

Table S1. Mean values of normative psychosocial stress among participants with low, moderate and high MPSP.

Normative Psychosocial Stress Category	Low (n = 104)		Moderate (n = 119)		High (n = 50)	
	Mean	SD	Mean	SD	Mean	SD
Prenatal Depression ^(a)	2.98	3.17	7.95	3.45	15.02	3.29
Pregnancy Related Anxiety ^(b)	4.75	1.69	6.00	1.94	8.10	2.63
Perceived Stress During Pregnancy ^(c)	31.25	6.40	37.80	5.49	44.22	5.07
State Anxiety During Pregnancy ^(d)	27.37	4.91	41.14	6.63	53.46	8.00
Trait Anxiety During Pregnancy ^(d)	28.09	4.85	40.85	5.07	54.06	5.70
Negative Stressful Events During Pregnancy ^(e)	0.89	1.37	1.47	1.57	3.56	2.87

^(a): measured by Edinburgh Postnatal Depression Scale (EPDS)

^(b): measured by Pregnancy Related Anxiety (PRAQ-R)

^(c): measured by Perceived Stress Scale (PSS-14)

^(d): measured by State/Trait Anxiety (STAI)

^(e): measured by the Psychiatric Epidemiology Research Interview Life Events Scale (LES)

Table S2. Effect size for birth weight across the low, moderate and high MPSP classes. See Figure 1 for additional info.

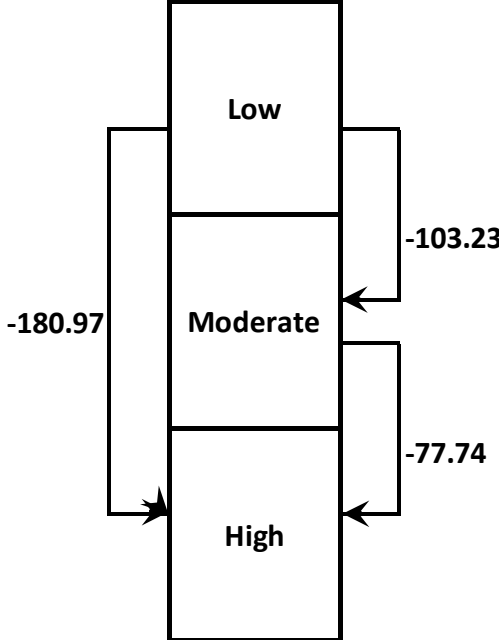


Table S3. List of the Imprinted genes whose expression has been tested.

Genes	Notes	Genes	Notes	Genes	Notes
<i>ABCA1</i>		<i>GPR1</i>	(1)	<i>OR11L1</i>	(2)
<i>ANKRD11</i>		<i>GRB10</i>		<i>OSBPL5</i>	
<i>ATP10A</i>		<i>GRIA1</i>	(2)	<i>PAX8</i>	
<i>BLCAP</i>		<i>H19</i>		<i>PCNA</i>	
<i>BMPR2</i>		<i>HLA-DPB2</i>		<i>PEG3</i>	
<i>CALCR</i>		<i>HYMAI</i>		<i>PEG10</i>	
<i>CCDC86</i>		<i>IGF2</i>		<i>PHLDA2</i>	
<i>CCNE1</i>		<i>IGF2AS</i>		<i>PLAGL1</i>	
<i>CD44</i>		<i>IGF2R</i>		<i>PPP1R9A</i>	
<i>CDKAL1</i>		<i>ILK</i>		<i>PRIM2</i>	
<i>CDKN1C</i>		<i>INPP5F</i>		<i>PSMD5-AS1</i>	(1)
<i>CERS4</i>		<i>INS</i>	(2)	<i>RB1</i>	
<i>COPG2</i>		<i>KCNK9</i>		<i>SDHD</i>	
<i>COPG2IT1</i>		<i>KCNQ1</i>	(2)	<i>SGCE</i>	
<i>CPA4</i>		<i>KCNQ1DN</i>		<i>SHANK2</i>	
<i>CPXM2</i>	(1)	<i>KCNQ1OT1</i>	(2)	<i>SLC22A18</i>	
<i>CTAG2</i>		<i>L3MBTL1</i>		<i>SLC22A18AS</i>	
<i>CTNNA3</i>		<i>LDB1</i>		<i>SLC22A3</i>	
<i>CTNND2</i>		<i>LIN28B</i>		<i>SNRPN</i>	
<i>CYR61</i>		<i>LRRTM1</i>		<i>SNRPN_VARIANT_2</i>	(2)
<i>DDC</i>	(2)	<i>MAGEL2</i>	(2)	<i>SNRPN_VARIANT_3/4/5</i>	(2)
<i>DHCR24</i>		<i>MCTS2P</i>		<i>SNURF/SNRPN_intron_1</i>	(2)
<i>DIRAS3</i>		<i>MEG3</i>		<i>TFPI2</i>	
<i>DLK1</i>		<i>MEST</i>		<i>THSD7A</i>	(1)
<i>DLX5</i>		<i>MESTIT</i>		<i>TRAPPC9</i>	(3)
<i>DOK7</i>		<i>MIMT1</i>	(2)	<i>UBE3A</i>	
<i>E2F7</i>		<i>MKRN3</i>		<i>VTRNA2-1</i>	(3)
<i>EPS15</i>		<i>MRAP2</i>	(2)	<i>ZBTB8B</i>	(2)(3)
<i>FAM50B</i>	(3)	<i>NAP1L5</i>		<i>ZC3H12C</i>	(3)
<i>GAA</i>		<i>NDN</i>		<i>ZDBF2</i>	(3)
<i>GABRA5</i>	(2)	<i>NEDD9</i>		<i>ZFAT</i>	(3)
<i>GABRG3</i>	(2)	<i>NGF</i>		<i>ZIM2</i>	
<i>GDNF</i>		<i>NHP2L1</i>	(3)	<i>ZNF264</i>	
<i>GFI1</i>		<i>NLRP2</i>		<i>ZNF331</i>	
<i>GLIS3</i>	(3)	<i>NNAT</i>		<i>ZNF597</i>	
<i>GNAS</i>		<i>NORAD</i>	(3)		
<i>GNASAS</i>		<i>NPAP1</i>	(2)		

(1): This gene is considered highly likely imprinted because of the allelic imbalanced expression detected in some tissues.

(2): Removed from the analysis because of inconsistent expression detected in more than 50% of the samples.

(3): This gene is considered highly likely imprinted because of the allele-specific expression detected in some tissues.

Table S4. Imprinted gene expression status, clustering analysis and association with MPSP and birth weight (Part I).

Gene	Expression and Factor Analysis	Prenatal Stress ⁽¹⁾						Birth Weight ⁽¹⁾	Mediation Effect Detected ⁽²⁾
		High Vs Moderate		High Vs Low		Moderate Vs Low			
		Dir	Eff Size	Dir	Eff Size	Dir	Eff Size		
<i>ABCA1</i>	Expression Cluster 1		0.082		0.076		-0.006		
<i>ANKRD11</i>	Expression Cluster 2		-0.052		-0.024		0.028	↑	
<i>ATP10A</i>	Not Clustered		-0.151		-0.019		0.132		
<i>BLCAP</i>	Expression Cluster 4		-0.052		0.019		0.071		
<i>BMPR2</i>	Expression Cluster 4		0.029		0.037		0.008		
<i>C15ORF2</i>	Inconsistent Expression								
<i>CALCR</i>	Expression Cluster 3	↑	0.495	↑	0.351		-0.144		
<i>CCDC86</i>	Expression Cluster 2		-0.066		0.008		0.073		
<i>CCNE1</i>	Expression Cluster 7	↑	0.193		0.056		-0.137	↓	
<i>CD44</i>	Expression Cluster 2		-0.15		-0.056		0.093	↑	
<i>CDKAL1</i>	Expression Cluster 2		-0.09		-0.075		0.015	↑	
<i>CDKN1C</i>	Expression Cluster 7		-0.021		-0.008		0.013		
<i>CERS4</i>	Expression Cluster 1	↑	0.394	↑	0.357		-0.038		
<i>COPG2</i>	Expression Cluster 1		0.023		0.051		0.028		
<i>COPG2IT1</i>	Expression Cluster 2		-0.208		-0.071		0.137		
<i>CPA4</i>	Expression Cluster 6		0.113		0.044		-0.07		
<i>CPXM2</i>	Expression Cluster 1		0.471	↑	0.721		0.25	↓	
<i>CTAG2</i>	Expression Cluster 5		0.162		0.164		0.003		
<i>CTNNA3</i>	Expression Cluster 6		-0.145		-0.068		0.077		
<i>CTNND2</i>	Expression Cluster 5		0.258		0.189		-0.069		
<i>CYR61</i>	Expression Cluster 6		-0.16		-0.044		0.116		
<i>DDC</i>	Inconsistent Expression								
<i>DHCR24</i>	Expression Cluster 3	↑	0.258		0.099		-0.158	↓	
<i>DIRAS3</i>	Expression Cluster 6		-0.086		-0.114		-0.029		
<i>DLK1</i>	Expression Cluster 3		0.033		0.059		0.027		
<i>DLX5</i>	Expression Cluster 1	↑	0.305		0.265		-0.04	↓	
<i>DOK7</i>	Expression Cluster 5		-0.197		-0.057		0.139		
<i>E2F7</i>	Not Clustered		-0.114		-0.106		0.009		
<i>EPS15</i>	Expression Cluster 3		0.025		0.015		-0.011		
<i>FAM50B</i>	Expression Cluster 2		-0.023		-0.055		-0.032		
<i>GAA</i>	Expression Cluster 1	↑	0.347	↑	0.316		-0.031	↓	
<i>GABRA5</i>	Inconsistent Expression								
<i>GABRG3</i>	Inconsistent Expression								
<i>GDNF</i>	Expression Cluster 6		0.08		0.138		0.057		
<i>GFI1</i>	Expression Cluster 5		0.064		0.067		0.004		
<i>GLIS3</i>	Expression Cluster 3		-0.037		-0.043		-0.006		
<i>GNAS</i>	Expression Cluster 4		-0.028		-0.014		0.013		
<i>GNASAS</i>	Not Clustered		0.075		0.125		0.05		
<i>GPR1</i>	Expression Cluster 5	↑	0.265	↑	0.278		0.013	↓	
<i>GRB10</i>	Expression Cluster 4		-0.048		0.006		0.054		
<i>GRIA1</i>	Inconsistent Expression								
<i>H19</i>	Expression Cluster 4	↑	-0.137		-0.014	↑	0.123		
<i>HLA-DPB2</i>	Not Clustered		-0.019		0.057		0.076		
<i>HYMAI</i>	Expression Cluster 6		-0.016		0.118		0.135		
<i>IGF2</i>	Expression Cluster 5		-0.199		-0.069		0.13	↑	
<i>IGF2AS</i>	Expression Cluster 4		-0.107		-0.052		0.055	↑	
<i>IGF2R</i>	Expression Cluster 1	↑	0.164	↑	0.186		0.023		
<i>ILK</i>	Expression Cluster 2		-0.083		-0.071		0.011		
<i>INPP5F</i>	Expression Cluster 1	↑	0.146		0.097		-0.049		
<i>INS</i>	Inconsistent Expression								
<i>KCNK9</i>	Inconsistent Expression								
<i>KCNQ1</i>	Expression Cluster 2		-0.016		-0.003		0.014	↑	
<i>KCNQ1DN</i>	Inconsistent Expression								
<i>KCNQ1OT1</i>	Expression Cluster 2		-0.033		0.028		0.061		
<i>L3MBTL1</i>	Expression Cluster 1		0.107		0.143		0.036		
<i>LDB1</i>	Expression Cluster 2		0.006		0.034		0.028		

Table S4. Imprinted gene expression status, clustering analysis and association with MPSP and birth weight (Part II).

Gene	Expression and Factor Analysis	Prenatal Stress ⁽¹⁾						Birth Weight ⁽¹⁾	Mediation Effect Detected ⁽²⁾
		High Vs Moderate		High Vs Low		Moderate Vs Low			
		Dir	Eff Size	Dir	Eff Size	Dir	Eff Size		
<i>LIN28B</i>	Expression Cluster 4		-0.041		-0.019		0.022		
<i>LRRTM1</i>	Inconsistent Expression								
<i>MAGEL2</i>	Expression Cluster 3		0.091		0.039		-0.052		
<i>MCTS2P</i>	Expression Cluster 2		0.025		-0.033		-0.057		
<i>MEG3</i>	Expression Cluster 2		-0.141		-0.027		0.114	↑	
<i>MEST</i>	Expression Cluster 3		0.01		0.016		0.006		
<i>MESTIT1</i>	Inconsistent Expression								
<i>MIMT1</i>	Expression Cluster 2		-0.118		-0.127		-0.01	↑	
<i>MKRN3</i>	Expression Cluster 1		0.178		0.042		-0.136		
<i>MRAP2</i>	Inconsistent Expression								
<i>NAP1L5</i>	Expression Cluster 3		0.138		0.165		0.027		
<i>NDN</i>	Expression Cluster 3		0.087		0.04		-0.047		
<i>NEDD9</i>	Expression Cluster 4		-0.079		-0.027		0.052		
<i>NGFB</i>	Expression Cluster 6		0.001		0.068		0.067		
<i>NHP2L1</i>	Expression Cluster 2		0.019		0.03		0.011		
<i>NLRP2</i>	Expression Cluster 1		0.17		0.182		0.012	↓	
<i>NNAT</i>	Expression Cluster 4		-0.026		-0.036		-0.01	↑	
<i>NORAD</i>	Expression Cluster 1		0.112	↑	0.181		0.07		
<i>OR11L1</i>	Inconsistent Expression								
<i>OSBPL5</i>	Expression Cluster 4		0.015		0.025		0.01		
<i>PAX8</i>	Not Clustered		0.051		0.068		0.017		
<i>PCNA</i>	Expression Cluster 5		0.113		0.065		-0.048		
<i>PEG10</i>	Expression Cluster 5		0.123		0.047		-0.076		
<i>PEG3</i>	Expression Cluster 1	↑	0.184		0.14		-0.045		
<i>PHLDA2</i>	Expression Cluster 7		-0.029		-0.102		-0.073		
<i>PLAGL1</i>	Expression Cluster 2		-0.085		0.041		0.126	↑	
<i>PPP1R9A</i>	Expression Cluster 2		-0.138		-0.055		0.083	↑	
<i>PRIM2</i>	Expression Cluster 3		0.043		-0.064	↓	-0.106		
<i>PSMD5-AS1</i>	Not Clustered		0.079		0.2		0.121		
<i>RB1</i>	Expression Cluster 4		-0.136		-0.104		0.032	↑	
<i>SDHD</i>	Expression Cluster 3	↑	0.139	↑	0.143		0.004		
<i>SGCE</i>	Expression Cluster 1		0.125	↑	0.155		0.03		
<i>SHANK2</i>	Expression Cluster 1	↑	0.399	↑	0.374		-0.025	↓	
<i>SLC22A18</i>	Expression Cluster 7		-0.029		-0.146		-0.116		
<i>SLC22A18AS</i>	Expression Cluster 7		0.099		-0.085	↓	-0.184		
<i>SLC22A3</i>	Expression Cluster 6		0.088		0.149		0.06	↑	
<i>SNRPN</i>	Expression Cluster 2		-0.13		-0.059		0.071	↑	
<i>SNRPN_VARIANT_2</i>	Inconsistent Expression								
<i>SNRPN_VARIANT_3/4/5</i>	Inconsistent Expression								
<i>SNURF/SNRPN_intron_1</i>	Inconsistent Expression								
<i>TFPI2</i>	Expression Cluster 1	↑	0.489		0.411		-0.078	↓	
<i>THSD7A</i>	Expression Cluster 1	↑	0.425	↑	0.44		0.015	↓	
<i>TRAPPC9</i>	Expression Cluster 2		0.018		-0.028		-0.046		
<i>UBE3A</i>	Expression Cluster 1		0.119	↑	0.148		0.029		
<i>VTRNA2-1</i>	Expression Cluster 2		-0.417		-0.233		0.184	↑	
<i>ZBTB8B</i>	Inconsistent Expression								
<i>ZC3H12C</i>	Expression Cluster 6		0.04		0.006		-0.034		
<i>ZDBF2</i>	Expression Cluster 1	↑	0.272		0.201		-0.071		
<i>ZFAT</i>	Expression Cluster 1		0.228		0.159		-0.069		
<i>ZIM2</i>	Expression Cluster 5		0.044		0.167		0.123		
<i>ZNF264</i>	Expression Cluster 1		0.111	↑	0.126		0.015		
<i>ZNF331</i>	Expression Cluster 2		-0.13		-0.03		0.1	↑	
<i>ZNF597</i>	Expression Cluster 2		-0.035		0.009		0.044		

⁽¹⁾: ↑ = for Prenatal Stress analysis, increase of the expression of the gene in the first vs the second category listed in the table header; for Birth Weight analysis, increase of the expression of the gene with increasing birth weight. ↓ = for Prenatal Stress analysis, decrease of the expression of the gene in the first vs the second category listed in the table header; for Birth Weight analysis, decrease of the expression of the gene with increasing birth weight (see Figures 2B and 3A for details).

⁽²⁾: limited to 5 of the 13 genes of groups I and II of the Prenatal Stress analysis that were also found associated with Birth Weight (see text for details)

Table S5. Average expression change (in log₂ format) for low, moderate and high MPSP categories. See Figure 2B for additional info.

Gene	Prenatal stress		
	Low	Moderate	High
<i>CALCR</i>	-0.0689	-0.2130	0.2820
<i>CERS4</i>	-0.1062	-0.1441	0.2503
<i>GAA</i>	-0.0948	-0.1260	0.2208
<i>GPR1</i>	-0.0972	-0.0840	0.1812
<i>IGF2R</i>	-0.0696	-0.0470	0.1166
<i>SDHD</i>	-0.0490	-0.0451	0.0941
<i>SHANK2</i>	-0.1161	-0.1414	0.2576
<i>THSD7A</i>	-0.1514	-0.1368	0.2882
<i>CPXM2</i>	-0.3238	-0.0735	0.3973
<i>NORAD</i>	-0.0838	-0.0140	0.0977
<i>SGCE</i>	-0.0617	-0.0319	0.0936
<i>UBE3A</i>	-0.0593	-0.0298	0.0891
<i>ZNF264</i>	-0.0472	-0.0317	0.0789
<i>CCNE1</i>	0.0272	-0.1098	0.0827
<i>DHCR24</i>	0.0196	-0.1386	0.1191
<i>DLX5</i>	-0.0748	-0.1152	0.1900
<i>INPP5F</i>	-0.0160	-0.0648	0.0807
<i>PEG3</i>	-0.0317	-0.0763	0.1080
<i>TFPI2</i>	-0.1110	-0.1890	0.3000
<i>ZDBF2</i>	-0.0432	-0.1144	0.1575
<i>PRIM2</i>	0.0568	-0.0497	-0.0071
<i>SLC22A18AS</i>	0.0895	-0.0941	0.0046
<i>H19</i>	-0.0365	0.0869	-0.0504

Table S6. List of the imprinted genes significantly associated with birth weight. The r and p values are provided. See Figure 3A for additional info.

Genes	r	p-value
<i>ANKRD11</i>	0.125	0.040
<i>CCNE1</i>	-0.272	<0.001
<i>CD44</i>	0.163	0.007
<i>CDKAL1</i>	0.142	0.019
<i>CPXM2</i>	-0.144	0.017
<i>DHCR24</i>	-0.173	0.004
<i>DLX5</i>	-0.189	0.002
<i>GAA</i>	-0.178	0.003
<i>GPR1</i>	-0.122	0.045
<i>IGF2</i>	0.139	0.022
<i>IGF2AS</i>	0.156	0.010
<i>MIMT1</i>	0.122	0.044
<i>KCNQ1</i>	0.142	0.019
<i>MEG3</i>	0.206	0.001
<i>NLRP2</i>	-0.175	0.004
<i>NNAT</i>	0.121	0.045
<i>PLAGL1</i>	0.145	0.016
<i>PPP1R9A</i>	0.162	0.007
<i>RB1</i>	0.217	<0.001
<i>SHANK2</i>	-0.243	<0.001
<i>SLC22A3</i>	0.148	0.015
<i>SNRPN</i>	0.162	0.007
<i>TFPI2</i>	-0.179	0.003
<i>THSD7A</i>	-0.152	0.012
<i>VTRNA2-1</i>	0.127	0.036
<i>ZNF331</i>	0.149	0.014

Table S7. Percent mediation between MPSP and birth weight explained by 5 of the 13 imprinted genes associated with both MPSP (only groups I and II) and birth weight. See text for details and Figure 4A for additional info.

Gene	Unadjusted	Adjusted
<i>CPXM2</i>	26%	0%
<i>GAA</i>	26%	22%
<i>GPR1</i>	0%	0%
<i>SHANK2</i>	28%	22%
<i>THSD7A</i>	16%	0%

Table S8. Cluster distribution of the imprinted genes whose expression has been associated with MPSP, birth weight or both. See Table 2 for additional info.

Cluster	Genes	Prenatal Stress				Birth Weight	
		All		Groups I&II		N.	%
		N.	%	N.	%		
1	21	15	65	10	77	7	27
2	21	-	-	-	-	11	42
3	11	4	18	2	15	1	4
4	11	-	-	-	-	3	11
5	9	1	4	1	8	2	8
6	9	-	-	-	-	1	4
7	5	3	13	-	-	1	4
ND	6	-	-	-	-	-	-
TOTAL	93	23	100	13	100	26	100

Table S9. Imprinted genes clusters association with birth weight. The r and p values are provided. See Figure 4C for additional info.

Cluster	r	p-value
1	-0.140	0.021
2	0.127	0.037
3	0.107	0.079
4	0.033	0.591
5	-0.065	0.285
6	0.019	0.754
7	-0.167	0.006

Table S10. Summary of the IPA analysis output providing basic information on top networks, top canonical pathways, molecular and cellular functions, physiological system development and function and top upstream regulators. See Figure 5 for additional info (Part I).

Top Networks

<u>Prenatal Stress</u>	Score	Molecules
Gene Expression, Cell Death and Survival, Cellular Assembly and Organization	55	21
Endocrine System Development and Function, Endocrine System Disorders, Nervous System Development and Function	3	1
<u>Birth Weight</u>		
Increased Levels of Alkaline Phosphatase, Organ Morphology, Organismal Injury and Abnormalities	37	16
Embryonic Development, Organismal Development, Cancer	6	4
Cardiovascular Disease, Cell Cycle, Cell Death and Survival	3	1
Endocrine System Development and Function, Endocrine System Disorders, Nervous System Development and Function	3	1
Cancer, Carbohydrate Metabolism, Cell Cycle	2	1

Top Canonical Pathways

<u>Prenatal Stress</u>	p-value
Myo-Inositol Biosynthesis	5.14E-03
PTEN Signaling	6.61E-03
Cholesterol Biosynthesis I, II (via 24,25-dihydrolanosterol), III (via Desmosterol)	1.33E-02
Glycogen Degradation III	1.43E-02
D-Myo-Inositol (1,4,5)-Triphosphate Degradation	1.84E-02
<u>Birth Weight</u>	
Estrogen-Mediated S-Phase Entry	3.57E-04
Antiproliferative Role of TOB in T Cell Signaling	4.20E-04
Cell Cycle Regulation by BTG Family Proteins	7.64E-04
Glioblastoma Multiforme Signaling	8.40E-04
Regulation of Cellular Mechanics by Calpain Protease	2.02E-03

Top Diseases and Biological Functions

<u>Prenatal Stress</u>	p-value	Molecules
Cancer	4.83E-02 - 1.09E-04	20
Organismal Injury and Abnormalities	4.83E-02 - 1.09E-04	21
Endocrine System Disorders	4.34E-02 - 1.20E-04	17
Gastrointestinal Disease	4.47E-02 - 1.20E-04	19
Hepatic System Disease	1.20E-04 - 1.20E-04	2
<u>Birth Weight</u>		
Gastrointestinal Disease	5.84E-03 - 2.15E-06	20
Organismal Injury and Abnormalities	5.84E-03 - 2.15E-06	23
Cancer	5.84E-03 - 7.77E-05	19
Tumor Morphology	5.27E-03 - 7.77E-05	5
Endocrine System Disorders	5.84E-03 - 8.48E-05	18

Table S10. Summary of the IPA analysis output providing basic information on top networks, top canonical pathways, molecular and cellular functions, physiological system development and function and top upstream regulators. See Figure 5 for additional info (Part II).

Molecular and Cellular Function

<u>Prenatal Stress</u>	p-value	Molecules
Gene Expression	2.68E-03 - 3.03E-10	6
Cell Cycle	4.24E-02 - 1.03E-03	4
Cell Morphology	4.19E-02 - 1.03E-03	7
Cell-To-Cell Signaling and Interaction	2.04E-02 - 1.03E-03	4
Cellular Assembly and Organization	4.14E-02 - 1.03E-03	4
<u>Birth Weight</u>		
Cell Cycle	5.84E-03 - 2.82E-06	5
Gene Expression	3.51E-03 - 1.07E-05	4
Cell Morphology	5.84E-03 - 1.31E-05	10
Cellular Development	5.84E-03 - 3.37E-05	12
Cellular Growth and Proliferation	5.84E-03 - 3.37E-05	12

Pshysiological System Development and Function

<u>Prenatal Stress</u>	p-value	Molecules
Behavior	4.73E-02 - 4.53E-05	5
Reproductive System Development and Function	4.63E-02 - 4.53E-05	7
Nervous System Development and Function	4.73E-02 - 6.53E-05	9
Organ Morphology	4.34E-02 - 6.53E-05	10
Organismal Development	4.53E-02 - 6.53E-05	11
<u>Birth Weight</u>		
Cardiovascular System Development and Function	5.84E-03 - 4.22E-05	8
Hair and Skin Development and Function	3.81E-03 - 4.71E-05	4
Connective Tissue Development and Function	5.84E-03 - 5.88E-05	7
Nervous System Development and Function	5.84E-03 - 5.89E-05	9
Reproductive System Development and Function	2.34E-03 - 6.17E-05	6

Top Upstream Regulators

<u>Prenatal Stress</u>	p-value of Overlap
<i>CDKN3</i>	7.86E-08
<i>ZFP57</i>	1.12E-07
D-tubocurarine	9.09E-05
<i>WDR5</i>	1.20E-04
<i>MECP2</i>	2.32E-04
<u>Birth Weight</u>	
<i>Butyric Acid</i>	5.12E-07
<i>IGF2BP3</i>	3.92E-06
<i>RPS6KB1</i>	1.35E-05
<i>MGEA5</i>	5.82E-05
<i>CAMK2N2</i>	5.85E-05

Table S11. Detailed table of the molecules that populate the networks scored by IPA for the imprinted genes associated with MPSP. See Figure 5A for additional info.

Network	Molecules in Network	Score	Input	Top Diseases and Functions
1	ADGRG6, Akt, Ang4, beta-estradiol, butyric acid, CALCR , caspase, CBX5, CCDC170, CCNE1 , CD3, CERS4 , CLYBL, COA4, CTNNA-CTNNB1-CTNNG-CDH5, CTNNB1, DEFB114, DHCR24 , DLX5 , E2F1, E2F1-HDAC-Rb, E2f1-Rb, ERK1/2, GAA , GPR1 , GPR88, GPR137, GPR139, GPR146, GPR160, GPR171, GPR173, GPR176, GUF1, H19, HCRTR2, HNF4A, HTR5A, IGF2R , INPP5F , INSL6, KIAA0141, P38 MAPK, PEG3 , PRIM2 , PROKR1, RB1, Rb-E2F-DP1, RBAK, RXFP3, SDHD , SFXN5, SGCE , SHANK2 , SIRT1, SLC22A18AS , Slpi (includes others), SOX2, SSR2, TAS1R2, TCEAL3, TFPI2 , Tgf beta, THSD7A , TNF, UBE3A , VN1R1, ZDBF2 , ZNF264 , ZNF137P	55	21	Gene Expression, Cell Death and Survival, Cellular Assembly and Organization
2	ARNT2, CPXM2 , OTX2, SIM1	3	1	Endocrine System Development and Function, Endocrine System Disorders, Nervous System Development and Function

Table S12. Detailed table of the molecules that populate the networks scored by IPA for the imprinted genes associated with birth weight. See Figures 5B and C for additional info.

Network	Molecules in Network	Score	Input	Top Diseases and Functions
1	2'-fucosyllactose, 24, 25-dihydroxyvitamin D3, 24R, 25-dihydroxyvitamin D3, Akt, ALK3-BMPR2, Alp, Androgen-AR, ANGPT4, ANGPTL1, ANKRD11 , caspase, CCNE1 , CD3, CD44 , Cgm4/Psg16, Cyp2j9, CYP4Z1, DBNDD1, DHCR24 , DLX5 , EGFR/PDGFR/IGFR, ERK, ERK1/2, estrogen receptor, ethylene glycol, ETV2, Focal adhesion kinase, FSH, GAA , Histone h3, IGF2 , IL22R1-IL10R2, Immunoglobulin, Insulin, isoleucine, Jnk, Jun-GABP, KCNQ1 , Mapk, MUC8, N-arachidonylglycine, NFkB (complex), NLRP2 , NNAT , Nrp-PlexinA, Omd, P38 MAPK, Pdgf (complex), PDGF BB, PI3K (complex), Pka, Pkc(s), PLAGL1 , PPP1R9A , Prl4a1, Ras, RB1 , Sh2b3, SHP2-PI3K-GAB2, SNRPN , TFPI2 , TMEM184A, TRAF1-TRAF2-TRAF3, Vegf, Vegfr dimer, Wfdc17/Wfdc18, Yap1, Ybx1-ps3, ZNF331 , ZNF675	37	16	Increased Levels of Alkaline Phosphatase, Organ Morphology, Organismal Injury and Abnormalities
2	ACAP1, adenine, ADGRB2, ADGRG2, ADGRL1, ADGRL2, ADRA2C, ADSS, BCCIP, C6, C21orf59, CCR10, CDKAL1 , CELSR1, CELSR2, CELSR3, CRAT, CRIP1, CTDNEP1, CTNNB1, CXADR, Cyp2d9 (includes others), DLGAP2, DLGAP3, EMX2, FANCF, FCAMR, FZD3, FZD6, FZD9, GNG5, GNS, GPR1 , GPR39, GPR45, GPR137, GPR146, GPR160, GPR137B, GPX2, GSTZ1, HNF4A, HSD17B2, LGR5, LHX6, LTB4R2, MINK1, MPZL2, NAT8, NCK1, NEURL2, NOP53, PPP1R15B, PRPF38B, PRX, PTK7, PTPN4, RAB18, RPL41, RXFP2, SEMA3C, SHANK2 , SLC22A3 , Slco1a1, SSTR1, SSTR4, STARD7, VEZT, VN1R1, YPEL3	6	4	Embryonic Development, Organismal Development, Cancer
3	MIMT1 , MYB	3	1	Cardiovascular Disease, Cell Cycle, Cell Death and Survival
4	ARNT2, CPXM2 , OTX2, SIM1	3	1	Endocrine System Development and Function, Endocrine System Disorders, Nervous System Development and Function
5	ASAP2, butyric acid, RAD21, SKIL, THSD7A	2	1	Cancer, Carbohydrate Metabolism, Cell Cycle
6	BAX, EIF2AK2, EIF2S1, EPHB6, SSB, VTRNA2-1	2	1	Cell Death and Survival, Cellular Compromise, Cellular Function and Maintenance
7	BMI1, GDF15, MDM2, MEG3 , TP53	2	1	Cell Cycle, Gene Expression, Immunological Disease

Table S13. Full list of the molecules that are common between network 1 of the MPSP IPA analysis and networks 1, 2 and 5 of the birth weight IPA analysis. See Figure 5D for additional info.

Prenatal Stress Network 1 & Birth Weight Network 1	Prenatal Stress Network 1 & Birth Weight Network 2	Prenatal Stress Network 1 & Birth Weight Network 5
Akt	<i>CTNNB1</i>	Butyric Acid
Caspase	<i>GPR1</i>	<i>THSD7A</i>
<i>CCNE1</i>	<i>GPR137</i>	
<i>CD3</i>	<i>GPR146</i>	
<i>DHCR24</i>	<i>GPR160</i>	
<i>DLX5</i>	<i>HNF4A</i>	
<i>ERK1/2</i>	<i>SHANK2</i>	
GAA	<i>VN1R1</i>	
<i>P38 MAPK</i>		
<i>RB1</i>		
<i>TFPI2</i>		

Table S14. List of the key canonical pathways scored by IPA from both the MPSP and birth weight analysis. Genes from the input list of the two analyses are listed. See Figure S5 for additional info.

Ingenuity Canonical Pathways	Prenatal Stress	Common	Birth Weight
Myo-Inositol Biosynthesis	<i>INPP5F</i>		
PTEN Signaling	<i>INPP5F, IGF2R</i>		
Cholesterol Biosynthesis I, II (via 24,25-Dihydrolanosterol), III (via Desmosterol)		<i>DHCR24</i>	
Glycogen Degradation III		<i>GAA</i>	
D-Myo-Inositol (1,4,5)-Trisphosphate Degradation	<i>INPP5F</i>		
GADD45 Signaling		<i>CCNE1</i>	
1D-Myo-Inositol Hexakisphosphate Biosynthesis II (Mammalian)	<i>INPP5F</i>		
D-Myo-Inositol (1,3,4)-Trisphosphate Biosynthesis	<i>INPP5F</i>		
DNA Damage-Induced 14-3-3s Signaling		<i>CCNE1</i>	
Osteoarthritis Pathway	<i>H19</i>	<i>DLX5</i>	
TCA Cycle II (Eukaryotic)	<i>SDHD</i>		
Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis	<i>CALCR</i>	<i>DLX5</i>	
Estrogen-Mediated S-Phase Entry		<i>CCNE1</i>	<i>RB1</i>
Superpathway of D-Myo-Inositol (1,4,5)-Trisphosphate Metabolism	<i>INPP5F</i>		
Antiproliferative Role of TOB in T Cell Signaling		<i>CCNE1</i>	<i>RB1</i>
Superpathway of Cholesterol Biosynthesis		<i>DHCR24</i>	
Cell Cycle Regulation by BTG Family Proteins		<i>CCNE1</i>	<i>RB1</i>
Inhibition of Matrix Metalloproteases		<i>TFPI2</i>	
Cell Cycle Control of Chromosomal Replication	<i>PRIM2</i>		
Stearate Biosynthesis I (Animals)		<i>DHCR24</i>	
Regulation of Cellular Mechanics by Calpain Protease		<i>CCNE1</i>	<i>RB1</i>
Cell Cycle: G1/S Checkpoint Regulation		<i>CCNE1</i>	<i>RB1</i>
Cyclins and Cell Cycle Regulation		<i>CCNE1</i>	<i>RB1</i>
Small Cell Lung Cancer Signaling		<i>CCNE1</i>	<i>RB1</i>
Prostate Cancer Signaling		<i>CCNE1</i>	<i>RB1</i>
Glioma Signaling	<i>IGF2R</i>		<i>RB1, IGF2</i>
Pancreatic Adenocarcinoma Signaling		<i>CCNE1</i>	<i>RB1</i>
Aryl Hydrocarbon Receptor Signaling		<i>CCNE1</i>	<i>RB1</i>
Glioblastoma Multiforme Signaling		<i>CCNE1</i>	<i>RB1, IGF2</i>
p53 Signaling			<i>RB1, PLAGL1</i>
Ovarian Cancer Signaling			<i>RB1, CD44</i>
Role of p14/p19ARF in Tumor Suppression			<i>RB1</i>

Table S15. List of all expressed imprinted genes and their inclusion in the co-expression modules from the whole-genome expression analysis. See Table 3 for additional info (Part I).

Gene	Module ⁽¹⁾	Clusters	Significant ⁽²⁾
<i>ABCA1</i>	blue	Cluster 1	
<i>ANKRD11</i>	turquoise	Cluster 2	BW
<i>ATP10A</i>	blue	Not Clustered	
<i>BLCAP</i>	pink	Cluster 4	
<i>BMPR2</i>	blue	Cluster 4	
<i>CALCR</i>	red	Cluster 3	PS
<i>CCDC86</i>	red	Cluster 2	
<i>CCNE1</i>	purple	Cluster 7	PS&BW
<i>CD44</i>	blue	Cluster 2	BW
<i>CDKAL1</i>	green	Cluster 2	BW
<i>CDKN1C</i>	pink	Cluster 7	
<i>CERS4</i>	turquoise	Cluster 1	PS
<i>COPG2</i>	grey	Cluster 1	
<i>COPG2IT1</i>		Cluster 2	
<i>CPA4</i>	blue	Cluster 6	
<i>CPXM2</i>	grey	Cluster 1	PS&BW
<i>CTAG2</i>	grey	Cluster 5	
<i>CTNNA3</i>		Cluster 6	
<i>CTNND2</i>		Cluster 5	
<i>CYR61</i>	blue	Cluster 6	
<i>DHCR24</i>	grey	Cluster 3	PS&BW
<i>DIRAS3</i>		Cluster 6	
<i>DLK1</i>	blue	Cluster 3	
<i>DLX5</i>	blue	Cluster 1	PS&BW
<i>DOK7</i>		Cluster 5	
<i>E2F7</i>		Not Clustered	
<i>EPS15</i>	blue	Cluster 3	
<i>FAM50B</i>	grey	Cluster 2	
<i>GAA</i>	turquoise	Cluster 1	PS&BW
<i>GDNF</i>		Cluster 6	
<i>GFI1</i>		Cluster 5	
<i>GLIS3</i>	grey	Cluster 3	
<i>GNAS</i>	yellow	Cluster 4	
<i>GNASAS</i>		Not Clustered	
<i>GPR1</i>	blue	Cluster 5	PS&BW
<i>GRB10</i>	blue	Cluster 4	
<i>H19</i>	blue	Cluster 4	PS
<i>HLA-DPB2</i>		Not Clustered	
<i>HYMAI</i>	turquoise	Cluster 6	
<i>IGF2</i>	blue	Cluster 5	BW
<i>IGF2AS</i>	blue	Cluster 4	BW
<i>IGF2R</i>	grey	Cluster 1	PS
<i>ILK</i>	black	Cluster 2	
<i>INPP5F</i>	red	Cluster 1	PS
<i>KCNQ1</i>	blue	Cluster 2	BW
<i>KCNQ1OT1</i>	turquoise	Cluster 2	
<i>L3MBTL1</i>	brown	Cluster 1	

Table S15. List of all expressed imprinted genes and their inclusion in the co-expression modules from the whole-genome expression analysis. See Table 3 for additional info (Part II).

Gene	Module ⁽¹⁾	Clusters	Significant ⁽²⁾
<i>LDB1</i>	brown	Cluster 2	
<i>LIN28B</i>	pink	Cluster 4	
<i>MAGEL2</i>		Cluster 3	
<i>MCTS2P</i>		Cluster 2	
<i>MEG3</i>	blue	Cluster 2	BW
<i>MEST</i>	pink	Cluster 3	
<i>MIMT1</i>		Cluster 2	BW
<i>MKRN3</i>	brown	Cluster 1	
<i>NAP1L5</i>		Cluster 3	
<i>NDN</i>	blue	Cluster 3	
<i>NEDD9</i>	blue	Cluster 4	
<i>NGF</i>		Cluster 6	
<i>NHP2L1</i>	turquoise	Cluster 2	
<i>NLRP2</i>	grey	Cluster 1	BW
<i>NNAT</i>	blue	Cluster 4	BW
<i>NORAD</i>		Cluster 1	PS
<i>OSBPL5</i>	blue	Cluster 4	
<i>PAX8</i>	turquoise	Not Clustered	
<i>PCNA</i>	cyan	Cluster 5	
<i>PEG10</i>	yellow	Cluster 5	
<i>PEG3</i>	yellow	Cluster 1	PS
<i>PHLDA2</i>	yellow	Cluster 7	
<i>PLAGL1</i>	blue	Cluster 2	BW
<i>PPP1R9A</i>	yellow	Cluster 2	BW
<i>PRIM2</i>	turquoise	Cluster 3	PS
<i>PSMD5-AS1</i>		Not Clustered	
<i>RB1</i>	blue	Cluster 4	BW
<i>SDHD</i>	turquoise	Cluster 3	PS
<i>SGCE</i>	turquoise	Cluster 1	PS
<i>SHANK2</i>	brown	Cluster 1	PS&BW
<i>SLC22A18</i>	pink	Cluster 7	
<i>SLC22A18AS</i>		Cluster 7	PS
<i>SLC22A3</i>	blue	Cluster 6	BW
<i>SNRPN</i>		Cluster 2	BW
<i>TFPI2</i>	grey	Cluster 1	PS&BW
<i>THSD7A</i>	grey	Cluster 1	PS&BW
<i>TRAPPC9</i>	brown	Cluster 2	
<i>UBE3A</i>	green	Cluster 1	PS
<i>VTRNA2-1</i>		Cluster 2	BW
<i>ZC3H12C</i>	turquoise	Cluster 6	
<i>ZDBF2</i>	greenyellow	Cluster 1	PS
<i>ZFAT</i>	brown	Cluster 1	
<i>ZIM2</i>		Cluster 5	
<i>ZNF264</i>	turquoise	Cluster 1	PS
<i>ZNF331</i>	salmon	Cluster 2	BW
<i>ZNF597</i>	green	Cluster 2	

⁽¹⁾: blank cells refers to genes not used for module construction because of low expression level

⁽²⁾: PS = Prenatal Stress; BW = Birth Weight

Table S16. Breakdown of the cross tabulation of the expressed imprinted genes by cluster and module. See Table 3 for additional info.

Module	Cluster 1				Cluster 2				Cluster 3				Cluster 4				Cluster 5				Cluster 6				Cluster 7				Total														
	Significant			All	Significant			All	Significant			All	Significant			All	Significant			All	Significant			All	Significant			All	Significant			All											
	PS	BW	Com		Tot	PS	BW		Com	Tot	PS		BW	Com	Tot		PS	BW	Com		Tot	PS	BW		Com	Tot	PS		BW	Com	Tot		PS	BW	Com	Tot							
turquoise	4	1	1	4	4	1	1	1	3	3	2	2	2	2	2																	6	2	1	7	11							
blue	1	1	1	1	2	4	4	4	4	4							1	3	4	8	8	1	2	1	2	2	2	1	1	3	3	3	3	11	2	12	22						
brown	1	1	1	1	4																										1	1	1	1	6								
yellow	1			1	1	1	1	1	1	1									1	1	1	1										1	1	1	2	5							
green	1			1	1	1	1	1	2	2																						1	1	2	3	3							
red	1			1	1				1	1	1	1	1	1	1																2	2	3	3	3								
black									1	1																										1							
pink														1	1				2	2										2				5									
magenta																																											
purple																																1	1	1	1	1							
greenyellow	1			1	1																											1	1	1	1	1							
tan																																											
salmon						1	1	1	1	1																						1	1	1	1	1							
cyan																					1	1														1							
midnightblue																																											
lightcyan																																											
grey60																																											
grey	4	4	3	5	6				1	1	1	1	1	1	2	2					1	1										5	5	4	6	10							
TOTAL	14	7	6	15	20	8	8	16	16	16	4	1	1	4	9	9	1	3	4	11	11	1	2	1	2	5	5	1	1	5	5	5	1	1	1	1	4	4	21	23	9	35	70