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**Supplementary Table 1.** Descriptive characteristics of the Early Autism Risk Longitudinal Investigation (EARLI) samples with placenta whole genome bisulfite sequencing measures

	<i>Number (%)</i>		<b>p-value</b>
	<b>Males (n=76)</b>	<b>Females (n=57)</b>	
<b><i>Neurodevelopmental diagnosis at age 3</i></b>			0.004 <sup>a</sup>
Typically Developing	17 (0.22)	20 (0.35)	
Non-Typically Developing	26 (0.34)	24 (0.42)	
Autism Spectrum Disorder	18 (0.24)	1 (0.02)	
Lost to follow up	15 (0.20)	12 (0.21)	
<b><i>Race</i></b>			0.467 <sup>a</sup>
White	43 (0.57)	26 (0.46)	
Black	6 (0.08)	4 (0.07)	
Asian	12 (0.16)	8 (0.14)	
Other/Missing	15 (0.20)	19 (0.33)	
<b><i>Mode of delivery</i></b>			0.290 <sup>a</sup>
Vaginal	38 (0.50)	30 (0.53)	
C-section	26 (0.34)	12 (0.21)	
Missing	12 (0.16)	15 (0.26)	
<b><i>Gestational Age (weeks)</i></b>			
Mean (range)	39.28 (35.99 - 42.43)	39.41 (33.86 - 41.57)	0.604 <sup>b</sup>

<sup>a</sup> chi square test p-value

<sup>b</sup> t-test p-value

**Supplementary Table 2.** BLAT results for ZNF300 DMR region. Results include BLAT results for reference sequence in DMR region and for source sequence of 9 450K probes that overlap this region.

<b>450k Probes Overlapping ZNF300 DMR</b>										
QUERY	SCORE	START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
cg19486756	50	1	50	50	100.00%	5	-	150281143	150281192	50
cg12346881	50	1	50	50	100.00%	5	-	150283837	150283886	50
cg04675542	50	1	50	50	100.00%	5	+	150284416	150284465	50
cg02343823	50	1	50	50	100.00%	5	-	150284419	150284468	50
cg08580836	50	1	50	50	100.00%	5	-	150284448	150284497	50
cg08580836	32	12	46	50	97.10%	6	+	1086171	1200162	113992
cg19014419	50	1	50	50	100.00%	5	+	150284456	150284505	50
cg11291313	50	1	50	50	100.00%	5	-	150284482	150284531	50
cg18237551	50	1	50	50	100.00%	5	-	150284552	150284601	50
cg21228005	50	1	50	50	100.00%	5	+	150284748	150284797	50
<b>chr5:150904274-150905870 under hg38</b>										
QUERY	SCORE	START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
hg38_dna	1597	1	1597	1597	100.00%	5	+	150904274	150905870	1597
hg38_dna	269	463	869	1597	83.50%	5	+	150946310	150946712	403
hg38_dna	30	1170	1254	1597	96.90%	1	+	154418956	154419188	233
hg38_dna	28	1199	1244	1597	66.70%	1	+	50659355	50659384	30
hg38_dna	26	1352	1381	1597	96.50%	10	+	461616	461660	45
hg38_dna	26	1352	1381	1597	96.50%	10	+	746531	746575	45
hg38_dna	26	810	836	1597	100.00%	1	+	193931671	193932153	483
hg38_dna	23	1182	1204	1597	100.00%	11	-	12070379	12070401	23
hg38_dna	23	1510	1533	1597	100.00%	1	+	176074721	176074745	25
hg38_dna	22	405	426	1597	100.00%	7	-	37414236	37414257	22
hg38_dna	22	1182	1203	1597	100.00%	12	-	100354201	100354222	22
hg38_dna	22	244	265	1597	100.00%	1	-	22907061	22907082	22
hg38_dna	21	182	202	1597	100.00%	12	-	70460496	70460516	21
hg38_dna	20	1182	1203	1597	95.50%	1	-	29551036	29551057	22

**Supplementary Table 3.** Association metrics for mean ZNF300 methylation levels and potential key confounders.

<b>Statistical model and confounder name</b>	<b>Coefficient (95% Confidence Interval)</b>	<b>p-value<sup>a</sup></b>
<i>Gestational Age:</i>		
$E(M_{\text{DMRmean}}) = \alpha + \beta_1 \text{GestationalAge} + \epsilon$	0.0025 (-0.0260, 0.0309)	0.861
<i>Genetic ancestry:</i>		
$E(M_{\text{DMRmean}}) = \alpha + \beta_2 \text{PC1} + \beta_2 \text{PC2} + \beta_3 \text{PC3} + \beta_4 \text{PC4} + \beta_5 \text{PC5} + \epsilon$		
PC1	-1.52 (-7.95, 4.91)	0.631
PC2	-2.09 (-9.05, 4.87)	0.541
PC3	1.29 (-12.34, 14.93)	0.846
PC4	-14.80 (-71.92, 42.31)	0.598
PC5	-2.73 (-13.71, 8.26)	0.613
<i>Mode of delivery:</i>		
$E(M_{\text{DMRmean}}) = \alpha + \beta_1 \text{ModeofDelivery} + \epsilon$	-0.032 (-0.165, 0.100)	0.619

PC: principal component

<sup>a</sup>from linear regression of mean across 45 CpG sites in ZNF300 DMR vs gestational age, the first 5 principal components from genotype data, and mode of delivery (vaginal vs C-section).

**Supplementary Table 4.** Candidate differentially methylated regions associated with fetal sex identified in our genome-wide screen of placentae from neurotypical children.

Chr	Start	End	Size (bp)	Mean_Males	Mean_Females	MeanDiff	fwer
5	150904274	150905870	1597	0.53969502	0.389863571	0.14983145	0.015
6	102904326	102905438	1113	0.36358626	0.480718729	-0.1171325	0.192
1	26817250	26817668	419	0.46238026	0.721890005	-0.2595097	0.319
8	3182959	3183686	728	0.29756636	0.394339137	-0.0967728	0.359
13	89087754	89088647	894	0.39849116	0.510989959	-0.1124988	0.371
22	33014021	33014861	841	0.1672423	0.314354614	-0.1471123	0.397
21	21024602	21025439	838	0.41402048	0.475943936	-0.0619235	0.454
5	62804346	62805039	694	0.56725629	0.412467734	0.15478855	0.504
7	47052929	47053330	402	0.25084429	0.405674256	-0.15483	0.524
21	21019803	21020643	841	0.36591433	0.416062629	-0.0501483	0.533
4	37001712	37002384	673	0.23213303	0.321256093	-0.0891231	0.672
18	30175567	30176200	634	0.2225856	0.366395684	-0.1438101	0.739
4	25506054	25506453	400	0.29781156	0.475505546	-0.177694	0.746
11	34346080	34346768	689	0.74035313	0.625274156	0.11507897	0.803
4	56433717	56434325	609	0.62517709	0.481522305	0.14365478	0.823
9	16869185	16869742	558	0.44334902	0.286416548	0.15693247	0.87
17	30823009	30823535	527	0.58974505	0.438174901	0.15157015	0.891
9	63859185	63859620	436	0.18865911	0.291493489	-0.1028344	0.904
3	33114982	33115497	516	0.59630619	0.441793945	0.15451224	0.918
7	25743955	25744332	378	0.22377351	0.351845682	-0.1280722	0.931
3	196163915	196164420	506	0.22882054	0.326757973	-0.0979374	0.946
8	4313287	4313811	525	0.40328952	0.450709515	-0.04742	0.948
2	60883035	60883593	559	0.40270084	0.240521326	0.16217951	0.955
7	43113076	43113374	299	0.35889834	0.213780459	0.14511788	0.956
9	5683764	5684207	444	0.66013324	0.794337795	-0.1342046	0.961
17	82228306	82228514	209	0.56440784	0.404294969	0.16011288	0.964
17	503023	503261	239	0.31963847	0.468408437	-0.14877	0.972
17	80832988	80833421	434	0.49849612	0.376316696	0.12217943	0.973
1	112957285	112957782	498	0.62968011	0.512139614	0.1175405	0.976
8	4643964	4644467	504	0.37603323	0.431062148	-0.0550289	0.976
22	47631852	47632172	321	0.29063687	0.418916495	-0.1282796	0.977
11	26114759	26115252	494	0.55515393	0.625585307	-0.0704314	0.977
2	55442125	55442427	303	0.65478068	0.785600569	-0.1308199	0.979
13	96947238	96947640	403	0.56990033	0.45208243	0.1178179	0.982
2	43218773	43219225	453	0.6417339	0.515743148	0.12599076	0.987
11	118788960	118789320	361	0.57662116	0.431160296	0.14546086	0.988
11	748309	748750	442	0.56287014	0.425001035	0.13786911	0.989
19	52536440	52536743	304	0.15673983	0.341667011	-0.1849272	0.991

11	23730361	23730589	229	0.3203217	0.44812786	-0.1278062	0.995
21	10119719	10119962	244	0.12107314	0.191750242	-0.0706771	0.997
21	20997548	20997812	265	0.14630042	0.220026114	-0.0737257	0.997
7	30596194	30596560	367	0.31803916	0.194787724	0.12325144	0.997
18	49017485	49017854	370	0.35070831	0.478526163	-0.1278179	0.997
5	150906191	150906538	348	0.59324673	0.487077205	0.10616953	0.998
22	10961644	10961748	105	0.2034263	0.282579507	-0.0791532	1
2	226835303	226835549	247	0.2530793	0.399235894	-0.1461566	1
4	6953213	6953403	191	0.79051205	0.656509643	0.1340024	1
8	6523620	6523876	257	0.57330059	0.738626583	-0.165326	1
12	68747362	68747557	196	0.47457651	0.358629776	0.11594673	1
11	95037869	95037965	97	0.15420386	0.27446568	-0.1202618	1
7	24977573	24977748	176	0.77516372	0.626604073	0.14855964	1
6	48069444	48069679	236	0.4746624	0.345747952	0.12891444	1
1	26863968	26864266	299	0.61154535	0.446746529	0.16479882	1
22	21569064	21569310	247	0.52440884	0.385207195	0.13920165	1
9	63708818	63708951	134	0.12622869	0.237047741	-0.1108191	1
5	39787881	39788013	133	0.5236956	0.656046628	-0.132351	1
1	27552048	27552178	131	0.66701315	0.776846896	-0.1098338	1
20	63641308	63641388	81	0.44121346	0.26799749	0.17321597	1
1	156436807	156436972	166	0.44166161	0.302576825	0.13908479	1
1	44794325	44794593	269	0.63957297	0.501941886	0.13763109	1
3	128490875	128491063	189	0.52224952	0.340747385	0.18150214	1
1	148844264	148844375	112	0.18319096	0.368005892	-0.1848149	1
18	12078	12161	84	0.43858114	0.56079891	-0.1222178	1
10	117373474	117373586	113	0.66364214	0.534971421	0.12867071	1
2	25216986	25217110	125	0.29588857	0.396137034	-0.1002485	1
9	133819210	133819365	156	0.46475588	0.559329468	-0.0945736	1
17	36658370	36658501	132	0.50973198	0.3657855	0.14394648	1
22	11618202	11618321	120	0.49343217	0.606624468	-0.1131923	1
7	72880605	72880834	230	0.69341631	0.552380268	0.14103604	1
3	157542604	157542648	45	0.2755862	0.383824841	-0.1082386	1
3	46845138	46845337	200	0.48711593	0.374539782	0.11257615	1
7	151460861	151461128	268	0.51639096	0.406896982	0.10949398	1
3	170909038	170909191	154	0.33495208	0.440143312	-0.1051912	1
7	44846295	44846413	119	0.57697319	0.458717672	0.11825552	1
9	136110285	136110367	83	0.68297503	0.515186473	0.16778856	1
2	3528256	3528357	102	0.71419382	0.555728818	0.158465	1
3	150703021	150703172	152	0.62033306	0.498521837	0.12181123	1
3	195659311	195659409	99	0.67656181	0.547707109	0.1288547	1
9	42636362	42636446	85	0.36246595	0.499199983	-0.136734	1

1	51877102	51877331	230	0.6328365	0.513548997	0.1192875	1
9	66269167	66269268	102	0.43975249	0.312889684	0.12686281	1
14	18966635	18966714	80	0.41976397	0.558251667	-0.1384877	1
11	95037404	95037492	89	0.13404375	0.251162466	-0.1171187	1
19	2428394	2428527	134	0.55021488	0.419253284	0.1309616	1
1	9183468	9183541	74	0.55327814	0.435611897	0.11766624	1
6	158939841	158939952	112	0.63060994	0.499820474	0.13078946	1
11	5937993	5938095	103	0.28469028	0.385370379	-0.1006801	1
7	155205469	155205605	137	0.42057054	0.254319313	0.16625123	1
1	246794195	246794381	187	0.51090202	0.384268641	0.12663338	1
3	9648787	9648886	100	0.47914683	0.594951797	-0.115805	1
7	91881387	91881554	168	0.29518391	0.426140411	-0.1309565	1
1	3538797	3538882	86	0.47672223	0.558948672	-0.0822264	1
16	69425919	69426137	219	0.77196256	0.624085947	0.14787661	1
14	59951529	59951675	147	0.30353118	0.482298425	-0.1787672	1
1	66931569	66931885	317	0.39192873	0.261945555	0.12998318	1
2	74530953	74531109	157	0.53756719	0.401683879	0.13588331	1
3	24522364	24522452	89	0.50086357	0.385242479	0.11562109	1
6	27630425	27630482	58	0.4420674	0.580163934	-0.1380965	1
16	68357089	68357286	198	0.69216437	0.789533419	-0.097369	1
16	71896786	71896916	131	0.58803064	0.472353201	0.11567744	1
20	38599875	38599894	20	0.46951431	0.587585335	-0.118071	1
16	75624202	75624266	65	0.29593336	0.420665851	-0.1247325	1
5	95960156	95960220	65	0.6281615	0.513862969	0.11429853	1
5	178087094	178087146	53	0.63132238	0.52194273	0.10937965	1
15	73221239	73221312	74	0.54046885	0.635315408	-0.0948466	1
6	33453156	33453403	248	0.64653333	0.471606606	0.17492672	1
1	143331925	143332013	89	0.51384825	0.766218557	-0.2523703	1
3	9916172	9916363	192	0.54078141	0.408062861	0.13271855	1
6	7313845	7313973	129	0.20787541	0.316457052	-0.1085816	1
15	74907469	74907697	229	0.61951186	0.505559664	0.1139522	1
21	10274090	10274234	145	0.62722703	0.424985944	0.20224108	1
7	44574706	44574745	40	0.41166986	0.530819084	-0.1191492	1
1	32499813	32499843	31	0.47055569	0.573593885	-0.1030382	1
1	91884479	91884576	98	0.54902255	0.425348841	0.12367371	1
4	37669799	37669900	102	0.57870869	0.425658962	0.15304973	1
15	55589346	55589409	64	0.40191328	0.286285847	0.11562744	1
14	59951010	59951115	106	0.40955544	0.610216582	-0.2006611	1
10	131972756	131972817	62	0.73230174	0.617520246	0.11478149	1
16	77527	77580	54	0.41594531	0.292566949	0.12337836	1
1	52663482	52663498	17	0.66321365	0.556284149	0.1069295	1

16	33516339	33516408	70	0.21562682	0.327995265	-0.1123684	1
1	144556793	144557065	273	0.50672015	0.663920838	-0.1572007	1
1	246793605	246793764	160	0.57924049	0.451079821	0.12816067	1
6	31701851	31702125	275	0.46163439	0.351559334	0.11007505	1
19	39406116	39406142	27	0.54559645	0.397974967	0.14762149	1
3	25662744	25662866	123	0.45914893	0.344636435	0.11451249	1
4	17811924	17812185	262	0.64039078	0.510493737	0.12989705	1
2	233867831	233867859	29	0.38082591	0.497871826	-0.1170459	1
6	116370081	116370221	141	0.60289399	0.487620281	0.11527371	1
19	54188248	54188433	186	0.55829196	0.427362155	0.1309298	1
1	54490242	54490348	107	0.56234151	0.431485684	0.13085582	1
5	175968949	175969073	125	0.69677009	0.574684422	0.12208567	1
1	148150643	148150756	114	0.50371152	0.389486313	0.11422521	1
3	61637971	61638111	141	0.67011876	0.54714846	0.1229703	1
11	65541703	65541746	44	0.23444536	0.336844875	-0.1023995	1
1	40980935	40980998	64	0.64091945	0.525332982	0.11558647	1
19	33195448	33195484	37	0.4894217	0.361151367	0.12827033	1
7	3914236	3914329	94	0.40727373	0.494978403	-0.0877047	1
1	17683690	17683702	13	0.48889576	0.561590693	-0.0726949	1
4	109561771	109561817	47	0.42410893	0.304901868	0.11920707	1
21	5156545	5156548	4	0.96610397	0.765822717	0.20028126	1
5	177517878	177517889	12	0.64105401	0.509999735	0.13105427	1
12	47904075	47904079	5	0.46911267	0.338785423	0.13032725	1
17	26593455	26593488	34	0.46786941	0.593773318	-0.1259039	1
21	21019221	21019408	188	0.3442985	0.376214985	-0.0319165	1
1	148246176	148246207	32	0.57935934	0.718871882	-0.1395125	1
6	27632298	27632400	103	0.66129806	0.552199735	0.10909833	1
19	43625504	43625562	59	0.26881748	0.408809886	-0.1399924	1
10	46378876	46378915	40	0.58147216	0.445863148	0.13560901	1
14	59950659	59950706	48	0.49916485	0.657172098	-0.1580072	1
5	178357743	178357761	19	0.4577331	0.326923447	0.13080966	1
17	83052683	83052706	24	0.69941798	0.574889102	0.12452887	1
10	80356201	80356313	113	0.49187432	0.377029589	0.11484473	1
1	93511123	93511212	90	0.41047113	0.51996816	-0.109497	1
1	35030799	35030804	6	0.59654116	0.488844218	0.10769694	1
1	26827742	26827791	50	0.52751101	0.416573137	0.11093787	1
12	51024867	51024885	19	0.42176187	0.297616293	0.12414558	1
1	224214105	224214193	89	0.55652502	0.438119016	0.11840601	1
19	48752175	48752198	24	0.46926756	0.340727212	0.12854035	1
6	73452503	73452508	6	0.3472082	0.248373512	0.09883469	1
3	172038972	172038989	18	0.46459088	0.563677592	-0.0990867	1



10	14579108	14579232	125	0.47160821	0.346163131	0.12544508	1
9	129738255	129738264	10	0.71937816	0.577432802	0.14194536	1
16	14909925	14909925	1	0.76295957	0.493747879	0.26921169	1
5	176239941	176239941	1	0.40962175	0.609286272	-0.1996645	1
3	141488485	141488485	1	0.48767862	0.343482291	0.14419633	1
14	64896891	64896891	1	0.60252301	0.762276118	-0.1597531	1
7	155345599	155345599	1	0.58876891	0.421927371	0.16684154	1
2	42013609	42013609	1	0.62957903	0.762344137	-0.1327651	1
7	102573673	102573673	1	0.52415798	0.351503911	0.17265407	1
14	56669487	56669487	1	0.71694676	0.557403479	0.15954328	1
22	42555032	42555032	1	0.48484988	0.623788462	-0.1389386	1
7	73157667	73157667	1	0.48097514	0.306001796	0.17497335	1
12	48106738	48106738	1	0.28632274	0.423368207	-0.1370455	1
9	41360138	41360138	1	0.60075944	0.742406304	-0.1416469	1
22	10571277	10571277	1	0.07631221	0.226366377	-0.1500542	1
4	138562248	138562248	1	0.58136789	0.700456576	-0.1190887	1
7	44122997	44122997	1	0.46375832	0.34881195	0.11494637	1
14	56668599	56668599	1	0.69761312	0.545062483	0.15255064	1
15	31390805	31390805	1	0.6136945	0.725216419	-0.1115219	1
5	141479035	141479035	1	0.34474105	0.218042163	0.12669888	1
8	132774577	132774577	1	0.57824679	0.694545031	-0.1162982	1
1	144811640	144811640	1	0.81487167	0.611641586	0.20323008	1
20	3172769	3172769	1	0.56526936	0.417757099	0.14751226	1
2	60884087	60884087	1	0.71727167	0.591259503	0.12601217	1
8	60516096	60516096	1	0.69144685	0.568598516	0.12284833	1
6	125987445	125987445	1	0.63931903	0.528588084	0.11073095	1
16	22161028	22161028	1	0.55505067	0.668965798	-0.1139151	1
16	67561316	67561316	1	0.75570437	0.630246893	0.12545748	1
15	32535114	32535114	1	0.74831672	0.607058895	0.14125783	1
10	47301071	47301071	1	0.46625522	0.337512243	0.12874298	1
3	185253475	185253475	1	0.34076158	0.228240374	0.1125212	1
1	149814128	149814128	1	0.66076446	0.555724691	0.10503977	1
9	35829998	35829998	1	0.65957111	0.544194128	0.11537698	1
9	26945818	26945818	1	0.41827689	0.294387977	0.12388891	1
2	91627174	91627174	1	0.40569202	0.510175384	-0.1044834	1
1	149102458	149102458	1	0.2077392	0.095397407	0.1123418	1
6	69866138	69866138	1	0.26873121	0.376107086	-0.1073759	1
9	4986535	4986535	1	0.55584205	0.447691365	0.10815069	1
11	3839901	3839901	1	0.61323566	0.46494706	0.1482886	1
17	42387217	42387217	1	0.36227666	0.248823696	0.11345297	1
6	691690	691690	1	0.7512944	0.650367472	0.10092693	1

6	128521514	128521514	1	0.62356283	0.519314497	0.10424833	1
22	50807836	50807836	1	0.16221806	0.149821874	0.01239618	1
2	126181612	126181612	1	0.67824842	0.549772994	0.12847542	1
3	128075246	128075246	1	0.32231602	0.218337287	0.10397873	1
1	40664754	40664754	1	0.50203857	0.622019586	-0.119981	1
6	2952096	2952096	1	0.7660068	0.650901061	0.11510574	1
15	65516307	65516307	1	0.57163284	0.467732622	0.10390022	1
2	169325251	169325251	1	0.42197327	0.522301529	-0.1003283	1
2	42013064	42013064	1	0.68388401	0.787728952	-0.1038449	1
21	44013979	44013979	1	0.63639722	0.513152493	0.12324472	1
20	38462914	38462914	1	0.2362895	0.413050671	-0.1767612	1
2	42974439	42974439	1	0.67467076	0.560916823	0.11375394	1
14	70254233	70254233	1	0.66226424	0.765156671	-0.1028924	1
17	51154571	51154571	1	0.55139713	0.444112232	0.1072849	1
6	27471878	27471878	1	0.40566709	0.305311989	0.1003551	1
19	3762180	3762180	1	0.45244129	0.327413649	0.12502764	1
1	235865757	235865757	1	0.45189121	0.353956541	0.09793467	1
3	134794466	134794466	1	0.19410446	0.266266354	-0.0721619	1
3	136750396	136750396	1	0.52884958	0.427662684	0.1011869	1
2	102737500	102737500	1	0.39819639	0.2828347	0.11536169	1
11	100481801	100481801	1	0.57406559	0.652814729	-0.0787491	1
6	79948856	79948856	1	0.34863754	0.248128244	0.1005093	1
16	67659354	67659354	1	0.72673198	0.615644515	0.11108746	1
20	25984970	25984970	1	0.22554291	0.349131263	-0.1235884	1
13	89162841	89162841	1	0.27718697	0.369332381	-0.0921454	1
1	29479899	29479899	1	0.3808028	0.48124185	-0.1004391	1
16	33516325	33516325	1	0.2331225	0.343133687	-0.1100112	1
16	33516312	33516312	1	0.23897963	0.34769418	-0.1087145	1
13	109141156	109141156	1	0.51847749	0.662891152	-0.1444137	1
1	152037550	152037550	1	0.65057056	0.545019567	0.10555099	1
13	89162879	89162879	1	0.27518599	0.366168118	-0.0909821	1
3	129427888	129427888	1	0.57537001	0.467229106	0.1081409	1

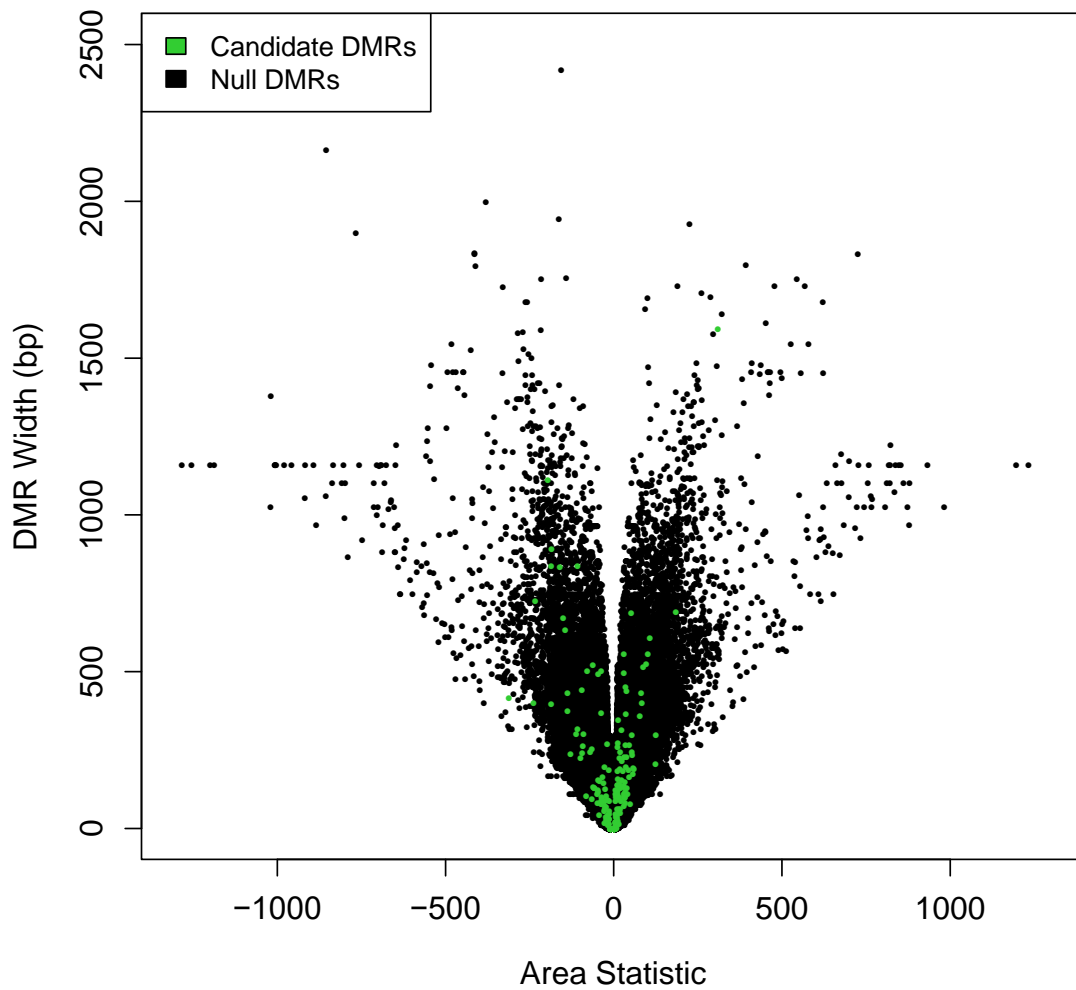
FWER: family wise error rate

<sup>a</sup>Mean difference value ('MeanDiff') calculated as (males –females methylation) across all measured positions in DMR region.

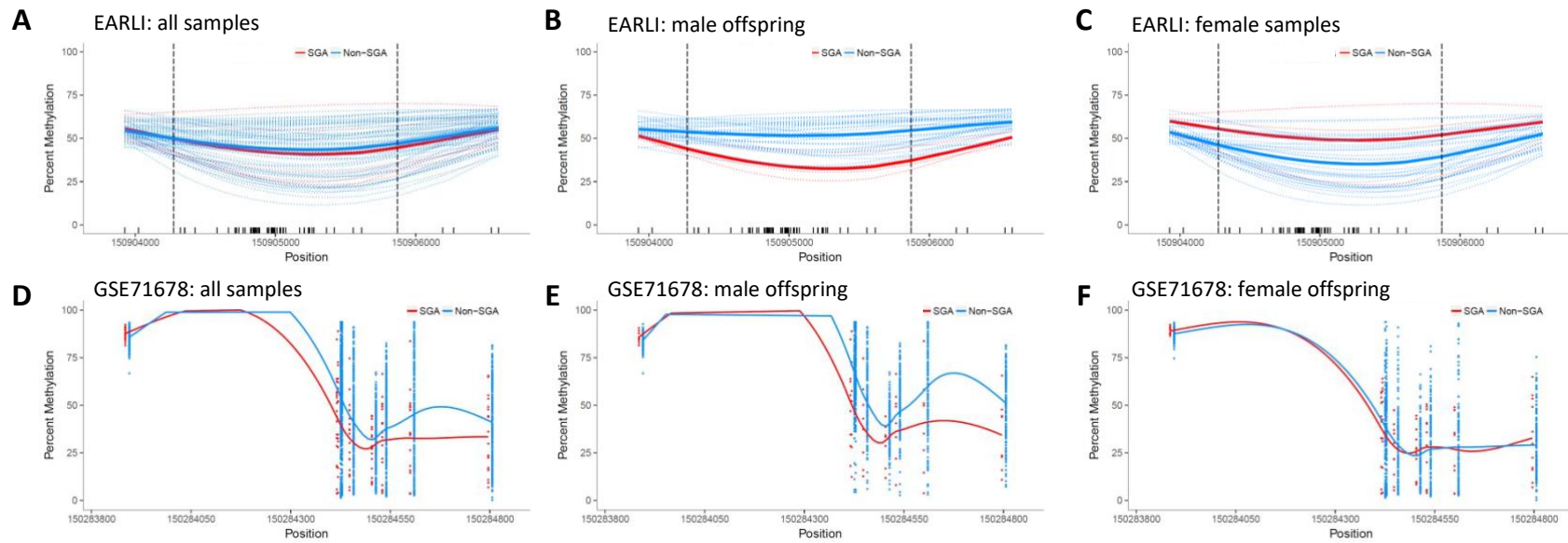
**Supplementary Table 5.** Summary of all data sets (discovery and replication) used in replication analyses.

<b>Dataset Name</b>	<b>Tissue Type</b>	<b>Measurement Platform</b>	<b>Cohort/GEO ID</b>	<b>N<sub>total</sub></b>	<b>N<sub>Males</sub></b>	<b>N<sub>Females</sub></b>
<b><i>Discovery:</i></b>						
<i>EARLI</i>	Placenta	WGBS	EARLI	37	17	20
<b><i>Replication:</i></b>						
<i>PR 1</i>	Placenta	WGBS	EARLI	50	26	24
<i>PR 2</i>	Placenta	450K	GSE75248	324	159	165
<i>PR 3</i>	Placenta	450K	GSE71678	342	184	158
<i>PR 4</i>	Placenta	450K	GSE75196	24	11	13
<i>PR 5</i>	Placenta	450K	Roifman et al. 2016	16	10	6
<i>PR 6</i>	Placenta	450K	GSE57767	12	6	6
<i>PR 7</i>	Placenta	450K	GSE93208	19	9	10
<b><i>Specificity Tissue 1</i></b>	Cord Blood	450K	EARLI	223	114	109
<b><i>Specificity Tissue 2</i></b>	Fetal Brain	450K	GSE58885	179	100	79
<b><i>Specificity Tissue 3</i></b>	Peripheral blood	450K	SEED	970	643	327

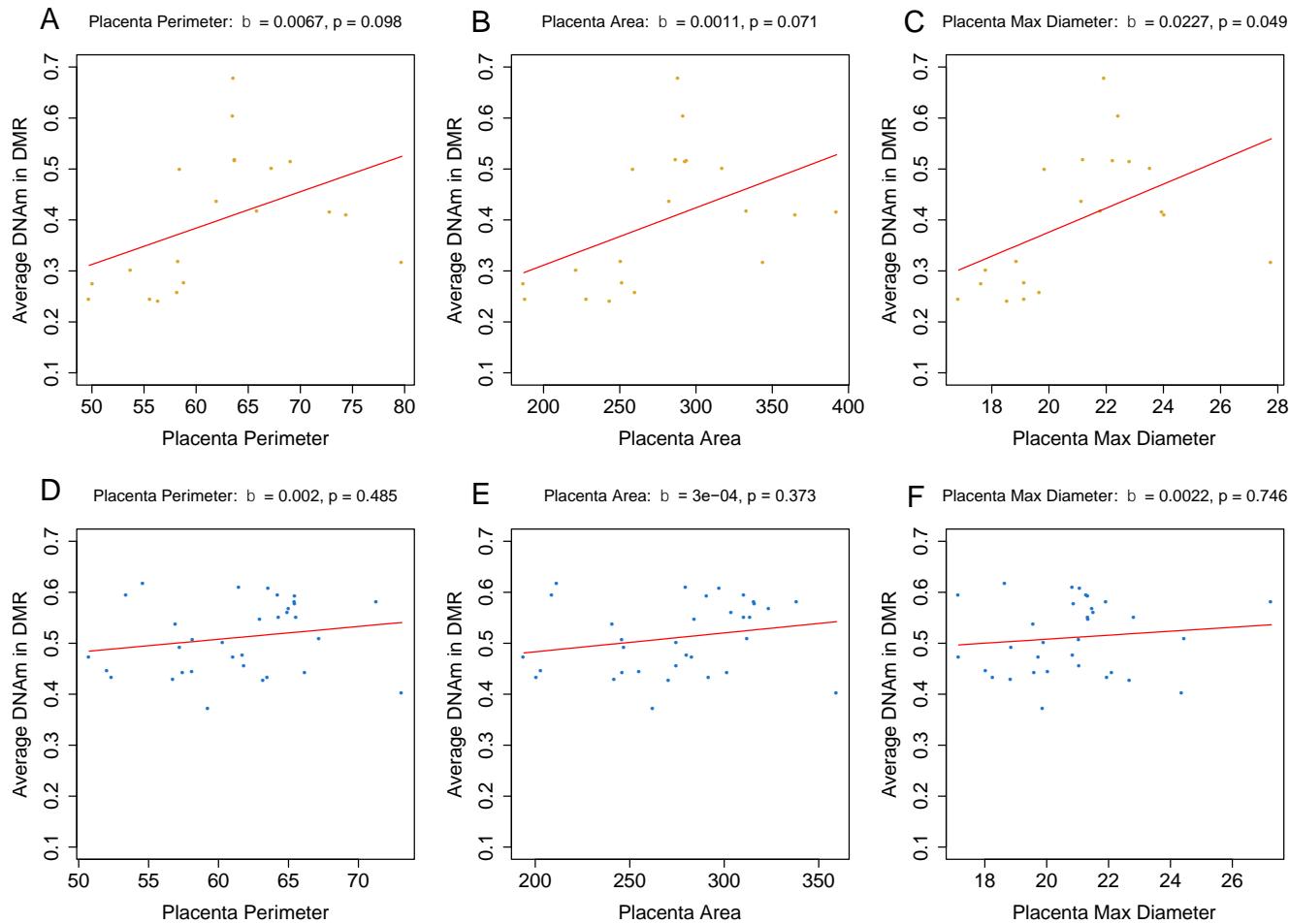
EARLI, Early Autism Risk Longitudinal Investigation; PR, placental replication; WGBS, whole genome bisulfite sequencing; 450K, Illumina 450K Methylation BeadChip



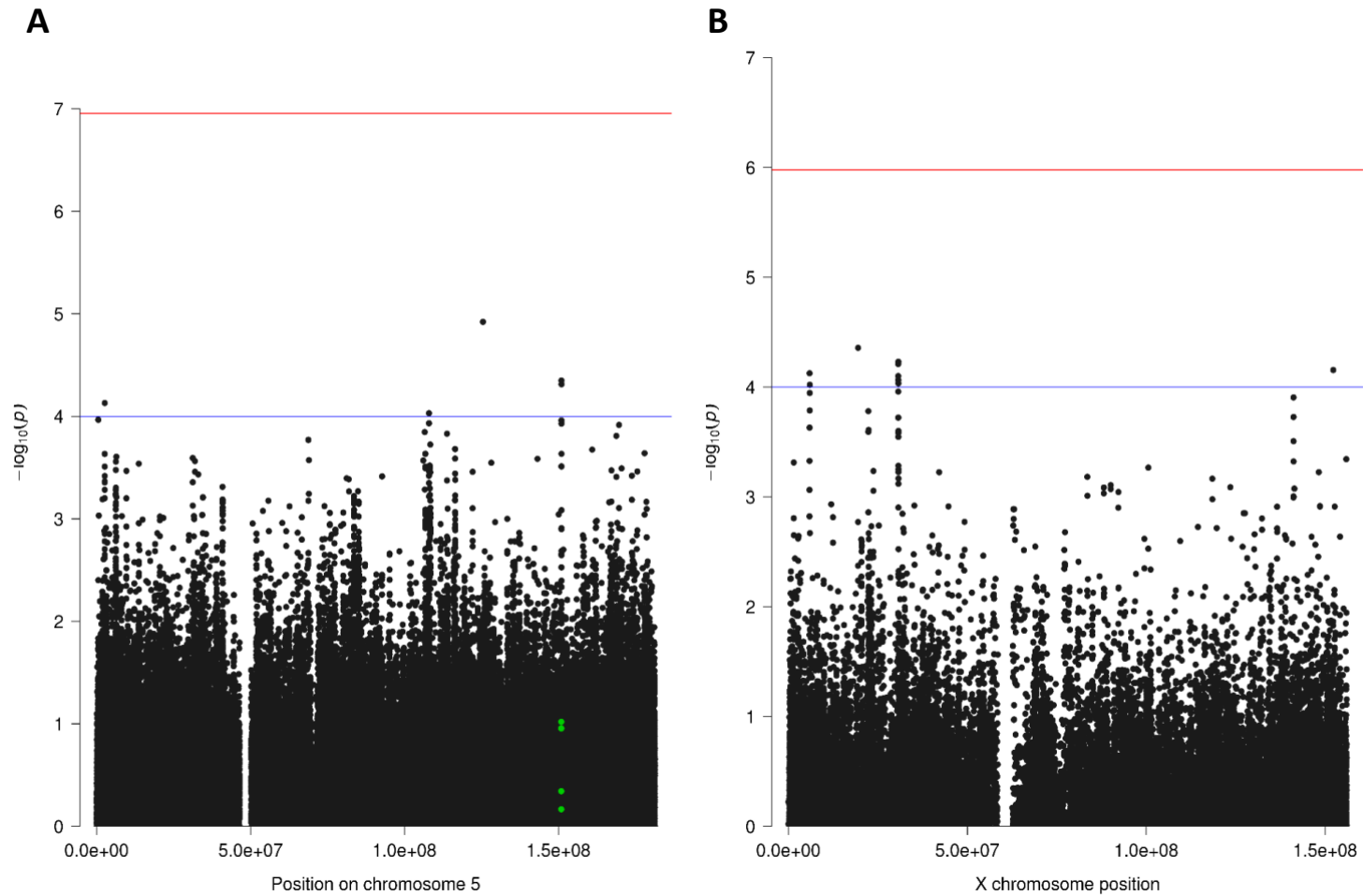
**Supplementary Figure S1:** Genome-wide results for identification of differentially methylated regions in placenta associated with fetal sex. Y-axis depicts width (bp) of null (black dots) or candidate (green dots) DMRs identified via BSmooth. X-axis depicts area statistics (sum of t-statistics in DMR) of null or candidate DMRs. Null DMRs are those generated across 1000 permutations.



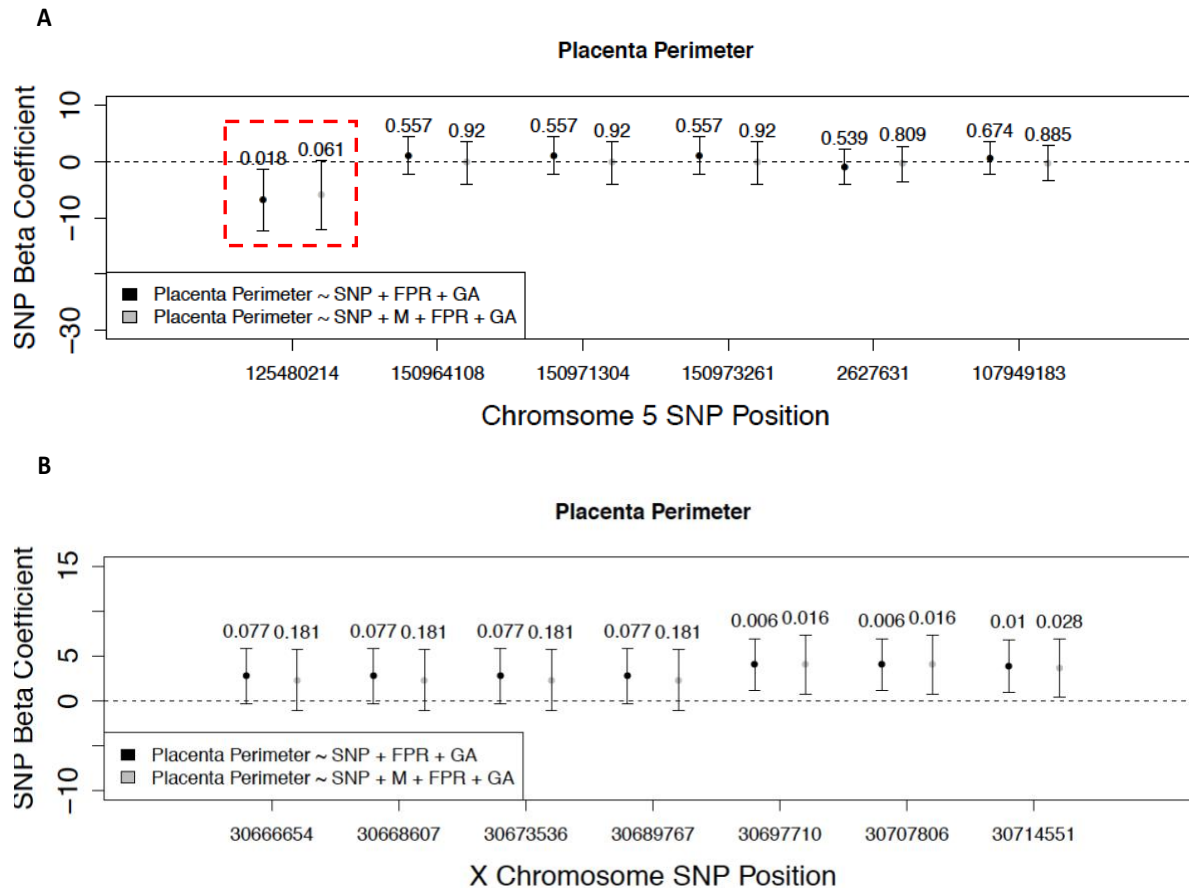
**Supplementary Figure 2: Inverse relationship between *ZNF300* promoter methylation and small for gestational age (SGA) between males and females.** Percent methylation (y-axis) vs genomic position (x-axis). Small for gestational age (SGA) is denoted in red and non-SGA in blue. EARLI study placenta whole genome bisulfite sequencing data (WGBS) from **A**, all samples (n=74); **B**, male offspring (n=34); **C**, female offspring (n=34). Illumina 450K DNA methylation data from replication set 3 (GSE71678) for **D**, all samples (n=338); **E**, male offspring (n=180); **F**, female offspring (n=158)



**Supplementary Figure 3: DNA methylation associations with placenta morphological features at *ZNF300* locus are observed in females but not males.** Mean methylation levels in DMR (y-axis) vs. placental perimeter (A,D), area (B,E), and maximum diameter (C,F), on the x-axis. P-values shown are for the regression of average methylation in the DMR onto each placental feature, adjusted for gestational age and FPR. A-C, among females (n=20; yellow points); D-F, among males (n=33; blue points).



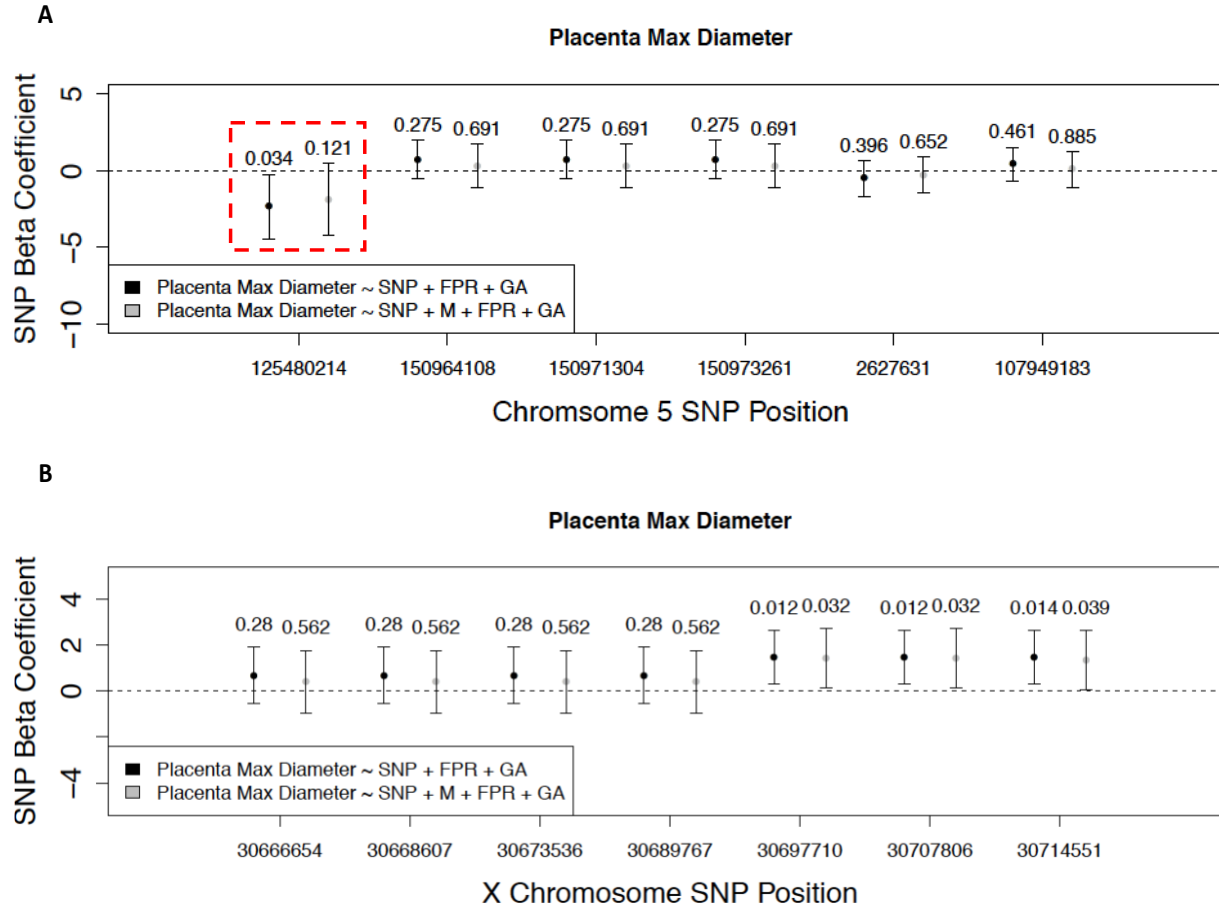
**Supplementary Figure 4: Manhattan plots showing SNP associations with DNA methylation at *ZNF300*.** **A**, chromosome 5 SNPs with green dots indicating SNPs that are located within the *ZNF300* differentially methylated region; **B**, SNPs on chromosome X that showed suggestive associations with methylation at *ZNF300*, in *trans*



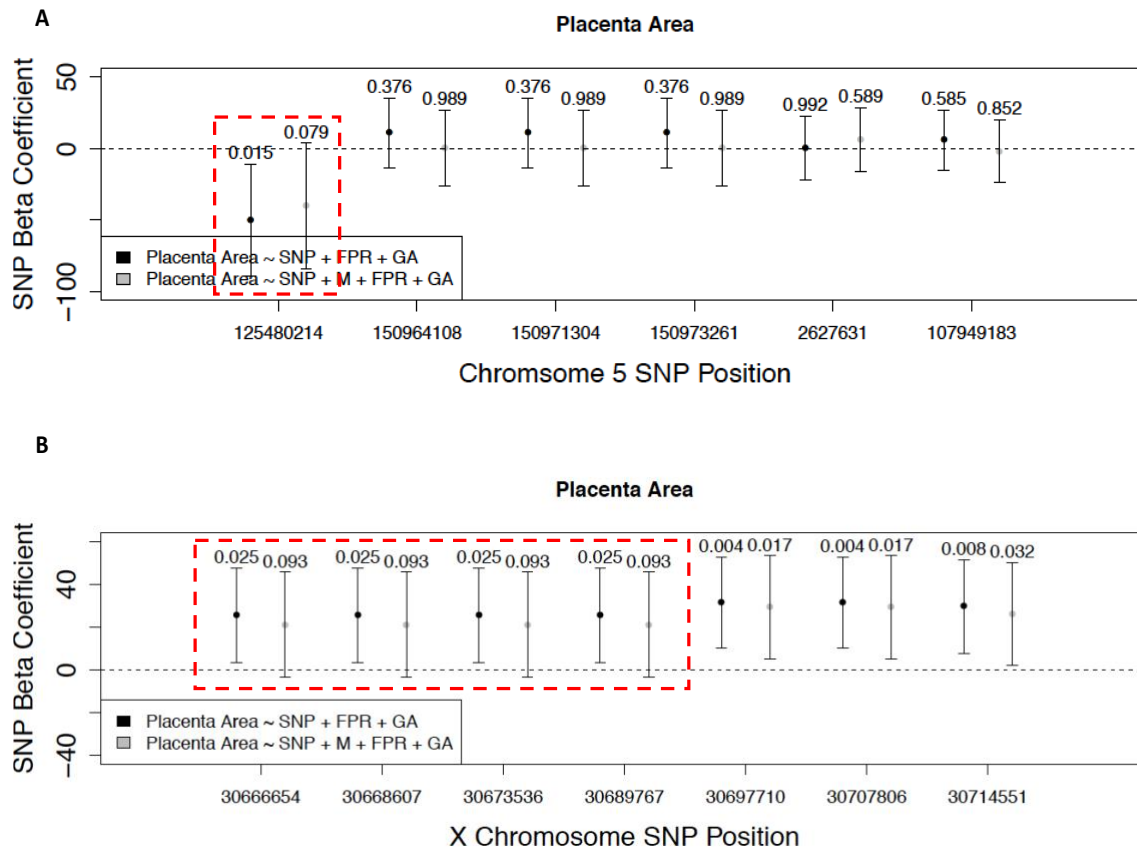
**Supplementary Figure 5: Causal inference testing reveals mediation of genetic variation on placenta perimeter by DNA methylation at the *ZNF300* locus.** Points indicate regression coefficients for SNP genotype terms in a model with the morphological phenotype as an outcome regressed onto the SNP, feto-placental weight ratio (FPR) and gestational age (GA) without (black) and with (gray) average methylation in the *ZNF300* DMR region. Corresponding p-values and error bars are also shown for each point. Red squares are drawn around SNPs showing evidence for mediation of SNP effects on placenta perimeter by *ZNF300* methylation. **A**) Results for chromosome 5 SNPs, and **B**) results from chromosome X SNPs.







**Supplementary Figure 6: Causal inference testing reveals mediation of genetic variation on placenta max diameter by DNA methylation at the *ZNF300* locus.** Points indicate regression coefficients for SNP genotype terms in a model with the morphological phenotype as an outcome regressed onto the SNP, fetoplacental weight ratio (FPR) and gestational age (GA) without (black) and with (gray) average methylation in the *ZNF300* DMR region. Corresponding p-values and error bars are also shown for each point. Red squares are drawn around SNPs showing evidence for mediation of SNP effects on placenta max diameter by *ZNF300* methylation. **A**) Results for chromosome 5 SNPs, and **B**) results from chromosome X SNPs.



**Supplementary Figure 7: Causal inference testing reveals mediation of genetic variation on placenta area by DNA methylation at the *ZNF300* locus.** Points indicate regression coefficients for SNP genotype terms in a model with the morphological phenotype as an outcome regressed onto the SNP, feto-placental weight ratio (FPR) and gestational age (GA) without (black) and with (gray) average methylation in the *ZNF300* DMR region. Corresponding p-values and error bars are also shown for each point. Red squares are drawn around SNPs showing evidence for mediation of SNP effects on placenta area by *ZNF300* methylation. **A**) Results for chromosome 5 SNPs, and **B**) results from chromosome X SNPs.