

Table S3. Pathways influenced by genes associated with DMR

	All Exposures	Pesticides	Plastics	Dioxin	Hydrocarbons
Number of unique genes in the list	479	351	191	47	33
Pathway Name	Number of affected genes in pathway				
Pathways in cancer	11	8	5	2	
MAPK signaling pathway	10	8	4	1	1
Cell adhesion molecules (CAMs)	9	7	5		1
Phagosome	9	7	4	1	1
Axon guidance	9	5	2	3	2
Endocytosis	9	4	5	1	2
Focal adhesion	8	8	3	1	
Regulation of actin cytoskeleton	8	6	3	2	
Neurotrophin signaling pathway	7	7	3	2	
Olfactory transduction	7	4	3	1	1
Antigen processing and presentation	7	3	3		2
Chemokine signaling pathway	6	5	3	3	
Protein processing in endoplasmic reticulum	6	4	2		1
Neuroactive ligand-receptor interaction	6	3	1	2	
Hypertrophic cardiomyopathy (HCM)	5	5	3		
Dilated cardiomyopathy	5	5	3		
Alzheimer's disease	5	5			
Insulin signaling pathway	5	4	2	2	1
Cell cycle	5	4	2		
Viral myocarditis	5	3	3		1
Purine metabolism	5	3	1	1	
Type I diabetes mellitus	5	2	2	1	1
<p>KEGG pathway enrichment for each exposure lineage regarding genes associated with differentially methylated regions (DMR) in F3 generation sperm. Top signaling and cellular pathways with 5 or greater total genes involved.</p>					