Supplementary table 2. Genes and their known functions. Gene IDs from NCBI gene database.

|  |  |  |  |
| --- | --- | --- | --- |
| Gene | Tissue | Methylation after exposure to high ppBMI/GWG | Known gene function |
| *ABCA1*ATP-binding cassette subfamily A member 1 | Offspring peripheral blood | Lower with GWG (1) | ABC-proteins transports various molecules across cellular membranes. In the cellular lipid removal pathway, the protein functions as a cholesterol efflux pump. (Gene ID: 19 (2)) |
| *ACACB*Acetyl-CoA carboxylase beta | Umbilical cord tissue | Higher with obesity (3) | ACC is a multifunctional enzyme system that catalyzes the carboxylation of A-CoA to malonyl-CoA, the rate-limiting step in fatty acid synthesis. (Malonyl-CoA inhibits Carnitine palmitoyltransferase I, the rate limiting step in the uptake and oxidation of fatty acids) (Gene ID: 32 (2)) |
| *ADIPOQ*Adiponectin, C1Q and collagen domain containing | Placenta | NS with ppBMI (4) | Exclusively expressed in adipose tissue. Encodes a protein with similarity to collagens X and VII and complement factor C1q. (Gene ID: 9370 (2)).  |
| Maternal adipose tissue | Higher with ppBMI (4) |
| *AHRR*Aryl-hydrocarbon receptor repressor | Umbilical cord blood | Higher with maternal 2.trimester BMI (5) | Involved in regulation of cell growth and differentiation, and participates in the aryl-hydrocarbon receptor signaling cascade, which mediates dioxin toxicity. (Gene ID: 57491 (2)).Involved in processing xenobiotics that could affect fetal development. (5) |
| *Alu elements* | Offspring peripheral mononuclear cells | NS with ppBMI or GWG (6) | Short interspersed elements that can generate copies of themselves in order to be inserted in other parts of the genome and thereby affect gene expression (7, 8).  |
| *ATP8B3*ATPase phospholipid transporting 8B3 | Offspring saliva | Higher with maternal BMI (9) | Aminophospholipid translocase that transport phosphatidyserine and phosphatidylethanolamine from one side of the bilayer to the other. (Gene ID: 148229 (2)) |
| *BAHCC1*BAH domain and coiled-coil containing 1 | Offspring blood | Lower with ppBMI (10) | (Gene ID: 57597 (2)) |
| *BCL1 (CCND1)*Cyclin D1 | Umbilical cord tissue | Higher with fat mass (11) | Regulates CDK4 or CDK6 that are required for cell cycle G1/S transition. Shown to interact with tumor suppressor protein Rb, and Rb regulates the gene expression positively. May contribute to tumorigenesis. (Gene ID: 595 (2)) |
| *BDNF*Brain derived neurotrophic facto | Umbilical cord blood | Higher with obesity (12) | Nerve growth factor. Promotes neuronal survival in the adult brain. May contribute in regulation of stress response and the biology of mood disorders (Gene ID: 627 (2)) |
| *CACNA1G*Calcium voltage-gated channel subunit alpha1 G | Umbilical cord blood | Higher with ppBMI (13) | Mediate the entry of calcium ions into excitable cells, and are also involved in a variety of calcium-dependent processes. (Gene ID: 8913 (2)) |
| *CAMK1*Calcium/calmodulin dependent protein kinase I | Umbilical cord blood monocytes | Lower with obesity (14) | Involved in metabolism (14) |
| *CBS*Cystathionine-beta-synthase | Offspring saliva | Higher with maternal BMI (9) | Catalyze the conversion of homocysteine to cystathionine. (Gene ID: 875 (2)) |
| *CCDC112*Coiled coil domain containing 112 | Umbilical cord blood | Higher with ppBMI (12) | Intracellular protein (Gene ID: 153733 (2)) |
| *CD59*CD59 molecule | Umbilical cord blood monocytes | Lower with obesity (14) | Defense response (14). Surface glycoprotein that regulates complement-mediated cell lysis and is involved in lymphocyte signal transduction.  |
| *CD101*CD101 molecule | Umbilical cord blood monocytes | Higher with obesity (14) | Immune gene (14) |
| *CDH5*Cadherin 5 | Umbilical cord blood monocytes | Lower with obesity (14) | Cell migration and adhesion in myeloid cells (14) |
| *CEP2*Cysteine proteinases superfamily protein  | Offspring saliva | Higher with maternal BMI (9) | (Gene ID: 823992 (2)) |
| *CERK*Ceramide kinase | Offspring blood | Lower with ppBMI (10) | Involved in sphingolipid metabolism and cellular processes (Gene ID: 64781 (2)) |
| *CLECL1*C-type lectin like 1 | Umbilical cord blood monocytes | Lower with obesity (14) | Initiating T-cell activation (14), enhances IL-4 production. (Gene ID: 16035 (2)) |
| *CMTM1*CKLF like MARVEL transmembrane domain containing 1 | Placenta  | Lower with obesity (15) | The protein encoded may be important in testicular development (Gene ID: 113540 (2)) |
| *CPT1A*Carnitine palmitoyltransferase 1A | Umbilical cord mesenchymal stem cells | Higher with obesity (3) | Carnitine palmitoyl transferase I at the outer membrane of the mitochondria initiate the oxidation of long chained fatty acids. It is the key enzyme in the carnitine-dependent transport across the mitochondrial inner membrane, this is the rate limiting step in uptake and oxidation. (Gene ID: 1374 (2)) |
| *CRYL1*Crystallin lambda 1 | Offspring saliva | Higher with maternal BMI (9) | Catalyze the dehydrogenation of L-gulonate to dehydro-L-gulonate in the urinate cycle, an alternative glucose metabolic pathway. (Gene ID: 51084 (2)) |
| *CSH1*Chorionic somatommamotropin hormone 1 | Placenta | Higher with obesity (15) | Growth control (Gene ID: 1442 (2)) |
| *CSH2*Chorionic somatommamotropin hormone 2 | Placenta | Higher with obesity (15) | Growth control (Gene ID: 1443 (2)) |
| *CSHL1*Chorionic somatommamotropin hormone like 1 | Placenta | Higher with obesity (15) | Growth control (Gene ID: 1444 (2)) |
| *CYP2S1*Cytochrome P450 family 2 subfamily S member 1 | Umbilical cord blood | Higher with obesity (12) | CYP450 are monooxygenases which catalyze many reactions involved in drug metabolism and cholesterol, steroid and lipid synthesis. (Gene ID: 29785 (2)) |
| *DAB1*DAB1, reelin adaptor protein | Umbilical cord tissue | Higher with fat mass (11) | The protein encoded is thought to be a signal transducer that interacts with protein kinase pathways to regulate neuronal positioning in the developing brain. (Gene ID: 1600 (2)) |
| *DCBLD1*Discodin, CUB and LCCL domain containing 1 | Offspring blood | Higher with ppBMI (10) | (Gene ID: 285761 (2)) |
| *DEFB1*Defensin beta 1 | Umbilical cord blood monocytes | Lower with obesity (14) | Defense response (14). Antimicrobial peptide implicated in the resistance of epithelial surfaces to microbial colonization (Gene ID: 1672 (2)) |
| *DDIT4*DNA damage inducible transcript 4 | Umbilical cord blood monocytes | Higher with obesity (14) | Stress response (14) |
| *DLC1*DLC1 Rho GTPase activating protein | Offspring saliva | Higher with maternal BMI (9) | Regulation of small GTP-binding proteins. Participate in signaling pathways that regulate cell processes involved in cytoskeletal changes. Tumor suppressor in many cancers. (Gene ID: 10395 (2)) |
| *DOK3*Docking protein 3 | Umbilical cord blood monocytes | Lower with obesity (14) | Defense response (14) |
| *ENO1*Enolase 1 | Umbilical cord blood monocytes  | Lower with obesity (14) | Involved in metabolism (14). Glycolytic enzyme (Gene ID: 2023 (2)). |
| *ESM1*Endothelial cell specific molecule 1 | Offspring blood | Lower with ppBMI (10) | Mainly expressed in lung and kidney tissues, expression is regulated by cytokines (Gene ID: 11082 (2)). |
| *ETV3*ETS variant 3 | Umbilical cord blood monocytes  | Higher with obesity (14) | Immune gene (14) |
| *FAH*Fumarylacetoacetate hydrolase | Umbilical cord blood | Higher with obesity (12) | The last enzyme in the tyrosine catabolism pathway. (Gene ID: 2184 (2)) |
| *FAM129B*family with sequence similarity 129 member B | Umbilical cord blood | Lower with BMI (12) | May play a role in apoptosis suppression. (Gene ID: 64855 (2)) |
| Offspring peripheral blood | Average early percentage change Higher with obese mothers (12) |
| *FGR*FGR proto-oncogene, Src family tyrosine kinase | Umbilical cord blood monocytes | Lower with obesity (14) | Cell migration and adhesion of myeloid cells (14). Negative regulator of cell migration and adhesion. (Gene ID: 2268 (2)) |
| *FOXA2*Forkhead box A2 | Umbilical cord tissue | Higher with fat mass (11) | Hepatocyte nuclear factors that are transcriptional activators for liver-specific genes, and also interact with chromatin. Similar DNA-binding family members have roles in regulation of metabolism and differentiation of the pancreas and liver in mice. The gene has been linked to maturity-onset diabetes of the young. (Gene ID: 3170 (2)) |
| *FOLR2*Folate receptor beta | Umbilical cord blood monocytes | Lower with obesity (14) | Involved in metabolism (14). High affinity for folic acid and its derivatives (Gene ID: 2350 (2)) |
| *FSTL1*Follistatin like 1 | Offspring saliva | Higher with maternal BMI (9) | Similar to follistatin, an activin-binding protein. Thought to be an autoantigen associated with rheumatroid arthritis. (Gene ID: 11167 (2)). |
| *FYN*FYN proto-oncogene, Src family tyrosine kinase | Umbilical cord tissue | Lower with fat mass (11) | Encodes a membrane-associated tyrosine kinase that is involved in regulating cell growth. (Gene ID: 2534 (2)) |
| *GH1*Growth hormone 1 | Placenta | Higher with obesity (15) | Growth control (Gene ID: 2688 (2)) |
| *GJB6*Gap junction protein beta 6 | Offspring blood | Lower with ppBMI (10) | Gap junctions (Gene ID: 10804 (2)) |
| *GLIPR1L2*GLIPR 1 like 2 | Umbilical cord blood | Higher with ppBMI (16) | Protein in the cysteine-rich secretory protein, antigen 5 and pathogenesis-related 1 superfamily, involved in processes such as cancer and immune defence (Gene ID: 144321 (2)) |
| *GNAI2*G protein subunit alpha i2 | Offspring blood | Lower with ppBMI (10) | Involved in the hormonal regulation of adenylate cyclase (Gene ID: 2771 (2)) |
| *GNRHR2*Gonadotropin releasing hormone receptor 2 | Offspring blood | Higher with ppBMI (10) | Pseudogene in humans (Gene ID: 114814 (2)) |
| *GRIN3A*Glutamate ionotropic receptor NMDA type subunit 3A | Offspring saliva | Lower with maternal BMI (9) | Subunit to a glutamate-regulated ion channel which function in physiological and pathological processes in the central nervous system. (Gene ID: 116443 (2)) |
| *GSX2*GS homebox 2 | Umbilical cord tissue | Lower with fat mass (11) | Neuronal development (Gene ID: 170825 (2)) |
| *H19*H19, imprinted maternally expressed transcript | Umbilical cord blood | NS (17) | Imprinted region near the IGF2-gene. Expressed only from the maternally inherited chromosome. Encodes a long non-coding RNA that functions as a tumor-suppressor. (Gene ID: 283120 (2)) |
| *HAPLN4*Hyaluronan and proteoglycan link protein 4 | Offspring blood | Higher with ppBMI (10) | (Gene ID: 404037 (2)) |
| *HES1*Hes family bHL transcription factor 1 | Umbilical cord tissue | Higher with fat mass (11) | The protein belongs to the helix-loop-helix family of transcription factors and is a repressor of genes that require a bHLH protein for their transcription. (Gene ID: 3280 (2)) |
| *HIF3A*Hypoxi inducible factor 3 subunit alpha | Umbilical cord blood | Lower with ppBMI (18) | One subunit of several heterodimeric transcription factors that regulate many adaptive responses to hypoxia. (Gene ID: 64344 (2)) |
| Offspring peripheral blood (adolescence) | NS (18) |
| Umbilical cord tissue | Higher with GWG in interaction with genotype (19) |
| *HLA-C*Major histocompability complex, class I, C | Umbilical cord blood monocytes | Higher with obesity (14) | Immune gene (14). HLA class I , presents peptides derived from endoplasmatic reticulum lumen. Expressed in nearly all cells (Gene ID: 3107 (2)). |
| *HLA-E*Major histocompability complex, class I, E | Umbilical cord blood monocytes | Higher with obesity (14) | Immune gene (14). HLA class I, binds a restricted subset of peptides derived from the leader peptides of other HLA class I molecules (Gene ID: 3133 (2)) |
| *ICA1*Islet cell autoanticen 1 | Umbilical cord blood monocytes  | Lower with obesity (14) | Involved in metabolism (14). Believed to be an autoantigen in insulin-dependent diabetes mellitus (Gene ID: 3382 (2)) |
| *IGDCC4*Immunoglobulin superfamily DCC subclass member 4 | Umbilical cord blood | Higher with ppBMI (13) | (Gene ID: 57722 (2)) |
| *IGF1R*Insulin like growth factor 1 receptor | Umbilical cord tissue | Lower with fat mass (11) | Binds IGF with high affinity. Critical role in transformation events. Highly overexpressed in malignant tissues as an anti-apoptotic agent. (Gene ID: 3480 (2)) |
| *IGF2*Insulin like growth factor 2 | Umbilical cord blood | Lower with obesity (20) | Involved in development and growth. Only expressed from the paternal allele (IGF1 from the maternal). Epigenetic changes are associated with Wilms tumor, Beckwith-Wiedmann syndrome, rhabdomyosarcoma and Silver-Russel syndrome. (Gene ID: 3481 (2)) |
| *IGFBP1*Insulin like growth factor binding protein 1 | Umbilical cord blood | Lower when IOM criteria met (17) | Circulates in plasma and binds both IGFs I and II, prolonging their half-lives and alters their interaction with cell surface receptors. Important in cell migration and metabolism. Low levels may be associated with impaired glucose tolerance, vascular disease and hypertension. (Gene ID: 3484 (2)). |
| *IL-1β*Interleukin 1 beta | Umbilical cord blood | Higher with obesity (21) | Produced as a proprotein by macrophages and is activated by caspase 1. Mediates inflammatory response and is involved in cellular activities such as cell proliferation, differentiation and apoptosis. (Gene ID: 3553 (2)) |
| *IL10*Interleukin 10 | Umbilical cord blood | Lower with obesity (21) | Cytokine produced primarily by monocytes. Pleiotropic effects in immunoregulation and inflammation, downregulates Th1, MHC class II Ags and costimulatory molecules on macrophages. Enhances B-cell survival, proliferation and antibody production. Can block NF-κB activity and regulate JAK-STAT signaling. (Gene ID: 3586 (2)) |
| *IRF5*Interferon regulatory factor 5 | Umbilical cord blood monocytes | Lower with obesity (14) | Defense response (14). Transcription factor involved in virus-mediated action of interferon, and modulation of cell growth, differentiation, apoptosis and immune system activity (Gene ID: 3663 (2)). |
| *ITGAX*Integrin subunit alpha X | Umbilical cord blood monocytes | Lower with obesity (14) | Cell migration and adhesion of myeloid cells (14). Adherence of neutrophils and monocytes to stimulated endothelium cells, and phagocytosis of complement coated particles (Gene ID: 3687 (2)) |
| *ITK*IL2 inducible T cell kinase | Umbilical cord blood monocytes | Higher with obesity (14) | Immune gene (14). Intracellular tyrosine kinase expressed in T-cells. Plays a role in T-cell proliferation and differentiation (Gene ID: 3702 (2)) |
| *KCNK4*Potassium two pore domain channel subfamily K member 4 | Umbilical cord blood | Higher with early GWG, could not be validated (22) | Involved in regulating the noxious input threshold in dorsal root ganglia neurons. (Gene ID: 50801 (2)).  |
| *KLHDC4*Kelch domain containing 4 | Offspring blood | Lower with ppBMI (10) | (Gene ID: 54758 (2)) |
| *LAMB3*Laminin subunit beta 3 | Umbilical cord blood monocytes | Lower with obesity (14) | Cell migration and adhesion of myeloid cells (14) |
| *LEP*Leptin | Placenta | NS (23, 24) | Major role in regulation of energy homeostasis. Promotes satiety and energy expenditure. Involved in regulating immune and inflammatory responses, hematopoiesis, angiogenesis, reproduction, bone formation and wound healing. (Gene ID: 3952 (2)) |
|  | Umbilical cord blood | Lower with higher BMI, Higher with excessive GWG (23) |
|  | Maternal blood | Lower with obesity (23) |
| *LDLRAD4*Low density lipoprotein receptor class A domaincontaining 4 | Umbilical cord blood monocytes | Lower with obesity (14) | Involved in metabolism (14).  |
| *Line-1 elements* | Offspring peripheral mononuclear cells | NS (6) | Long interspersed elements that can generate copies of themselves in order to be inserted in other parts of the genome and thereby affect gene expression (7, 8). |
| Placenta | NS (25) |
| Umbilical cord blood | NS (25) |
| Umbilical cord blood | Lower with early pregnancy BMI (17) |
| *LMX1A*LIM homebox transcription factor 1 alpha | Umbilical cord tissue | Higher with fat mass (11) | The encoded gene is a transcription factor that acts as a positive regulator of insulin gene transcription, and also plays a role in development of dopamine producing neurons during embryogenesis (Gene ID: 4009 (2)) |
| *LOC256880* | Umbilical cord blood | Higher with obesity (12) | Uncharacterized (Gene ID: 256880 (2)) |
| *MAD1L1*Mitotic arrest deficient 1 like 1 | Wharton’s jelly mesenchymal stromal cells | Differential with obesity (26) | Component of the mitotic spindle assembly checkpoint that prevents the onset of anaphase until all chromosome are aligned at the metaphase plate. May play a role in cell cycle control and alternative splicing. (Gene ID: 8379 (2)) |
| *MCOLN3*Mucolipin 3 | Umbilical cord blood | Higher with ppBMI (12) | Mucolipin cation channel protein. Similar protein in mice is found in cochlea hair cells. (Gene ID: 55283 (2)) |
| *MEG3*Maternally expressed gene 3 | Umbilical cord blood | Lower with obesity (27) |  |
| *MFSD1*Major facilitator superfamily domain containing 1 | Umbilical cord blood | Lower with obesity (16) | (Gene ID: 64747 (2)) |
| *MFSD6*Major facilitator superfamily domain containing 6 | Offspring blood | Lower with ppBMI (10) | (Gene ID: 54842 (2)) |
| *MMP7*Matrix mellopeptidase 7 | Umbilical cord blood | Higher with early GWG, could not be validated (22)  | Involved In the breakdown of extracellular matrix in normal physiological processes. (Gene ID: 4316 (2)). |
| *MTG2*Mitochondrial ribosome associated GTPase 2 | Offspring blood | Lower with ppBMI (10) | G-proteins act as molecular switches regulating cellular processes (Gene ID:26164 (2)) |
| *NFE2L3*nuclear factor, erythroid 2 like 3 | Umbilical cord blood | Higher with obesity (16) | Protein involved in the leucine zipper family of transcription factors (Gene ID: 9603 (2)) |
| *NFKB1*Nuclear factor kappa B subunit 1 | Umbilical cord blood | Higher with early GWG, could not be validated (22) | NFKB is a transcription regulator involved in many biological functions, cell growth and immune cell development included. (Gene ID: 100467906 (2)) |
| *NKX2-1*NK2 homebox 1 | Umbilical cord tissue | Higher with fat mass (11) | Encodes thyroid-specific transcription factor that binds to the thyroglobulin promoter and regulates the expression of thyroid-specific genes. It also regulates genes involved in morphogenesis. (Gene ID: 7080 (2)) |
| *NLRC3*NLR family CARD domain containing 3 | Umbilical cord blood monocytes | Lower with obesity (14) | Initiating T-cell activation (14). Cytosolic regulator of innate immunity (Gene ID: 197358 (2)) |
| *NRF1*Nuclear respiratory factor 1 | Offspring saliva | Higher with maternal BMI (9) | Transcription factor of metabolic genes regulating cell growth and genes required for respiration, heme biosynthesis and mitochondrial DNA transcription and replication. (Gene ID: 4899 (2)) |
| *NXPH1*Neurexophilin 1 | Offspring saliva | Lower with maternal BMI (9) | Neuroxiphilin proteins forms a tight complex with alpha neurexins, a group of proteins that promote adhesion between dendrites and axons. (Gene ID: 30010 (2)) |
| *ODZ4 (TENM4)*Teneurin transmembrane protein 4 | Offspring saliva | Higher with maternal BMI (9) | Plays a role in establishing proper neuronal connectivity during development. (Gene ID: 26011 (2)) |
| *PAQR8*Progestin and adipoQ receptor family member 8 | Umbilical cord blood monocytes | Lower with obesity (14) | Involved in metabolism (14) |
| *PDE6A*Phosphodiesterase 6A | Offspring blood | Lower with ppBMI (10) | Encodes a part of the cyclic-GMP-specific phosphodiesterase, and has functions in retinal rods (Gene ID: 5145 (2)) |
| *PLAGL1*Pleiomorphic adenoma gene-like 1 | Umbilical cord blood | Higher (27) | Zinc finger protein that functions as a suppressor of cell growth (Gene ID: 5325 (2)). |
| *PPARG*Peroxisome proliferator activated receptor gamma | Offspring white blood cells | NS (28) | Nuclear receptor that form heterodimer with retinoid X receptors and thereby regulate transcription of a variety of genes. PPARƴ, is a regulator of monocyte/machrophage (14) and adipocyte differentiation, and has been implicated in the pathology of many diseases; obesity, diabetes, atherosclerosis and cancer (Gene ID: 5468 (2))  |
| Umbilical cord blood monocytes | Lower with obesity (14) |
| Maternal white blood cells | NS (28) |
| *PPARGC1A*PPARG coactivator 1 alpha | Umbilical cord tissue | Higher with ppBMI (29) | Transcriptional coactivator that regulates the genes involved in energy metabolism. Interacts with PPARƴ, interact with and regulate activities of CREB, NRFs.May be involved in controlling blood pressure, regulating cellular cholesterol homeostasis and the development of obesity. (Gene ID: 10891 (2)) |
| *PPARGC1B*PPARG coactivator 1 beta | Offspring saliva | Higher with maternal BMI (9) | Stimulates the activity of several transcription factors and nuclear receptors (estrogen receptor alpha, NRF1 and glucocorticoid receptor). May be involved in fat oxidation, non-oxidative glucose metabolism and energy expenditure regulation. Downregulated in predeabetic and T2DM patients. (Gene ID: 133522 (2)) |
| *PRKAG2*Protein kinase AMP-activated non-catalytic subunit gamma 2 | Umbilical cord mesenchymal stem cells | Higher with obesity, but not confirmed by pyrosequencing (3) | AMPK is an important energy-sensing enzyme that can inactivate key enzymes involved in regulating de novo fatty acid- and cholesterol synthesis. (Gene ID: 51422 (2)) |
| *PSG1*Pregnancy specific beta-1-glycoprotein 1 | Placenta | Higher with obesity (15) | Proteins mainly produced by placental syncytiotrophoblasts during pregnancy Belongs to the immunoglobulin superfamily of genes. (Gene ID: 5669 (2)) |
| *PSG5*Pregnancy specific beta-1-glycoprotein 5 | Placenta | Higher with obesity (15) |
| *PSG6*Pregnancy specific beta-1-glycoprotein 6 | Placenta | Higher with obesity (15) |
| *PSG7*Pregnancy specific beta-1-glycoprotein 7 | Placenta | Higher with obesity (15) |
| *PSG11*Pregnancy specific beta-1-glycoprotein 11 | Placenta | Higher with obesity (15) |
| *PSG2*Pregnancy specific beta-1-glycoprotein 2 | Placenta | Higher with obesity (15) |
| *R3HDM1*R3H domain containing 1 | Umbilical cord blood | Higher with obesity (12) | Gene onthology has related this gene to nucleic acid binding. (Gene ID: 23518 (2)) |
| *RBPMS*RNA binding protein, mRNA processing factor | Umbilical cord blood | Higher with obesity (12) | RNA-binding protein. (Gene ID: 11030 (2)) |
| *RDH10*Retinol dehydrogenase 10 | Umbilical cord blood | Higher with obesity (12) | Retinol dehydrogenase converts all-trans-retinol to all-trans-retinal. Studies in mice suggests this protein is essential for synthesis of embryonic retinoic acid and is required for limb, craniofacial and organ development (Gene ID: 157506 (2)) |
| *RHOH*Ras homolog family member H | Umbilical cord blood monocytes | Higher with obesity (14) | Immune gene (14). Expressed in hematopoietic cells, functions as a negative regulator of cell growth and survival (Gene ID: 399 (2)).  |
| *RP11*pre-mRNA processing factor 31 | Umbilical cord blood | Decrased with obesity (16) | Protein incolced in the spliceosome complex, and is a renitis pigmentosa-causing gene (Gene ID 26121 (2)). |
| *RXRA*Retinoid X receptor alpha | Umbilical cord blood | NS (30) | Nuclear receptor that mediate the biological effects of retinoids. (Gene ID: 6256 (2)) |
| *S100B*S100 calcium binding protein B | Umbilical cord blood monocytes | Higher with obesity (14) | Immune gene (14). Involved in cell cycle progression and differentiation. Altered expression in several diseases, including T1DM (Gene ID: 6285 (2)). |
| *SDHC*Succinate dehydrogenase complex subunit C | Umbilical cord tissue | Higher with obesity, but not confirmed with pyrosequencing (3) | Encodes 1 of 4 subunits that make succinate dehydrogenase (mitochondrial complex II), a key enzyme in the citric acid cycle and aerobic respiratory chains of the mitochondria. (Gene ID: 6391 (2)) |
| *SHANK2*SH3 and multiple ankyrin repeat domains 2 | Offspring saliva | Higher with maternal BMI (9) | Synaptic protein that may function as molecular scaffolds in the postsynaptic density of excitatory synapses. (Gene ID: 22941 (2)) |
| *SIGLEC14*Sialic acid binding Ig like lectin 14 | Umbilical cord blood | Higher with obesity (12) | Related to innate immune system and RET signaling. Involved in carbohydrate binding (Gene ID: 100049587 (2)). |
| *SORCS2*Sortilin related VPS10 domain containing receptor 2 | Offspring saliva | Higher at one CpG with maternal BMI (9) | Vacuolar protein sorting 10 domain-containing receptor protein. (Gene ID: 57537 (2)) |
| Lower at one CpG with maternal BMI (9) |
| *SUCLG2*Succinate-CoA ligase GDP-forming beta subunit | Umbilical cord blood | Lower with obesity (12) | GTP-specific subunit of succinyl-CoA synthase. Catalyzes the formation of succinyl-CoA and succinate. (Gene ID: 8801 (2)) |
| Offspring peripheral blood | Average early percentage change Higher with obese mothers (12) |
| *SWAP70*Switching B cell complex subunit | Umbilical cord blood | Higher with obesity (12) | Related pathway is NF-κB signaling. Involved in calcium ion binding. (Gene ID: 23075 (2)) |
| *TAPBP*TAP binding protein | Umilical cord blood | Higher with obesity (16) | Mediates interaction between MHC class I and TAP, which mediates antigen transportion across endoplasmatic reticulum membrane in order to get optimal peptide loading on the MHC I (Gene ID: 6892 (2)) |
| *TNFRSF25*TNF receptor superfamily member 25 | Umbilical cord blood monocytes | Higher with obesity (14) | Immune gene (14). TNF-receptor that may play a role in regulating lymphocyte homeostasis (Gene ID: 8718 (2)). |
| *TREM1* | Umbilical cord blood monocytes | Lower with obesity (14) | Defense response (14). |
| *TRIM10*Tripartite motif containing 10 | Wharton’s jelly mesenchymal stromal cells | Differential with obesity (26) | The protein localizes to cytoplasmic bodies. Might play a role in erythroid differentiation. (Gene ID: 10107 (2)) |
| *TRIM40*Tripartite motif containing 40 | Umbilical cord blood monocytes | Lower with obesity (14) | Defense response (14). |
| *TRPM5*Transient receptor potential cation channel subfamily M member 5 | Umbilical cord blood | Higher with early GWG, could not be validated (22) | Calcium- and temperature activated, non-selective cation channel important in taste transduction. (Gene ID: 29850 (2)) |
| *TXNIP*Thioredoxin interacting protein | Umbilical cord blood monocytes | Higher with obesity (14) | Stress response (14) Protects cells from oxidative stress, and also(Gene ID: 10628 (2)) |
| *UNC13A*Unc-13 homolog A | Offspring saliva | Lower with BMI (9) | UNC13 proteins are important in neutrotransmitter release at synapses. (Gene ID: 23025 (2)) |
| *WDR35*WD repear domain 35 | Umbilical cord blood | Higher with obesity (12) | Involved in cell cycle progression, signal transduction, apoptosis and gene regulation. (Gene ID: 57539 (2)) |
| *XDH*Xanthine dehydrogenase | Offspring blood | Lower with ppBMI (10) | Involved in oxidative metabolism of purines (Gene ID: 7498 (2)) |
| *ZC3HAV1*Zinc finger CCCH-type containing, antiviral 1 | Umbilical cord blood | Higher with obesity (12) | Thought to prevent infection by retroviruses. (Gene ID: 56829 (2)) |
| *ZCCHC10*Zinc finger CCHC-type containing 10 | Umbilical cord blood | Higher with ppBMI (31) | Involved in nucleic acid binding. (Gene ID: 54819 (2)) |
| *ZNF804A*Zinc finger protein 804A | Offspring saliva | Higher with BMI (9) | Zinc finger binding protein. (Gene ID: 91752 (2)) |
| *ZPF36L1* | Umbilical cord blood monocytes | Higher with obesity (14) | Immune gene (14) |
| NS: Not Significant |

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