Table S3. Process gene ontologies with significant enrichment in the gene sets with differential methylation.

		Corrected p-value		
GOID	TERM	ETBF epithelium	Mock tumor	ETBF tumors
GO:0048568	embryonic organ development			7.69E-11
GO:0048562	embryonic organ morphogenesis			2.13E-10
GO:0048598	embryonic morphogenesis			3.44E-09
GO:0030851	granulocyte differentiation		1.35E-04	1.24E-08
GO:0048513	animal organ development		1.80E-04	1.63E-08
GO:1903707	negative regulation of hemopoiesis		2.04E-04	1.83E-08
GO:0009888	tissue development		2.74E-04	2.88E-08
GO:0045646	regulation of erythrocyte differentiation		2.93E-04	4.51E-08
GO:0048731	system development		7.76E-05	4.71E-08
GO:0032774	RNA biosynthetic process		3.86E-04	5.86E-08
GO:0006355	regulation of transcription, DNA-templated		1.22E-03	2.24E-07
GO:1903506	regulation of nucleic acid-templated transcription		2.01E-03	5.99E-07
GO:0051252	regulation of RNA metabolic process		2.17E-03	6.43E-07
GO:2001141	regulation of RNA biosynthetic process		1.30E-04	1.13E-06
GO:0048534	hematopoietic or lymphoid organ development			1.21E-06
GO:0009887	animal organ morphogenesis		6.62E-03	3.03E-06
GO:0006351	transcription, DNA-templated			3.40E-06
GO:0002682	regulation of immune system process			4.25E-06
GO:0097659	nucleic acid-templated transcription		7.35E-04	4.93E-06
GO:0042471	ear morphogenesis			6.89E-06
GO:0007275	multicellular organism development		8.03E-04	7.55E-06
GO:0048469	cell maturation		7.81E-05	8.53E-06
GO:0030097	hemopoiesis			8.71E-06
GO:0002520	immune system development			9.47E-06
GO:1903706	regulation of hemopoiesis			9.49E-06
GO:0042127	regulation of cell proliferation			1.38E-05
GO:2000112	regulation of cellular macromolecule biosynthetic process		4.98E-04	1.72E-05
GO:0044707	single-multicellular organism process		1.18E-03	2.05E-05
GO:0048856	anatomical structure development		1.89E-06	3.35E-05
GO:0030099	myeloid cell differentiation		1.73E-03	3.85E-05
GO:0044767	single-organism developmental process		7.74E-05	3.93E-05
GO:0033599	regulation of mammary gland epithelial cell proliferation		2.76E-03	4.19E-05
GO:0042472	inner ear morphogenesis		2.22E-03	4.77E-05
GO:0048518	positive regulation of biological process		1.17E-04	4.91E-05
GO:0032502	developmental process			7.02E-05
GO:0002683	negative regulation of immune system process			1.03E-04
GO:0048522	positive regulation of cellular process			1.04E-04
GO:0032609	interferon-gamma production			1.29E-04
GO:0010556	regulation of macromolecule biosynthetic process			1.43E-04
GO:0034654	nucleobase-containing compound biosynthetic process		6.07E-05	1.71E-04
GO:0018130	heterocycle biosynthetic process			1.83E-04
GO:0019438	aromatic compound biosynthetic process			2.07E-04
GO:1901362	organic cyclic compound biosynthetic process			2.39E-04
GO:0048706	embryonic skeletal system development		2.31E-03	2.47E-04
GO:0001501	skeletal system development			3.56E-04
GO:0034645	cellular macromolecule biosynthetic process			3.91E-04
GO:0048704	embryonic skeletal system morphogenesis			4.51E-04
GO:0022008	neurogenesis			4.75E-04
GO:0007399	nervous system development	3.29E-03		4.97E-04
GO:0048468	cell development		1.85E-04	5.22E-04
GO:0010468	regulation of gene expression	7.06E-03	1.48E-03	5.47E-04
GO:0048699	generation of neurons			6.05E-04
GO:0051321	meiotic cell cycle			6.22E-04
GO:0048869	cellular developmental process			6.43E-04
GO:0016070	RNA metabolic process		1.02E-04	7.06E-04
GO:0009653	anatomical structure morphogenesis		1.65E-04	7.06E-04
GO:0030154	cell differentiation			7.51E-04
GO:1903046	meiotic cell cycle process			8.04E-04
GO:0007126	meiotic nuclear division		1.09E-04	8.05E-04
GO:0007129	synapsis		1.95E-03	8.13E-04
GO:0022414	reproductive process			1.22E-03
GO:0000003	reproduction			1.48E-03
GO:0009059	macromolecule biosynthetic process			1.55E-03
GO:0030182	neuron differentiation			1.67E-03
GO:0019219	regulation of nucleobase-containing compound metabolic process			1.72E-03

GO:0050808	synapse organization		1.78E-03
GO:0031326	regulation of cellular biosynthetic process		1.96E-03
GO:0007268	chemical synaptic transmission		1.96E-03
GO:0098916	anterograde trans-synaptic signaling		2.06E-03
GO:0099536	synaptic signaling		2.11E-03
GO:0099537	trans-synaptic signaling		2.15E-03
GO:0043009	chordate embryonic development		2.25E-03
GO:0090304	nucleic acid metabolic process	1.36E-06	2.48E-03
GO:0009792	embryo development ending in birth or egg hatching		2.56E-03
GO:0051171	regulation of nitrogen compound metabolic process		2.67E-03
GO:0034587	piRNA metabolic process		2.76E-03
GO:0009889	regulation of biosynthetic process		2.77E-03
GO:0016043	cellular component organization		2.83E-03
GO:0050804	modulation of synaptic transmission		2.98E-03
GO:0048666	neuron development		3.08E-03
GO:0044260	cellular macromolecule metabolic process		3.14E-03
GO:0045143	homologous chromosome segregation		4.16E-03
GO:0010467	gene expression		4.25E-03
GO:0044702	single organism reproductive process		4.34E-03
GO:0007127	meiosis I		4.38E-03
GO:0007267	cell-cell signaling		5.49E-03
GO:0000122	negative regulation of transcription from RNA polymerase II promoter		5.73E-03
GO:0003002	regionalization		6.40E-03
GO:0006357	regulation of transcription from RNA polymerase II promoter	1.35E-03	6.87E-03
GO:0006366	transcription from RNA polymerase II promoter		8.57E-03
GO:0007389	pattern specification process		8.79E-03
GO:0044249	cellular biosynthetic process	9.69E-07	
GO:0044271	cellular nitrogen compound biosynthetic process	1.82E-06	
GO:0045165	cell fate commitment	8.85E-06	
GO:0045595	regulation of cell differentiation	5.20E-05	
GO:0045596	negative regulation of cell differentiation	2.04E-04	
GO:0045892	negative regulation of transcription, DNA-templated	3.89E-04	
GO:0045893	positive regulation of transcription, DNA-templated	4.58E-04	
GO:0045934	negative regulation of nucleobase-containing compound metabolic process	4.74E-04	
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	4.87E-04	
GO:0048523	negative regulation of cellular process	5.27E-04	
GO:0048705	skeletal system morphogenesis	1.08E-03	
GO:0051093	negative regulation of developmental process	1.69E-03	
GO:0051216	cartilage development	1.69E-03	
GO:0051253	negative regulation of RNA metabolic process	1.69E-03	
GO:0051254	positive regulation of RNA metabolic process	1.69E-03	
GO:0060255	regulation of macromolecule metabolic process	2.48E-03	
GO:0060429	epithelium development	4.74E-03	
GO:0061448	connective tissue development	5.11E-03	
GO:0090596	sensory organ morphogenesis	5.45E-03	
GO:1901576	organic substance biosynthetic process	5.68E-03	
GO:1902679	negative regulation of RNA biosynthetic process	5.87E-03	
GO:1902680	positive regulation of RNA biosynthetic process	6.20E-03	
GO:1903507	negative regulation of nucleic acid-templated transcription	7.46E-03	
GO:1903508	positive regulation of nucleic acid-templated transcription	7.47E-03	
GO:2000113	negative regulation of cellular macromolecule biosynthetic process	8.84E-03	