Supplemental Information

Table S1. Select genes that are potentially responsive to EDCs (endocrine disrupting compound-responsive genes; EDCRGs) in *M. beryllina*

Gene	Gene Name	Specific Function	Source
17β-hsd	17-beta-hydroxysteroid dehydrogenase 14	Steroidogenesis	(DeCourten *et al.* in revision)
3β-hsd	3 beta-hydroxysteroid dehydrogenase delta 5--	Steroidogenesis	(DeCourten *et al.* in revision)
aad-a	alpha-aspartyl dipeptidase	Proteolysis	(Jeffries *et al.* 2015)
acad11	acyl- dehydrogenase family member 11	Metabolism; Fatty acid beta-oxidation	(Jeffries *et al.* 2015)
aimp1	aminoacyl trna synthase complex-interacting multifunctional protein 1-like	Inflammation	(Jeffries *et al.* 2015)
akt1	rac-beta serine threonine-protein kinase-like		(Frank *et al.* 2019)
alas1	5-aminolevulinate mitochondrial-like	Lipid metabolism	(Jeffries *et al.* 2015)
alox5ap	arachidonate 5-lipoxygenase-activating protein	Leukotriene synthesis	(Jeffries *et al.* 2015)
app1	protein app1-like	Cytoskeleton	(Jeffries *et al.* 2015)
arg	arginase- mitochondrial-like	Arginine metabolism associated with the urea cycle	(Jeffries *et al.* 2015)
ar	androgen receptor alpha	Hormone receptor	(DeCourten *et al.* in revision)
atnb233	sodium potassium-transporting atpase subunit beta-233	Osmoregulation	(Jeffries *et al.* 2015)
atp1a1	sodium potassium-transporting atpase alpha-1 subunit	Osmoregulation	(Jeffries *et al.* 2015)
atp1a1b	sodium potassium atpase alpha subunit	Osmoregulation	(Jeffries *et al.* 2015)
atp1A2	sodium potassium-transporting atpase subunit alpha-2-like	Osmoregulation	(Jeffries *et al.* 2015)
atp1a3	sodium potassium-transporting atpase subunit alpha-3-like	Osmoregulation	(Jeffries *et al.* 2015)
bccip	protein bccip homolog	May promote cell cycle arrest and DNA repair	(Jeffries *et al.* 2015)
bmf	bcl-2-modifying factor-like	Apoptosis	(Jeffries *et al.* 2015)
c1qtnf5	complement c1q tumor necrosis factor-related protein 5-like	Structural; Collagen	(Jeffries *et al.* 2015)
c4bpa	c4b-binding protein alpha chain precursor	Controls complement activation	(Jeffries *et al.* 2015)
calr	calreticulin precursor	Protein folding; Calcium binding	(Jeffries *et al.* 2015)
camkk	calcium calmodulin-dependent protein kinase kinase 1-like	Calcium signaling; Neurodevelopment	(Frank *et al.* 2019)
casp3	caspase-3 precursor	Activates apoptosis cascade	(Jeffries *et al.* 2015)
cbr1	carbonyl reductase	Prostaglandin synthesis	(Jeffries *et al.* 2015)
ccl28	c-c motif chemokine 28 precursor	Immune function; Cellular calcium regulation; Epithelial chemokine	(Jeffries *et al.* 2015)
chg	choriogenin l		
cnot6	ccr4-not transcription complex subunit 6-like	Transcription	(Jeffries *et al.* 2015)
coi	cytochrome c oxidase subunit mitochondrial-like	Metabolism	(Jeffries *et al.* 2015)
cops6	cop9 signalosome complex subunit 6	Proteosomal degradation; Regulator of the ubiquitin conjugation pathway	(Jeffries *et al.* 2015)
cp	ceruloplasmin precursor	Oxidative stress	(Jeffries *et al.* 2015)
creb	cyclic amp-dependent transcription factor atf-4-like	Calcium signaling; Neurodevelopment	(Frank *et al.* 2019)
cs056	upf0139 membrane protein c19orf56 homolog	unknown	(Jeffries *et al.* 2015)
cyba	cytochrome b-245 light chain-like	Oxidative stress; Component of membrane-bound oxidase of phagocytes that generates superoxide	(Jeffries *et al.* 2015)
cyp19b	brain aromatase	Steroid metabolism	(DeCourten *et al.* in revision)
cyp1a1	cytochrome p450 1a	Metabolism, cholesterol synthesis	(DeCourten *et al.* in revision)
cyt1l	type i enveloping like	Cytoskeleton	(Jeffries *et al.* 2015)
ddit3	dna damage-inducible transcript 3	Apoptosis; Response to endoplasmic reticulum stress	(Jeffries *et al.* 2015)
dmrt1	doublesex and mab-3-related transcription factor 3	Sex determination	
dnmt1	dna (cytosine-5)-methyltransferase 1-like	DNA Methylation	(DeCourten *et al.* in revision)
dnmt3a	dna (cytosine-5)-methyltransferase 3a-like	DNA Methylation	(DeCourten *et al.* in revision)
dnmt3b	dna (cytosine-5)-methyltransferase 3b-like	DNA Methylation	(DeCourten *et al.* in revision)

Table S1 Continued

Gene	Gene Name	Specific Function	Source
eef1d	elongation factor 1-delta	Translation	(JEFFRIES *et al.* 2015)
eif4e	eukaryotic translation initiation factor 4e	Calcium signaling; Neurodevelopment	(FRANK *et al.* 2019)
esr1	estrogen receptor alpha	Hormone receptor	(DECOURTEN *et al.* in revision)
esr2	estrogen receptor beta	Hormone receptor	(DECOURTEN *et al.* in revision)
esr3	estrogen receptor beta 2	Hormone receptor	(DECOURTEN *et al.* in revision)
fabp6	fatty acid-binding protein 6	Lipid metabolism	(JEFFRIES *et al.* 2015)
fau	ubiquitin-like protein fubi	Proteosomal degradation; Belongs to the ubiquitin family	(JEFFRIES *et al.* 2015)
fbxl18	f-box lrr-repeat protein 18-like	Proteosomal degradation; Component of ubiquitin ligase complex	(JEFFRIES *et al.* 2015)
fermt1	fermitin family homolog 1-like	Cell adhesion	(JEFFRIES *et al.* 2015)
fshr	follicle stimulating hormone receptor	Hormone receptor	
galectin-1	beta-galactoside-binding lectin-like	May regulate apoptosis, cell proliferation and cell differentiation	(JEFFRIES *et al.* 2015)
ghrb	growth hormone receptor 2	Hormone receptor	(DECOURTEN *et al.* in revision)
gimap4	gtpase imap family member 4-like	GTPase activity; Involved in immunity	(JEFFRIES *et al.* 2015)
gnrhr	gonadotropin-releasing hormone receptor 1	Hormone receptor	(DECOURTEN *et al.* in revision)
gpr30	g-protein coupled estrogen receptor 1-like	Hormone receptor	(DECOURTEN *et al.* in revision)
gr	glutathione reductase	Oxidative stress; Cell redox homeostasis	(JEFFRIES *et al.* 2015)
hpgd	15-hydroxyprostaglandin dehydrogenase	Prostaglandin synthesis	(JEFFRIES *et al.* 2015)
htra3	serine protease htra3-like	Proteolysis; Cleaves several extracellular matrix proteins	(JEFFRIES *et al.* 2015)
igf2	insulin-like growth factor ii	Growth factor	(DECOURTEN *et al.* in revision)
inha	inhibin alpha subunit		
krt13	type i cytoskeletal 13-like	Structural; Cytoskeleton	(JEFFRIES *et al.* 2015)
lta4h	leukotriene a-4 hydrolase	Leukotriene synthesis	(JEFFRIES *et al.* 2015)
mapk14	mitogen-activated protein kinase 11-like	Cell proliferation	(DECOURTEN *et al.* in revision)
mlst8	target of rapamycin complex subunit lst8-like		(FRANK *et al.* 2019)
mmp9	matrix metalloproteinase 9	Immune Function; Gelatinase	(JEFFRIES *et al.* 2015)
mtor	serine threonine-protein kinase mtor	Calcium signaling; Neurodevelopment	(FRANK *et al.* 2019)
nag1	glucosamine-6-phosphate isomerase	Carbohydrate metabolism	(JEFFRIES *et al.* 2015)
nccrp1	non-specific cytotoxic cell receptor protein 1 homolog	Promotes cell proliferation	(JEFFRIES *et al.* 2015)
noa1	nitric oxide-associated protein 1-like	Regulates mitochondrial protein translation	(JEFFRIES *et al.* 2015)
nr0b2	nuclear receptor subfamily 0 group b member 2	Transcription	(JEFFRIES *et al.* 2015)
pdlim1	pdz and lim domain protein 1	Cytoskeleton	(JEFFRIES *et al.* 2015)
phlda2	pleckstrin homology-like domain family a member 2-like	Binds phosphoinositides; Associated with cell membranes	(JEFFRIES *et al.* 2015)
plac8l1	plac8-like protein 1	unknown	(JEFFRIES *et al.* 2015)
ppdpf-b	pancreatic progenitor cell differentiation and proliferation factor b	Involved in cell differentiation	(JEFFRIES *et al.* 2015)
prr15la	proline-rich protein 15-like protein a-like	May have a role in cell proliferation or differentiation	(JEFFRIES *et al.* 2015)
psma7	proteasome subunit alpha type-7	Proteosomal degradation; Protein polyubiquination	(JEFFRIES *et al.* 2015)
psmc4	26s protease regulatory subunit 6b	Proteosomal degradation	(JEFFRIES *et al.* 2015)
ptges3	prostaglandin e synthase 3	Prostaglandin synthesis	(JEFFRIES *et al.* 2015)
ptgr1	prostaglandin reductase 1-like	Prostaglandin synthesis	(JEFFRIES *et al.* 2015)
ptgs1	prostaglandin g h synthase 1-like	Prostaglandin synthesis	(JEFFRIES *et al.* 2015)
ptgs2	prostaglandin g h synthase 2-like	Prostaglandin synthesis	(JEFFRIES *et al.* 2015)
rab21	ras-related protein rab-21-like	Protein transport; May regulate cell adhesion	(JEFFRIES *et al.* 2015)
rheb	gtp-binding protein rheb-like	GTP-ase activity	(FRANK *et al.* 2019)
rps13	40s ribosomal protein s13	Translation	(JEFFRIES *et al.* 2015)
Rps16	40s ribosomal protein s16	Translation	(JEFFRIES *et al.* 2015)
Rps6	40s ribosomal protein s6	Translation	(FRANK *et al.* 2019)
ryr1	ryanodine receptor 1-like	Calcium signaling; Neurodevelopment	(FRANK *et al.* 2019)

Table S1 Continued

Gene	Gene Name	Specific Function	Source
ryr2	ryanodine receptor 2-like	Calcium signaling; Neurodevelopment	(FRANK *et al.* 2019)
ryr3	ryanodine receptor 3-like	Calcium signaling; Neurodevelopment	(FRANK *et al.* 2019)
slc39a14	zinc transporter zip14-like	Preferentially binds to zinc	(JEFFRIES *et al.* 2015)
smpd3	sphingomyelin phosphodiesterase 3-like	Lipid metabolism; mediates many cellular processes	(JEFFRIES *et al.* 2015)
sod2	manganese superoxide dismutase	Mitochondrial superoxide response	(JEFFRIES *et al.* 2015)
star	steroidogenic acute regulatory protein		
stat1	signal transducer and activator of transcription 1	Immune function; Inflammation	(JEFFRIES *et al.* 2015)
stat2	signal transducer and activator of transcription 2	Inflammation	(JEFFRIES *et al.* 2015)
svep1	von willebrand factor type egf and pentraxin domain-containing protein 1-like	Cell adhesion	(JEFFRIES *et al.* 2015)
tbt-bp1	tributyltin binding protein type 1	Protein binding; Binds endogenous and exogenous compounds	(JEFFRIES *et al.* 2015)
tead3	transcriptional enhancer factor tef-5-like	Hippo signaling pathway	(JEFFRIES *et al.* 2015)
tgfb	transforming growth factor beta-1-like isoform 1	Growth factor, immune function	(FRANK *et al.* 2019)
tmed10	transmembrane emp24 domain-containing protein 10 precursor	Protein trafficking; Secretory pathway	(JEFFRIES *et al.* 2015)
tra	thyroid hormone receptor alpha	Hormone receptor	(DECOURTEN *et al.* in revision)
trb	thyroid hormone receptor beta	Hormone receptor	(DECOURTEN *et al.* in revision)
txnl4a	thioredoxin-like protein 4a	RNA processing and cell cycle	(JEFFRIES *et al.* 2015)
unc-89	muscle m-line assembly protein unc-89-like	Structural component of muscle	(JEFFRIES *et al.* 2015)
uqcrb	cytochrome b-c1 complex subunit 7	Metabolism	(JEFFRIES *et al.* 2015)
usp42	ubiquitin carboxyl-terminal hydrolase 42-like	Proteosomal degradation; Deubiquitinating enzyme	(JEFFRIES *et al.* 2015)
vtg	vitellogenin a	Egg yolk protein	(DECOURTEN *et al.* in revision)
ywhab	14-3-3 protein beta alpha-1-like	Regulates many signaling pathways	(JEFFRIES *et al.* 2015)

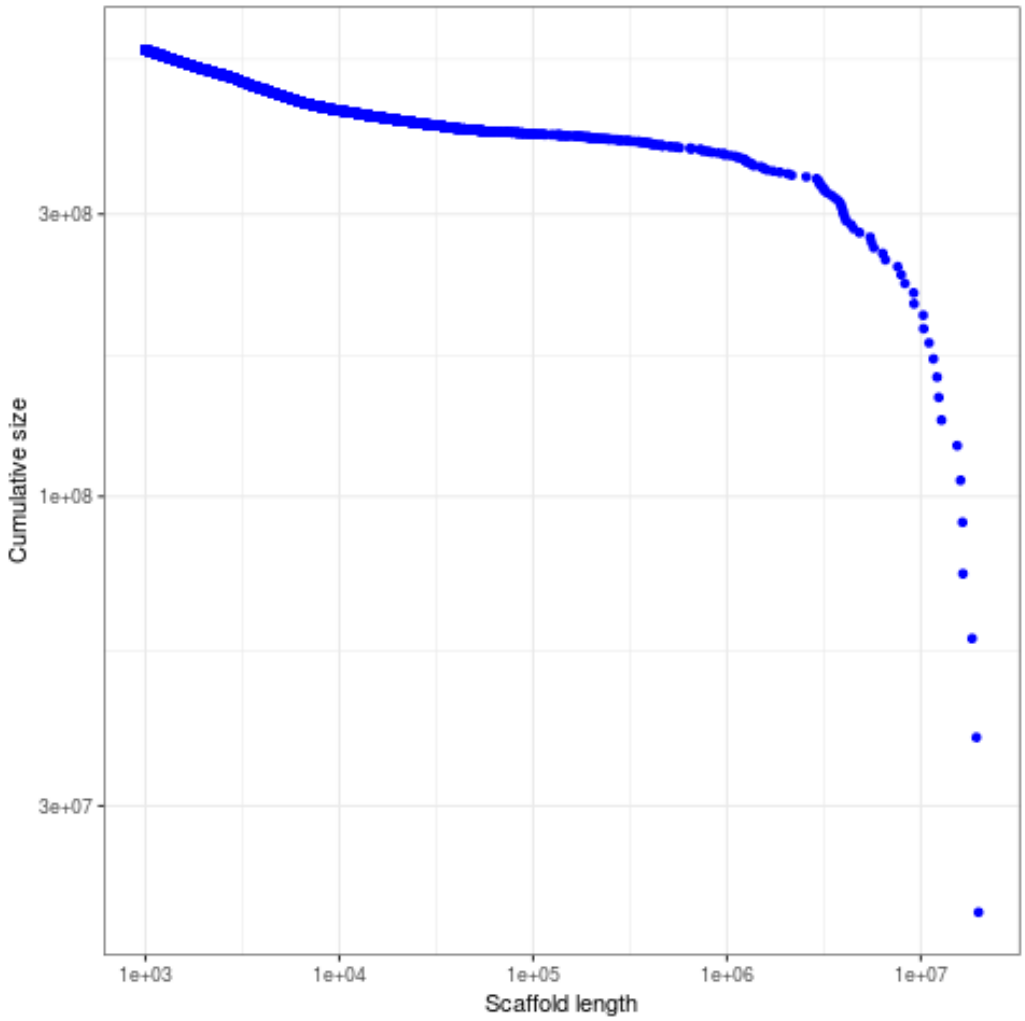

Figure S2. Distribution of scaffold length as a result of *M. beryllina* genome assembly.

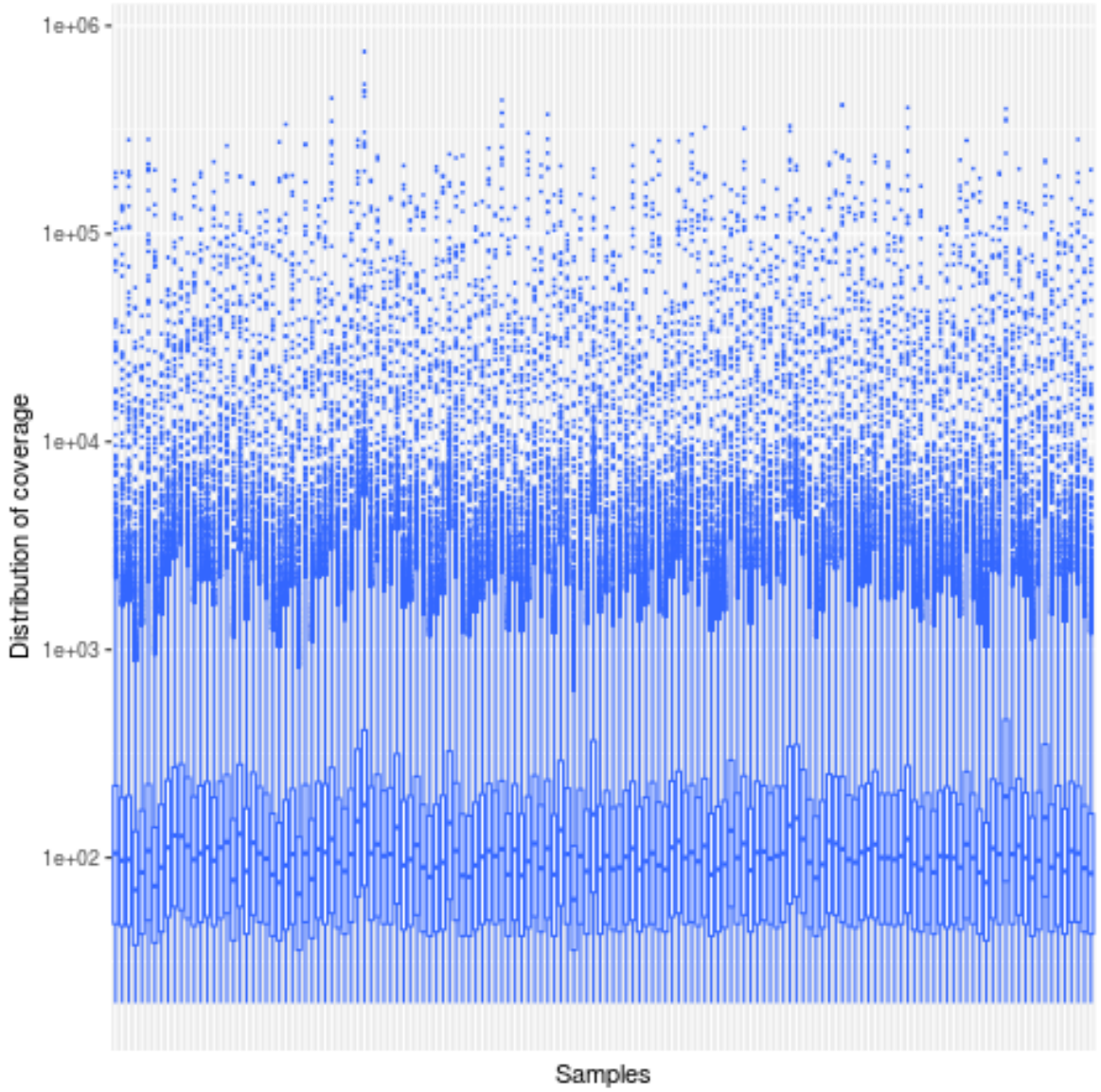

Figure S3. RRBS coverage by sample.

Table S4. Full listing of enriched Gene Ontology (GO) Terms (biological processes) for all treatments and generations, by gene region (promoter or gene body) and differential methylation state relative to the control (hyper, hypo). Values are Fisher's exact test p-values.

				Bif			EE2			Levo			Tren		
GO.ID	Term	Region	Hyper/Hypo	F0	F1	F2	F0	F1	F2	F0	F1	F2	F0	F1	F2
GO:0000122	negative regulation of transcription by ...	Gene body	Hyper											4.80E-04	
			Hypo									9.50E-03			
GO:0001502	cartilage condensation	Promoter	Hyper	5.00E-04											
			Hypo			1.04E-03								5.30E-04	
GO:0001570	vasculogenesis	Gene body	Hyper									3.20E-03			
GO:0001840	neural plate development	Gene body	Hypo						8.35E-03						
GO:0001946	lymphangiogenesis	Gene body	Hyper						6.59E-03						
GO:0001955	blood vessel maturation	Promoter	Hypo							6.00E-03					
GO:0002042	cell migration involved in sprouting ang...	Gene body	Hyper									4.00E-03			
GO:0002062	chondrocyte differentiation	Promoter	Hyper				8.13E-03						8.75E-03		
GO:0002063	chondrocyte development	Gene body	Hyper												7.00E-03
GO:0003007	heart morphogenesis	Promoter	Hyper		8.40E-03										
GO:0003157	endocardium development	Gene body	Hypo				8.80E-05								
GO:0006189	'de novo' IMP biosynthetic process	Gene body	Hypo			2.80E-03									
GO:0006275	regulation of DNA replication	Gene body	Hypo					9.60E-03							
GO:0006355	regulation of transcription, DNA-templat...	Promoter	Hypo									6.90E-03			
		Gene body	Hyper						9.34E-03						
GO:0006433	prolyl-tRNA aminoacylation	Gene body	Hyper							2.90E-03			3.00E-03		
			Hypo			8.20E-03									8.20E-03
GO:0006525	arginine metabolic process	Gene body	Hyper										7.80E-03		
GO:0006560	proline metabolic process	Gene body	Hypo												6.70E-03
GO:0006582	melanin metabolic process	Gene body	Hyper						7.04E-03						
GO:0006662	glycerol ether metabolic process	Promoter	Hyper	3.60E-03											2.30E-03
			Hypo		2.70E-03	7.41E-03	3.72E-03	4.00E-03			2.80E-03			3.84E-03	
GO:0006754	ATP biosynthetic process	Promoter	Hyper								4.20E-03				
GO:0006754		Gene body	Hypo				5.70E-03								
GO:0006777	Mo-molybdopterin cofactor biosynthetic p...	Gene body	Hypo				5.80E-03								
GO:0006851	mitochondrial calcium ion transmembrane ...	Gene body	Hyper								2.68E-03				
GO:0006888	ER to Golgi vesicle-mediated transport	Gene body	Hypo		5.50E-03										
GO:0006911	phagocytosis, engulfment	Promoter	Hyper											5.90E-03	
GO:0006955	immune response	Gene body	Hypo								6.30E-03				
GO:0006978	DNA damage response, signal transduction...	Gene body	Hyper							5.70E-03	5.30E-04			1.60E-04	
			Hypo	4.26E-03					7.10E-04						
GO:0007084	mitotic nuclear envelope reassembly	Gene body	Hypo			8.20E-03			9.40E-03					4.30E-03	
GO:0007156	homophilic cell adhesion via plasma memb...	Promoter	Hyper						3.20E-03						
		Gene body	Hyper					7.09E-03							
GO:0007199	G protein-coupled receptor signaling pat...	Gene body	Hyper											3.48E-03	
GO:0007229	integrin-mediated signaling pathway	Promoter	Hypo						8.10E-03						
GO:0007409	axonogenesis	Promoter	Hypo								9.60E-03				
GO:0008016	regulation of heart contraction	Promoter	Hyper		5.10E-03										
GO:0008045	motor neuron axon guidance	Promoter	Hypo												7.50E-03
GO:0008630	intrinsic apoptotic signaling pathway in...	Gene body	Hyper		7.10E-03					9.40E-03	1.28E-03			3.90E-04	
			Hypo	6.40E-04					3.20E-04			2.40E-03			
GO:0009186	deoxyribonucleoside diphosphate metaboli...	Gene body	Hypo			8.20E-03									
GO:0009206	purine ribonucleoside triphosphate biosy...	Gene body	Hyper		7.00E-04										
GO:0009411	response to UV	Gene body	Hyper								4.14E-03			1.28E-03	
			Hypo						3.20E-04						
GO:0009950	dorsal/ventral axis specification	Promoter	Hyper				7.21E-03			9.56E-03					
GO:0009952	anterior/posterior pattern specification	Promoter	Hypo											1.82E-03	
GO:0010165	response to X-ray	Gene body	Hyper							9.40E-03	1.28E-03			3.90E-04	
			Hypo	6.97E-03					1.70E-03						
GO:0010172	embryonic body morphogenesis	Promoter	Hyper	2.50E-05											
			Hypo			3.55E-03								1.83E-03	
		Gene body	Hyper								4.14E-03				
GO:0010212	response to ionizing radiation	Gene body	Hyper		9.30E-03										
GO:0010332	response to gamma radiation	Gene body	Hyper							2.90E-03	7.77E-03			3.48E-03	
			Hypo	2.17E-03			5.80E-03		9.40E-03			5.40E-03			8.20E-03
GO:0010923	negative regulation of phosphatase activ...	Promoter	Hypo											1.31E-03	

Table S4. Continued

				Bif			EE2			Levo			Tren		
GO.ID	Term	Region	Hyper/Hypo	F0	F1	F2	F0	F1	F2	F0	F1	F2	F0	F1	F2
GO:0014036	neural crest cell fate specification	Promoter	Hyper	2.90E-03											
			Hypo			5.98E-03								3.09E-03	
GO:0015672	monovalent inorganic cation transport	Promoter	Hyper								8.20E-03				
GO:0016339	calcium-dependent cell-cell adhesion via...	Gene body	Hyper			8.59E-03									
GO:0016573	histone acetylation	Promoter	Hyper	4.40E-03											
			Hypo			3.50E-04								4.67E-03	
GO:0016573	histone acetylation	Gene body	Hyper		3.60E-03										
GO:0016578	histone deubiquitination	Promoter	Hyper	5.00E-04							1.10E-03				
			Hypo												1.10E-03
GO:0017038	protein import	Gene body	Hyper					5.91E-03							
GO:0018279	protein N-linked glycosylation via aspar...	Promoter	Hypo											9.55E-03	
GO:0019674	NAD metabolic process	Gene body	Hyper	3.10E-03											
GO:0021514	ventral spinal cord interneuron differen...	Gene body	Hypo		3.50E-03							5.40E-03			
GO:0021517	ventral spinal cord development	Promoter	Hyper												7.40E-03
GO:0021548	pons development	Gene body	Hypo			4.50E-03									
GO:0021754	facial nucleus development	Gene body	Hypo		6.90E-03										
GO:0021756	striatum development	Gene body	Hyper						7.04E-03						3.60E-03
GO:0021797	forebrain anterior/posterior pattern spe...	Promoter	Hyper							1.27E-03					
GO:0021879	forebrain neuron differentiation	Promoter	Hyper				2.68E-03						6.83E-03		
GO:0021881	Wnt-activated signaling pathway involved...	Promoter	Hyper							8.50E-04					
			Hypo												1.80E-03
		Gene body	Hyper							9.40E-03					
GO:0030042	actin filament depolymerization	Promoter	Hypo											9.55E-03	
GO:0030111	regulation of Wnt signaling pathway	Gene body	Hyper							1.10E-03					
GO:0030178	negative regulation of Wnt signaling pat...	Promoter	Hypo											3.37E-03	
GO:0030183	B cell differentiation	Gene body	Hyper					6.00E-05			2.46E-03				
GO:0030901	midbrain development	Gene body	Hypo						1.86E-03						7.60E-03
GO:0031016	pancreas development	Promoter	Hypo						4.40E-03						
GO:0031101	fin regeneration	Promoter	Hyper				4.50E-04						5.20E-04		
GO:0031571	mitotic G1 DNA damage checkpoint	Gene body	Hyper							9.40E-03					
			Hypo	6.97E-03											
GO:0031581	hemidesmosome assembly	Gene body	Hypo							7.70E-04					
GO:0032012	regulation of ARF protein signal transdu...	Gene body	Hypo									3.80E-03			
GO:0032228	regulation of synaptic transmission, GAB...	Promoter	Hyper							9.39E-03					7.30E-03
GO:0032331	negative regulation of chondrocyte diffe...	Gene body	Hypo	2.17E-03											
GO:0032438	melanosome organization	Promoter	Hypo											9.55E-03	
GO:0033077	T cell differentiation in thymus	Promoter	Hyper					9.60E-03							
		Gene body	Hyper					2.60E-04							
GO:0033209	tumor necrosis factor-mediated signaling...	Promoter	Hyper									8.00E-03			
GO:0033334	fin morphogenesis	Gene body	Hyper												6.20E-03
GO:0033339	pectoral fin development	Gene body	Hyper												8.50E-03
GO:0033578	protein glycosylation in Golgi	Promoter	Hyper				8.12E-03					8.00E-03			
			Hypo					9.70E-03			8.10E-03				
GO:0034644	cellular response to UV	Gene body	Hyper							9.40E-03					
			Hypo	6.97E-03											
GO:0035089	establishment of apical/basal cell polar...	Gene body	Hyper										3.00E-03		
			Hypo												8.20E-03
GO:0035166	post-embryonic hemopoiesis	Gene body	Hypo								5.30E-03				
GO:0035249	synaptic transmission, glutamatergic	Promoter	Hypo								8.10E-03				
GO:0035329	hippo signaling	Promoter	Hypo				5.10E-04								
GO:0035567	non-canonical Wnt signaling pathway	Gene body	Hyper											2.27E-03	
GO:0036071	N-glycan fucosylation	Promoter	Hyper				8.12E-03					8.00E-03			
			Hypo					9.70E-03			8.10E-03				
GO:0042068	regulation of pteridine metabolic proces...	Promoter	Hypo								8.10E-03				
GO:0042073	intraciliary transport	Promoter	Hyper								6.10E-03				
GO:0042074	cell migration involved in gastrulation	Promoter	Hyper		5.70E-03										
GO:0042246	tissue regeneration	Promoter	Hyper							1.37E-03					
GO:0042542	response to hydrogen peroxide	Gene body	Hypo			8.20E-03			9.40E-03						
GO:0043066	negative regulation of apoptotic process	Gene body	Hypo			7.90E-03									
GO:0043114	regulation of vascular permeability	Promoter	Hyper					1.80E-03							

Table S4. Continued

GO.ID	Term	Region	Hyper/Hypo	Bif			EE2			Levo			Tren		
				F0	F1	F2	F0	F1	F2	F0	F1	F2	F0	F1	F2
GO:0043281	regulation of cysteine-type endopeptidas...	Gene body	Hyper											5.46E-03	
GO:0043488	regulation of mRNA stability	Gene body	Hypo						8.35E-03						
GO:0043508	negative regulation of JUN kinase activi...	Gene body	Hyper							2.90E-03					
			Hypo		3.50E-03						1.60E-03			4.30E-03	8.20E-03
GO:0043523	regulation of neuron apoptotic process	Gene body	Hyper								9.88E-03			2.31E-03	
GO:0043704	photoreceptor cell fate specification	Gene body	Hyper				4.60E-03						6.00E-03		7.00E-03
GO:0044333	Wnt signaling pathway involved in digest...	Gene body	Hyper										6.00E-03		
GO:0045603	positive regulation of endothelial cell ...	Gene body	Hyper									7.80E-03			
GO:0045813	positive regulation of Wnt signaling pat...	Promoter	Hyper											5.90E-03	
GO:0046103	inosine biosynthetic process	Promoter	Hypo							6.00E-03					
GO:0046548	retinal rod cell development	Gene body	Hyper				4.60E-03						6.00E-03		7.00E-03
GO:0046549	retinal cone cell development	Gene body	Hyper				7.50E-03						9.70E-03		
GO:0046578	regulation of Ras protein signal transdu...	Gene body	Hyper		9.30E-03										
GO:0048484	enteric nervous system development	Promoter	Hyper										8.75E-03		
GO:0048702	embryonic neurocranium morphogenesis	Gene body	Hypo				8.90E-05								8.20E-03
GO:0048741	skeletal muscle fiber development	Gene body	Hypo				6.10E-03								
GO:0048769	sarcomerogenesis	Promoter	Hyper		7.30E-03										
			Hypo			5.98E-03									
GO:0048854	brain morphogenesis	Gene body	Hypo										1.90E-03		
GO:0048884	neuromast development	Gene body	Hypo				9.70E-03								
GO:0048886	neuromast hair cell differentiation	Gene body	Hypo								5.30E-03				
GO:0048919	posterior lateral line neuromast develop...	Promoter	Hyper	7.10E-03						7.34E-03					
GO:0048923	posterior lateral line neuromast hair ce...	Gene body	Hyper	5.60E-03			4.60E-03								
GO:0050821	protein stabilization	Gene body	Hypo	6.97E-03									8.20E-03		
GO:0050847	progesterone receptor signaling pathway	Gene body	Hypo									1.90E-03			
GO:0050919	negative chemotaxis	Gene body	Hyper			1.60E-04			1.20E-04		7.77E-03				
			Hypo			8.20E-03	5.80E-03	6.90E-05				5.40E-03	2.60E-03		8.20E-03
GO:0051046	regulation of secretion	Gene body	Hyper						2.86E-03						
GO:0051056	regulation of small GTPase mediated sign...	Gene body	Hypo	5.98E-03									8.90E-03		
GO:0051262	protein tetramerization	Gene body	Hyper								7.30E-04			1.50E-04	
			Hypo						1.05E-03						
GO:0055114	oxidation-reduction process	Promoter	Hypo							5.80E-03					
GO:0060017	parathyroid gland development	Gene body	Hypo					9.60E-03			3.20E-03				
GO:0060028	convergent extension involved in axis el...	Promoter	Hypo									8.70E-03			
GO:0060042	retina morphogenesis in camera-type eye	Promoter	Hyper			8.30E-03									
GO:0060047	heart contraction	Gene body	Hyper				1.40E-03								
GO:0060055	angiogenesis involved in wound healing	Promoter	Hypo				9.39E-03								
GO:0060214	endocardium formation	Gene body	Hyper									7.80E-03			
GO:0060216	definitive hemopoiesis	Gene body	Hyper								1.78E-03			2.89E-03	
			Hypo				7.30E-03		2.73E-03						
GO:0060319	primitive erythrocyte differentiation	Gene body	Hypo						3.26E-03						
GO:0060729	intestinal epithelial structure maintena...	Gene body	Hyper										2.40E-03		
GO:0060854	branching involved in lymph vessel morph...	Promoter	Hypo		8.00E-03			9.70E-03							
GO:0060855	venous endothelial cell migration involv...	Promoter	Hypo		8.00E-03			9.70E-03							
GO:0060956	endocardial cell differentiation	Gene body	Hypo												8.20E-03
GO:0061337	cardiac conduction	Promoter	Hyper									6.20E-05			
			Hypo										6.00E-05		
GO:0061371	determination of heart left/right asymme...	Promoter	Hyper		8.20E-03										
GO:0070278	extracellular matrix constituent secreti...	Gene body	Hypo		6.90E-03			9.60E-03							
GO:0070654	sensory epithelium regeneration	Gene body	Hyper											4.07E-03	
GO:0070838	divalent metal ion transport	Gene body	Hypo										4.10E-03		
GO:0072017	distal tubule development	Gene body	Hyper						7.04E-03						
GO:0090090	negative regulation of canonical Wnt sig...	Promoter	Hyper				6.34E-03								
GO:0090129	positive regulation of synapse maturatio...	Promoter	Hyper								6.10E-03				
			Hypo									3.10E-03			
GO:1902117	positive regulation of organelle assembl...	Gene body	Hyper					2.10E-04							
GO:2001243	negative regulation of intrinsic apoptot...	Promoter	Hyper							9.39E-03			8.43E-03		
			Hypo					9.70E-03			8.10E-03	9.50E-03			

Table S5. Full listing of enriched Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways for all treatments and generations, by gene region (promote or gene body) and differential methylation state relative to the control (hyper, hypo). Values are Fisher's exact test p-values.

				Bif			EE2			Levo			Tren		
path_code	pathway	Region	Hyper/ Hypo	F0	F1	F2	F0	F1	F2	F0	F1	F2	F0	F1	F2
path:dre00010	Glycolysis / Gluconeogenesis	Promoter	Hyper										4.68E-03		
		Gene body	Hyper		8.04E-04										
			Hypo			2.91E-03									
path:dre00020	Citrate cycle (TCA cycle)	Gene body	Hypo							8.46E-03					
path:dre00051	Fructose and mannose metabolism	Gene body	Hypo			3.25E-04	2.82E-03		5.37E-03						5.37E-03
path:dre00061	Fatty acid biosynthesis	Gene body	Hyper						7.69E-03					4.25E-03	
			Hypo					5.84E-03							
path:dre00062	Fatty acid elongation	Gene body	Hypo							8.46E-03					
path:dre00100	Steroid biosynthesis	Gene body	Hyper				2.68E-03								
path:dre00230	Purine metabolism	Gene body	Hyper			2.35E-06									7.20E-05
			Hypo			6.73E-03									
path:dre00260	Glycine, serine and threonine metabolism	Gene body	Hypo												6.10E-03
path:dre00270	Cysteine and methionine metabolism	Gene body	Hypo			7.78E-03	5.09E-03								
path:dre00310	Lysine degradation	Gene body	Hyper		6.02E-03										
			Hypo			2.91E-03									
path:dre00440	Phosphonate and phosphinate metabolism	Promoter	Hypo							6.70E-03					
path:dre00480	Glutathione metabolism	Gene body	Hyper									4.30E-03			
			Hypo		2.67E-03	1.09E-03		4.81E-03						3.82E-03	
path:dre00500	Starch and sucrose metabolism	Gene body	Hypo						3.24E-03						
path:dre00513	Various types of N-glycan biosynthesis	Promoter	Hyper				1.59E-03								
path:dre00515	Mannose type O-glycan biosynthesis	Gene body	Hypo										5.10E-03		
path:dre00561	Glycerolipid metabolism	Gene body	Hyper		3.48E-03										
			Hypo											5.24E-03	
path:dre00562	Inositol phosphate metabolism	Gene body	Hypo												9.17E-04
path:dre00564	Glycerophospholipid metabolism	Gene body	Hypo		1.31E-03	7.61E-03								2.08E-04	
path:dre00600	Sphingolipid metabolism	Promoter	Hypo				4.27E-03								
path:dre00603	Glycosphingolipid biosynthesis - globo and isoglobo series	Promoter	Hypo										9.59E-03		
path:dre00630	Glyoxylate and dicarboxylate metabolism	Gene body	Hyper		5.02E-03										
path:dre00640	Propanoate metabolism	Gene body	Hyper		3.95E-03										
			Hypo	8.19E-03		2.21E-03				8.46E-03					
path:dre00770	Pantothenate and CoA biosynthesis	Gene body	Hypo						5.78E-03						
path:dre03013	RNA transport	Gene body	Hyper					1.20E-07			3.95E-03			1.11E-03	
			Hypo			7.48E-03									
path:dre03015	mRNA surveillance pathway	Gene body	Hyper		9.96E-03										
			Hypo	5.54E-03					8.72E-04						
path:dre03018	RNA degradation	Gene body	Hyper		9.21E-03										
path:dre03022	Basal transcription factors	Gene body	Hypo			3.53E-03						2.11E-03			
path:dre03030	DNA replication	Gene body	Hypo					1.36E-03	3.78E-03						
path:dre03040	Spliceosome	Gene body	Hyper	3.72E-03											
path:dre03410	Base excision repair	Gene body	Hyper				9.97E-03	3.76E-03							
			Hypo	9.65E-03		2.82E-03		1.26E-03	3.51E-03						3.51E-03
path:dre03430	Mismatch repair	Gene body	Hypo	3.48E-03				7.04E-03							
path:dre03460	Fanconi anemia pathway	Gene body	Hypo				4.57E-03		8.36E-04						
path:dre04010	MAPK signaling pathway	Promoter	Hyper					7.59E-03							
			Hyper								8.56E-04				
path:dre04012	ErbB signaling pathway	Promoter	Hyper												5.31E-03
		Gene body	Hyper		5.09E-04	7.94E-03		2.93E-04			6.84E-04				8.74E-06
			Hypo												2.57E-04
path:dre04020	Calcium signaling pathway	Promoter	Hyper					3.07E-03							
		Gene body	Hyper			5.74E-03		8.40E-04			2.30E-05	1.17E-03			
path:dre04068	FoxO signaling pathway	Gene body	Hyper					3.08E-03							
path:dre04110	Cell cycle	Gene body	Hyper											5.05E-03	
			Hypo			4.53E-03		8.87E-03							
path:dre04114	Oocyte meiosis	Promoter	Hyper					3.50E-03						9.85E-03	
			Hypo												2.89E-03
		Gene body	Hyper		4.82E-04	4.64E-03		3.68E-05			5.87E-06				4.31E-03
			Hypo			1.39E-04			7.42E-03						2.22E-04
path:dre04115	p53 signaling pathway	Gene body	Hyper		1.02E-04			5.66E-04							
			Hypo		6.06E-03	3.28E-05			5.04E-05		1.69E-03			8.61E-03	

Table S5. Continued

				Bif			EE2			Levo			Tren		
path_code	pathway	Region	Hyper/ Hypo	F0	F1	F2	F0	F1	F2	F0	F1	F2	F0	F1	F2
path:dre04120	Ubiquitin mediated proteolysis	Gene body	Hyper											5.44E-03	
			Hypo				2.58E-03								
path:dre04122	Sulfur relay system	Promoter	Hyper												8.15E-03
path:dre04141	Protein processing in endoplasmic reticulum	Gene body	Hypo										8.60E-03		
path:dre04142	Lysosome	Gene body	Hypo												7.42E-03
path:dre04144	Endocytosis	Gene body	Hyper	3.54E-03	2.83E-03		1.76E-03				4.54E-03				
			Hypo					9.38E-03							
path:dre04145	Phagosome	Promoter	Hyper		5.85E-03			4.14E-03							
			Hypo			1.99E-04	1.19E-04								2.68E-03
		Gene body	Hypo												1.88E-03
path:dre04146	Peroxisome	Gene body	Hyper		1.47E-03										
path:dre04150	mTOR signaling pathway	Gene body	Hyper		2.03E-03	5.01E-04		5.33E-03			1.52E-03		2.38E-04		
			Hypo	1.13E-04			7.95E-03		9.75E-04			1.31E-03			4.74E-03
path:dre04210	Apoptosis	Gene body	Hypo						2.73E-03						
path:dre04217	Necroptosis	Promoter	Hyper		8.68E-03										
		Gene body	Hyper		3.10E-04			8.71E-04							
path:dre04218	Cellular senescence	Gene body	Hyper		8.49E-03			5.19E-03			1.48E-03				1.56E-03
path:dre04261	Adrenergic signaling in cardiomyocytes	Promoter	Hypo				5.41E-03					4.22E-03			8.88E-03
		Gene body	Hyper			5.87E-03		5.93E-04			3.33E-03				3.16E-03
			Hypo					8.94E-03							2.40E-03
path:dre04310	Wnt signaling pathway	Promoter	Hypo			5.19E-03									
		Gene body	Hyper		4.45E-04	8.65E-05		2.22E-04			5.29E-09	4.11E-03	1.86E-03	4.32E-05	2.48E-05
			Hypo						4.99E-03			7.41E-03			3.03E-05
path:dre04330	Notch signaling pathway	Promoter	Hypo		7.27E-05									5.30E-03	
path:dre04350	TGF-beta signaling pathway	Promoter	Hyper												6.75E-03
path:dre04510	Focal adhesion	Promoter	Hypo						9.32E-03						
		Gene body	Hyper												4.90E-03
			Hypo		5.78E-03										
path:dre04512	ECM-receptor interaction	Promoter	Hypo				9.17E-03								
		Gene body	Hypo	4.62E-04	8.18E-04					5.81E-03					
path:dre04621	NOD-like receptor signaling pathway	Gene body	Hyper		4.54E-03			2.73E-03						8.57E-03	
			Hypo			1.64E-03									
path:dre04625	C-type lectin receptor signaling pathway	Promoter	Hypo								6.67E-03				
		Gene body	Hyper								8.61E-03				
path:dre04810	Regulation of actin cytoskeleton	Gene body	Hyper								2.08E-03	3.97E-03			7.45E-03
path:dre04910	Insulin signaling pathway	Gene body	Hypo				4.98E-03								
path:dre04912	GnRH signaling pathway	Gene body	Hyper					4.44E-03			1.48E-03				
path:dre04914	Progesterone-mediated oocyte maturation	Gene body	Hypo			1.88E-04									
path:dre04916	Melanogenesis	Promoter	Hypo						1.97E-03						2.52E-03
		Gene body	Hyper			8.14E-05		1.91E-04			3.11E-08		3.95E-03	4.93E-03	4.07E-05
			Hypo									2.02E-03			1.64E-04
path:dre04920	Adipocytokine signaling pathway	Gene body	Hyper					7.52E-03							
			Hypo						9.64E-04						
path:dre05132	Salmonella infection	Promoter	Hypo				9.77E-03							9.25E-03	
		Gene body	Hypo		9.22E-03										
path:dre05168	Herpes simplex virus 1 infection	Gene body	Hyper					5.47E-03							
			Hypo				8.13E-03		1.82E-04			1.35E-03			

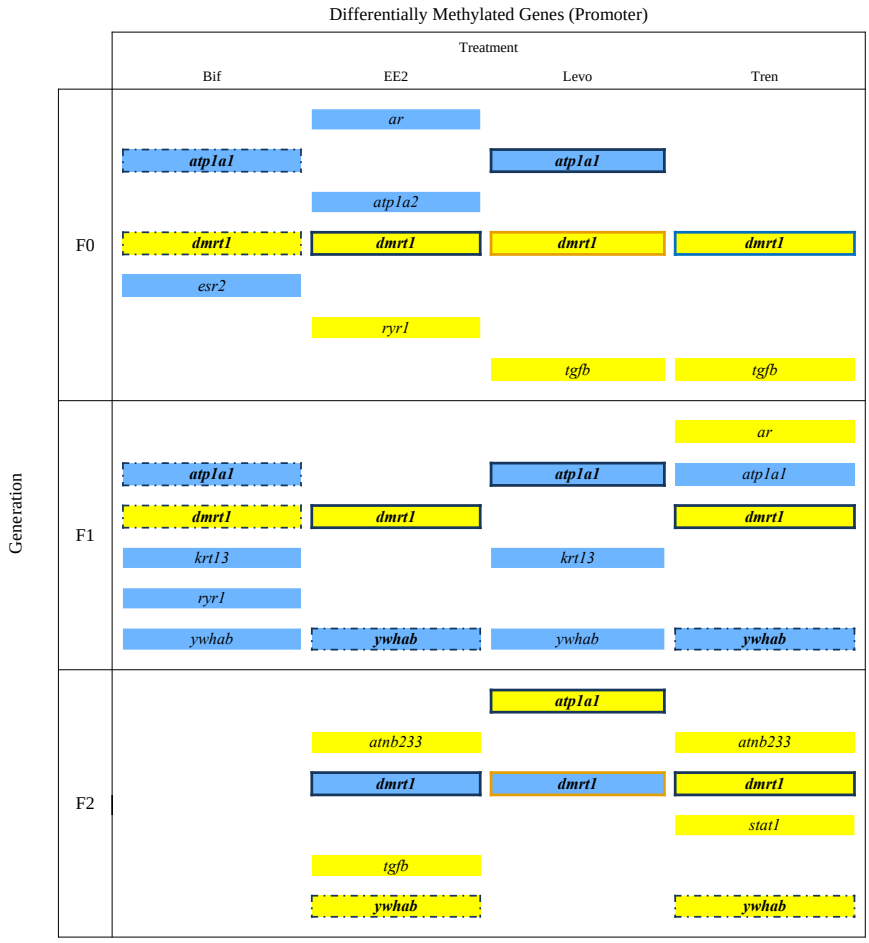

Figure S6. Differential methylation gene 'fingerprints' for a set of 109 potentially endocrine disrupting compound-responsive genes (EDCRGs) relative to controls for the promoter region by treatment and generation. Gene abbreviations denote genes that were significantly (adj.p <0.05) hyper- (blue shading) or hypo- (yellow shading) methylated relative to controls. Gene absence indicates that no significant methylation changes were noted for that gene. Colored outlines around genes indicate differential methylation across all three generations (solid blue), two sequential generations (dashed blue), or two non-sequential generations (solid orange) for each region.

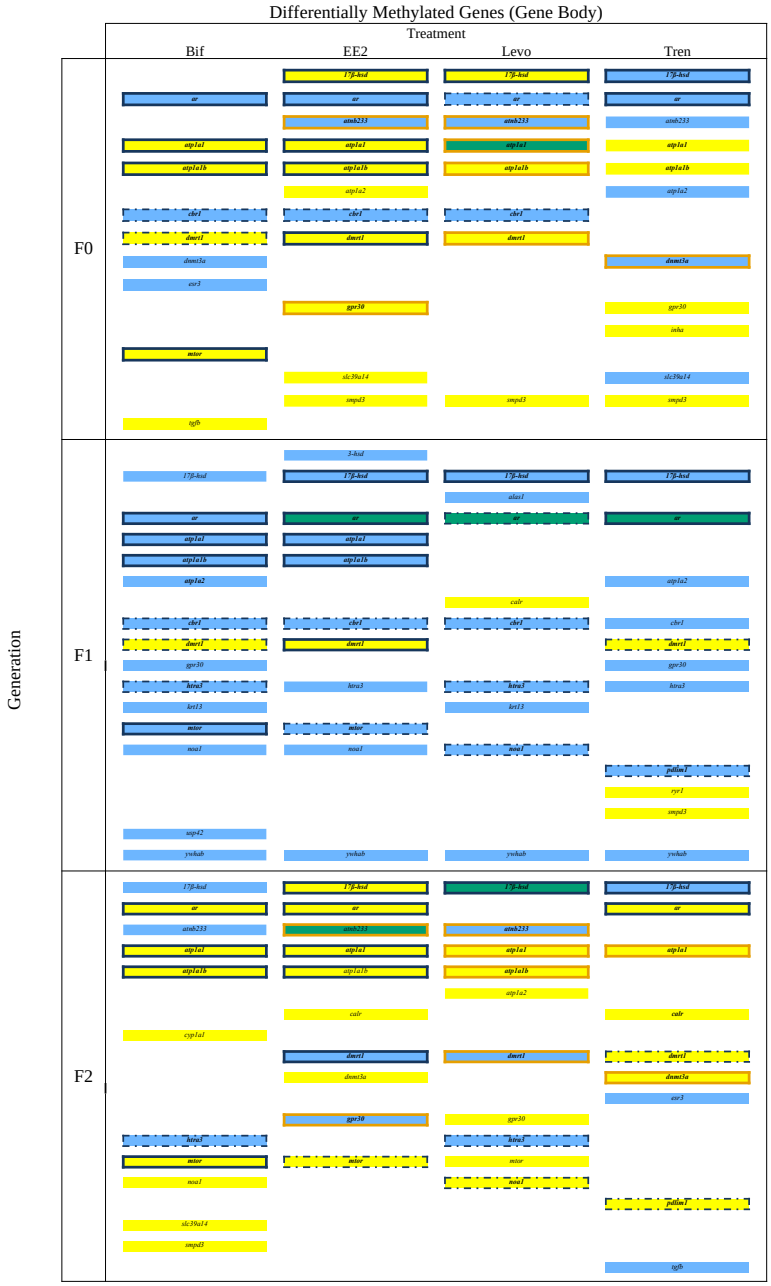

Figure S7. Differential methylation gene ‘fingerprints’ for a set of 109 potentially endocrine disrupting compound-responsive genes (EDCRGs) relative to controls for the gene body region by treatment and generation. Gene abbreviations denote genes that were significantly (adj.p <0.05) hyper- (blue shading), hypo- (yellow shading), or hyper and hypo- (green shading) methylated relative to controls. Gene absence indicates that no significant methylation changes were noted for that gene. Colored outlines around genes indicate differential methylation across all three generations (solid blue), two sequential generations (dashed blue), or two non-sequential generations (solid orange) for each region.

Table S8. Differential gene body methylation for significantly ($p < 0.05$) differentially methylated EDC-responsive genes (EDCRGs) as organized by gene, region (promoter or gene body), treatment, and generation. Each line represents a differentially methylated segment.

Gene Abbrev.	Region	Treatment	Gen	Segment Length (bp)	No. CpG	Methylation Relative to Control	Adjusted p-value
17ß-hsd	Gene body	Bif	F1	287	33	hyper	0.00E+00
			F1	296	32	hyper	0.00E+00
			F2	296	32	hyper	4.73E-04
		EE2	F0	296	32	hypo	0.00E+00
			F1	287	33	hyper	0.00E+00
			F1	296	32	hyper	0.00E+00
			F2	287	33	hypo	1.80E-06
		Levo	F0	287	33	hypo	0.00E+00
			F0	296	32	hypo	0.00E+00
			F1	287	33	hyper	0.00E+00
			F2	287	33	hypo	0.00E+00
			F2	296	32	hyper	1.27E-05
		Tren	F0	287	33	hyper	7.30E-11
			F1	287	33	hyper	4.13E-05
			F2	296	32	hyper	0.00E+00
3-hsd	Gene body	EE2	F1	267	12	hyper	5.31E-03
		Tren	F2	338	31	hypo	3.32E-03
alas1	Gene body	Levo	F1	190	13	hyper	2.55E-02
ar	Promoter	EE2	F0	291	13	hypo	2.65E-05
		Tren	F1	291	13	hypo	1.93E-03
	Gene body	Bif	F0	111	11	hyper	0.00E+00
			F1	111	11	hyper	3.82E-02
			F2	193	15	hypo	0.00E+00
			F2	111	11	hypo	1.57E-04
		EE2	F0	111	11	hyper	7.65E-04
			F1	342	23	hypo	1.84E-02
			F1	111	11	hyper	0.00E+00
			F2	193	15	hypo	0.00E+00
			F2	111	11	hypo	1.19E-02
		Levo	F0	193	15	hyper	4.31E-07
			F1	193	15	hypo	0.00E+00
			F1	111	11	hyper	0.00E+00
		Tren	F0	111	11	hyper	5.53E-10
			F1	409	27	hypo	8.63E-04
			F1	111	11	hyper	0.00E+00
			F2	193	15	hypo	0.00E+00
atnb233	Promoter	EE2	F2	339	14	hypo	1.36E-05
		Tren	F2	339	14	hypo	6.22E-04
	Gene body	Bif	F2	281	20	hyper	4.01E-10
		EE2	F0	281	20	hyper	8.19E-03
			F2	259	20	hypo	4.72E-05
			F2	281	20	hyper	3.50E-05
		Levo	F0	281	20	hyper	6.99E-03
			F0	259	20	hyper	1.25E-05
			F2	281	20	hyper	0.00E+00
		Tren	F0	281	20	hyper	1.21E-03
			F0	259	20	hyper	8.38E-03
atp1a1	Promoter	Bif	F0	372	29	hyper	8.25E-05
			F1	372	29	hyper	1.76E-04
		Levo	F0	239	20	hyper	4.59E-02
atp1a1 (cont'd)	Promoter	Levo	F1	372	29	hyper	4.50E-02
			F2	372	29	hypo	1.02E-10
		Tren	F1	372	29	hyper	0.00E+00
	Gene body	Bif	F1	332	33	hyper	1.02E-02
			F1	372	40	hyper	1.22E-02
			F2	372	40	hypo	3.53E-04
		EE2	F1	372	40	hyper	5.85E-08
			F2	372	40	hypo	1.75E-02
		Levo	F0	239	20	hyper	4.59E-02
		Tren	F2	374	35	hypo	2.01E-02
atp1b, atp1a1	Gene body	Bif	F0	323	31	hypo	5.84E-11
			F1	323	31	hyper	0.00E+00
			F2	323	31	hypo	0.00E+00
		EE2	F0	323	31	hypo	1.38E-06
			F1	323	31	hyper	0.00E+00
			F2	323	31	hypo	0.00E+00
		Levo	F0	323	31	hypo	4.24E-04
			F2	323	31	hypo	0.00E+00
		Tren	F0	491	26	hypo	2.58E-02
atp1a2	Promoter	EE2	F0	162	13	hypo	3.08E-09
	Gene body	Bif	F1	243	17	hyper	1.88E-02
		EE2	F0	162	13	hypo	3.08E-09
		Levo	F2	359	19	hypo	2.89E-06
		Tren	F0	109	6	hyper	2.77E-05
			F1	243	17	hyper	1.50E-04
calr	Gene body	EE2	F2	294	9	hypo	3.07E-06
		Levo	F1	451	20	hypo	1.17E-03
		Tren	F2	451	20	hypo	4.79E-04
cbr1	Gene body	Bif	F0	197	22	hyper	5.49E-05
			F1	197	22	hyper	4.31E-11
		EE2	F0	197	22	hyper	0.00E+00
			F1	197	22	hyper	0.00E+00
		Levo	F0	197	22	hyper	6.89E-07
			F1	197	22	hyper	0.00E+00
		Tren	F1	197	22	hyper	0.00E+00
cyp1a1	Gene body	Bif	F2	250	14	hypo	8.61E-03
dmrt1	Promoter	Bif	F0	307	24	hypo	0.00E+00
			F0	331	30	hypo	2.48E-10
			F1	307	24	hypo	0.00E+00
			F1	331	30	hypo	0.00E+00
		EE2	F0	307	24	hypo	0.00E+00
			F0	331	30	hypo	0.00E+00
			F1	307	24	hypo	0.00E+00
			F1	331	30	hypo	0.00E+00
			F2	307	24	hyper	0.00E+00
			F2	331	30	hyper	2.16E-10
		Levo	F0	307	24	hypo	0.00E+00
			F0	331	30	hypo	0.00E+00
			F2	307	24	hyper	1.97E-02
			F2	331	30	hyper	0.00E+00

Table S8. Continued

Gene Abbrev.	Region	Treatment	Gen	Segment Length (bp)	No. CpG	Methylation Relative to Control	Adjusted p-value
dmrt1 (cont'd)	Promoter	Tren	F0	307	24	hypo	0.00E+00
			F1	331	30	hypo	1.56E-08
			F2	307	24	hypo	5.57E-06
noa1 (cont'd)		Levo	F1	231	20	hyper	2.53E-06
			F2	231	20	hypo	7.91E-08
pdlim1	Gene body	Tren	F1	242	11	hyper	5.55E-08

			F2	331	30	hypo	0.00E+00
	Gene body	Bif	F0	331	30	hypo	2.48E-10
			F1	331	30	hypo	0.00E+00
		EE2	F0	331	30	hypo	0.00E+00
			F1	331	30	hypo	0.00E+00
			F2	331	30	hyper	2.16E-10
		Levo	F0	331	30	hypo	0.00E+00
			F2	331	30	hyper	0.00E+00
		Tren	F1	331	30	hypo	1.56E-08
			F2	331	30	hypo	0.00E+00
dmrt3a	Gene body	Bif	F0	346	11	hyper	5.42E-05
		EE2	F2	346	11	hypo	2.12E-08
		Tren	F0	346	11	hyper	4.38E-11
			F2	346	11	hypo	1.12E-04
esr2	Promoter	Bif	F0	385	36	hyper	2.85E-06
esr3	Gene body	Bif	F0	429	19	hyper	2.53E-03
		Tren	F2	280	14	hyper	2.52E-02
gpr30	Gene body	Bif	F1	386	22	hyper	4.70E-03
		EE2	F0	282	40	hypo	3.24E-03
			F0	278	9	hypo	1.04E-02
			F2	73	4	hyper	2.55E-03
		Levo	F2	282	40	hypo	0.00E+00
		Tren	F0	278	9	hypo	3.20E-03
			F1	386	22	hyper	2.90E-02
htra3	Gene body	Bif	F1	269	13	hyper	4.59E-03
			F2	269	13	hyper	1.12E-06
		EE2	F1	269	13	hyper	3.33E-09
		Levo	F1	269	13	hyper	0.00E+00
			F2	269	13	hyper	0.00E+00
		Tren	F1	269	13	hyper	1.79E-05
inha	Gene body	Tren	F0	308	36	hypo	4.49E-02
krt13	Promoter	Bif	F1	350	13	hyper	8.60E-07
		Levo	F1	350	13	hyper	1.17E-04
	Gene body	Bif	F1	350	13	hyper	8.60E-07
		Levo	F1	350	13	hyper	1.17E-04
mtor	Gene body	Bif	F0	168	8	hypo	8.96E-07
			F1	168	8	hyper	0.00E+00
			F2	168	8	hypo	0.00E+00
		EE2	F1	168	8	hyper	0.00E+00
			F2	168	8	hypo	0.00E+00
		Levo	F2	168	8	hypo	1.10E-02
noa1	Gene body	Bif	F1	231	20	hyper	0.00E+00
			F2	231	20	hypo	1.89E-07
		EE2	F1	231	20	hyper	0.00E+00
			F2	242	11	hypo	0.00E+00
ryr1	Promoter	Bif	F1	103	9	hyper	1.74E-02
		EE2	F0	103	9	hypo	2.91E-11
	Gene body	Tren	F1	350	19	hypo	3.37E-05
slc39a14	Gene body	Bif	F2	256	11	hypo	3.98E-02
			F2	406	19	hypo	6.64E-07
		EE2	F0	256	11	hypo	4.39E-03
		Tren	F0	406	19	hyper	2.19E-05
smpd3	Gene body	Bif	F2	389	24	hypo	0.00E+00
		EE2	F0	389	24	hypo	4.70E-03
		Levo	F0	389	24	hypo	5.22E-08
		Tren	F0	389	24	hypo	1.14E-02
			F1	192	17	hypo	3.50E-03
stat1	Promoter	Tren	F2	492	21	hypo	6.99E-03
tgfb	Promoter	EE2	F2	216	15	hypo	5.23E-04
		Levo	F0	216	15	hypo	9.91E-10
		Tren	F0	216	15	hypo	1.21E-04
	Gene body	Bif	F0	142	7	hypo	4.88E-02
		Tren	F2	451	25	hyper	2.09E-02
usp42	Gene body	Bif	F1	441	26	hyper	9.36E-04
ywhab	Promoter	Bif	F1	409	22	hyper	1.88E-04
		EE2	F1	409	22	hyper	3.61E-04
			F2	250	21	hypo	7.78E-06
		Levo	F1	409	22	hyper	3.05E-05
		Tren	F1	409	22	hyper	1.81E-06
			F2	250	21	hypo	1.05E-03
	Gene body	Bif	F1	409	22	hyper	1.88E-04
		EE2	F1	409	22	hyper	3.61E-04
		Levo	F1	409	22	hyper	3.05E-05
		Tren	F1	409	22	hyper	1.81E-06
		Levo	F1	231	20	hyper	2.53E-06

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