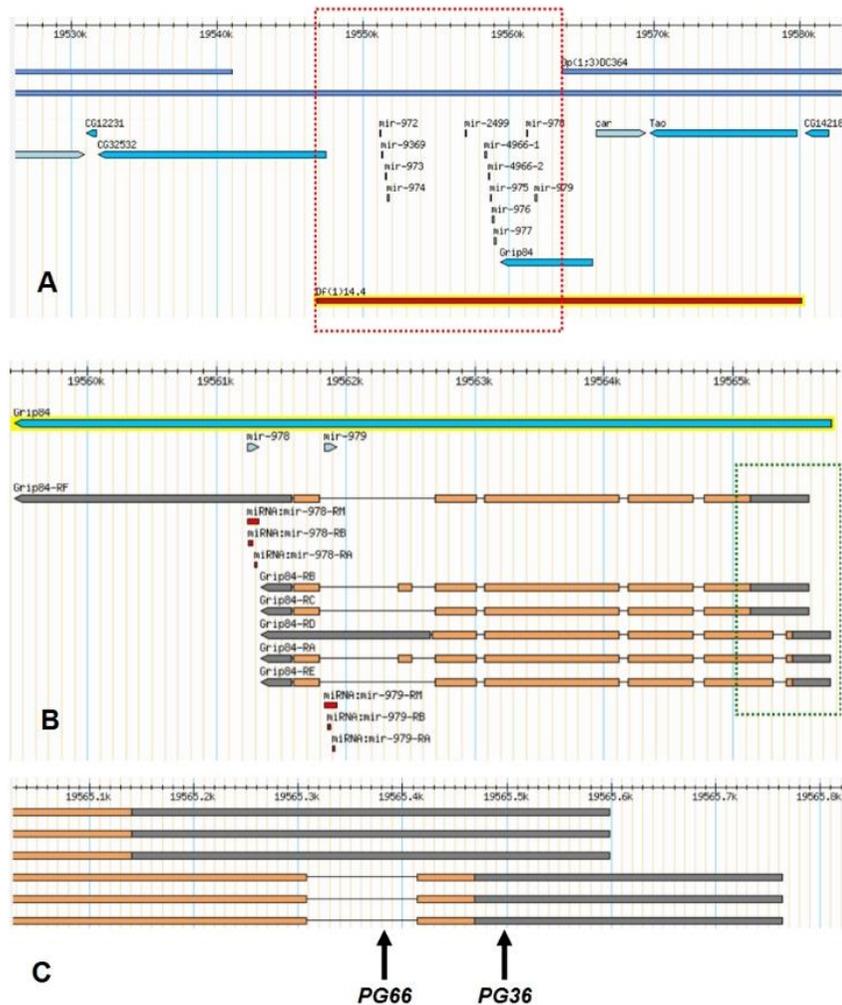


Supplementary Table S1. Raw count and percentage of larvae with mutated (MUT) (defined as head width < -2SD below average) or wildtype (WT) phenotype. Statistical significance for microcephalic forms (MUT) obtained in KD vs RESCUE experiments: Multiple comparisons one-way ANOVA; * : $P \leq 0.05$; **: $P \leq 0.01$. This includes Sidak's amendment test for multiple comparisons.

Number of embryos with WT or MUT phenotype	Replicate 1		Replicate 2		Replicate 3		Overall		Statistics
	WT	MUT	WT	MUT	WT	MUT	WT	MUT	
Trans MO 4nM (n=153) KD	2 (3%)	60 (97%)	14 (30%)	33 (70%)	4 (9%)	40 (91%)	20 (13%)	133 (87%)	
Trans MO 4nM + mRNA 25pg (n=207) RESCUE	27 (40%)	41 (60%)	38 (61%)	24 (32%)	27 (35%)	50(65%)	92 (44%)	115 (56%)	0,043 *
Splice MO 4nM (n=147) KD	13 (27%)	36 (73%)	2 (3%)	58 (97%)	2 (2%)	36 (0.95%)	17 (12%)	130 (88%)	
Splice MO 4nM + mRNA 25pg (n=157) RESCUE	19 (42%)	26 (58%)	32 (53%)	28 (47%)	22 (42%)	30 (58%)	73 (46%)	84 (54%)	0,0039 **



Supplementary Figure S1. Organisation of the *Grip84* gene in *Drosophila melanogaster*. (A) Genomic region surrounding the gene, showing a small deficiency, *Df(1)14.4* and left part of the duplication *Dp(1;3)DC364*. In the stock including both the deficiency and the duplication, the region in a red dashed rectangle is missing, therefore *Grip84* should be eliminated. Micro RNAs and *cg32532* are also eliminated. (B) structure of the gene, including alternatively used exons, the fragment in the dashed, green rectangle is magnified in (C) together with precise positions of two P elements.