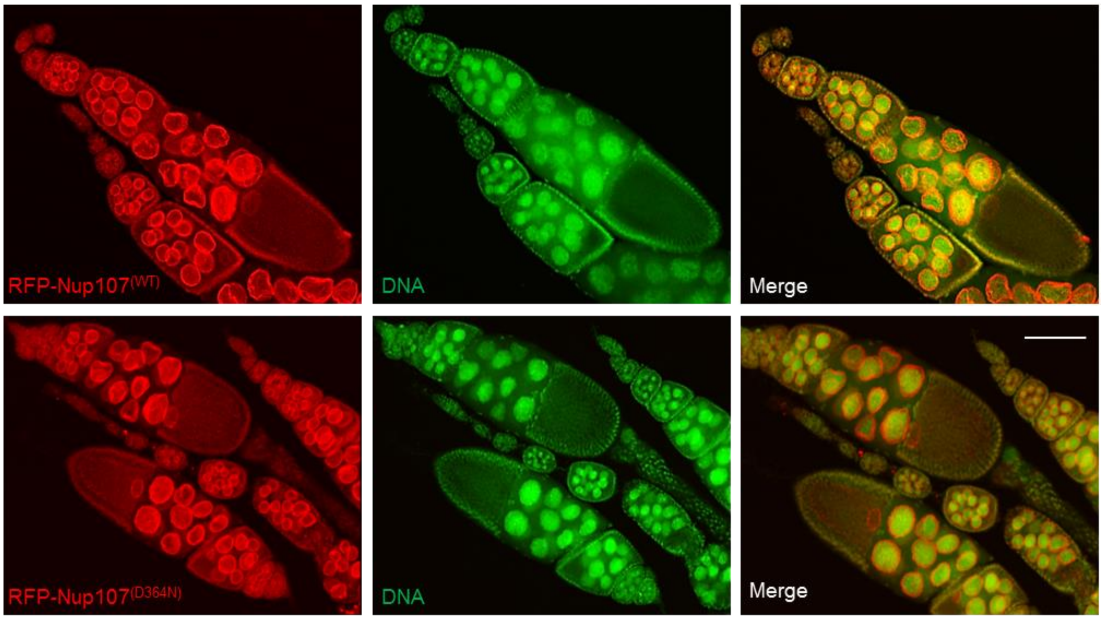

Figure S1. RFP-Nup107 WT and mutant D364N protein localization. Both transgenic WT RFP-Nup107$^{(WT)}$ (upper panel) and mutant RFP-Nup107$^{(D364N)}$ (bottom panel) are correctly localized to the nuclear membrane rim, as indicated in **Red** by the RFP-Nup107 protein, which envelops the nuclear DNA (Sytox, **Green**). Scale bar: 100µm.

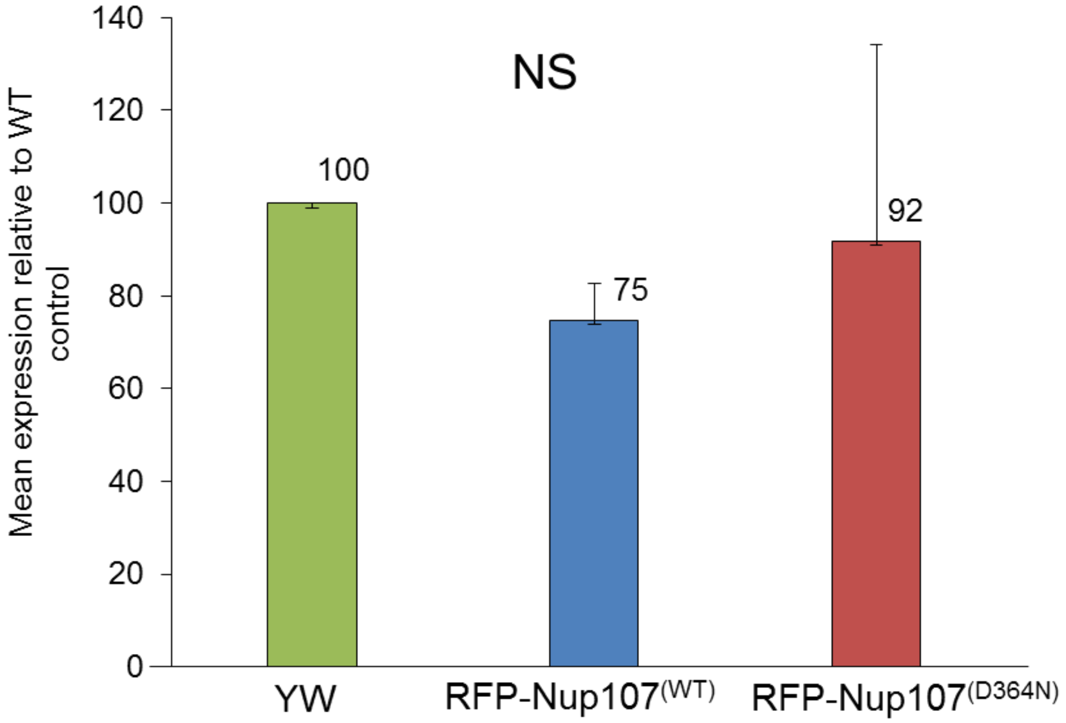

Figure S2. Nup107 transcript levels in ovaries from wild type and transgenic flies. Endogenous and transgenic Nup107 transcripts are expressed at comparable levels. Quantitative real-time PCR using Taqman assays (see methods) was performed on pooled RNA from 10 ovaries of each genotype and normalized to the ovarian house-keeping gene *RpS17*. Results shown are the mean of four experiments, each conducted in triplicate. NS- Not significant. Statistical significance was assessed by a two-tailed, unpaired Student's t-test.

Table S1- Next Generation Sequencing data analysis:

Data filtering criteria	Affected individual (Figure 1A)	
	IV-1	IV-5
Total variants	48,000	47,948
Variants with Read depth ≥ 5	43,106	42,255
Coding / Splicing variants *	21,120	20,109
Homozygous variants	6,265	6,286
Shared among both affected	832	
Frequency ≤ 1%	207	
Polyphen2 score ≥ 0.6, SIFT score ≤ 0.05	72	
Co-segregation in additional relatives**: homozygous in additional affected females IV-6 & IV-7 and not homozygous for the same alleles in healthy female IV-2	1	

* Missense, nonsense, splicing, frameshift, codon insertion/deletion

** Based on SNP array data (see Methods)