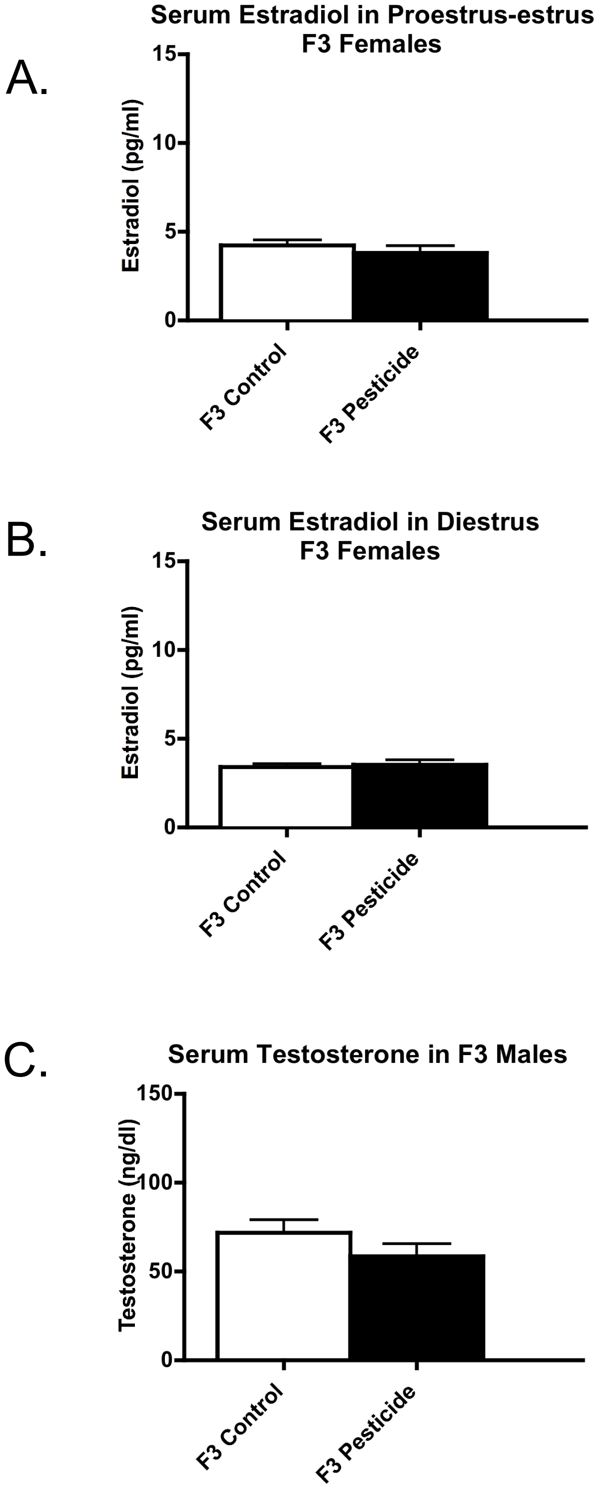
Supplementary Figure Legends

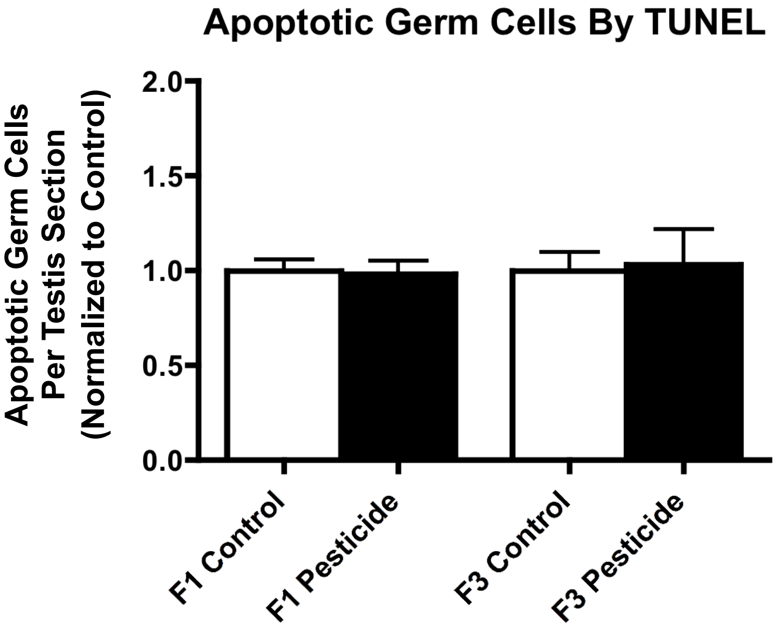
Supplemental Figure S1. (A). Serum estradiol concentrations in proestrus-estrus in F3 generation control and pesticide lineage females. (B). Serum estradiol concentrations in diestrus in F3 generation control and pesticide lineage females. (C). Serum testosterone concentrations in F3 generation control and pesticide lineage males. There were no significant alterations in hormone concentrations of pesticide lineage rats. The means ± SEM for control (66 animals) and pesticide lineage (75 animals) for each analysis are presented.

Supplemental Figure S2. Testicular spermatogenic cell apoptosis as assessed by Terminal deoxynucleotidyl transferase dUTP nick end labeling (TUNEL) in F1 and F3 generation control (white bars) and pesticide lineage (black bars) rats. Number of apoptotic germ cells was normalized to control means. The means ± SEM for three different experiments are presented with relative differences from control lineage.

Supplementary Figure S1



Supplementary Figure S2



Supplemental Table S1A. Body Weight and Organ Weights in Control and Pesticide F1 and F3 Generation Female Rats (Mean ± Standard Error).

Generation	Treatment	Sex	Body Weight (grams)	Ovaries (% of BW)	Uterus (% BW)	Kidney (% BW)
F1	Control	F	310.9 ± 6.15	0.0532 ± 0.0032	0.2589 ± 0.0209	0.3276 ± 0.0127
F1	Pesticide	F	304.1 ± 11.21	0.0486 ± 0.0037	0.2794 ± 0.0330	0.3351 ± 0.0110
F3	Control	F	293.6 ± 2.31	0.0501 ± 0.0011	0.3883 ± 0.0150	0.3567 ± 0.0036
F3	Pesticide	F	303.0* ± 4.00	0.0497 ± 0.0021	0.3208* ± 0.0143	0.3499 ± 0.0052

Asterisks (*, **), if present, indicate statistically significant differences between means of Control and Pesticide generation rats ($P<0.05$, $P<0.01$ respectively).

Supplemental Table S1B. Body Weight and Organ Weights in Control and Pesticide F1 and F3 Generation Male Rats (Mean ± Standard Error).

Generation	Treatment	Sex	Body Weight (grams)	Testis (% BW)	Prostate (% BW)	Seminal Vesicle (% BW)	Epididymis (% BW)	Kidney (% BW)
F1	Control	M	545.3	0.7599	0.2239	0.1395	0.2585	0.3821
			± 8.66	± 0.0154	± 0.0076	± 0.0092	± 0.0045	± 0.0092
F1	Pesticide	M	538.0	0.7480	0.1985	0.1331	0.2415*	0.3365**
			± 12.61	± 0.0209	± 0.0138	± 0.0098	± 0.0072	± 0.0064
F3	Control	M	515.80	0.8153	0.1970	0.1330	0.2628	0.3791
			± 6.09	± 0.0102	± 0.0041	± 0.0038	± 0.0028	± 0.0010
F3	Pesticide	M	531.4	0.7948	0.2010	0.1286	0.2543	0.3599
			± 8.00	± 0.0126	± 0.0048	± 0.0042	± 0.0042	± 0.0072

Asterisks (*, **), if present, indicate statistically significant differences between means of Control and Pesticide generation rats (P<0.05, P<0.01 respectively).

Supplemental Table S2A. Individual disease incidence in F1 generation female rats of control and pesticide lineages.

Animal	Animal ID	Sex	Age	Puberty	PFL	PCO	Kidney	Tumor	Obesity	Total Disease
C1	DCS0-1-1-1	F	1 Yr	-	-	-	-	-	-	
C2	DCS0-1-1-2	F	1 Yr	-			-	-	-	
C3	DCS0-1-1-3	F	1 Yr	-			+	-	-	1
C4	DCR1-1-2-1	F	1 Yr	-	-	-	-	-	-	
C5	DCR1-1-2-2	F	1 Yr	-			-	-	-	
C6	DCR1-1-2-3	F	1 Yr	-				+	-	1
C7	DCB1-1-3-1	F	1 Yr	-			-	-	-	
C8	DCB1-1-3-2	F	1 Yr	-				-	-	
C9	DCF1-1-4-1	F	1 Yr	-	-	-	-	+	-	1
C10	DCF1-1-4-2	F	1 Yr	-	-	-	-	-	-	
C11	DCF1-1-4-3	F	1 Yr	-	-	-	+	-	-	1
C12	DCL1-1-5-1	F	1 Yr	-	+	-	+	-	-	2
C13	DCL1-1-5-2	F	1 Yr	-			-	-	-	
C14	DCL1-1-5-3	F	1 Yr	-	-	-	-	-	-	
C15	DCM2-1-6-1	F	1 Yr	-	-	-	-	-	-	
C16	DCM2-1-6-2	F	1 Yr	+			-	-	-	1
C17	DCM2-1-6-3	F	1 Yr	+	-	-	-	-	-	1
C18	DCF0-1-7-1	F	1 Yr	-			-	-	-	
C19	DCF0-1-7-2	F	1 Yr	-			-	-	-	
C20	DCF0-1-7-3	F	1 Yr	-			-	-	-	

Animal	Animal ID	Sex	Age	Puberty	PFL	PCO	Kidney	Tumor	Obesity	Total Disease
P1	DPM2-1-1-1	F	1 Yr	+	+	-	-	-	-	2
P2	DPM2-1-1-2	F	1 Yr	-	-	+		-	-	1
P3	DPS1-1-2-1	F	1 Yr	+	+	+	+	-	-	4
P4	DPS1-1-2-2	F	1 Yr	+	+	+	+	-	-	4
P5	DPS1-1-2-3	F	1 Yr	+	+	+	-	-	-	3
P6	DPZ0-1-4-1	F	1 Yr	-	+	+	-	-	-	2
P7	DPZ0-1-4-2	F	1 Yr	-	+	-	+	-	-	2
P8	DPZ0-1-4-3	F	1 Yr	+	+	+	+	-	-	4

A ‘+’ indicates the presence of disease; A ‘-‘ indicates the absence of disease; A blank cell indicates ‘not evaluated.’ Animal IDs with a ‘C’ belong to control lineage and those with a ‘P’ belong to pesticide lineage. PFL = Primordial follicle loss; PCO= Polycystic ovarian disease. See ‘Materials and Methods’ section for disease assessment in rats. The number of animals per litter (litter representation) mean ± SEM used for each specific disease/abnormality was found not to be statistically different between the control versus pesticide lineage animals.

Supplemental Table S2B. Individual disease incidence in F1 generation male rats of control and pesticide lineages.

Animal	Animal ID	Sex	Age	Puberty	Testis	Prostate	Kidney	Tumor	Obesity	Total Disease
C1	DCS0-1-1-5	M	1 Yr	-	+	-	-	-	-	1
C2	DCS0-1-1-6	M	1 Yr	-	-	-	-	-	-	
C3	DCR1-1-2-5	M	1 Yr	-	-	-	-	-	-	
C4	DCR1-1-2-6	M	1 Yr	-		-	-	-	-	
C5	DCR1-1-2-7	M	1 Yr	-		+	-	-	-	1
C6	DCR1-1-2-8	M	1 Yr	-	-	-	-	-	-	
C7	DCB1-1-3-3	M	1 Yr	-	+	-	-	-	-	1
C8	DCB1-1-3-4	M	1 Yr	-	-	-	-	-	-	
C9	DCF1-1-4-6	M	1 Yr	-	-	-	-	-	-	
C10	DCF1-1-4-7	M	1 Yr	+	-	+	-	-	-	2
C11	DCF1-1-4-8	M	1 Yr	-	-	-	-	-	-	
C12	DCF1-1-4-9	M	1 Yr	+	-	-	-	-	-	1
C13	DCL1-1-5-6	M	1 Yr	-	-	-	-	-	-	
C14	DCL1-1-5-7	M	1 Yr	-	-	+	-	-	-	1
C15	DCL1-1-5-8	M	1 Yr	-	-	-	-	-	-	
C16	DCL1-1-5-9	M	1 Yr	-	-	+	-	-	-	1
C17	DCM2-1-6-7	M	1 Yr	+	-	+	-	-	-	2
C18	DCM2-1-6-9	M	1 Yr	+	+	-	-	-	-	2
C19	DCM2-1-6-10	M	1 Yr	-	+	-	-	-	-	1
C20	DCF0-1-7-5	M	1 Yr	-		-	-	-	-	
C21	DCF0-1-7-6	M	1 Yr	-	-	-	+	-	-	1
C22	DCF0-1-7-7	M	1 Yr	-	-	-	-	-	-	

Animal	Animal ID	Sex	Age	Puberty	Testis	Prostate	Kidney	Tumor	Obesity	Total Disease
P1	DPM2-1-1-3	M	1 Yr	+	+	-	-	-	-	2
P2	DPM2-1-1-4	M	1 Yr	+	-	-	+	-	-	2
P3	DPS1-1-2-7	M	1 Yr	-	-	+	-	-	-	1
P4	DPS1-1-2-8	M	1 Yr	-	+	-	-	-	-	1
P5	DPS1-1-2-11	M	1 Yr	-	-	-	+	-	-	1
P6	DPK1-1-3-1	M	1 Yr	-	+	-	+	-	-	2
P7	DPK1-1-3-2	M	1 Yr	+		-	-	-	-	1
P8	DPZ0-1-4-6	M	1 Yr	-	+	+	-	-	-	2
P9	DPZ0-1-4-7	M	1 Yr	-	-	-	-	-	-	
P10	DPZ0-1-4-8	M	1 Yr	-	+	+		-	-	2
P11	DPZ0-1-4-9	M	1 Yr	+	+	+	+	-	-	4

A ‘+’ indicates the presence of disease; A ‘-‘ indicates the absence of disease; A blank cell indicates ‘not evaluated.’ Animal IDs with a ‘C’ belong to control lineage and those with a ‘P’ belong to pesticide lineage. See ‘Materials and Methods’ section for disease assessment in rats. The number of animals per litter (litter representation) mean ± SEM used for each specific disease/abnormality was found not to be statistically different between the control versus pesticide lineage animals.

Supplemental Table S3A. Individual Disease Incidence in F3 Generation Control and Pesticide Female Rats.

Animal	Animal ID	Sex	Age	Puberty	PFL	PCO	Kidney	Tumor	Obesity	Total Disease
C1	DCF1-3-1-2	F	1 Yr	-			-	-	-	
C2	DCF1-3-1-3	F	1 Yr	-			-	-	-	
C3	DCF1-3-1-4	F	1 Yr	-			-	-	-	
C4	DCF1-3-1-5	F	1 Yr	-				-	-	
C5	DCS0-3-2-2	F	1 Yr	-			-	-	-	
C6	DCS0-3-2-3	F	1 Yr	-	-	-	-	-	-	
C7	DCS0-3-2-4	F	1 Yr	-				-	-	
C8	DCS0-3-2-5	F	1 Yr	-				-	-	
C9	DCL1-3-3-2	F	1 Yr	-	-	-	+	-	-	1
C10	DCL1-3-3-3	F	1 Yr	-				+	-	1
C11	DCB1-3-4-2	F	1 Yr	-			-	-	-	
C12	DCB1-3-4-3	F	1 Yr	-			-	-	-	
C13	DCB1-3-4-4	F	1 Yr	-			-	-	-	
C14	DCB1-3-4-5	F	1 Yr	-	-	-		-	-	
C15	DCB1-3-4-6	F	1 Yr	-				-	-	
C16	DCS0-3-5-2	F	1 Yr	-			+	-	-	1
C17	DCS0-3-5-3	F	1 Yr	-			-	-	-	
C18	DCS0-3-5-4	F	1 Yr	-			-	-	-	
C19	DCS0-3-5-5	F	1 Yr	-			-	-	-	
C20	DCS0-3-5-6	F	1 Yr	-	-	-		-	-	
C21	DCS0-3-6-2	F	1 Yr	-			+	-	-	1
C22	DCS0-3-6-3	F	1 Yr	-	+	-	-	-	-	1
C23	DCB1-3-7-2	F	1 Yr	-	-	-		-	-	

Animal	Animal ID	Sex	Age	Puberty	PFL	PCO	Kidney	Tumor	Obesity	Total Disease
C24	DCB1-3-7-3	F	1 Yr	-			-	-	-	
C25	DCB1-3-7-4	F	1 Yr	-				-	-	
C26	DCB1-3-7-5	F	1 Yr	-				-	-	
C27	DCB1-3-7-6	F	1 Yr	-				-	-	
C28	DCR1-3-8-2	F	1 Yr	-	-	-		-	-	
C29	DCR1-3-8-3	F	1 Yr	-			-	-	-	
C30	DCR1-3-8-4	F	1 Yr	-			-	-	-	
C31	DCR1-3-8-5	F	1 Yr	-				-	-	
C32	DCF1-3-9-2	F	1 Yr	-	-	-		-	-	
C33	DCF1-3-9-3	F	1 Yr	-			-	-	-	
C34	DCF1-3-9-4	F	1 Yr	+			-	-	-	1
C35	DCF1-3-9-5	F	1 Yr					-	-	
C36	DCB1-3-10-2	F	1 Yr	-				-	-	
C37	DCB1-3-10-3	F	1 Yr	-	-	-	-	-	-	
C38	DCB1-3-10-4	F	1 Yr	-			-	-	-	
C39	DCL1-3-11-2	F	10 m.	-				+	-	1
C40	DCL1-3-11-3	F	1 Yr	-			-	-	-	
C41	DCL1-3-11-4	F	1 Yr	-			-	-	-	
C42	DCL1-3-11-5	F	1 Yr	-			-	-	-	
C43	DCL1-3-11-6	F	1 Yr	-				-	-	
C44	DCL1-3-11-8	F	11 m.	-				+	-	1
C45	DCB1-3-12-2	F	1 Yr	-				-	-	
C46	DCB1-3-12-3	F	1 Yr	-			-	-	-	
C47	DCL1-3-13-1	F	1 Yr	-			-	-	-	
C48	DCL1-3-13-2	F	1 Yr	-				-	-	

Animal	Animal ID	Sex	Age	Puberty	PFL	PCO	Kidney	Tumor	Obesity	Total Disease
C49	DCL1-3-13-3	F	1 Yr	-			-	-	-	
C50	DCS0-3-14-2	F	1 Yr	-				-	-	
C51	DCS0-3-14-3	F	1 Yr	-			-	-	-	
C52	DCL1-3-15-2	F	1 Yr	+			-	-	-	1
C53	DCL1-3-15-3	F	1 Yr	+			+	-	-	2
C54	DCL1-3-15-4	F	1 Yr	+			+	-	-	2
C55	DCL1-3-15-5	F	1 Yr	-				-	-	
C56	DCS0-3-16-2	F	1 Yr	-				-	-	
C57	DCS0-3-16-3	F	1 Yr	-			-	-	-	
C58	DCS0-3-16-4	F	1 Yr	-			-	-	-	
C59	DCS0-3-16-5	F	1 Yr	-				-	-	
C60	DCR1-3-17-1	F	1 Yr	-				-	-	
C61	DCR1-3-17-2	F	1 Yr	-			-	-	-	
C62	DCR1-3-17-3	F	1 Yr	-			-	-	-	
C63	DCR1-3-17-4	F	1 Yr	+				-	-	1
C64	DCS0-3-18-2	F	1 Yr					-	-	
C65	DCS0-3-18-3	F	1 Yr				-	-	-	
C66	DCS0-3-18-4	F	1 Yr				-	-	-	
C67	DCF1-3-19-1	F	1 Yr	-				-	-	
C68	DCF1-3-19-2	F	1 Yr	-			-	-	-	
C69	DCF1-3-19-3	F	11 m.	-				+	-	
P1	DPS1-3-1-3	F	1 Yr	-			-	-	-	
P2	DPS1-3-1-4	F	6 m.	-				+	-	1
P3	DPS1-3-1-5	F	1 Yr	+	+	+	-	-	-	3

Animal	Animal ID	Sex	Age	Puberty	PFL	PCO	Kidney	Tumor	Obesity	Total Disease
P4	DPS1-3-1-6	F	1 Yr	-				-	-	
P5	DPS1-3-2-3	F	1 Yr	-	+	+	-	-	-	2
P6	DPM2-3-3-3	F	1 Yr	+	+	+	-	-	-	3
P7	DPS1-3-4-2	F	1 Yr	-			-	-	-	
P8	DPS1-3-4-3	F	1 Yr	-	+	+	-	-	-	2
P9	DPM2-3-5-2	F	1 Yr	-	+	+	-	-	-	2
P10	DPM2-3-6-3	F	1 Yr	+	+	+	-	-	-	3
P11	DPS1-3-7-3	F	1 Yr	+			-	-	-	1
P12	DPS1-3-7-4	F	1 Yr	+			-	-	-	1
P13	DPS1-3-7-5	F	1 Yr	+	+	+	-	-	-	3
P14	DPS1-3-7-6	F	1 Yr	+				-	-	1
P15	DPZ0-3-8-3	F	1 Yr	+			-	-	-	1
P16	DPZ0-3-8-5	F	1 Yr	+			-	-	-	1
P17	DPZ0-3-8-6	F	1 Yr	+	+	+	-	-	-	3
P18	DPZ0-3-9-2	F	1 Yr	+			-	-	-	1
P19	DPZ0-3-9-3	F	1 Yr	+	+	+	-	-	-	3
P20	DPZ0-3-9-4	F	8 m.	+				+	-	2
P21	DPZ0-3-9-5	F	1 Yr	+			-	-	-	1
P22	DPS1-3-10-2	F	1 Yr	-			-	-	-	
P23	DPS1-3-10-3	F	11 m.	-				+	-	1
P24	DPS1-3-10-4	F	1 Yr	-			-	-	-	
P25	DPS1-3-10-5	F	1 Yr	-			-	-	-	
P26	DPS1-3-10-6	F	11 m.	-				+	-	1
P27	DPZ0-3-11-1	F	1 Yr				-	-	-	
P28	DPZ0-3-11-2	F	1 Yr				-	-	-	

Animal	Animal ID	Sex	Age	Puberty	PFL	PCO	Kidney	Tumor	Obesity	Total Disease
P29	DPZ0-3-11-3	F	1 Yr				-	-	-	
P30	DPM2-3-12-1	F	1 Yr	-			-	-	-	
P31	DPM2-3-12-2	F	1 Yr	-			-	-	-	
P32	DPM2-3-12-3	F	1 Yr	-			-	-	-	
P33	DPM2-3-13-1	F	1 Yr	+				-	-	1
P34	DPM2-3-13-3	F	1 Yr	+				-	-	1
P35	DPM2-3-13-5	F	1 Yr	+				-	-	1
P36	DPM2-3-13-6	F	1 Yr	+				-	-	1
P37	DPM2-3-13-7	F	1 Yr	-				-	-	

A '+' indicates the presence of disease; A '-' indicates the absence of disease. A blank cell indicates 'not evaluated.' Animal IDs with a 'C' belong to Control lineage and those with a 'P' belong to Pesticide lineage. PFL = Primordial Follicle Loss; PCO = Polycystic Ovarian Disease. See 'Materials and Methods' section for disease assessment in rats. The number of animals per litter (litter representation) mean ± SEM used for each specific disease/abnormality was found not to be statistically different between the control versus pesticide lineage animals.

Supplemental Table S3B. Individual Disease Incidence in F3 Generation Control and Pesticide Male Rats.

Animal	Animal ID	Sex	Age	Pubertal	Testis	Prostate	Kidney	Tumor	Obesity	Total Disease
C1	DCF1-3-1-8	M	1 Yr	-	+		-	-	-	1
C2	DCF1-3-1-9	M	1 Yr	-		-	-	-	-	
C3	DCF1-3-1-10	M	1 Yr	-		-	+	-	-	1
C4	DCS0-3-2-11	M	1 Yr	-	-	-	-	-	-	
C5	DCS0-3-2-12	M	1 Yr	-	-	-	-	-	-	
C6	DCS0-3-2-13	M	1 Yr	-	-		-	-	-	
C7	DCL1-3-3-6	M	1 Yr	-	-	-		-	-	
C8	DCL1-3-3-7	M	1 Yr	-	-	-		-	-	
C9	DCB1-3-4-9	M	1 Yr	-	-	+	-	-	-	1
C10	DCB1-3-4-10	M	1 Yr	-	-	-	-	-	-	
C11	DCB1-3-4-11	M	1 Yr	-	-	-	-	-	-	
C12	DCB1-3-4-12	M	1 Yr	-				-	-	
C13	DCB1-3-4-13	M	1 Yr	-				-	-	
C14	DCS0-3-5-9	M	1 Yr	-	-		-	-	-	
C15	DCS0-3-5-10	M	1 Yr	-	-	-	-	-	-	
C16	DCS0-3-5-11	M	1 Yr	-	-	-	-	-	-	
C17	DCS0-3-6-6	M	1 Yr	-	-		-	-	-	
C18	DCS0-3-6-7	M	1 Yr	-	-	-	-	-	-	
C19	DCS0-3-6-8	M	1 Yr	-	+	-	-	-	-	1
C20	DCB1-3-7-9	M	1 Yr	-	-		+	-	-	1
C21	DCB1-3-7-10	M	1 Yr	-	-	-	-	-	-	
C22	DCB1-3-7-11	M	1 Yr	-	-	-	-	-	-	
C23	DCR1-3-8-7	M	1 Yr	-	-	-	-	-	-	
C24	DCR1-3-8-8	M	1 Yr	-	-	-	-	-	-	

Animal	Animal ID	Sex	Age	Pubertal	Testis	Prostate	Kidney	Tumor	Obesity	Total Disease
C25	DCF1-3-9-11	M	1 Yr	-	-	-		-	-	
C26	DCF1-3-9-12	M	1 Yr	-	-			-	-	
C27	DCF1-3-9-13	M	1 Yr	+	-			-	-	1
C28	DCB1-3-10-9	M	9 m.	-	-	-	-	+	-	1
C29	DCB1-3-10-10	M	1 Yr	-		-	-	-	-	
C30	DCB1-3-10-11	M	1 Yr	-	-	-	-	-	-	
C31	DCB1-3-10-12	M	1 Yr	-	+	-	-	-	-	1
C32	DCB1-3-10-13	M	11m.	-		-		+	-	1
C33	DCL1-3-11-9	M	1 Yr	-	-		-	-	-	
C34	DCL1-3-11-10	M	1 Yr	-	-	+	-	-	-	1
C35	DCL1-3-11-11	M	1 Yr	-	-	-	-	-	-	
C36	DCB1-3-12-6	M	1 Yr	-	-	-	-	-	-	
C37	DCB1-3-12-7	M	1 Yr	-	+	+	-	-	-	2
C38	DCB1-3-12-8	M	1 Yr	-	+	-	-	-	-	1
C39	DCL1-3-13-4	M	1 Yr	-	-	-	-	-	-	
C40	DCS0-3-14-5	M	1 Yr	-	-	-	-	-	-	
C41	DCS0-3-14-6	M	1 Yr	-	-	-		-	-	
C42	DCS0-3-14-7	M	1 Yr	-	-	-	-	-	-	
C43	DCL1-3-15-7	M	1 Yr	+	-	-	-	-	-	1
C44	DCL1-3-15-8	M	1 Yr	+	-	+	-	-	-	2
C45	DCL1-3-15-9	M	1 Yr	+	-	-	-	-	-	1
C46	DCS0-3-16-9	M	1 Yr	-	-	-	-	-	-	
C47	DCS0-3-16-10	M	1 Yr	-	-	-	-	-	-	
C48	DCS0-3-16-11	M	1 Yr	-	-	-	-	-	-	
C49	DCS0-3-16-13	M	1 Yr	-				-	-	

Animal	Animal ID	Sex	Age	Pubertal	Testis	Prostate	Kidney	Tumor	Obesity	Total Disease
C50	DCR1-3-17-6	M	1 Yr	-		-	-	-	-	
C51	DCS0-3-18-10	M	1 Yr			-	+	-	-	1
C52	DCS0-3-18-11	M	1 Yr		+	-	+	-	-	2
C53	DCS0-3-18-12	M	1 Yr		-		-	-	-	
C54	DCF1-3-19-4	M	1 Yr	-	-		-	-	-	
C55	DCF1-3-19-5	M	1 Yr	-	-	-		-	-	
C56	DCF1-3-19-6	M	1 Yr	-	-	-	-	-	-	
P1	DPS1-3-1-10	M	1 Yr	-	+	-	-	-	-	1
P2	DPS1-3-1-11	M	1 Yr	-	-	-	-	-	-	
P3	DPS1-3-1-12	M	1 Yr	-	-	-	-	-	-	
P4	DPS1-3-2-7	M	1 Yr	-	-	-	+	-	-	1
P5	DPS1-3-2-8	M	1 Yr	+	-	-	+	-	-	2
P6	DPS1-3-2-9	M	1 Yr	-	-	+	-	-	-	1
P7	DPM2-3-3-7	M	1 Yr	-	-	-	-	-	-	
P8	DPM2-3-3-8	M	1 Yr	-	-	-	+	-	-	1
P9	DPM2-3-3-9	M	1 Yr	-	-	-	-	-	-	
P10	DPM2-3-3-10	M	1 Yr	-				-	-	
P11	DPS1-3-4-6	M	1 Yr	-	+	-	-	-	-	1
P12	DPZ0-3-5-4	M	1 Yr	-	-	-	-	-	-	
P13	DPZ0-3-5-5	M	1 Yr	-	-	-	-	-	-	
P14	DPZ0-3-5-6	M	1 Yr	-		-	-	-	-	
P15	DPM2-3-6-6	M	1 Yr	-	+	-	-	-	-	1
P16	DPM2-3-6-7	M	1 Yr	-	+	-	-	-	-	1
P17	DPM2-3-6-8	M	1 Yr	-	-	-	-	-	-	
P18	DPS1-3-7-11	M	1 Yr	-	-	+	-	-	-	1

Animal	Animal ID	Sex	Age	Pubertal	Testis	Prostate	Kidney	Tumor	Obesity	Total Disease
P19	DPS1-3-7-12	M	1 Yr	+	+	-	-	-	-	2
P20	DPS1-3-7-13	M	1 Yr	+	-	+	-	-	-	2
P21	DPZ0-3-8-9	M	1 Yr	+	-	-	+	-	-	2
P22	DPZ0-3-8-10	M	1 Yr	+	-	-	-	-	-	1
P23	DPZ0-3-9-8	M	1 Yr	-	+	-	-	-	-	1
P24	DPZ0-3-9-9	M	1 Yr	-	-	-	-	-	-	
P25	DPZ0-3-9-10	M	1 Yr	-	+	-	-	+	-	2
P26	DPS1-3-10-8	M	8 m.	-				+	-	1
P27	DPZ0-3-11-6	M	1 Yr		+		-	-	-	1
P28	DPZ0-3-11-7	M	1 Yr		+		-	-	-	1
P29	DPZ0-3-11-8	M	1 Yr		+	-	-	-	-	1
P30	DPM2-3-12-10	M	1 Yr	-	+	-	-	-	-	1
P31	DPM2-3-12-11	M	1 Yr	-	-	-	-	-	-	
P32	DPM2-3-12-12	M	1 Yr	-	-	-	-	-	-	
P33	DPM2-3-12-13	M	1 Yr	-				-	-	
P34	DPM2-3-12-14	M	1 Yr	-				-	-	
P35	DPM2-3-13-12	M	1 Yr	-	-	+	-	-	-	1
P36	DPM2-3-13-13	M	1 Yr	-	-	+	+	-	-	2
P37	DPM2-3-13-14	M	1 Yr	-	-	-		-	-	

A ‘+’ indicates the presence of disease; A ‘-‘ indicates the absence of disease. A blank cell indicates ‘not evaluated.’ Animal IDs with a ‘C’ belong to Control lineage and those with a ‘P’ belong to Pesticide lineage. See ‘Materials and Methods’ section for disease assessment in rats. The number of animals per litter (litter representation) mean ± SEM used for each specific disease/abnormality was found not to be statistically different between the control versus pesticide lineage animals.

Supplemental Table S4. List of rat sperm differential DNA methylation regions (DMR) found in F3-generation Pesticide linege

Gene Symbol	Chr	Start	Stop	Gene ID	min p-value	Gene Title
Apoptosis						
Pdcd11	1	252412922	252413522	309458	1.3E-09	programmed cell death 11
Siva1	6	137630549	137631439	362791	1.2E-12	SIVA1, apoptosis-inducing factor
Card10	7	116767137	116768035	315120	8.7E-08	caspase recruitment domain family, member 10
Tnfrsf12a	10	12940938	12942568	302965	5.2E-23	tumor necrosis factor receptor superfamily, member 12a
Higd2a	17	16084041	16084831	290999	2.4E-14	HIG1 hypoxia inducible domain family, member 2A
Tnfaip8	18	45084538	45085228	307428	1.8E-13	tumor necrosis factor, alpha-induced protein 8
Cell Cycle						
Cep55	1	242381886	242382486	294074	3.8E-15	centrosomal protein 55kDa
Cdk9	3	11677067	11677767	362110	4.1E-08	cyclin-dependent kinase 9
Cdk5	4	6116554	6117864	140908	9.6E-10	cyclin-dependent kinase 5
Cdk2	7	2006927	2007527	362817	6.1E-09	cyclin dependent kinase 2
Dock6	8	20894272	20895262	367039	4.2E-20	dedicator of cytokinesis 6
Gas8	19	53834037	53834839	361438	2.4E-09	growth arrest specific 8
Pak3	X	34841200	34842210	29433	4.9E-10	p21 protein (Cdc42/Rac)-activated kinase 3
Cytoskeleton-ECM						
Clec11a	1	94792412	94793122	29313	8.0E-08	C-type lectin domain family 11, member a
Actn3	1	207492038	207492749	171009	7.4E-10	actinin alpha 3
Add3	1	259452730	259453611	25230	2.7E-13	adducin 3 (gamma)
Lmo1	1	166741881	166742882	245979	3.4E-08	LIM domain only 1
Krtcap2	2	181416132	181417032	295243	1.2E-10	keratinocyte associated protein 2
Actl6a	2	118918849	118919939	361925	9.2E-14	actin-like 6A
Flg	2	186309317	186310200	24641	5.6E-12	filaggrin
Cercam	3	8877244	8878133	296616	2.7E-10	cerebral endothelial cell adhesion molecule
LOC313641	5	156333892	156334783	313641	1.6E-10	perlecan
Tpm2	5	60003516	60004592	500450	2.1E-09	tropomyosin 2, beta
Icam5	8	20966220	20967039	313785	7.6E-09	intercellular adhesion molecule 5, telencephalin
Cspg5	8	114620901	114621591	50568	7.1E-09	chondroitin sulfate proteoglycan 5
LOC100363366	8	30972488	30973193	100363366	1.0E-12	amyloid beta (A4) precursor-like protein 2-like
Tpm1	8	71356826	71357726	24851	2.3E-13	tropomyosin 1, alpha
Lasp1	10	86551715	86552513	29278	5.6E-08	LIM and SH3 protein 1
Mapt	10	93411242	93412032	29477	1.9E-07	microtubule-associated protein tau

Gene Symbol	Chr	Start	Stop	Gene ID	min p-value	GeneTitle
Mprip	10	45975563	45976456	116504	7.5E-16	myosin phosphatase Rho interacting protein
Snip	10	86320851	86321529	56029	1.0E-10	SNAP25-interacting protein
Snip	10	86323498	86324403	56029	9.7E-10	SNAP25-interacting protein
Ncam2	11	20423008	20423897	288280	7.4E-08	neural cell adhesion molecule 2
Vcl	15	3575689	3576884	305679	1.1E-11	vinculin
Fat1	16	50588806	50589905	83720	2.4E-13	FAT tumor suppressor homolog 1 (Drosophila)
Tubb2a	17	37138997	37140410	498736	2.5E-17	tubulin, beta 2a
Vim	17	87847877	87848477	81818	1.8E-09	vimentin
Pcdhb15	18	30286538	30287330	291646	1.1E-11	protocadherin beta 15
Cdh11	19	2225447	2226147	84407	3.1E-08	cadherin 11
Lrg1	Un/9	25672410	25673300	367455	2.1E-15	leucine-rich alpha-2-glycoprotein 1
Plin5	Un/9	25672410	25673300	501283	2.1E-15	perilipin 5
Development						
Dmpk	1	78450272	78451687	308405	2.0E-23	dystrophia myotonica-protein kinase
Ggn	1	84303670	84304575	292765	1.7E-07	gametogenetin
Ttyh1	1	69482346	69483230	292597	5.4E-13	tweety homolog 1 (Drosophila)
Six5	1	78450272	78451687	308406	2.0E-23	SIX homeobox 5
Usmg5	1	252412922	252413522	171069	1.3E-09	up-regulated during skeletal muscle growth 5 homolog (mouse)
Dkk2	2	229541018	229541911	295445	1.4E-09	dickkopf homolog 2 (Xenopus laevis)
Sv2c	2	26554389	26554989	29643	2.6E-07	synaptic vesicle glycoprotein 2c
Disp2	3	105283894	105284775	311324	7.9E-09	dispatched homolog 2 (Drosophila)
Lhx6	3	15214211	15214897	311901	5.8E-08	LIM homeobox 6
Ntng2	3	8228607	8229412	311836	3.4E-18	netrin G2
Qser1	3	90155661	90156556	311266	1.4E-09	glutamine and serine rich 1
SPATA2	3	158640784	158641479	114210	1.1E-14	spermatogenesis associated 2
SMO	4	56653034	56653704	25273	1.8E-13	smoothened homolog (Drosophila)
Lbx2	4	117298557	117299157	500224	9.8E-11	ladybird homeobox 2
Bspry	5	79471177	79472257	64027	1.5E-08	B-box and SPRY domain containing
Vwa1	5	172630371	172631649	298683	1.5E-09	von Willebrand factor A domain containing 1
Npc2	6	108814526	108815606	286898	1.1E-45	Niemann-Pick disease, type C2
Bre	6	24791954	24793149	362704	2.0E-09	brain and reproductive organ-expressed protein
Pmel	7	2006927	2007527	362818	6.1E-09	premelanosome protein
Trps1	7	87076226	87077245	299897	3.5E-15	trichorhinophalangeal syndrome I homolog (human)
Tmie	8	115269400	115270189	501061	5.3E-13	transmembrane inner ear
Mll1	8	47836284	47837266	315606	1.4E-08	myeloid/lymphoid or mixed-lineage leukemia 1

Gene Symbol	Chr	Start	Stop	Gene ID	min p-value	GeneTitle
Aamp	9	73610303	73611481	301512	3.2E-08	angio-associated, migratory cell protein
Nlgn2	10	56675163	56676245	117096	9.4E-13	neuroligin 2
Nlgn2	10	56678345	56679370	117096	4.8E-11	neuroligin 2
Hoxb6	10	85032294	85033194	497986	5.8E-18	homeo box B6
Auts2	12	25400693	25401534	498173	2.4E-14	autism susceptibility candidate 2
Pbx1	13	84115851	84116728	304947	3.6E-09	pre-B-cell leukemia homeobox 1
Myog	13	47243170	47244059	29148	3.9E-08	myogenin
Pinx1	15	43125066	43125666	305963	1.1E-14	PIN2-interacting protein 1
Unc13a	16	18853366	18853966	64829	2.4E-08	unc-13 homolog A (C. elegans)
Irx2	17	746309	746989	306657	8.4E-20	iroquois homeobox 2
Irx5	19	15751735	15752521	498918	1.2E-09	iroquois homeobox 5
Nodal	20	29546601	29547322	294503	1.9E-18	nodal homolog (mouse)
Bex2	X	123323586	123324186	363498	7.7E-09	brain expressed X-linked 2
Bex4	X	123441916	123442626	501624	8.9E-09	brain expressed gene 4
DNA Repair						
Rad54l2	8	111984966	111985566	363135	3.7E-07	Rad54 like 2 (S. cerevisiae)
Electron Transport						
Cox6b2	1	67810664	67811751	654441	3.1E-08	cytochrome c oxidase subunit VIb polypeptide 2
Prdx5	1	209585932	209587138	113898	7.6E-17	peroxiredoxin 5
Cyp24a1	3	161553659	161554660	25279	1.3E-13	cytochrome P450, family 24, subfamily a, polypeptide 1
Cyp4f5	7	13119902	13120699	286905	6.6E-25	cytochrome P450, family 4, subfamily f, polypeptide 5
Nxnl1	16	18769847	18771129	306342	5.1E-13	nucleoredoxin-like 1
Epigenetics						
Suv420h2	1	67823420	67824426	308345	5.8E-10	suppressor of variegation 4-20 homolog 2 (Drosophila) <histone-lysine N-methyltransferase SUV420H2>
Eed	1	146589901	146590900	293104	7.2E-08	embryonic ectoderm development
Smarca2	1	230016032	230016827	361745	2.8E-11	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
CXXC4	2	231704355	231705138	83824	3.5E-08	CXXC finger 4
Setd5	4	148949953	148951038	297514	3.4E-12	SET domain containing 5
H1f0	7	117001353	117002342	24437	1.3E-12	H1 histone family, member 0
Cbx6	7	118069182	118069782	315136	3.4E-10	chromobox homolog 6
Satb2	9	55824749	55825838	501145	3.2E-13	SATB homeobox 2
Kdm6b	10	56204571	56206172	363630	1.4E-16	lysine (K)-specific demethylase 6B
Phf15	10	37379987	37381795	303113	1.2E-13	PHD finger protein 15
Tbx2	10	74084425	74085225	303398	5.3E-33	T-box 2

Gene Symbol	Chr	Start	Stop	Gene ID	min p-value	GeneTitle
ASMT	12	16815952	16816847	246281	8.8E-18	acetylserotonin O-methyltransferase
Asmtl	12	16824308	16825214	288527	1.0E-09	acetylserotonin O-methyltransferase-like
Kdm2b	12	34672184	34673309	304495	3.8E-14	lysine (K)-specific demethylase 2B
Gadd45g	17	19231639	19232721	291005	1.3E-18	growth arrest and DNA-damage-inducible, gamma
Hist1h2bn	17	50352153	50352753	291157	3.1E-17	histone cluster 1, H2bn
Hdac3	18	30875498	30876184	84578	3.2E-14	histone deacetylase 3
Golgi Apparatus						
B3gnt8	1	80834920	80835615	308440	4.7E-09	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8
Mgat4b	10	35775455	35776055	303100	7.2E-12	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B
Growth Factors						
Gdnf	2	57403318	57404513	25453	3.4E-22	glial cell derived neurotrophic factor
MDK	3	76310613	76312125	81517	1.4E-13	midkine
Sspo	4	76528498	76529282	474348	3.1E-12	SCO-spondin
Ntf3	4	162504664	162505639	81737	3.7E-12	neurotrophin 3
WNT10B	7	137545980	137547070	315294	1.3E-13	wingless-type MMTV integration site family, member 10B
Dlk2	9	10243248	10244843	316232	4.1E-07	delta-like 2 homolog (Drosophila)
VEGFA	9	10521846	10522726	83785	1.8E-07	vascular endothelial growth factor A
Wnt3	10	92946863	92947763	24882	9.3E-11	wingless-type MMTV integration site family, member 3
Sept5	11	84364223	84365013	116728	2.4E-08	septin 4
Vgf	12	20905109	20906021	29461	4.9E-10	VGF nerve growth factor inducible
Hgfac	14	81353598	81354616	58947	4.2E-15	hepatocyte growth factor activator
Sept11	14	16548270	16549455	305227	9.4E-19	septin 11
LTB	20	3667367	3668263	361795	4.9E-07	lymphotoxin beta (TNF superfamily, member 3)
Immune Response						
Igsf10	2	148733771	148734471	310448	1.1E-10	immunoglobulin superfamily, member 10
Cd82	3	77875422	77876242	83628	1.0E-10	Cd82 molecule

Gene Symbol	Chr	Start	Stop	Gene ID	min p-value	GeneTitle
Cd276	8	62361422	62362307	315716	1.5E-11	Cd276 molecule
Spag7	10	57548762	57549583	303260	4.8E-07	sperm associated antigen 7
Spag7	10	57549874	57551068	303260	1.2E-13	sperm associated antigen 7
Fcgr2a	13	86913190	86913875	116591	1.7E-13	Fc fragment of IgG, low affinity IIa, receptor (CD32)
RT1-CE7	20	3416588	3417188	368153	8.1E-18	RT1 class I, locus CE7
RT1_CE13	20	89064	90548	414790	1.1E-12	RT1 class I, locus CE13
Metabolism & Transport						
Apoe	1	79005645	79006565	25728	2.3E-12	apolipoprotein E
Syt3	1	94866084	94867099	25731	2.5E-10	synaptotagmin III
Sult2b1	1	96264926	96265526	292915	2.2E-06	sulfotransferase family, cytosolic, 2B, member 1
Scd	1	249358774	249359374	83792	6.1E-07	stearoyl-CoA desaturase (delta-9-desaturase)
Syt7	1	212877078	212877873	59267	9.0E-09	synaptotagmin VII
Dhdpsl	1	248805982	248806667	293949	2.2E-06	dihydrodipicolinate synthase-like, mitochondrial
Fah	1	140875689	140876469	29383	2.7E-13	fumarylacetoacetate hydrolase
Slc1a1	1	232487265	232487865	25550	2.8E-11	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1
Kcnn3	2	181715756	181716441	54263	4.8E-13	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3
Slc25a31	2	127697443	127698323	689108	1.2E-10	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31
Slc30a5	2	31636928	31637528	294698	2.4E-09	solute carrier family 30 (zinc transporter), member 5
Slc7a14	2	116461907	116462597	499587	1.4E-09	solute carrier family 7 (cationic amino acid transporter, y+ system), member 14
Acoxl	3	115365654	115366254	296138	2.2E-09	acyl-Coenzyme A oxidase-like
Clstn3	4	160665157	160666372	171393	1.1E-10	calsyntenin 3
Gapdh	4	161285353	161286243	24383	3.7E-06	glyceraldehyde-3-phosphate dehydrogenase
Mat2a	4	105744927	105745527	171347	6.9E-15	methionine adenosyltransferase II, alpha
Magi2	4	11440081	11441061	113970	3.7E-15	membrane associated guanylate kinase, WW and PDZ domain containing 2
Sh3bgrl3	5	152877492	152878472	298544	1.3E-10	SH3 domain binding glutamic acid-rich protein-like 3
Echdc2	5	129265151	129266066	298381	7.1E-09	enoyl Coenzyme A hydratase domain containing 2

Gene Symbol	Chr	Start	Stop	Gene ID	min p-value	GeneTitle
Clstn1	5	166671398	166672378	313717	1.5E-16	calsyntenin 1
Decr1	5	30519336	30520146	117543	2.3E-07	2,4-dienoyl CoA reductase 1, mitochondrial
Pusl1	5	172749107	172749787	362681	1.4E-10	pseudouridylate synthase-like 1
Rbks	6	24791954	24793149	362706	2.0E-09	ribokinase
Srd5a2	6	21452565	21453390	64677	3.8E-09	steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 2)
Pygl	6	92340725	92341524	64035	2.3E-08	phosphorylase, glycogen, liver
Rtn1	6	94681088	94681888	116644	1.3E-12	reticulon 1
SLC39A3	7	10171471	10172556	314637	5.2E-08	solute carrier family 39 (zinc transporter), member 3
Cacnb3	7	137383447	137384546	25297	2.1E-10	calcium channel, voltage-dependent, beta 3 subunit
Carm1	8	20650587	20651612	363026	8.2E-15	coactivator-associated arginine methyltransferase 1
Pkm2	8	63486309	63487492	25630	2.5E-11	pyruvate kinase, muscle
Stt3a	8	38016123	38016924	500972	1.4E-10	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)
Accn4	9	74724160	74724955	63882	2.2E-10	amiloride-sensitive cation channel 4, pituitary
Gnptg	10	14488661	14489341	287134	9.5E-11	N-acetylglucosamine-1-phosphate transferase, gamma subunit
Plscr3	10	56687180	56687875	360549	1.4E-09	phospholipid scramblase 3
KCNH4	10	89696676	89697576	114032	2.2E-08	potassium voltage-gated channel, subfamily H (eag-related), member 4
Slc9a3r1	10	105236801	105237401	59114	8.0E-08	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1
Clcn2	11	82426660	82427380	29232	3.9E-07	chloride channel 2
Clcn2	11	82429579	82430269	29232	1.0E-08	chloride channel 2
Atp6v1a	11	58125901	58126716	685232	2.1E-09	ATPase, H+ transporting, lysosomal V1 subunit A
Acads	12	42765275	42765875	64304	1.1E-11	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain
Gltp	12	43194112	43195012	288707	7.0E-08	glycolipid transfer protein
Mepce	12	19853018	19853828	304361	7.0E-11	methylphosphate capping enzyme
Nmnat2	13	67969800	67970695	289095	2.4E-23	nicotinamide nucleotide adenylyltransferase 2
Tomm40b	13	87111787	87112902	304971	5.8E-16	translocase of outer mitochondrial membrane 40 homolog B (yeast)
Rhbdd3	14	85758629	85759334	289753	1.7E-09	rhomboid domain containing 3
Enoph1	14	10859038	10860028	305177	1.6E-18	enolase-phosphatase 1

Gene Symbol	Chr	Start	Stop	Gene ID	min p-value	GeneTitle
Qdpr	14	70741367	70742367	64192	3.7E-11	quinoid dihydropteridine reductase
Dpysl2	15	46412626	46413517	25416	1.6E-11	dihydropyrimidinase-like 2
Slc6a7	18	56976220	56977132	117100	1.8E-09	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7
Best2	19	24802086	24803166	364973	2.2E-14	bestrophin 2
Gpt2	19	22914732	22915711	307759	1.2E-08	glutamic pyruvate transaminase (alanine aminotransferase) 2
Gstt2	20	13218263	13218863	29487	2.7E-07	glutathione S-transferase, theta 2
Tap1	20	4789651	4790543	24811	2.9E-10	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)
Proteolysis						
Ctsd	1	202632820	202633700	171293	8.6E-21	cathepsin D
Psma1	1	172248407	172249402	29668	4.0E-16	proteasome (prosome, macropain) subunit, alpha type 1
Serpinh1	1	156673475	156674287	29345	1.9E-07	serine (or cysteine) peptidase inhibitor, clade H, member 1
Ubxn11	5	152877492	152878472	192207	1.3E-10	UBX domain protein 11
Ubxn2b	5	19629204	19629903	312965	1.3E-12	UBX domain protein 2B
Adamts15	7	10873782	10874784	300474	8.7E-17	ADAM metallopeptidase with thrombospondin type 1 motif, 15
Prssl1	7	11424819	11425640	408241	5.9E-15	protease, serine-like 1
Xpnpep3	7	119728411	119729114	685823	4.7E-07	X-prolyl aminopeptidase (aminopeptidase P) 3, putative
Ubl5	8	19661648	19662660	500954	3.3E-08	ubiquitin-like 5
AMZ2	10	98899341	98900231	360650	1.5E-07	archaelysin family metallopeptidase 2
Tmub2	10	91364446	91365238	303567	2.4E-07	transmembrane and ubiquitin-like domain containing 2
Mmp17	12	28171455	28172150	288626	2.6E-13	matrix metallopeptidase 17
Gene Symbol	Chr	Start	Stop	Gene ID	min p-value	GeneTitle
Mmp2	19	15274320	15274920	81686	3.5E-10	matrix metallopeptidase 2
Psmb8	20	4789651	4790543	177046	2.9E-10	proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7)
Pi16	20	7642807	7643887	294312	5.6E-12	peptidase inhibitor 16
Receptors & Binding Proteins						
Pvrl2	1	79058741	79060044	308417	1.2E-14	poliovirus receptor-related 2
Nccrp1	1	83656823	83657423	292755	1.5E-07	non-specific cytotoxic cell receptor protein 1 homolog (zebrafish)
Olr168	1	162485084	162485684	293315	5.0E-07	olfactory receptor 168

Gene Symbol	Chr	Start	Stop	Gene ID	min p-value	GeneTitle
P2RY6	1	158376135	158377025	117264	1.0E-13	pyrimidinergic receptor P2Y, G-protein coupled, 6
Osbp	1	214811944	214812740	365410	4.2E-13	oxysterol binding protein
Ranbp3l	2	58725068	58726193	294789	1.0E-11	RAN binding protein 3-like
Olr414	3	163798239	163798839	56821	6.5E-07	olfactory receptor 414
Spsb2	4	160931316	160932317	297592	6.6E-23	splA/ryanodine receptor domain and SOCS box containing 2
Sec23a	6	79706895	79707495	58817	1.6E-08	Sec23 homolog A (S. cerevisiae)
KISS1R	7	11291511	11292218	78976	5.5E-10	KISS1 receptor
Igfbp2	9	71966094	71967073	25662	2.2E-09	insulin-like growth factor binding protein 2
Olr1415	10	44132028	44132628	405059	1.1E-06	olfactory receptor 1415
Il1rap	11	76225521	76226241	25466	5.2E-08	interleukin 1 receptor accessory protein
Pvrl3	11	55842225	55843130	288124	2.4E-08	poliovirus receptor-related 3
IL3RA	12	16829845	16831365	246144	2.6E-09	interleukin 3 receptor, alpha
Opn3	13	91426959	91427559	498289	8.1E-12	opsin 3
Aebp1	14	86524798	86525695	305494	1.2E-07	AE binding protein 1
Heatr1	17	68654760	68655860	361262	3.9E-09	HEAT repeat containing 1
Necab2	19	49691211	49692111	170928	2.3E-11	N-terminal EF-hand calcium binding protein 2
Prrt1	20	4220107	4221198	406167	7.8E-20	proline-rich transmembrane protein 1
Olr1687	20	4259416	4260219	309574	3.1E-07	olfactory receptor 1687
Olr1684	20	3497439	3498621	294151	1.8E-10	olfactory receptor 1684
Signaling						
Brsk1	1	67876013	67876613	499073	3.0E-08	BR serine/threonine kinase 1
Rabac1	1	80274216	80275308	83583	1.3E-14	Rab acceptor 1 (prenylated)
Inppl1	1	159291743	159292748	65038	7.0E-12	inositol polyphosphate phosphatase-like 1
Calca	1	172690039	172691119	24241	9.8E-19	calcitonin-related polypeptide alpha
Shank1	1	94792412	94793122	78957	8.0E-08	SH3 and multiple ankyrin repeat domains 1
Cnksr3	1	37957713	37958623	308113	9.8E-18	Cnksr family member 3
Gene Symbol	Chr	Start	Stop	Gene ID	min p-value	GeneTitle
Gng8	1	77218978	77219578	245986	3.0E-21	guanine nucleotide binding protein (G protein), gamma 8
Mrgprg	1	204155989	204156589	309133	2.2E-10	MAS-related GPR, member G
Cks1b	2	181615695	181616678	499655	3.2E-11	CDC28 protein kinase regulatory subunit 1B
RAB13	2	182460590	182461570	81756	7.6E-27	RAB13, member RAS oncogene family
Shc1	2	181615695	181616678	85385	3.2E-11	SHC (Src homology 2 domain containing) transforming protein 1
Ankrd34a	2	191395150	191396232	295283	5.7E-20	ankyrin repeat domain 34A

Gene Symbol	Chr	Start	Stop	Gene ID	min p-value	GeneTitle
ANP32E	2	190715161	190716362	361999	5.7E-18	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
Egflam	2	56666235	56667515	365691	3.6E-11	EGF-like, fibronectin type III and laminin G domains
Notch2	2	192855441	192856541	29492	1.5E-19	Notch homolog 2 (Drosophila)
Ywhab	3	154925245	154926019	56011	2.1E-11	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide
Tyro3	3	106308759	106310151	25232	1.3E-08	TYRO3 protein tyrosine kinase
Ptprz1	4	49267340	49268020	25613	1.7E-09	protein tyrosine phosphatase, receptor-type, Z polypeptide 1
Acap3	5	172749107	172749787	313772	1.4E-10	ArfGAP with coiled-coil, ankyrin repeat and PH domains 3
LOC683719	5	86273089	86273964	683719	1.2E-11	similar to RAS and EF hand domain containing
Lpar1	5	76571751	76572551	116744	2.0E-13	lysophosphatidic acid receptor 1
Pink1	5	157102069	157102960	298575	4.5E-09	PTEN induced putative kinase 1
Akap6	6	73042917	73043604	64553	9.4E-61	A kinase (PRKA) anchor protein 6
Itga7	7	2229865	2231454	81008	4.2E-11	integrin, alpha 7
Palm	7	11424819	11425640	170673	5.9E-15	paralemmin
Shc2	7	11583824	11584614	314612	2.4E-16	SHC (Src homology 2 domain containing) transforming protein 2
Grina	7	114277254	114278461	266668	2.9E-19	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)
Mapk11	7	127449653	127450253	689314	2.4E-17	mitogen-activated protein kinase 11
MAPK8IP2	7	127772817	127773697	315220	3.0E-08	mitogen-activated protein kinase 8 interacting protein 2
Shank3	7	127816023	127816717	59312	1.7E-26	SH3 and multiple ankyrin repeat domains 3
Itga5	7	142276341	142277241	315346	5.0E-11	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
Anp32a	8	66488052	66489373	25379	1.6E-08	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A
Calml4	8	67005516	67006116	691455	1.7E-25	calmodulin-like 4
Snx33	8	60673757	60674357	315696	1.4E-27	sorting nexin 33
Efnb3	10	56378095	56379587	360546	2.0E-28	ephrin B3
Anxa6	10	40438545	40439245	79125	7.7E-11	annexin A6
PLEKHH3	10	90191441	90192426	360634	2.2E-10	pleckstrin homology domain containing, family H (with MyTH4 domain) member 3

Gene Symbol	Chr	Start	Stop	Gene ID	min p-value	GeneTitle
Ywhae	10	63072423	63073223	29753	9.8E-07	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide
Camk2n2	11	82519950	82520632	59314	4.5E-09	calcium/calmodulin-dependent protein kinase II inhibitor 2
Akap17a	12	16824308	16825214	288526	1.0E-09	A kinase (PRKA) anchor protein 17A
Gnb2	12	19601090	19602388	81667	8.9E-22	guanine nucleotide binding protein (G protein), beta polypeptide 2
Ptprg	15	15129826	15130718	171357	1.2E-07	protein tyrosine phosphatase, receptor type, G
Dda1	16	18640032	18640843	688813	1.8E-08	DET1 and DDB1 associated 1
Gtpbp3	16	18656594	18657490	290633	2.7E-08	GTP binding protein 3
Dusp26	16	64958383	64959068	306527	1.3E-09	dual specificity phosphatase 26 (putative)
Psd2	18	28594728	28596406	307500	2.5E-07	pleckstrin and Sec7 domain containing 2
Pdp2	19	31389541	31390235	246311	2.4E-09	pyruvate dehyrogenase phosphatase catalytic subunit 2
Ppp1r10	20	2984086	2984883	65045	2.8E-26	protein phosphatase 1, regulatory subunit 10
Gucy1a2	Un	47455432	47456222	66012	8.1E-11	guanylate cyclase 1, soluble, alpha 2
Ptprs	Un	25300105	25300805	25529	2.5E-16	protein tyrosine phosphatase, receptor type, S
Gprasp1	X	1331319	1331919	171407	4.1E-08	G protein-coupled receptor associated sorting protein 1
Transcription						
Mypop	1	78344996	78345976	499090	8.1E-08	Myb-related transcription factor, partner of profilin
Cic	1	80557664	80558744	308435	6.2E-20	capicua homolog (Drosophila)
Clip3	1	85238795	85239697	308493	6.2E-08	CAP-GLY domain containing linker protein 3
Scaf1	1	95488479	95489374	56081	2.8E-11	SR-related CTD-associated factor 1
Zc3h12d	1	250472051	250472651	308266	2.0E-06	zinc finger CCCH type containing 12D
PITX3	1	251356410	251357495	29609	4.3E-42	paired-like homeodomain 3
Nr2f2	1	125286094	125286799	113984	4.3E-10	nuclear receptor subfamily 2, group F, member 2
Pax2	1	249895584	249896463	293992	2.3E-09	paired box 2
Zfp687	2	189914894	189915882	310660	2.0E-12	zinc finger protein 687
Mov10	2	200075206	200076102	310756	1.9E-08	Moloney leukemia virus 10
Nras	2	198292829	198293429	24605	3.1E-18	neuroblastoma ras oncogene
Rai14	2	60059148	60059838	294804	8.4E-09	retinoic acid induced 14
Nfe2l2	3	58393873	58394894	83619	1.5E-10	nuclear factor, erythroid derived 2, like 2
Nr4a2	3	38872480	38873296	54278	3.1E-08	nuclear receptor subfamily 4, group A, member 2

Gene Symbol	Chr	Start	Stop	Gene ID	min p-value	GeneTitle
Scrt2	3	142434466	142435066	366229	1.1E-07	scratch homolog 2, zinc finger protein (Drosophila)
Sp5	3	52695364	52696343	296510	1.2E-09	Sp5 transcription factor
Abtb1	4	122936490	122937308	297432	4.9E-09	ankyrin repeat and BTB (POZ) domain containing 1
Ing3	4	48255109	48255809	312154	2.0E-19	inhibitor of growth family, member 3
Ahdc1	5	152101596	152102486	362617	9.3E-15	AT hook, DNA binding motif, containing 1
Fbxo2	5	165237874	165238963	85273	4.9E-19	F-box protein 2
Med8	5	138890220	138890995	362575	1.3E-09	mediator complex subunit 8
NR4A3	5	64719277	64719987	58853	5.2E-16	nuclear receptor subfamily 4, group A, member 3
RGD1563216	6	108814526	108815606	500694	1.1E-45	similar to HESB like domain containing 1
Sp8	6	146168329	146168929	299499	2.1E-08	Sp8 transcription factor
Dnajc14	7	2104216	2104816	114481	9.4E-11	DnaJ (Hsp40) homolog, subfamily C, member 14
Scx	7	114503595	114504375	680712	8.6E-20	scleraxis
Dnajc22	7	137872861	137874254	362998	1.1E-13	DnaJ (Hsp40) homolog, subfamily C, member 22
Zfp385a	7	142249435	142250435	685474	4.4E-12	zinc finger protein 385A
Nr4a1	7	140012571	140013171	79240	1.6E-18	nuclear receptor subfamily 4, group A, member 1
Arid3b	8	61607737	61608550	367092	5.6E-09	AT rich interactive domain 3B (Bright like)
Bcl9l	8	47449901	47450705	300673	5.0E-14	B-cell CLL/lymphoma 9-like
Klhdc3	9	10051392	10053207	363192	5.2E-11	kelch domain containing 3
Foxp4	9	8507797	8508795	363185	1.2E-09	forkhead box P4
HOXB7	10	85016559	85017435	497985	4.9E-07	homeo box B7
Nfe2l1	10	85586351	85587341	360610	3.5E-12	nuclear factor, erythroid derived 2,-like 1
Scand3	12	27861394	27861994	288622	1.8E-09	SCAN domain containing 3
Higd2al1	12	1366187	1366787	688606	3.9E-10	HIG1 hypoxia inducible domain family, member 2A-like 1
Ewsr1	14	85758629	85759334	289752	1.7E-09	Ewing sarcoma breakpoint region 1
Ndrg2	15	27346566	27347666	171114	4.8E-28	N-myc downstream regulated gene 2
Zic5	15	107598237	107599053	361095	2.9E-10	Zic family member 5 (odd-paired homolog, Drosophila)
Id4	17	22528169	22528964	291023	4.3E-13	inhibitor of DNA binding 4
Arid4b	17	59458282	59459273	84481	9.8E-09	AT rich interactive domain 4B (Rbp1 like)
Gata6	18	2502507	2503598	29300	2.8E-09	GATA binding protein 6
LOC685382	18	15772845	15773445	685382	8.9E-13	similar to Proline-rich nuclear receptor coactivator 1
Znf521	18	5147539	5148225	307579	3.5E-08	zinc finger protein 521
LYL1	19	25113855	25114855	304663	7.9E-22	lymphoblastic leukemia derived sequence 1

Gene Symbol	Chr	Start	Stop	Gene ID	min p-value	GeneTitle
Nudt7	19	41441292	41442411	361413	3.4E-15	nudix (nucleoside diphosphate linked moiety X)-type motif 7
Armcx2	X	122265349	122266438	367903	4.0E-29	armadillo repeat containing, X-linked 2
Zmym3	X	89491287	89491987	317260	3.0E-09	zinc finger, MYM-type 3
Translation & Protein Modification						
Tarsl2	1	120049966	120051055	308701	4.0E-13	threonyl-tRNA synthetase-like 2
Ptrh1	3	11749922	11750919	362113	7.0E-11	peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae)
Rps8	5	137468053	137469043	65136	2.4E-08	ribosomal protein S8
Padi2	5	159761520	159762334	29511	6.7E-12	peptidyl arginine deiminase, type II
Rpl8	7	114953948	114955044	26962	1.0E-10	ribosomal protein L8
Syncrip	8	93822110	93822710	363113	9.8E-12	synaptotagmin binding, cytoplasmic RNA interacting protein
Igf2bp1	10	84714285	84715211	303477	1.6E-12	insulin-like growth factor 2 mRNA binding protein 1
Npm1	10	18062093	18062873	25498	2.0E-19	nucleophosmin (nucleolar phosphoprotein B23, numatrin)
Eif4g1	11	82470316	82471209	287986	1.6E-12	eukaryotic translation initiation factor 4 gamma, 1
Hnrpdl	14	10859038	10860028	305179	1.6E-18	heterogeneous nuclear ribonucleoprotein D-like
Aars	19	38413210	38414035	292023	1.1E-07	alanyl-tRNA synthetase
Mrps18b	20	2984086	2984883	294230	2.8E-26	mitochondrial ribosomal protein S18B
Rpl36	Un	25163917	25164597	58927	4.1E-24	ribosomal protein L36
Miscellaneous & Unknown						
RGD1565346	1	93660805	93661590	499139	1.0E-10	similar to expressed sequence C80587
RGD1565305	1	93866197	93866982	499141	9.8E-10	similar to RIKEN cDNA 4931406B18
Tmem160	1	76716621	76717399	292654	1.3E-07	transmembrane protein 160
Trim3	1	163361976	163362576	83616	5.1E-08	tripartite motif-containing 3
Tsku	1	155621658	155622558	308843	6.0E-36	tsukushin
NSCAN pred chr1.1565.a	1	176442929	176443636		1.1E-07	
RGD1307615	3	3780798	3781496	362084	9.2E-11	similar to hypothetical protein FLJ13045
RGD1311517	5	172951361	172952061	313775	1.4E-07	similar to RIKEN cDNA 9430015G10
Gene Symbol	Chr	Start	Stop	Gene ID	min p-value	GeneTitle
Wdr8	5	171103703	171104382	366515	5.4E-08	WD repeat domain 8
NSCAN pred chr5.714.a	5	125316795	125317615		1.6E-07	
Birc6	6	20847680	20848580	313876	3.5E-13	baculoviral IAP repeat-containing 6
Crip	6	138159304	138160009	691657	2.4E-10	cysteine-rich intestinal protein

Gene Symbol	Chr	Start	Stop	Gene ID	min p-value	GeneTitle
Wdr35l	6	32462311	32462988	503018	5.7E-10	WD repeat domain 35-like
NSCAN pred chr6.1025.a	6	143691197	143692302		5.8E-12	
NSCAN pred chr8.1119.a	8	123867973	123869170		3.3E-11	
NSCAN pred chr8.784.a	8	85203182	85203992		2.3E-07	
NSCAN pred chr8.1047.a	8	114860374	114861274		6.7E-13	
Nme3	10	14145576	14146376	85269	1.5E-09	non-metastatic cells 3, protein expressed in
Tmem95	10	56720709	56721596	691982	3.7E-09	transmembrane protein 95
Fam117a	10	84021838	84023150	497983	8.9E-09	family with sequence similarity 117, member A
RGD1565744	10	14488661	14489341	360494	9.5E-11	similar to RIKEN cDNA 0610007P22
RGD1311899	12	42954418	42955018	288704	2.7E-09	similar to RIKEN cDNA 2210016L21 gene
RGD1560846	12	6095843	6096542	498133	3.5E-13	similar to hypothetical protein MGC40178
rCG21620-like	12	34588608	34589612	100359816	3.0E-12	rCG21620-like
NSCAN pred chr12.007.a	12	1019708	1020388		5.4E-10	
Fam72a	13	44451758	44452849	681249	1.1E-10	family with sequence similarity 72, member A
RGD1307161	13	99339499	99340519	305031	2.0E-22	similar to 0610010K06Rik protein
NSCAN pred chr14.352.a	14	49589568	49590168		2.2E-11	
NSCAN pred chr17.082.a	17	12540665	12541742		7.5E-11	
RGD1562080	18	12945779	12946669	498827	7.3E-11	similar to Hypothetical protein CBG10141
NSCAN pred chr19.598.a	19	56135908	56136508		4.5E-08	
NSCAN chr20.066.a	20	3442365	3443350		8.6E-23	
RGD1560927	X	7709114	7709808	501507	6.1E-09	RGD1560927
NSCAN pred chrX.046.a	X	7961753	7962453		3.4E-09	
NSCAN pred chrX.568.a	X	90946064	90947069		1.6E-09	
EST's						
RGD1561205	5	149686351	149687140	500557	1.1E-07	
RGD1562342	7	2104216	2104816	500762	9.4E-11	similar to RIKEN cDNA 1110012D08
RGD1563441	10	56132674	56133469	497935	3.0E-07	similar to RIKEN cDNA A030009H04
TL0ABA42YC21 mRNA sequence	20	6067533	6068428		7.7E-12	

Supplementary Table S5. Top KEGG Pathways Enriched with Pesticide lineage gene lists

Pathway Name	# Genes Affected	# Genes in Pathway	Impact Factor
MAPK signaling pathway	8	253	2.11
Focal adhesion	8	187	5.7
Pathways in cancer	8	321	1.9
Phagosome	7	191	NA
Cell adhesion molecules (CAMs)	7	151	5.5
Neurotrophin signaling pathway	7	129	NA
Regulation of actin cytoskeleton	6	204	2.9
HTLV-I infection	6	296	NA
Chemokine signaling pathway	5	178	NA
Axon guidance	5	123	3.8
Glutamatergic synapse	5	130	NA
Alzheimer's disease	5	213	1.3
Herpes simplex infection	5	207	NA
Transcriptional misregulation in cancers	5	182	NA
Hypertrophic cardiomyopathy (HCM)	5	85	NA
Dilated cardiomyopathy	5	94	NA
ErbB signaling pathway	4	83	3.7
Cytokine-cytokine receptor interaction	4	193	1.4
Cell cycle	4	117	1.6
Protein processing in endoplasmic reticulum	4	165	NA
Endocytosis	4	231	NA
Cardiac muscle contraction	4	81	3.4
Wnt signaling pathway	4	142	2.1
VEGF signaling pathway	4	69	4.3

Pathway Name	# Genes Affected	# Genes in Pathway	Impact Factor
Adherens junction	4	73	3.6
Tight junction	4	128	1.9
Gap junction	4	90	2.8
Natural killer cell mediated cytotoxicity	4	98	2.7
Leukocyte transendothelial migration	4	116	2.2
Olfactory transduction	4	732	0.003
Insulin signaling pathway	4	130	2.9
Parkinson's disease	4	157	1.7
Bacterial invasion of epithelial cells	4	72	NA
Arrhythmogenic right ventricular cardiomyopathy (ARVC)	4	73	NA
Purine metabolism	3	169	NA
Ribosome	3	77	2.1
Neuroactive ligand-receptor interaction	3	259	0.2
Oocyte meiosis	3	115	NA
p53 signaling pathway	3	67	NA
Lysosome	3	124	NA
Hedgehog signaling pathway	3	51	2.9
ECM-receptor interaction	3	74	2.2
Antigen processing and presentation	3	100	2.0
T cell receptor signaling pathway	3	110	1.3
Cholinergic synapse	3	112	NA
Serotonergic synapse	3	132	NA
Dopaminergic synapse	3	132	NA
GnRH signaling pathway	3	91	1.7

Pathway Name	# Genes Affected	# Genes in Pathway	Impact Factor
Melanogenesis	3	96	1.6
Tuberculosis	3	69	NA
Renal cell carcinoma	3	69	2.2
Glioma	3	64	2.4
Prostate cancer	3	91	1.7
Basal cell carcinoma	3	51	3.0
Bladder cancer	3	36	3.8
Chronic myeloid leukemia	3	78	2.1
Systemic lupus erythematosus	3	114	1.6
Rheumatoid arthritis	3	90	NA
Viral myocarditis	3	109	NA

The KEGG pathway with number of associated DMR genes, total number of genes in pathway, and calculated impact factor (Wayne State University, Intelligent Systems and Bioinformatics Laboratory, www.vortex.cs.wayne.edu/ontoexpress) presented. The NA indicates not available.