Supporting Information

Supplemental Tables

Table S1. miRNA mapping

Sample	# Total	# Mapped	Rate
mouse_MAX10.5_1.cutadapt	8,285,943	5,729,779	0.692
mouse_MAX10.5_2.cutadapt	9,396,466	7,842,924	0.835
mouse_MAX11.5_1.cutadapt	16,406,467	12,318,940	0.751
mouse_MAX11.5_2.cutadapt	20,784,494	17,406,631	0.837
mouse_MAX12.5_1.cutadapt	20,971,137	18,758,701	0.895
mouse_MAX12.5_2.cutadapt	17,777,426	15,336,544	0.863
mouse_MAX13.5_1.cutadapt	3,664,072	3,284,924	0.897
mouse_MAX13.5_2.cutadapt	4,395,308	4,078,095	0.928
mouse_MAX14.5_1.cutadapt	11,650,387	10,875,216	0.933
mouse_MAX14.5_2.cutadapt	28,728,299	25,273,975	0.880

Table S2. Differentially expressed nodes

Molecules	E11.5 vs E10.5	E12.5 vs E11.5	E13.5 vs E12.5	E14.5 vs E13.5
Genes	466	470	414	70
TFs	23	20	13	1
miRNAs	13	11	34	10

Table S3. The detailed information of miRNA-target databases for mice

Category	Database	Version	# Total Pairs	# miRNAs	# targets
Validated	miRTarBase	Release 7.0: Sept. 15, 2017	40,681	959	7280
Predicted	miRanda	August 2010 Release	631,947	238	18,779
	PITA	version 6 (31-Aug-08)	143,635	491	9,239
	TargetScan	Release 7.2, August 2018	378,188	580	15,044

Table S4. Regulation pairs in the databases

Regulation type	**# Genes**	**# TFs**	**# miRNAs**	**# Pairs**
TF-gene	1141	435	N/A	121,746
TF-miRNA	N/A	432	789	110,246
miRNA-gene	6,468	N/A	778	21,970
miRNA-TF	N/A	343	464	2176

Supplemental Figures

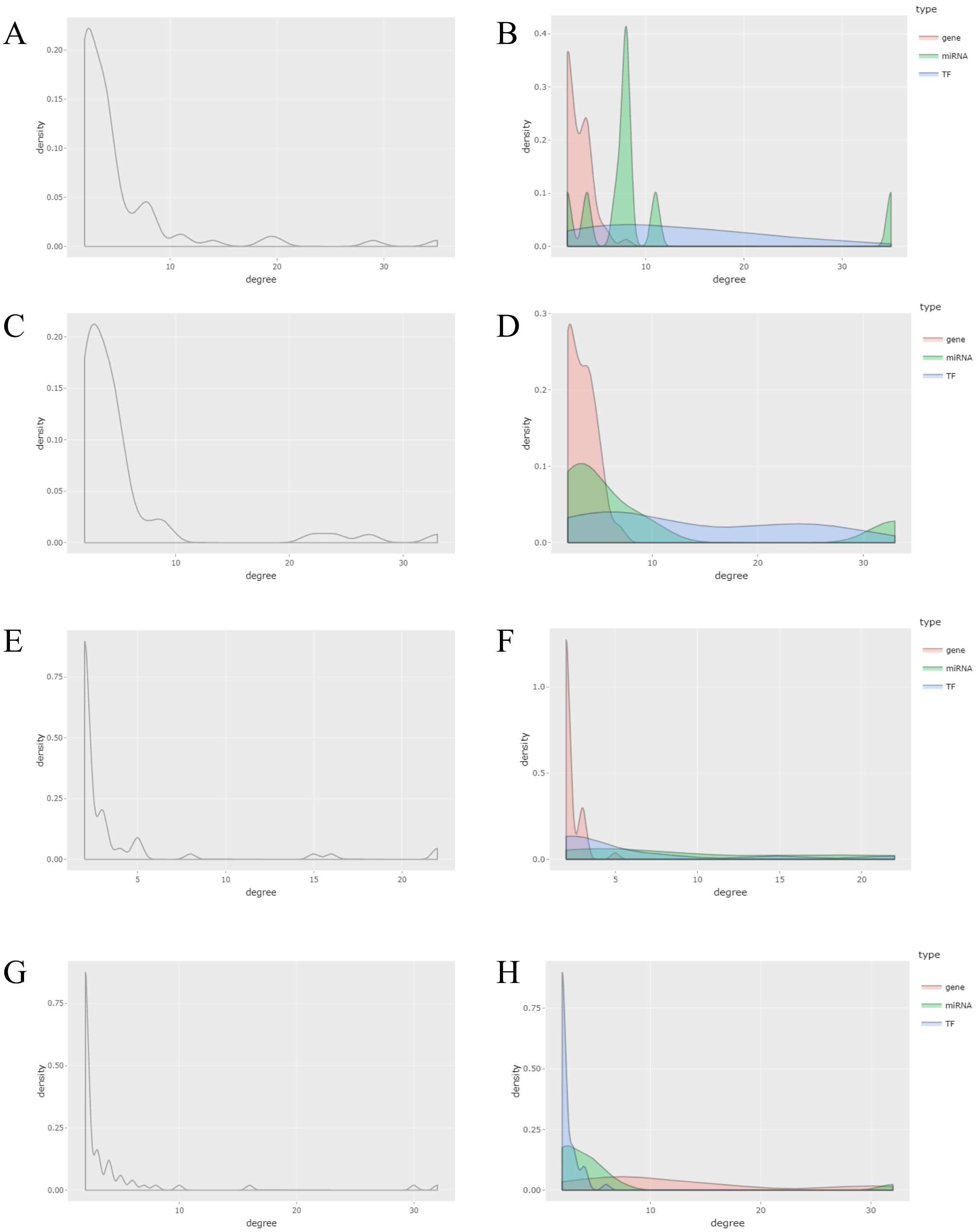

Figure S1. Distribution of nodes in the regulatory network from (AB) E10.5 to E11.5, (CD) E11.5 to E12.5, (EF) E12.5 to E13.5, and (GH) E13.5 to E14.5. Line in red correspond to degree distribution of genes, line in green correspond to degree distribution of miRNAs, and line in blue correspond to degree distribution of transcription factors.