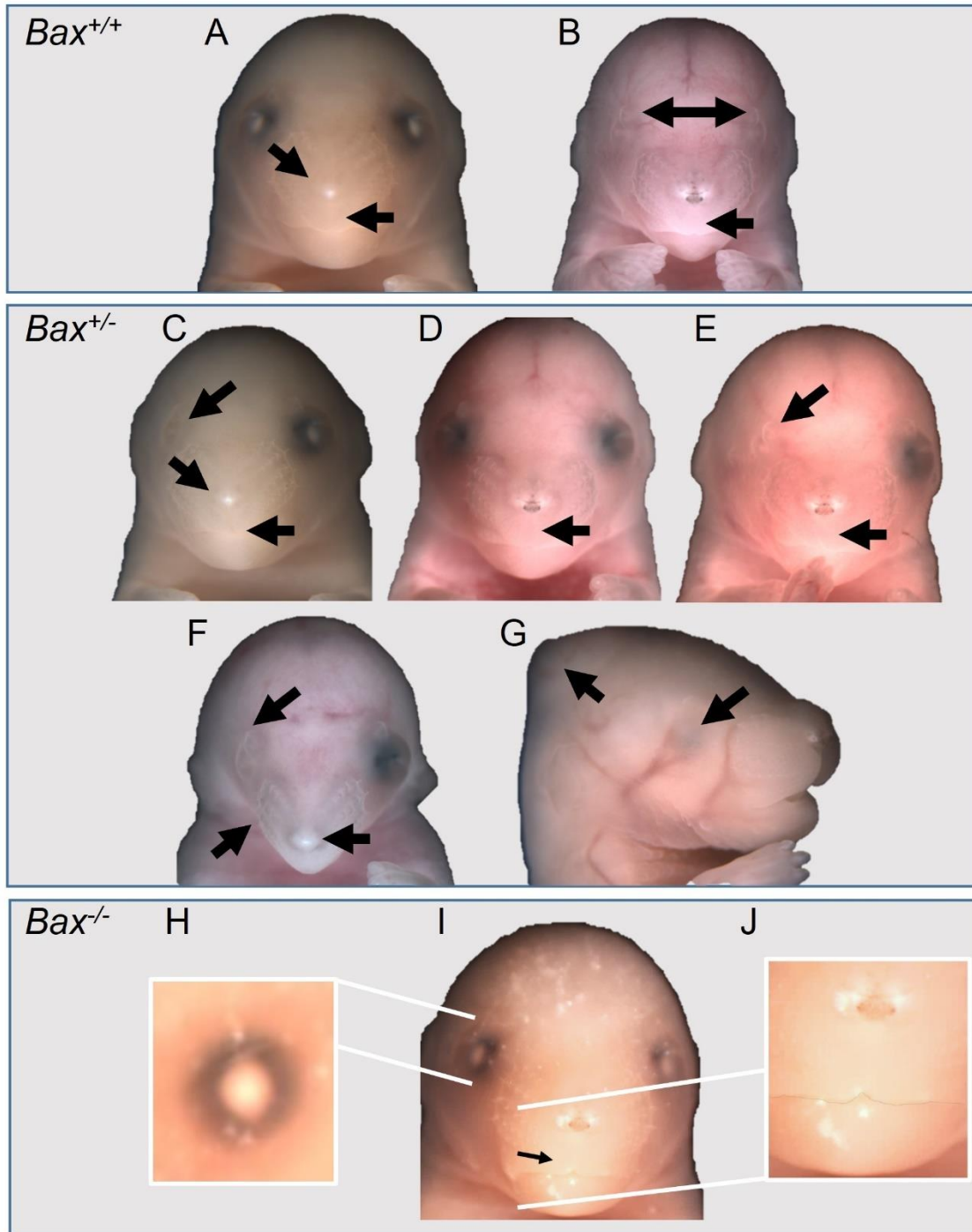
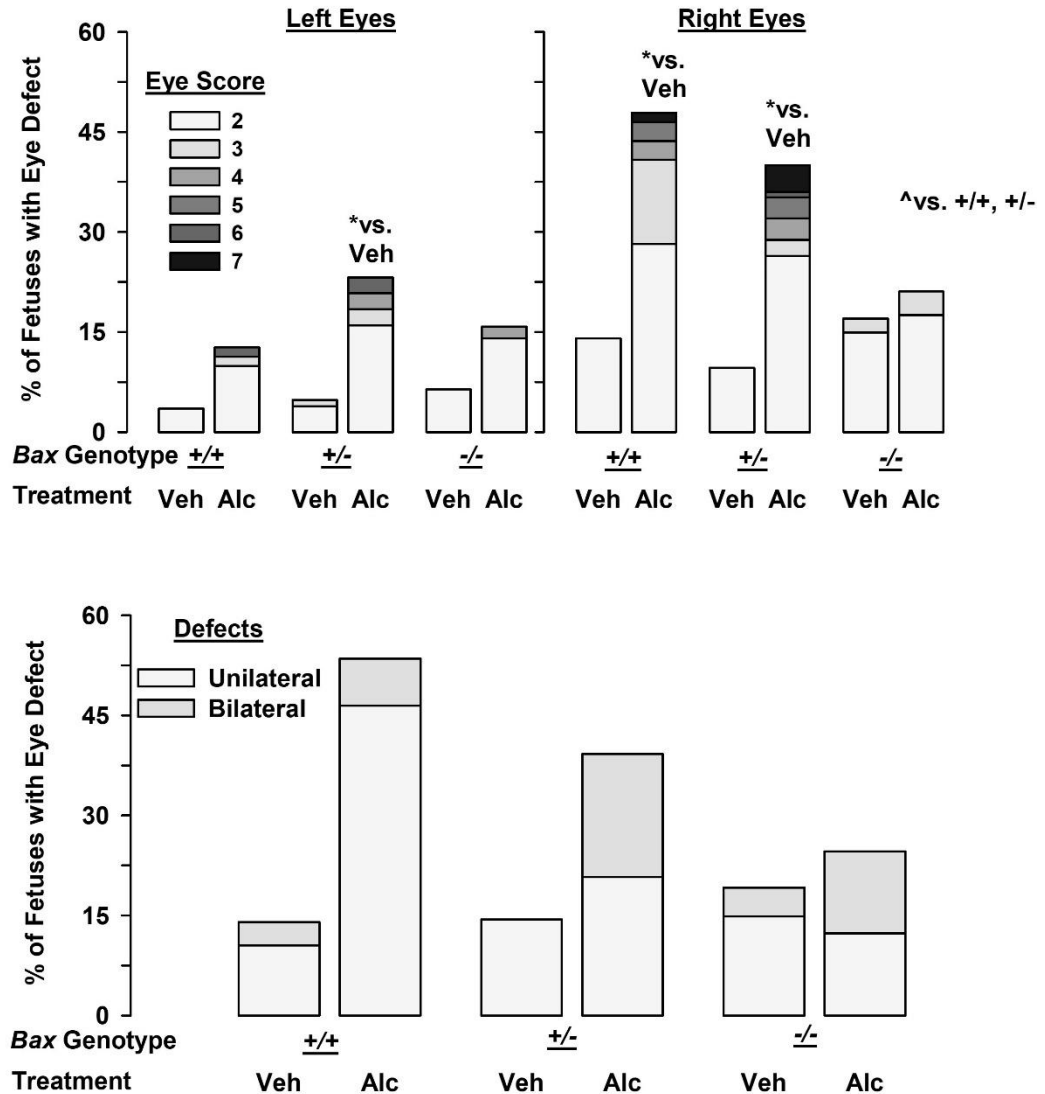


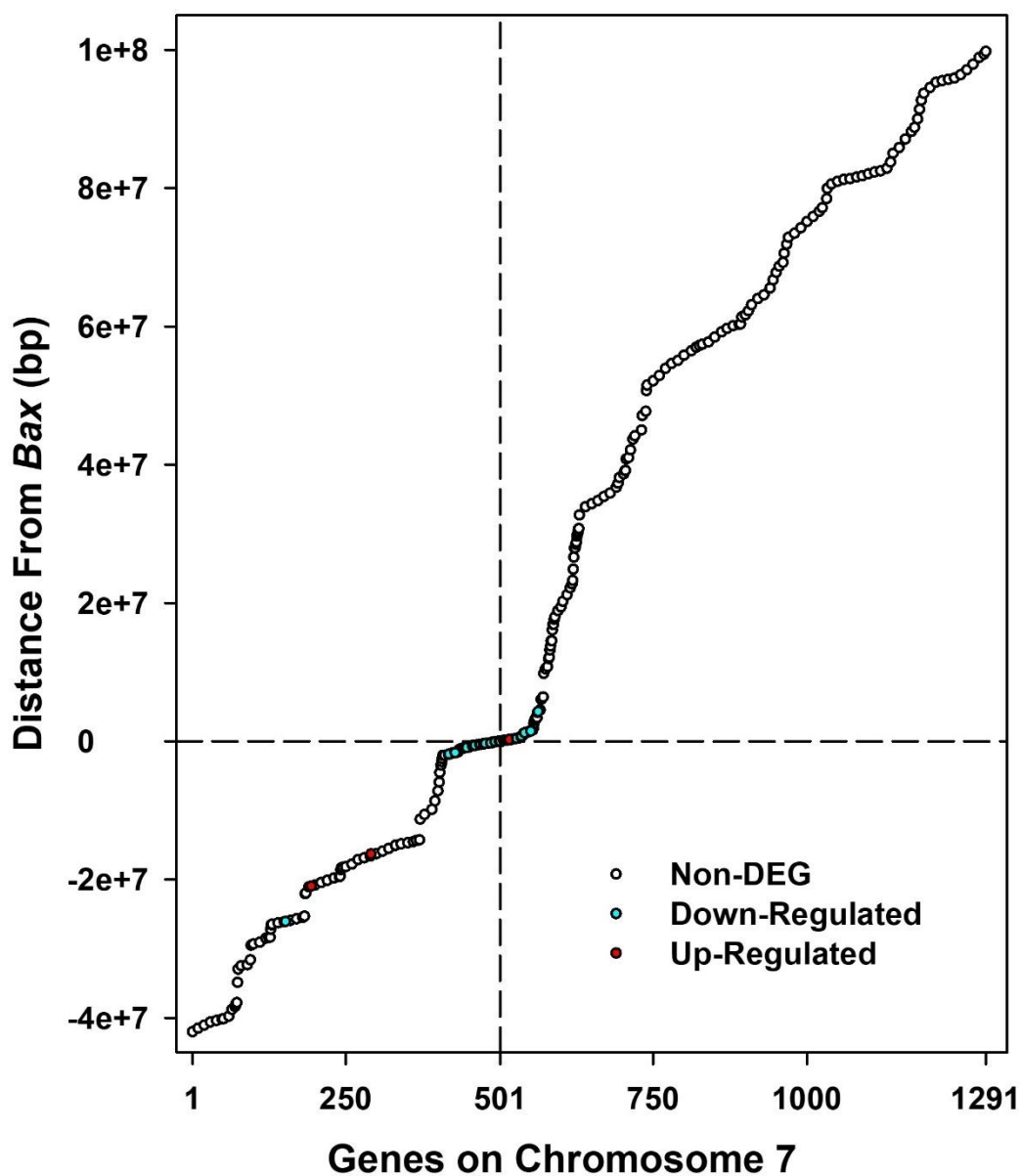
Supplemental Figure 1. Comparison of spontaneously occurring and alcohol-induced minor right eye defects. The *left and center sets of bars* portray the mean size (\pm SEM) of the lens and globe, respectively for vehicle (*open bars*) and alcohol (*filled bars*) treated $Bax^{+/+}$ and $Bax^{-/-}$ fetuses. The *right set of bars* portrays the mean (\pm SEM) lens area expressed as a percent of the entire globe. * denotes significance ($p < 0.05$) vs. unaffected control eyes (eye score 1).



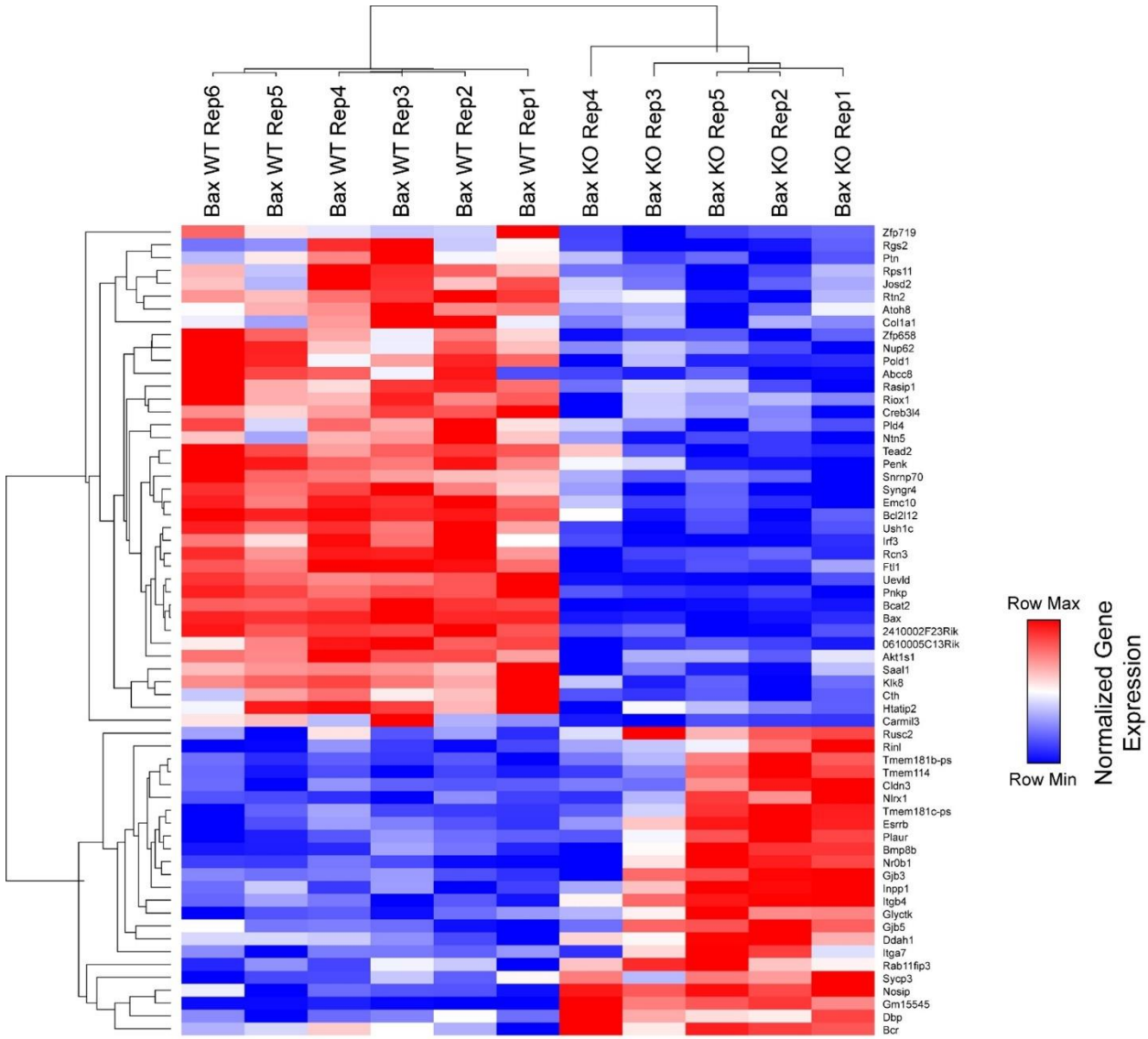
Supplemental Figure 2. Cases of craniofacial dysmorphology in alcohol-treated, *Bax*^{+/+}, *Bax*^{+/-}, and *Bax*^{-/-} fetuses. Shown here are photographs of either live (B, D, E, F, & G), or formalin-fixed (A, C, & H) fetuses. The *Bax*^{-/-} fetus had evidence for a smaller lip notch that was not noticed upon the initial evaluation. The upper lip has been outlined in J to highlight the lip notch. In contrast to the other cases of craniofacial dysmorphology, this fetus had only a minor shape alteration in the right pupil (H). The speckled appearance of this fetus is caused by prolonged fixation.



Supplemental Figure 3. Effects of *Bax* genotype and alcohol on the sidedness of fetal eye defects. Panel A portrays the percent of fetuses with defects in the left or the right eye, plotted separately in the left and right figures. *Stacked bars* indicate the percent of fetuses with an eye categorized as a 2 (smaller globe or minor change in pupil shape) to 7 (complete anophthalmia) for *Bax*^{+/+}, *Bax*^{+/-}, and *Bax*^{-/-} fetuses (*left, center, and right sets of bars*, respectively). Panel B portrays the incidence of unilateral (*light gray bars*) and bilateral (*gray bars*) for *Bax*^{+/+}, *Bax*^{+/-}, and *Bax*^{-/-} fetuses (*left, center, and right sets of bars*, respectively). * denotes significance vs. vehicle treated fetuses of the same genotype, while the ^ denotes significance (*p*<0.05) vs. alcohol-treated the *Bax*^{+/+} and *Bax*^{+/-} fetuses.

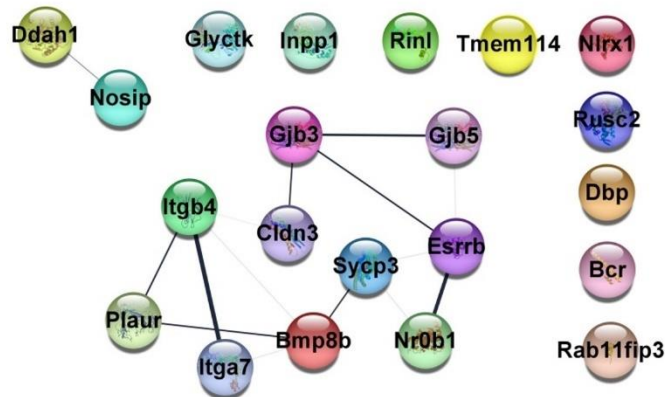


Supplemental Figure 4. Depiction of gene expression changes on chromosome 7. *Circles* represent all genes across chromosome 7, with the *y-axis* indicating distance (in base pairs) between the gene and *Bax* (gene 501, intersection between the *vertical* and *horizontal* hatched lines). *Open circles* represent genes that are not differentially expressed, whereas genes with significantly lower- and higher-expression in the *Bax*^{-/-} embryos are shown in *cyan* and *red circles*, respectively. For genes earlier on the chromosome compared to *Bax* (genes 1-500), distance between *Bax* and a given gene is designated as the number of base pairs between the 3' end of *Bax* and the nearest end (5' or 3') for that particular gene. For genes later on the chromosome relative to *Bax* (genes 502-1291), distance is designated as the number of base pairs from the 5' end of *Bax* and the nearest end (5' or 3') for that particular gene. Gene location was determined by using the Mouse Genome Informatics database. N.B., for clarity, and to avoid extensively overlapping symbols, circles for non-differentially expressed genes can represent between one and ten genes.

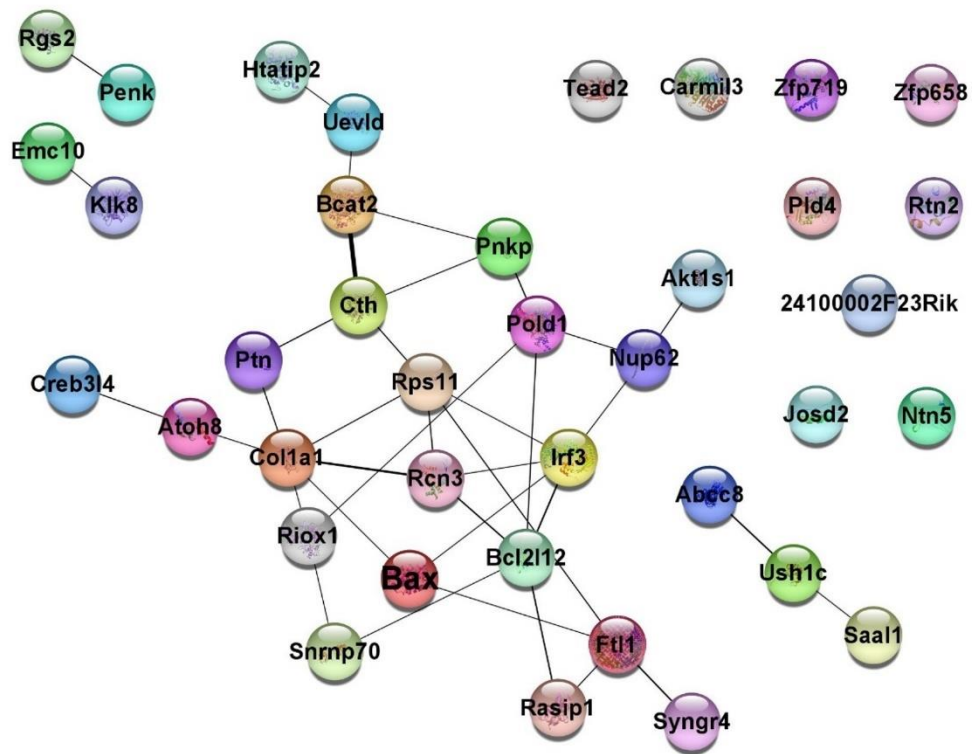


Supplemental Figure 5. Heat map showing differentially expressed genes in individual *Bax*^{+/+} and *Bax*^{-/-} embryos. Red-shaded boxes indicate greater expression, while blue-shaded boxes indicate lower expression. Note that *Bax_KO_rep4* (left-most KO column) had an expression pattern of certain genes that were expressed more like the *Bax*^{+/+} embryos (*Bax_WT*) than the other *Bax*^{-/-} embryos

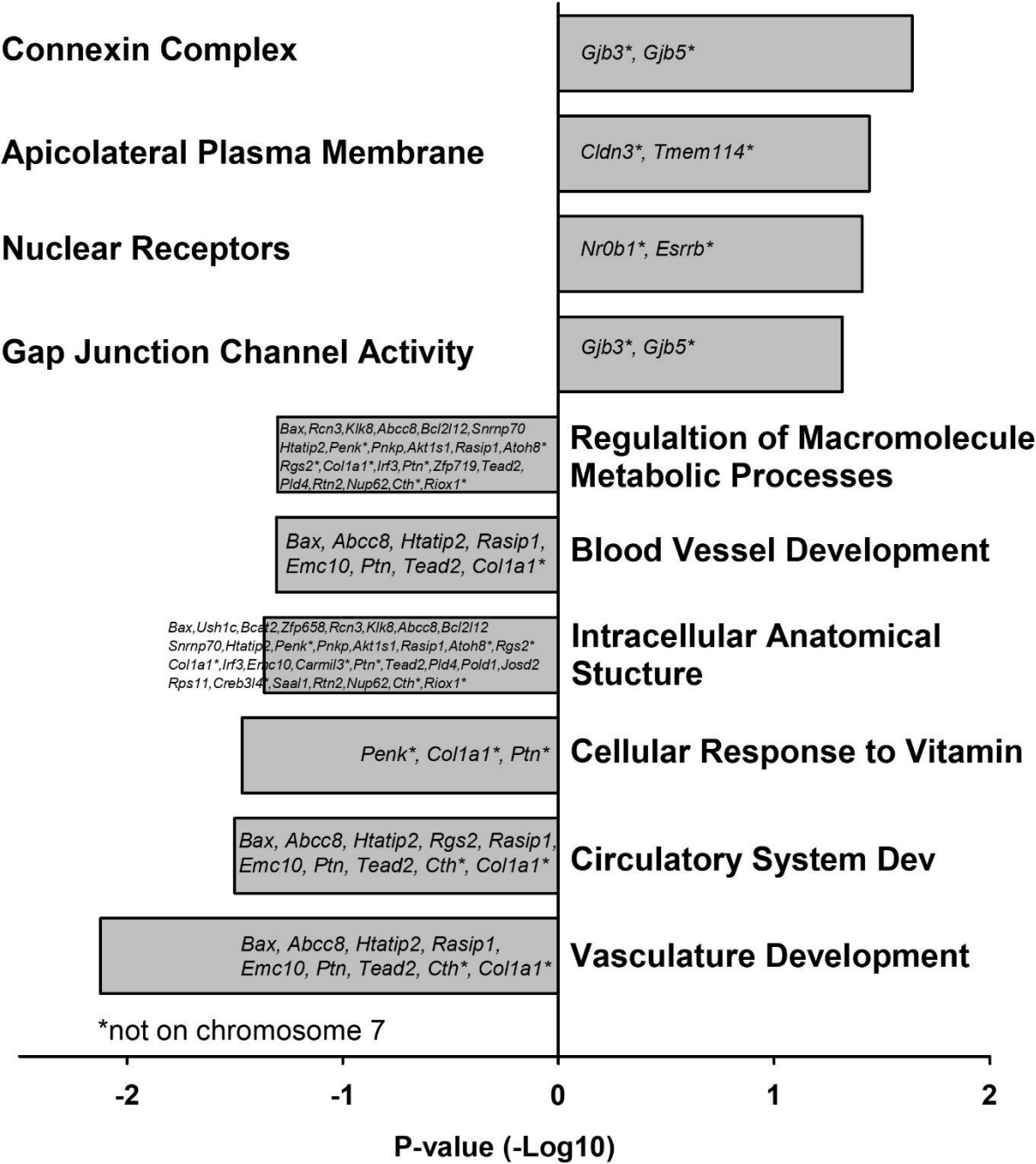
A Gene Expression Up-Regulated in *Bax*^{-/-} Embryos



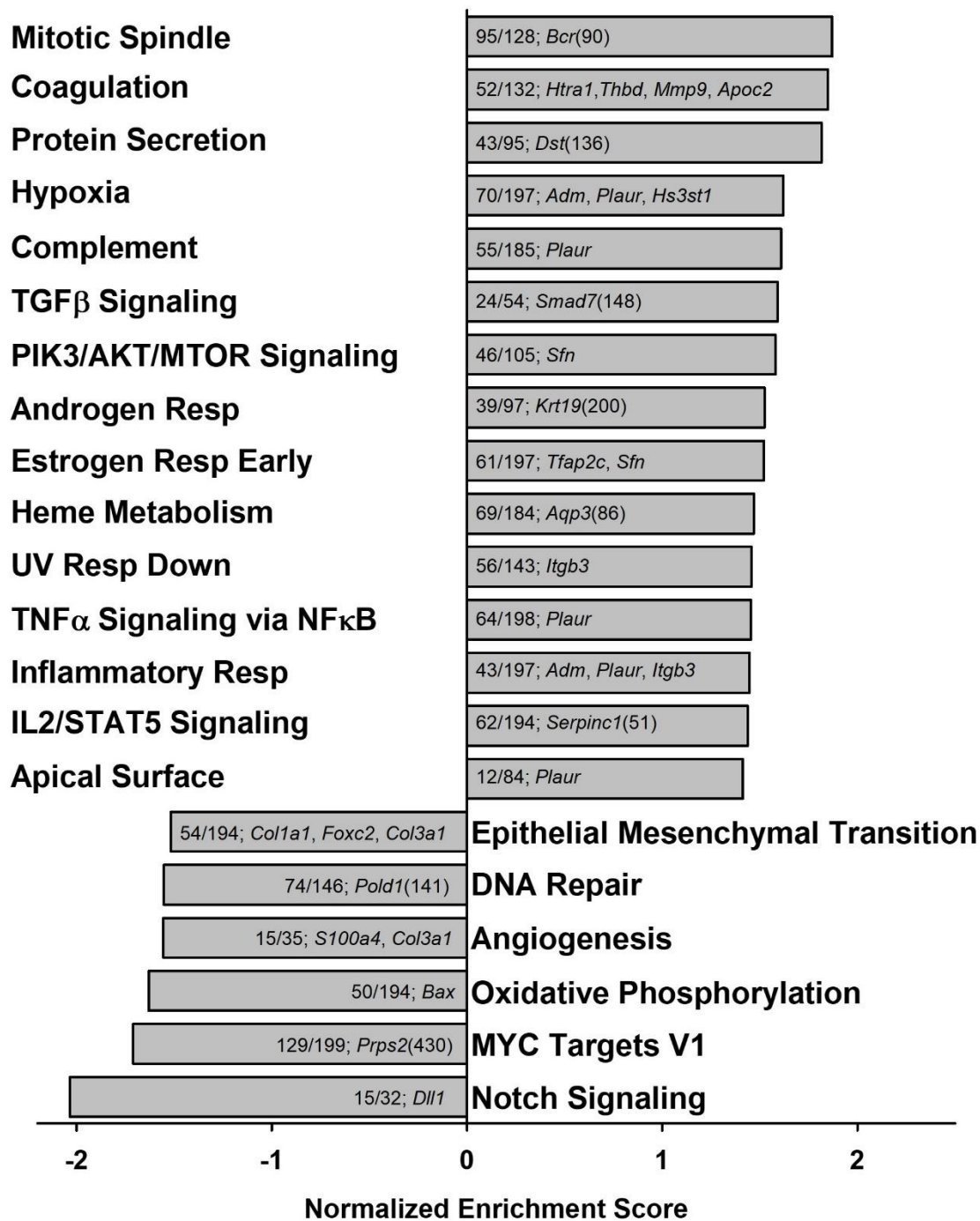
B Gene Expression Down-Regulated in *Bax*^{-/-} Embryos



Supplemental Figure 6. Cytoscape-generated gene network map between differentially expressed genes that are up-regulated and down-regulated in untreated *Bax*^{-/-} vs. *Bax*^{+/+} embryos. Line thickness denotes relative strength of associations between genes.



Supplemental Figure 7. g:profiler analysis of significantly dysregulated pathways in *Bax*^{-/-} vs *Bax*^{+/+} embryos. Differentially expressed genes within each pathway are inset in each bar. * indicates genes that are not located on chromosome 7.



Supplemental Figure 8. Dysregulated pathways in *Bax*^{-/-} vs. *Bax*^{+/+} embryos following GSEA Hallmarks analysis. *Inset text* indicates number of genes with core-enrichment/total genes in gene set, and the top ranked enriched genes. Genes are ranked in the top 50, unless otherwise noted in parentheses.

Table S1. Differentially Expressed Genes that are Up-regulated in *Bax*^{-/-} vs *Bax*^{+/+} Embryos

Gene	Protein	Chrom.	Function	Log2 Fold Change	Adj p-value
<i>Gm15545</i>	Predicted gene 15545	7	– Unknown	2.3	5.2x10 ⁻⁵⁷
<i>Itgb4</i>	Integrin beta 4	11	– Forms heterodimer with Itga6. – Laminin receptor, binds NRG1, IGF1, IGF2. – Important for cell adhesion and migration. – Role in cancer, epidermolysis bullosa, trophoblast invasion, anti-inflammatory effects in lung	1.1	9.3x10 ⁻⁹
<i>Nr0b1 (Dax1)</i>	Nuclear receptor subfamily 0, group B, member 1	X	– Interacts with Esrrb. – Limits embryonic stem cell pluripotency. – Suppresses testes development, promotes ovary development	0.79	1.2x10 ⁻⁴
<i>Gjb3</i>	Gap junction beta 3 (Connexin 31)	4	– Formation of gap junctions. – Critical embryonic role. Expressed in trophoblasts.	0.75	0.001
<i>Plaur</i>	Urokinase plasminogen activator surface receptor	7	– Role in vascular development, cancer, inflammation, extracellular matrix degradation. – Stimulates proliferation and inhibits apoptosis.	0.75	2.8x10 ⁻⁴
<i>Rinl</i>	Ras and Rab interactor-like protein	7	– Endocytosis	0.73	0.001
<i>Sycp3</i>	Synaptonemal complex protein 3	10	– Formation of synaptonemal complex during meiosis. – Expressed in cancer cells and may induce homologous recombination defect.	0.69	0.006
<i>Gjb5</i>	Gap junction beta 5 (Connexin 31.1)	4	– Formation of gap junctions. – Critical embryonic role. – Expressed in trophoblasts. – Affects pluripotency	0.66	0.005
<i>Nlr1</i>	NOD-like receptor family X1	9	– Role in inflammation. – Down-regulated in cancer. – Found in placenta	0.66	0.007
<i>Cldn3</i>	Claudin-3	5	– Formation of tight junctions. – Critical for neural tube closure. Role in cancer.	0.65	0.014
<i>Bmp8b</i>	Bone morphogenic protein 8b	4	– Important for osteogenesis, primordial germ cells, and	0.64	0.004

			metabolism through brown adipose tissue. – Role in liver disease		
<i>Tmem114</i>	Transmembrane protein 114	16	– Important for eye development. – Down-regulation can cause microphthalmia. – Upregulated in cataracts	0.64	0.004
<i>Inpp1</i>	Inositol polyphosphate 1-phosphatase	1	– Hyperactive in certain cancers. – Gene variants associated with psychiatric disease and lithium responses.	0.62	0.006
<i>Esrrb</i>	Estrogen-related receptor 2	12	– Transcription factor affecting embryonic and trophoblast cells through FGF and Wnt signaling. – Involved in pluripotency and expressed in primordial germ cells. – Promotes oxidative phosphorylation. – Interacts with Nr0b1.	0.59	8.6x10 ⁻⁴
<i>Tmem181b-ps</i>	Predicted gene	?	– Unknown	0.58	0.003
<i>Ddah1</i>	N(g),N(g)-dimethylarginine dimethylaminohydrolase 1	3	– Hydrolyzes ADMA and MMA which are inhibitors of NOS. – Critical for embryonic development. – May protect against apoptosis, can upregulate Bcl-2	0.57	0.014
<i>Dbp</i>	D site-binding protein-transcriptional activator	7	– Modulator of clock output genes. – Under circadian control in placenta, but unknown embryonic role	0.57	0.014
<i>Rusc2</i>	Iporin	4	– Interacts with Rab1, Rab 35, GM130, EGFR. – May inhibit Shh signaling	0.56	0.035
<i>Itga7</i>	Integrin alpha-7	10	– Laminin receptor. – Important for cell adhesion, vascular development	0.52	0.032
<i>Nosip</i>	Nitric oxide synthase-interacting protein	7	– Negative regulator of nitric oxide. – Modulates PP2a and may protect against eye defects, holoprosencephaly, midline facial defects.	0.52	3.4x10 ⁻⁸
<i>Glyctk</i>	Glycerate kinase	9	– Deficiency in humans causes d-glyceric aciduria, which has range of effects.	0.51	0.006
<i>Bcr</i>	Breakpoint cluster region protein	10	– Oncoprotein.	0.51	0.032

			<ul style="list-style-type: none"> - Activated by tyrosine kinase. - Can activate NFkB. Modulates GTP-binding proteins, RAC1, RAC2, CDC42. - Fusion with ABL causes forms of leukemia. - Inhibition of apoptosis? 		
<i>Rab11fip3</i>	Rab11 family-interacting protein 3	17	- Involved in endocytic traffic	0.45	0.027
<i>Tmem181c-ps</i>	Transmembrane protein 181c-pseudogene	17	- Unknown	0.40	0.047

Table S2. Differentially Expressed Genes that are Down-Regulated in *Bax*^{-/-} vs *Bax*^{+/+} Embryos

Gene	Protein	Chrom.	Function	Log2 Fold Change	Adj <i>p</i> -value
<i>Riox1</i>	Ribosomal oxygenase 1. Nucleolar protein 66.	12	<ul style="list-style-type: none"> - Histone lysine demethylase and ribosomal histidine hydroxylase. - Osteoblast differentiation, ribosome biogenesis. - Role in cancer via anti-apoptotic, proliferative effect. - Important for sensitivity to alcohol (<i>Drosophila</i>). 	-0.29	0.022
<i>Cth</i>	Cystathione gamma-lyase	3	<ul style="list-style-type: none"> - Catalyzing methionine to cysteine. - Crucial for protection from reactive oxygen species. - Regulated by PI3K/AKT pathway 	-0.32	0.022
<i>Nup62</i>	Nucleoporin 62	7	<ul style="list-style-type: none"> - Protein recruitment to centrosome after nuclear breakdown. - Role in autophagy 	-0.33	0.034
<i>Rtn2</i>	Reticulon-2	7	<ul style="list-style-type: none"> - Inhibits amyloid precursor protein processing. - Traffics intracellular membranes to cell membrane. - Lipid metabolism. - Formation of ER 	-0.37	0.027
<i>Saal1</i>	Serum amyloid A-like 1	7	<ul style="list-style-type: none"> - Enhances proliferation. - Possible role in arthritis and cancer 	-0.42	4.4x10 ⁻⁴
<i>Creb3l4</i>	Cyclic AMP-response element binding protein 3-like protein 4	3	<ul style="list-style-type: none"> - Upregulated in cancers. - Associated with reduced apoptosis. - May affect male germ cell development. 	-0.47	0.035
<i>Rps11</i>	40s ribosomal protein s11	7	<ul style="list-style-type: none"> - Protects against apoptosis in certain cancers. - Higher expression predicts worse outcomes in glioblastoma. 	-0.47	0.003
<i>Josd2</i>	Josephin-2	7	<ul style="list-style-type: none"> - Deubiquitinating enzyme. Positive regulator of cancer cell proliferation 	-0.48	0.003
<i>Pold1</i>	DNA polymerase delta catalytic subunit	7	<ul style="list-style-type: none"> - High fidelity genome replication. - Mutated in cancers. 	-0.49	3.2x10 ⁻⁵

			<ul style="list-style-type: none"> – Role in embryonic development. – May inhibit apoptosis 		
<i>Pld4</i>	5'-3' exonuclease PLD4.	12	<ul style="list-style-type: none"> – Regulates inflammatory cytokine responses 	-0.51	0.041
<i>Tead2</i>	Transcriptional enhancer factor TEF-4	7	<ul style="list-style-type: none"> – Hippo pathway. – Restricts proliferation and promotes apoptosis. – Embryonic role in neural tube closure 	-0.52	1.2x10 ⁻⁴
<i>Zfp719</i>	Zinc finger protein 719	7	<ul style="list-style-type: none"> – Unknown 	-0.55	0.010
<i>Ptn</i>	Pleiotrophin	6	<ul style="list-style-type: none"> – Growth factor involved in cell proliferation, survival, growth, and differentiation in neurons and bone. – Upregulated in cancer and by alcohol exposure 	-0.58	0.038
<i>Carmil3</i>	Capping protein, Arp2/3 and myosin-I linker protein 3.	14	<ul style="list-style-type: none"> – Role in tumor migration, cell adhesions, epithelia-mesenchymal transition. – Regulates proinflammatory cytokines associated with apoptosis 	-0.59	0.028
<i>Emc10</i>	ER membrane protein complex subunit 10.	7	<ul style="list-style-type: none"> – Incorporation of proteins into ER membrane. – Angiogenesis. 	-0.60	7.7x10 ⁻¹¹
<i>Irf3</i>	Interferon regulatory factor 3	7	<ul style="list-style-type: none"> – Innate immune responses. – Regulates transcription of IFN-α and IFN-β. – Important for alcoholic liver disease. – Associates with BAX to affect apoptosis. 	-0.60	6.1x10 ⁻⁷
<i>Colla1</i>	Collagen alpha-1(1) chain	11	<ul style="list-style-type: none"> – Role in osteogenesis, fibrogenesis, cancer, extracellular matrix accumulation in glaucoma, extraembryonic membrane rupture. – Linked to mandibular prognathism 	-0.62	0.032
<i>Rgs2</i>	Regulator of G-protein signaling 2	1	<ul style="list-style-type: none"> – Inhibits signal transduction. – Loss of Rgs2 impairs neural crest development. – Increased by ischemic stress to enhance apoptosis 	-0.62	0.025
<i>Ntn5</i>	Netrin-5	7	<ul style="list-style-type: none"> – Neurogenesis 	-0.66	0.006

<i>Syngn4</i>	Synaptogyrin-4	7	– Increased levels associated with ALS.	-0.66	4.2x10 ⁻⁴
<i>Atoh8 (Math6)</i>	Atonal homolog 8	6	– Key embryonic role in somitogenesis, neural crest, bone development, placentation, mesenchymal-epithelial transition. – Tumor suppressor in cancer	-0.69	0.006
<i>Rasip1</i>	Ras-interacting protein 1	7	– Angiogenesis, cell adhesion, endothelial cell morphogenesis	-0.71	1.2x10 ⁻⁴
<i>Akt1s1</i>	Proline-rich AKT1 substrate 1 (Pras)	7	– Subunit of mTORC1. – Augments activation of PI3K/AKT. – Inhibits apoptosis	-0.71	9.5x10 ⁻⁷
<i>Pnkp</i>	Bifunctional polynucleotide phosphatase/kinase	7	– Repair of DNA damage. – Appears to inhibit apoptosis. – Inhibitors sensitize cells to chemotherapies. – Knockdown causes microcephaly	-0.72	3.2x10 ⁻²¹
<i>Penk</i>	Preproenkephalin. Proenkephalin-A	4	– Precursor to Met- and Leu-enkephalin. – Involved in apoptosis, associated with Huntington's disease. – Hypermethylated in pancreatic cancer. – Tumor suppressor gene.	-0.72	3.1x10 ⁻⁵
<i>Htatip2</i>	Oxioductase HTATIP2. Also, Tip30/CC3	7	– Redox sensor required for tumor suppression. – Role in cancer and HIV. – Overexpression also upregulates p27, Bax, p53, caspase 3/9, downregulates cyclin D1, Bcl-2, Bcl-xL.	-0.73	0.002
<i>Snrnp70</i>	U1 small nuclear ribonucleoprotein 70kDa.	7	– Spliceosome, removes introns from pre-mRNA	-0.75	4.0x10 ⁻⁸
<i>Bcl2l12</i>	BCL2-like 12	7	– Inhibits apoptosis by dimerizing with Bax, inhibiting Tp53	-0.84	2.2x10 ⁻¹⁰
<i>Abcc8 (Sur1)</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	7	– Important for K ⁺ channels. – Mutated in diabetes, monogenic cause of neonatal diabetes	-0.85	2.8x10 ⁻⁵
<i>Klk8</i>	Kallikrein-8, Neuropsin	7	– Serine protease cleaves casein, fibrinogen, kininogen, fibronectin,	-0.93	2.7x10 ⁻⁹

			collagen type 4, L1CAM (linked to fetal alcohol syndrome). – May be oncogenic		
<i>2410002F23Rik</i>	?	7	– Unknown	-0.98	3.0×10^{-25}
<i>Rcn3</i>	Reticulocalbin-3	7	– Molecular chaperone, biosynthesis and transport in ER. – Regulates collagen fibrillogenesis	-0.98	1.8×10^{-20}
<i>Zfp658</i>	Zinc finger protein 658	7	– Unknown	-1.1	4.0×10^{-9}
<i>Bcat2</i>	Branched chain aminotransferase, mitochondrial	7	– Associated with diabetes and nutrient signaling.	-1.8	2.0×10^{-59}
<i>Ftl1</i>	Ferritin light chain 1	7	– Iron storage and delivery. – Role in ferroptosis.	-1.3	4.9×10^{-23}
<i>Ush1c</i>	Harmonin	7	– Anchoring/scaffolding protein. – Important in cochlear hair cells and brush border differentiation. – Mutated in Usher syndrome	-1.6	3.3×10^{-20}
<i>0610005C13Rik</i>	?	7	– Unknown	-1.7	2.5×10^{-22}
<i>Uevld</i>	Ubiquitin-conjugating enzyme E2 variant 3	7	– Negative regulator of polyubiquitination	-2.2	2.0×10^{-38}
<i>Bax (Bcl-2l4)</i>	Bcl-2-associated X protein	7	– Activates apoptosis	-4.3	4.7×10^{-183}

Supplemental Table S3. Gene Ontology (GSEA) Sets Positively Enriched in *Bax*^{-/-} Embryos vs *Bax*^{+/+} Embryos

Gene Set	Enriched/ Total Genes	Normalized Enrichment Score	Adj <i>p</i> -value	High-Ranked Genes (rank- metric ≥ 0.1)
<i>Gene Sets Related to Placental Development</i>				
Placenta development*	35/133	2.0	0.017	<i>Wnt7a, Adm,</i>
Cell differentiation in embryonic placental development*	9/23	1.9	0.036	<i>Htra1, Gjb3, Gjb5, Plac1,</i>
Embryonic placenta development*	24/78	2.1	0.009	<i>Etv2, Igf2, Tfeb, Gata2, Fosl1, Ascl2, Hand1</i>
<i>Gene Sets Related to Apoptosis</i>				
Negative regulation of endothelial cell apoptotic process*	11/32	2.0	0.012	<i>Gata2, Cdh5, Fga</i>
Negative regulation of epithelial cell apoptotic process*	17/48	1.9	0.032	
Endothelial cell apoptotic process	17/59	1.9	0.037	<i>Gata2, Faslg, Cdh5, Fga</i>
<i>Gene Sets Related to Coagulation</i>				
Regulation of coagulation*	23/70	2.0	0.013	<i>Plaur, Thbd,</i>
Negative regulation of coagulation*	16/53	2.0	0.014	<i>Procr, Serpinc1,</i>
Fibrinolysis*	9/25	1.9	0.028	<i>Ubash3b, Fga</i>
<i>Gene Sets Related to Membranes and Permeability</i>				
Establishment of endothelial barrier	21/48	1.9	0.035	<i>Wnt7a, Cldn3, Cdh5, Pecam1</i>
Regulation of vascular permeability	25/41	1.8	0.044	<i>Adm, Nppb, Ddah1, Cdh5</i>
Vacuolar membrane	126/390	1.9	0.034	<i>Thbd, Tfeb, Mreg, Myo6, C3ar1, Dram1</i>
Brush border membrane	23/59	1.9	0.031	<i>Pdzk1</i>
Microvillus membrane	13/24	1.8	0.043	<i>Itgb3, Slc7a8, Pdzk1</i>
Sulfur compound transport	23/49	1.8	0.049	<i>Slc13a3, Slc44a4</i>
Sulfur compound transmembrane transporter activity	24/47	1.9	0.031	<i>Slc13a3, Slc44a4, Abcc6</i>
<i>Genes Sets Related to Gene Expression or Replication</i>				
DNA methylation involved in gamete generation*	11/19	1.9	0.020	<i>Dnmt3l, Pw1l2,</i>
DNA methylation or demethylation*	34/88	1.9	0.045	<i>Mov10l1</i>
Regulation of gene expression by genetic imprinting	5/15	1.9	0.034	<i>Igf2, Dnmt3l</i>
Regulation of translation, NCRNA-mediated	12/67	2.3	0.002	
Mitotic spindle pole	14/33	1.8	0.044	

Gene Sets Related to Receptor Binding and Channel Activity

Quaternary ammonium group binding	15/29	1.9	0.036	<i>Apoa2, 4, 5, Pltp</i>
Phosphatidylinositol phosphate phosphatase activity*	16/31	1.8	0.043	
Phosphatidylinositol dephosphorylation*	14/29	1.9	0.025	
Negative regulation of receptor-mediated endocytosis	12/33	1.9	0.023	<i>Itgb3, Apoc2</i>
Receptor serine threonine kinase binding	5/25	1.8	0.042	<i>Bmp4, Bmp8b, Cdh5</i>
Calcium release channel activity	10/17	1.8	0.042	<i>Mcoln2</i>

Gene Sets Related to Cellular Organelles

Microtubule end	13/32	1.9	0.033	
Actin filament depolymerization	23/55	1.8	0.043	
Negative regulation of actin filament bundle assembly	18/33	2.0	0.017	<i>Tacstd2</i>

Gene Sets Related to Other Processes

Negative regulation of kidney development	6/17	1.9	0.044	<i>BMP4, MMP9, Tacstd2, Hnf1b</i>
Positive regulation of vascular-associated smooth muscle cell migration	10/21	1.9	0.035	
Keratinocyte migration	6/18	1.9	0.036	<i>Mmp9</i>
Hydrogen peroxide biosynthetic process	4/15	1.8	0.042	<i>Duoxa2, Duox2</i>
Positive regulation of ROS biosynthetic process	11/50	1.9	0.035	<i>Duoxa2, H19, Ddah1</i>
Regulation of hormone metabolic process	6/32	1.9	0.038	<i>Duox2, Adm,</i>
Regulation of urine volume	5/20	1.8	0.042	<i>Adm, Nppb</i>
Response to thyroid hormone*	14/22	2.0	0.017	
Response to acidic pH	11/23	1.8	0.044	
Lipase inhibitor activity	7/17	1.9	0.040	<i>Apoc2, Apoa2</i>

*Indicates significant clustering of adjacent gene sets

Supplemental Table S4. Gene Ontology (GSEA) Sets Negatively Enriched in *Bax*^{-/-} Embryos vs *Bax*^{+/+} Embryos

Gene Set	Enriched/ Total Genes	Normalized Enrichment Score	Adj p-value	High-Ranked Genes (rank- metric ≥ 0.1)
<i>Gene Sets Related Apoptosis</i>				
Apoptotic process involved in development*	12/35	-2.3	0.008	<i>Bax, Cryab, Foxc2,</i>
Apoptotic process involved in morphogenesis*	9/23	-2.3	0.013	<i>Hand2, Fgf4</i>
HSP70 protein binding	5/39	-2.2	0.017	<i>Bax</i>
Response to salt stress	3/23	-2.2	0.033	<i>Bax</i>
<i>Gene Sets Related to Cellular Organelles</i>				
Regulation of ER unfolded protein response	3/28	-2.1	0.033	<i>Bax</i>
ER calcium ion homeostasis	2/25	-2.1	0.046	<i>Bax</i>
Mitochondrial fusion	2/28	-2.2	0.025	<i>Bax</i>
<i>Gene Sets Related to Development</i>				
Somite development*	31/83	-2.2	0.020	<i>Foxc2, Pcdh8,</i>
Somitogenesis*	21/64	-2.3	0.009	<i>Dll1, Wnt3a,</i> <i>Aldh1a2, Mesp2,</i> <i>Tbx6, Hes7</i>
Ovarian follicle development	17/52	-2.2	0.021	<i>Bax</i>
<i>Gene Sets Related to Remodeling</i>				
Blood vessel remodeling	12/43	-2.1	0.049	<i>Bax, Foxc2, Bgn</i>

*Indicates significant clustering of adjacent gene sets