

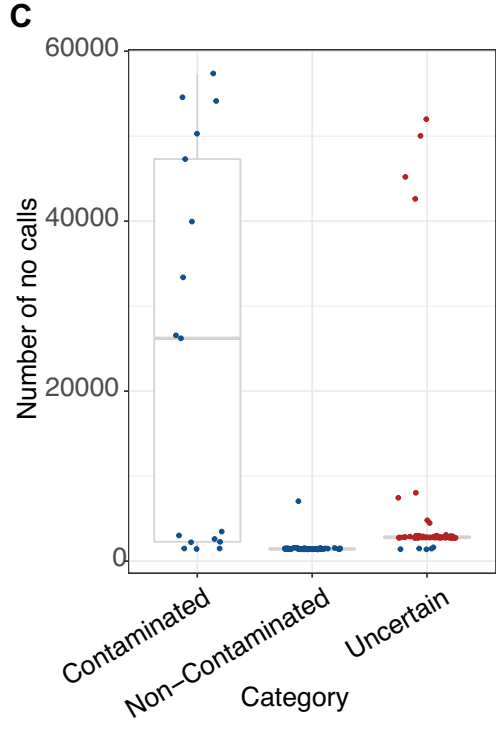
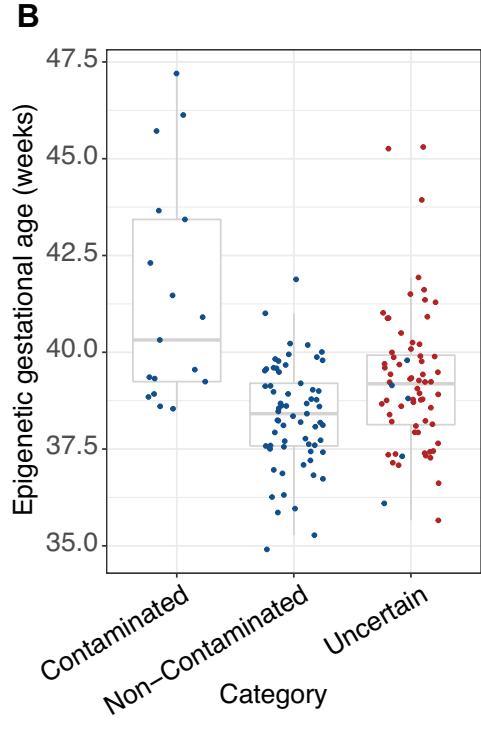
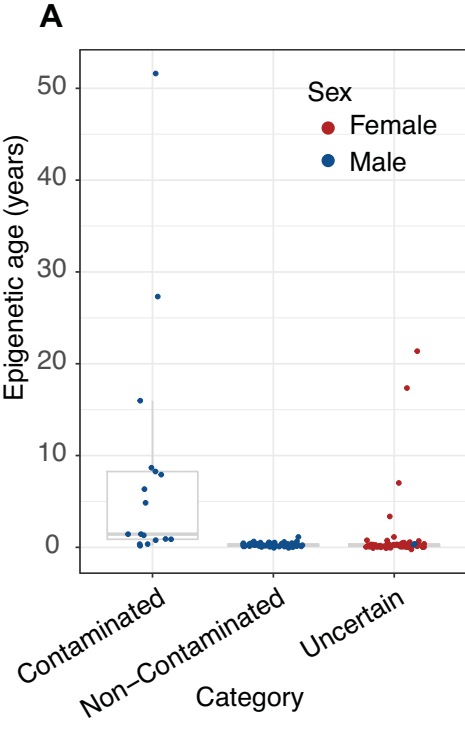
Tables

Table 1: Primer sequences used for pyrosequencing

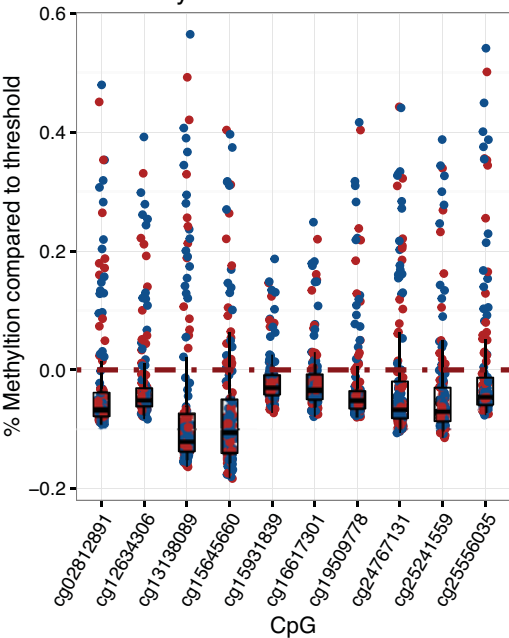
Primer name	Sequence
cg25556035 F	AGTTTTTGTTTTTTAGGGTAGGTATTGATA
cg25556035 R-biot	AACTCCAACACAAACTATTTACAC
cg25556035 Seq	GTTTTTTTTTTTTTTTTAGTATTAATTAATTTAAG
cg15931839 F	TAGATTTTATTTTAAAGTTAGGGTGTGTGG
cg15931839 R-biot	AACCAAACCATATTTAAAACCTTATTC
cg15931839 Seq	GAATAGAAAAAAATTAGTTAGGAG
cg002812891 F-biot	ATGGTGTAGTAGGTGAGTTTGT
cg002812891 R	TACAACCCACCTCTACTCCATCCTAAC
cg002812891 Seq	AACTACCACCCCATACCATCCC

Table 2: Beta value thresholds used for DNA methylation arrays and pyrosequencing

	Array-SWAN	Array-BMIQ	Pyrosequencing
cg25556035	0.123726	0.085192	0.057375
cg13138089	0.18849	0.214598	
cg12634306	0.128539	0.140893	
cg25241559	0.209688	0.230536	
cg02812891	0.107235	0.102181	0.029425
cg15645660	0.267049	0.279702	
cg19509778	0.117568	0.062266	
cg15931839	0.14165	0.084144	0.081525
cg16617301	0.159146	0.106105	
cg24767131	0.145945	0.185700	

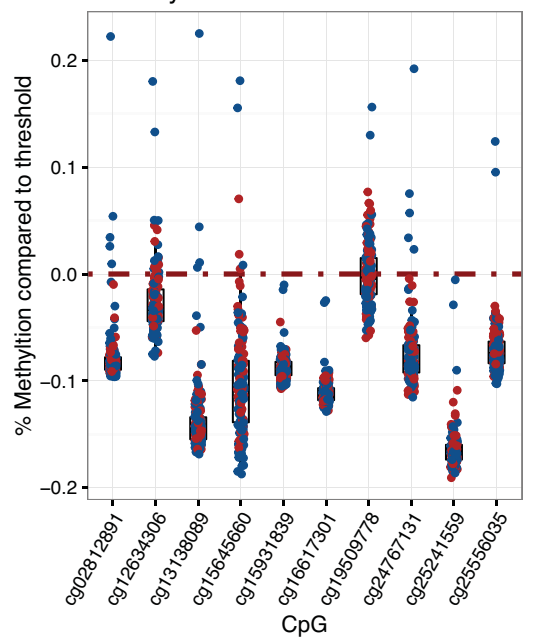


Array Residuals First Cohort

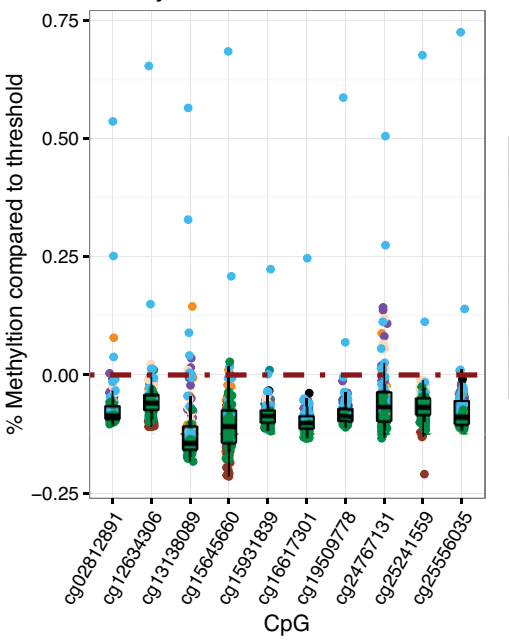


Sex
 Female
 Male

Array Residuals Second Cohort



Array residuals GEO Datasets



Array residuals Predo

