

F1 Generation: DMC and DMR count in Female and Male Offspring									
Differentially Methylated CpGs (DMCs)									
5mC	10 ppb iAs				245 ppb iAs				
	Female		Male		Female		Male		
Hypermethylated	259	66%	299	65%	157	61%	265	64%	
Hypomethylated	132	34%	196	42%	99	39%	151	36%	
Total	391		462		256		416		
Differentially Methylated Regions (DMRs)									
5mC	10 ppb iAs				245 ppb iAs				
	Female		Male		Female		Male		
Hypermethylated	4	80%	3	43%	-	0%	9	82%	
Hypomethylated	1	20%	4	57%	-	0%	2	18%	
Total	5		7		-		11		
F2 Generation: DMC and DMR count in Female and Male Grand-Offspring									
Differentially Methylated CpGs (DMCs)									
5mC	10 ppb iAs				245 ppb iAs				
	Female		Male		Female		Male		
Hypermethylated	320	60%	140	54%	156	43%	144	52%	
Hypomethylated	217	40%	118	46%	208	57%	133	48%	
Total	537		258		364		277		
Differentially Methylated Regions (DMRs)									
5mC	10 ppb iAs				245 ppb iAs				
	Female		Male		Female		Male		
Hypermethylated	9	56%	1	100%	1	20%	1	100%	
Hypomethylated	7	44%	-	-	4	80%	-	-	
Total	16		1		5		1		

Table 1 *Differential Methylation Across Generation, Sex, and Dose in Liver by RRBS Data* Liver tissue from F1 and F2 offspring at exposures 10 ppb and 245 ppb were assessed for differential DNA methylation as a result of in utero exposure. RRBS differential methylation was identified by *DSS* package in R studio.