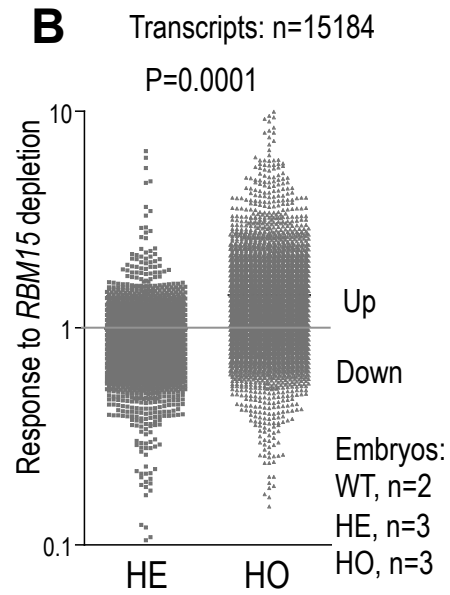
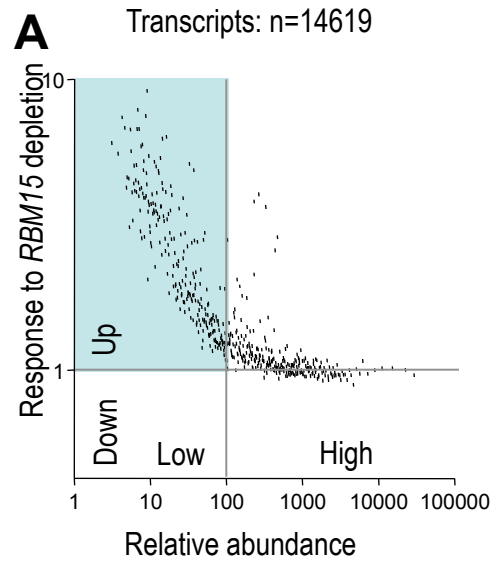


## Supplemental Figure Legend

Figure 1. *A*, Embryos at E11.5 were analyzed on mRNA microarrays, leading to high confidence detection of 33167 transcripts. Values corresponding to RefSeq-annotated transcripts (n=14619, for complete datasets see <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE11785>) are presented. Plotted on the X-axis (*Relative abundance*) are the log levels of each transcript (raw intensity units), averaged over WT and HE embryos (n=5). Plotted on the Y-axis (*Response to RBM15 depletion*) are log intensity ratios that represent, for each transcript, its level found in a typical HO embryo, divided by its *Relative abundance* value. Data were subjected to pruning, so that each symbol on the plot represents 20 transcripts. *Down* and *Up*, the down and upregulated transcripts in HO embryo. *Low* and *High*, the low and high abundance transcripts, arbitrarily defined. *B*, For each low abundance transcript, its average level obtained in HE (n=3) or HO (n=3) embryos was normalized to that in WT (n=2) and plotted on the Y-axis (*Response to RBM15 depletion*). These values are significantly different in HE and HO animals (n=15184, P=0.0001,  $\alpha=0.05$ , Mann-Whitney test). Similar results were obtained when studying the *RBM15*<sup>XK135</sup> allele in mice with different genetic backgrounds (not shown). *C*, The top transcript categories, according to *Molecular Function* (PANTHER classification system, <http://www.pantherdb.org>) that are nonrandomly represented ( $\alpha=0.05$ , Mann-Whitney test) in HO as compared to HE embryos. For each RefSeq-annotated transcript (n=14619), we divided its average level in HO embryos (n=3) by that in HE (n=3), and analyzed these ratios using the PANTHER expression tools online.

# Supplementary Figure 1



**C**

Molecular Function	number	P-value	Regulation
G-protein coupled receptor	589	2.00E-12	up
Nucleic acid binding	1682	7.60E-11	down
Ribonucleoprotein	57	6.38E-08	down
Ribosomal protein	142	7.88E-08	down
mRNA splicing factor	69	2.53E-06	down
mRNA processing factor	96	1.63E-05	down