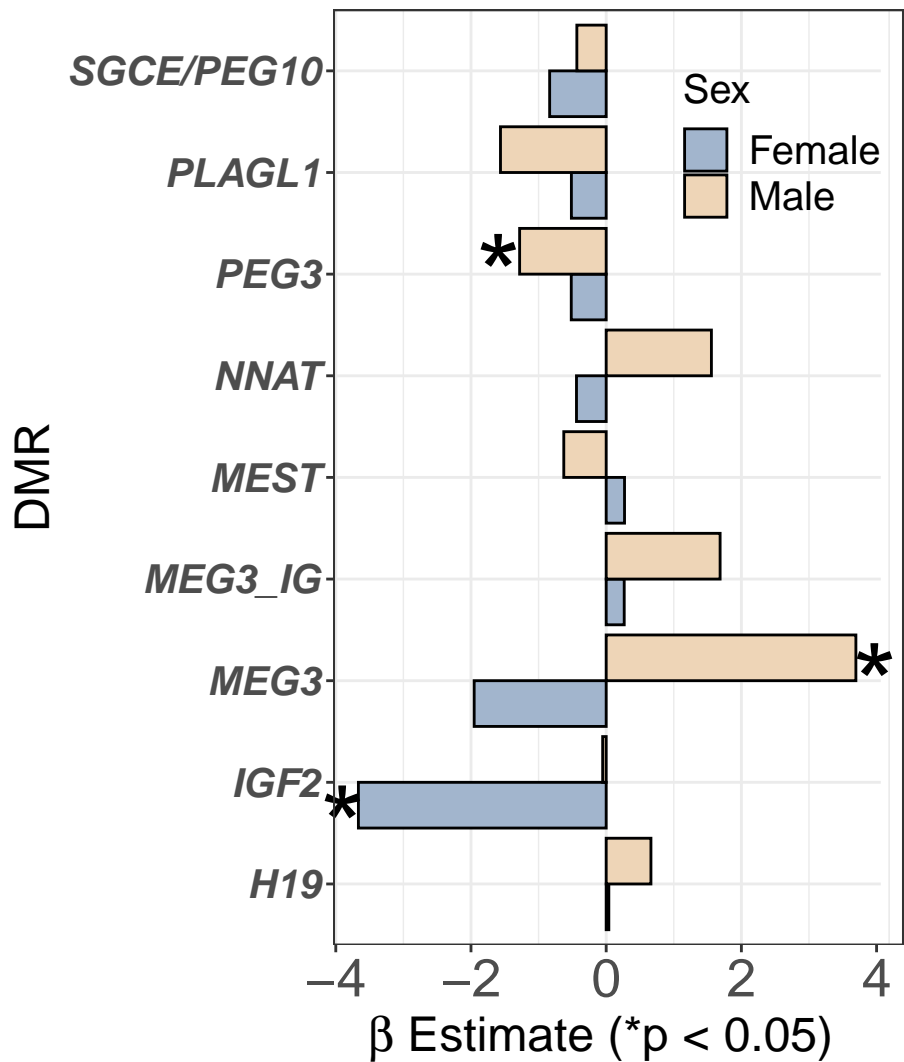


ART ET/ICSI and Offspring Methylation

Change in Mean Methylation %



	Cases(n)	Controls(n)	Estimate(95%CI)	Pvalue
<i>SGCE/PEG10-M</i>	10	182	-0.43 (-1.99, 1.12)	0.582
<i>SGCE/PEG10-F</i>	12	169	-0.84 (-2.36, 0.69)	0.281
<i>PLAGL1-M</i>	9	191	-1.56 (-5.17, 2.05)	0.394
<i>PLAGL1-F</i>	13	178	-0.51 (-3.92, 2.89)	0.766
<i>PEG3-M</i>	8	184	-1.28 (-2.45, -0.11)	0.032
<i>PEG3-F</i>	13	159	-0.52 (-1.81, 0.78)	0.432
<i>NNAT-M</i>	9	170	1.56 (-2.51, 5.62)	0.451
<i>NNAT-F</i>	11	157	-0.44 (-3.82, 2.94)	0.797
<i>MEST-M</i>	10	174	-0.63 (-3.29, 2.03)	0.642
<i>MEST-F</i>	12	166	0.27 (-2.07, 2.61)	0.819
<i>MEG3_IG-M</i>	9	229	1.69 (-0.35, 3.72)	0.105
<i>MEG3_IG-F</i>	14	194	0.27 (-1.71, 2.24)	0.790
<i>MEG3-M</i>	11	248	3.69 (0.10, 7.29)	0.044
<i>MEG3-F</i>	12	227	-1.95 (-5.55, 1.65)	0.286
<i>IGF2-M</i>	6	146	-0.05 (-4.27, 4.17)	0.981
<i>IGF2-F</i>	9	143	-3.67 (-6.79, -0.55)	0.022
<i>H19-M</i>	6	149	0.66 (-2.06, 3.38)	0.631
<i>H19-F</i>	13	150	0.04 (-1.75, 1.83)	0.966

Linear regression for ART 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 ART (*p < 0.05). **Bolded** values in table represent outlier removal (+/- 3sd from mean).