Supplementary Table S1. Complementation status of *l(3)tb* with cytologically mapped deletion lines

S.No.	Bloomington Stock Number	Deletion Lines	Estimated Cytological Break points	Status of Complementation
1.	BL: 6554	*Df(3L)XG8*	71C3-D1;71F2-5	No
2.	BL:6548	*Df(3L)XG1*	71C3-D1;71F2-5	No
3.	BL:6603	*Df(3L)X-21.2*	71F1;72A2	No
4.	BL:6157	$Df(3L)D\text{-}5rv12,e^{1}$	70C2;72A1	No
5.	BL:6558	*Df(3L)XG15*	71A3;71F4	Yes
6.	BL:3641	$Df(3L)th^{102},h^{1},kni^{ri\text{-}1},e^{1}$	72A2;72D10	Yes

Supplementary Table S2. Complementation analysis of *l(3)tb* with lethal transposon insertion lines

S. No.	Stock	Symbol	Gene Affected/ Estimated cytology*	Genomic Sequence Coordinates*	Complementation Status
1.	18573	*PBac{WH}DCX-EMAP^{f02655}*	*DCX-EMP* 71A2	3L:14933115..14933115	**YES**
2.	12791	*P{GT1}mnd^{BG01434}*	*minidiscs (mnd)* 71A4	3L:14980561..14980561	**YES**
3.	17084	*P{EP}Prosbeta2^{EP3067}*	*Proteosome β2 subunit* 71B1	3L:14993119..14993119	**YES**
4.	12089	*P{lacW}cp309^{s2172}*	*cp309* 71B3	3L:15072574..15072574	**YES**
5.	21206	*P{EPgy2}cp309^{EY16376}*	*cp309* 71B3	3L:15072713..15072713	**YES**
6.	16007	*P{EPgy2}Aats-gly^{EY09021}*	*Glycil tRNA synthetase* 71B4	3L:15088255..15088255	**YES**
7.	12090	*P{lacW}l(3)j2A2^{j2A2}*	*lethal(3)j2A2* 71B5	3L:15134670..15134670	**YES**
8.	34467	*Mi{MIC}Toll-6^{MI02127}*	*Toll-6* 71C2	3L:15332734	**YES**
9.	16100	*PBac{5HPw[+]}CG7841^{A372}*	*CG7841* 71D3	3L:15500292..15500292	**YES**
10.	21095	*P{EPgy2}CrebA^{EY13494}*	*CrebA* 71E1	3L:15529167..15529167	**YES**
11.	10183	*P{PZ}CrebA^{03576}*	*CrebA* 71E1	3L:15537388..15537388	**YES**
12.	12091	*P{lacW}l(3)s1754^{s1754}*	*lethal(3)s1754* 71E1	3L:15556710..15556710	**YES**
13.	12092	*P{lacW}RhoGAP71Ej6B9*	*RhoGAP71E* 71E1	3L:15582004..15582004	**YES**
14.	15523	*P{EPgy2}mrn^{EY01615}*	*marionette* 71E1	3L:15573609..15573609	**YES**
15.	12100	*P{lacW}RhoGAP71Es1629a*	*RhoGAP71E* 71E1	3L:15582004..15582004	**YES**
16.	17134	*P{EP}RhoGAP71E^{EP3492}*	*RhoGAP71E* 71E1	3L:15586701..15586701	**YES**
17.	22649	*P{EPgy2}CG7650^{EY23633}*	*CG7650* 71E2	3L:15603462..15603462	**YES**
18.	23596	*Mi{ET1}CG7579^{MB02986}*	*CG7579* 71F1	3L:15676129..15676129	**YES**
19.	16186	*PBac{5HPw^{+}}B259*	71F2	3L:15700304..15700457	**YES**
20.	17644	*P{EPgy2}comm^{EY10154}*	*commissureless* 71F2	3L:15721560..15721560	**YES**
21.	21983	*P{EPg}fwe^{HP35545}*	*flower*	3L:15809466..158	

			72A1	09466	**YES**
22.	12794	*P{GT1}DCP2*^{BG01766}	*Decapping protein2* 72A1	3L:15819332..15819332	**NO**
23.	23591	*Mi{ET1}CG32150*^{MB02846}	CG32150 72A2	3L:15834442..15834442	**YES**
24.	25339	*Mi{ET1}pHCl*^{MB06931}	*pHCl* 72A3	3L:15863723..15863723	**YES**
25.	22126	*P{EPg}HP36806*	72B2	3L:15948256..15948256	**YES**

Allele of *Decapping protein 2* (*P{GT1}DCP2*^{BG01766}), reported to be semi-lethal in the FlyBase showed non-complementation to the mutation in *l(3)tb*. *Designates the current annotation and cytological positions and molecular insertion sites as per FlyBase (R5).

Supplementary Table S3. Primers used for characterizing deletion in *Df(3L)RM95*.

Primer	Primer Details						PARAMETER Ta (°C) / Ext. (Sec)
	PRIMER (10 pmol/µL)	SEQUENCE (5'→3')	Molecular Positions (Flybase, R5)	Tm (°C)	'GC' (%)	Amplicon Size (In Bp)	
Custom A	FOR	GCACCAACTGAGCTGTATC	15525318-	54.1	52.6	420	54^0C/ 30sec
PRY4	REV	CAATCATATCGCTGTCTCACTCA		60.3	43.5		
W7500D	FOR	GTCCGCCTTCAGTTGCACTT		62.7	55.0	1600	6^0C/ 1min
W11678U	REV	TCATCGCAGATCAGAAGCGG		64.9	55.0		
3.PRY4	FOR	CAATCATATCGCTGTCTCACTCA	-15948402	60.3	43.5	360	54^0C / 1min
Custom B	REV	TAGTCCACGTAAGGTGCAC		54.3	55.6		

Custom A and custom B primers were designed from the genomic region upstream and downstream to the region where the P{RS5} and P{RS3} progenitor element localized so that with the combination of PRY4, could give 420 bp and 360 bp amplicon respectively.

Supplementary Table S4. Overlapping set of primers for *DCP2* and thermal cycler conditions of annealing temperature and extension time for each primer pair to amplify the genomic region of *DCP2* gene in the homozygous *l(3)tb* mutant.

PRIMER SYMBOL	PRIMER DETAILS					
	PRIMER (10 pmol/µL)	SEQUENCE (5'→3')	MOLECULAR POSITIONS (FlyBase, R5)	Tm (°C)	'GC' (%)	AMPLICON SIZE (in bp)
DCP2_P1	FOR	AGGCTTCTCTCCCCCGTAACT	15813182-15813746	62.7	57.1	565
	REV	CTGCGGGGCGAGAACACGAT		70.0	65.0	
DCP2_P2	FOR	TTCATAGGTGGGGGCGGGCA	15813671-15814201	71.8	65.0	531
	REV	ACGTTAGGGAACCACAAACACACCT		65.9	48.0	
DCP2_P3	FOR	TGTGCTGAGCGGAAGACTCTCGTTT	15814054-15814635	69.5	52.0	582
	REV	GCAGCAGCTGGGAATCGACTTTACG		70.7	56.0	
DCP2_P4	FOR	ATTTGGCGTAAAGTCGATTC	15814605-15815184	56.9	40.0	580
	REV	CAAGCAATGAGAAGGTGAGT		55.4	45.0	
DCP2_P5	FOR	AGGATTTTGACTGGCTGCTG	15814960-15815231	60.4	50.0	272
	REV	GCGTCAACTGTTCCATAGCC		60.7	55.0	
DCP2_P6	FOR	GGAACAGTTGACGCTTCGAG	15815218- 15815640	61.0	55.0	423
	REV	GCCTGAAGAAGTGGGTGAAC		59.7	55.0	
DCP2_P7	FOR	CTTATTGCGTTTCCCATTGC	15815330-15815709	60.5	45.0	380
	REV	ATGCCATATCAAAGGCCAAG		59.9	45.0	
DCP2_P8	FOR	AGCCTTCCGATCGTTCACCCAC	15815609-15815909	68.8	59.1	301
	REV	GGTTTATGAGGAGACCGGGTTCG		66.9	56.5	
DCP2_P9	FOR	ATGTTTCGCACCACGTACAG	15815802- 15816213	59.6	50.0	412
	REV	GCTATCGGTGCCCACTTATG		60.5	55.0	
DCP2_P10	FOR	ATAGCGCCATAAGTGGGCACCGATA	15816187-15816720	69.9	52.0	534
	REV	ACTCCTCCTACGGCAGCTCATCATC		68.0	56.0	
DCP2_P11	FOR	GATGATGAGCTGCCGTAGGAGGAGT	15816696-15817147	68.0	56.0	452
	REV	CTATCAGTTTCTTGGGGCCGTGTGC		70.4	56.0	
DCP2_P12	FOR	GCACACGGCCCCAAGAAACTG	15817123-15817595	69.2	61.9	473
	REV	AGGCTCTTACAAAGGGTGCTTATCGAA		66.9	44.4	

DCP2_P13	FOR	TCGATAAGCACCCTTTGTAAGAGCCT		15817570-15817972	66.2	46.2	403
	REV	CACCAGTCTACGTTATCGGGGTCGT			68.2	56.0	
DCP2_P14	FOR	AGTGCTGCAGTACGACCCCGATA		15817937-15818367	67.1	56.5	431
	REV	ACAATCAGAATATCTCCCACCCAGCA			67.7	46.2	
DCP2_P15	FOR	TGCTGGGTGGGAGATATTCTGATTGT		15818342-15818617	67.7	46.2	276
	REV	CGTCTCTGCCTCTGCTAGCGT			64.4	61.9	
DCP2_P16	FOR	ACGCTAGCAGAGGCAGAGAC		15818597- 15818806	59.9	60.0	210
	REV	CAGAGAGAGACGCGAATGTG			59.7	55.0	
DCP2_P17	FOR	AGAGGCAGAGGCTGTGACGAC		15818623-15819021	64.4	61.9	399
	REV	TTCGTGCGACAAAAGCGGACG			70.7	57.1	
DCP2_P18	FOR	TGCAATCGTCCGCTTTTGTCGCA		15818995-15819495	73.6	52.2	501
	REV	AGAGGAAGGCGAGTTTTGAGCAGT			65.9	50.0	
DCP2_P19	FOR	TGCTCACCGAACTTTTTCGCGATCT		15819379-15819751	70.7	48.0	373
	REV	GTGCAACGGAAGGGAATCTAACTGTG			67.8	50.0	
DCP2_P20	FOR	CACAGTTAGATTCCCTTCCGTTGCAC		15819726- 15820171	67.8	50.0	446
	REV	ACAAAGCACGTCCAGGGCCA			68.4	60.0	

Supplementary Table S5. Overlapping set of primers to amplify the genomic region in *DCP2* gene for the region covered by the DCP2_P19 set of primers in the homozygous *l(3)tb* mutant.

PRIMER SYMBOL	PRIMER DETAILS							
	PRIMER (10 pmol/µL)	SEQUENCE (5'→3')	TEMPLATE STRAND	LENGTH (in ntd.)	MOLECULAR POSITIONS (FlyBase, R5)	Tm (°C)	'GC' (%)	
DCP2_P19_1	FOR	TAAATTGCCTTTATTTACACGTTGC	PLUS (+)	25	15819403-15819518	60.6	32.0	
	REV	ACTATTTCTATACGCGACGCTGAAG	MINUS(-)	25		62.1	44.0	
DCP2_P19_2	FOR	ACTATTTAACGGGCTTTTCAACTG	PLUS (+)	24	15819452-15819569	60.0	37.5	
	REV	CGGTATATTTTGGTATCTTAGTGAGC	MINUS(-)	26		58.7	38.5	
DCP2_P19_3	FOR	CAGCGTCGCGTATAGAAATAGTATG	PLUS (+)	25	15819497-15819622	67.7	46.2	
	REV	AGTACATTTATCACAGAGCCAACTG	MINUS(-)	25		58.8	40.0	
DCP2_P19_4	FOR	GCTCACTAAGATACCAAAATATACCG	PLUS (+)	26	15819544-15819657	58.7	38.5	
	REV	AAAATAAGCAAATAACGTAAGACAGG	MINUS(-)	26		58.5	30.8	
DCP2_P19_5	FOR	AAGCCTGTCTTACGTTATTTGCTTA	PLUS (+)	25	15819629-15819764	59.8	36.0	
	REV	CAACTACAAGTAAGTGCAACGGAAG	MINUS(-)	25		61.4	44.0	

Supplementary Table S6. Overlapping set of primers to amplify the complete 5'UTR of genomic region in *DCP2* gene in the homozygous *l(3)tb* mutant. The table also documents the thermal cycler conditions of annealing temperature and extension time for each primer pair. Genomic region amplified by primer pair is also mentioned.

PRIMER SYMBOL	PRIMER DETAILS					
	PRIMER (10 pmol/µL)	SEQUENCE (5'→3')	MOLECULAR POSITIONS (FlyBase, R5)	Tm (°C)	'GC' (%)	AMPLICON SIZE (in bp)
DCP2_5'UTR1	FOR	GTACTCTAGTTATTCCATCGGTTGC	15819051-15819563	59.5	44.0	513
	REV	ATTTTGGTATCTTAGTGAGCAGCAT		59.6	36.0	
DCP2_5'UTR2	FOR	TTTTGCTATTGTTCTCTCGATTTTC	15819085-15819652	60.1	32.0	568
	REV	AAGCAAATAACGTAAGACAGGCTTT		60.8	36.0	
DCP2_5'UTR3	FOR	AAGCCTGTCTTACGTTATTTGCTTA	15819629-15820187	59.8	36.0	459
	REV	TCTGTTCTCTACGGATACAAAGCAC		61.0	44.0	