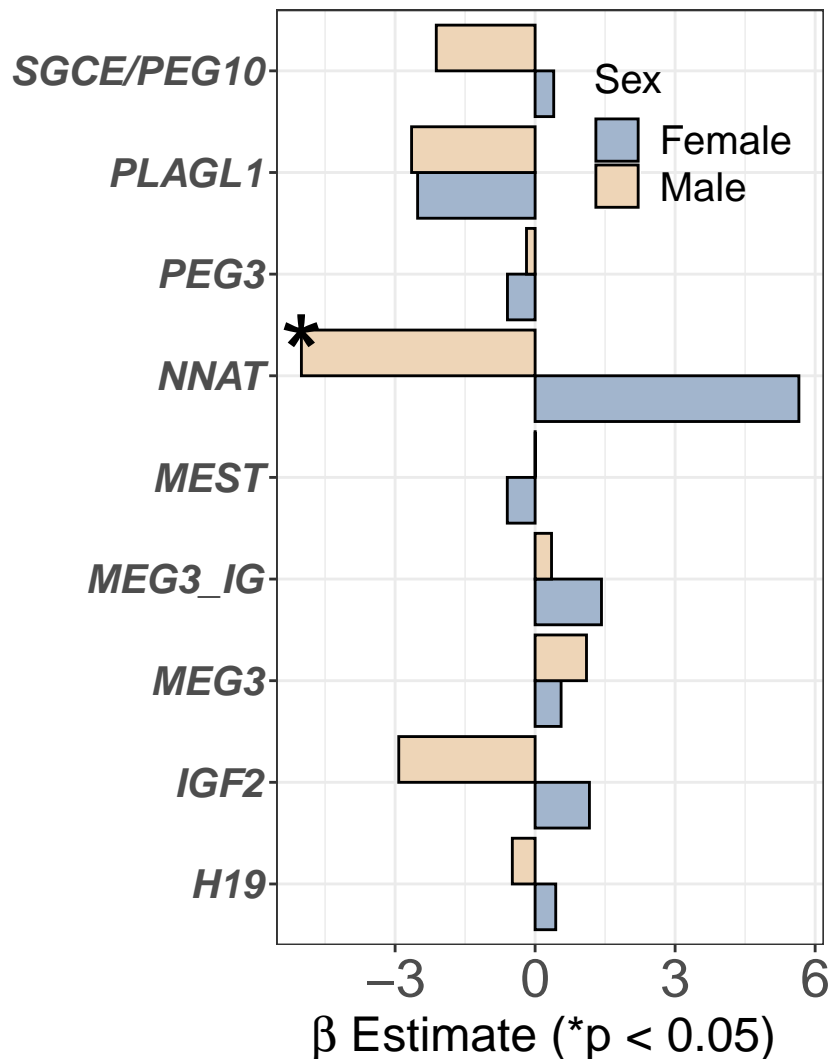


# Clomifene and Offspring Methylation

Change in Mean Methylation %

DMR



	Cases(n)	Controls(n)	Estimate(95%CI)	Pvalue
<i>SGCE/PEG10-M</i>	11	94	-2.12 (-4.75, 0.52)	0.114
<i>SGCE/PEG10-F</i>	7	<b>77</b>	0.40 (-2.56, 3.36)	0.788
<i>PLAGL1-M</i>	10	101	-2.65 (-8.10, 2.81)	0.337
<i>PLAGL1-F</i>	8	<b>86</b>	-2.52 (-8.66, 3.62)	0.416
<i>PEG3-M</i>	10	<b>95</b>	-0.18 (-1.57, 1.20)	0.791
<i>PEG3-F</i>	8	<b>70</b>	-0.59 (-2.28, 1.10)	0.485
<i>NNAT-M</i>	11	<b>83</b>	-5.01 (-9.80, -0.22)	0.041
<i>NNAT-F</i>	8	<b>66</b>	5.65 (-0.61, 11.91)	0.076
<i>MEST-M</i>	10	<b>90</b>	0.00 (-3.92, 3.92)	0.999
<i>MEST-F</i>	7	<b>77</b>	-0.60 (-5.23, 4.04)	0.798
<i>MEG3_IG-M</i>	11	<b>137</b>	0.35 (-3.35, 4.05)	0.851
<i>MEG3_IG-F</i>	10	<b>107</b>	1.42 (-1.39, 4.24)	0.318
<i>MEG3-M</i>	9	<b>157</b>	1.10 (-5.33, 7.53)	0.736
<i>MEG3-F</i>	10	<b>134</b>	0.56 (-4.05, 5.16)	0.811
<i>IGF2-M</i>	9	102	-2.92 (-7.12, 1.27)	0.170
<i>IGF2-F</i>	7	86	1.16 (-3.14, 5.46)	0.591
<i>H19-M</i>	9	92	-0.49 (-3.12, 2.14)	0.713
<i>H19-F</i>	6	83	0.44 (-2.22, 3.10)	0.741

Linear regression for Clomifene use for the index pregnancy and mean CpG methylation. We stratified models by sex and adjusted for pyrosequencing batch, pre-pregnancy maternal BMI, race, maternal age, diabetes, and parity. Estimates represent the mean percentage of methylation change associated with maternal use of Clomifene (\*p < 0.05). Bolded values in table represent outlier removal (+/- 3sd from mean).