

**Additional file 4 Results from ubiquitous knockdown studies of UAS-RNAi lines with and without *DmManf* overexpression.**

UAS-RNAi line	Without <i>DmManf</i> OE				With <i>DmManf</i> OE			
	Tb+	Tb-	pupal-%	adult-%	Tb+	Tb-	pupal-%	adult-%
UAS- <i>bora</i> -RNAi <sup>1</sup>	20	612	6%	0%	6	461	3%	0%
UAS- <i>betaTry</i> -RNAi	126	118	97%	109%	53	107	104%	98%
UAS- <i>dome</i> -RNAi	102	118	87%	103%	68	109	120%	75%
UAS- <i>Hsp68</i> -RNAi	1	166	1%	0%	0	139	0%	0%
UAS- <i>l (2) 37Bb</i> -RNAi <sup>2</sup>	0	91	0%	0%	0	80	0%	0%
UAS- <i>ND75</i> -RNAi	0	218	0%	0%	0	94	0%	0%
UAS- <i>Aats-phe</i> -RNAi	0	133	0%	0%	0	103	0%	0%
UAS- <i>pABp</i> -RNAi	0	76	0%	0%	0	116	0%	0%
UAS- <i>Spn27A</i> -RNAi	110	115	92%	1%	72	117	119%	1%
UAS- <i>Taf5</i> -RNAi	0	185	0%	0%	0	95	0%	0%
UAS- <i>timeout</i> -RNAi <sup>1,2</sup>	282	495	112%	0%	205	381	108%	0%
UAS- <i>Tom20</i> -RNAi <sup>1,2</sup>	1	376	1%	100%	1	340	1%	100%
UAS- <i>Ts</i> -RNAi	28	104	40%	0%	11	63	46%	0%
UAS- <i>Fip1</i> -RNAi	0	186	0%	0%	0	178	0%	0%
UAS- <i>Cdk12</i> -RNAi	0	172	0%	0%	0	203	0%	0%
UAS- <i>CG9249</i> -RNAi	0	127	0%	0%	0	128	0%	0%
UAS- <i>CG7277</i> -RNAi	151	153	94%	77%	82	164	104%	98%
UAS- <i>CG30493</i> -RNAi	1	115	2%	0%	1	70	4%	0%
UAS- <i>CG32174</i> -RNAi	113	79	111%	85%	49	89	111%	96%
UAS- <i>Irbp</i> -RNAi <sup>1,2</sup>	0	457	0%	0%	2	522	1%	100%
UAS- <i>COQ7</i> -RNAi <sup>1</sup>	153	376	48%	0%	0	226	0%	0%
UAS- <i>CG9613</i> -RNAi <sup>1</sup>	217	523	53%	0%	22	249	24%	0%
UAS- <i>CSN3</i> -RNAi <sup>1</sup>	285	304	93%	0%	107	487	55%	0%

*tub*-GAL4/TM6 Tb Sb females were crossed to UAS-*x*-RNAi(/SM6-TM6) (without *DmManf* OE) and UAS-*x*-RNAi ; UAS-*DmManf*-OE/SM6-TM6 (with *DmManf* OE) males. Columns: Tb<sup>+</sup> and Tb<sup>-</sup>, amounts of Tb<sup>+</sup> and Tb<sup>-</sup> pupae in crosses; pupal-%, normalized proportion of Tb<sup>+</sup> of all pupae, wild type or wild type/SM6-TM6 were used to normalize proportions (see Additional file 7); adult-%, proportion of emerged adults out of Tb<sup>+</sup> pupae. OE, overexpression. n of analysed vials = 2 (except <sup>1</sup>, n = 6 vials, see Methods). Without *DmManf* overexpression, homozygous UAS-*x*-RNAi lines were used expect <sup>2</sup> which were balanced with SM6-TM6.