

Additional file 8 Results from ubiquitous knockdown of UAS-*DmManf*-RNAi.

UAS line	Tb ⁺	Tb ⁻	pupal-%	adult-%
wild type *	489	423	100%	106%
wild type/SM6-TM6 *	138	279	100%	106%
UAS- <i>DmManf</i> -RNAi	11	504	5%	0%
UAS- <i>DmManf</i> -RNAi ; UAS- <i>DmManf</i> -OE/SM6-TM6	148	293	103%	86%
UAS- <i>DmManf</i> -RNAi ; UAS-mCD8-GFP	11	467	5%	17%
UAS- <i>DmManf</i> -RNAi ; UAS- <i>HsMANF</i> -OE/SM6-TM6	193	402	100%	93%
UAS- <i>DmManf</i> -RNAi ; UAS- <i>HsCDNF</i> -OE/SM6-TM6	199	349	113%	82%
UAS- <i>DmManf</i> -RNAi ; <i>DmManf</i> ^{Δ96} /SM6-TM6	0	304	0%	0%
UAS- <i>DmManf</i> -OE *	444	359	102%	93%

tub-GAL4/TM6 Tb Sb females were crossed to males of indicated phenotypes. Columns: Tb⁺ and Tb⁻, amounts of Tb⁺ and Tb⁻ pupae in crosses; pupal-%, normalized proportion of Tb⁺ of all pupae, wild type or wild type/SM6-TM6 were used to normalize proportions; adult-%, proportion of emerged adults out of Tb⁺ pupae. OE, overexpression. n of analysed vials = 6. * Wild type and UAS-*DmManf*-OE data has been previously reported in [13].