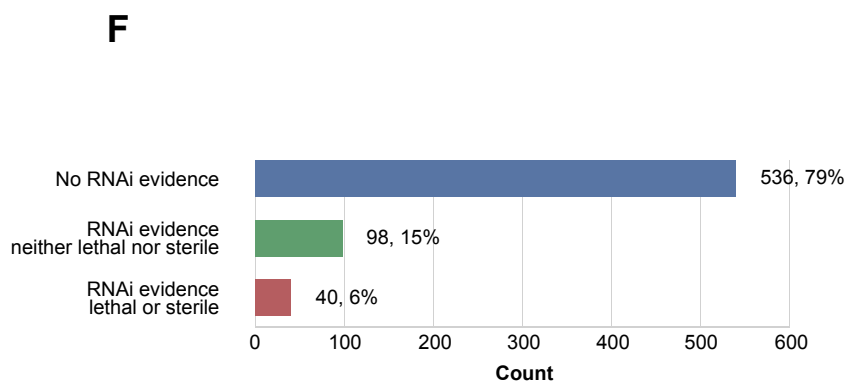
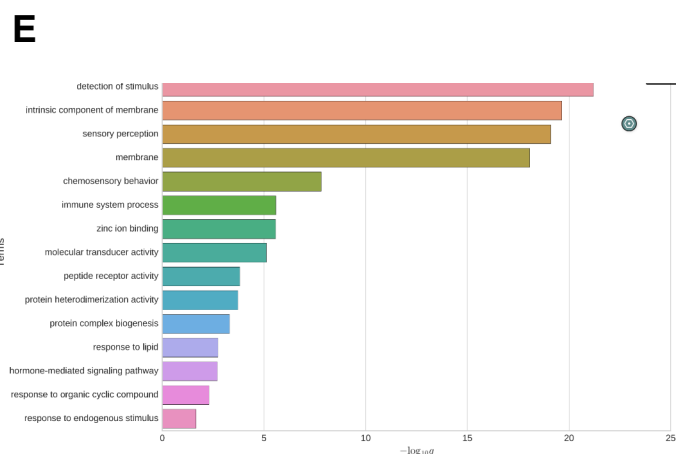
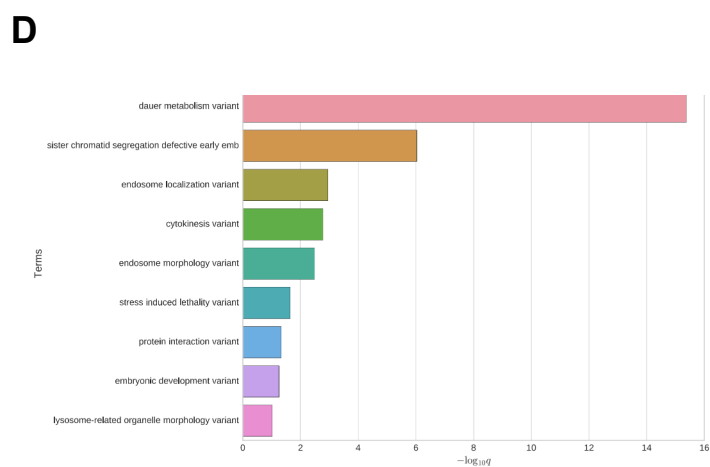
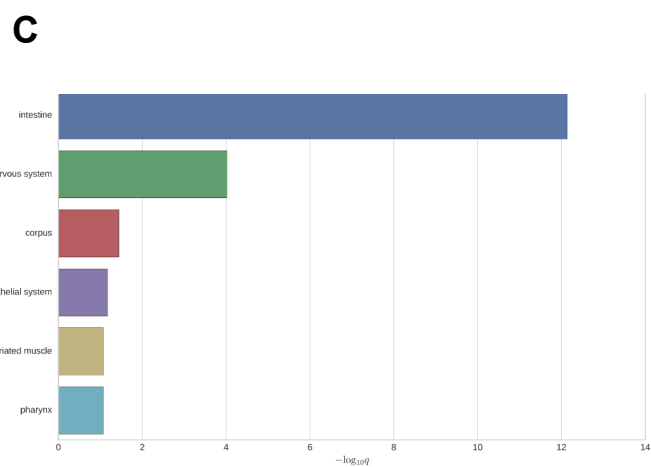


B

	CGH1-specific	CGH2-specific	Intersection (CGH1 & CGH2)
High impact gene	5	64	49
Pseudogene	1	26	9
No_clue	2	18	2
Total	8	108	60



Supplemental Figure S9. Quality and gene ontology analysis of N2-specific genes. (A) N2-specific genes (completely deleted genes) compared with two CGH data. CGH1: Maydan et al., 2007, CGH2: Maydan et al., 2010. (B) Analysis of CGH specific genes. 67% of the genes that were reported as deleted by CGH analyses but were not confirmed as N2-specific genes are actually high impact genes in CB4856, and 20% of them were pseudogenes. (C-F) Enrichment analysis of tissue, phenotype and GO in N2-specific genes. (C) Tissue Enrichment Analysis of high-impact SV genes. (D) Phenotype Enrichment Analysis of high-impact SV genes. (E) Gene Ontology Enrichment Analysis of high-impact SV genes. (F) RNAi evidence of lethal and sterile phenotype in N2-specific genes.