Supplementary material to:

**IMPRINTING GENES ASSOCIATED WITH ENDOMETRIOSIS**

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**Paternally expressed and maternally imprinted genes: These genes are imprinted, with preferential expression from the paternal allele.**

**NDUFA4P1, NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa, pseudogene 1**

NDUFA4 is a component of the cytochrome c oxidase (CCO), which is the terminal oxidase of the mitochondrial electron transport chain (http://www.ncbi.nlm.nih.gov/gene/360165) (Balsa et al., 2012; Srinivasan and Avadhani, 2012). CCO dysfunction or a reduced expression leads to mitochondrial reactive oxygen species production and cellular oxidative stress, and is affected in a wide variety of diseases including preeclampsia, neurodegenerative diseases, myocardial ischemia/reperfusion, bone and skeletal diseases, diabetes and cancer (He et al., 2004).

**GFI1, growth factor independent 1 transcription repressor**

GFI1 is a transcriptional repressor that plays a critical role in hematopoiesis and lymphomagenesis (http://www.ncbi.nlm.nih.gov/gene/2672) (Du et al., 2013). It is repressed by p53 and inhibits DNA damage-induced apoptosis (Du et al., 2013).

**DIRAS3, DIRAS family, GTP-binding RAS-like 3**

DIRAS3 is a member of the Ras superfamily, and appears to be a putative tumor suppressor gene (http://www.ncbi.nlm.nih.gov/gene/9077). Up-regulation of DIRAS3 expression is associated with infertility and endometriosis (Li et al., 2011).

**FUCA1, fucosidase, alpha-L-1, tissue**

This protein is a lysosomal enzyme involved in the degradation of fucose-containing glycoproteins and glycolipids (http://www.ncbi.nlm.nih.gov/gene/2517). The alpha-fucosidase activity was increased in patients with infertility (Brandelli and Passos, 1998).

**BMP8B, bone morphogenetic protein 8b**

BMP is a part of the transforming growth factor-beta (TGFβ) superfamily that induces ectopic bone growth (http://www.ncbi.nlm.nih.gov/gene/656). Progesterone-dependent Ihh, Wnt, and BMP signaling pathways within the endometrium play a role in decidualization, implantation and embryo attachment (Wetendorf and DeMayo, 2012).

**RPL22, ribosomal protein L22**

This protein is a component of the 60S subunit and acts as a cytoplasmic ribosomal protein (http://www.ncbi.nlm.nih.gov/gene/6146).
PRDM16, PR domain containing 16
PRDM16, PPARγ and C/EBPa are master regulators of adipocyte development and regulate the process of adipogenesis that include adiponectin secretion and insulin-dependent glucose uptake (http://www.ncbi.nlm.nih.gov/gene/63976) (Kajimura et al., 2010; Farmer, 2008).

OBSCN, obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
OBSCN has a role in the organization of myofibrils and is essential for normal muscle function (http://www.ncbi.nlm.nih.gov/gene/84033).

OR11L1, olfactory receptor, family 11, subfamily L, member 1
The olfactory receptor proteins are members of a large family of G-protein-coupled receptors (GPCR) (http://www.ncbi.nlm.nih.gov/gene/391189).

LRRTM1, leucine rich repeat transmembrane neuronal 1
This protein is predominantly expressed in thalamus, hippocampus and limbic cortex and functions as a synaptic cell adhesion molecule that influences synaptic excitation (http://www.ncbi.nlm.nih.gov/gene/347730). Lack of LRRTM1 presumably causes the abnormality in behavior (Soler-Llavina et al., 2013).

CCDC85A, coiled-coil domain containing 85A
CCDC85A expression is association with age at menarche, a landmark of the late stage of pubertal development, in the Japanese population. Multiple factors and the interactions between genetic and environmental factors influence the age at which menarche occurs (http://www.ncbi.nlm.nih.gov/gene/114800).

CYP1B1, cytochrome P450, family 1, subfamily B, polypeptide 1
The cytochrome P450 metabolizes procarcinogens and synthesizes cholesterol, steroids and other lipids (http://www.ncbi.nlm.nih.gov/gene/1545). This enzyme is involved in eye development. The gene polymorphisms of CYP1B1 in exon 2 codon 119 are also an associated risk factor for endometriosis (Li and Wang 2009).

GPR1, G protein-coupled receptor 1
GPR1 is regulated in the process of the development of a chronic inflammatory disease such as atherosclerosis (http://www.ncbi.nlm.nih.gov/gene/2825) (Karagiannis et al., 2013).

TIGD1, tigger transposable element derived 1
This protein belongs to the superfamiliy of DNA-mediated transposons in humans and is similar to the major mammalian centromere protein B (CENP-B) (http://www.ncbi.nlm.nih.gov/gene/200765). CENP-B is a centromeric satellite DNA-binding protein and functions in the assembly of centromeric nucleosomes (Tachiwana et al., 2013).

MYEOV2, myeloma overexpressed 2
MYEOV2 expression is associated with the development of multiple myeloma (http://www.ncbi.nlm.nih.gov/gene/150678) (Ebina et al., 2013).
HES1, hairy and enhancer of split 1
This protein belongs to the transcriptional repressor gene family that requires a basic helix-loop-helix protein for their transcription (http://www.ncbi.nlm.nih.gov/gene/3280). The HES1 gene regulatory networks play a central role in the timing of somitogenesis and can become deregulated in human cancer (Sturrock et al., 2013).

SPON2, spondin 2, extracellular matrix protein
SPON2 is known as mindin. SPON2 is an extracellular matrix protein and can modify the production of proinflammatory cytokines. Aberrant DNA methylation of SPON2 gene was observed in prostate cancer (Kim et al., 2012).

NAP1L5, nucleosome assembly protein 1-like 5
Nucleosome assembly protein 1 (NAP-1) is an integral component associated with the establishment, maintenance, and dynamics of eukaryotic chromatin and its modification states (Park and Luger, 2006). NAP1L5 plays a role for transcriptional interference (Park and Luger, 2006).

GAB1, GRB2-associated binding protein 1
Members of the GAB family are expressed in T cells, B cells, macrophages and mast cells. GAB acts as a downstream effector of receptor-tyrosine kinase-triggered signal transduction and plays a central role in growth, transformation and apoptosis (http://www.ncbi.nlm.nih.gov/gene/2549). GAB1 is also a mediator of branching renal tubulogenesis.

CDH18, cadherin 18, type 2
CDH18 is expressed in the central nervous system and is involved in calcium-dependent synaptic adhesion, axon outgrowth, guidance, neural circuitry and mature synaptic function (http://www.ncbi.nlm.nih.gov/gene/1016). CDH18 is of special interest in the pathogenesis of neuropsychiatric disease (Redies et al., 2012).

FAM50B, family with sequence similarity 50, member B
FAM50B plays a role in spermatogenesis (Zhang et al., 2011).

MRAP2, melanocortin 2 receptor accessory protein 2
MRAP2 modulates energy balance, glucose homeostasis and the development of obesity (Liu et al., 2013a).

LIN28B, lin-28 homolog B
This gene is highly expressed in fetal liver, testis and placenta (http://www.ncbi.nlm.nih.gov/gene/389421). Pubertal timing is under strong genetic control (Leinonen et al., 2012). LIN28B is the puberty-associated gene and influences adult adiposity-related traits, including obesity, type 2 diabetes and cardiovascular disease (Leinonen et al., 2012).

PLAGL1, pleiomorphic adenoma gene-like 1
This protein is a zinc finger protein with DNA-binding activities (http://www.ncbi.nlm.nih.gov/gene/5325). It functions as a tumor suppressor. Overexpression of this gene during fetal development is linked to developmental disorders such as transient neonatal diabetes mellitus, which is a rare disease characterized by intrauterine growth retar-
dation, dehydration, and failure to thrive due to a lack of normal insulin secretion (Abdollahi, 2007). Transient neonatal diabetes mellitus type 1 frequently recurs in later life.

**HYMAI, hydatidiform mole associated and imprinted**
This gene encodes a non-protein coding transcript (http://www.ncbi.nlm.nih.gov/gene/57061). HYMAI is one of the causative genes for transient neonatal diabetes mellitus (Mackay and Temple, 2010). Diabetes frequently recurs in later life. It is caused by overexpression of the imprinted genes PLAGL1 and HYMAI on human chromosome 6q24 (Mackay and Temple, 2010).

**PEG10, paternally expressed 10**
Four imprinted genes, two paternally expressed (IGF2 and PEG10) and two maternally expressed (PHLDA2 and CDKN1C), play a role in fetal growth and placental development (Dória et al., 2010). Gene expression pattern of IGF2, PHLDA2, PEG10 and CDKN1C imprinted genes is associated with pregnancy loss such as spontaneous miscarriages or fetal deaths (Dória et al., 2010). Overexpression of the PEG10 gene is also associated with hepatocellular carcinomas (http://www.ncbi.nlm.nih.gov/gene/23089).

**SGCE, sarcoglycan, epsilon**
Sarcoglycans are components of the dystrophin-glycoprotein complex, which link the actin cytoskeleton to the extracellular matrix (http://www.ncbi.nlm.nih.gov/gene/8910). Myoclonus-dystonia is a common clinical sign in many neurogenetic disorders. Mutations in the SGCE gene and its variant (c.1295G > A, p.Ser432His) may have contributed to the development of dystonia (Kurtis et al., 2010).

**MEST, mesoderm specific transcript**
The encoded protein plays a role in development (http://www.ncbi.nlm.nih.gov/gene/4232). Decreased MEST methylation was observed in gestational diabetes mellitus groups or in adults with morbid obesity compared with controls (El Hajj et al., 2013). The loss of imprinting of MEST gene has been linked to certain types of cancer.

**COPG2IT1, COPG2 imprinted transcript 1**
COPG2IT1 is a transcript located within intron of COPG2 that is located telomeric to MEST at human chromosome 7q32 in fetal tissues. Embryonic stem cells express COPG2IT1 gene.

**MESTIT1, MEST intronic transcript 1, antisense RNA**
This gene encodes a non-protein coding antisense RNA and is located in an intron of MEST gene (http://www.ncbi.nlm.nih.gov/gene/317751).

**DLGAP2, discs, large (Drosophila) homolog-associated protein 2**
The product of this gene is a membrane-associated guanylate kinase and plays a role in synapse organization and signalling in neuronal cells (http://www.ncbi.nlm.nih.gov/gene/9228). DLGAP2 was also associated with eating behavior and obesity (Do et al., 2013).

**ZFAT, zinc finger and AT hook domain containing ZFAT-AS1, ZFAT antisense RNA 1**
The encoded protein, ZFAT, is a DNA binding protein and functions as a transcriptional regulator involved in cell survival and apoptosis (http://www.ncbi.nlm.nih.gov/gene/57623). SNPs of the ZFAT gene are associated with an increased risk of autoimmune thyroid disease. ZFAT
expressed in syncytiotrophoblasts is downregulated in placentas from preeclampsia (Barbaux et al., 2012). The ZFAT-AS1 gene encodes a small antisense RNA that regulates the sense strand locus, ZFAT (http://www.ncbi.nlm.nih.gov/gene/594840).

**GLIS3, GLIS family zinc finger 3**
This gene encodes a transcriptional nuclear protein with zinc finger domains (http://www.ncbi.nlm.nih.gov/gene/169792). GLIS3 regulates the development of pancreatic beta cells, thyroid, eye, liver and kidney. Mutations in this gene are well known to cause neonatal diabetes and congenital hypothyroidism. GLIS3 is a candidate gene for type 1 diabetes (Santin and Eizirik, 2013).

**INPP5F, inositol polyphosphate-5-phosphatase F**
The encoded protein is an inositol 1,4,5-trisphosphate (InsP3) 5-phosphatase (http://www.ncbi.nlm.nih.gov/gene/22876). INPP5F modulates cardiac myocyte size and cardiac hypertrophy (Zhu et al., 2009).

**KCNQ1OT1, KCNQ1 opposite strand/antisense transcript 1**
The KCNQ1OT1 transcript is the antisense to the KCNQ1 gene and is a long non-coding RNA (http://www.ncbi.nlm.nih.gov/gene/10984). It interacts with chromatin and regulates transcription of multiple target genes through epigenetic modifications. KCNQ1OT1 plays an important role in patients with Beckwith-Wiedemann syndrome and in colorectal carcinogenesis. Beckwith-Wiedemann syndrome is a loss-of-imprinting syndrome characterized by macrosomia, macroglossia, and abdominal wall defects, which is referred to as genetic overgrowth disorder or large offspring syndrome.

**INS, insulin**
Insulin (INS) stimulates glucose uptake through the insulin receptor. The INS and insulin-like growth factor-2 (IGF-2) region on chromosome 11p15.5 has been associated with the metabolic syndrome, type 2 diabetes and coronary heart disease (Osada, 2009).

**IGF2AS, IGF2 antisense RNA**
The IGF2AS gene encodes an antisense transcript of the IGF2 gene (http://www.ncbi.nlm.nih.gov/gene/51214). The transcript is overexpressed in Wilms tumor. Both IGF2 and IGF2AS appear to be part of the same chromatin domain. IGF2 (G13790C and Apal) and IGF2AS (A1364C and G11711T) are associated with muscle damage (Devaney et al., 2007).

**IGF2, insulin-like growth factor 2 (somatomedin A)**
The IGF2 gene is involved in cell proliferation, growth, migration, differentiation and survival. Epigenetic changes at this locus are associated with Wilms tumour, Beckwith-Wiedemann syndrome, rhabdomyosarcoma, Silver-Russell syndrome and cardiovascular disease (Bergman et al., 2013) (http://www.ncbi.nlm.nih.gov/gene/3481).

**ZC3H12C, zinc finger CCCH-type containing 12C**
ZC3H12C suppresses the inflammatory response in endothelial cells through inhibition of NF-kappaB activation and subsequent pro-inflammatory gene expression (Liu et al., 2013b).
**DLK1, delta-like 1 homolog**
The encoded protein is involved in the suppression of brown adipocyte differentiation (Hudak and Sul, 2013) (http://www.ncbi.nlm.nih.gov/gene/8788).

**MAGEL2, MAGE-like 2**
This gene lies in the Prader-Willi syndrome chromosomal region 15q11-q12 (http://www.ncbi.nlm.nih.gov/gene/54551). Disruption of this gene at this locus contributes to Prader-Willi syndrome. Prader-Willi Syndrome exhibits neonatal hypotonia, developmental delay, and childhood-onset obesity and is caused by the loss of function of several genes, including MAGEL2. Mice lacking Magel2 display obesity and hypothalamic deficiency (Mercer et al., 2013).

**MKRN3, makorin ring finger protein 3**
MKRN3 is localized to close proximity, 15q11-q13, to the Prader-Willi syndrome imprinting center on the paternal chromosome (Rodriguez-Jato et al., 2013) (http://www.ncbi.nlm.nih.gov/gene/7681).

**SNORD64, small nucleolar RNA, C/D box 64**
**SNORD107, small nucleolar RNA, C/D box 107**
**SNORD108, small nucleolar RNA, C/D box 108**
**SNORD109A, small nucleolar RNA, C/D box 109A**
**SNORD109B, small nucleolar RNA, C/D box 109B**
**SNORD115-48, small nucleolar RNA, C/D box 115-48**
**SNORD115@, small nucleolar RNA, C/D box 115 cluster**
**SNORD116@, small nucleolar RNA, C/D box 116 cluster**
**SNORD116-1, also known as PWCR1, Prader-Willi syndrome chromosome region 1**
Box C/D class small nucleolar RNAs (snoRNAs) are involved in site-specific methylation of preribosomal RNA precursors and RNA processing (http://www.ncbi.nlm.nih.gov/gene/?term=SNORD107). SNORDs are expressed predominantly in the brain (http://www.ncbi.nlm.nih.gov/gene/347686). The loss of SNORD115 or SNORD116 expression at the locus 15q11.2 has been implicated as a cause for the Prader-Willi syndrome (Zhang et al., 2012, Kishore et al., 2010). Therefore, loss of expression of the snoRNAs confers much or all of the phenotype of Prader-Willi syndrome (Gallagher et al., 2002).

**SNRPN, small nuclear ribonucleoprotein polypeptide N**
**SNURF, SNRPN upstream reading frame**
Alternative splicing or deletion in the region 15q11.2 is responsible for Angelman syndrome or Prader-Willi syndrome (Plagge, 2012) (http://www.ncbi.nlm.nih.gov/gene/6638, http://www.ncbi.nlm.nih.gov/gene/8926).

**NDN, necdin, melanoma antigen (MAGE) family member**
Loss of expression of this intronless gene, NDN, may result in the phenotype of Prader-Willi syndrome (http://www.ncbi.nlm.nih.gov/gene/4692).
ZIM2, zinc finger, imprinted 2
Human chromosome 19q13.4 contains several imprinted gene clusters including PEG3 (paternally expressed gene 3) and ZIM2 (http://www.ncbi.nlm.nih.gov/gene/23619). This transcript is expressed in the brain and testis.

MIMT1, MER1 repeat containing imprinted transcript 1
MIMT1 is a non-protein coding gene that forms part of the imprinted PEG3 (paternally expressed gene 3) domain. Loss of paternal MIMT1 expression results in the phenotype of late term abortion and stillbirth in cattle (Flisikowski et al., 2010).

PEG3, paternally expressed 3
Tuman PEG3 protein belongs to the zinc finger protein family (http://www.ncbi.nlm.nih.gov/gene/5178). The imprinted gene PEG3 plays a role in p53-mediated apoptosis and tumor suppressor activity. PEG3 has shown tumorigenesis in glioma and ovarian cells. PEG3 confers sexual behaviors, alters growth and development, and regulates apoptosis (Jiang et al., 2010).

MIR371A, microRNA 371a
MicroRNAs (miRNAs) recognize target mRNAs and result in translational inhibition of the target mRNA. There is no research linking MIR371A to human phenotype.

PSIMCT-1, malignant T cell amplified sequence 1 pseudogene
PSIMCT-1 is a pseudogene for MCT-1. The MCT-1 oncogene was identified as an amplified gene on chromosome Xq22-24 in a T-cell lymphoma and in a subset of diffuse large B-cell lymphoma (DLBCL), a common form of Non-Hodgkin's Lymphoma (NHL).

NNAT, neuronatin
This protein regulates ion channels during normal brain development (http://www.ncbi.nlm.nih.gov/gene/4826). NNAT plays a role in forming and maintaining the structure of the nervous system. Similar to IGF2, aberrant expression of NNAT gene results in the phenotype of a variety of embryonic neoplasms, including Wilms tumor (Hubertus et al., 2013).

MCTS2, malignant T cell amplified sequence 2
The retrogene MCTS2 is a functional gene resulting from retrotransposition of a mRNA molecule into the genome. There is no research linking MCTS2 to human phenotype.

L3MBTL, l(3)mbt-like 1
The encoded protein functions to regulate gene activity, via chromatin modification. L3MBTL is necessary for mitosis (http://www.ncbi.nlm.nih.gov/gene/26013). Deletion of L3MBTL is a characteristic of myeloid malignancies (Li et al., 2004).

GNASAS, GNAS antisense RNA 1, also known as SANG
Prenatal growth restriction is associated with different epigenetic changes that may lead to later health outcomes, including obesity and metabolic syndrome (Tobi et al., 2011). DNA methylation of GNASAS gene might be associated with small for gestational age and myocardial infarction among women (Tobi et al., 2011). Loss of imprinting of the GNASAS gene is also a cause of pseudohypoparathyroidism (http://www.ncbi.nlm.nih.gov/gene/149775).
MIR296, microRNA 296
MIR298, microRNAs 298
Several miRNAs including MIR296 are found to be dysregulated in placenta of preeclampsia patients (Choi et al., 2013). MIR296 is important for the pathogenesis of preeclampsia (Choi et al., 2013). MIR296 and MIR298 lie within the GNASAS transcription units (Robson et al., 2012).

**Maternally expressed and paternally imprinted genes: These genes are imprinted, with preferential expression from the maternal allele.**

**DVL1, dishevelled segment polarity protein 1**
Wnt stimulation induces recruitment of DVL to the G-protein coupled frizzled (FZD) receptors (Kawano et al., 2011). DVL plays a key role in relaying cellular information for several developmental pathways such as cell proliferation, migration, polarity, terminal differentiation, and the self-renewal of stem cells (Dillman et al., 2013). DVL1 encodes a cytoplasmic phosphoprotein and is a substrate of NR1I2 (nuclear receptor subfamily 1, group I, member 2), which is a family of serine/threonine kinases that have been associated with differentiation of epithelial and neuronal cells (Elbert et al., 2006). Charcot-Marie-Tooth disease has been mapped to the same region as DVL1. This disease is the hereditary neuropathy characterized by muscular atrophy and weakness in the distal parts of the legs (Ostern et al., 2013). Failures in Wnt signalling are a cause of infertility and endometriosis (Sonderegger et al., 2010).

**TP73, tumor protein p73**
TP53, TP63, and TP73 genes encode a member of the p53 family of transcription factors (Ozdemir et al., 2012). TP73 is involved in cellular responses to stress and development. Aberrant methylation of gene promoter regions including TP73 and cyclin-dependent kinase inhibitor 2B (CDKN2B) is important for inactivation of tumor suppressor genes in ovarian cancer (Ozdemir et al., 2012).

**WRAP73, WD repeat containing, antisense to TP73**
The WRAP73 gene encodes a member of the Trp-Asp (WD) motif repeat protein family (Ozdemir et al., 2012). WRAP73, a member of the WD family, is involved in a variety of cellular processes, including cell cycle progression, signal transduction, apoptosis, gene regulation and ossification.

**PEX10, peroxisomal biogenesis factor 10**
Peroxisomes have an important role in lipid metabolism and the homeostasis of reactive oxygen species (Ozdemir et al., 2012). PEX10 is involved in import of peroxisomal matrix proteins. Mutations in the PEX10 gene are closely associated with the Zellweger spectrum, ranging from neonatal adrenoleukodystrophy to a lethal neurometabolic disorder, Zellweger syndrome (Steinberg et al., 2009).

**HSPA6, heat shock 70kDa protein 6**
The heat shock proteins are chaperones with central roles in processes of polypeptide remodeling events. HSPA6 induction is associated with cellular stress (Ozdemir et al., 2012).
PTPN14, protein tyrosine phosphatase, non-receptor type 14
The protein encoded by the PTPN14 gene is a member of the protein tyrosine phosphatase (PTP) family (http://www.ncbi.nlm.nih.gov/gene/5784). PTPs are known to be signaling molecules that regulate cell growth, differentiation, mitotic cycle, and oncogenic transformation.

HIST3H2BB, histone cluster 3, H2bb
This gene encodes a member of the histone H2B family (http://www.ncbi.nlm.nih.gov/gene/128312). Hypoacetylation of the histone family within promoter regions of candidate genes (e.g., HOXA10, ESR1, CDH1, and p21 WAF1/Cip1) is downregulated in endometriosis (Monteiro et al., 2013).

VAX2, ventral anterior homeobox 2
This gene encodes a homeobox protein and is expressed in the retina during development (http://www.ncbi.nlm.nih.gov/gene/25806). The VAX2 gene was required for the patterning of the eye and the development of optic fissure and retina (Liu et al., 2008).

OTX1, orthodenticle homeobox 1
The OTX1 and OTX2 homeobox genes are crucial for the brain development (http://www.ncbi.nlm.nih.gov/gene/5013) (Larsen et al., 2010). Both genes are important in neuronal cell development and differentiation: OTX1 in the neocortex, and OTX2 in the archicortex, diencephalon, rostral brain stem, and cerebellum (Larsen et al., 2010).

ABCG8, ATP-binding cassette, sub-family G (WHITE), member 8
ABCG5 and ABCG8 form a complex (G5G8) and are expressed in liver to promote the excretion of cholesterol into bile (http://www.ncbi.nlm.nih.gov/gene/64241) (Li and Wang, 2009). G5G8 influences the development of diet-induced obesity phenotypes (Li and Wang, 2009).

ZFP36L2, ZFP36 ring finger protein-like 2
This nuclear transcription factor regulates the response to growth factors (http://www.ncbi.nlm.nih.gov/gene/678). Dysregulation of ZFP36L2 function may play a role in the pathophysiology of certain types of leukemia (Iwanaga et al., 2011).

ALDH1L1, aldehyde dehydrogenase 1 family, member L1
The encoded protein belongs to the aldehyde dehydrogenase family and is essential for cell growth regulation (http://www.ncbi.nlm.nih.gov/gene/10840). Loss of function or expression of the ALDH1L1 gene is associated with increased cell motility, decreased apoptosis and cancer progression.

ZIC1, Zic family member 1
The ZIC1 gene encodes a transcription factor with zinc finger domains that can transactivate the apolipoprotein E gene (http://www.ncbi.nlm.nih.gov/gene/7545). ZIC1 is linked to the process of neural development. Overexpression of ZIC1 results in inactivation of Shh (sonic hedgehog), PI3K and MAPK signaling pathways, which in turn has been implicated in the process of gastric cancer (Zhong et al., 2012).
FGFRL1, fibroblast growth factor receptor-like 1
FGFRL1 influences mitogenesis and differentiation (http://www.ncbi.nlm.nih.gov/gene/53834). The FGF2 754C/G polymorphism may be closely associated with a risk of developing endometriosis (Kang et al., 2010). This gene stimulates cell proliferation at the ectopic endometriotic site.

KIAA1530, also known as UVSSA, UV-stimulated scaffold protein A
The KIAA1530 gene is important for ubiquitination and dephosphorylation of RNA polymerase II subunits (http://www.ncbi.nlm.nih.gov/gene/57654). UVSSA regulates nucleotide excision repair activity and repairs DNA damage (Schwertman et al., 2013).

ADAMTS16, ADAM metallopeptidase with thrombospondin type 1 motif, 16
This gene encodes a member of the ADAMTS (a disintegrin and metalloproteinase with thrombospondin motifs) protein family (http://www.ncbi.nlm.nih.gov/gene/170690). ADAMTS16 acts as a downstream target of WT1 (Jacobi et al., 2013). This gene has been implicated in the process of branching morphogenesis of the kidneys and regulating blood pressure during urogenital development (Jacobi et al., 2013).

CSF2, colony stimulating factor 2 (granulocyte-macrophage)
This cytokine controls the differentiation and function of granulocytes and macrophages (http://www.ncbi.nlm.nih.gov/gene/1437). Tumor necrosis factor (TNF)-induced overexpression of CSF2 is associated with the etiology of asthma, likely due to stimulation of macrophages and neutrophils during inflammation (Burkhardt et al., 2012).

BTNL2, butyrophilin-like 2 (MHC class II associated)
BTNL2 may be closely associated with the process of two inflammatory diseases, myositis and sarcoidosis (Arnett et al., 2007). This gene down-regulates T cell activation and is implicated in resetting the balance of the immune response in the gut.

SLC22A2, solute carrier family 22 (organic cation transporter), member 2
SLC22A3, solute carrier family 22 (organic cation transporter), member 3
Transporters are essential for elimination of endogenous organic cations, environmental toxins and drugs (http://www.ncbi.nlm.nih.gov/gene/6582). SLC22A2 (expressed in kidney, lung and brain) and SLC22A3 (expressed in skeletal muscle, liver, placenta, kidney and heart) are downstream targets of IGF2R (Burger et al., 2010). They play a role in the detoxification (Burger et al., 2010). SLC22A2 could be a susceptibility gene for aspirin intolerance in asthmatics (Park et al., 2011).

MAGI2, membrane associated guanylate kinase, WW and PDZ domain containing 2
MAGI2 is responsible for recruitment of neurotransmitter receptors such as AMPA- and NMDA-type glutamate receptors (Koide et al., 2012). The MAGI2 protein interacts with atrophin-1 and is involved in dentatorubral and pallidoluysian atrophy (http://www.ncbi.nlm.nih.gov/gene/9863). Schizophrenia is a psychiatric disorder characterized by positive symptoms, negative symptoms, and cognitive impairment. MAGI2 SNPs may confer an excess risk of cognitive impairment in schizophrenic patients (Koide et al., 2012).
PPP1R9A, protein phosphatase 1, regulatory subunit 9A
PPP1R9A is maternally expressed in embryonic skeletal muscle and neuronal tissues (http://www.ncbi.nlm.nih.gov/gene/55607). This protein controls actin cytoskeleton reorganization (Nakabayashi et al., 2004). It is also a neural tissue specific F-actin-binding protein and functions as a key candidate molecule in synaptic formation and function in brain (Nakabayashi et al., 2004). Changes in expression of several genes including PPP1R9A were observed in patients with Huntington disease (Becanovic et al., 2010).

TFPI2, tissue factor pathway inhibitor 2
The TFPI2 protein is a member of the Kunitz-type serine proteinase inhibitor family (http://www.ncbi.nlm.nih.gov/gene/7980). This protein inhibits a variety of serine proteases including factor VIIa/tissue factor, factor Xa, plasmin, trypsin, chymotrypsin and plasma kallikrein. This gene has been identified as a tumor suppressor gene in several types of cancer, including endometriosis-associated clear cell carcinoma (Arakawa et al., 2013).

DLX5, distal-less homeobox 5
The DLX5 gene encodes a member of a homeobox transcription factor gene family working in neurogenesis (http://www.ncbi.nlm.nih.gov/gene/1749). DLX5 is a candidate gene for some of the autistic spectrum disorder patients (Nakashima et al., 2010). The encoded protein also plays a role in bone development.

CPA, carboxypeptidase A4
The CPA gene is implicated in the histone hyperacetylation pathway (http://www.ncbi.nlm.nih.gov/gene/51200). CPA has a potential role in cell proliferation and differentiation and is a strong candidate gene for prostate cancer aggressiveness. Changes in CPA cluster expression on human chromosome 7q32-qter increase risk of intrauterine growth restriction associated with Silver-Russell syndrome (Bentley et al., 2003).

KLF14, Kruppel-like factor 14
This intronless gene encodes a member of the Kruppel-like family of transcription factors (http://www.ncbi.nlm.nih.gov/gene/136259). The KLF14 locus is associated with metabolic disease risk (Small et al., 2011). The type 2 diabetes locus on the chromosome 7q32.3 including KLF14 gene acts as a regulator of adipose gene expression (Small et al., 2011).

KCNK9, potassium channel, subfamily K, member 9
KCN functions as a pH-dependent potassium channel, with preferential expression in the brain (http://www.ncbi.nlm.nih.gov/gene/51305). Mutations in this gene were associated with Birk-Barel mental retardation dysmorphism syndrome characterized by mental retardation, hypotonia, and unique dysmorphism with elongated face (Barel et al., 2008). Overexpression of this gene has been observed in several types of human cancer.

KCNQ1DN, potassium channel, subfamily Q, member 1 downstream neighbor
The KCNQ1DN gene is located between CDKN1C (p57, KIP2) and KCNQ1 (KvLQT1) of chromosome 11p15.5 within the WT2 region (Xin et al., 2000). A maternal-specific loss of heterozygosity on the WT2-related chromosome 11p15.5 has been observed in Wilms and other embryonal tumors (Xin et al., 2000). Mouse model of Wilms tumor has been developed using Igf2 biallelic expression and Wt1 knockout. KCNQ1DN existing far from the H19/IGF2 region may play some role in Wilms tumorigenesis along with IGF2.
**KCNQ1, potassium channel, subfamily Q, member 1**
KCNQ1 within the 11p15.5 imprinted domain has been implicated in the process of congenital growth (Travers et al., 2013). KCNQ1, KCNQ1OT1 and CDKN1C mediate diabetes susceptibility at the KCNQ1 locus (Travers et al., 2013).

**OSBPL5, oxysterol binding protein-like 5**
The OSBPL5 gene encodes a member of the oxysterol-binding protein (OSBP) family, a group of intracellular lipid receptors that play a key role in the maintenance of cholesterol balance in the body (http://www.ncbi.nlm.nih.gov/gene/114879). A cluster of genes on chromosome 11 (SLC22A18, PHLDA2, NAP1L4, SNORA54, CARS, and OSBPL5) is an important foci involved in alcohol dependence (Edenberg et al., 2010).

**SLC22A18, solute carrier family 22, member 18**
Alterations or mutations in the SLC22A18 region have been implicated in the process of the Beckwith-Wiedemann syndrome, Wilms tumor, rhabdomyosarcoma, adrenocortical carcinoma, and lung, ovarian, and breast cancer. This protein acts as a transporter of organic cations (Lambertini et al., 2012). SLC22A18 demonstrated the positive correlation with the fetal head circumference (Lambertini et al., 2012).

**PHLDA2, pleckstrin homology-like domain, family A, member 2**
The PHLDA2 gene is located on chromosome 11p15.5, which harbors a cluster of imprinted genes and is considered to be an important tumor suppressor gene region (http://www.ncbi.nlm.nih.gov/gene/7262). Alterations in this region may be associated with the Beckwith-Wiedemann syndrome, Wilms tumor, rhabdomyosarcoma, adrenocortical carcinoma, and lung, ovarian, and breast cancer. Overexpression of the PHLDA2 gene has strong correlation with lower birth weight phenotype (Ishida et al., 2012).

**CDKN1C, cyclin-dependent kinase inhibitor 1C (p57, Kip2)**
The encoded protein is a strong G1 cyclin/Cdk-dependent inhibitor and a negative regulator of cell proliferation, suggesting a tumor suppressor candidate (http://www.ncbi.nlm.nih.gov/gene/1028). Mutations in this gene are implicated in sporadic cancers and Beckwith-Wiedemann syndrome. CDKN1C plays a role in endometrial stromal cell differentiation in the process of decidualization (Qian et al., 2005).

**H19, imprinted maternally expressed transcript (non-protein coding)**
The H19 gene is located in an imprinted region of chromosome 11 near the IGF2 gene (http://www.ncbi.nlm.nih.gov/gene/283120). The H19 gene expresses a non-coding RNA, and functions as a tumor suppressor. H19 and IGF2 are only expressed from the maternally- and paternally-inherited chromosome, respectively. H19 and IGF2 compete for a common enhancer element located in an imprinted domain of chromosome 11. Mutations in these genes are associated with Beckwith-Wiedemann Syndrome and Wilms tumorigenesis.

**RBP5, retinol binding protein 5, cellular**
Retinol-dependent physiological processes are mediated by retinol-binding proteins (RBPs) and their receptors through regulating cell proliferation and differentiation (Ho et al., 2007). Retinol can prevent potentially malignant disorders. RBP5 down-regulation in hepatocellular carcinoma was associated with aggressive tumor features, suggesting an important role of RBP5 in cancer progression (Ho et al., 2007).
**RB1, retinoblastoma 1**
The protein encoded by this gene is a negative regulator of the cell cycle and acts as a tumor suppressor gene (http://www.ncbi.nlm.nih.gov/gene/5925). The active form of RB1 protein binds E2F transcription factor 1 (E2F1). Defects in this gene result in the phenotype of childhood cancer retinoblastoma (RB), bladder cancer, and osteogenic sarcoma.

**MEG3, maternally expressed 3 (non-protein coding)**
The MEG3 gene is a long non-coding RNA (lncRNA) (http://www.ncbi.nlm.nih.gov/gene/55384). The MEG3 locus is frequently deregulated in hepatocellular carcinoma (Anwar et al., 2012). MEG3 interacts with the tumor suppressor p53 and regulates p53 target gene expression. MEG3 inhibits cell proliferation and angiogenesis. Its expression is lost in multiple cancers.

**UBE3A, ubiquitin protein ligase E3A**
The UBE3A gene encodes an E3 ubiquitin-protein ligase, part of the ubiquitin protein degradation system (http://www.ncbi.nlm.nih.gov/gene/7337). This imprinted gene is maternally expressed in brain. Deletion of this gene causes Angelman Syndrome, characterized by severe motor and intellectual retardation, ataxia, hypotonia, epilepsy, absence of speech, and characteristic facies (Mabb et al., 2011). UBE3A also interacts with high risk subtype HPV16 early oncoprotein E6, resulting in ubiquitination and proteolysis of tumor protein p53.

**ATP10A, ATPase, class V, type 10A**
The encoded ATP10A protein belongs to the family of P-type cation transport ATPases (http://www.ncbi.nlm.nih.gov/gene/57194). The ATP10A gene maps within the interval of deletion responsible for Angelman syndrome.

**NAA60, N(alpha)-acetyltransferase 60, NatF catalytic subunit**
NatF is important for normal chromosome segregation (Van Damme et al., 2011).

**ZNF597, zinc finger protein 597**
ZNF597 is associated with brain development and maintenance (Tanabe et al., 2010).

**TCEB3C, transcription elongation factor B polypeptide 3C (elongin A3)**
The elongin transcription elongation factor complex enhances the rate of transcription elongation by RNA polymerase II (http://www.ncbi.nlm.nih.gov/gene/162699). The TCEB3C gene encodes elongin subunit A3.

**NLRP2, Nucleotide-binding oligomerization domain, Leucine rich Repeat and Pyrin domain containing 2**
NLRP proteins, such as NLRP2, are involved in the activation of caspase-1 by Toll-like receptors (http://www.ncbi.nlm.nih.gov/gene/55655). They may be involved in activation of proinflammatory caspases.
REFERENCES

Abdollahi A. LOT1 (ZAC1/PLAGL1) and its family members: mechanisms and functions. J Cell Physiol 2007;210:16-25.

Anwar SL, Krech T, Hasemeier B, Schipper E, Schweitzer N, Vogel A, Kreipe H, Lehmann U. Loss of imprinting and allelic switching at the DLK1-MEG3 locus in human hepatocellular carcinoma. PLoS One 2012;7:e49462.

Arakawa N, Miyagi E, Nomura A, Morita E, Ino Y, Ohtake N, Miyagi Y, Hirahara F, Hirano H (2013) Secretome-Based Identification of TFPI2, A Novel Serum Biomarker for Detection of Ovarian Clear Cell Adenocarcinoma. J Proteome Res 2013 Aug 29.

Arnett HA, Escobar SS, Gonzalez-Suarez E, Budelsky AL, Steffen LA, Boiani N et al. BTNL2, a butyrophilin/B7-like molecule, is a negative costimulatory molecule modulated in intestinal inflammation. J Immunol 2007;178:1523-33.

Balsa E, Marco R, Perales-Clemente E, Szklarczyk R, Calvo E, Landázuri MO et al. NDUFA4 is a subunit of complex IV of the mammalian electron transport chain. Cell Metab 2012;16:378-86.

Barbaux S, Gascoin-Lachambre G, Buffat C, Monnier P, Mondon F, Tonanny MB et al. A genome-wide approach reveals novel imprinted genes expressed in the human placenta. Epigenetics 2012;7:1079-90.

Barel O, Shalev SA, Ofir R, Cohen A, Zlotogora J, Shorer Z et al. Maternally inherited Birk Barel mental retardation dysmorphism syndrome caused by a mutation in the genomically imprinted potassium channel KCNK9. Am J Hum Genet 2008; 83:193-9.

Becanovic K, Pouladi MA, Lim RS, Kuhn A, Pavlidis P, Luthi-Carter R et al. Transcriptional changes in Huntingdon disease identified using genome-wide expression profiling and cross-platform analysis. Hum Mol Genet 2010;19:1438-52.

Bentley L, Nakabayashi K, Monk D, Beechey C, Peters J, Birjandi Z et al. The imprinted region on human chromosome 7q32 extends to the carboxy-peptidase A gene cluster: an imprinted candidate for Silver-Russell syndrome. J Med Genet 2003;40:249-56.

Bergman D, Halje M, Nordin M, Engström W. Insulin-like growth factor 2 in development and disease: a mini-review. Gerontology 2013;59:240-9.

Brandelli A, Passos EP. Glycosidases in the peritoneal fluid from infertile women with and without endometriosis. Clin Biochem 1998;31:181-6.

Burkhardt J, Kirsten H, Wolfram G, Quente E, Ahnert P. Differential allelic expression of IL13 and CSF2 genes associated with asthma. Genet Mol Biol 2010;33:567-74.

Burger H, Zoumaro-Djayoon A, Boersma AW, Hellemans J, Berns EM, Mathijssen RH et al. Differential transport of platinum compounds by the human organic cation transporter OCT2 (hSLC22A2). Br J Pharmacol 2010;159:898-908.

Choi SY, Yun J, Lee OJ, Han HS, Yeo MK, Lee MA et al. MicroRNA expression profiles in placenta with severe preeclampsia using a PNA-based microarray. Placenta 2013;34:799-804.

Devaney JM, Hoffman EP, Gordish-Dressman H, Kearns A, Zambraski E, Clarkson PM. IGF-II gene region polymorphisms related to exertional muscle damage. J Appl Physiol 2007;102:1815-23.

Dillman AR, Minor PJ, Sternberg PW. Origin and evolution of dishevelled. G3 (Bethesda). 2013;3:251-62.

Do DN, Strathe AB, Osterson T, Jensen J, Mark T, Kardarmideen HN. Genome-wide association study reveals genetic architecture of eating behavior in pigs and its implications for humans obesity by comparative mapping. PLoS One 2013;8:e71509.

Dória S, Sousa M, Fernandes S, Ramalho C, Brandão O, Matias A et al. Gene expression pattern of IGFI, PHLDA2, PEG10 and CDKN1C imprinted genes in spontaneous miscarriages or fetal deaths. Epigenetics 2010;5:444-50.

Du P, Tang F, Qiu Y, Dong F. GF11 is repressed by p53 and inhibits chromatin damage-induced apoptosis. PLoS One 2013;8:e73542.

El Hajj N, Pliushch G, Schneider E, Dittrich M, Müller T, Korenkov M et al. Metabolic programming of MEST DNA methylation by intrauterine exposure to gestational diabetes mellitus. Diabetes 2013;62:1320-8.

Elbert M, Cohen D, Müsch A. PAR1b promotes cell-cell adhesion and inhibits dishevelled-mediated transformation of Madin-Darby canine kidney cells. Mol Biol Cell 2006;17:3345-55.
Farmer SR. Molecular determinants of brown adipocyte formation and function. Genes Dev 2008;22:1269-75.

Flisikowski K, Venhoranta H, Nowacka-Woszuk J, McKay SD, Flyckt A, Taponen J et al. A novel mutation in the maternally imprinted PEG3 domain results in a loss of MIMT1 expression and causes abortions and stillbirths in cattle (Bos taurus). PLoS One 2010;5:e15116.

Gallagher RC, Pils B, Albalwi M, Francke U. Evidence for the role of PWCR1/HBII-85 C/D box small nucleolar RNAs in Prader-Willi syndrome. Am J Hum Genet 2002;71:669-78.

He L, Wang Z, Sun Y. Reduced amount of cytochrome c oxidase subunit I messenger RNA in placentas from pregnancies complicated by preeclampsia. Acta Obstet Gynecol Scand 2004;83:144-8.

Ho JC, Cheung ST, Poon WS, Lee YT, Ng IO, Fan ST. Down-regulation of retinol binding protein 5 is associated with aggressive tumor features in hepatocellular carcinoma. J Cancer Res Clin Oncol 2002;133:929-36.

Hubertus J, Zitzmann F, Trippel F, Müller-Höcker J, Stehr M, von Schweinitz D et al. Selective methylation of CpGs at regulatory binding sites controls NNAT expression in Wilms tumors. PLoS One 2013;8:e67605.

Hudak CS, Sul HS. Pref-1, a gatekeeper of adipogenesis. Front Endocrinol (Lausanne) 2013;4:79.

Ishida M, Monk D, Duncan AJ, Abu-Amero S, Chong R, Ring SM et al. Maternal inheritance of a promoter variant in the imprinted PHLDA2 gene significantly increases birth weight. Am J Hum Genet 2012;90:715-9.

Kang S, Li SZ, Wang N, Zhou RM, Wang T, Wang DJ et al. Association between genetic polymorphisms in fibroblast growth factor (FGF1) and FGF2 and risk of endometriosis and adenomyosis in Chinese women. Hum Reprod 2010;25:1806-11.

Karagiannis GS, Weile J, Bader GD, Minta J. Integrative pathway dissection of molecular mechanisms of moxLDL-induced vascular smooth muscle phenotype transformation. BMC Cardiovasc Disord 2013;13:4.

Kawano Y, Nasu K, Li H, Tsuno A, Abe W, Takai N et al. Application of the histone deacetylase inhibitors for the treatment of endometriosis: histone modifications as pathogenesis and novel therapeutic target. Hum Reprod 2011;26:2486-98.

Kim JW, Kim ST, Turner AR, Young T, Smith L, Liu W et al. Identification of new differentially methylated genes that have potential functional consequences in prostate cancer. PLoS One 2012;7:e48545.

Kishore S, Khanna A, Zhang Z, Hui J, Balwierz PJ, Stefan M et al. The snoRNA MBII-52 (SNORD 115) is processed into smaller RNAs and regulates alternative splicing. Mol Hum Genet 2010;19:1153-64.

Koide T, Banno M, Aleksic B, Yamashita S, Kikuchi T, Kohmura K et al. Common variants in MAGI2 gene are associated with increased risk for cognitive impairment in schizophrenic patients. PLoS One 2012;7:e36836.

Kurtis MM, San Luciano M, Yu Q, Goodman RR, Ford B, Raymond D et al. Clinical and neurophysiological improvement of SGCE myoclonus-dystonia with G Pi deep brain stimulation. Clin Neurol Neurosurg 2010;112:149-52.

Lambertini L, Marsit CJ, Sharma P, Macconi M, Ma Y, Hu J et al. Imprinted gene expression in fetal growth and development. Placenta 2012;33:480-6.

Larsen KB, Lutterodt MC, Møllgård K, Møller M. Expression of the homeobox genes OTX2 and OTX1 in the early developing human brain. J Histochem Cytochem 2010;58:669-78.

Leinonen JT, Surakka I, Haukilahti A, Kettunen J, Luoto R, Salomaa V et al. Association of LIN28B with adult adiposity-related traits in females. PLoS One 2012;7:e48785.

Li YG, Wang X. Association of the CYP1B1 gene polymorphism with susceptibility to endometriosis. Zhonghua Yi Xue Yi Chuan Xue Za Zhi 2009;26:66-9.
Li J, Bench AJ, Vassiliou GS, Fourouclas N, Ferguson-Smith AC, Green AR. Imprinting of the human L3MBTL gene, a polycomb family member located in a region of chromosome 20 deleted in human myeloid malignancies. Proc Natl Acad Sci USA 2004;101:7341-6.

Li J, Wang SJ, Sun L, Li YL. Differential expression of the anti-oncogene ARHI between patients with and without endometriosis. Nan Fang Yi Ke Da Xue Xue Bao 2011;31:796-800.

Liu M, Liu Y, Liu Y, Lupo G, Lan L, Barsacchi G et al. A role for Xvax2 in controlling proliferation of Xenopus ventral eye and brain progenitors. Dev Dyn 2008;237:3387-93.

Liu T, Elmquist JK, Williams KW. Mrap2: an accessory protein linked to obesity. Cell Metab 2013a;18:309-11.

Liu L, Zhou Z, Huang S, Guo Y, Fan Y, Zhang J et al. Zc3h12c inhibits vascular inflammation by repressing NF-κB activation and pro-inflammatory gene expression in endothelial cells. Biochem J 2013b;451:55-60.

Mabb AM, Judson MC, Zylka MJ, Philpot BD. Angelman syndrome: insights into genomic imprinting and neurodevelopmental phenotypes. Trends Neurosci 2011;34:293-303.

Mackay DJ, Temple IK. Transient neonatal diabetes mellitus type 1. Am J Med Genet C Semin Med Genet 2010;154C:335-42.

Merce RE, Michaelson SD, Chee MJ, Atallah TA, Wervick R, Colmers WF. Mage\(\text{2}\) is required for leptin-mediated depolarization of POMC neurons in the hypothalamic arcuate nucleus in mice. PLoS Genet 2013;9:e1003207.

Monteiro JB, Colón-Díaz M, García M, Gutierrez S, Colón M, Seto E et al. Endometriosis is characterized by a distinct pattern of histone 3 and histone 4 lysine modifications. Reprod Sci 2014;21:305-18.

Nakabayashi K, Makino S, Minagawa S, Smith AC, Bamforth JS, Stanier P et al. Genomic imprinting of PPP1R9A encoding neurabin I in skeletal muscle and extra-embryonic tissues. J Med Genet 2004;41:601-8.

Nakashima N, Yamagata T, Mori M, Kuwajima M, Suwa K, Momoi MY. Expression analysis and mutation detection of DLX5 and DLX6 in autism. Brain Dev 2011;32:98-104.

Osada H. Association between polymorphisms in genes related to common adult diseases and fetal growth. Clin Med Pediatr 2009;3:11-8.

Ostern R, Fagerheim T, Hjellnes H, Nygård B, Mellgren SI, Nilsson O. Diagnostic laboratory testing for Charcot Marie Tooth disease (CMT): the spectrum of gene defects in Norwegian patients with CMT and its implications for future genetic test strategies. BMC Med Genet 2013;14:94.

Ozdemir F, Altinisik J, Karateke A, Coksuer H, Buyru N. Methylation of tumor suppressor genes in ovarian cancer. Exp Ther Med 2012;4:1092-6.

Park YJ, Luger K. The structure of nucleosome assembly protein 1. Proc Natl Acad Sci USA 2006;103:1248-53.

Park TJ, Kim JH, Bae JS, Park BL, Cheong HS, Chun JY et al. Possible association of SLC22A2 polymorphisms with aspirin-intolerant asthma. Int Arch Allergy Immunol 2011;155:395-402.

Plagge A. Non-coding RNAs at the Gnas and Snrpn-Ube3a imprinted gene loci and their involvement in hereditary disorders. Front Genet 2012;3:264.

Qian K, Chen H, Wei Y, Hu J, Zhu G. Differentiation of endometrial stromal cells in vitro: down-regulation of suppression of the cell cycle inhibitor p57 by HOXA10? Mol Hum Reprod 2005;11:245-51.

Redies C, Hertel N, Hübner CA. Cadherins and neuropsychiatric disorders. Brain Res 2012:1470:130-44.

Robson JE, Eaton SA, Underhill P, Williams D, Peters J. MicroRNAs 296 and 298 are imprinted and part of the GNAS/Gnas cluster and miR-296 targets IKBKE and Tmed9. RNA 2012;18:135-44.

Rodriguez-Jato S, Shan J, Khadake J, Heggestad AD, Ma X, Johnston KA et al. Regulatory elements associated with paternally-expressed genes in the imprinted murine Angelman/Prader-Willi syndrome domain. PLoS One 2013;8:e52390.

Santin I, Eizirik DL. Candidate genes for type 1 diabetes modulate pancreatic islet inflammation and β-cell apoptosis. Diabetes Obes Metab 2013;15(Suppl 3):71-81.

Schwertman P, Vermeulen W, Marteijn JA. UVSSA and USP7, a new couple in transcription-coupled DNA repair. Chromosoma 2013;122:275-84.

Solé-Llavina GJ, Artikaitis P, Morishita W, Ahmad M, Südhof TC, Malenka RC. Leucine-rich repeat transmembrane proteins are essential for maintenance of long-term potentiation. Neuron 2013;79:439-46.

Small KS, Hedman AK, Grundberg E, Nica AC, Thorleifsson G, Kong A et al. Identification of an imprinted master trans regulator at the KLF14 locus related to multiple metabolic phenotypes. Nat Genet 2011;43:561-4.
Sonderegger S, Pollheimer J, Knöfler M. Wnt signalling in implantation, decidualisation and placental differentiation--review. Placenta 2010;31:839-47.

Srinivasan S, Avadhani NG. Cytochrome c oxidase dysfunction in oxidative stress. Free Radic Biol Med 2012;53:1252-63.

Steinberg SJ, Snowden A, Braverman NE, Chen L, Watkins PA, Clayton PT et al. A PEX10 defect in a patient with no detectable defect in peroxisome assembly or metabolism in cultured fibroblasts. J Inherit Metab Dis 2009;32:109-19.

Sturrock M, Hellander A, Matzavinos A, Chaplain MA. Spatial stochastic modelling of the Hes1 gene regulatory network: intrinsic noise can explain heterogeneity in embryonic stem cell differentiation. J R Soc Interface 2013;10:20120988.

Tachiwana H, Miya Y, Shono N, Ohzeki J, Osakabe A, Otake K et al. Nap1 regulates proper CENP-B binding to nucleosomes. Nucleic Acids Res 2013;41:2869-80.

Tanabe Y, Hirano A, Iwasato T, Itohara S, Araki K, Yamaguchi T et al. Molecular characterization and gene disruption of a novel zinc-finger protein, HIT-4, expressed in rodent brain. J Neurochem 2010;112:1035-44.

Tobi EW, Heijmans BT, Kremer D, Putter H, Delemarre-van de Waal HA, Finken MJ et al. DNA methylation of IGF2, GNASAS, INSIGF and LEP and being born small for gestational age. Epigenetics 2011;6:171-6.

Travers ME, Mackay DJ, Dekker Nitert M, Morris AP, Lindgren CM, Berry A et al. Insights into the molecular mechanism for type 2 diabetes susceptibility at the KCNQ1 locus from temporal changes in imprinting status in human islets. Diabetes 2013;62:987-92.

Van Damme P, Hole K, Pimenta-Marques A, Helsens K, Vandenbroucke J, Martinho RG et al. NatF contributes to an evolutionary shift in protein N-terminal acetylation and is important for normal chromosome segregation. PLoS Genet 2011;7:e1002169.

Wetendorf M, DeMayo FJ. The progesterone receptor regulates implantation, decidualization, and glandular development via a complex paracrine signaling network. Mol Cell Endocrinol 2012;357:108-18.

Wisniewska M, Karlberg T, Lehtio L, Johansson I, Kotenyova T, Moche M et al. Crystal structures of the ATPase domains of four human Hsp70 isoforms: HSPA1L/Hsp70-hom, HSPA2/Hsp70-2, HSPA6/Hsp70B', and HSPA5/BiP/GRP78. PLoS One 2010;5:e8625.

Xin Z, Soejima H, Higashimoto K, Yatsuki H, Zhu X, Satoh Y et al. A novel imprinted gene, KCNQ1DN, within the WT2 critical region of human chromosome 11p15.5 and its reduced expression in Wilms' tumors. J Biochem 2000;128:847-53.

Zhang A, Skaar DA, Li Y, Huang D, Price TM, Murphy SK et al. Novel retrotransposed imprinted locus identified at human 6p25. Nucleic Acids Res 2011;39:5388-400.

Zhang Q, Bouma GJ, McClellan K, Tobet S. Hypothalamic expression of snoRNA Snord116 is consistent with a link to the hyperphagia and obesity symptoms of Prader-Willi syndrome. Int J Dev Neurosci 2012;30:479-85.

Zhong J, Chen S, Xue M, Du Q, Cai J, Jin H et al. ZIC1 modulates cell-cycle distributions and cell migration through regulation of sonic hedgehog, PI(3)K and MAPK signaling pathways in gastric cancer. BMC Cancer 2012;12:290.

Zhu W, Trivedi CM, Zhou D, Yuan L, Lu MM, Epstein JA. Inpp5f is a polyphosphoinositide phosphatase that regulates cardiac hypertrophic responsiveness. Circ Res 2009;105:1240-7.