAF2004
EG6699, <i>rrrSi474</i> [<i>Plin-29A(act-1 5'UTR exon)::gfp(pest)/h2b::unc-54 3'UTR(mab-10 condensed 3'UTR mut-res), unc-119(+)</i>] II	This study	RAF2005
<i>lin-41(rrr3)</i> (I); <i>rrrSi367</i> [<i>Plin-41::FLAG-GFP-TEV-LIN-41::lin-41 full-length 3'UTR; unc-119(+)</i>] (II)	Tocchini et al., 2014 ²	RAF1587

Supplementary Table 5: RNA sequences used for fluorescence polarization. Related to Methods

Name	Length	Sequence	Description
L1	13	GGAGUCCAACUCC	lin-29A 5'UTR SL I
Ctrl	13	GCUGACCAACUCC	a stem-loop with 5 nucleotides in the loop
L1.1 (Mut1)	13	GGAGUCC <u>U</u> ACUCC	Loop III (A->U) mutation in L1
L1.2 (Mut2)	13	GGAGUCC <u>C</u> ACUCC	Loop III (A->C) mutation in L1
L1.3 (Mut3)	13	GGAGUCC <u>G</u> ACUCC	Loop III (A->G) mutation in L1
L1.4 (Mut4)	13	GGAG <u>ACCA</u> <u>U</u> CUCC	Stem -1/+1 (U-A->A-U) mutation in L1
L1.5 (Mut5)	13	GGAG <u>CCCAG</u> CUCC	Stem -1/+1 (U-A->C-G) mutation in L1
L1.6 (Mut6)	13	GGAG <u>GCCA</u> <u>C</u> CUCC	Stem -1/+1 (U-A->G-C) mutation in L1

Mutations are marked in red.

The predicted secondary structures for *lin-29A* 5'UTR, parts of *mab-10* 3'UTR and the condensed *mab-10* 3'UTR are shown in dot-bracket notation. Several models are shown for each sequence and their minimum free energies are indicated. Sequence regions that fold into tri-loop SLs with a U-A base pair at stem position 1 are highlighted in green. Other tri-loop SLs are highlighted in yellow. The loop nucleotides are shown in red. Alternative secondary structures of these regions are highlighted in gray. The yellow SLs in part 2 and part 3 of the *mab-10* 3'UTR arise from overlapping sequences and hence will never form simultaneously in the context of whole *mab-10* 3'UTR.

Part 2 - nucleotides 151 – 350

Part 3 - nucleotides 301 – 500

[illegible]

C. elegans mab-10 3'UTR

Part 4 - nucleotides 451 – 650

[illegible]

***C. elegans mab-10* condensed 3'UTR (217 nucleotides)**

[illegible]

***C. elegans* lin-29A 5'UTR exon 1 (194 nucleotides)**

[illegible]

Supplementary Note 2: Multiple sequence alignment of NHL domains of various NHL domain-containing proteins.

Alignment positions with a conserved residue in 60% or more of the proteins analyzed are highlighted in cyan.

BratDrosophilamelanogaster	KMIYHCKF-GEFGVM----	EGQFTEPSGAVNA-QNDIIVADTNN-HRIQIF-DKEGRFKFQFGECKG-----	RDSQLLYPNRVAVVR-----	NSGDIIIVTERS
BratisoformX1Papiliomachao	KMIYHCKF-GEFGVM----	EGQFTEPSGAVNA-QNDIIVADTNN-HRIQIF-DKEGRFKFQFGECKG-----	RDGQLLYPNRVAVVR-----	TSGDIIIVTERS
BratApismellifera	KMIYHCKF-GEFGVM----	EGQFTEPSGAVNA-QNDIIVADTNN-HRIQIF-DKEGRFKFQFGECKG-----	RDGQLLYPNRVAVVR-----	TSGDIIIVTERS
BratMyzuspersicae	KMIYHCKF-GEFGAM----	EGQFTEPSGAVNA-QNDIIVADTNN-HRIQIF-DKEGRFKFQFGECKG-----	RDGQLLYPNRVAVVK-----	PSGDIIIVTERS
BratParasteatodatepidariorum	KMIYHCKF-GEFGVM----	EGQFTEPSGAVNA-QNDIIVADTNN-HRIQIF-DKEGRFKFQFGECKG-----	RDGQLLYPNRVAVVK-----	NSGDIIIVTERS
NCL1-likeParasteatodatepidariorum	KMIYHCKF-GEFGVM----	EGQFTEPSGAVNA-QNDIIVADTNN-HRIQIF-DKEGRFKFQFGECKG-----	RDGQLLYPNRVAVVK-----	TSGDIIIVTERS
NCL1Ascarissuum	KMIYHCKF-GEFGVM----	EGQFTEPSGAVNA-QNDIIVADTNN-HRIQIF-DKEGRFKFQFGECKG-----	RDGQLLYPNRVAVNR-----	VTGDFIVTERS
NCL1Brugiamalayi	KMIYHCKF-GEFGVM----	EGQFTEPSGAVNA-QNDIIVADTNN-HRIQIF-DKEGRFKFQFGECKG-----	RDGQLLYPNRVAVNR-----	LTGDFIVTERS
NCL1Caenorhabditiselegans	KMIYHCKF-GEFGVM----	EGQFTEPSGAVNG-QGDIVVADTNN-HRIQVF-DKEGRFKFQFGECKG-----	RDGQLLYPNRVAVNR-----	TTGDFVVTTERS
BratAscarissuum	DLILRWHI-GGIGVG----	PGQFNSPHGFCCLGC-DDEILVADTNN-HRIQIL-SKQGMVMQF6IAGT-----	DDGHLFYPKKVVALRPRASLPDGGYIVVDKG	
NHL2Caenorhabditiselegans	KVHSVFGT-SQQGST----	IRELHCPSGFCLSD-TDDILVADTNN-HRVVVC-GPPHP--WKIGRPGT-----	DDGQLCFPRKVIALLR-----	GEAVRVVVLDDKG
Brat-likeApismellifera	PMHIRCKF-GQLGPG----	KGQFSSPHGFCLSA-DEEIIIVADTNN-HRIQIF-EKTGIFKFQF6VPGK-----	EEGQLWYPRKVAVMR-----	NSGKFVVCDRG
NCL1-likeMyzuspersicae	SMDIVAKF-GQMGSG----	LGQFNSPHGFCCLSP-TEDIVVADTNN-HRIQVF-EKDGTYKTEFGREGK-----	EDGYLFYPRKVVFNL-----	HNQIVVCDRG
Brat-likePapiliomachao	PMHIRCKF-GQLGGG----	KGQFNSPHGFCCLGN-DEEIIIVADTNN-HRIEIV-DKMGALKFQF6VAGK-----	EEGQLWYPRKVAVVR-----	ATGKFVVCDRG
Brat-likeCapitellateleta	AMQIRCKF-GQLGPG----	KSQFNSPHGFCCLGM-DEEIIIVADTNN-HRIQVF-EKSGEFKYQF6IPGK-----	EEGQLWYPRKVAVMR-----	HCGKYVVCDRG
Brat-likeParasteatodatepidariorum	TMQIRCKF-GQLGPG----	KSQFNSPHGFCCLGM-DEEIIIVADTNN-HRIQVF-EKTDGFKYQF6VAGK-----	EEGQLWYPRKVAVIR-----	SSGKFVICDRG
Mei-P26Drosophilamelanogaster	PMQIRCKF-GSLGTA----	KGQFNSPHGFCCLGV-DEEIIIVADTNN-HRIEIV-DKMGALKFQF6VAGK-----	EEGQLWYPRKVAVMH-----	NNGKFVVCDRG
NHL1Ascarissuum	KSKPRLVF-GKKGSK----	EGDLNWPBGVTAIC-GTEFAVCDSSN-HRVCFI-NTQGRLLRVF6KYGT-----	GEGLDLSAAGICCN-----	RFRQLIVSDRY
NHL1isoformCBrugiamalayi	KGKPKLVF-GKKGSK----	EGELNWPBGVLAIG-GNEFAVCDSSN-HRVCFI-NTQGRLLRMF6KYGT-----	GDAQLDLSAAGICYS-----	RYKHLIVSDRY
NHL1Caenorhabditiselegans	RGRPRAVF-GRKGAK----	DGELNWPBGICALS-GGLVATCDSSN-HRVCFI-DKDGKFRVQF6GGYGA-----	GAGQLDLSAAGLASS-----	KLRVIVSDRY
NHL1Capitellateleta	KKNPVMKFGGGERGSA----	EGQFKLPBGVAISPQDGTIVADSSN-HRAQVF-DQHGOYVRTF6SYGD-----	SDGEFDCLAGVAISQ-----	SGDVIADRY
NHL1isoformX2Apismellifera	KRRQLFKF-GMRGSE----	PGCFTWPRGLAVGP-DNSIVVADSSN-HRVQVF-DCNNGFMKEF6SYGS-----	GEGEFDCLAGVAVNR-----	IGQYIADRY
NHL1-likeAplysiacalifornica	KGTAVVRF-GDRGSE----	PKSFTWPRGVAVSPMDDHIFVSDSSN-HRVQVF-DNSGKYLKSF6TYGQ-----	GNGEFDCLAGIAING-----	LGQIIIADRY
NHL1Parasteatodatepidariorum	KGKSCFKF-GSRGTE----	HGCFITWPRGVSVDGT-DNTIIVADSSN-HRVQVF-SASGKYQF6TYGS-----	ADGEFDCLAGVTVNR-----	IGQFIVSDRY
NHL1isoformX1Myzuspersicae	KRQLLFKI-GGRGSE----	PGYFTWPRGVAVGP-DNLIVVADSSN-HRIQVF-DNSGKIFKDF6SYGN-----	SEGEFDCLAGVAVNR-----	IGQYIADRY
NHL1isoformX1Papiliomachao	KRRLLQFSV-GSRGSE----	PGYFTWPRGIAVGP-DNTMVVADSSN-HRVQVF-DMNGIFZKEF6YGS-----	GEGEFDCLAGVAVNR-----	IGQYIADRY
AbbaDrosophilamelanogaster	KRQQLFQL-GGRGSE----	PGSFTWPRGLAVGP-DNSIVVADSSN-HRVQVF-DSNGIFVKEF6EYGN-----	GEGEFDCLAGVAVNR-----	IGQYIADRY
NHL1isoformX1Parasteatodatepidariorum	KRRMLMKI-GSRGSD----	SSNFTWPRGVAVGP-DNSIVVADSSN-HRIQVF-DSIGKFSFEF6TYGS-----	GDGEFDCLAGVAVNR-----	IGQFIVSDRY
WechCeratitis capitata	MLTPTISF-ATEGHD----	DGQVSRPWGLCVDK-FGNVVISDRRN-HRIQVF-SLEGMKLF6GRKGV-----	GNGEFDLPAGICVDM-----	DNRIVVDDKD
WechBombyxmori	PGVPMFSF-GREGQD----	EGQVSRPWGLCVDK-EGNIIIVADRRN-NRIQIF-NSRGEFKMMF6SGKT-----	GSGEFDLPAGITTTD-----	YGRIVVDDKD
WechisoformAclunio marinus	ALVPLTTF-CFDGHE----	DGEVSRPWGICVKN-NNEIIVADRRN-NRIQVF-FADGGFKF6GVKGT-----	GSQFDLPAGVATDQ-----	NNRIIVVDDKD
WechisoformX1Aedesaegypti	AVGPSTTF-GFDGHE----	DGQVSRPWGIAVDK-DGHVLVADRRN-NRVQVF-YPDGTFLKF6SGKT-----	ANGQFDLPAGICTDG-----	QNRIVVDDKD
WechMuscadomestica	SNALSLSF-ATEGHE----	DGQVSRPWGLCVDK-MGHVLVSDRRN-NRVQVF-NPDGSLKFKF6GRKGV-----	GNGEFDLPAGICVDI-----	DNRIVVDDKD
WechDrosophilamelanogaster	SNALSLSF-ATEGHE----	DGQVSRPWGLCVDK-MGHVLVSDRRN-NRVQVF-NPDGSLKFKF6GRKGV-----	GNGEFDLPAGICVDV-----	DNRIVVDDKD
TRIM71Daniorerio	VGLPMASF-GGEGDG----	DGQLCRPWGICVDK-EGYVVVADRSN-NRVQVF-KPCGTFFHKKF6TLGS-----	RPQFDRPAGVACDS-----	QRRIVVADKD
TRIM71isoformX1Apismellifera	SVTPLRIT-GNDGPN----	QDNLCRPWGICADR-EGHIIIVADRSN-NRIQIF-FQDGSLFRRF6THGT-----	APQFDRPAGVAVDA-----	RRRIVVADKD
TRIM71Cionaintestinalis	AGTPVLTTF-GKEGSK----	DGELCRPWGICDSD-QGHLIVADRSN-NRLQIF-NYDGFHHKF6TSGS-----	RPQFDRPAGVTNKN-----	QGQIVVADKD
TRIM71-likeParasteatodatepidariorum	TRIM71-likeParasteatodatepidariorum	TRIM71-likeParasteatodatepidariorum	TRIM71-likeParasteatodatepidariorum	TRIM71-likeParasteatodatepidariorum
TRIM71Capitellateleta	VGSVLSLF-GVEGSA----	DGELCRPWGICTHR-DGYIIVADRSN-NRIQIF-TQEGKFFHKKF6AAGS-----	RNGQFDRPAGVACNA-----	QGQIVVADKD
TRIM71isoformXenopus laevis	IGLPTLSF-GGEGDH----	DGKLCRPWGVCDVR-EGYIVVADRSN-NRVQVF-KPCGTFFHKKF6SLGS-----	RPQFDRPAGVACDS-----	SRRIVVADKD
TRIM71Homo sapiens	IGLPLGSF-GSEGDS----	DGKLCRPWGVSDK-EGYIIVADRSN-NRVQVF-KPCGAFFHKKF6TLGS-----	RPQFDRPAGVACDA-----	SRRIVVADKD
TRIM71Ornithorhynchusanatinus	VGLPLGSF-GSEGDN----	DGKLCRPWGVSDK-EGYIIVADRSN-NRVQVF-KPCGAFFHKKF6TLGS-----	RPQFDRPAGVACDA-----	SRRIVVADKD
Lin41Caenorhabditiselegans	AKGPILTF-GKEGSG----	DGELCRPWGICVDQ-RGRVIVADRSN-NRVQVF-DKDNFISKF6TSGN-----	RPQFDRPAGITTNS-----	LNNIVVADKD
Lin41Ascarissuum	RTGPVFSF-GSEGTA----	DGQVCRPWGICCDN-KGRILVADRSN-NRIQVF-DKDGKFLMKF6SPGV-----	RSQFDRPAGIAVNS-----	MNEIVVADKD
Lin41isoformCBrugiamalayi	RTGPPLFSF-GSEGSA----	DGQFCRPWGICCDN-KGRILVADRSN-NRIQIF-DKEGNFLHKKF6SPGT-----	RPQFDRPAGIAVNS-----	MNEIVVADKD
NHL3Daniorerio	EDELIVRV-ITRGRE----	KGEFTNLQGISASI-SGRVIVADSN-QCIQVF-TNDGQKARF6VRGR-----	SPGQLQRPTGVAVDT-----	NGDYIVADYD
TRIM2Parasteatodatepidariorum	EDDLILTKI-GHRGRG----	RGDFSNPQGVCCCTT-DGHIIIVADSN-QCQVQFSDTTGEFHLR6SRGR-----	APGEMQRPTGVTTLP-----	NGNYIVADYE
TRIM2Capitellateleta	EDDLVLSV-GMKGRA----	KGEFTNPQGVCCYK--DRVIVADSN-QCQVQF-TCGGDFLKR6FTRGR-----	QVQQLQRPTGVAVTL-----	NGNYIVADYD
TRIM2isoformX1Daniorerio	EDDLIFRI-GTKGRN----	KGEFTNLQGVAAST-VGKVLADSN-QCQVQF-SNDGQFKSRF6IRGR-----	SPGQLQRPTGVAVHP-----	SGDIIIADYD
TRIM2isoformX1Ornithorhynchusanatinus	EDDLIFRV-GTKGRN----	KGEFTNLQGVAAST-NGKILVADSN-QCQVQF-SNDGQFKSRF6IRGR-----	SPGQLQRPTGVAVHP-----	SGDIIIADYD
TRIM2Mus musculus	EDDLIFRV-GTKGRN----	KGEFTNLQGVAAST-SGKILVADSN-QCQVQF-SNDGQFKSRF6IRGR-----	SPGQLQRPTGVAVHP-----	SGDIIIADYD
TRIM2Homo sapiens	EDDLIFRV-GTKGRN----	KGEFTNLQGVAAST-NGKILVADSN-QCQVQF-SNDGQFKSRF6IRGR-----	SPGQLQRPTGVAVHP-----	SGDIIIADYD

TRIM2LhomeologXenopuslaevis
 TRIM3ShomeologXenopuslaevis
 TRIM3isoformX1Daniorerio
 TRIM3Musmusculus
 TRIM3HomoSapiens
 TRIM32HomoSapiens
 TP0421Treponemapallidum
 BB0236Borreliaburgdorferi
 NHL3Caenorhabditiselegans
 PGal-1Caenorhabditiselegans
 Pal2Drosophilamelanogaster
 Pal1Drosophilamelanogaster
 PamRattusnorvegicus
 AMDHomoSapiens
 Pamm-1Caenorhabditiselegans
 MT3624Mycobacteriumtuberculosis
 PKNDMycobacteriumtuberculosis
 NHLRC1HomoSapiens
 TRIM56HomoSapiens

EDDLIFRV-GTKGRN----KGEFTNLQGVAAST-NGKILADSN-NCVQIF-SNDGQFKSRFGIRGR-----SPGQLQRPTGVAVHP-----SGDIIIADYD
 EDEMILRV-CSRGRD----KGEFSNLQGIISTSC-NNRIVVADSN-NCIQVF-TNDGLFKLRFVGRGR-----SPGQLQRPTGVAVDM-----NGDIVVADYD
 EDELIFRV-GTRGRE----RGEFSNLQGIISTTS-SGRIVVADSN-NCIQVF-SNDGQFKLFGVGRGR-----SPGQLQRPTGVAVDM-----NGDIVVADYD
 EDELVFRV-CSRGRE----KGEFTNLQGVSAAS-SGRIVVADSN-NCIQVF-SNEGQFKFRFGVGRGR-----SPGQLQRPTGVAVDT-----NGDIVVADYD
 EDELVFRV-CSRGRE----KGEFTNLQGVSAAS-SGRIVVADSN-NCIQVF-SNEGQFKFRFGVGRGR-----SPGQLQRPTGVAVDT-----NGDIVVADYD
 QCLFLKKM-GAKGST----PGMFNLVPSLYVTS-QGEVLVADRGN-YRIQVF-TRKGFLKEIRRSPSGIDSVF-----LSFLGADLPNLTPLSVAMNC-----QGLIGVTDYSY
 HFSESESF-HAVRRG----TVLFRRLSLCALA-DGTFWMSAYGS-NELLRF-DVNGRVRZARTRGPV-----EGFDRPFDVQTR-----SGDLLVSEFA
 ELNFKKLV-KVASLDNSIYKRPBGVQITSLRADK-YGGYYAANFVG-NEILYF-DVNNVNVALVKDGF-----SYLKSPLYDVIEA-----NNLLYVTLYS
 AFRIDSFH-AYDWMQ----PVTFKYPTKCMWDEPTKRMFVLDSDGN-KRVRVL-RDNGDVITDVRN-----DEFKSGTVGMVYLG-----NEELVVLWSQ
 VFEQDREL-IGLFNP----SKEIGQVSGLAVNK-NGHIVAFHRSG-RVWDEK-SFNDHETFNKDLGVNNKTAIIS-REKKVIDEFGAGLFYMPHGLTIDN-----NGDYVVTDVG
 SVPTPVLV-ENWPE-----QHSFGQVTAIVADP-QGSPVVFHRAE-RYWDVN-TFNESNIYYLIEYGPIKENTIIYVLDAKTGAIKSGWGSNMFMYPHGLTIDL-----HGNVYITDVA
 LNNYVYVQ-NAWPAN-----NVKLGAVTAVSFDK-AGNVVIFHRVN-RVWQOT-TFDNRNQYQEKYRGPPIRESTILALEPATGKVQYDWGKNFFYMPHGLTVDP-----EDNVVLTDVA
 GDFHVEEE-LDWPVG----YLLPGQVSGVALDS-KNNLVIFHRGD-HVWDGN-SFDSKFVYQQRGLPIEEDTILVIDPNNAEILQSSGKNLFYLPHGLSIDT-----DGNVYVTDVA
 GDFHMEEA-LDWPVG----YLLPGQVSGVALDP-KNNLVIFHRGD-HVWDGN-SFDSKFVYQQRGLPIEEDTILVIDPNNAEILQSSGKNLFYLPHGLSIDK-----DGNVYVTDVA
 PFGIVQEA-IHENLG----GVKLQVAGLAFNN-EQQLLVFQRAQ-RVWDAS-TFDNYNTLLKKLPADPVILVISYSGNQTLLERLGGGQFYLPHGIVYDK-----DGFVYTTDVG
 TSGQAASP-TTSPSPSQVVPVIDLWNPBGVTVDL-ADAVYVADSGH-KRLKLK-PAGSNTPTTLPF-----TDIGPGGAVNS-----NRDYYVIDED
 SGQTVLPF-TG-----IDFLRSPSGVAVDS-AGNVYVTSEGMVGRVVKL-ATGSTGTTLVFP-----NGLYQPGQLAVDG-----AGTVYVTDNF
 SAPGALT-HHTFGG----WGTLVNPSTGLALCPKTRGVVVHDDR-RVKLIF-DSGGGCAHQFGEKD-----AAQDIRYPVDVITITN-----DCHVVLTDAAG
 RPIFYCSF-PTRMPPG----DKRSPRITGLCPFG-PREILVADEON-RALKRF-SLNGDYKGTVPVP-----EGCSPCSVAAL-----QSAVAFSA

BratDrosophilamelanogaster
 BratisoformX1Papiiomachao
 BratApismellifera
 BratMyzuspersicae
 BratParasteatodatepidariorum
 NCL1-likeParasteatodatepidariorum
 NCL1Ascarissuum
 NCL1Brugiamalayi
 NCL1Caenorhabditiselegans
 BratAscarissuum
 NHL2Caenorhabditiselegans
 Brat-likeApismellifera
 NCL1-likeMyzuspersicae
 Brat-likePapiiomachao
 Brat-likeCapitellateleta
 Brat-likeParasteatodatepidariorum
 Mei-P26Drosophilamelanogaster
 NHL1Ascarissuum
 NHL1isoformCBrugiamalayi
 NHL1Caenorhabditiselegans
 NHL1Capitellateleta
 NHL1isoformX2Apismellifera
 NHL1-likeAplysiacalifornica
 NHL1Parasteatodatepidariorum
 NHL1isoformX1Myzuspersicae
 NHL1isoformX1Papiiomachao
 AbbaDrosophilamelanogaster
 NHL1isoformX1Parasteatodatepidariorum
 WechCeratitis capitata
 WechBombyxmori
 WechisoformACLuniomarinus
 WechisoformX1Aedesaegypti
 WechMuscadomestica
 WechDrosophilamelanogaster
 TRIM71Daniorerio
 TRIM71isoformApismellifera
 TRIM71Cionaintestinalis
 TRIM71-likeParasteatodatepidariorum
 TRIM71Capitellateleta
 TRIM71isoformXenopuslaevis
 TRIM71HomoSapiens

P--THQIQIYN-QYQG-FVRKFGAT-----ILQHPRGVTVDNK--GRIIVVECK-VMRVII--FDQNG---NVLHKFGCSK-----HLE-----
 P--THQIQIYN-QYQG-FVRKFGAN-----ILQHPRGVTVDNK--GRIVVVECK-VMRVII--FDQVG---NVLQKFGCSK-----HLE-----
 P--THQIQIYN-QYQG-FVRKFGAN-----ILQHPRGVTVDNK--GRIVVVECK-VMRVII--FDQAG---IVLQKFGCSK-----HLE-----
 P--THQIQIYN-QYQG-FVRKFGAN-----ILQHPRGITVDNK--GRIVVVECK-VMRVII--FDQAG---NVLVKFGCSK-----HLE-----
 P--THQIQIYN-QYQG-FVRKFGAN-----ILQHPRGVTVDNK--GLIIVAECK-VMRVII--FDQEG---NVMHKFGCSK-----HLE-----
 P--THQIQIYN-QYQG-FVRKFGAN-----ILQHPRGVTVDNK--GRIVVVECK-VMRVII--FDQLG---NVLQKFGCSK-----HLE-----
 P--THQIQIYN-QYQG-FLRKFGAN-----ILQHPRGVVDNK--GRIIVIECK-VMRVII--FDMFG---NILQKFGCSR-----YLE-----
 P--THQIQIYN-QYQG-FLRKFGAN-----ILQHPRGVVDNK--GRIIVIECK-VMRVII--FDMFG---NILQKFGCSR-----YLE-----
 P--THQIQIYN-QYQG-FLRKFGAN-----ILQHPRGVVDNK--GRIIVIECK-VMRVII--FDMFG---NILQKFGCSR-----YLE-----
 P--THQIQIYN-QYQG-FLRKFGAN-----ILQHPRGVVDNK--GRIIVIECK-VMRVII--FDMFG---NILQKFGCSR-----YLE-----
 D-NKARLQLFS-KVGE-FIKKIVA-----SYIEYVSALTVDNA--GHVVVFNST-SAMFVL--DVDQGPAAKILKWADCGK-----MLC-----
 GDGKTRAQIE-ARGE-FVKRLNMA-----LVPRGGIEVSAAATPN--GQLLLVDTA-GFVYSI--DVDAP---RVTFWFDAST-----QLG-----
 N-ERSRMQIFT-KSGH-FIKKIAI-----RYIDIVAGLAVTSE--GHILAVDSV-SPTVVF--ISDTG---DLLRWFDCE-----YMR-----
 S-DRSRVQIFEYPTGK-FIKKIQV-----QFIEIVAGVAVTAN--GHILAVDSV-HPTVFLVNVNEDN--GIMKWFDCA-----YME-----
 N-ERSRMQIFT-KNGH-FLKKIAV-----RFIDIVAGLAVTAE--GLIIVAECK-VMRVII--LSEEG---DLMSWFDCE-----CMR-----
 N-ERSRMQIFT-KNGH-FIKKIAI-----RYIDIVAGLAVTAE--GHILAVDSV-SPTVVF--IGETG---ELVWFDCE-----YMR-----
 S-ERSRMQIFT-KTGH-FLKKIAI-----RYIDIVAGLAVTAE--GHILAVDSV-SPTVVF--ISETG---DLLHWFDCE-----YMR-----
 N-ERSRMQIFS-KCGH-FMKKIAI-----RYIDIVAGLAVTAE--GHILAVDSV-SPTVVF--ISEEG---ELVWFDCE-----YMR-----
 N--HRIVIFD-QLGQ-FIKAFGGHG-----PSSGRFNNPWGVCVDET--GIYVADKD-NHRVQV--FDSNG---QFVSKFGSMGP-----GPGQLH-----
 N--HRIMIFD-QDGH-CVRKFGGHG-----PSNGRFNNPWGVAVDNM--GMIYVADKD-NHRVQV--FDSKG---QFAGKFGTNGP-----GISQFH-----
 N--HRISVFG-LEGD-HLFSFGHG-----QGNKFNPNPWGVAVDNL--GSIYVADKD-NHRVQV--FDKNG---QFIKFGSGFGH-----LPGQLN-----
 N--HRIQIFD-SNFN-FKLKFGSEG-----SSDGKFKYVPGVTVDEH--GLVYVCDKE-NHRVQV--FGADG---TFLRRFGSTGN-----QPGKLE-----
 N--HRIQVLD-PSGR-FLRAFSGQG-----TADGRFNYPWGITTAL--GFIYVCDKE-NHRVQV--FQSDG---TFVGKFGSGCS-----GRGQLE-----
 N--HRVQVLD-RNGR-FQCSFGSEG-----SSEGQLNYPWGVACDNM--GFIYVCDKE-NHRVQV--FQSDG---AFVRTFGHYGN-----RSQFEE-----
 N--HRLQVFD-PNGR-FIRAFGHEG-----RSDGKFNYPWGVATDNL--GFIYVCDKE-NHRVQV--FQGDG---TYVTKFGGIGQ-----RPGELE-----
 N--HRIQVLD-PSGR-FLRSFGSGQG-----SSDGRFNYPWGITTAL--GFIYVCDKE-NHRVQV--FQSDG---TFVGKFGSNGN-----KIGQLE-----
 N--HRIQVFD-PAGR-FLRSFGSGQG-----TGDGKFNYPWGITTAL--GFIYVCDKE-NHRVQV--FQSDG---TFVGKFGSGFS-----KLQGLE-----
 N--HRIQVLD-PQGR-FLRAFSGQG-----TADGKFNYPWGITTAL--GFIYVCDKE-NHRVQV--FQSDG---SFVGKFGSGCR-----GEGGLE-----
 N--YRVQLFD-PTGR-FLRAFSGQG-----RTDGRFNYPWGITTAL--GFIYVCDKE-NHRVQV--FQSDG---TFVGKFGSLGS-----RPGQLE-----
 N--HRVQIFT-ANGL-FLLKFGSYG-----KEYGQFYPPWDVAVNSR--RQIVVDSR-NHRVQV--FDSEG---RFIRQVIFDNH-----GLNKGTIA-----
 N--HRVQIFT-SSGN-FILKFGSGF-----KEGQFYPPWDVAVNSR--GNIIVTDSR-NHRVQV--FTSDG---TYITKFVFEGANP-----AKMLKGT-----
 N--HRVQVFS-ASGA-FILKFGSYG-----KELNQFMYPWACAVNSK--SQILVDSR-NHRVQV--FSPDG---NFISRFSGDGVNH-----SRYLKGLT-----
 N--HRVQVFS-TNGL-FLLKFGSYG-----KDCGQFYPPWDVAVNSK--GEILVDSR-NHRVQV--FNSEG---QFISRFSGDGVNH-----SRYLKGLT-----
 N--HRVQIFT-STGA-FLLKFGSYG-----KEYGQFYPPWDVAVNSR--RQIVVDSR-NHRVQV--FDSEG---RFIRQVIFDNH-----SNKGTIA-----
 N--HRVQIFT-ASGV-FLLKFGSYG-----KEYGQFYPPWDVAVNSR--RQIVVDSR-NHRVQV--FDSEG---RFIRQVIFDNH-----QTKGTIA-----
 N--HRIQIFT-FDQV-FLLKFGSEG-----TKNGQFNYPWDVAVNSE--GKILVSDTR-NHRVQV--FGPDG---TFLNKYGFEGA-----LWKHFD-----
 N--HRIQVLT-MEGL-FLLCFGEKG-----CRAGQFNYPWDVAVNSE--CQIVVSDTR-NHRVQV--FSPDG---VFLRKYGESSP-----NMWKHFD-----
 N--HRIQIFC-FDGT-FVGMFGERG-----SKSGQFNYPWDVAVNSV--GMIIVTDSR-NHRVQV--FSPDG---TFLNKYGFEGA-----LWKHFD-----
 N--HRIQIFD-GDGN-FILKFGERG-----SKNGQFNYPWDVAVNSV--GHILVSDTR-NHRVQV--FGSDG---SFINKYGFDDG-----LWKHFD-----
 N--HRIQIFA-FDGT-FLLKFGSEG-----SKNGQFNYPWDVAVNSE--GRVLSVDSR-NHRVQV--FSSDG---QFINKYGFEGS-----LWKHFD-----
 N--HRVQIFT-FEQV-FLLKFGSEG-----TKNGQFNYPWDVAVNSE--GKILVSDTR-NHRVQV--FGPDG---TFLNKYGFEGA-----LWKHFD-----
 N--HRIQIFT-FEQV-FLLKFGSEG-----TKNGQFNYPWDVAVNSE--GKILVSDTR-NHRVQV--FGPDG---VFLNKYGFEGA-----LWKHFD-----

BratDrosophilamelanogaster
BratISOformX1Papiliomachaon
BratApismellifera
BratMyzuspersicae
BratParasteatodatepidariorum
NCL1-likeParasteatodatepidariorum
NCL1Ascarissuum
NCL1Brugiamalayi
NCL1Caenorhabditiselegans
BratAscarissuum
NHL2Caenorhabditiselegans
Brat-likeApismellifera
NCL1-likeMyzuspersicae
Brat-likePapiliomachaon
Brat-likeCapitellatelela
Brat-likeParasteatodatepidariorum
Mei-P26Drosophilamelanogaster
NHL1Ascarissuum
NHL1ISOformcBrugiamalayi
NHL1Caenorhabditiselegans
NHL1Capitellatelela
NHL1ISOformX2Apismellifera
NHL1-likeAplysialcalifornica
NHL1Parasteatodatepidariorum
NHL1ISOformX1Myzuspersicae
NHL1ISOformX1Papiliomachaon
AbbaDrosophilamelanogaster
NHL1ISOformX1Parasteatodatepidariorum
WechCeratitis capitata
WechBombuxmori

--FPMGVVNDK-QEIFISDNR-----AHCVKVFNYEQ-YLRQIGGE-----GITNYPIGVGINSNGEILADNHNN--FNLTIFTQDG-QLVSALESK-----
--FPMGVVNDK-QEIFISDNR-----AHCVKVFNYEGI-YLRQIGGE-----GVTNYPIGVGINASGEILADNHNN--FNLTIFTQEG-QLVSALESK-----
--FPMGVVNDK-QEIFISDNR-----AHCVKVFNYEGA-YLRQIGGE-----GITNYPIGVGINAVEGILADNHNN--FNLTIFTQDG-QLVSALESK-----
--FPMGVVNDK-QEIFISDNR-----AHCVKVFNYEQ-YLRQIGSQ-----GITNYPIGVGINASGEILADNHNN--FNLTIFTQEG-QLVSALESK-----
--FPMGVVNDK-QEIFISDNR-----AHCVKVFDEYGH-FLRQIGGE-----GLTNYPIGVCINTHEGILVADNHNN--FNITVFTQDG-QLVSALESK-----
--FPMGVVNDK-QEIFISDNR-----AHCVKVFNYDGV-FLRQIGGE-----GLTNYPIGVCINQGEILVADNHNN--FNITIFTQDG-QLVSALESK-----
--FPMGVCTNDK-QEILISDNR-----AHCIKVFNYDQG-FARQIGGE-----GITNYPIGVGINSAGEVVDADNHNN--FNLTVFSQDG-TMLSALESK-----
--FPMGVCTNHK-QEILISDNR-----AHCIKVFNYDQG-FVRQIGGE-----GITNYPIGVGINYAGDVVDADNHNN--FNLTVFSQDG-TMLSALESK-----
--FPMGVCTNDK-NEILISDNR-----AHCIKVFSYEQ-YLRQIGGE-----GVTNYPIGVGINSLEGEVVDADNHNN--FNLTVFSQDG-TMLGALESK-----
--EASDVSVFE-GLYYVTDYK-----QHCVVVLITDGD-LVRRFGAF-----EHTPYPIGVDSKTDGVLVADSHGNH--FHILVCSKTG-QRLQDFECT-----
--EASDVAMFD-NLIYITDFK-----HHCVVYVTSSEK-FIRKMGEF-----SQTPYPIGIDSVKAGEVLVADTHGNH--LHVVFSDQG-QHIHSFTHN-----
--EPSDIAISG-KEYFVCDFK-----GHCVVVFNEEGK-FLRRIGGD-----NVTNFPNGIDISDAGDVLIGDSHGHR--FHAVVFSRQG-SLISEFECF-----
--EPSDIIVRD-DDYVYVDFK-----GHSIVVFNDGEV-CLRRIGGE-----YITSFPNGIDISENGEILVGDSHGHR--FHAVVFSHDG-THLTDLCEP-----
--EPSDIAISG-KEYFVCDFK-----GHCVVVFDEEGR-FLRRIGCE-----NVTNFPNGIDVSDAGDVLIGDSHGHR--FHAVVFSRQG-VLVTEFECF-----
--EPSDIAISG-KEYFVCDFK-----GHCVVVFNEEDQ-FMRIGICE-----NITNYPNGIDISDAGDVLIGDSHGHR--FHAVVFSRQG-SLISEFECF-----
--EPSDIAVSD-KEYFYCDFK-----GHCVIVFSEEGK-FLRKIGSE-----NVTNFPNGIDISDSDGVLVGDSHGHR--FHIVVFSRQGDTLSEFECF-----
--EPSDIAIRD-NDFYVDFK-----GHCVAVFQDDGT-FLRYIGNE-----KYVTCFNGIDISNAGDVLIGDSHGHR--FHVACYSRQG-ALQSEFECF-----
--NPQFIAYHKQTHLYVTDSS-----NHRVCVFDHNGN-PVFQFQGEF-----HNGQLKFPGRGIAVDDQGFIVADSGN--NRVQIFYPDG-RFMHSFGTWGN-----
--HPQFIAVNKRTHNIYVTDSS-----NHRVCIFDHNNGN-PIFQFQSEGF-----QNGQMKFPRGIAVDDQGFIVADSGN--NRVQIFYPDG-RYMHSFGTWGN-----
--SPLFIASVRVTHHVVYDSS-----NHRISVFDPHGV-HLFSFGEFG-----HGQGFKFPGRGIAIDSQENLIADSGN--NRVQVFDAGQ-QFVSSFGTWGN-----
--NPYYITVGHD-RNIYVSDTH-----NNRIQVFTSGG-VNVSFGPGD-----QDGKFKHPGKITVDHNGFMVVDADSGN--HRIQVLRSDG-TFLVAKFGTKGR-----
--HPHYIAVSNT-NRVIVSDGN-----NHRIQIFDVNGR-VLTSFGSEGS-----DEGQFKFPRGVAVDDQGYIVVADSGN--NRIQIFSPDG-AFLKSF6GWS-----
--NPHYIAVSPD-NKVVYDSS-----NHRIQVFSIYGR-LDFSFGTGT-----LRGQMKFPRGLAIDHQGFVVDADSGN--NRIQIFRHDG-RFYTFMG6GWS-----
--HPHYIAVSTT-NRVIVSDSN-----NHRIQIYDVNGR-LSTFTGTEGS-----EEGQFKYPRGVAVDDQGYIVVADSGN--NRIQIFPDG-TFLKAFGTWS-----
--HPHYIAVSNT-NRVIVSDCN-----NHRIQIFDVNGR-VISSFGTEGS-----ENGQFKFPGKVAVDDQGYIVVADSGN--NRIQIFHSDG-TFLRAF6GWS-----
--HPHYIAVSTT-NRVIVSDSN-----NHRIQVFDVNGR-VLSSFGEES-----EDGQFKFPRGVAVDDQGYIVVADSGN--NRIQIFPDG-TFLRAF6GWS-----
--HPHYIAVSNT-NRVIVSDSN-----NHRIQIFDVNGK-VLSTVFGEGS-----DDGQFKFPRGVAVDDQGYIVVADSGN--NRIQIFPDG-SFLKTF6GWS-----
--HPHYIAVTNT-NRVVTDTN-----NHRVQIFDVNGR-LSTFTGSEGS-----DEGHFKFPGKIAVDDQGYIVVADSGN--NRIQIFPDG-TFLRCF6GTG-----
--SPRGVCYTPA-GNIIVSDFD-----NHCLLVLDDPDVNVLSAKHGEGS-----GAQEENRPSGTCDDDGRITVADSKN--QRVIVHSPD-DYLSWIDIRPSN-----
--TPRGVCYTPA-GNIIVSDFE-----NHRLLVMDPTLTKVLHCVGREGS-----GIGELNRPSTGTVDDGRIVVADSKN--HRIVLTSSEL-RLVAVDLKSP-----

WechisoformAClunioamarinus --TPRGAAFNQ-PGNIISDFE-----NHRLILIDASMSKILATKGHEGS-----ALHEFCRPSGICCCDDGRIVVADSKN----QRLVIFSPML-EFLWTVEIRPSAR
WechisoformX1Aedesaegypti --TPRGACFTPQ-GDVIISDFE-----NHRLLLIDATLTKVLAAGHEGT-----AVHEFSRPSGICCCDDGRIVVADSKN----QRLVIFSPQL-EFLWAVEIRPSSN
WechMuscadomestica --SPRGVCYTPP-GNIIIVSDFD-----NHCLYLIDPDNDILSAKGHEGS-----GFQEFNRPSSGICCCDDGRIVVADSKN----QRIVYVSPTL-DYLDWIEIRPSLN
WechDrosophilamelanogaster --SPRGVCYTPP-GNIIIVSDFD-----NHCLYLIDPDNDILSVKGHEGS-----GFHEFNRPSSGLCCDDEGRIVVADSKN----QRIIVFNQNL-DFMWDIEVVRPSIN
TRIM71Daniorerio --SPRGVAFNQE-GHLVVTDFN-----NHRLLVIRPDCQ-SARFLGSEGT-----GNGQFLRPQGVAVDQEDRIIVADSRN----HRIQVFEPNG-NFLCKFGTHGN--
TRIM71isoformApismellifera --SPRGVAFNPD-GNIVTTDFN-----NHRLVIIDSDVF-HARVLECESP-----GAPKQFLRPQGLVIDDEGNIIIVADSRN----HRIQIFDSTG-TLQWRFGNYGK--
TRIM71Cionaintestinalis --SPRGVAFSHD-RRIIVTDFN-----NHRLVIIIEPDLQ-SARYLGSEGN-----QALQFLRPQGVAVDEEGNIIVVADSRN----HRIQVFTPTG-GLIAVFGGASTT--
TRIM71-likeParasteatodatepidariorum --SPRGVSFTSD-GHMMVVTDFN-----NHRLIVVHPNFQ-SARFLGQEGS-----NNGHFLRPQGVAVDPEGHIIVADSRN----HRIQIFHPNG-HFLCKFGTYGV--
TRIM71Capitellateleta --SPRGVCFNNE-GHMMVVTDFN-----NHRLLVIIHPDQ-SARFLGSEGS-----ANGQFLRPQGVAVDQEGNIIVADSRN----HRIQVFPNG-NFLCKFGTPGS--
TRIM71isoformXenopuslaevis --SPRGVAFSQD-GYLVVTDFN-----NHRLLIKIPDCQ-SAFFLGTGEGT-----GNGQFLRPQGVAVDQEGRIIVADSRN----HRVQIFEPNG-SFLCKFGTQGS--
TRIM71Homo sapiens --SPRGVAFNHE-GHLVVTDFN-----NHRLLVIIHPDQ-SARFLGSEGT-----GNGQFLRPQGVAVDQEGRIIVADSRN----HRVQMFESNG-SFLCKFGAQGS--
TRIM7110rnithorhynchusanatinus --SPRGVTFNHE-GHLVVTDFN-----NHRLLVIIHPDQ-SARFLGSEGT-----GNGQFLRPQGVAVDQEGRIIVADSRN----HRVQIFESNG-SFLCKFGTQGG--
Lin41Caenorhabditiselegans --SPRGCLCYLPD-GQLLITDFN-----NHRLAVLSPRNMSEMKVYVSGEGD-----GDGMFVRPQGVVIDPEGHILVCDSRN----NRVQVFASDD-MRFIGSFG---LG
Lin41Ascarissuum --SPRGVCFLPD-GLLVITDFN-----NHRLAVVSSRGPTMKCFGSEGE-----GDGCFCRPQGVTTDSEGHILVCDSRN----NRVQVLSAED-MHCVATFGGSPVS
Lin41isoformBrugiamalayi --SPRGVCFLPD-GQLLITDFN-----NHRLVMMSSRGTVDMKMYGSEGED-----SEGSCFRPQGVITTDNEGHILVCDSRN----NRIQVLNLDG-MQCVASFGGAGLG
NHL3Daniorerio --GPHFVAVNNK-NEIIVTDFH-----NHSVKVYSADGE-FLFKFGSHGE-----GNGQFNAPTGVAVDVNGNIIVADWGN----SRIQVFDAG-SFLSYINTS----
TRIM2Parasteatodatepidariorum --GPHYAAVNSK-NQIVVSDFH-----GHCIKIFDAEGS-FITSFSGNGE-----GNGQFNAPTGVITDDQNIIVADWGN----CRIQVFDING-SFLSFINTF----
TRIM2Capitellateleta --GPHFCAINSR-NDIIVSDFH-----NHCVKVYDCEGT-FITSFSGNGE-----GNGQFNAPTGVAVDKNDNIIVADWGN----SRIQVFDSSG-SFLSYINTA----
TRIM2isoformX1Daniorerio --GPHFAAVNQ-NEIIVTDFH-----NHSVKVFSPEGE-FILKFGSNGE-----GNGQFNAPTGVAVDANGNIIVADWGN----SRIQVFDSSG-SFLSYINTS----
TRIM2isoformX10rnithorhynchusanatinus --LDGPHFAAVNS-NEIIVTDFH-----NHSVKVFNQEGE-FMLKFGSNGE-----GNGQFNAPTGVAVDSNGNIIVADWGN----SRIQVFDSSG-SFLSYINTS----
TRIM2Musmusculus --GPHFAAVNS-NEIIVTDFH-----NHSVKVFNQEGE-FMLKFGSNGE-----GNGQFNAPTGVAVDSNGNIIVADWGN----SRIQVFDSSG-SFLSYINTS----
TRIM2Homo sapiens --GPHFAAVNS-NEIIVTDFH-----NHSVKVFNQEGE-FMLKFGSNGE-----GNGQFNAPTGVAVDSNGNIIVADWGN----SRIQVFDSSG-SFLSYINTS----
TRIM2LhomeologXenopuslaevis --GPHFAAVNS-NEIIVTDFH-----NHSVKVFNQEGE-FMLKFGSNGE-----GNGQFNAPTGVAVDSNGNIIVADWGN----SRIQVFDSSG-SFLSYINTS----
TRIM3ShomeologXenopuslaevis --LDGPHFVAVNNK-NEIIVTDFH-----NHSVKVYSADGE-FLFKFGSHGE-----GNGQFNAPTGVAVDSNGNIIVADWGN----SRIQVFDSSG-SFLSYINTM----
TRIM3isoformX1Daniorerio --AFSPHFVAINNK-NEIIVTDFH-----NHSVKVYNADGE-FLFKFGSHGE-----GNGQFNAPTGVAVDGNNGNIIVADWGN----SRIQVFDSSG-SFLSYINTT----
TRIM3Musmusculus --GPHFVAVNNK-NEIIVTDFH-----NHSVKVYSADGE-FLFKFGSHGE-----GNGQFNAPTGVAVDSNGNIIVADWGN----SRIQVFDSSG-SFLSYINTS----
TRIM3Homo sapiens --GPHFVAVNNK-NEIIVTDFH-----NHSVKVYSADGE-FLFKFGSHGE-----GNGQFNAPTGVAVDSNGNIIVADWGN----SRIQVFDSSG-SFLSYINTS----
TRIM32Homo sapiens --RPKFVTCDAE-GTVYFTQGLGLNLENRQNEHLEGFSIKGSGVDPDQ-LGRQISHFFS-----ENEDFRCLAGMCVDARGDLIVADSSR----KEILHFPKGG-GYSVLIREG---
TP0421Treponemapallidum --APGGIAILD-ELVYVADAL-----KGAIVVFDTAGN-VYRTLVAEGT-----LKHVESVRAW-NGRLLVSLPN-----EVMVVDVGL-ASLHTIARL---
BB0236Borreliaburgdorferi --GPTGTGYTLN-ENIYVADSL-----RNTIEVFDTSN-HLYSVFTS-----IEGIEGLSSDFVGNVIVSSKD-----GVYKISIAK-HITITILKA---
NHL3Caenorhabditiselegans --EVKCVGVGLD-DDVIIVGTT-----DELLLYDGAGK-MLRKLNVSPPGTVMKVGGRFNITVTCDVTTGQIVVIFTDKKMDRTNIGIVISYKG-DFLYSIEPGP---
PGal-1Caenorhabditiselegans --VPHSLSLIEDMNVICVADRE-----NQRVQCFSAGLS-EGDRTLPTGI-----PITSATDIGRVFAIREREHYLIGVTGN-SEDEAQMFSIDM-QTGKTETF-----
Pal2Drosophilamelanogaster --VPHAITLLEHLDDLCCIADRE-----NMVVCPKAGLI-SSHGEPEAA-----TIQEPDLGRVFGVASFGDIIVFVNGP-TSMLPVRGFTIDP-RSETIIGH-----
Pal1Drosophilamelanogaster --IPHALTLVPELQLLCAADRE-----NGRVQCFLSSNG-TFHSQYHNL-----IGDRLFSMAYTPAAGGQLVIVNGP-PTAELGIHPEHY-NEVHGFLVLSMRSK
PamRattusnorvegicus --VPHSLALVPHLDQLCVADRE-----NGRIQCFTDITK-EFVREIKHASF-----GRNVFAISYIPGFLFAVNGKPYFGDQEP---VQGFVMNFSS-GEIIDVFKPV---
AMDHomo sapiens --VPHSLALVPLLGLQCVADRE-----NGRIQCFTDITK-EFVREIKHASF-----GRNVFAISYIPGFLFAVNGKPYFGDQEP---VQGFVMNFSS-GEIIDVFKPV---
Pamm-1Caenorhabditiselegans --LPHDIYSDSA-GRLLVTDRE-----NGRVQHMTTQGH-VIEEFKSTMF-----TNIYSAASHEDYVFMVPGRPIMGHETE-GIAVFGVRSRGTG-LIEYAFGPTTKGK
MT3624Mycobacteriumtuberculosis --HPYDVAVDGA-GTVYVTDSE-----HNRVVALTAGSA-TPVHLPSA-----DLSFPAAGVTVDKDDSVYVADLNN---NRVLKLAGS-NAQSQLPFTG---
PKNDMycobacteriumtuberculosis --DPDGVAVDNS-GNVYVTDTD-----NNRVVKLEASN-NQVLLPFT-----DITAPWGIAVDEAGTVYVTEHNT---NQVVKLAGS-TTSTVLPFTG---
NHLRC1Homo sapiens --NPRGVAVSWLTGAIAVLEHPLALG-----TGVCSTRVKVFSSSMQ-LVGQVDTFGL-----SLYFSPKITASAVTFDHQGNVIVADTSG---PAILCLGKPE-EFPVPKPMV---
TRIM56Homo sapiens --ALVFLTTSPQ-GHVFVGSWDQ-----QNSVVICDGLGQ-VVGEYKGPGL-----HGCQPGSVSVDKKGYIFLTLREV---NKVVILDPKG-SLLGDFLTA---

BratDrosophilamelanogaster -----VKHAQCFDVALMDDG-SVVLASKDY-----RLYIYRYV-----
BratisoformX1Papiliomachaon -----VKHAQCFDVALMDDG-SVVLASKDY-----RLYIYRYV-----
BratApismellifera -----VKHAQCFDVALMDDG-SVVLASKDY-----RLYIYRYV-----
BratMyzuspersicae -----VKHAQCFDVALMDDG-SVVLASKDY-----RLYIYRYI-----
BratParasteatodatepidariorum -----VKHAQCFDVALMDDG-SVVLASKDY-----RLYIYRYM-----
NCL1-likeParasteatodatepidariorum -----VKHAQCFDVALMDDG-SVVLASKDY-----RLYIYRYM-----
NCL1Ascarissuum -----VKHAQCFDVALVEDG-SVVLASKDY-----RLYLYRYAP-----
NCL1Brugiamalayi -----VKHAQCFDVALVEDG-SVVLASKDY-----RLYLYRY-----
NCL1Caenorhabditiselegans -----VKHAQCFDVALVDDG-SVVLASKDY-----RLYLYRFLP-----
BratAscarissuum -----QLKVSRCVGLRITSEG-NIVSISKNNH---NVLMFNTLY-----
NHL2Caenorhabditiselegans -----EFRLSRCVGLRIAKSG-HIVTLCKNNH---TLFVFKPLI-----
Brat-likeApismellifera -----YKVSRCCLKITSEG-YIVTLAKNNH---HVLVLNTLY-----
NCL1-likeMyzuspersicae -----YKVSRCCLKITSEG-HIVTLAKNNH---HVLVLNTATV-----
Brat-likePapiliomachaon -----YKVSRCCLKITSEG-YIVTLAKNNH---HVLVLNTLY-----
Brat-likeCapitellateleta -----YKVSRCCLKITSEG-HVVTAKNNH---HVLVLNTLY-----
Brat-likeParasteatodatepidariorum -----YKVSRCCLKITSEG-YVVTAKNNH---HVLVLNTLY-----
Mei-P26Drosophilamelanogaster -----YKVSRCCLKITSEG-YVVTAKNNH---HVLVLNTLY-----
NHL1Ascarissuum -----GPGQLKLEDITL-CDK-TIVVSDRENH---RIQLF-----
NHL1isoformBrugiamalayi -----APGQLKGEVAVL-IDT-TIVVTDRENH---RIQLF-----

NHL1Caenorhabditiselegans	-----GAGQLKGVEDVCTADG-SIVVTDRENH----	RIQIF-----
NHL1Capitellateleta	-----GEGQLRDPEGIAITPDG-KILVADKDNV----	RILMF-----
NHL1isoformX2Apismellifera	-----GDGEFKGLEGVAVTSTG-NIVVCDRENH----	RVQVF-----
NHL1-likeAplysiaacalifornica	-----ENGHFKGLEGVAILANG-NIVVSDRENH----	RIQIF-----
NHL1Parasteatodatepidariorum	-----GDGEFKLEGIAVSPTG-QILACDRENH----	RIQVF-----
NHL1isoformX1Myzuspersicae	-----GDGEFKLEGIAVMSNG-NILVCDRENH----	RVQVF-----
NHL1isoformX1Papiiliomachaon	-----SDGEFKLEGIAVMSGG-NIIVCDRENH----	RVQVF-----
AbbaDrosophilamelanogaster	-----GDSEFKLEGVAIMSNG-NILVCDRENH----	RVQVF-----
NHL1isoformX1Parasteatodatepidariorum	-----SDGEFKGLEGLAVTTGG-SIACDRENH----	RVQVF-----
WechCeratitis capitata	R-----LMPPTIDEKDRTCDAVLPDG-RIVFLIELSP----	DSKEGTSPIYKRFVHIF
WechBombyxmori	-----GLDDKDRPSDVALTPEG-YLVVLFETLP----	DTARDVSSHGKQYIKVY
WechisoformACLuniomarinus	N-----VLTSNMDEKDRPSDVALNDG-RLVVMVETSP----	DSREAI SHNKT FVQVY
WechisoformX1Aedesaegypti	N-----LLTMGMEKDRPSDVALPDG-RLVVMVETSP----	DARDQCSPQKTFIQIY
WechMuscadomestica	P-----LMPPTLDEKDRTCDAVLPDG-RIVFLIELSP----	DSKEGSNPIYKRFVHVF
WechDrosophilamelanogaster	P-----LMPPTLDEKDRTCDAVIMPDG-RIVFLIELSP----	DSKEGSNPIY-----
TRIM71Daniorerio	-----GFGQMDRPSGIAVTPDG-VIVAVDFGNN----	RILMF-----
TRIM71isoformX1Apismellifera	-----DDNEMDRPSGIALCPDG-RIVIVDFGNN----	RVLLI-----
TRIM71Cionaintestinalis	-----NGSALMDRPSGIVTTPHG-HIAVVDGNN----	RVIVF-----
TRIM71-likeParasteatodatepidariorum	-----GPDQMDRPSGVCVSPEG-YIIVDFGNN----	RIQVF-----
TRIM71Capitellateleta	-----GVGQLDRPSGLCLSSDG-AILVVDGNN----	RVQIF-----
TRIM71isoformX1Xenopuslaevis	-----GFGQLDRPSGIAVTPDG-TIVVVDGNN----	RILAF-----
TRIM71Homosapiens	-----GFGQMDRPSGIAITPDG-MIVVVDGNN----	RILVF-----
TRIM71Ornithorhynchusanatinus	-----GFGQMDRPSGIAVTPDG-MIVVVDGNN----	RILIF-----
Lin41Caenorhabditiselegans	PVPNSGFQMP---QELPAPYSSLGGPFGAPAFSSAPTP--LTPSPRQLLDRPTDLAVGPDG-RIVVVDGNN----	CIRVF-----
Lin41Ascaris suum	ASCGGKMG I-----ASSTRSSPQSSGNDAVTLDRPTDICVSPEG-TIIVVDGFSN----	CIRVY-----
Lin41isoformfBrugiamalay	PTLASGVGNASGGESTITPLASMPATHTTVKTSSAQLPTSTNVPKHLVLRPTDLCVSPDG-LIIVVDGFS--	CIRVY-----
NHL3Daniorerio	-----ADPLYGPGGLALTS DG-HVVVADSGNH----	CFKVYRYLQ-----
TRIM2Parasteatodatepidariorum	-----GDPLYGPGGLAMTSDG-HVVVSDSGNH----	CFKIYKYLQ-----
TRIM2Capitellateleta	-----GGPLYGPGGLDISPEG-QVIVADSGNH----	CLKMYKYLQ-----
TRIM2isoformX1Daniorerio	-----ADPLYGPGGLALTS DG-HVVVADSGNH----	CFKVYRYLQ-----
TRIM2isoformX1Ornithorhynchusanatinus	-----ADPLYGPGGLALTS DG-HVVVADSGNH----	CFKVYRYLQ-----
TRIM2Mus musculus	-----ADPLYGPGGLALTS DG-HVVVADSGNH----	CFKVYRYLQ-----
TRIM2Homosapiens	-----ADPLYGPGGLALTS DG-HVVVADSGNH----	CFKVYRYLQ-----
TRIM2LhomeologXenopuslaevis	-----ADPLYGPGGLSLTS DG-HVVVADSGNH----	CFKVYRYLQ-----
TRIM3ShomeologXenopuslaevis	-----GDPLYGPGGLSLTS DG-HVVVADSGNH----	CFKVYRYLQ-----
TRIM3isoformX1Daniorerio	-----ADPLYGPGGLALTS DG-HVAVADSGNH----	CFKVYRYLQ-----
TRIM3Mus musculus	-----AEPLYGPGGLALTS DG-HVVVADAGNH----	CFKAYRYLQ-----
TRIM3Homosapiens	-----AEPLYGPGGLALTS DG-HVVVADAGNH----	CFKAYRYLQ-----
TRIM32Homosapiens	-----LTCPVGIALTPKG-QLLVLDWDH----	CIKIYSYHL-----
TP0421Treponemapallidum	-----GNAPIRLTAAPVDANG-NVLLADYKNE----	RIEIVSRIS-----
BB0236Borrelia burgdorferi	-----DKMNSKISSSILDANN-QMIVSDFNNA----	KVSVYKSDA-----
NHL3Caenorhabditiselegans	-----HEKFMAPCGIFVHKN--KAFVTD FERN----	TVRSYKYK-----
PGal-1Caenorhabditiselegans	-----AKGVRNTHALAI AADG-VMFVSQLEPS----	RILEIRLL-----
Pal2Drosophilamelanogaster	-----WGEFKNPHSMAVSVNGSALYVTEIGTNHQTNRVWKYVLA-----	
Pal1Drosophilamelanogaster	QLV-----SKFGPNLQFQNP HDVAVTADGNEIYVAELNPM----	RIHKFVHRS-----
PamRattus norvegicus	-----RKHFDMPHDIVASEDG-TVYIGDAHTN----	TVWKFTLTE-----
AMDHomosapiens	-----RKHFDMPHDIVASEDG-TVYIGDAHTN----	TVWKFTLTE-----
Pamn-1Caenorhabditiselegans	-----REQMPQFGQPHCLRVCPDGGHIFVGDIAEG----	KARLWQFKI-----
MT3624Mycobacterium tuberculosis	-----LFSPTDVAVDNDG-AVYVIDFYNR----	MLKLPTA-----
PKNDMycobacterium tuberculosis	-----LNTPLAVAVDS DR-TVYVADRGND----	RVVKLTS-----
NHLRC1Homosapiens	-----THGLSHPVALTFTKEN-SLLVLDTASH----	SIKVYKVDW-----
TRIM56Homosapiens	-----YHGLEKP-RVTTMVDG-RYLVSLSNG----	TIHIFRVS-----

Supplementary References

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2. Tocchini, C. *et al.* The TRIM-NHL protein LIN-41 controls the onset of developmental plasticity in *Caenorhabditis elegans*. *PLoS Genet* 10, e1004533 (2014).