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Top Organisms [Tree]

[Mus musculus \(4445\)](#)[Homo sapiens \(2784\)](#)[Danio rerio \(373\)](#)[Rattus norvegicus \(249\)](#)[Drosophila melanogaster \(243\)](#)GEO DataSet ▾ embryo X[Summary](#) [500 per page](#) [Sort by Default order](#)

Search results

Items: 1 to 500 of 9102Filters activated: Expression profiling by array. [Clear all](#) to show 585856 items. [Bradykinin promotes immune responses in differentiated embryonic neurospheres carrying APP swe and PS1](#)1. [dE9 mutations](#)

(Submitter supplied) Neural stem cells (NSCs) can be cultivated from developing brains, reproducing many of the processes that occur during neural development. They can be isolated from a variety of animal models, such as transgenic mice carrying mutations in amyloid precursor protein (APP) and presenilin 1 and 2 (PSEN 1 and 2), characteristic of familial Alzheimer's Disease (AD). Modulating the development of these cells with inflammation-related peptides, like bradykinin (BK) and its antagonist HOE-140, enables the understanding of the impact of such molecules on the genetic load of treated neurospheres. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL13912 12 Samples

Download data: [TXT](#)

Series Accession: GSE246792 ID: 200246792

 [Characterization of mast cells from human umbilical cord blood](#)

2. (Submitter supplied) Mast cells are tissue-resident innate immune cells that express high affinity to receptor immunoglobulin E and responsible for host defense and array of diseases relate to immune system. We aim to characterize the function of human umbilical cord blood-dervied mast cells (hCBMCs).

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL6244 5 Samples

Download data: [CEL](#)

Series Accession: GSE201473 ID: 200201473

 [Gene expression profiles of depletion of Daxx and HOTAIR](#)

3. (Submitter supplied) In this study, we found that Daxx may modulate HOTAIR stability, and therefore, regulate H3K27me3 levels. To further examine the possible mechanism and biological consequence, we separately knocked down Daxx and HOTAIR with a lentivirus plasmid constructed with short hairpin RNA and siRNA oligonucleotides, respectively. We then used microarray analysis to identify several candidate genes regulated under the Daxx-HOTAIR axis.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL14550 12 Samples

[Download data: TXT](#)

Series Accession: GSE35792 ID: 200035792

 [Endometrial transcriptomic changes after application of seminal plasma: a randomized controlled trial](#)

4. (Submitter supplied) We hypothesized that seminal plasma, the acellular seminal fluid component, influences the endometrium stimulating the immune system and facilitating the implantation. We designed a randomized, double-blinded, placebo-controlled trial, and we used microarray analysis to evaluate differences in the endometrial transcriptomic profile after vaginal seminal plasma application. Differential gene pathways analysis showed an upregulation of pathways associated with the immune response, cell viability, proliferation and cellular movement, implantation, **embryo** development, oocyte maturation and angiogenesis. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL23126 9 Samples

[Download data: CEL](#)

Series Accession: GSE241134 ID: 200241134

 [Single cell microarray analysis of mouse primordial germ cells with Prdm14 mutation.](#)

5. (Submitter supplied) Prdm14 is a critical gene for specifying mouse primordial germ cells (PGCs). The changes in expression in mouse PGCs caused by mutations of the Prdm14 gene were investigated at the single-cell level using microarray analysis.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL1261 30 Samples

[Download data: CEL](#)

Series Accession: GSE233342 ID: 200233342

 [Gene expression profiling of human fresh and cryopreserved sperm](#)

6. (Submitter supplied) Cryopreservation process deregulates the expression of pathways important for fertility in human spermatozoa Study design, size, duration (max. 75 words): Semen samples were obtained from 20 normospermic men from April to May 2022. Each sample was divided in two aliquots. From one aliquot total RNA was immediately extracted. The second aliquot was slowly cryopreserved and after a week of storage in liquid nitrogen total RNA was extracted. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL10332 11 Samples

[Download data: TXT](#)

Series Accession: GSE225320 ID: 200225320

 [Early Host Immune Responses in Human Gallbladder to Salmonella Typhi Strains from Patients with Acute and](#)[7. Chronic Infections](#)

(Submitter supplied) *Salmonella enterica* serovar Typhi (*S. Typhi*), a human-restricted pathogen, enters the host through the gut to cause typhoid fever. Recent calculations of the typhoid fever burden estimated that more than 20 million new typhoid fever cases occur in low and middle-income countries, resulting in 129,000-223,000 deaths yearly. Interestingly, upon the resolution of acute disease, 1%-5% of patients become asymptomatic chronic carriers of *S. Typhi*. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL32993 35 Samples

[Download data: RCC](#)

Series Accession: GSE253700 ID: 200253700

 [Identification of HTRA4 as a transcriptional target of P63 in trophoblast](#)

8. (Submitter supplied) The placenta plays a crucial role in pregnancy success. deltaNp63alpha (p63), a transcription factor from the TP53 family, is highly expressed in villous cytotrophoblasts (CTBs), the epithelial stem cells of the human placenta,

and has been shown to be involved in CTB maintenance and differentiation. In this study, we set out to identify mechanism(s) of action of p63, by identifying its downstream targets. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL10558 12 Samples

Download data: IDAT, TXT

Series Accession: GSE251742 ID: 200251742

[Effects of Apigenin and Rutaecarpine on Gene Expression Profiling of Human BMSC-derived osteoblasts](#)

9. [\[Microarray\]](#)

(Submitter supplied) Aging causes dysfunctional changes to the bone microenvironment that lead to osteoporosis development. Osteoporosis is a serious bone health issue that is characterized by decreased bone formation and increased bone resorption. The aim of this study is to evaluate the effects of natural compounds, Apigenin and Rutaecarpine on osteoblast differentiation and examine if Apigenin and Rutaecarpine can rescue osteogenesis in aging-context. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL14550 9 Samples

Download data: TXT

Series Accession: GSE252845 ID: 200252845

[Effect of group III phospholipase A2 deletion on gene expression in bronchial epithelial cells in an antigen-induced asthma model.](#)

10. [\[Microarray\]](#)

(Submitter supplied) Asthma is a chronic inflammatory disease of the airways characterized by recurrent episodes of airway obstruction, hyperresponsiveness, remodeling, and eosinophilia. Phospholipase A2s (PLA2s), which release fatty acids and lysophospholipids from membrane phospholipids, have been implicated in exacerbating asthma by generating pro-asthmatic lipid mediators, but an understanding of the association between individual PLA2 subtypes and asthma is still incomplete. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL10333 4 Samples

Download data: TXT

Series Accession: GSE249135 ID: 200249135

[Effect of group III phospholipase A2 deletion in antigen-induced asthma modeled lung](#)

11. [\[Microarray\]](#)

(Submitter supplied) Asthma is a chronic inflammatory disease of the airways characterized by recurrent episodes of airway obstruction, hyperresponsiveness, remodeling, and eosinophilia. Phospholipase A2s (PLA2s), which release fatty acids and lysophospholipids from membrane phospholipids, have been implicated in exacerbating asthma by generating pro-asthmatic lipid mediators, but an understanding of the association between individual PLA2 subtypes and asthma is still incomplete. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL10333 4 Samples

Download data: TXT

Series Accession: GSE249134 ID: 200249134

[Ablation of Max expression induces meiotic onset in sexually undifferentiated germ cells](#)

12. [\[Microarray\]](#)

(Submitter supplied) MAX (MYC Associated Factor X) is generally known as a mandatory partner for MYC transcription factor, which activates various genes involved in cell growth and metabolism. On the other hand, MAX, when interacting with MGA, forms the polycomb repressive complex (PRC) 1.6, one of the subtypes of PRC1, which directs the transcriptionally repressed chromatin state. Although physiological significance is not known at present, we have previously demonstrated that mouse embryonic stem cells (ESCs) bear a potential to onset meiosis, albeit not germ cells, and PRC1.6 prevent ESCs from their ectopic onset of meiosis (Suzuki et al., 2016, Nat. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL20258 4 Samples

Download data: CEL

Series Accession: GSE233556 ID: 200233556

[Gene expression profiles of mouse derived esophagus and stomach epithelial stem cells 3D organoids](#)

13. (Submitter supplied) The gastroesophageal squamocolumnar junction (GE-SCJ) is a critical tissue interface between the esophagus and stomach, with significant relevance in the pathophysiology of gastrointestinal diseases. Despite this, the molecular mechanisms underlying GE-SCJ development remain unclear. Using single-cell transcriptomics, organoids, and spatial analysis, we examine the cellular heterogeneity and spatiotemporal dynamics of GE-SCJ development from embryonic to adult mice. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL13912 6 Samples

Download data: TXT

Series Accession: GSE181409 ID: 200181409

[Molecular analysis of the subaortic hematopoietic stem cell niche](#)

14. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus

Type: **Expression profiling by array**; Expression profiling by high throughput sequencing

Platforms: GPL20710 GPL23092 GPL24247 24 Samples

Download data: CEL, MTX, TSV

Series Accession: GSE159592 ID: 200159592

[Molecular analysis of the subaortic hematopoietic stem cell niche \[E12.5\]](#)

15. (Submitter supplied) Hematopoietic stem cells (HSCs) are formed in the Aorta-Gonad-Mesobephros (AGM) region of mouse midgestation embryos. This process is tightly regulated in time and space by surrounding cells inculding mesenchymal cells located underneath the dorsal aorta. We combined laser microdissection and microarrays to isolate the dorsal and ventral aortic tissues at three developmental stages and to explore their gene expression profiling.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL23092 8 Samples

Download data: CEL

Series Accession: GSE159591 ID: 200159591

[Molecular analysis of the subaortic hematopoietic stem cell niche \[E11.5\]](#)

16. (Submitter supplied) Hematopoietic stem cells (HSCs) are formed in the Aorta-Gonad-Mesobephros (AGM) region of mouse midgestation embryos. This process is tightly regulated in time and space by surrounding cells inculding mesenchymal cells located underneath the dorsal aorta. We combined laser microdissection and microarrays to isolate the dorsal and ventral aortic tissues at three developmental stages and to explore their gene expression profiling.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL20710 6 Samples

Download data: CEL

Series Accession: GSE159590 ID: 200159590

[Molecular analysis of the subaortic hematopoietic stem cell niche \[E10.5_2\]](#)

17. (Submitter supplied) Hematopoietic stem cells (HSCs) are formed in the Aorta-Gonad-Mesobephros (AGM) region of mouse midgestation embryos. This process is tightly regulated in time and space by surrounding cells inculding mesenchymal cells located underneath the dorsal aorta. We combined laser microdissection and microarrays to isolate the dorsal and ventral aortic tissues at three developmental stages and to explore their gene expression profiling.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL23092 2 Samples

[Download data: CEL](#)

Series Accession: GSE159589 ID: 200159589

[Molecular analysis of the subaortic hematopoietic stem cell niche \[E10.5_1\]](#)

18. (Submitter supplied) Hematopoietic stem cells (HSCs) are formed in the Aorta-Gonad-Mesobephros (AGM) region of mouse midgestation embryos. This process is tightly regulated in time and space by surrounding cells inculding mesenchymal cells located underneath the dorsal aorta. We combined laser microdissection and microarrays to isolate the dorsal and ventral aortic tissues at three developmental stages and to explore their gene expression profiling.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL23092 6 Samples

[Download data: CEL](#)

Series Accession: GSE159588 ID: 200159588

[Resistance to Naïve and Formative Pluripotency Conversion in RSeT Human Embryonic Stem Cells](#)

19. (Submitter supplied) One of the most important properties of human embryonic stem cells (hESCs) is related to their primed and naïve pluripotent states. Our previous meta-analysis indicates the existence of heterogeneous pluripotent states derived from diverse naïve protocols. In this study, we have characterized a commercial medium (RSeT)-based pluripotent state under various growth conditions. Notably, RSeT hESCs can circumvent hypoxic growth conditions as required by naïve hESCs, in which some RSeT cells (e.g., H1 cells) exhibit much lower single cell plating efficiency, having altered or much retarded cell growth under both normoxia and hypoxia. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL6480 24 Samples

[Download data: TXT](#)

Series Accession: GSE217275 ID: 200217275

[Serum exosomal miRNA profile in pregnancies with gestational diabetes based on pancreatic β-cell function](#)

20. (Submitter supplied) Pancreatic β-cell function impairment is a key mechanism for developing gestational diabetes mellitus (GDM). Maternal and placental exosomes regulate maternal and placental responses during hyperglycemia. Studies have associated exosomal micro RNAs (miRNAs) with GDM development. To date, no studies have been reported that evaluate the profile of miRNAs present in maternal and placental exosomes in the early stages of gestation from pregnancies that develop GDM. [more...](#)

Organism: synthetic construct; Homo sapiens

Type: **Expression profiling by array**

Platform: GPL21572 28 Samples

[Download data: CEL, CHP](#)

Series Accession: GSE243374 ID: 200243374

[Generation of induced pluripotent stem \(iPS\) cells using non-viral magnet-based nanofection](#)

21. (Submitter supplied) Using magneto-nanofection, iPS cells were efficiently generated by the transient expression of iPS genes in MEF (mouse embryonic fibroblast), suggesting that the non-viral magneto-nanofection method can be used for the efficient generation of iPS cells.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6481 10 Samples

[Download data: TXT](#)

Series Accession: GSE21357 ID: 200021357

[Agents which upregulate CD55 \[decay accelerating factor \(DAF\)\] expression \[Array\]](#)

22. (Submitter supplied) (Submitter supplied) Identification of transcription factors (TFs) which upregulate human CD55 expression. CD55 was originally described as a cellular complement regulator that protects self-cells from autologous complement attack. It is now known as cellular regulator which controls many functions of cells, as examples T cell

commitment to T effector cells vs Foxp3+ T regulatory cells, B2 cell Ab production, and receptor tyrosine kinase (RTK) growth factor receptor function. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL570 9 Samples

[Download data](#)

Series Accession: GSE255080 ID: 200255080

[Crosslinked elastin-like polypeptides mediate direct cardiac differentiation of mouse embryonic and induced](#)

23. [pluripotent stem cells without use of cardiac differentiation factors](#)

(Submitter supplied) Elastin-like polypeptides (ELPs) are promising for biomedical applications due to their unique thermos-responsive and elastic properties. ELP-based biomaterial has been produced through enzymatic crosslinking of modified ELPs. We investigated the role of elastin like polypeptide in cardiomyocyte proliferation and differentiation in mouse ES cells

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL4134 12 Samples

[Download data: TXT](#)

Series Accession: GSE145623 ID: 200145623

[Maternal Exercise Prior to and During Gestation Induces Sex-Specific Alterations in the Mouse Placenta](#)

24. (Submitter supplied) Examined the role of maternal voluntary wheel running commencing 10 weeks prior to gestation, and throughout pregnancy, on placental transcriptome in late gestation. While exercise (EX) is beneficial during pregnancy for both mother and child, little is known about the mechanisms by which maternal (MAT EX) mediates changes in utero. We hypothesized that effects of MAT EX prior to and during gestation will be evident in transcriptomic signatures in the placenta and will be sexually dimorphic. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL1261 12 Samples

[Download data: CEL, XLS](#)

Series Accession: GSE243228 ID: 200243228

[Class A capsid assembly modulator apoptotic elimination of hepatocytes with high HBV core antigen level in](#)

25. [vivo is dependent on de novo core protein translation](#)

(Submitter supplied) Treatment with hepatitis B virus (HBV) capsid assembly modulators that induce the formation of aberrant HBV core protein structures (CAM-A) leads to programmed cell death, apoptosis, of HBV-infected hepatocytes and subsequent reduction of HBV antigens, which differentiates CAM-A from other CAMs. The effect is dependent on the de novo synthesis and high levels of core protein.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL33894 92 Samples

[Download data: CEL](#)

Series Accession: GSE246563 ID: 200246563

[Human induced pluripotent stem cells are resistant to human cytomegalovirus infection primarily at the](#)

26. [attachment level due to the reduced expression of cell-surface heparan sulfate](#)

(Submitter supplied) Cytomegalovirus (CMV), a type of herpes virus, is the predominant cause of congenital anomalies due to intrauterine infections in humans. Adverse outcomes related to intrauterine infections with human CMV (HCMV) vary widely depending on factors, such as fetal infection timing, infection route, and viral virulence. The precise mechanism underlying HCMV susceptibility remains unclear. In this study, we compared the susceptibility of neonatal human dermal fibroblast cells (NHDFCs) and human induced pluripotent stem cells (hiPSCs) derived from NHDFCs, which are genetically identical to HCMV, using immunostaining, microarray, in situ hybridization, quantitative PCR, and scanning electron microscopy. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL21185 6 Samples

Download data: [TXT](#)

Series Accession: GSE241636 ID: 200241636

[The impact of selective HDAC inhibitors on the transcriptome of early mouse embryos](#)

27. (Submitter supplied) Histone acetylation, which is regulated by histone acetyltransferases (HATs) and histone deacetylases (HDACs), plays a crucial role in the control of gene expression. HDAC inhibitors (HDACi) have shown potential in cancer therapy; however, the specific roles of HDACs in early embryos remain unclear. Moreover, although some pan-HDACi have been used to maintain cellular undifferentiated states in early embryos, the specific mechanisms underlying their effects remain unknown. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL10787 39 Samples

Download data: [TXT](#)

Series Accession: GSE238124 ID: 200238124

[THE BITTER TASTE RECEPTOR AGONIST DENATONIUM INHIBITS STEMNESS CHARACTERISTICS IN](#)

28. [HEMATOPOIETIC STEM CELLS](#)

(Submitter supplied) Bone marrow microenvironmental stimuli profoundly impact hematopoietic stem cell fate and biology. As G protein-coupled receptors, the bitter taste receptors (T2Rs) are key in transmitting extracellular stimuli into an intracellular response, within the oral cavity but also in extraoral tissues. Their expression in the bone marrow (BM)-derived cells suggests their involvement in sensing the BM microenvironmental fluctuation. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL23159 4 Samples

Download data: [CEL](#)

Series Accession: GSE220210 ID: 200220210

[Placental gene expression data from human fetuses with isolated spina bifida and fetuses with no congenital anomalies](#)

29. (Submitter supplied) Fetal spina bifida can associate with reduced fetal growth. However, little is known about placental development and function in pregnancies with fetal spina bifida, despite that the placenta is a critical regulator of fetal growth. We used data from a case-control study to determine how the placental transcriptome differs in fetuses with isolated spina bifida (cases), compared to fetuses without any congenital anomalies (controls).

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL23126 33 Samples

Download data: [CEL, CHP](#)

Series Accession: GSE252552 ID: 200252552

[Cortical miR-709 links glutamatergic signaling to NREM sleep EEG slow waves in an activity-dependent manner](#)

30. [manner](#)

(Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus

Type: **Expression profiling by array**; Non-coding RNA profiling by array; Expression profiling by high throughput sequencing

[4 related Platforms](#) [50 Samples](#)

Download data: [RCC, TXT](#)

Series Accession: GSE189353 ID: 200189353

[Understanding Bovine Embryo Elongation: A Transcriptomic Study of Trophoblastic Vesicles](#)

31.

(Submitter supplied) Background: During the process of elongation, the **embryo** increases in size within the uterus while the extra-embryonic tissues (EET) develop and differentiate in preparation for implantation. As it grows, the ovoid **embryo** changes shape into first a tubular and then a filamentous form. This process is directed by numerous genes and pathways, the expression of which may be altered in the case of developmental irregularities such as when the conceptus is shorter than expected or when the **embryo** develops after splitting. [more...](#)

Organism: Bos taurus

Type: **Expression profiling by array**

Platform: [GPL7417](#) 24 Samples

[Download data: TXT](#)

Series Accession: GSE146768 ID: 200146768

[Gene expression dynamics reveal Sprouty mediated regulation of Wnt pathway genes](#)

32. (Submitter supplied) Sprouty genes (Spry) are feedback regulators of receptor tyrosine kinase signaling, and are genes with known tumor suppressing activity. The impact of Spry induction is ligand specific, but it is well-understood to be a negative feedback regulator of the mitogen-activated protein kinase pathway in response to fibroblast growth factor (FGF). However, the precise impact Spry has on transcription resulting in tumor suppression remains unknown. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: [GPL6885](#) 32 Samples

[Download data: TXT](#)

Series Accession: GSE124923 ID: 200124923

[Transcriptome analysis for differentiated gene expression analysis of TU2218, Vactosertib, and Ramucirumab on VEGF-induced endothelial cell anergy condition](#)

33. (Submitter supplied) Transcriptome analysis of HUVECs treated with TGF β RI or VEGFR2 inhibitors on endothelial cell anergy condition In this study, the dual inhibitory mechanism of TU2218 was identified using an in vitro analysis mimicking the tumor microenvironment and its anti-tumor effects were analyzed using in vivo mouse syngeneic tumor models. TU2218 directly normalized the activity of damaged T lymphocytes and natural killer cells from TGF β and suppressed the activity and viability of regulatory T cells. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL16686](#) 18 Samples

[Download data: CEL, CHP, XLSX](#)

Series Accession: GSE239760 ID: 200239760

[Gene expression in the placenta, and cerebral cortex of the brain of offspring mice; effect of maternal exposure to carbon black nanoparticle and ascorbic acid pre-treatment](#)

34. (Submitter supplied) To investigate the effects of administration of carbon black nanoparticle (CB-NP) to pregnant mice on the brain development in infantile mice, we have employed whole-genome microarray expression profiling to identify genes which show dose-dependent differential expression with astrogliosis in the frontal cortex of offspring mice. Some pregnant mice were pretreated with ascorbic acid to investigate the mechanism underlying the CB-NP effect. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: [GPL13912](#) 32 Samples

[Download data: TXT](#)

Series Accession: GSE250286 ID: 200250286

[The expression data from mandibular arch and tongue primordia in mouse embryos.](#)

35. (Submitter supplied) The mouse hypoglossal nerve originates from the occipital motor nuclei and projects a long distance, reaching the vicinity of the tongue primordia, the lateral lingual swelling, at E11.5. However, the details of how the hypoglossal nerve correctly projects to the primordia are not well understood. To investigate the molecular basis of hypoglossal nerve elongation, we employed cDNA microarray technology and screened for candidate genes involved in the axon guidance event.

Organism: Mus musculus
 Type: **Expression profiling by array**
 Platform: GPL21163 4 Samples
[Download data: TXT](#)
 Series Accession: GSE249490 ID: 200249490

[Comparison of E14.5 embryonic kidney transcriptomes \(Grb2 ureteric-specific knockout vs wild-type\)](#)

36. (Submitter supplied) Grb2 is a small SH2-SH3 adaptor molecule that interacts with activated tyrosine kinase receptors (RTKs), providing a crucial link towards downstream activation of pro-proliferative and pro-survival ERK and Akt signaling pathways. Ret and FGFR2, two RTKs that interact with Grb2, play important roles in ureteric branching and the proper establishment of the renal collecting duct system, but it is unclear whether Grb2 is required in this process. [more...](#)

Organism: Mus musculus
 Type: **Expression profiling by array**
 Platform: GPL16570 8 Samples
[Download data: CEL, CHP](#)
 Series Accession: GSE163040 ID: 200163040

[Pro-inflammatory T cells-derived cytokines enhance the maturation of the human fetal intestinal barrier](#)

37. (Submitter supplied) In this data set we aimed to interrogate the milestones of human functional gut development from 13-20 weeks post gestation for proximal intestinal segments and 15-35 weeks gestation for distal intestinal segments

Organism: Homo sapiens
 Type: **Expression profiling by array**
 Platform: GPL24324 45 Samples
[Download data: CEL](#)
 Series Accession: GSE247523 ID: 200247523

[lncRNA expression profile in placenta of diabetic macrosomia and normal birth weight newborn](#)

38. (Submitter supplied) LncRNAs and mRNAs expression in placenta of diabetic macrosomia were detected by microarray profile.

Organism: Homo sapiens
 Type: **Expression profiling by array**; Non-coding RNA profiling by array
 Platform: GPL16956 8 Samples
[Download data: TXT](#)
 Series Accession: GSE162173 ID: 200162173

[Fam46a is a regulator for gene expression in secretory tissues and plays an important role in development and](#)

39. [homeostasis](#)

(Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Xenopus laevis; Homo sapiens
 Type: **Expression profiling by array**
 Platforms: GPL16686 GPL10756 22 Samples
[Download data: CEL](#)
 Series Accession: GSE108692 ID: 200108692

[Fam46a is a regulator for gene expression in secretory tissues and plays an important role in development and](#)

40. [homeostasis \[FAM46A-shRNA\]](#)

(Submitter supplied) In early embryonic development, the organiser functions in multiple developmental processes, including neural induction, dorsoventral patterning of the mesoderm, and formation of the axial mesoderm. Chordin is a central molecule for the activity of the Spemann's organiser and abundantly secreted from the Spemann's organiser in Xenopus laevis. However, so far, a whole picture of the gene expression profile regulated by Chordin has not been examined. [more...](#)

Organism: Homo sapiens
 Type: **Expression profiling by array**
 Platform: GPL16686 6 Samples

[Download data: CEL](#)

Series Accession: GSE108691 ID: 200108691

- [Fam46a is a regulator for gene expression in secretory tissues and plays an important role in development and homeostasis \[Fam46a-MO1\]](#)
- 41.

(Submitter supplied) In early embryonic development, the organiser functions in multiple developmental processes, including neural induction, dorsoventral patterning of the mesoderm, and formation of the axial mesoderm. Chordin is a central molecule for the activity of the Spemann's organiser and abundantly secreted from the Spemann's organiser in *Xenopus laevis*. However, so far, a whole picture of the gene expression profile regulated by Chordin has not been examined. [more...](#)

Organism: *Xenopus laevis*Type: **Expression profiling by array**

Platform: GPL10756 12 Samples

[Download data: CEL](#)

Series Accession: GSE108686 ID: 200108686

- [Fam46a is a regulator for gene expression in secretory tissues and plays an important role in development and homeostasis \[Chordin\]](#)
- 42.

(Submitter supplied) In early embryonic development, the organiser functions in multiple developmental processes, including neural induction, dorsoventral patterning of the mesoderm, and formation of the axial mesoderm. Chordin is a central molecule for the activity of the Spemann's organiser and abundantly secreted from the Spemann's organiser in *Xenopus laevis*. However, so far, a whole picture of the gene expression profile regulated by Chordin has not been examined. [more...](#)

Organism: *Xenopus laevis*Type: **Expression profiling by array**

Platform: GPL10756 4 Samples

[Download data: CEL](#)

Series Accession: GSE108684 ID: 200108684

- [Attenuated retinoic acid signaling is among the early responses in mouse uterus approaching embryo attachment](#)
- 43.

(Submitter supplied) The uterus is transiently receptive for **embryo** implantation. It remains to be understood why the uterus does not reject semi-allogeneic or allogeneic embryos for implantation. Uterine early response genes at the time approaching **embryo** attachment may provide insights. Uteri from C57BL/6 pseudo-pregnant (PP) mice and pregnant (P) mice approaching **embryo** attachment on day 3 post-coitum (D3) @22 h were analyzed for early response genes by microarray. [more...](#)

Organism: *Mus musculus*Type: **Expression profiling by array**

Platform: GPL6246 8 Samples

[Download data: CEL](#)

Series Accession: GSE247638 ID: 200247638

- [Keloid Transcriptome](#)

44. (Submitter supplied) Eevaluation of intra- and inter-keloid fibroblast heterogeneity by analyzing their gene expression using transcriptomic analysis

Organism: *Homo sapiens*Type: **Expression profiling by array**

Platform: GPL23126 29 Samples

[Download data: CEL](#)

Series Accession: GSE218007 ID: 200218007

- [Single-cell CRISPR screens in vivo map T cell fate regulomes in cancer](#)

45. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus
 Type: Expression profiling by high throughput sequencing; Genome binding/occupancy profiling by high throughput sequencing; **Expression profiling by array**
 Platforms: GPL21103 GPL23038 89 Samples
 Download data: CEL, CSV, TAR
 Series Accession: GSE216800 ID: 200216800

[Single-cell CRISPR screens in vivo map T cell fate regulomes in cancer \[microarray\]](#)

46. (Submitter supplied) The gene regulatory network (GRN) underlying CTL differentiation and whether Tex responses can be functionally reinvigorated are incompletely understood. Here, we systematically mapped causal GRNs via single-cell CRISPR (scCRISPR) screens in vivo and discovered checkpoints for CTL differentiation.

Organism: Mus musculus
 Type: **Expression profiling by array**
 Platform: GPL23038 15 Samples
 Download data: CEL
 Series Accession: GSE216749 ID: 200216749

[Irisin deficiency exacerbates diet-induced insulin resistance and cardiac dysfunction and promotes ischemia](#)

47. [and reperfusion injury](#)

(Submitter supplied) The myokine irisin is involved in the regulation of a variety of physiological conditions, metabolism, and survival. We and others have demonstrated that recombinant irisin contributes critically to modulation of insulin resistance and cardiac function. However, the molecular mechanisms by which irisin exerts its physiological effects on cardiac function and insulin sensitivity remain unclear. We utilized the CRISPR/Cas9 genome editing system to delete irisin. [more...](#)

Organism: Mus musculus
 Type: **Expression profiling by array**
 Platform: GPL17791 6 Samples
 Download data: CEL
 Series Accession: GSE231597 ID: 200231597

[Expression data from mice hematopoietic progenitor cells](#)

48. (Submitter supplied) Nfatc1 short isoform-specific KO mice are embryonic lethal. This isoform is essential for osteoclast differentiation and is responsible for the gene expression of various osteoclast markers, including the isoform itself. We used clariom s assay to explore genes showing altered expression during osteoclast differentiation in cultured hematopoietic progenitor cells from KO mice.

Organism: Mus musculus
 Type: **Expression profiling by array**
 Platform: GPL23038 4 Samples
 Download data: CEL
 Series Accession: GSE225882 ID: 200225882

[Expression data from Lund Human Mesencephalic cells \(LUHMES\) exposed to acute and persistent oxidative DNA damage](#)

49. (Submitter supplied) Oxidative DNA damage in neurons activates a DNA damage response (DDR) to promote repair. Under a chronic oxidative environment these processes may be altered and promote accumulation of unrepaired DNA damage and continued activation of a DDR, leading to apoptosis or senescence activation. Accumulation of oxidative DNA damage are features of brain ageing and neurodegeneration but the effects of persistent DNA damage in neurons are not well characterised. [more...](#)

Organism: Homo sapiens
 Type: **Expression profiling by array**
 Platform: GPL570 9 Samples
 Download data: CEL, CHP
 Series Accession: GSE160841 ID: 200160841

- [Discovery of diagnostic biomarker and molecular mechanisms of placenta accreta spectrum](#)
50. (Submitter supplied) Transcriptome analysis of FFPE placenta of placenta accreta spectrum, over increta. Pre-diagnosis is essential to safely deal with placenta accrete spectrum, but definitive diagnostic markers have not yet been established. We conducted a transcriptome analysis of FFPE placenta to establish early diagnostic markers for placenta accreta.
- Organism: Homo sapiens
Type: **Expression profiling by array**
Platform: GPL16686 11 Samples
Download data: CEL, CHP
Series Accession: GSE189267 ID: 200189267
- [Modeling the Progression of Placental Transport from Early- to Late-Stage Pregnancy by Tuning Trophoblast Differentiation and Vascularization](#)
51. (Submitter supplied) The aim of this work was to compare the syncytiotrophoblast differentiation capacity of placental stem cells (PSCs) to the BeWo b30 trophoblast cell line. Syncytiotrophoblast markers were analyzed, as well as drug, hormone and nutrient transporters.
- Organism: Homo sapiens
Type: **Expression profiling by array**
Platform: GPL23159 15 Samples
Download data: CEL
Series Accession: GSE245763 ID: 200245763
- [Gene expression changes in cord blood-derived ECFCs in response to in vitro senescence stimuli](#)
52. (Submitter supplied) Senescent endothelial cells accumulate in blood vessels during aging and produce the senescence-associated secretory phenotype (SASP). Age-related cardiovascular disease is promoted by SASP chronic inflammation. SASP establishment has been attributed to DNA damage and cGAS activation through cytoplasmic chromatin fragments. Therefore, DNA sensing has been extensively studied in cellular senescence; RNA sensing, on the other hand, remains unexplored. [more...](#)
- Organism: Homo sapiens
Type: **Expression profiling by array**
Platform: GPL21827 15 Samples
Download data: TXT
Series Accession: GSE160166 ID: 200160166
- [Prenatal Diagnosis and Clinical Analysis of Talipes Equinovarus by Chromosomal Microarray Analysis](#)
53. (Submitter supplied) With the advancement of molecular technology, fetal talipes equinovarus (TE) is believed to be not only associated with chromosome aneuploidy, but also related to chromosomal microdeletion and microduplication. The study aimed to explore the molecular etiology of fetal TE and provide more information for the clinical screening and genetic counseling of TE by CMA. This retrospectively study included 131 fetuses with TE identified by ultrasonography. [more...](#)
- Organism: Homo sapiens
Type: **Expression profiling by array**
Platform: GPL18637 131 Samples
Download data: CEL, CYCHP
Series Accession: GSE230532 ID: 200230532
- [Stem cell technology provides novel tools to understand the impact of human variation on malaria](#)
54. (Submitter supplied) Plasmodium falciparum parasites have a complex life cycle, but the most clinically relevant stage of the disease is the invasion of erythrocytes and the proliferation of the parasite in the blood. The influence of human genetic traits on malaria has been known for a long time, however understanding the role of the proteins involved is hampered by the anuclear nature of erythrocytes that makes them inaccessible to genetic tools. [more...](#)
- Organism: Homo sapiens
Type: **Expression profiling by array**
Platform: GPL28270 100 Samples
Download data: IDAT, XLSX
Series Accession: GSE245735 ID: 200245735

- [Transcriptome analysis of human mononuclear blood cells post UC-MSC treatment](#)
55. (Submitter supplied) Studying the safety and efficacy of two treatment protocols for Multiple sclerosis (MS) patients using Mesenchymal Stromal/Stem Cells MSCs subtype derived from the umbilical cord; UC-MSCs and their secretome
- Organism: Homo sapiens
Type: Expression profiling by array
Platform: GPL17586 12 Samples
Download data: CEL, CHP
Series Accession: GSE235689 ID: 200235689
- [Consequences of Nkiras deficiency for the EGF response](#)
56. (Submitter supplied) Cancer is a disease of aberrant intracellular signaling. The NF- κ B family of transcription factors and the Ras family of small GTPases have emerged as particularly important mediators of the pro-proliferative signaling that drives tumorigenesis and carcinogenesis. The κ B-Ras proteins, encoded by the genes Nkiras1 and Nkiras2, were previously shown to inhibit both NF- κ B and Ras pathway activation through independent molecular mechanisms, implicating them as tumor suppressors with potentially broad relevance to human cancers. [more...](#)
- Organism: Mus musculus
Type: Expression profiling by array
Platform: GPL15639 4 Samples
Download data: PAIR
Series Accession: GSE216127 ID: 200216127
- [Microglia response to allergic airway inflammation during early postnatal period in mice](#)
57. (Submitter supplied) We examined how allergic inflammation in early postnatal period influences microglia using a short- and long-term airway allergy model. Male mice (C57BL/6) were immunized by intraperitoneal injection with aluminum hydroxide and ovalbumin (OVA) or phosphate-buffered saline (PBS) (control) at postnatal days (P) 3, 7, and 11, followed by intranasal challenge with OVA or PBS solution twice a week until P30 or P70. [more...](#)
- Organism: Mus musculus
Type: Expression profiling by array
Platform: GPL20258 4 Samples
Download data: CEL
Series Accession: GSE159463 ID: 200159463
- [Expression Data from HUVEC and HUAEC](#)
58. (Submitter supplied) To assess if HUVEC and HUAEC differ in susceptibility to inflammation and inflammation resolution, the cells were stimulated for 24 hrs with TNF followed by RNA isolation. Two additional groups were first stimulated with TNF (24 hr) followed by TNF removal (12 and 24 hrs). Expression profiles were compared to basal conditions, i.e. cells cultured in normal medium. We used micro-arrays to assess if Gene-expression profiles between HUVEC and HUAEC differ under inflammatory conditions and under conditions of inflammation resolution
- Organism: Homo sapiens
Type: Expression profiling by array
Platform: GPL24989 24 Samples
Download data: CEL
Series Accession: GSE179478 ID: 200179478
- [Dual targeted extracellular vesicles regulating oncogenic genes in pancreatic cancer \[Mouse Array\]](#)
59. (Submitter supplied) Pancreatic ductal adenocarcinoma (PDAC) tumours carry multiple gene mutations and respond poorly to treatments. There is currently an unmet need for drug carriers that can deliver multiple gene cargoes to high solid tumour burden like PDAC. Here, we report a dual-targeted extracellular vesicle (EV) carrying high loads of RNA that effectively suppresses large PDAC tumours in mice. The EV surface contains a CD64 protein that has a tissue targeting peptide and a humanized monoclonal antibody. [more...](#)
- Organism: Mus musculus
Type: Expression profiling by array
Platform: GPL13912 14 Samples
Download data: TXT

Series Accession: GSE223408 ID: 200223408

 [Dual targeted extracellular vesicles regulating oncogenic genes in pancreatic cancer](#)

60. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Homo sapiens; Mus musculus

Type: Non-coding RNA profiling by high throughput sequencing; **Expression profiling by array**[4 related Platforms](#) [43 Samples](#)[Download data: FA, TXT](#)

Series Accession: GSE223409 ID: 200223409

 [Transcriptomic profiling reveals differential cellular response of copper oxide nanoparticles and polystyrene](#)

- 61.
- [nanoplastics in perfused human placenta](#)

(Submitter supplied) Concerns about the potential risks to human health due nanoparticulate pollution have been emerging. However, the risks to sensitive populations, such as pregnant individuals and their unborn children are poorly characterised. With increasing evidence of environmental particles passing the placenta, their potential adverse effects on pregnancy and fetal development need to be assessed. Here, we investigated the impact of copper oxide (CuO) and polystyrene (PS) nanoparticle exposure on gene expression in ex vivo perfused human placental tissue.

Organism: Homo sapiens

Type: **Expression profiling by array**[Platform: GPL16699](#) [16 Samples](#)[Download data: TXT](#)

Series Accession: GSE220756 ID: 200220756

 [Dgcr8 function in the anterior second heart field](#)

62. (Submitter supplied) Morphogenesis of the heart is a complex process that relies on the precise gene expression and gene expression regulators during embryonic development. Dgcr8 is a gene involved in cardiac morphogenesis and it is in the chromosomal region deleted in 22q11.2DS patients. In order to study Dgcr8 function on heart development, we inactivated this gene in the cardiac progenitor cells of mouse embryos and did expression profiling of the long RNAs and miRNAs.

[more...](#)

Organism: Mus musculus; synthetic construct

Type: **Expression profiling by array**; Non-coding RNA profiling by array[Platforms: GPL19117](#) [GPL6246](#) [30 Samples](#)[Download data: CEL, TSV, TXT](#)

Series Accession: GSE186064 ID: 200186064

 [Differentiated embryonic neurospheres from familial Alzheimer's disease model show Innate Immune and Glial](#)

- 63.
- [Cell Responses](#)

(Submitter supplied) Proteins involved in the Alzheimer's disease (AD), such as amyloid precursor protein (APP) and presenilin-1 (PS1), play critical roles in early development of the central nervous system (CNS), as well as in innate immune and glial cell responses. However, it is unknown whether these alterations start on development of the CNS of carriers of APPswe and PS1dE9 mutations , associated with familial AD. Using microarray technology we studied the genome-wide gene expression profiles in the differentiated neural progenitor cells (NPCs) from wild-type (WT) and APPswe/PS1dE9 **embryo** telencephalon. Differential gene expression analysis indicated the occurrence of strong innate immune and glial cell responses in APPswe/PS1dE9 neurospheres, involving mainly microglial cells, inflammatory mediators and chemokines. APPswe/PS1dE9 cells expressed up to 100-fold more CCL12, CCL5, CCL3, C3, CX3CR1, TLR2 and TNF-alpha, which was confirmed by real time PCR. The expression of activated microglia marker Iba-1 was also 20-fold upregulated in APPswe/PS1dE9 cells. The secretome of APPswe/PS1dE9 differentiated NPCs increased the chemoattraction of peripheral blood mononuclear cells (PBMCs) compared to the secretome of WT cells. Taken together, our results demonstrated that neurogenic niche obtained from differentiation of embryonic APPswe/PS1dE9 neurospheres is an excellent model for AD in vitro, since this culture spontaneously presents several alterations observed in the adult-brain with this pathology. Moreover, our data strengthen pathophysiological hypotheses that propose an early neurodevelopmental origin for familial AD.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: [GPL13912](#) 4 Samples

[Download data: TXT](#)

Series Accession: GSE227002 ID: 200227002

[CircRNA profiling in laminar shear stress-treated human umbilical vein endothelial cells.](#)

64. (Submitter supplied) Laminar shear stress (LSS) suppresses endothelial inflammation and protects the arteries from atherosclerosis. Circular RNAs (circRNAs) are powerful regulators of vascular homeostasis and atherosclerosis; however, their roles in mediating the effects of LSS remain unexplored. To identify the changes in circRNA expression patterns after shear stress stimulation, we conducted circRNA microarray analysis using RNA extracted from HUVECs cultured for 24 h under static or LSS conditions.

Organism: Homo sapiens

Type: **Expression profiling by array**; Non-coding RNA profiling by array

Platform: [GPL21825](#) 6 Samples

[Download data: TXT, XLS](#)

Series Accession: GSE228636 ID: 200228636

[Nanostring of gene expression in intrahepatic leukocytes from mice fed a high-fat, -fructose, and -cholesterol](#)

65. [\(FFC\) diet](#)

(Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: [GPL19964](#) 17 Samples

[Download data: RCC](#)

Series Accession: GSE243295 ID: 200243295

[Nanostring of gene expression in intrahepatic leukocytes from wild type \(WT\) or myeloid-specific RAGE](#)

66. [knockout \(RAGE-MKO\) mice fed a chow or high-fat, -fructose, and -cholesterol \(FFC\) diet](#)

(Submitter supplied) Intrahepatic macrophages in nonalcoholic steatohepatitis (NASH) are heterogenous and include proinflammatory recruited monocyte derived macrophages. RAGE is expressed on macrophages and can be activated by damage associated molecular patterns (DAMPs) upregulated in NASH, yet the role of macrophage-specific RAGE signaling in NASH is unclear. Therefore, we hypothesized that a subset of RAGE expressing macrophages are proinflammatory and mediate liver inflammation in NASH. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: [GPL19964](#) 8 Samples

[Download data: RCC](#)

Series Accession: GSE243294 ID: 200243294

[Gene expression data from differentiating 3T3-L1 cells](#)

67. (Submitter supplied) The MED1 subunit has been shown to mediate ligand-dependent binding of the Mediator coactivator complex to multiple nuclear receptors, including the adipogenic PPAR γ , and to play an essential role in ectopic PPAR γ -induced adipogenesis of mouse embryonic fibroblasts. However, the precise roles of MED1, and its various domains, at various stages of adipogenesis and in adipose tissue have been unclear. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: [GPL16570](#) 19 Samples

[Download data: CEL, CHP](#)

Series Accession: GSE158083 ID: 200158083

[HEY1-NCOA2 interacts with RUNX2 to induce mesenchymal chondrosarcoma](#)

68. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus

Type: **Expression profiling by array**; Genome binding/occupancy profiling by high throughput sequencing

Platforms: [GPL16417](#) [GPL11180](#) 46 Samples

[Download data: CEL, TDF](#)

Series Accession: GSE163588 ID: 200163588

[HEY1-NCOA2 interacts with RUNX2 to induce mesenchymal chondrosarcoma \[Array\]](#)

69. (Submitter supplied) Mesenchymal chondrosarcoma is a high-grade malignant neoplasm characterized by biphasic growth of poorly differentiated small round cells and well differentiated cartilage. Mesenchymal chondrosarcoma affects adolescents and young adults, and the HEY1-NCOA2 fusion gene is causally associated with most cases. Here we generate a mouse model for mesenchymal chondrosarcoma by introducing HEY1-NCOA2 into mouse embryonic chondrogenic progenitors followed by subcutaneous transplantation into nude mice. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: [GPL11180](#) 35 Samples

[Download data: CEL](#)

Series Accession: GSE163291 ID: 200163291

[Increased hyaluronan by naked mole-rat HAS2 extends healthspan in mice](#)

70. (Submitter supplied) Abundant high molecular weight hyaluronic acid (HMW-HA) contributes to cancer resistance and possibly longevity of the longest-lived rodent, the naked mole-rat^{1,2}. To study whether the benefits of increased HMW-HA could be transferred to other animal species, we generated a transgenic mouse overexpressing naked mole-rat hyaluronic acid synthase 2 gene (nmrHAS2). nmrHAS2 mice showed increase in hyaluronan levels in several tissues, and lower incidence of spontaneous and induced cancer, extended lifespan and improved healthspan. [more...](#)

Organism: Mus musculus; Rattus norvegicus; Homo sapiens

Type: **Expression profiling by array**; Methylation profiling by array

Platform: [GPL28271](#) 19 Samples

[Download data: IDAT](#)

Series Accession: GSE234154 ID: 200234154

[Gene Expression data of MTA1-deficient human cord blood-derived HSCs](#)

71. (Submitter supplied) Human CB HSC enriched cells were transduced with shRNAs targeting MTA1 to identify changes in global transcription programme and understand the mechanisms behind MTA1 knock down induced phenotype.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL16686](#) 9 Samples

[Download data: CEL](#)

Series Accession: GSE206083 ID: 200206083

[Analysis of the effect of prenatal alcohol exposure on the Placenta—Cortex transcriptomic signature](#)

72. (Submitter supplied) Although alcohol consumption during pregnancy is a major cause of behavioral and learning disabilities, most FASD infants are late- or even misdiagnosed due to clinician's difficulties achieving early detection of alcohol-induced neurodevelopmental impairments. Neuroplacentology has emerged as a new field of research focusing on the role of the placenta in fetal brain development. Several studies have reported that prenatal alcohol exposure (PAE) dysregulates a functional placenta–cortex axis, which is involved in the control of angiogenesis and leads to neurovascular-related defects. However, these studies were focused on PIGF, a pro-angiogenic factor. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: [GPL11202](#) 16 Samples

[Download data: TXT](#)

Series Accession: GSE241836 ID: 200241836

[Inflammation-inducible promoters to overexpress immune inhibitory factors by MSCs](#)

73.

(Submitter supplied) Umbilical cord mesenchymal stromal cells (UC-MSCs) were treated with different concentration with HIL10 and the influences on the secretome analyzed

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL26355 12 Samples

Download data: CSV, TXT

Series Accession: GSE224735 ID: 200224735

[CD44 connects autophagy decline and aging in the vascular endothelium](#)

74. (Submitter supplied) The decline of endothelial autophagy is closely related to vascular senescence and disease, although the molecular mechanisms connecting these outcomes in vascular endothelial cells (VECs) remain unclear. Here, we identify a crucial role for CD44, a multifunctional adhesion molecule, in controlling autophagy and aging in VECs. The CD44 intercellular domain (CD44ICD) negatively regulates autophagy by reducing PIK3R4 and PIK3C3 levels and disrupting STAT3-dependent PtdIns3K complexes. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL17586 3 Samples

Download data: CEL, XLSX

Series Accession: GSE236523 ID: 200236523

[Elevated Dietary Non-Esterified Fatty Acid Levels Impact BeWo Trophoblast Metabolism and Lipid Processing:](#)

75. [A Multi-OMICS Outlook](#)

(Submitter supplied) Maternal obesity and gestational diabetes mellitus (GDM) are associated with adverse intrauterine environments that are high in circulating nutrients. These adverse environments facilitate impairments in placental mitochondrial function and nutrient processing that ultimately leads to an increased risk of the exposed offspring developing non-communicable cardiometabolic health disorders (e.g. obesity, type 2 diabetes, metabolic syndrome). [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL23159 20 Samples

Download data: CEL, CHP

Series Accession: GSE197385 ID: 200197385

[Using Genomic Signatures to Elucidate Individual and Mixture Effects of Inorganic Arsenic and Manganese in](#)

76. [Placental Trophoblasts](#)

(Submitter supplied) HTR-8/SVneo human placental trophoblast cells were exposed to low-level environmentally relevant concentrations of iAs, Mn, and iAs-Mn mixtures. A microarray assay was performed to understand the changes and differences in gene expression in relation to single-metal and metal-mixtures

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL23159 30 Samples

Download data: CEL, CHP

Series Accession: GSE240673 ID: 200240673

[Comparative study of 3D vs. 2D cell culture transcriptional changes of murine embryonic stem cells, stromal](#)

77. [cells and lung cancer cells](#)

(Submitter supplied) Transcriptional profiling of 3D and 2D condition on mouse embryonic stem cells, stromal cells (M210B4) and Lewis lung cancer cells (LLC).

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL16570 6 Samples

Download data: CEL

Series Accession: GSE99942 ID: 200099942

- [Gene expression profiles of EpiSC-derived neural stem cell lines in comparison with EpiSC and embryonic CNS](#)
78. (Submitter supplied) Epiblast stem cells (EpiSCs) maintained in the medium with activin were freed from activin to elicit neural development, exposed to various strengths of Wnt signals, which may provide the initial stage of anteroposterior regional specificities, and placed in the culture condition to arrest neural development but expand cells as neural stem cells (NSCs) with epidermal growth factor (EGF) and fibroblast growth factor 2 (FGF2).

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL21163 22 Samples

Download data: [TXT](#)

Series Accession: GSE237042 ID: 200237042

- [Side-population trophoblasts from first and third trimester pregnancies](#)

79. (Submitter supplied) Gene expression microarrays investigating the transcriptome of matched populations of human side-population trophoblasts and cytотrophoblasts isolated from first and third trimester placentae

Organism: Homo sapiens

Type: **Expression profiling by array**; Third-party reanalysis

Platform: GPL16043 10 Samples

Download data: [CEL](#), [XLS](#)

Series Accession: GSE123555 ID: 200123555

- [Expression data from adult Drosophila melanogaster virgin males](#)

80. (Submitter supplied) We used microarrays to investigate the transcriptome of male flies exposed to either a rich or a poor nutrient environment during development. Further we investigated transcriptome of their offspring and grand-offspring also developed at poor or rich diet. The ability of organisms to cope with poor quality nutrition is essential for their persistence. For species with short generation time, the nutritional environments can transcend generations, making it beneficial for adults to prime their offspring to particular diets. [more...](#)

Organism: Drosophila melanogaster

Type: **Expression profiling by array**

Platform: GPL20842 30 Samples

Download data: [CEL](#)

Series Accession: GSE236807 ID: 200236807

- [Endothelial CD34 expression and regulation of immune cell response in-vitro](#)

81. (Submitter supplied) Endothelial cells cover the lining of different blood vessels and lymph nodes, and have major functions including the transport of blood, homeostasis, inflammatory responses, control of infiltration of circulating cells into the tissues, and formation of new blood vessels. Therefore, understanding these cells is of major interest. The morphological features, phenotype and function of endothelial cells varies according to the vascular bed examined. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL17586 6 Samples

Download data: [CEL](#), [XLSX](#)

Series Accession: GSE236137 ID: 200236137

- [Transdifferentiating alveolar macrophages characterized by Placenta-expressed transcript 1 \(Plet1\) expression](#)

82. (Submitter supplied) This experiment is performed to analyse the differential expression of genome pattern on both M1 and M2 macrophages during infection in vivo. This experiment could provide us the key genes that regulate the phenotype of macrophages and the difference in expression of pro-survival and anti-apoptotic genes during influenza virus induced acute lung injury. The animals are infected with (PR8) influenza virus and the bronchoalveolar lavage samples are collected with PBS+EDTA and stained with antibodies. [more...](#)

Organism: Mus; Mus musculus

Type: **Expression profiling by array**

Platform: GPL13912 8 Samples

Download data: [GPR](#)

Series Accession: GSE208000 ID: 200208000

- [Hyaluronic Acid Induction Promotes the Differentiation of Human Neural Crest-like Cells into Periodontal Ligament Stem-like Cells](#)
- 83.

(Submitter supplied) Periodontal ligament (PDL) stem-like cells (PDLSCs) are considered to be promising for the regeneration of periodontium because they demonstrate multipotency, high proliferative capacity, and potential to regenerate bone, cementum, and PDL tissue. However, the transplantation of autologous PDLSCs is restricted by limited availability and the need for tooth extraction to isolate these cells. PDLSCs are derived from neural crest cells (NCs) in early vertebrate development and NCs persist in adult PDL tissue. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL21185 2 Samples

Download data: [TXT](#)

Series Accession: GSE235864 ID: 200235864

- [Expression data of Tubb3+ cells from E4 chicken neural tube](#)

- 84.
- (Submitter supplied) The specification of the different neuronal subtypes is associated with a profound morphological transformation, involving processes common to most neurons and others characteristic of each neuronal subtype. To study the Tcf-dependent genes that were active during commissural neuron differentiation, we compared the genes in differentiating neurons (Tubb3+ cells) after the repression of Tcf-dependet transcription in chichen neural tube from E3 to E4, period when mostly commissural neurons are differentiating. [more...](#)

Organism: Gallus gallus

Type: **Expression profiling by array**

Platform: GPL3213 6 Samples

Download data: [CEL](#), [CHP](#)

Series Accession: GSE234518 ID: 200234518

- [Defining the Sox2-independent reprogramming steps to pluripotency](#)

- 85.
- (Submitter supplied) Several Sox family members, small molecules, and inhibitors of the TGF- β pathway can replace exogenous Sox2 during the generation of induced pluripotent stem cells (iPSCs), suggesting that SOX2 is dispensable for initiation of reprogramming. However, the time point at which the endogenous Sox2 locus is activated in these conditions was not thoroughly evaluated. To identify the Sox2-independent reprogramming steps, we excluded Sox2 from the reprogramming cocktail and used Sox2-deficient mouse embryonic fibroblasts. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6885 16 Samples

Download data: [TXT](#)

Series Accession: GSE59372 ID: 200059372

- [Exploring the functional roles of telomere maintenance 2 in the tumorigenesis of Glioblastoma multiforme and drug responsiveness to temozolomide](#)
- 86.

(Submitter supplied) Glioblastoma multiforme (GBM) is a grade IV human glioma and is the most malignant primary central nervous system tumor in adults, accounting for around 15% of intracranial neoplasms and 40–50% of all primary malignant brain tumors. However, the median survival time of GBM patients is still less than 15 months, even after treatment with surgical resection, concurrent chemoradiotherapy, and adjuvant chemotherapy with temozolomide (TMZ). [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL21282 12 Samples

Download data: [GPR](#)

Series Accession: GSE231503 ID: 200231503

- [Transcriptomic comparison of two selective retinal cell ablation paradigms in zebrafish reveals shared and cell-specific regenerative responses](#)
- 87.

(Submitter supplied) Retinal Müller glia (MG) can act as stem-like cells to generate new neurons in both zebrafish in mice. In zebrafish, retinal regeneration is innate and robust, resulting in the replacement of lost neurons and restoration of visual

function. In mice, exogenous stimulation of MG is required to reveal a dormant and, to date, limited regenerative capacity. Zebrafish studies have been key in revealing factors that promote regenerative responses in the mammalian eye. [more...](#)

Organism: Danio rerio

Type: **Expression profiling by array**

Platform: GPL1319 138 Samples

[Download data: CEL, XLSX](#)

Series Accession: GSE234646 ID: 200234646

[The active form of Mef2c promotes maturation of induced cardiomyocytes](#)

88. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus

Type: **Expression profiling by array**; Expression profiling by high throughput sequencing

Platforms: [GPL19057](#) [GPL23038](#) 22 Samples

[Download data: CEL, CHP](#)

Series Accession: GSE222870 ID: 200222870

[The active form of Mef2c promotes maturation of induced cardiomyocytes with p300 in direct cardiac](#)

89. [reprogramming](#)

(Submitter supplied) Direct cardiac reprogramming converts fibroblasts into induced cardiomyocytes (iCMs) with the minimal combination of transcription factors, Gata4 (G), Mef2c (M), and Tbx5 (T). However, the induction of functional mature iCMs is inefficient and the mechanisms remain elusive. Mef2c is a central transcription factor in direct cardiac reprogramming. We investigated the effect of Mef2c isoforms(M1, M2, M6) and transcriptional activity (M2TAD) on cardiac reprogramming on cardiac reprogramming. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: [GPL23038](#) 7 Samples

[Download data: CEL, CHP](#)

Series Accession: GSE196293 ID: 200196293

[The transcription factor Bcl6 represses active Notch signalling in fetal thymocytes](#)

90. (Submitter supplied) We used Affymetrix microarrays to understand the genome wide differences between DMSO and Bcl6 inhibitor (79-6) anti-CD3 treated Rag1-/ E17.5 thymocytes (n=2) .

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: [GPL6246](#) 6 Samples

[Download data: CEL](#)

Series Accession: GSE152577 ID: 200152577

[Prospective identification and characterization of multipotent peripheral neural stem cells out of mammalian](#)

91. [central nervous system](#)

(Submitter supplied) It has been widely accepted that mammalian neural stem cells (NSCs) only exist in central nervous system (CNS). Here, we challenge this concept and show that peripheral NSCs (pNSCs) could be isolated out of CNS from mouse embryonic limbs, postnatal tail and adult lung tissues. Derived-pNSCs express multiple NSC-specific markers, exhibit cell morphology, self-renewing capacity, genome-wide transcriptional profile, epigenetic features similar to those of brain control NSCs. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: [GPL6885](#) 12 Samples

[Download data: TXT](#)

Series Accession: GSE151649 ID: 200151649

[Expression data from human kidney organoids treated with the Hedgehog agonist SAG](#)

92.

(Submitter supplied) The kidney, similar to non-renal tissue, is adversely affected by increased Hedgehog signaling. We treated human kidney organoids with the Hedgehog activator SAG in order to study the effects of constitutive active Hedgehog signaling on human kidney development. We used microarrays to identify gene expression changes in human kidney tissue following Hedgehog activation.

Organism: Homo sapiens

Type: Expression profiling by array

Platform: GPL16686 6 Samples

Download data: CEL

Series Accession: GSE205957 ID: 200205957

[Deciphering the cardiovascular potential of human CD34+ stem cells](#)

93. (Submitter supplied) Ex vivo monitored human CD34+ stem cells (SCs) injected into myocardium scar tissue have shown real benefits for the recovery of patients with myocardial infarctions. They have been used previously in clinical trials with hopeful results and are expected to be promising for cardiac regenerative medicine following severe acute myocardial infarctions. However, some debates on their potential efficacy in cardiac regenerative therapies remain to be clarified.
[more...](#)

Organism: Homo sapiens

Type: Expression profiling by array

Platform: GPL17077 20 Samples

Download data: TXT

Series Accession: GSE221650 ID: 200221650

[Gene expression profiles of OT-1 T cells co-cultured with MHC-I Negative Tumors and Antigen Loaded](#)

94. [Macrophages](#)

(Submitter supplied) OT-1 T-cells were co-cultured either alone in T-cell media supplemented with IL-2 (50IU/mL IL-2), with OVA loaded macrophages, or with both OVA loaded macrophages and CT2A-TRP2- β 2mKO tumor cells. Cells were cultured at a 5:1 T-cell to tumor ratio, and 2:1 T-cell to macrophage ratio. After 24 h of co-culture, CD8 T-cells were FACS sorted, and RNA extracted (RNeasy Mini Kit, Qiagen). RNA was analyzed on an nCounter MAX Analysis System (Nanostring) with the PanCancer Immune profiling panel (Nanostring) according to manufacturer instructions. [more...](#)

Organism: Mus musculus

Type: Expression profiling by array

Platform: GPL25652 9 Samples

Download data: CSV, RCC

Series Accession: GSE220960 ID: 200220960

[Identification of KLF4 regulated transcriptional features in breast cancer](#)

95. (Submitter supplied) Kruppel-like factor 4 (KLF4), as a eukaryotic transcription factor, participates in the regulation of cell proliferation, differentiation, embryonic development and other important life processes. KLF4 is also closely related to the occurrence and development in variety types of tumor. To determine the functions of KLF4 in breast cancer, we over-expressed KLF4 in breast cancer LM2-4175 cells and used gene expression profiling to identify KLF4 regulated genes.

Organism: Homo sapiens

Type: Expression profiling by array

Platform: GPL570 6 Samples

Download data: CEL

Series Accession: GSE175844 ID: 200175844

[Adoptive transfer of type 2 diabetes by hematopoietic stem cells reprogrammed in utero by vitamin D deficiency](#)

96. (Submitter supplied) This study demonstrates that transplantation of fetal liver hematopoietic stem cells (FL-HSCs) from fetuses subjected to vitamin D (VD) deficiency in utero induced persistent insulin resistance to VD sufficient recipient mice. Transcriptional changes associated with intrauterine vitamin D deficiency where identified through microarray analysis of mouse BMMS from vitamin D deficient and sufficient conditions.

Organism: Mus musculus

Type: Expression profiling by array

Platform: GPL6246 10 Samples

[Download data: CEL](#)

Series Accession: GSE158763 ID: 200158763

- [Targetable programs of adult cancer are ontogenically rooted within early cell fate trajectories of human pluripotent state \[array\]](#)
- 97.

(Submitter supplied) Recognized molecular similarities between pluripotency and cancer have recently been underscored with multi-omics campaigns revealing stemness networks that are shared between human pluripotent stem cells (hPSCs) and tumors, where tumors types cluster based on tissue origins. Informed by these *in silico* studies, we now demonstrate hPSCs serve as a source of networks that define properties of adult tissue oncogenesis. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL16686 22 Samples

[Download data: CEL](#)

Series Accession: GSE133041 ID: 200133041

- [Expression data of human induced pluripotent stem cells \(hiPSCs\), human embryonic stem cells \(hESCs\) and those differentiated cells.](#)
- 98.

(Submitter supplied) We examined hiPSCs, hESCs and those differentiated cells to identify pluripotent signature genes, differentiation marker genes and relationship between expression and phenotypes. Additionally, we performed microarray experiments to examine gene expression in human tissues. This data was used for comparison with hESCs, hiPSCs and those differentiated cells. A total of 22 tissues (bone marrow, cerebellum, colon, cortex, fetal brain, heart, kidney, liver, lung, pancreas, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testes, thymus, thyroid, trachea and uterus) were examined.

Organism: Homo sapiens

Type: **Expression profiling by array**; Third-party reanalysis

Platform: GPL570 77 Samples

[Download data: CEL](#)

Series Accession: GSE39144 ID: 200039144

- [Competing endogenous RNA expression profiling in decidua after LPS treatment](#)

- 99.
- (Submitter supplied) To investigate the competing endogenous RNA expression changes in decidua under the inflammatory reaction, LPS (100 µg/kg body weight) was intraperitoneally injected into the mice at 15 days of pregnancy. Premature births has been found after approximately 48 h of treatment. When bleeding found in vagina, the decidua were selected in asepsis condition, and total RNA was isolated to analyze the expression of competing endogenous RNA compared with cesarean sections.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL28498 6 Samples

[Download data: TXT](#)

Series Accession: GSE150066 ID: 200150066

- [Differential gene expression profile analysis of parental, Cas9-p15 control, and MELK knockout cells](#)

- 100.
- (Submitter supplied) Triple-negative breast cancer (TNBC) has high relapse and metastasis rates and a high proportion of cancer stem-like cells (CSCs), which possess self-renewal and tumor initiation capacity. MELK (maternal embryonic leucine zipper kinase), a protein kinase of the Snf1/AMPK kinase family, is known to promote CSC maintenance and malignant transformation. Our study showed that MELK knockdown using siRNA or MELK inhibition using the MELK inhibitor MELK-In-17 significantly reduced invasiveness, reversed epithelial-to-mesenchymal transition (EMT), and reduced CSC self-renewal and maintenance in TNBC cells. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL17586 12 Samples

[Download data: CEL, XLSX](#)

Series Accession: GSE227774 ID: 200227774

[Gene Expression Changes after Coumestrol Stimulation of Human Trophoblast Cells](#)

101. (Submitter supplied) Coumestrol is a potent isoflavone found in spinach and soy. To examine whether consuming large amounts of coumestrol during pregnancy affects the development of the placenta, human trophoblast cells (HTR8/Svneo) were treated with vehicle or coumestrol. Upon treatment, 3,079 genes were differentially regulated.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL23159 6 Samples

Download data: CEL

Series Accession: GSE183072 ID: 200183072

[Oncofetal gene reactivation drives EZH2-mutant myeloid leukemia pathogenesis](#)

102. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus

Type: Expression profiling by high throughput sequencing; Genome binding/occupancy profiling by high throughput sequencing; **Expression profiling by array**

Platforms: GPL23038 GPL21103 GPL24247 59 Samples

Download data: BW, CEL

Series Accession: GSE173497 ID: 200173497

[Expression data of freshly isolated and sorted HSC populations from murine fetal liver or adult bone marrow](#)

103. [\[array\]](#)

(Submitter supplied) We isolated murine fetal liver and murine adult bone marrow and FACS sorted LT-HSCs, ST-HSCs and MPPs. We used global expression analysis by microarray to compare regulated genesets in different HSC populations in fetal and adult.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL23038 18 Samples

Download data: CEL

Series Accession: GSE173158 ID: 200173158

[Gene Expression Changes in Soleus Muscle in Mice after Pericytes-Deletion](#)

104. (Submitter supplied) Pericytes(PCs) are mural cells embedded in the capillary basal lamina. Some PC populations exhibit multipotency, similar to mesenchymal stem cells. Here, the process of adaptation was investigated by determining changes in transcript profiles when NG2 positive PCs were deleted. PC-deletion was induced by using NG2CreER(+/-)/diphtheria toxin fragment A(DTA) transgenic mice. Cre recombinase was induced by tamoxifen(Tam) treatment(intraperitoneally, 100mg/kg body weight per day) for 5days. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL22438 1 Sample

Download data: TXT

Series Accession: GSE229364 ID: 200229364

[Time-course transcriptome of developing brown adipose tissue](#)

105. (Submitter supplied) Transcriptome of brown adipose tissues from E18, 4 and 10 days old, and 4 and 8 weeks old C57BL6/N mice were examined to describe the development of the tissue.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL13912 16 Samples

Download data: TXT

Series Accession: GSE221113 ID: 200221113

[A cardiac developmental defect prevents thyroid hormone induced tachycardia in the syndrome of resistance to](#)

106. [thyroid hormone alpha](#)

(Submitter supplied) Purpose: the objective of this study was to determine cardiac gene expression profile in the mice heart of mutated thyroid receptor alpha 1 (TR α 1R384C+/m) male offspring of control dams as well as of dams treated with 3,3',5-triiodo-L-thyronine (T3) from embryonic day 12.5 to 18.5

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL23038 24 Samples

Download data: CEL, CHP

Series Accession: GSE227847 ID: 200227847

[Development of an osteosarcoma model with MYCN amplification and TP53 mutation in hiPS cell-derived](#)

107. [neural crest cells](#)

(Submitter supplied) Osteosarcoma, derived from mesenchymal stem cells or osteoblasts, is the most common malignant bone tumor and the highly metastatic malignant phenotypes often with poor prognosis are related to modulation of TP53- and cell cycle-related pathways. MYC, which regulates the transcription of cell-cycle modulating genes, e.g. CCNE1, is used as a representative prognostic marker. MYCN, a member of MYC oncogene family, is highly expressed in a subset of osteosarcoma, however, its roles in osteosarcoma have not been elucidated extensively. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL17077 12 Samples

Download data: TXT

Series Accession: GSE201511 ID: 200201511

[Different expression profiles of mRNAs in preeclampsia and normal placenta \(mRNA\)](#)

108. (Submitter supplied) Preeclampsia (PE), which results from abnormal placentation, acts as a primary cause of maternal and neonatal morbidity and mortality. However, the cause of abnormal development of placenta remain poorly understood. Recently, it has been proposed that the genes that are differentially expressed between PE and normal placenta tissues are associated with PE pathogenesis. To further elucidate the pathogenesis, we conducted transcriptional profiling of mRNA between PE and normal placenta tissues.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL21282 6 Samples

Download data: XLS

Series Accession: GSE149812 ID: 200149812

[IL15 Deficiency in Rats](#)

109. (Submitter supplied) NK cells are a major immune cell in the uterus during pregnancy. IL15 is required for the maturation of these cells, therefore a mutation in the IL15 gene results in a lack of NK cells. In this study, implantation sites were collected from gestational day 9.5 pregnant IL15 deficient or WT Sprague-Dawley Holtzman rats. RNA was collected, and a Clariom S microarray was performed to elucidate differences in gene expression at the developing placenta and uterus between mutants and WT dams.

Organism: Rattus norvegicus; Rattus

Type: **Expression profiling by array**

Platform: GPL23040 6 Samples

Download data: CEL

Series Accession: GSE216395 ID: 200216395

[Genome wide expression analysis of Caenorhabditis elegans mdt-15\(tm2182\) null mutants \(vs. WT N2 worms\)](#)

110. (Submitter supplied) MDT-15/MED15 is a subunit of the Mediator complex and is known to regulate specific gene programs. We had previously profiled gene expression in C. elegans following mdt-15 depletion by RNAi. To complement this, we also performed gene expression profiling of the mdt-15(tm2182) hypomorphic mutant to identify MDT-15 regulated genes and developmental and/or physiological gene programs.

Organism: Caenorhabditis elegans

Type: **Expression profiling by array**

Platform: GPL11346 8 Samples

[Download data: TXT](#)

Series Accession: GSE220955 ID: 200220955

 [Arabidopsis thaliana seedlings: Control vs Erwinia amylovora microbial Volatile Organic Compounds](#)

111. (Submitter supplied) Arabidopsis seedling were exposed in co-culture to E. amylovora mVOC and data show that mVOCs promote plant growth and early responses

Organism: Arabidopsis thaliana

Type: **Expression profiling by array**

Platform: GPL9020 4 Samples

[Download data: TXT](#)

Series Accession: GSE223760 ID: 200223760

 [Differential Effects of Estradiol on Progenitor -Smooth Muscle Cell and -Endothelial Cell Growth and Gene](#)

112. [Response](#).

(Submitter supplied) Coronary artery disease is the leading cause of mortality in women. Abnormal growth of smooth muscle cells and endothelial damage contributes to the thickening of the blood vessels and vascular occlusion. Estradiol prevents vascular remodeling by promoting EC growth and inhibiting SMC growth. Recent studies suggest that circulating (bone marrow derived) progenitor cells also contribute to the vascular remodeling process. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL16329 12 Samples

[Download data: CEL](#)

Series Accession: GSE171709 ID: 200171709

 [Gene expression data from 3D spheroids of human amniotic epithelial stem cell \(hAESC\) treated with 20 uM](#)

113. [Carnosic Acid](#)

(Submitter supplied) Gene expression profiling reveals multiple tissue-specific functionality of carnosic acid in a stem-based tool. We evaluated the effects of carnosic acid on human amniotic epithelial stem cells. We performed an untargeted whole-genome transcriptome analysis to explore functionality of carnosic acid in a stem cell-based tool.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL23159 4 Samples

[Download data: CEL, CHP](#)

Series Accession: GSE228408 ID: 200228408

 [Alteration of m6A epitranscriptome profile in the bleomycin-treated mouse model of scleroderma](#)

114. (Submitter supplied) The exploration of m6A methylation in scleroderma remains in its infancy. We aimed to reveal the landscape of m6A methylated long noncoding RNAs (lncRNAs) and small RNAs in scleroderma.

Organism: Mus musculus

Type: **Expression profiling by array**; Non-coding RNA profiling by array

Platform: GPL25915 16 Samples

[Download data: TXT, XLSX](#)

Series Accession: GSE226331 ID: 200226331

 [The steroid hormone estriol \(E3\) regulates epigenetic programming of fetal mouse brain and reproductive tract](#)

115. [\[Affymetrix\]](#)

(Submitter supplied) We identify an unexpected functional role for E3 in fetal reproductive system and brain. We further identify a novel mechanism of estrogen action, through recruitment of epigenetic modifiers to estrogen receptors and their target genes, which doesn't correlate with the traditional view of estrogen potency.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL20775 8 Samples

[Download data: CEL, CHP](#)

Series Accession: GSE199174 ID: 200199174

 [Expression data from a human primary syncytiotrophoblast model in response to double-stranded RNA](#)

116. (Submitter supplied) Differentiated primary human cytotrophoblasts were stimulated with synthetic double-stranded RNA, poly I:C. Gene expression was profiled using Agilent microarray.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL21185 2 Samples

Download data: [TXT](#)

Series Accession: GSE224785 ID: 200224785

 [DNA Methylation Explains a Subset of Placental Gene Expression Differences Based on Ancestry and altitude](#)

117. (Submitter supplied) Investigation of how gene expression and epigenetics contribute to conservation of birth weight at high altitudes by examining mRNA and DNA methylation differences between placentas of indigenous Andeans and placentas of European descent residing at high and low altitude

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL10558 45 Samples

Download data: [IDAT, TXT](#)

Series Accession: GSE100988 ID: 200100988

 [Transcripts identified by microarray analysis that were deregulated in GFP positive cells of E11.5](#)

118. [Tbx18\(GFP/GFP\) and Tbx18\(cre/+\);HPRT\(Tbx18VP16\) kidney rudiments.](#)

(Submitter supplied) Evaluation of the transcriptional changes in E11.5 ureter mesenchyme cells upon loss of Tbx18 or overexpression of an activator version of Tbx18, respectively.

Organism: Mus musculus

Type: **Expression profiling by array**

Platforms: GPL24228 GPL19795 8 Samples

Download data: [TXT](#)

Series Accession: GSE198129 ID: 200198129

 [Expression data from mothers, placentas, and newborns in the Democratic Republic of Congo](#)

119. (Submitter supplied) Maternal stress has long been associated with lower birthweight but mechanisms remain elusive. This study explored how maternal stress may impact changes in gene expression within a cohort of mother-placenta-newborn triads in the eastern Democratic Republic of Congo. We used microarrays to detail the global programme of gene expression underlying the impact of maternal stress on newborn birthweight and identified that global placental gene expression may partially mediate the negative impact of maternal war stress on newborn birthweight.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL23126 279 Samples

Download data: [CEL, CHP, CSV](#)

Series Accession: GSE226993 ID: 200226993

 [Skeletal muscle mitochondrial dysfunction in spinal muscular atrophy](#)

120. (Submitter supplied) The survival motor neuron 1 (SMN1) gene is the causative gene for the spinal muscular atrophy (SMA) disease, the first genetic cause of infant mortality. It affects primarily motor neurons which are the targets of the approved genetic therapies aimed to compensate for the loss of SMN1. However, the limitations of these therapies are now evident since they are not cures, and alternative strategies need to be investigated. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL10787 27 Samples

Download data: [TXT](#)

Series Accession: GSE207890 ID: 200207890

[Hematopoietic stem and progenitor cell formation in a BCR-ABL inducible expression embryonic stem cell](#)

121. [model](#)

(Submitter supplied) Generating hematopoietic stem cells from pluripotent stem cells (PSC) has been a long lasting quest in the field of hematology. Previous studies suggested that the enforced expression of BCR-ABL, the oncogenic driver of chronic myeloid leukemia (CML), in hematopoietic cells derived from mouse embryonic stem cells (ESCs) is sufficient to confer on them in vivo long-term repopulating potential. To uncover more precisely the events regulated by BCR-ABL expression during the course of ESC differentiation, we engineered a doxycycline inducible system to modulate BCR-ABL expression.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL16570 12 Samples

Download data: CEL

Series Accession: GSE198018 ID: 200198018

[ESRG, a novel target of OCT4, maintains self-renewal and pluripotency of human pluripotent stem cells in](#)

122. [collaboration with MCM2](#)

(Submitter supplied) Long non-coding RNA ESRG was first identified in our previous study, but its physiological function, regulatory and action mechanisms in human pluripotent stem cells (hPSCs) remain largely unexplored. Here, we found that ESRG is specifically and highly expressed in hPSCs, and its transcription is directly regulated by OCT4, suggesting that ESRG may be an integral component of the core regulatory circuit regulating the pluripotent state of hPSCs. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL10558 2 Samples

Download data: IDAT, TXT

Series Accession: GSE190957 ID: 200190957

[Genome activity during the emergence of mouse embryonic totipotency](#)

123. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL7202 55 Samples

Download data: GPR

Series Accession: GSE64650 ID: 200064650

[Genome activity during the emergence of mouse embryonic totipotency \(time course\)](#)

124. (Submitter supplied) Fertilization transforms sperm and egg into a totipotent **embryo** but the underlying mechanisms are unknown. We here report that gene expression initiates during the gamete-to-**embryo** transition in mouse embryos. Meiotic exit induced by sperm entry enhances a transcriptionally-permissive epigenetic landscape. Time-course analysis of single embryos revealed a succession of genome-wide transcription 'ripples' initiating within 2 hours. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL7202 24 Samples

Download data: GPR

Series Accession: GSE64649 ID: 200064649

[Genome activity during the emergence of mouse embryonic totipotency \(morpholino\)](#)

125. (Submitter supplied) Fertilization transforms sperm and egg into a totipotent **embryo** but the underlying mechanisms are unknown. We here report that gene expression initiates during the gamete-to-**embryo** transition in mouse embryos. Meiotic exit induced by sperm entry enhances a transcriptionally-permissive epigenetic landscape. Time-course analysis of single embryos revealed a succession of genome-wide transcription 'ripples' initiating within 2 hours. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL7202 31 Samples

[Download data: GPR](#)

Series Accession: GSE64648 ID: 200064648

[Expression data in Heart Tissue associated with Tetralogy of Fallot](#)

126. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Homo sapiens

Type: **Expression profiling by array**; Genome binding/occupancy profiling by high throughput sequencing

Platforms: GPL20115 GPL28148 GPL20712 27 Samples

[Download data: TXT](#)

Series Accession: GSE146220 ID: 200146220

[lncRNA and mRNA expression data in Heart Tissue associated with Tetralogy of Fallot](#)

127. (Submitter supplied) The aim of the study is to identify the global messenger RNA (mRNA) and long noncoding RNA (lncRNA) expression profiling in tissue samples of the right ventricular outflow tract of 5 TOF children with no other intracardiac and extracardiac malformations and 5 normal fetuses.

Organism: Homo sapiens

Type: **Expression profiling by array**; Non-coding RNA profiling by array

Platform: GPL20115 9 Samples

[Download data: TXT](#)

Series Accession: GSE146218 ID: 200146218

[Expression data of GFP-GnRH neurons during rat embryonic development](#)

128. (Submitter supplied) During development, gonadotropin releasing hormone (GnRH) neurons are born in the nasal placode and migrate to the hypothalamus, where they position to regulate sexual reproduction. Defective GnRH neuron development may lead to GnRH deficiency (GD) which is characterized by absent or delayed puberty. Several GD causative genes have been identified so far, but half of the cases are still idiopathic. The identification of candidate genes is also hampered by the difficulty in isolating and studying GnRH neurons, which are small in number, develop in a short developmental window and lack specific markers. Gene expression profiles of GnRH neurons are lacking, as obtaining primary GnRH neurons is challenging and no reports on gene expression profiles during the whole developmental process of GnRH neurons are available. In this work, we obtained the transcriptomic profile of sorted GFP-positive and unsorted GFP-negative cells from Gnrh1-GFP rat embryos at three developmental stages, representing the initiation (embryonic day (E)14), the peak (E17) and the completion of GnRH neuronal migration (E20).

Organism: Rattus norvegicus

Type: **Expression profiling by array**

Platform: GPL6247 6 Samples

[Download data: CEL](#)

Series Accession: GSE174896 ID: 200174896

[Monocyte signature as a predictor of chronic lung disease in the preterm infant](#)

129. (Submitter supplied) The early changes in innate immunity associated with BPD (bronchopulmonary dysplasia) development are incompletely understood. Transcriptome analyses from cord blood of preterm infants indicate a monocyte-centered, profibrotic signature at birth confirming TNFalpha as a critical upstream regulator for the development of BPD.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL33162 61 Samples

[Download data: TXT](#)

Series Accession: GSE225881 ID: 200225881

[Effect of Nrf2 deletion on developmental lung transcriptomics in mice](#)

130. (Submitter supplied) Background: NRF2 is an essential cytoprotective transcription factor inducing antioxidant response element (ARE)-bearing genes. However, association of NRF2 with lung development has not been examined. Human lungs are not fully developed until 2-3 years of age and they are fully matured at about 8 years. Murine lungs at birth are immature (at saccular stage of lung development) and have been used to study developmental lung disorders. [more...](#)

Organism: Mus musculus
Type: **Expression profiling by array**
Platform: GPL1261 66 Samples
Download data: CEL, CHP
Series Accession: GSE197587 ID: 200197587

[Expression data from chordoma and notochord \(microarray\)](#)

131. (Submitter supplied) Chordoma is a rare malignant tumor thought to originate from embryonic notochord. However, no molecular comparison of chordoma and notochord has been performed to date, leaving the identities of dysregulated pathways unclear. Absence of a molecular description of a control tissue clouds our understanding of chordoma. Thus, we conducted an unbiased comparison of chordoma and notochord using gene expression profiling to clarify chordoma's tissue of origin and identify novel drug targets

Organism: Homo sapiens
Type: **Expression profiling by array**
Platform: GPL570 11 Samples
Download data: CEL
Series Accession: GSE224776 ID: 200224776

[Activin pathway gene expression atlas in rainbow trout](#)

132. (Submitter supplied) The genome of many plant and animal species are heavily influenced by ancestral whole genome duplication (WGD) events. These events transform the regulation and function of gene networks, yet the evolutionary forces at work on duplicated genomes are not fully understood. Genes involved in cell surface signaling pathways are commonly retained following WGD. To understand the mechanisms driving functional evolution of duplicated cell signaling pathways, we performed the activin receptor signaling pathway in rainbow trout (RBT). [more...](#)

Organism: Oncorhynchus mykiss
Type: **Expression profiling by array**
Platform: GPL33095 70 Samples
Download data: RCC, XLSX
Series Accession: GSE224617 ID: 200224617

[Expression data from chordoma and notochord](#)

133. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Homo sapiens
Type: Expression profiling by high throughput sequencing; **Expression profiling by array**
Platforms: GPL9115 GPL570 22 Samples
Download data: CEL, TAB
Series Accession: GSE205458 ID: 200205458

[Round or columnar and hypertrophic chondrocytes of Tric-b-KO mice](#)

134. (Submitter supplied) To survey altered gene expression in round, columnar and hypertrophic chondrocytes of Tric-b-KO mice, total RNA preparations from round chondrocytes and columnar/hypertrophic chondrocytes were subjected to gene microarray analysis. Results provide insight into the transcriptional profile of each Tric-b-KO chondrocyte and provide further insight into their functions.

Organism: Mus musculus
Type: **Expression profiling by array**
Platform: GPL1261 2 Samples
Download data: CEL, CHP
Series Accession: GSE223776 ID: 200223776

[Expression data from human fetal and adult neutrophils](#)

135. (Submitter supplied) Fetal neutrophils from early embryonic stages display a reduced capacity to react to inflammatory stimuli, therefore this study aimed to investigate the underlying molecular mechanisms regulating fetal neutrophil function during ontogeny. Whole transcriptome analysis of human fetal cord blood-derived neutrophils from premature (<37 weeks of

gestation) and mature (>37 weeks of gestation) infants, comparing their gene expression profiles to neutrophils from healthy adult donors

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL570 9 Samples

Download data: CEL

Series Accession: GSE222156 ID: 200222156

- [The impact of Mmu17 non-Hsa21 orthologous genes in the Ts65Dn mouse model of Down syndrome: the “gold standard” refuted](#)
136.

(Submitter supplied) Background: Despite successful preclinical treatment studies to improve neurocognition in the Ts65Dn mouse model of Down syndrome (DS), translation to humans has failed. This raises questions about the appropriateness of the Ts65Dn mouse as the “gold standard” for DS research. Here we used the novel Ts66Yah mouse that carries both an extra chromosome and the identical segmental Mmu16 trisomy as Ts65Dn without the Mmu17 non-orthologous region.

[more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL24242 89 Samples

Download data: CEL

Series Accession: GSE222355 ID: 200222355

- [Genomic Glucocorticoid Action in Embryonic Mouse Neural Stem Cells](#)

137. (Submitter supplied) The goal of this study was to measure genome-wide expression in primary mouse neural stem/progenitor cell (NSPC) cultures to determine if SOX2 ablation alters the transcriptomic response which occurs following glucocorticoid receptor activation by the synthetic glucocorticoid, Dexamethasone. Neurosphere cultures of SOX2 knock out (KO) NSPCs and control non-deleted wild-type (WT) NSPCs (C57BL/6) derived from the fetal telencephalon were established at postnatal day zero (P0).

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL23038 26 Samples

Download data: CEL

Series Accession: GSE222392 ID: 200222392

- [Reprogramming of fish somatic cells for nuclear transfer is primed by Xenopus egg extract](#)

138. (Submitter supplied) Somatic cell reprogramming in vitro prior to nuclear transfer is one strategy expected to improve clone survival during development. In this study, we investigated the reprogramming extent of fish fin somatic cells after in vitro exposure to Xenopus egg extract and subsequent culture. Using a cDNA microarray approach, we observed drastic changes in the gene expression profile of the treated cells. Several actors of the TGFbeta and Wnt/beta-catenin signaling pathways, as well as some mesenchymal markers, were inhibited in treated cells, while several epithelial markers were upregulated. [more...](#)

Organism: Carassius auratus

Type: **Expression profiling by array**

Platform: GPL32340 12 Samples

Download data: TXT, XLSX

Series Accession: GSE205854 ID: 200205854

- [The impact of hyperglycemia upon BeWo trophoblast cell metabolic function: A multi-OMICS and functional metabolic analysis](#)
139.

(Submitter supplied) Pre-existing and gestationally-developed diabetes mellitus during pregnancy have been linked to impaired metabolic function in the villous trophoblast layer of the placenta. These metabolic impairments have been thought to mediate an increased risk of early life metabolic disease development in the exposed offspring. Previous research using the BeWo trophoblast cell line has suggested that independently, hyperglycemia is an important modulator of placental metabolic function in diabetic pregnancies. [more...](#)

Organism: Homo sapiens
Type: **Expression profiling by array**
Platform: GPL23159 10 Samples
Download data: CEL, CHP
Series Accession: GSE190025 ID: 200190025

[Expression analysis of Chd7 in mouse hematopoietic stem and progenitor cells \[microarray\]](#)

140. (Submitter supplied) Hematopoietic stem and progenitor cell (HSPC) formation and lineage differentiation involve gene expression programs orchestrated by transcription factors and epigenetic regulators. Knockdown of the chromatin remodeler chromodomain-helicase-DNA-binding protein 7 (CHD7) expanded phenotypic HSPCs, erythroid, and myeloid lineages in zebrafish and mouse embryos. CHD7 acts to suppress hematopoietic differentiation in a cell autonomous manner in the **embryo** and adult. [more...](#)

Organism: Mus musculus
Type: **Expression profiling by array**
Platform: GPL16570 8 Samples
Download data: CEL
Series Accession: GSE84127 ID: 200084127

[Non-conventional β-catenin activity is essential for Notch1-driven T-cell leukemia](#)

141. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Homo sapiens; Mus musculus
Type: **Expression profiling by array**; Genome binding/occupancy profiling by high throughput sequencing
Platforms: GPL6246 GPL11154 GPL16570 26 Samples
Download data: BEDGRAPH, CEL
Series Accession: GSE69158 ID: 200069158

[Gene expression analyses of E14.5 fetal liver Lin-Sca1+ckit+ \(LSK\) cells from wild-type, β-Catenin-KO, N1IC+ and N1IC+β-Catenin-KO embryos.](#)

(Submitter supplied) Notch activation is instrumental in the development of most T-cell acute lymphoblastic leukemia (T-ALL) cases, yet Notch mutations alone are not sufficient to recapitulate the full human disease in animal models. Using multiple *in vivo* and *in vitro* T-ALL models we here demonstrate that β-Catenin is essential for Notch-driven T-cell leukemic initiation. Transcriptome analyses of leukemic initiating cells revealed a switch in β-Catenin activity that was Notch-context dependent. [more...](#)

Organism: Mus musculus
Type: **Expression profiling by array**
Platform: GPL16570 12 Samples
Download data: CEL
Series Accession: GSE69154 ID: 200069154

[Phenological transcriptomic profile of double-crested cormorants during embryonic development](#)

143. (Submitter supplied) In this study, we tracked the phenology of the transcriptome during double-crested cormorant (*Nannopterum auritum*) embryogenesis. Fresh eggs were collected from a reference site and artificially incubated from collection until four days prior to hatching. Embryos were periodically sampled throughout incubation for a total of seven time points. A custom microarray was designed for cormorants (over 14,000 probes) and used for transcriptome analysis in whole body (days 5, 8) and liver tissue (days 12, 14, 16, 20, 24). [more...](#)

Organism: Phalacrocorax auritus
Type: **Expression profiling by array**
Platform: GPL32286 32 Samples
Download data: TXT
Series Accession: GSE204670 ID: 200204670

[A member of transcription/export complex \(TREX\), THOC5 controls elongation rate by recruiting CDK12.](#)

- 144.

(Submitter supplied) THOC5, a member of the THO complex that is a subcomplex of Transcription/export complex (TREX) 1, is essential for 3' processing of slow kinetics IEGs, and for export of only a subset of genes. Applying nanopore mRNA-sequence technology, we show here that upon depletion of THOC5, 50% of mRNAs showed alteration of 3' end cleavage sites. Moreover, polymerase-II (Pol II)-CHIP-sequencing data reveals that upon depletion of THOC5 Pol II density was increased at gene body and 3'UTR. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL29692](#) 2 Samples

Download data: [TXT](#)

Series Accession: GSE166115 ID: 200166115

[Profiling ERRb-target genes in mouse ES cells](#)

145. (Submitter supplied) We found ERRb activates the transcription through two molecular pathways, which are interaction to AF2-region binding PGC-1a/cofactors and general transcription factor TFIID. To analyze the significance of these pathways in cells, we first identified ERRb-target genes in ES cells. Estrogen-related receptors (ERR α /b/g) are orphan nuclear receptors that function in a number of energy-demanding physiological processes, as well as in development and stem cell maintenance, but mechanisms underlying target gene activation are largely unknown. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: [GPL16570](#) 12 Samples

Download data: [CEL](#), [CHP](#)

Series Accession: GSE164633 ID: 200164633

[Modeling the initiation of Ewing sarcoma tumorigenesis in human Embryonic Stem Cells](#)

146. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Homo sapiens

Type: **Expression profiling by array**; Expression profiling by high throughput sequencing

Platforms: [GPL16791](#) [GPL16686](#) 16 Samples

Download data: [CEL](#)

Series Accession: GSE141889 ID: 200141889

[Modeling the initiation of Ewing sarcoma tumorigenesis in human Embryonic Stem Cells \[expression array\]](#)

147. (Submitter supplied) Ewing sarcoma family of tumors (ESFT) is a uniquely human, highly aggressive bone and soft tissue malignancy peaking during adolescence characterized by EWSR1/ETS rearrangements. EWSR1/FLI1 expression is only tolerated in embryonic and mesenchymal stem cells (hESC and hMSC, respectively) that, although acquire ESFT transcriptional signatures, are devoid of tumorigenic potential. Here we report that ectopic EWSR1/FLI1 expression in hESC allows *in vivo* differentiation towards the three germ layers. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL16686](#) 10 Samples

Download data: [CEL](#)

Series Accession: GSE140328 ID: 200140328

[Comparative gene expression in synergid cells and antipodal cells at anthesis](#)

148. (Submitter supplied) Synergid cells represent the receptor cell type of angiosperm gametophytes that attract and receive the male pollen tube and are implicated in the transfer of the sperm cells to the target egg and central cells prior to double fertilization. The antipodals represent an accessory cell type that typically degenerates after fertilization; in rice it may initially have a short-lived nutritional role prior to endosperm establishment. [more...](#)

Organism: Oryza sativa; Oryza sativa Japonica Group

Type: **Expression profiling by array**

Platform: [GPL2025](#) 6 Samples

Download data: [CEL](#)

Series Accession: GSE56108 ID: 200056108

[Comparative gene expression in mature egg cell, fertilized egg cell \(1-1.5 hap\) and fertilized zygote \(2.5-3 hap\)](#)

149. (Submitter supplied) Egg cells represent the female partner that fuses with the sperm cell during fertilization in all multicellular eukaryotic organisms—and, in flowering plants, is a founder of the **embryo**. We examined the transcriptome of *Oryza sativa* ssp. *japonica* (cv Katy) using the Affymetrix 57K rice genome GeneChip to provide an overview of genes activated in the maternal gamete, transcripts transmitted by the paternal genome, and changes in transcript up- and down-regulation during fertilization. [more...](#)

Organism: *Oryza sativa* Japonica Group; *Oryza sativa*

Type: **Expression profiling by array**

Platform: GPL2025 9 Samples

Download data: CEL

Series Accession: GSE27400 ID: 200027400

[The transcriptional signature for Hepatocyte Growth Factor-driven invasive growth predicts poor prognosis of human hepatocellular carcinoma.](#)

(Submitter supplied) During embryogenesis, Hepatocyte Growth Factor (HGF) elicits a distinctive morphogenetic program, the invasive growth, by the activation of MET, whose aberrant activation in cancer drives metastatic progression. Aim of this work is to define and characterize the transcriptional signature of invasive growth, and to verify its activation in human cancers. Global expression profiling was carried out on mouse liver stem/progenitor cells (MLP-29) stimulated for different times, one, six and twenty-four hours, in vitro with HGF to define the invasive growth signature. [more...](#)

Organism: *Mus musculus*

Type: **Expression profiling by array**

Platform: GPL6885 8 Samples

Download data: TXT

Series Accession: GSE43393 ID: 200043393

[Gene expression analysis of control and Dnd1-cKO germ cells at E12.5 and E13.5.](#)

151. (Submitter supplied) The present investigation was to identify transcriptomic changes of control and Dnd1-cKO PGCs at E12.5 and E13.5 by microarray comparison. We identified 1470 upregulated and 924 downregulated genes in Dnd1-cKO PGCs.

Organism: *Mus musculus*

Type: **Expression profiling by array**

Platform: GPL21163 12 Samples

Download data: CSV, TXT

Series Accession: GSE218744 ID: 200218744

[Fetal and maternal liver expression post gestational exposure to perfluorooctanoic acid \(PFOA\) or hexafluoropropylene oxide-dimer acid \(HFPO-DA or GenX\) in CD-1 mice](#)

(Submitter supplied) Multiple per- and polyfluoroalkyl substances (PFAS) have been associated with adverse liver outcomes in adult humans and toxicological models, but effects on the developing liver or biologic pathways involved are not known. We performed whole-transcriptome gene expression analysis to investigate the molecular mechanisms of liver toxicity in the dam and female fetuses after exposure to two different PFAS, perfluorooctanoic acid (PFOA) and its replacement, hexafluoropropylene oxide-dimer acid (HFPO-DA, commonly referred to as GenX).

Organism: *Mus musculus*

Type: **Expression profiling by array**

Platform: GPL20775 50 Samples

Download data: CEL

Series Accession: GSE199233 ID: 200199233

[Zygotic genome activation by the totipotency pioneer factor Nr5a2](#)

153. (Submitter supplied) Life begins with a switch in genetic control from the maternal to the embryonic genome during zygotic genome activation (ZGA). Despite its importance, the essential regulators of ZGA remain largely unknown in mammals. Based on de novo motif searches, we identified the orphan nuclear receptor Nr5a2 as a key activator of major ZGA in mouse 2-cell embryos. Nr5a2 is required for progression beyond the 2-cell stage. [more...](#)

Organism: Mus musculus
 Type: **Expression profiling by array**
 Platform: GPL19057 398 Samples
[Download data](#)
 Series Accession: GSE178661 ID: 200178661

[Lymphatic endothelial cell identity is controlled by a GATA2 bound enhancer](#)

154. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus
 Type: Expression profiling by high throughput sequencing; **Expression profiling by array**
 Platforms: [GPL19057](#) [GPL6246](#) 22 Samples
[Download data: CEL, TSV](#)
 Series Accession: GSE184046 ID: 200184046

[Lymphatic endothelial cell identity is controlled by a GATA2 bound enhancer \(Microarray\)](#)

155. (Submitter supplied) This study investigates the transcriptome of primary dermal lymphatic endothelial cells compared with blood vascular endothelial cells using samples isolated from wildtype embryos at defined points (E14.5, E16.5 and E18.5) during mouse embryonic development.

Organism: Mus musculus
 Type: **Expression profiling by array**
 Platform: [GPL6246](#) 18 Samples
[Download data: CEL](#)
 Series Accession: GSE184045 ID: 200184045

[A clinical-grade HLA haplobank of human induced pluripotent stem cells derived from Japanese donors](#)

156. (Submitter supplied) We constructed a clinical-grade haplobank of 27 induced pluripotent stem cells (iPSCs) lines prepared in accordance with good manufacturing practice regulations from seven donors who were homozygous for one of the four most frequent human leukocyte antigen (HLA)-haplotypes in Japan. The haplobank could provide HLA-matched iPSCs lines to ~40% of the Japanese population. Since the first release in 2015, these iPSC lines have been used in more than 12 clinical studies. [more...](#)

Organism: Homo sapiens
 Type: **Expression profiling by array**
 Platforms: [GPL14550](#) [GPL32205](#) 391 Samples
[Download data: TXT](#)
 Series Accession: GSE201468 ID: 200201468

[Gene expression profile of s-spheroids and t-spheroids differentiated from iPS cells](#)

157. (Submitter supplied) For definitive endoderm differentiation, iPS cells (day0) were treated with 100 ng/ml-1 activin A and 3 μ M CHIR99021 for 1 day and 100 ng/ml-1 activin A for the following two days. Definitive endoderm was subsequently treated with 3 μ M CHIR99021 and 500ng/ml-1 FGF4 for mid/hindgut differentiation. Mid/hindgut floating spheroids (fl; t-Spheroids) were collected from culture medium from day6 to day 8. On day6, mid/hindgut cells were dissociated into single cells and seeded onto EZSPHERE plate to generate suspension spheroids(EZ; s-Spheroids). [more...](#)

Organism: Homo sapiens
 Type: **Expression profiling by array**
 Platform: [GPL22439](#) 12 Samples
[Download data: TXT](#)
 Series Accession: GSE182230 ID: 200182230

[Single cell expression data from ICM cells of mouse blastocysts](#)

158. (Submitter supplied) Transcriptional reactivation of the paternal X chromosome occurs in specific cells of the mouse blastocyst between E(mbryonic day)3.5 and E4.5 during pre- to peri-implantation development. While the trophectoderm (TE) and the primitive endoderm (PE) maintain Xist RNA expression and thereby imprinted silencing of genes on the Xp, the epiblast (EPI) cells within the inner cell mass (ICM) gradually downregulate Xist and undergo XCR. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL1261 14 Samples

Download data: CEL, XLSX

Series Accession: GSE208430 ID: 200208430

[Integrated Expression Profiling of MicroRNAs and Messenger RNAs in the Developing Neural Tube](#)

159. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus; synthetic construct

Type: **Expression profiling by array**; Non-coding RNA profiling by array

Platforms: GPL1261 GPL14613 24 Samples

Download data: CEL, CHP

Series Accession: GSE140777 ID: 200140777

[Expression data \(messenger RNA\) from developing Neural Tubes of mouse embryos](#)

160. (Submitter supplied) Morphogenesis of the mammalian neural tube (NT) is reliant on precise, spatio-temporal expression of numerous genes and coordinated interaction of signal transduction and gene regulatory networks, disruption of which may contribute to the etiology of neural tube defects (NTDs). MicroRNAs (miRNAs) as well as their downstream messenger RNA (mRNA) targets are key modulators of cell and tissue differentiation. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL1261 12 Samples

Download data: CEL, CHP

Series Accession: GSE140775 ID: 200140775

[Transcripts identified by microarray analysis that were deregulated in E18.5 Sox2\(creERT2\);Tbx2\(f/f\) \(Sox2-](#)

161. [Tbx2LOF\) organ of Corti.](#)

(Submitter supplied) Evaluation of transcriptional changes in the E18.5 organ of Corti upon tamoxifen-induced loss of Tbx2.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL27545 4 Samples

Download data: TXT

Series Accession: GSE180501 ID: 200180501

[Transcripts identified by microarray analysis that were deregulated in E14.5 Sox2\(creERT2\);Tbx2\(f/f\) \(Sox2-](#)

162. [Tbx2LOF\) cochlear duct.](#)

(Submitter supplied) Evaluation of transcriptional changes in the E14.5 cochlear duct epithelium upon tamoxifen-induced loss of Tbx2 in prosensory cells.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL27545 4 Samples

Download data: TXT

Series Accession: GSE180500 ID: 200180500

[Loss of GM-CSF-dependent instruction of alveolar macrophages in COVID-19 provides a rationale for inhaled](#)

163. [GM-CSF treatment](#)

(Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Homo sapiens; Mus musculus; Mus

Type: Expression profiling by high throughput sequencing; **Expression profiling by array**

Platforms: GPL6246 GPL24676 46 Samples

Download data: CEL, H5

Series Accession: GSE216705 ID: 200216705

[Loss of evolutionary conserved GM-CSF-dependent signature in pulmonary macrophages in COVID-19](#)164. [provides a rationale for inhaled GM-CSF treatment \(microarray\)](#)

(Submitter supplied) Alveolar GM-CSF is required for monocytes to differentiate into alveolar macrophages (AM) that control alveolar homeostasis and dampen inflammation. By mapping cross-species AM development stages to clinical lung samples, we discovered that COVID-19 is marked by defective GM-CSF-dependent AM instruction and accumulation of proinflammatory macrophages. In a multi-center, open-label, randomized, controlled trial in 81 non-ventilated COVID-19 patients with respiratory failure, we found that inhalation of rhu-GM-CSF did not improve mean oxygenation parameters compared with standard treatment. [more...](#)

Organism: Mus; Mus musculus

Type: **Expression profiling by array**

Platform: GPL6246 27 Samples

Download data: CEL, TXT

Series Accession: GSE216701 ID: 200216701

 [Expression data from mouse embryonic fibroblasts](#)

165. (Submitter supplied) We use microarray to measure the global gene expression of mouse embryonic fibroblasts cells

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6246 10 Samples

Download data: TXT

Series Accession: GSE185370 ID: 200185370

 [An organoids-on-a-chip model of human ARPKD](#)

166. (Submitter supplied) Microarray of kidney organoids derived from PKHD1 mutant human pluripotent stem cells.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL13915 6 Samples

Download data: TXT

Series Accession: GSE190272 ID: 200190272

 [Expression analysis of WT, dnmt3bb.2-/- and dnmt3aa-/-](#)

167. (Submitter supplied) To investigate the effects of gene expression by dnmt3bb.2 and dnmt3aa mutations in zebrafish, expression array analyses were performed.

Organism: Danio rerio

Type: **Expression profiling by array**

Platform: GPL14688 45 Samples

Download data: TXT

Series Accession: GSE202646 ID: 200202646

 [Differential Gene expression after peroxiredoxin2 downregulation in human extravillous cytotrophoblast-derived](#)168. [cell line HTR8](#)

(Submitter supplied) The study was designed to explore the differential gene expression after peroxiredoxin2 (Prdx2) downregulation by siRNAs transfection in human trophoblast cell line HTR8 compared with negative control.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL21185 6 Samples

Download data: TXT

Series Accession: GSE215845 ID: 200215845

 [Lipid metabolism genes in first trimester placenta](#)

169. (Submitter supplied) Placentas of obese women have low mitochondrial beta-oxidation of fatty acids (FA) and accumulate lipids in late pregnancy. This creates a lipotoxic environment, impairing placental efficiency. We assessed expression of key regulators of FA metabolism in first trimester placentas of lean and obese women. Expression of genes associated with FA

oxidation (FAO; ACOX1, CPT2, AMPK α), FA uptake (LPL, LIPG, MFSD2A), FA synthesis (ACACA) and storage (PLIN2) were significantly reduced in placentas of obese compared to lean women. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL32346 32 Samples

[Download data: RCC, XLSX](#)

Series Accession: GSE206037 ID: 200206037

[Functional effects on HUVEC of CD63+ and MHC class 1+ subsets of extracellular vesicle produced by wild type and CD47-deficient T cells](#)

170. (Submitter supplied) The present study revealed that CD63+ and MHC-1+ EVs from CD47-deficient T cells are enriched in small non-coding RNAs relative to the respective EVs from WT cells. CD47-deficient T cells secrete more CD63+ and MHC-1+ EVs, but MHC-1+ EVs are selectively taken up more by human umbilical vein endothelial cells. Microarray analysis of endothelial cells treated with CD63+ or MHC-1+ EVs showed surface marker- and CD47-dependent changes in gene expression in the target cells. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL6244 18 Samples

[Download data: CEL, CHP](#)

Series Accession: GSE185918 ID: 200185918

[Variation of DNA methylation on the IRX1/2 genes is responsible for the neural differentiation propensity in human induced pluripotent stem cells](#)

171. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Homo sapiens

Type: **Expression profiling by array**; Methylation profiling by genome tiling array

Platforms: GPL21145 GPL20844 74 Samples

[Download data: IDAT, TXT](#)

Series Accession: GSE214022 ID: 200214022

[Expression data from human endometrial stromal cells \(HESCs\) treated with PRP](#)

172. (Submitter supplied) In IVF treatment, the effects of intrauterine platelet-rich plasma (PRP) infusion with increasing rate of successful pregnancy have been reported; however, the mechanisms that support **embryo** implantation remain unclear. In the undifferentiated HESCs, PRP was found to strongly promote the gene expression associated with cell growth, tissue regeneration, proinflammatory response, and antibiotic effects. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL16686 16 Samples

[Download data: CEL](#)

Series Accession: GSE213873 ID: 200213873

[Transcriptome of EpoR-/ CFU-E cells](#)

173. (Submitter supplied) During erythropoiesis, erythroid progenitor cells proliferate in response to erythropoietin (Epo) and progressively differentiate, which encompasses an increasing accumulation of iron-bound hemoglobin. The impact of Epo on these dynamic processes remained to be resolved. By combining the development of a time-collapsed super SILAC method with transcriptome analysis we examined Epo-induced alterations in the proteome of erythroid progenitor cells at the colony-forming unit erythroid stage (CFU E). [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL1261 2 Samples

[Download data: CEL](#)

Series Accession: GSE108696 ID: 200108696

- [Clinical and pathological findings in neurolymphomatosis: preliminary association with gene expression profiles in sural nerves.](#)
174. [in sural nerves.](#)

(Submitter supplied) Although inflammation appears to play a role in neurolymphomatosis (NL), the mechanisms leading to degeneration in the peripheral nervous system are poorly understood. The purpose of this exploratory study was to identify molecular pathways underlying NL pathogenesis, combining clinical and neuropathological investigation with gene expression (GE) studies. Based on the neuropathic symptoms and signs, NL patients were classified into three forms of neuropathy: chronic symmetrical sensorimotor polyneuropathy (SMPN, n=3), multiple mononeuropathy (MN, n=4) and acute motor-sensory axonal neuropathy (AMSAN, n=1). [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL13369 16 Samples

Download data: [TXT](#)

Series Accession: GSE213455 ID: 200213455

- [Transcripts identified by microarray analysis that were deregulated in E14.5](#)

175. [Tbx18\(cre/+\);FGFR1\(f/f\);FGFR2\(f/f\);\(Fgfr1/2cDKO\) ureters](#)

(Submitter supplied) Evaluation of the transcriptional changes in E14.5 ureters upon loss of Fgfr1 and Fgfr2 in the ureteric mesenchyme.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL27545 4 Samples

Download data: [TXT](#)

Series Accession: GSE197369 ID: 200197369

- [Transcripts identified by microarray analysis that were deregulated in E15.5+6d](#)

176. [Tbx18\(cre/+\);FGFR1\(f/f\);FGFR2\(f/f\);\(Fgfr1/2cDKO\) ureter cultures](#)

(Submitter supplied) Evaluation of the transcriptional changes in E15.5+6d ureter cultures upon loss of Fgfr1 and Fgfr2 in the ureteric mesenchyme.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL24228 2 Samples

Download data: [TXT](#)

Series Accession: GSE197368 ID: 200197368

- [PRC2 molecule EED is a target of epigenetic therapy of neuroblastoma](#)

177. (Submitter supplied) Epigenetic modification by polycomb repressive complex (PRC) molecules appears to have a role in tumorigenesis and aggressiveness of neuroblastoma (NB). Embryonic Ectoderm Development (EED) is a member of PRC2 complex and binds the H3K27me3 mark deposited by EZH2, via propagation on adjacent nucleosomes. Here we studied the molecular roles of EED in MYCN-amplified neuroblastoma cells by using EED-knocked down shRNAs, EED-knocked out sgRNAs, and EED small molecule inhibitor EED226. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL16699 10 Samples

Download data: [TXT](#)

Series Accession: GSE183369 ID: 200183369

- [Identification of the differentially expressed genes in the mouse embryonic dorsal spinal cord from E10.5 to](#)

178. [E12.5](#)

(Submitter supplied) To identify differentially expressed genes in the developmental mouse dorsal spinal cord, we characterized the global gene expression profiling of mouse embryonic dorsal spinal cord commissural neurons at E10.5, E11.5 and E12.5. We used the Affymetrix Mouse Exon 1.0 ST Array platform to analyze the gene expression profiling. We included the gene expression data obtained from dorsal spinal cord commissural neuron at different embryonic stage. [more...](#)

Organism: Mus musculus
 Type: **Expression profiling by array**
 Platform: GPL6096 6 Samples
[Download data: CEL](#)
 Series Accession: GSE169448 ID: 200169448

[Expression Profile Analysis of Long non-coding RNAs in Mouse Liver](#)

179. (Submitter supplied) In the present study, the lncRNA expression profile of mouse fetal and adult liver was analyzed by ArrayStar LncRNA Array 3.0. Differentially expressed lncRNAs with statistical significance were identified through Volcano Plot filtering between two groups. Pathway analysis and GO analysis were applied to determine the roles of these differentially expressed lncRNAs played in these biological pathways or GO terms. [more...](#)

Organism: Mus musculus
 Type: **Expression profiling by array**; Non-coding RNA profiling by array
 Platform: GPL19286 6 Samples
[Download data: TXT](#)
 Series Accession: GSE117540 ID: 200117540

[circRNA, lncRNA and mRNA profiles of umbilical cord blood exosomes from preterm newborns showing](#)

180. [bronchopulmonary](#)

(Submitter supplied) Purpose: The purpose of this study was to detect the expression profiles of circRNAs, lncRNAs and mRNAs in umbilical cord blood (UCB) exosomes from BPD infants. Methods: Microarray analysis was performed to compare the RNA profiles of UCB-derived exosomes from preterm newborn with and without BPD. Then, circRNA/lncRNA-miRNA-mRNA co-expression networks were built to determine their associations with BPD. Results: A total of 317 circRNAs, 104 lncRNAs, 135 mRNAs showed significant differential expression in UCB-derived exosomes from BPD preterm infants compared with the NBPD group. [more...](#)

Organism: Homo sapiens
 Type: **Expression profiling by array**; Non-coding RNA profiling by array
 Platform: GPL30862 16 Samples
[Download data: TXT](#)
 Series Accession: GSE190215 ID: 200190215

[Expression data from AZA treated megakaryocytic cells under TPO-RA stimulation](#)

181. (Submitter supplied) Thrombocytopenia is an independent prognostic indicator in patients with MDS (de Swart, L. et al, Br J Haematol, 2015) and we sought to evaluate the contribution of azacitidine to the worsening of this condition in patients with MDS and acute myeloid leukemia (AML). Since MDS/AML may have lower amounts of residual healthy cells, we sought to model this effect of AZA on healthy cord blood derived megakaryocytic cells. [more...](#)

Organism: Homo sapiens
 Type: **Expression profiling by array**
 Platform: GPL23126 15 Samples
[Download data: CEL, XLS](#)
 Series Accession: GSE144410 ID: 200144410

[Comparative expression of embryonic medial- and lateral/caudal-ganglionic eminence cells migrating in the](#)

182. [mouse cerebral cortex](#)

(Submitter supplied) Cortical interneurons originate in the medial and caudal ganglionic eminence and migrate into the cortex during embryogenesis. We purified cells migrating within the cortex at different embryonic stages and compared their transcriptome to identify transcriptional programmes underlying distinct cortical interneuron fates.

Organism: Mus musculus
 Type: **Expression profiling by array**
 Platform: GPL1261 12 Samples
[Download data: CEL](#)
 Series Accession: GSE207506 ID: 200207506

- [Assessment of unique behavioral, morphological, and molecular alterations in the comparative developmental toxicity profiles of PFBA using the zebrafish model system](#)
- 183.

(Submitter supplied) Perfluoroalkyl substances (PFAS) are a class of synthetic chemicals that are persistent in the environment. Due to concerns linked with longer chain PFAS, shorter chain chemicals were used as replacements, but developmental toxicity assessments of the shorter chain chemicals are limited. The aim of this study was to compare the developmental toxicity of three perfluoroalkyl acids (PFAAs): perfluorooctanoic acid (PFOA), composed of 8 carbon (C8), perfluorohexanoic acid (PFHxA, C6), and perfluorobutanoic acid (PFBA, C4) using the zebrafish (*Danio rerio*). [more...](#)

Organism: *Danio rerio*

Type: **Expression profiling by array**

Platform: GPL23074 16 Samples

Download data: [TXT](#), [XLS](#)

Series Accession: GSE211172 ID: 200211172

- [Assessment of unique behavioral, morphological, and molecular alterations in the comparative developmental toxicity profiles of PFHxA using the zebrafish model system](#)
- 184.

(Submitter supplied) Perfluoroalkyl substances (PFAS) are a class of synthetic chemicals that are persistent in the environment. Due to concerns linked with longer chain PFAS, shorter chain chemicals were used as replacements, but developmental toxicity assessments of the shorter chain chemicals are limited. The aim of this study was to compare the developmental toxicity of three perfluoroalkyl acids (PFAAs): perfluorooctanoic acid (PFOA), composed of 8 carbon (C8), perfluorohexanoic acid (PFHxA, C6), and perfluorobutanoic acid (PFBA, C4) using the zebrafish (*Danio rerio*). [more...](#)

Organism: *Danio rerio*

Type: **Expression profiling by array**

Platform: GPL23074 16 Samples

Download data: [TXT](#), [XLS](#)

Series Accession: GSE211171 ID: 200211171

- [Assessment of unique behavioral, morphological, and molecular alterations in the comparative developmental toxicity profiles of PFOA using the zebrafish model system](#)
- 185.

(Submitter supplied) Perfluoroalkyl substances (PFAS) are a class of synthetic chemicals that are persistent in the environment. Due to concerns linked with longer chain PFAS, shorter chain chemicals were used as replacements, but developmental toxicity assessments of the shorter chain chemicals are limited. The aim of this study was to compare the developmental toxicity of three perfluoroalkyl acids (PFAAs): perfluorooctanoic acid (PFOA), composed of 8 carbon (C8), perfluorohexanoic acid (PFHxA, C6), and perfluorobutanoic acid (PFBA, C4) using the zebrafish (*Danio rerio*). [more...](#)

Organism: *Danio rerio*

Type: **Expression profiling by array**

Platform: GPL23074 16 Samples

Download data: [TXT](#), [XLS](#)

Series Accession: GSE211169 ID: 200211169

- [Gene expression data of mRNA from liver sample of F2 population based German Landrace \(DL\) and Pietrain \(Pi\) pig breeds](#)
- 186.

(Submitter supplied) 47,880 probe-sets were screened, in the first part of this study pig embryos at 63 days post conception (dpc)

Organism: *Sus scrofa*

Type: **Expression profiling by array**

Platform: GPL16569 24 Samples

Download data: [CEL](#)

Series Accession: GSE202677 ID: 200202677

- [Gene expression profiles of Wnt4 high and Wnt4 low populations of murine islets at postnatal day 1 \(P1\).](#)
187. (Submitter supplied) To find the differences between β cells expressing Wnt4 and those that do not express it (or express it at low levels) at neonatal stage, murine islets at postnatal day 1 (P1) were collected. Based on a reporter expressing Cre

recombinase from the Wnt4 locus, we observed that Wnt4 expression starts in a small subset of β cells at embryonic day (E) 18.5. At neonatal stages, around 50% of β cells express Wnt4 at P0 and most of cells express it by P5. more...

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL21163 6 Samples

Download data: [TXT](#)

Series Accession: GSE210237 ID: 200210237

[HUVEC cell transcriptome response to Zaire Ebola virus \(EBOV\) and mutant lacking the mucin domain](#)

188. [\(deltamucin-EBOV\)](#)

(Submitter supplied) The purpose is to obtain samples for mRNA analysis in HUV-EC-C cells, a human endothelial cell line isolated from the vein of the umbilical cord, using the following viruses obtained by reverse genetics: Zaire Ebola virus wild-type in the Δ VP30 background (Δ VP30-WT) and mutant lacking the mucin domain (Δ VP30-deltamucin).

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL13497 75 Samples

Download data: [TXT](#)

Series Accession: GSE210189 ID: 200210189

[Transformed cells after senescence give rise to more severe tumor phenotypes than transformed non-](#)

189. [senescent cells](#)

(Submitter supplied) Oncogenic stress-induced senescence initially inhibits tumor initiation by blocking proliferation. If these cells are not eliminated they may resume proliferation upon loss-of-tumor suppressors, and be at risk of transformation. During tumor formation, depending on the sequence of events of gain-of-oncogenes and/or loss-of-tumor suppressors, cancer cells may emerge from senescent cells. The goal of this study is to determine if transformed cells after senescence (TS) display more aggressive tumorigenic features, with a greater capacity to migrate and a higher resistance to anti-tumoral drugs than cells having undergone transformation without senescence. more...

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL11202 12 Samples

Download data: [TXT](#)

Series Accession: GSE210060 ID: 200210060

[A maternal high-fat diet induces fetal origins of NASH-HCC in mice](#)

190. (Submitter supplied) Maternal overnutrition affects offspring susceptibility to nonalcoholic steatohepatitis (NASH). Male offspring from high-fat diet (HFD)-fed dams developed a severe form of NASH, leading to highly vascular tumor formation. The cancer/testis antigen HORMA domain containing protein 1 (HORMAD1), one of 146 upregulated differentially expressed genes in fetal livers from HFD-fed dams, was overexpressed with hypoxia-inducible factor 1 alpha (HIF-1alpha) in hepatoblasts and in NASH-based hepatocellular carcinoma (HCC) in offspring from HFD-fed dams at 15 weeks old. more...

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL21163 4 Samples

Download data: [TXT](#)

Series Accession: GSE183360 ID: 200183360

[Expression data from WT and BMPR2 knockout hematopoietic stem cells extracted from mice.](#)

191. (Submitter supplied) Abstract copied in below, from Warsi et al. 2021 BMP signaling is required for postnatal murine hematopoietic stem cell self-renewal, published in Haematologica. DOI 10.3324/haematol.2019.236125 Life-long production of blood from hematopoietic stem cells (HSCs) is a process of strict modulation. Intrinsic and extrinsic signals govern fate options like self-renewal - a cardinal feature of HSCs. Bone morphogenetic proteins (BMP) have an established role in embryonic hematopoiesis, but less is known about its functions in adulthood. more...

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6246 8 Samples

Download data: CEL, XLSX

Series Accession: GSE209862 ID: 200209862

- [Gene expression of the Dnmt1/3a/3b TKO ESCs which ubiquitously express full-length DNMT1\(TKO_FL\) or a deletion mutant DNMT1 lacking the N-terminal 602 amino acids\(TKO_602\).](#)
192.

(Submitter supplied) Gene expression analysis of TKO_FL ESCs and TKO_602 ESCs(day 0), differentiated cells from each ESCs(day4 and day7).

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL1261 6 Samples

Download data: CEL

Series Accession: GSE201306 ID: 200201306

- [Cerebellar gene expression changes in Pdgfc and Pdgfra mutant](#)

193. (Submitter supplied) Platelet-derived growth factor-C (PDGF-C) is one of three known ligands for the tyrosine kinase receptor PDGFR-alpha. Analysis of Pdgfc null mice has demonstrated roles for PDGF-C in palate closure and the formation of cerebral ventricles, but redundancy with other PDGFR-alpha ligands might hide additional functions. In search of further developmental roles for PDGF-C, we generated mice that were double mutants for Pdgfc -/- and Pdgfra GFP/+.[more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6246 16 Samples

Download data: CEL

Series Accession: GSE77049 ID: 200077049

- [PI3K \$\beta\$ and \$\beta\$ -Catenin mediate EZH2 removal from promoters controlling human ESC stemness and primitive streak gene expression](#)
194.

(Submitter supplied) The mechanism governing the transition of human embryonic stem cells towards differentiated cells is only partially understood. To explore this transition, the activity and expression of the ubiquitous phosphoinositide-3-kinase (PI3K α and β) were modulated. This study reports a pathway that dismantles the repression imposed by the EZH2 polycomb repressor on an essential stemness gene, NODAL, and on transcription factors required at differentiation to trigger primitive streak formation. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL10332 12 Samples

Download data: TXT

Series Accession: GSE202163 ID: 200202163

- [Allergic sensitization and exposure to ambient air pollution beginning early in life leads to a COPD-like phenotype in young adult mice](#)
195.

(Submitter supplied) The perinatal period and early infancy are considered critical periods for lung development, and adversities during this period are believed to impact lung health in adulthood. The main factors affecting postnatal lung development and growth include environmental exposures, cigarette smoking, (viral) infections, allergic sensitization, and asthma. Therefore, we hypothesized that concomitant exposure in the early postnatal period in mice would cause more profound alterations in lung alveolarization and growth in adult life, quantified by stereology, and differently modulate lung inflammation and gene expression than either insult alone. Five-day-old male mice were immunized intraperitoneally (i.p.) with 10 μ g of ovalbumin (OVA). [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL16570 12 Samples

Download data: CEL, CHP

Series Accession: GSE195996 ID: 200195996

[Transcription analysis of blastocyst form oocyte exposed to the high level of NEFAs with cocultured of monolayer of GCs](#)
196.

(Submitter supplied) The transcriptome pattern in blastocyst that developed from oocytes exposed to the high level of NEFAs with cocultured of monolayer of GSs was investigated. Genome-wide transcriptome analysis was performed by micro array using EDMA platform.

Organism: Sus scrofa

Type: **Expression profiling by array**

Platform: GPL28870 4 Samples

Download data: [TXT](#)

Series Accession: GSE154836 ID: 200154836

 [Role of YAP/TAZ-TEAD in human trophoblast](#)

197. (Submitter supplied) During placentation, placental cytotrophoblast cells differentiate into syncytiotrophoblast cells and extravillous trophoblast cells. In placenta, the expression of various genes is regulated by the Hippo pathway through the transcriptional coactivator YAP/TAZ-TEAD activity. To examine the effect of YAP/TAZ and/or TEAD on trophoblast differentiation, knockdown experiments were performed. Microarray analysis were performed to identify YAP/TAZ and/or TEAD target genes in human trophoblast.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL23159 9 Samples

Download data: [CEL](#), [CHP](#)

Series Accession: GSE182900 ID: 200182900

 [Gene expression differences between Gata2cko and wt mouse midbrain](#)

198. (Submitter supplied) Transcription factor Gata2 has been shown to regulate the development of the GABAergic neurons in the mouse midbrain. To gain information about the possible target genes of the Gata2 transcription factor, we used cDNA microarrays to compare gene expression in the embryonic day 12.5 (E12.5) wild-type and Gata2 mutant embryos. In this dataset, gene expression in control and Gata2cko dorsal and ventral midbrain tissues is reported. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6887 18 Samples

Download data: [TXT](#)

Series Accession: GSE208110 ID: 200208110

 [Apyrase-mediated amplification of secretory IgA promotes intestinal homeostasis](#)

199. (Submitter supplied) Morphogenesis of epithelial tissues relies on the precise developmental control of cell polarity and architecture. In the early Drosophila **embryo**, the primarSecretory IgA (SIgA) interaction with commensal bacteria regulates the composition and function of the microbiota, contributing to gut ecosystem homeostasis. However, mechanisms regulating the reciprocal control of microbiota and SIgA are not defined. [more...](#)

Organism: Mus; Mus musculus

Type: **Expression profiling by array**

Platform: GPL23038 23 Samples

Download data: [CEL](#), [XLSX](#)

Series Accession: GSE203433 ID: 200203433

 [MCF-7 Cell Derived Soluble Factors Define Growth of Vascular and Lymphatic Endothelial Cells: Modulatory Role of miR193a](#)

(Submitter supplied) Angiogenesis and Lymphangiogenesis plays a key role in promoting tumor growth and breast cancer progression as well as metastasis. Active angiogenic process within the tumor tissue is known to promote cancer/tumor growth via nutrient supply, moreover, soluble molecules secreted by lymphatic endothelial cells (ECs) promotes tumor growth. Hence is feasible that paracrine factors generated by breast cancer cells play a role in regulating tumor neovascularization by lymphatic and vascular ECs. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL23159 8 Samples](#)

Download data: [CEL](#), [XLSX](#)

Series Accession: GSE189084 ID: 200189084

[Analysis of porcine blastocyst from oocyte exposed to the high level of NEFAs](#)

201. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Sus scrofa

Type: **Expression profiling by array**; Methylation profiling by array

Platforms: [GPL28869](#) [GPL28870 8 Samples](#)

Download data: [TXT](#)

Series Accession: GSE154433 ID: 200154433

[Transcriptomic analysis of porcine blastocyst from oocyte exposed to the high level of NEFAs](#)

202. (Submitter supplied) The transcriptome pattern in blastocyst that developed from oocytes exposed to the high level of NEFAs was investigated. Genome-wide transcriptome analysis was performed by micro array using EDMA platform.

Organism: Sus scrofa

Type: **Expression profiling by array**

Platform: [GPL28870 4 Samples](#)

Download data: [TXT](#)

Series Accession: GSE154432 ID: 200154432

[Transcriptomic analysis of undifferentiated hESC, hESC -derived cell populations and human Embryonic Liver](#)

203. [\(EL\) cell populations.](#)

(Submitter supplied) RNA microarrays technology was used to compare hESC-derived cell populations to undifferentiated hESC and to human EL cell populations. Microarrays confirmed the hematoendothelial, endothelial and hematopoietic identity of hPSC-derived CD144+-EBs, BCs and ECs, respectively, and the similarities between hESC-derived cell populations and human EL equivalent populations.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL16686 29 Samples](#)

Download data: [CEL](#)

Series Accession: GSE194372 ID: 200194372

[miR-515-5p suppresses trophoblast cell invasion and proliferation through XIAP regulation in preeclampsia](#)

204. (Submitter supplied) MicroRNAs (miRNAs) are non-coding small RNA molecules that can be secreted into the circulation and which exist in remarkably stable forms. Circulating miRNAs regulates numerous regulations of biological process and aberrantly expressed in pathological status. Differentially expressed circulating miRNAs have received attention as potential biomarkers for many diseases. In this study, we revealed that miR-515-5p was significantly upregulated in maternal serum from preeclampsia (PE) patients in comparison to normal pregnant women. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL29077 6 Samples](#)

Download data: [TXT](#)

Series Accession: GSE206763 ID: 200206763

[HDAC3 Inhibition Causes the Impairment in Development of Neocortical VIP Interneurons via dysregulation of](#)

205. [Notch Signaling and Autism-like Behaviors](#)

(Submitter supplied) Autism spectrum disorders (ASDs) are a neurodevelopmental disorder characterized by impairments in social interactions and stereotyped behaviors. While ASD has a strong genetic background, environmental factors including toxins, pesticides, infection and drugs are also known to confer autism susceptibility, likely by inducing epigenetic changes. Exposure to Valproic acid (VPA), a drug for epilepsy and bipolar disorders, during pregnancy is highly associated with the risk of ASD children. [more...](#)

Organism: Mus musculus
Type: **Expression profiling by array**
Platform: GPL19127 6 Samples
[Download data: TXT](#)
Series Accession: GSE133932 ID: 200133932

[Human umbilical vein endothelial cells: Control vs. Uninfected Groups](#)

206. (Submitter supplied) Experiments compared uninfected ECV304 cells with ECV304 cells infected with HSV-2, and both were tested for differential genes by microarray with the goal of determining the effect of HSV-2 on gene expression in ECV304 cells.

Organism: Homo sapiens
Type: **Expression profiling by array**
Platform: GPL887 2 Samples
[Download data: TXT](#)
Series Accession: GSE206320 ID: 200206320

[Sex-specific modulation of the host transcriptome in the spleen of Schistosoma mansoni infected mice](#)

207. (Submitter supplied) Intestinal Schistosomiasis, caused by the helminth Schistosoma mansoni, results in fibroproliferative disease triggered by liver trapped parasite eggs. Characteristic of the infection is a chronic course of disease with progressive periportal fibrosis, spleno- and hepatomegaly, and portal hypertension. Despite significant progress in understanding the complex immunological processes involved in the host-pathogen relationship, there is currently no effective vaccine against the infection nor antifibrotic drugs, increasing the pressure to find new targets for schistosome drugs and vaccine candidates. [more...](#)

Organism: Mus musculus
Type: **Expression profiling by array**
Platform: GPL23038 10 Samples
[Download data: CEL, CHP](#)
Series Accession: GSE197804 ID: 200197804

[Enhancers of host immune tolerance to bacterial infection discovered using linked computational and experimental approaches](#)

208. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Xenopus laevis
Type: **Expression profiling by array**
Platform: GPL10756 67 Samples
[Download data: CEL](#)
Series Accession: GSE196425 ID: 200196425

[Enhancers of host immune tolerance to bacterial infection discovered using linked computational and experimental approaches II](#)

(Submitter supplied) Current therapeutic strategies against bacterial infections focus on reduction of pathogen load using antibiotics; however, stimulation of host tolerance to infection in the presence of pathogens might offer an alternative approach. We used computational transcriptomics and Xenopus laevis embryos to discover infection response pathways, identify potential tolerance inducer drugs, and validate their ability to induce broad tolerance. [more...](#)

Organism: Xenopus laevis
Type: **Expression profiling by array**
Platform: GPL10756 27 Samples
[Download data: CEL](#)
Series Accession: GSE196424 ID: 200196424

[Enhancers of host immune tolerance to bacterial infection discovered using linked computational and experimental approaches I](#)

(Submitter supplied) Current therapeutic strategies against bacterial infections focus on reduction of pathogen load using antibiotics; however, stimulation of host tolerance to infection in the presence of pathogens might offer an alternative approach. We used computational transcriptomics and *Xenopus laevis* embryos to discover infection response pathways, identify potential tolerance inducer drugs, and validate their ability to induce broad tolerance. [more...](#)

Organism: *Xenopus laevis*

Type: **Expression profiling by array**

Platform: GPL10756 40 Samples

Download data: CEL

Series Accession: GSE196422 ID: 200196422

[IncRNA and mRNA expression of HUVECs under H/R and normal conditions](#)

211. (Submitter supplied) To have a global view of transcriptional change of hypoxia/reoxygenation (H/R) condition compared with normal condition, we collected human umbilical vein endothelial cells (HUVECs) from both conditions. The expression profiles of HUVECs were detected by microarray, and two conditions were compared to detect significantly changed lncRNAs and mRNAs.

Organism: *Homo sapiens*

Type: **Expression profiling by array**; Non-coding RNA profiling by high throughput sequencing

Platform: GPL20115 6 Samples

Download data: TXT

Series Accession: GSE193047 ID: 200193047

[Expression profiling of retinoic acid targets in lateral mesoderm from *Xenopus laevis* embryos](#)

212. (Submitter supplied) Renal precursors of the *Xenopus* pronephros arise from dorso-lateral mesoderm at the early neurula stage. This process is under the control of retinoic acid (RA). We have used microarrays to identify RA targets in dorso-lateral mesoderm by performing differential expression analysis between control and RA-depleted situations

Organism: *Xenopus laevis*

Type: **Expression profiling by array**

Platform: GPL10756 18 Samples

Download data: CEL

Series Accession: GSE205827 ID: 200205827

[Gene expression profiling of hepatocyte-like cells from human mesenchymal stem cells](#)

213. (Submitter supplied) We established a protein-based artificial transcription system and successfully engineered human hepatocyte-like cells from human umbilical cord-derived mesenchymal stem cells (MSC-UCs). We utilized four artificial transcription factors (ATFs) that targeted hepatocyte nuclear factor (HNF)1 α , HNF3 γ , HNF4 α and GATA4 (4F), and found that treatment with 4F for 5 days converted MSC-UCs to hepatocyte-like cells (4F-Heps). [more...](#)

Organism: *Homo sapiens*

Type: **Expression profiling by array**

Platform: GPL21185 9 Samples

Download data: TXT

Series Accession: GSE205543 ID: 200205543

[Chronic allergic asthma alters m6A epitranscriptomic tagging of mRNAs and lncRNAs in the lung](#)

214. (Submitter supplied) Chronic allergic asthma alters the lung m6A epitranscriptome, suggesting functional implications in the pathophysiology of refractory asthma. Methylated IL17RB mRNA possibly become a new therapeutic target for chronic allergic asthma.

Organism: *Mus musculus*

Type: **Expression profiling by array**; Non-coding RNA profiling by array

Platform: GPL25915 12 Samples

Download data: TXT

Series Accession: GSE205471 ID: 200205471

[HUVEC T Cell Irradiation Study](#)

- 215.

(Submitter supplied) Question Addresses: What is the gene expression profile from human umbilical vein endothelial cells (HUVEC) and human Jurkat T cells after irradiation (IR)? What, if any, is the effect of co-culturing these two cell types on gene expression? There are eight experimental conditions for this experiment: (1) non-irradiated HUVEC; (2) irradiated HUVEC; (3) non-irradiated Jurkat; (4) irradiated Jurkat; (5) non-irradiated HUVEC + non-irradiated Jurkat+; (6) non-irradiated HUVEC + irradiated Jurkat; (7) irradiated HUVEC + non-irradiated Jurkat; (8) irradiated HUVEC + irradiated Jurkat. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL10332 18 Samples

[Download data](#)

Series Accession: GSE39019 ID: 200039019

[Transcriptional profiling in neurons of C. elegans : comparison between ahr-1 mutant and wild-type animals.](#)

216. (Submitter supplied) The Aryl hydrocarbon Receptor (AhR) is a transcription factor well known in vertebrate to play an essential role as xenobiotic sensor. On the contrary, no ligand has been identified to date for invertebrate AhR. In some model organisms such as *D. melanogaster* and *C. elegans*, AhR orthologs have physiological functions and their inability to bind prototypical ligands of vertebrate AhR such as tetrachlorodibenzo-p-dioxin (TCDD) suggests that the detoxification role of the receptor could be an adaptation acquired during evolution. [more...](#)

Organism: Caenorhabditis elegans

Type: **Expression profiling by array**

Platform: GPL31292 4 Samples

[Download data: GPR, XLSX](#)

Series Accession: GSE195728 ID: 200195728

[Gene expression and Targeted protein expression analysis of skewed or drug-treated mouse T cells, and of](#)

217. [serum from first disease vs flare in a model of Cutaneous Lupus Erythematosus](#)

(Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus

Type: **Expression profiling by array**; Protein profiling by protein array

Platforms: GPL30820 GPL30876 28 Samples

[Download data: RCC](#)

Series Accession: GSE186096 ID: 200186096

[Directional capacity of human mesenchymal stem cells to support hematopoietic stem cell proliferation in vitro](#)

218. (Submitter supplied) Objectives: Hematopoietic stem cells (HSCs) reside in a specialised microenvironment in the bone marrow, which is majorly composed of mesenchymal stem cells (MSCs) and its' derivatives. This study aimed to investigate the regulatory role of MSCs to decipher the cellular and humoral communications on HSCs' proliferation, self-renewal, and differentiation at the transcriptomic level. Materials and methods: Microarray assay was employed to analyse the gene expression profile of HSCs that imparted by MSCs during co-culture. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL16699 8 Samples

[Download data: TXT](#)

Series Accession: GSE176002 ID: 200176002

[Analysis of Amniotic Fluid-derived lncRNAs and mRNAs in Fetuses with ventricular septal defect](#)

219. (Submitter supplied) Ventricular septal defect (VSD) is one of the most prevalent birth defects. The pathogenesis of VSD remains unknown. to analyze the expression of AF-derived lncRNAs and their roles in VSD development, Arraystar Human LncRNA Microarray V5.0 is employed for the global profiling of human lncRNAs and protein-coding transcripts.

Organism: Homo sapiens

Type: **Expression profiling by array**; Non-coding RNA profiling by array

Platform: GPL26963 10 Samples

[Download data: TXT](#)

Series Accession: GSE204935 ID: 200204935

[Genome-wide analysis of Wild Type and Relb-/ MEFs](#)

220. (Submitter supplied) Recent studies indicated that the NF- κ B RelB subunit may play roles beyond immune modulations. The molecular mechanism that may allow RelB to engage in such diverse physiological activities remains unclear. To better understand the RelB-driven transcriptome, therefore, we subjected wild type and Relb-/ mouse embryonic fibroblast (MEF) to microarray analyses using Illumina MouseRef-8 v2.0 Expression BeadChip. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL15097 4 Samples

Download data: [TXT](#)

Series Accession: GSE176446 ID: 200176446

 [Whole genome expression profile of human decidual PMN-MDSC and autologous neutrophils in normal](#)

221. [pregnancy](#)

(Submitter supplied) It is suggested that decidual polymorphonuclear myeloid-derived suppressor cell (PMN-MDSCs) are a group of activated suppressive neutrophils. Decidual microenvironment can facilitate circulating neutrophils with phenotypes and functions of PMN-MDSCs. The mechanism of PMN-MDSCs differentiation induced by decidual microenvironment has not been fully understood. Here we performed whole genome expression profile of 3 decidual PMN-MDSCs and autologous neutrophils from normal early pregnancy. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL21185 6 Samples

Download data: [TXT](#)

Series Accession: GSE192850 ID: 200192850

 [Role of Amh and Activin B in testis development](#)

222. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL20775 27 Samples

Download data: [CEL, CHP](#)

Series Accession: GSE196842 ID: 200196842

 [Microarray analysis of embryonic E12.5 mouse gonads from control male, female and Amh; Inhbb dKO males](#)

223. (Submitter supplied) Fate determination and maintenance of fetal testes in most mammals occur cell autonomously as a result of the action of key transcription factors in Sertoli cell. In the mouse testis AMH and Activin B are required for the maintenance of Sertoli cell fate. By E12.5, the testis of the dKO male are comparable with the control testis as Amh and Activin B are not required for the initial testis differentiation. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL20775 12 Samples

Download data: [CEL, CHP](#)

Series Accession: GSE196841 ID: 200196841

 [Microarray analysis of embryonic E15 mouse gonads from control male, female and Amh; Inhbb dKO males](#)

224. (Submitter supplied) Fate determination and maintenance of fetal testes in most mammals occur cell autonomously as a result of the action of key transcription factors in Sertoli cell. In the mouse testis AMH and Activin B are required for the maintenance of Sertoli cell fate. In the absence of both AMH and Activin B initial testis differentiation (E12.5) occurs normally but, by embryonic day 15.5, Sertoli cells at the testis poles transdifferentiate into granulosa cells.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL20775 15 Samples

Download data: [CEL, CHP](#)

Series Accession: GSE196826 ID: 200196826

- [Post-transcriptionally regulated genes are essential for pluripotent stem cell survival](#)
225. (Submitter supplied) The effects of transcription factors on the maintenance and differentiation of pluripotent stem cells (PSCs) have been well studied. However, the importance of post-transcriptional regulatory mechanisms, which cause the quantitative dissociation of mRNA and protein expression, is still little known. Here, by combining transcriptome and proteome profiling, we identified 228 post-transcriptionally regulated genes with strict upregulation at the protein amounts in PSCs. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL30657 15 Samples

[Download data: TXT](#)

Series Accession: GSE184546 ID: 200184546

- [Epigenome-wide association study of bronchopulmonary dysplasia in preterm infants](#)

226. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Homo sapiens

Type: **Expression profiling by array; Methylation profiling by genome tiling array**

Platforms: GPL14951 GPL13534 130 Samples

[Download data: IDAT](#)

Series Accession: GSE189582 ID: 200189582

- [Cord blood gene expression profiles of bronchopulmonary dysplasia in preterm infants](#)

227. (Submitter supplied) Bronchopulmonary dysplasia (BPD) is a lung disease in premature infants characterized by impaired pulmonary development which persists into later life. While advances in neonatal care have improved survival rates of premature infants, cases of BPD have been increased. Therapeutic options are limited for prevention and treatment. This study was designed to explore differentially expressed genes associated with BPD. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL14951 23 Samples

[Download data: IDAT](#)

Series Accession: GSE188944 ID: 200188944

- [A molecular circuit that creates the phloem pattern](#)

228. (Submitter supplied) The vascular system of plants consists of xylem, phloem and procambium in a specific pattern. The phloem consists of sieve elements, the apparatus for bulk flow of photo-assimilates, and companion cells, which mediate transport of photo-assimilates between the sieve elements and surrounding cells and support the biological activities of the sieve element cells. The regulatory mechanisms of vascular development are being uncovered. [more...](#)

Organism: Arabidopsis thaliana

Type: **Expression profiling by array**

Platform: GPL17416 12 Samples

[Download data: CEL](#)

Series Accession: GSE166182 ID: 200166182

- [BAF complex cooperates with c-Myc to orchestrate early fate decisions of CD8 T cells \(Microarray\)](#)

229. (Submitter supplied) We found cBAF and c-Myc co-assort asymmetrically to the two daughter nuclei, such that daughter cells with low c-Myc and cBAF display a cell fate trajectory towards memory T cell differentiation. Moreover, cBAF complex and c-Myc physically interact with each other, and act in establishing the chromatin landscape in activated CD8 T cells.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL23038 16 Samples

[Download data: CEL](#)

Series Accession: GSE184587 ID: 200184587

- [BAF complex cooperates with c-Myc to orchestrate early fate decisions of CD8 T cells](#)

230. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus

Type: Genome binding/occupancy profiling by high throughput sequencing; Expression profiling by high throughput sequencing; **Expression profiling by array**

Platforms: [GPL24247](#) [GPL23038](#) 101 Samples

[Download data: BED, BIGWIG, CEL, TAB](#)

Series Accession: GSE183619 ID: 200183619

[Microarray-based Gene Expression Analysis of WA09 human cerebral organoids with CRISPR-KO of NGLY1](#)

231. (Submitter supplied) Analysis of human cerebral organoids developed from both WA09 human embryonic stem cells with CRISPR-KO of NGLY1. The hypothesis tested was that NGLY1 is key to normal human brain development and when knocked out would alter cerebral development of organoids through the differential expression of various key genes.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL10558](#) 54 Samples

[Download data: IDAT, TXT](#)

Series Accession: GSE169696 ID: 200169696

[Investigation of genetic compensation in tdp1-/ zebrafish embryos](#)

232. (Submitter supplied) Tdp1, tyrosyl-DNA phosphodiesterase 1, is an enzyme responsible for the repair of DNA breaks resulting from aberrant topoisomerase 1 activity, called Top1 cleavage complexes (Top1-CCs). Mutation of Tdp1 leads to a progressive neurodegenerative disorder spinocerebellar ataxia with axonal neuropathy 1 (SCAN1). We have generated tdp1-/ zebrafish as a model for SCAN1. The adult fish have a behavioral defect and hypersensitivity to camptothecin (CPT), a Top1 poison. [more...](#)

Organism: Danio rerio

Type: **Expression profiling by array**

Platform: [GPL16933](#) 6 Samples

[Download data: CEL, CHP](#)

Series Accession: GSE148923 ID: 200148923

[High efficient serum free differentiation of endothelial cells from human iPS cells without sorting](#)

233. (Submitter supplied) Introduction: Endothelial cells (ECs) form the inner lining of all blood vessels of the body, play important roles in vascular tone regulation, hormone secretion, anticoagulation, regulation of blood cell adhesion and immune cell extravasation. Limitless ECs sources are required to further in-vitro investigations of ECs' physiology and pathophysiology as well as for tissue engineering approaches. Ideally, the differentiation protocol avoids animal derived components such as fetal serum and yields ECs at efficiencies that make further sorting obsolete for most applications. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL23159](#) 21 Samples

[Download data: CEL](#)

Series Accession: GSE200399 ID: 200200399

[Covid-19 Infection During Pregnancy Induces Differential Gene Expression in Human Cord Blood Cells from](#)

234. [Term Neonates](#)

(Submitter supplied) Exposure to COVID-19 during pregnancy induces differential gene expression in cord blood cells. The early exposure and associated differentially expressed genes may potentially contribute to cardiac, hepatic, renal and immunological disorders in offspring. These findings lead to a further understanding of the effects of COVID-19 exposure at an early stage of life and its potential long-term consequences as well as therapeutic targets. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL23159](#) 16 Samples

[Download data: CEL](#)

Series Accession: GSE195938 ID: 200195938

- [Temporal Changes in Transcripts of MITE Transposable Elements during Rice Endosperm Development](#)
235. (Submitter supplied) Repression of transposable elements (TEs) by DNA methylation is necessary for host plants to maintain genome integrity and prevent from harmful mutations. However, under certain circumstances, TEs are thought to escape from the host defense system and therefore activate their transcription. In *A. thaliana* and *O. sativa*, DNA demethylase targets to the sequence derived from TEs in the central cell, a progenitor cell of endosperm in the female gametophyte. [more...](#)

Organism: Oryza sativa Japonica Group; Oryza sativa

Type: **Expression profiling by array**

Platform: GPL17507 30 Samples

Download data: [TXT](#)

Series Accession: GSE185870 ID: 200185870

- [A Positive Regulatory Feedback Loop Between EKLF/ KLF1 and TAL1/SCL Sustaining the Erythropoiesis](#)

236. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus

Type: **Expression profiling by array**; Genome binding/occupancy profiling by genome tiling array

Platforms: GPL13412 GPL1261 10 Samples

Download data: [CEL](#), [CHP](#), [PAIR](#)

Series Accession: GSE171289 ID: 200171289

- [Microarray expression level comparison between WT and KO fetal liver cells](#)

237. (Submitter supplied) The erythroid Krüppel-like factor EKLF/KLF1 is a hematopoietic transcription factor binding to CACCC DNA motif and participating in the regulation of erythroid differentiation. With combined use of microarray-based gene expression profiling and promoter-based ChIP-chip assay of E14.5 fetal liver cells from wild type (WT) and EKLF-knockout (*Eklf*-/-) mouse embryos, we have identified the pathways and direct target genes activated or repressed by EKLF. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL1261 8 Samples

Download data: [CEL](#), [CHP](#)

Series Accession: GSE171200 ID: 200171200

- [Differences in fetal liver gene expression between low and high maternal nutrition](#)

238. (Submitter supplied) To investigate the impact of maternal nutrient restriction on gene expression in the fetal liver, we profiled gene expression in the liver of Japanese Black fetal calves in high and low nutrient condition of pregnant maternal cows .

Organism: Bos taurus

Type: **Expression profiling by array**

Platform: GPL11649 8 Samples

Download data: [TXT](#)

Series Accession: GSE191179 ID: 200191179

- [Gene expression profiles of variants of B16OVA melanoma cells established from different host immunological conditions](#)
239. (Submitter supplied) To establish cancer cells escaping from host immunity, we used murine B16 melanoma cell line expressing ovalbumin (B16OVA) and inoculated into mice immunized with OVA. Using this model, we established cell lines after the *in vivo* passage through distinct immunological condition. B16OVA tumor exposed to OVA-specific CD8+ T cell immunity in OVA-immunized B6 mice were isolated and established five variants (IMM1, 2, 8). [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL16570 10 Samples

Download data: [CEL](#), [XLSX](#)

Series Accession: GSE199573 ID: 200199573

[Human placental tissues:control group vs non-diabetic fetal macrosomia \(NDFMS\) group](#)

240. (Submitter supplied) To investigate whether aberrant lncRNA expression in the placenta is involved in the pathogenesis of NDFMS and to elucidate its biological mechanisms. The expression profile of lncRNAs in the placentas of pregnant women with NDFMS was investigated using an Agilent Human LncRNA Microarray. Differentially expressed lncRNAs were selected for validation using reverse transcription-quantitative polymerase chain reaction (RT-qPCR).

Organism: Homo sapiens

Type: **Expression profiling by array**; Non-coding RNA profiling by array

Platform: GPL20115 2 Samples

Download data: [TXT](#), [XLS](#)

Series Accession: GSE199148 ID: 200199148

[ZNF521 enhances MLL-AF9-dependent hematopoietic stem cell transformation in acute myeloid leukemias by](#)

241. [altering the gene expression landscape](#)

(Submitter supplied) Leukemias derived from the MLL-AF9 rearrangement rely on deranged transcriptional networks. ZNF521, a transcription co-factor implicated in the control of hematopoiesis, has been proposed to sustain leukemic transformation in collaboration with other oncogenes. We demonstrate here that ZNF521 mRNA levels correlate with specific genetic aberrations: in particular, the highest expression is observed in AMLs bearing MLL rearrangements, while the lowest is detected in AMLs with FLT3-ITD, NPM1 or CEBPa double mutations. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL23126 10 Samples

Download data: [CEL](#)

Series Accession: GSE181006 ID: 200181006

[Target-agnostic discovery of Rett Syndrome therapeutics by coupling computational network analysis and](#)

242. [CRISPR-enabled in vivo disease modeling](#)

(Submitter supplied) It is difficult to develop effective treatments for neurodevelopmental genetic disorders, such as Rett syndrome, which are caused by a single gene mutation but trigger changes in numerous other genes, and thereby also severely impair functions of organs beyond the central nervous system (CNS). This challenge is further complicated by the lack of sufficiently broad and biologically relevant drug screens, and the inherent complexity in identifying clinically relevant targets responsible for diverse phenotypes. [more...](#)

Organism: Xenopus laevis

Type: **Expression profiling by array**

Platform: GPL10756 13 Samples

Download data: [CEL](#)

Series Accession: GSE199049 ID: 200199049

[OFCD \(Occulofciocardiodental\) patient's PDL \(periodontal ligament cells\) and Healthy control PDL cells](#)

243. (Submitter supplied) Transcriptional profiling of mouse embryonic stem cells comparing Mutant PDL cells and healthy PDL cells to study Radiculomegaly (excessive dental root elongation) Two-condition experiment, Mutant vs. Healthy PDL cells, technological triplicate

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL32064 2 Samples

Download data: [TXT](#)

Series Accession: GSE198708 ID: 200198708

[Maternal folic acid mild over consumption in mice leads to sex-specific transcriptional alterations in E17.5](#)

244. [embryonic cerebrum](#)

(Submitter supplied) Food fortification of folic acid (FA) and increased use of vitamin supplements have raised concerns over high folate intake periconceptionally. We reported that diet containing 5-fold higher FA than recommended for mice (5xFASD) during pregnancy, resulted in neurobehavioral abnormalities (hyperactivity and short-term memory impairment) in

newborns. Our goal was to determine the origins of these changes and the underlying mechanisms by examining potential transcription changes in E17.5 embryonic cerebrum. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL23038 16 Samples

Download data: CEL, XLS, XLSX

Series Accession: GSE193352 ID: 200193352

[Exon Level Expression Profiling:HTA 2.0 array](#)

245. (Submitter supplied) Transcriptome analysis of RNA samples extracted from human placenta FFPE sample RNA expression level comparison

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL17586 2 Samples

Download data: CEL, CHP

Series Accession: GSE198252 ID: 200198252

[Differential gene expression in leukemic blasts and leukemic stem cells \(LSC\) sorted from pediatric AML](#)

246. [patients compared to control myeloblasts and hematopoietic stem cells \(HSC\) sorted from cord blood](#)

(Submitter supplied) Purpose: Currently, only few reports address the molecular abnormalities of LSC compared to HSC in pedAML. Identifying LSC aberrations is crucial to tackle the high relapse rate and to develop therapeutic targeting strategies for LSC elimination, while ensuring salvage of normal HSCs. Methods: Blasts and stem cells were separated based on CD38 expression (positive and negative, respectively). Leukemic blasts (n=4), LSCs (n=3) and lymphocytes (n=4) were sorted from 4 de novo pedAML patients (two FLT3-ITD, two FLT3 WT). [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL18641 15 Samples

Download data: TXT

Series Accession: GSE128103 ID: 200128103

[Lysophosphatidic acid Shifts Metabolic and Transcriptional Landscapes to Induce a Novel Cellular State in](#)

247. [Human Embryonic Stem Cells](#)

(Submitter supplied) Pluripotent stem cells can be maintained in a continuum of cellular states with distinct features.

Exogenous lipid supplements are commonly utilized to shift the balance of global metabolism relieving the dependence on de novo lipogenesis. However, it is largely unexplored how specific lipid components regulate metabolism and pluripotency state. In this study, we investigate the impact of lipid supplements on human embryonic stem cells (hESCs), and report that signaling lipid lysophosphatidic acid (LPA) is the key component to shift the metabolic landscape in lipid supplement AlbuMAX. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL10558 12 Samples

Download data: TXT

Series Accession: GSE198007 ID: 200198007

[Protein Kinase C Establishes the Signaling Boundary Between Mesodermal and Extraembryonic Lineages in](#)

248. [Human Embryonic Stem Cell Differentiation](#)

(Submitter supplied) The interplay among mitogenic signaling pathways is crucial for proper embryogenesis. These pathways collaboratively act through intracellular master regulators to determine specific cell fates. Identifying the master regulators is critical to understanding embryogenesis and to developing new applications of pluripotent stem cells. In this report, we demonstrate protein kinase C (PKC) as an intrinsic master switch between embryonic and extraembryonic cell fates in the differentiation of human pluripotent stem cells (hPSCs). [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL10558 24 Samples

[Download data: TXT](#)

Series Accession: GSE198006 ID: 200198006

 [Transcriptome Alterations in ASMT Knockout-Induced Depression-Like Behaviors and Exercise Effects](#)

249. (Submitter supplied) Sleep disorder caused by abnormal circadian rhythm is one of the main symptoms and risk factors of depression. N-acetylserotonin methyltransferase (ASMT), the last rate-limiting enzyme of melatonin (MT, a known hormone regulating circadian rhythms), has been reportedly associated with depression. Exercise can regulate circadian rhythm and play an important role in depression treatment. Recently, gene chip has been widely used in depression research. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL21163 12 Samples

[Download data: TXT](#)

Series Accession: GSE197888 ID: 200197888

 [Gene expression changes in NCU10K cells lacking Nedd4](#)

250. (Submitter supplied) Nedd4 is an E3 ubiquitin ligase that has essential roles in neural crest cell development. This study aimed to detect the gene expression changes induced by removing Nedd4 in the neural crest cell line, NCU10K, to define the molecular pathways regulated by Nedd4.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6246 6 Samples

[Download data: CEL](#)

Series Accession: GSE197631 ID: 200197631

 [Single-cell sequencing reveals PDFGR \$\alpha\$ + stromal cell subpopulations that promote proacinar differentiation in embryonic salivary gland organoids](#)

(Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus

Type: **Expression profiling by array**; Expression profiling by high throughput sequencing

4 related Platforms 15 Samples

[Download data: CEL, MTX, TSV](#)

Series Accession: GSE181430 ID: 200181430

 [Expression data from E16 mouse embryonic organoids - grown with epithelium and stroma in the presence or absence of FGF2 \[Mes\]](#)

(Submitter supplied) FGF2 signals BMP7 expression and TGFB/myofibroblast gene inhibition that promotes proacinar differentiation. We have characterized these stromal factors affecting the epithelium using a combination of scRNA Sequencing of whole tissue and transcriptional profiling of the organoid cell compartments.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL20775 6 Samples

[Download data: CEL](#)

Series Accession: GSE181424 ID: 200181424

 [Expression data from E16 mouse embryonic organoids - grown with epithelium and stroma in the presence or absence of FGF2 \[Epi\]](#)

(Submitter supplied) FGF2 signals BMP7 expression and TGFB/myofibroblast gene inhibition that promotes proacinar differentiation. We have characterized these stromal factors affecting the epithelium using a combination of scRNA Sequencing of whole tissue and transcriptional profiling of the organoid cell compartments.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL23038 6 Samples

[Download data: CEL](#)

Series Accession: GSE181423 ID: 200181423

 [Dedifferentiation of human adult Sertoli cells in cross talk with seminoma cells in vitro](#)

254. (Submitter supplied) Germ cell neoplasia in situ (GCNIS) is the noninvasive precursor of testicular germ cell tumors type II (TGCT), the most common cancer in young men. GCNIS originates from embryonic germ cells blocked in their maturation. The causes are unknown. GCNIS is associated with impaired Sertoli cells that express fetal marker keratin 18 (KRT18) and pluripotency factor SOX2. According to the spread theory of the origin of GCNIS, these impaired Sertoli cells are prepubertal cells arrested in their maturation due to genetic anomalies and/ or environmental anti-androgens. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**Platforms: [GPL6480](#) [GPL17077](#) 16 Samples[Download data: GPR](#)

Series Accession: GSE169557 ID: 200169557

 [Transcriptional profile of pericytes and stromal cells in bleomycin lung injury](#)

255. (Submitter supplied) We previously showed that pericyte-like cells derived from the FoxD1-lineage contribute to myofibroblasts following bleomycin-induced lung injury. However, their functional significance in lung fibrosis remains unknown. In this study, we used a model of lung pericyte-like cell ablation to test the hypothesis that pericyte-like cell ablation attenuates lung fibrosis in bleomycin-induced lung injury. Methods: Lung fibrosis was induced by intratracheal instillation of bleomycin. To ablate pericyte-like cells in the lung, diphtheria toxin (DT) was administered to Foxd1-Cre;Rosa26-iDTR mice at two different phases of bleomycin-induced lung injury. For early ablation, we co-administered bleomycin with DT and harvested mice at days 7 and 21. To test the effect of ablation after acute injury, we delivered DT 7 days after bleomycin administration. We assessed fibrosis by lung hydroxyproline content and semiquantitative analysis of picrosirius red-staining. We performed bronchoalveolar lavage to determine cell count and differential. We also interrogated genome-wide mRNA expression at day 7 post injury in whole lung RNA. We focused on the following cell populations for the transcriptional profiling experiments: FoxD1-derived+/Coll-GFP- pericytes (Peri), FoxD1-derived+/Coll-GFP+ pericytes (PeriFibro), and FoxD1-derived-/Coll-GFP+ stromal fibroblasts (Fibro). Results: Compared to DT-insensitive littermates where pericyte-like cells were not ablated, DT-sensitive animals exhibited no difference in fibrosis at day 21 both in the early and late pericyte ablation models. However, early ablation of pericytes reduced acute lung inflammation, as indicated by decreased inflammatory cells. Our data confirm a role for pericytes in regulating pulmonary inflammation in early lung injury.

Organism: Mus musculus

Type: **Expression profiling by array**Platform: [GPL6887](#) 14 Samples[Download data: TXT](#)

Series Accession: GSE184761 ID: 200184761

 [Effects of zinc ions and HrasG12V-activated signaling on gene expression of rat embryonic fibroblasts](#)256. [maintained in serum-free media](#)

(Submitter supplied) To identify intracellular events affected by HrasG12V and zinc ion availability, gene expression profiling was performed with Rat-1·RasValA1, a stably transfected cell line where oncogenic mutant HrasG12V is expressed under the control of an IPTG-inducible promoter. Rat-1·RasValA1 cells were treated for 24 h with or without 5 mM IPTG in serum-free DMEM in the presence or absence of ZnCl₂ supplementation at 3 microm. [more...](#)

Organism: Rattus norvegicus

Type: **Expression profiling by array**Platform: [GPL22440](#) 4 Samples[Download data: TXT](#)

Series Accession: GSE182481 ID: 200182481

 [Identifying target genes for the long noncoding RNA, GATA2-AS1](#)

257. (Submitter supplied) We have identified a set of endothelial-enriched long noncoding RNAs (lncRNAs) in another experiment. In this experiment, we aim to identify genes that are regulated by the GATA2-AS1 lncRNA. We have depleted GATA2-AS1 using two distinct siRNA in human umbilical vein endothelial cells (HUVEC)

Organism: Homo sapiens

Type: **Expression profiling by array**; Non-coding RNA profiling by array

Platform: GPL16956 9 Samples

Download data: [TXT](#)

Series Accession: GSE197376 ID: 200197376

[Contribution of the hedgehog-signaling pathway to Wolffian Duct development.](#)

258. (Submitter supplied) Introduction and objectives: Proper In utero Wolffian duct (WD) development requires androgens and is essential to epididymis formation and male fertility. However, non-hormonal factors that control WD homeostasis and development remain largely unknown. In this study, we investigated the contribution of Hedgehog signaling pathway to Wolffian duct development by combining pharmacological approaches on organotypic cultures of WD with microarray profiling. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL23038 10 Samples

Download data: [CEL](#)

Series Accession: GSE145816 ID: 200145816

[Transcriptomic analysis in Caenorhabditis elegans exposed to organic and inorganic forms of arsenic or mercury](#)

259. (Submitter supplied) Arsenic and mercury are known chemical hazards. The differences in effects from organic and inorganic forms of these toxic elements is less well understood, however. The nematode *Caenorhabditis elegans* (*C. elegans*) is a suitable model to investigate the toxicity of environmental hazards. In this study, the transcriptomic profiles of *C. elegans* exposed to inorganic mercury chloride ($HgCl_2$) and sodium (meta)arsenite ($NaAsO_2$) were assessed alongside organic methylmercury chloride (me $HgCl$) and dimethylarsinic acid (DMA). [more...](#)

Organism: Caenorhabditis elegans

Type: **Expression profiling by array**

Platform: GPL10094 16 Samples

Download data: [TXT](#)

Series Accession: GSE196891 ID: 200196891

[Signal requirement for cortical potential of transplantable human neuroepithelial stem cells \[array\]](#)

260. (Submitter supplied) The cerebral cortex develops from dorsal forebrain neuroepithelial progenitor cells. Initial expansion of the progenitor cell pool is followed by the generation of neurons of all the cortical layers and later, astrocytes and oligodendrocytes. However, the regulatory pathways that control the expansion and maintenance of the neuroepithelial progenitor cell pool are currently unknown. Here we define six basic pathway components that regulate proliferation of cortically specified human neuroepithelial stem cells (cNESC)s in vitro without the loss of developmental potential. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL17586 28 Samples

Download data: [CEL](#)

Series Accession: GSE185258 ID: 200185258

[Microarray Analysis of GCNF mutant and wt E9.0 embryos in Mus musculus](#)

261. (Submitter supplied) Neural crest cells are migratory progenitor cells that contribute to nearly all tissues and organs throughout the body. Their formation, migration and differentiation are regulated by a multitude of signaling pathways, that when disrupted can lead to disorders termed neurocristopathies. While work in avian and amphibian species has revealed essential factors governing the specification and induction of neural crest cells during gastrulation and neurulation in non-mammalian species, their functions do not appear to be conserved in mice, leaving major gaps in our understanding of neural crest cell formation in mammals. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL1261 4 Samples

Download data: [CEL](#)

Series Accession: GSE166458 ID: 200166458

[Analysis of gene expression in uniparental mouse blastocysts produced in different culture media](#)

262. (Submitter supplied) In the field of in vitro **embryo** production it is generally thought that the culture media are not as good as the oviductal fluid, resulting in detrimental changes of embryonic gene expression. Yet in vitro **embryo** culture (IVC) is one of the pillars of the assisted reproductive technologies. Therefore, unintended effects on gene expression may impact on the health of ART babies (PMID 27554442). Granted, human ART has many more components than just the culture media, but, the practice of **embryo** culture superimposes with the phase of life when cellular totipotency is present - that's why **embryo** culture media receive special attention. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL20775 15 Samples

Download data: CEL

Series Accession: GSE111112 ID: 20011112

 [LIF-responsive genes in monocytes from healthy donors](#)

263. (Submitter supplied) LIF has an important role in immunosuppression in different scenarios, such as in **embryo** implantation in the uterus, autoimmune disease or organ transplantation. In tumor progression it has been largely demonstrated the importance of immune system. The fact that LIF is highly expressed in certain tumor types, in addition to its immunomodulatory properties, led us to hypothesize that tumors expressing high levels of LIF might be promoting an immune-tolerant microenvironment precluding the anti-tumor immune response. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL17692 5 Samples

Download data: CEL

Series Accession: GSE79851 ID: 200079851

 [Primordial germ cells identified as one potential cell of origin of MYC rhabdoid tumors](#)

264. (Submitter supplied) Rhabdoid tumors (RT) are rare and highly aggressive pediatric neoplasms. Their epigenetically-driven intertumoral heterogeneity is well described; however, the cellular origin of RT remains an enigma. Here, we established and characterized different genetically engineered mouse models driven under the control of distinct promoters and being active in early progenitor cell types with diverse embryonic onsets. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL16570 41 Samples

Download data: CEL

Series Accession: GSE188654 ID: 200188654

 [Microarray analysis of Replicative senescence and TNF- \$\alpha\$ induced senescence in Human umbilical vein](#)

265. [endothelial cells \(HUVECs\)](#)

(Submitter supplied) Cellular senescence is a dynamic tumor suppression mechanism that limits the proliferation of impaired cells, by executing a stable cell cycle arrest. Understanding the molecular pathways and regulatory circuits that are involved in the process of senescence is presently incomplete. In this study, we determined the changes in gene expression during the establishment of replicative senescence, by comparing the expression profiles of young and senescent human umbilical vein endothelial cells (HUVECs). [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL6244 12 Samples

Download data: CEL, TXT

Series Accession: GSE195517 ID: 200195517

 [Exosomal RNA expression profiles and their prediction performance in gestational diabetes mellitus patients](#)

266. [with macrosomia](#)

(Submitter supplied) Exosomal RNAs in cord blood may allow intercellular communication between maternal and fetus. We aimed to establish exosomal RNA expression profiles in cord blood exosomes from gestational diabetes mellitus (GDM)

patients with macrosomia. We used microarray technology to establish the differential mRNA, lncRNA and circRNA expression profiles in cord blood exosomes from GDM patients with macrosomia compared with normal controls. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**; Non-coding RNA profiling by array

Platform: GPL22120 6 Samples

Download data: [TXT](#), [XLSX](#)

Series Accession: GSE194119 ID: 200194119

[Expression profiling of Ciona intestinalis initial tailbud stage embryos expressing mutant forms of the](#)

267. [transcription factor Ci-XBP1 in the notochord.](#)

(Submitter supplied) XBP transcription factors are well-known regulators of the unfolded protein response and are required for plasma cell differentiation. However, recent studies have shown that the XBP1 gene is also expressed in the developing notochord of Ciona and various vertebrates, and to date its role in the formation of this organ is largely uncharacterized. We identified putative targets of Ci-XBP1 through a microarray screen, using RNAs extracted from embryos expressing mutant forms of this transcriptional regulator in the notochord. [more...](#)

Organism: Ciona intestinalis

Type: **Expression profiling by array**

Platform: GPL15657 9 Samples

Download data: [CEL](#)

Series Accession: GSE46751 ID: 200046751

[Expression data of LX2 transfected with Adenoviruses overexpressing Gata4 or GFP](#)

268. (Submitter supplied) Deactivation of aHSCs has emerged as a novel and promising therapeutic approach for liver fibrosis. However, our knowledge of the master regulators involved in the deactivation of fibrotic HSCs is still limited. The transcription factor GATA4 has been previously shown to play an important role in embryonic hepatic stellate cells quiescence. We aim to evaluate whether GATA4 is able to revert the active phenotype of LX2 cells. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL16686 6 Samples

Download data: [CEL](#), [CHP](#)

Series Accession: GSE168818 ID: 200168818

[Expression data of shDIDO1 and shCtrl HUVEC cell lines](#)

269. (Submitter supplied) DIDO1(Death inducer-obliterator) gene localizes in the nucleus and cytosol, which is required in the early steps during the tumor progression and metastasis. We analyzed the GeneChip expression profiles of human umbilical vein endothelial cells transfected by RNAi lentiviral vectors, shDIDO1 cell line and shCtrl cell lines

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL15207 14 Samples

Download data: [CEL](#)

Series Accession: GSE156713 ID: 200156713

[Integrative transcriptomics reveals activation of innate immune responses and inhibition of inflammation during](#)

270. [oral immunotherapy for egg allergy in children](#)

(Submitter supplied) The objective of the study was to investigate how oral immunotherapy (OIT) for food allergy modulates inflammation and immune cell responses. The blood cell transcriptome of 50 children receiving egg OIT was profiled using peripheral blood mononuclear cell (PBMC) samples obtained at baseline and after 3 and 8 months of OIT.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL21185 176 Samples

Download data: [XLSX](#)

Series Accession: GSE178460 ID: 200178460

[Effect of prenatal sulforaphane \(SUL\) on Nrf2+/+ and Nrf2-/+ placenta](#)

271. (Submitter supplied) Results: In Nrf2+/+ placenta, genes involved in estrogen receptor signaling and reproductive system development (e.g., Med subfamily, Igf1r, Ncor2), vasculature and embryonic development (e.g., Adamdec1, Pdgfrb, Col8a2, Sema3g, Krt5, Lce1a1), and inhibition of prenatal death and cell morbidity (e.g., Dnmt3a, Col4a2) were regulated by SFN. Multiple granzyme isozymes (Gzmd, Gzmg, Gzmf, Gzmc) and oxidoreduction genes (e.g., Gstt1, Gstt2, Prdx5, Hao3, Hsd17b10, Pecr) were suppressed in Nrf2+/+ placenta treated with SFN. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL1261 12 Samples

Download data: CEL, CHP

Series Accession: GSE164700 ID: 200164700

[Effect of prenatal sulforaphane \(SUL\) on hyperoxia-induced lung injury in Nrf2+/+ and Nrf2-/+ neonates](#)

272. (Submitter supplied) Results: Prenatal SUL altered baseline lung genes involved in organ/cell development and growth (e.g., Ibsp, Ctsk, Igfbp5) and ARE responses (e.g., Aldh3a1, Maff, Mafg) in Nrf2+/+ neonates and in cell morphogenesis and cell death and organismal injury/abnormality inhibition (e.g., Neat1, Nox4, Vegfa, Igfbp2, Trp53) in Nrf2-/+ neonates. In hyperoxia-exposed lung, prenatal SUL increased organogenesis/development genes (e.g., Prss35, Cep128) and decreased inflammatory genes (H2-D1, Cd40, Lcn2, Cdh22) in Nrf2+/+ pups. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL1261 21 Samples

Download data: CEL, CHP

Series Accession: GSE164699 ID: 200164699

[Transcripts identified by microarray analysis that were deregulated in P4 Tbx18\(cre/+\);Rbpj\(fx/fx\) \(Rbpj-cKO\) ureters](#)

273. ureters

(Submitter supplied) Evaluation of transcriptional changes in the P4 ureters upon loss of Rbpj in the ureteric mesenchyme.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL27545 2 Samples

Download data: TXT

Series Accession: GSE184597 ID: 200184597

[Transcripts identified by microarray analysis that were deregulated in E13.5 Pax-2cre;Fgfr1\(fl/?\);Fgfr2\(fl/fl\) \(Egfr2cKO\) ureters.](#)

274. (Egfr2cKO) ureters.

(Submitter supplied) Evaluation of the transcriptional changes in E13.5 ureters upon loss of Fgfr2 (and reduction of Fgfr1) in the ureteric epithelium.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL27545 2 Samples

Download data: TXT

Series Accession: GSE178093 ID: 200178093

[Transcripts identified by microarray analysis that were deregulated in E14.5 Tbx18\(cre/+\);Gata6\(fl/fl\) \(Gata6cKO\) ureters](#)

275. (Gata6cKO) ureters

(Submitter supplied) Evaluation of the transcriptional changes in E14.5 ureters upon loss of Gata6 in the ureteric mesenchyme.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL27545 2 Samples

Download data: TXT

Series Accession: GSE174614 ID: 200174614

[Transcripts identified by microarray analysis that were deregulated in E18.5 Tbx18\(cre/+\);Rbpj\(f/f\) \(Rbpj-cKO\)](#)276. [ureters](#)

(Submitter supplied) Evaluation of the transcriptional changes in E18.5 ureters upon loss of Rbpj in the ureteric mesenchyme.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL11202 2 Samples

Download data: [TXT](#)

Series Accession: GSE169662 ID: 200169662

 [Transcripts identified by microarray analysis that were deregulated in E14.5 Tbx18\(cre/+\);Rbpj\(f/f\) \(Rbpj-cKO\)](#)277. [ureters](#)

(Submitter supplied) Evaluation of the transcriptional changes in E14.5 ureters upon loss of Rbpj in the ureteric mesenchyme.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL27545 2 Samples

Download data: [TXT](#)

Series Accession: GSE169661 ID: 200169661

 [Gene expression profiles from the cardiac tissue of HIPK2-knockout and Wild Type \(WT\) mice](#)

278. (Submitter supplied) We use Affymetrix Gene Chip Array to screen the targets of HIPK2 in heart. Total RNA was extracted from 8-week-old HIPK2-knockout and Wild Type (WT) mice.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL21163 10 Samples

Download data: [TXT](#)

Series Accession: GSE169429 ID: 200169429

 [Caliban regulates mitochondrial morphology and redox state in enterocytes to maintain intestinal homeostasis in Drosophila](#)279. [in Drosophila](#)

(Submitter supplied) Precise regulation of stem cell activity is crucial for tissue homeostasis. In Drosophila, intestinal stem cells (ISCs) maintain the midgut epithelium and respond to oxidative challenges by increasing proliferation rates. However, the connection between intestinal homeostasis and redox signaling remains obscure. Here we identify Caliban (Clbn) as a novel mitochondrial protein involved in regulating the cellular redox state in enterocytes (ECs) and the proliferative activity of ISCs. [more...](#)

Organism: Drosophila melanogaster

Type: **Expression profiling by array**

Platform: GPL1322 6 Samples

Download data: [CEL](#)

Series Accession: GSE125032 ID: 200125032

 [Evolutionary Origin of Vertebrate Oct4/POUV Functions in Supporting Pluripotency](#)280. (Submitter supplied) Pluripotency is the capacity of early embryonic cells to make all the future lineages of the organism, and the existence of a pluripotent population of cells is important to both germ cell function and the pool of progenitor cells that enable vertebrate development to proceed over time through the process of gastrulation. Oct4, a class V POU transcription factor, is required for maintenance of pluripotency in embryonic stem cells (ESCs) and induction of pluripotency via transcription factor reprogramming. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL13912 6 Samples

Download data: [TXT](#)

Series Accession: GSE183049 ID: 200183049

[Analysis of mouse monozygotic twin blastocysts produced in two different culture media](#)

281. (Submitter supplied) Following fertilization in mammals, it is generally accepted that totipotent cells are exclusive to the zygote and to each of the two blastomeres originating from the first mitotic division. We counter that this classic view needs to be revised, because we have presented compelling evidence the sister blastomeres are both totipotent in only a subset of 2-cell stage mouse embryos (PMID 28811525). Building on our previous findings, we here ask the question if the differences between sister blastomeres can be modulated experimentally. [more...](#)

Organism: Mus musculus

Type: Expression profiling by array

Platform: GPL20775 30 Samples

Download data: CEL

Series Accession: GSE110735 ID: 200110735

 [In Vivo Organ Regeneration via Stroma-Dependent Adult Lineage Reprogramming](#)

282. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Drosophila melanogaster; Gallus gallus; Rattus norvegicus; Mus musculus; Caenorhabditis elegans; Danio rerio; Homo sapiens

Type: Expression profiling by array; Non-coding RNA profiling by array

Platforms: GPL7202 GPL13992 24 Samples

Download data: TXT

Series Accession: GSE37309 ID: 200037309

 [In Vivo Organ Regeneration via Stroma-Dependent Adult Lineage Reprogramming \(mRNA\)](#)

283. (Submitter supplied) Remarkable progress has been made in cell fate reprogramming by forced expression of a small number of transcription factors. Major challenges remain, however, in regenerative medicine regarding how to target multiple cell types and direct them to form a functional organ *in vivo*. Here, we demonstrate that, by changing their stromal microenvironment, adult differentiated cells of endodermal origin can be reprogrammed to generate a functional ectodermal organ. [more...](#)

Organism: Mus musculus

Type: Expression profiling by array

Platform: GPL7202 12 Samples

Download data: TXT

Series Accession: GSE37289 ID: 200037289

 [Expression data from HUVEC treated with combinations of IL-1 plus P. santalinus extract](#)

284. (Submitter supplied) HUVEC respond to pro-inflammatory stimuli such as IL-1 by expressing several hundreds of genes including cytokines, chemokines, cell adhesion molecules, and those involved in coagulation, survival/apoptosis, and metabolism. Extract of *P. santalinus* inhibited the expression of certain genes, while leaving other unaffected; thereby a set of responsive and non-responsive genes could be defined, to be further analyzed by bioinformatics.

Organism: Homo sapiens

Type: Expression profiling by array

Platform: GPL23159 4 Samples

Download data: CEL

Series Accession: GSE178106 ID: 200178106

 [Placental Immune alterations in early-onset preeclampsia and late-onset preeclampsia](#)

285. (Submitter supplied) Preeclampsia is a severe placenta-related pregnancy disorder that is generally divided into two subtypes named early-onset preeclampsia (onset <34 weeks of gestation), and lateonset preeclampsia (onset ≥34 weeks of gestation), with distinct pathophysiological origins. Both forms of preeclampsia have been associated with maternal systemic inflammation. However, alterations in the placental immune system have been less well characterized. [more...](#)

Organism: Homo sapiens

Type: Expression profiling by array

Platform: GPL31059 32 Samples

Download data: XLSX

Series Accession: GSE190639 ID: 200190639

- [A balanced Oct4 protein interaction network is crucial for maintaining pluripotency](#)
286. (Submitter supplied) Oct4 is considered a master transcription factor for pluripotent cell self-renewal and **embryo** development. It primarily collaborates with other transcriptional factors or coregulators to maintain pluripotency. However, it is still unclear how Oct4 interacts with its partners. Here, we show that the Oct4 linker interface mediates competing and balanced Oct4 protein interactions which are crucial for maintaining pluripotency. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6885 10 Samples

Download data: [TXT](#)

Series Accession: GSE144305 ID: 200144305

- [γH2A.X Modulates Self-renewal and Differentiation of Human Pluripotent Stem Cells.](#)

287. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platforms: GPL6244 GPL16686 12 Samples

Download data: [CEL](#)

Series Accession: GSE92649 ID: 200092649

- [γH2A.X Modulates Self-renewal and Differentiation of Human Pluripotent Stem Cells. \[HuGene-1_0-st\]](#)

288. (Submitter supplied) Histone variants are important epigenetic regulators known to play a role in governing the processes of self-renewal and lineage specific differentiation . Phosphorylation of the histone variant H2A.X (γH2A.X) has historically been associated with DNA damage response, but more recent investigations have further demonstrated it's role in cell cycle, aging and early development. Through both genetic and chemical targeting approaches, we now reveal a direct involvement of γH2A.X in hPSC self-renewal and differentiation decisions in vitro and in vivo. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL6244 6 Samples

Download data: [CEL](#)

Series Accession: GSE92643 ID: 200092643

- [γH2A.X Modulates Self-renewal and Differentiation of Human Pluripotent Stem Cells. \[HuGene-2_0-st\]](#)

289. (Submitter supplied) Histone variants are important epigenetic regulators known to play a role in governing the processes of self-renewal and lineage specific differentiation . Phosphorylation of the histone variant H2A.X (γH2A.X) has historically been associated with DNA damage response, but more recent investigations have further demonstrated it's role in cell cycle, aging and early development. Through both genetic and chemical targeting approaches, we now reveal a direct involvement of γH2A.X in hPSC self-renewal and differentiation decisions in vitro and in vivo. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL16686 6 Samples

Download data: [CEL](#)

Series Accession: GSE92642 ID: 200092642

- [Analysis of gene expression of hESCs upon genetic modification with EBNA and S/MAR episomal vectors](#)

290. (Submitter supplied) Analysis of the episomal backbone's influence on gene expression. The first hypothesis tested in the present study is that the episomal EBNA vectors, which rely on the EBNA-1 oncprotein for episomal maintenance, have a greater influence on the cells' expression profiles than S/MAR vectors. The second hypothesis tested was that when bacterial sequences are removed from the episomal vector backbone, the gene disturbance is minimal.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL10558 12 Samples

Download data: [TXT](#)

Series Accession: GSE142299 ID: 200142299

- [Investigation of gene expression in murine Shh-Medulloblastoma, ocular lesions of Rax-creERT2::Ctnnb1\(ex3\)Fl/+SmoM2 Fl/+ \(RBS\) mice and healthy murine eyes.](#)
291. [Investigation of gene expression in murine Shh-Medulloblastoma, ocular lesions of Rax-creERT2::Ctnnb1\(ex3\)Fl/+SmoM2 Fl/+ \(RBS\) mice and healthy murine eyes.](#)

(Submitter supplied) The objective of this study was to compare gene expression of RBS ocular lesions with human intraocular medulloepithelioma (IO-MEPL), using murine and human Shh-Medulloblastomas as a reference.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL28581 12 Samples

Download data: RCC

Series Accession: GSE173758 ID: 200173758

- [Terahertz Exposure Enhances Neuronal Synaptic Transmission and Oligodendrocyte Differentiation in vitro](#)

292. (Submitter supplied) Terahertz (THz) frequency occupies a large portion of the electromagnetic spectrum that is between the infrared and microwave region. Recent advances in THz application have stimulated interests regarding the biological effects associated with this frequency range. In current study, we report that irradiation with a single-frequency THz laser on primary mice cortical neuron cultures and oligodendrocyte cultures results in dose dependent irradiation specific changes in cellular function and gene expression. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL21163 6 Samples

Download data: TXT

Series Accession: GSE178729 ID: 200178729

- [Alveolar organoid model](#)

293. (Submitter supplied) Rationale: Alveolar epithelial type 2 (AT2) cells are stem/progenitor cells in the adult lung and their maintenance and regulation is achieved through their interaction with mesenchymal cells which constitute their niches. However, the precise identity of the niche cells is still elusive. Objectives: To characterize the niche cells capable of supporting the self-renewal of AT2 stem cells in the murine model. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL21810 8 Samples

Download data: GPR

Series Accession: GSE162859 ID: 200162859

- [Nicotinamide promotes human pluripotent stem cells differentiation into cardiomyocytes \[2\]](#)

294. (Submitter supplied) Nicotinamide, the amide form of vitamin B3, is essential to maintain the human fetal development. It benefits the ectoderm and endoderm development, but its influence in mesoderm differentiation is elusive. In this study, we reported that nicotinamide regulated the gene expression of cardiovascular system, and it induced functional cardiomyocytes which was independent of canonical WNT signaling. Through a kinase screening, we found that nicotinamide inhibited the activity of P38δ to promote cardiomyocyte differentiation. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL10558 4 Samples

Download data: TXT

Series Accession: GSE154454 ID: 200154454

- [Nicotinamide promotes human pluripotent stem cells differentiation into cardiomyocytes \[1\]](#)

295. (Submitter supplied) Nicotinamide, the amide form of vitamin B3, is essential to maintain the human fetal development. It benefits the ectoderm and endoderm development, but its influence in mesoderm differentiation is elusive. In this study, we reported that nicotinamide regulated the gene expression of cardiovascular system, and it induced functional cardiomyocytes which was independent of canonical WNT signaling. Through a kinase screening, we found that nicotinamide inhibited the activity of P38δ to promote cardiomyocyte differentiation. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL10558 2 Samples

[Download data: TXT](#)

Series Accession: GSE154453 ID: 200154453

 [Nicotinamide promotes human pluripotent stem cells differentiation into cardiomyocytes](#)

296. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL10558 6 Samples

[Download data](#)

Series Accession: GSE154455 ID: 200154455

 [Gene analysis of tumor cells from mice with the Treg-specific deletion of Blimp1 compared to WT mice](#)297. [\(NanoString Cancer\)](#)

(Submitter supplied) We observed that mice with the Treg-specific deletion of Blimp1 had delayed and smaller tumor growth associated with the activation of tumor-infiltrating immune effector cells. To determine what extent disruptions of Treg suppressive activity by a specific deletion of Blimp1 could impact on the tumor, we assessed the gene expression of sorted tumor cells by NanoString analysis.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL28581 4 Samples

[Download data: XLSX](#)

Series Accession: GSE178134 ID: 200178134

 [Gene analysis of tumor cells from mice with the Treg-specific deletion of Blimp1 compared to WT mice](#)298. [\(NanoString Immune\)](#)

(Submitter supplied) We observed that mice with the Treg-specific deletion of Blimp1 had delayed and smaller tumor growth associated with the activation of tumor-infiltrating immune effector cells. To determine what extent disruptions of Treg suppressive activity by a specific deletion of Blimp1 could impact on the tumor, we assessed the gene expression of sorted tumor cells by NanoString analysis.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL29428 5 Samples

[Download data: XLSX](#)

Series Accession: GSE178133 ID: 200178133

 [Expression data from proximal tubular cells of proximal tubular cell-specific KAT5 knockout mice](#)

299. (Submitter supplied) Isolated proximal tubular cells from proximal tubular cell-specific KAT5 knockout mice for RNA extraction and hybridization on Affymetrix microarrays. We sought to obtain the physiological significance of KAT5 in proximal tubular cells.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL23038 2 Samples

[Download data: CEL, CHP](#)

Series Accession: GSE168535 ID: 200168535

 [Transcriptional impacts of lipids on hESC](#)

300. (Submitter supplied) Pluripotent stem cells can be maintained in a continuum of cellular states with distinct features.

Exogenous lipid supplements are commonly utilized to shift the balance of global metabolism relieving the dependence on de novo lipogenesis. However, it is largely unexplored how specific lipid components regulate metabolism and pluripotency state. In this study, we investigate the impact of lipid supplements on human embryonic stem cells (hESCs), and report that signaling lipid lysophosphatidic acid (LPA) is the key component to shift the metabolic landscape in lipid supplement AlbuMAX. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL10558](#) 7 Samples

Download data: [TXT](#)

Series Accession: GSE165892 ID: 200165892

- [Expression data from ethanol extract of Aurantiochytrium Sp. \(EEA\)-treated human amnion epithelial cells \(hAECS\)](#)
- 301.

(Submitter supplied) Gene expression profiling reveals a potential role of EEA in neural induction and neuronal differentiation of hAECS. hAECS were isolated from discarded term placenta and were treated with EEA at the concentration of 20 µg/ml for seven days. Microarray gene expression profiling was conducted for three biological replicates of EEA-treated and untreated control cells.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL13667](#) 6 Samples

Download data: [CEL](#), [CHP](#), [TXT](#)

Series Accession: GSE188411 ID: 200188411

- [Effect of maternal iron deficiency on placental gene expression on gestational day 18.5 in rats](#)

302. (Submitter supplied) Iron deficiency occurs when iron demands chronically exceed intake, and is particularly prevalent in pregnant women. Iron deficiency during pregnancy poses health risks for the baby. The placenta serves as the interface between a pregnant mother and her baby; thus, maternal iron deficiency may indirectly impact fetal growth and development by altering placental function. In this study, pregnant Sprague-Dawley rats were fed either a low-iron or iron-replete diet starting two weeks before mating. [more...](#)

Organism: Rattus norvegicus

Type: **Expression profiling by array**

Platform: [GPL23040](#) 8 Samples

Download data: [CEL](#)

Series Accession: GSE163226 ID: 200163226

- [R4 RGS subfamily proteins regulates human hematopoietic stem cell engraftment](#)

303. (Submitter supplied) We have employed whole genome microarray expression profiling to identify genes differentially expressed in human cord blood CD34+ cells overexpressing Regulator of G protein Signaling (RGS) proteins.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL16686](#) 16 Samples

Download data: [CEL](#)

Series Accession: GSE98453 ID: 200098453

- [Expression data from hepatocyte-like cells \(HLCs\) differentiated from human induced pluripotent stem cells \(iPSCs\)](#)

304. (Submitter supplied) We devised two hepatocyte differentiation methods, namely Method 1 (M1) and Method 2 (M2), through modifying existing well-known hepatocyte differentiation strategies, and compared the resultant cells phenotypically, functionally and transcriptomically at different stages of hepatocyte differentiation. !Series_summary =We used microarrays to compare the global gene expression of the HLCs differentiated using the two methods, M1 and M2.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL15207](#) 15 Samples

Download data: [CEL](#), [CHP](#)

Series Accession: GSE187011 ID: 200187011

- [Sperm transcriptome of infertile men](#)

305. (Submitter supplied) Infertility is a widespread health problem, with rising incidence worldwide. Whether the infertility is caused by genetic or environmental factors, the reason for inability to reproduce can be the too low number of sperm or

morphological or functional abnormality of the sperm. Therefore there can be a certain possibility that divergent causes would converge in common mechanisms impairing sperm functionality. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL17692 24 Samples

Download data: CEL

Series Accession: GSE160749 ID: 200160749

[Sphere-derived multipotent progenitor cells obtained from human oral tissue neural crest-derived cells](#)

306. (Submitter supplied) The purpose of this study was to isolate neural crest stem cells from apical papilla, periodontal ligament and oral mucosa.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL21185 9 Samples

Download data: TXT

Series Accession: GSE164327 ID: 200164327

[Gene expression changes induced in mouse bone marrow by placenta growth factor \(PIGF\) overexpression.](#)

307. (Submitter supplied) Placenta growth factor (PIGF) is a member of the vascular endothelial growth factor family and plays an important role in adult pathological angiogenesis. To further investigate PIGF functions in tumor growth and metastasis formation, we used transgenic mice overexpressing PIGF. Recent studies demonstrate that tumor vascularization does not exclusively rely on preexisting vessels but also depends on bone marrow derived progenitor cells. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL8321 8 Samples

Download data: CEL

Series Accession: GSE52414 ID: 200052414

[Porphyromonas gingivalis alters gene expressions in the liver and brown adipose tissue, and induces](#)

308. [gestational obesity and underweight of fetus in pregnant mice \[Liver\]](#)

(Submitter supplied) The aim of this study was to evaluate the effect of oral and intravenous administration of sonicated P.gingivalis to the liver and brown adipose tissue tissueof pregnant mice

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL21163 8 Samples

Download data: TXT

Series Accession: GSE180189 ID: 200180189

[Porphyromonas gingivalis alters gene expressions in the liver and brown adipose tissue, and induces](#)

309. [gestational obesity and underweight of fetus in pregnant mice \[BAT\]](#)

(Submitter supplied) The aim of this study was to evaluate the effect of oral and intravenous administration of sonicated P.gingivalis to the liver and brown adipose tissue tissueof pregnant mice

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL21163 8 Samples

Download data: TXT

Series Accession: GSE180115 ID: 200180115

[Linc1548 promotes the transition of epiblast stem cells into neural progenitors by engaging OCT6 and SOX2](#)

310. (Submitter supplied) The transition of embryonic stem cells from the epiblast stem cells (EpiSCs) to neural progenitor cells (NPCs), name as the neural induction process, is crucial for cell fate determination of neural differentiation. However, the mechanism of this transition is unclear. Here, we identified a long non-coding RNA (linc1548) as a critical regulator of neural differentiation of mouse embryonic stem cells (mESCs). [more...](#)

Organism: Mus musculus
 Type: **Expression profiling by array**
 Platform: GPL21810 2 Samples
[Download data: TXT, XLSX](#)
 Series Accession: GSE163870 ID: 200163870

[Expression factors for oxalate stimulation in HEK293T cells](#)

311. (Submitter supplied) parental HEK293T were challenged with 1064 µg/cm² calcium oxalate monohydrate (COM) or sodium oxalate (NaOx) 4mM or vehicle for 24 hours and DNA microarray was performed. We observed and selected two-fold upregulation of laminin, beta 3 (LAMB3), early growth response 1 (EGR1), gremlin 1, DAN family BMP antagonist, Ca⁺⁺-dependent secretion activator 2, Ras association domain family member 3, interleukin 33 and bone morphogenetic protein 8a , and two-fold down-regulation of interleukin 37 and intercellular adhesion molecule 1 in COM lord compared to vehicle.

Organism: Homo sapiens
 Type: **Expression profiling by array**
 Platform: GPL20844 3 Samples
[Download data: TXT, XLSX](#)
 Series Accession: GSE186676 ID: 200186676

[Intrauterine hyponutrition reduces fetal testosterone production and postnatal sperm count in the C57BL/6N](#)

312. (Submitter supplied) There has been growing interest in the relationship between maternal undernutrition and reproductive disorders in male offspring. In the present study, we determined the effects of maternal calorie restriction throughout the critical period for in utero development of the male reproductive system, termed the “masculinization programming window” on the reproductive system of mice. The intratesticular testosterone concentration of the fetuses of calorie-restricted (R) dams was lower than in control fetuses at 17.5 days post coitum. [more...](#)

Organism: Mus musculus
 Type: **Expression profiling by array**
 Platform: GPL21810 10 Samples
[Download data: TXT](#)
 Series Accession: GSE186345 ID: 200186345

[Mechanistic Target of Rapamycin Complex 2 \(mTORC2\) regulation of the primary human trophoblast cell](#)

313. [transcriptome](#)

(Submitter supplied) Differential gene expression following the silencing of rictor and raptor to identify genes regulated by mTORC2 in primary human trophoblast (PHT) cells.

Organism: Homo sapiens
 Type: **Expression profiling by array**
 Platform: GPL10558 12 Samples
[Download data: IDAT, TXT](#)
 Series Accession: GSE185949 ID: 200185949

[Enhanced glucose metabolism through activation of HIF-1α covers the energy demand in a rat embryonic heart](#)

314. [primordium after heartbeat initiation.](#)

(Submitter supplied) The initiation of heartbeat is an essential step in cardiogenesis in the heart primordium, but it remains unclear how intracellular metabolism responds to increased energy demands after heartbeat initiation. In this study, embryos in Wistar rats at embryonic day 10, at which heartbeat begins in rats, were divided into two groups by the heart primordium before and after heartbeat initiation and their metabolic characteristics were assessed. [more...](#)

Organism: Rattus norvegicus
 Type: **Expression profiling by array**
 Platform: GPL15084 6 Samples
[Download data: TXT](#)
 Series Accession: GSE185702 ID: 200185702

[Myeloid amino acid metabolism supports solid tumor malignancy](#)

315. (Submitter supplied) Cancer immunosuppression involves cellular pathways appropriated by tumors to escape immune surveillance but are normally required for tissue homeostasis and repair, self-tolerance, and successful transplantation. Among these pathways, enzymes that degrade tryptophan and arginine are thought to suppress activated T cells in the tumor microenvironment and are therefore attractive drug targets. However, how amino acid metabolism controls the development and progression of cancer has remained elusive, since commonly used implantable tumor models may not faithfully recapitulate the complex cellular and biochemical interactions within tumor microenvironments. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL16570 6 Samples

Download data: CEL

Series Accession: GSE126024 ID: 200126024

[Changes of gene expression related to cellular senescence in human umbilical cord-derived mesenchymal](#)

316. [stem cells](#)

(Submitter supplied) Mesenchymal stem cells (MSCs) are recognized as potential treatments for multiple degenerative and inflammatory disorders as a number of animal and human studies have indicated their therapeutic effects. There are also several approved medicinal products manufactured using these cells. For large-scale manufacturing requirements, the in vitro expansion of harvested MSCs is essential. Multiple subculturing of MSCs, however, provokes cellular senescence process which is known to deteriorate the therapeutic efficacy of the cells. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL16686 4 Samples

Download data: CEL

Series Accession: GSE183995 ID: 200183995

[Agilent zebrafish V3 array 4'44K microarray-Aflatoxin B1 treated with 6-48 hpf zebrafish embryos](#)

317. (Submitter supplied) To investigate the effects of Aflatoxin B1 on gene expressions in zebrafish embryos.

Organism: Danio rerio

Type: **Expression profiling by array**

Platform: GPL14664 2 Samples

Download data: TXT

Series Accession: GSE121125 ID: 200121125

[Inhibition of vascular growth by modulation of the AEA/FAAH axis](#)

318. (Submitter supplied) Inhibition of FAAH and AEA accumulation reduces angiogenesis.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL10558 12 Samples

Download data: IDAT, TXT

Series Accession: GSE152552 ID: 200152552

[A molecular framework for control of oriented cell division in the Arabidopsis embryo](#)

319. (Submitter supplied) Premitotic control of cell division orientation is critical for plant development, as cell walls prevent extensive cell remodelling or migration. Whilst many divisions are proliferative and add cells to existing tissues, some divisions are formative, and generate new tissue layers or growth axes. Such formative divisions are often asymmetric in nature, producing daughters with different fates. We have previously shown that in the *Arabidopsis thaliana* **embryo**, developmental asymmetry is correlated with geometric asymmetry, creating daughter cells of unequal volume. [more...](#)

Organism: Arabidopsis thaliana

Type: **Expression profiling by array**

Platform: GPL22599 7 Samples

Download data: CEL

Series Accession: GSE165986 ID: 200165986

[The role of transcriptome and proteome in developmental competence of eggs of Sander lucioperca](#)

320. (Submitter supplied) Molecular profiling of the eggs is an excellent approach aiming at understanding biological processes and mechanisms conditioning developmental competence in finfishes and, consequently, reproductive fitness. Despite many efforts, it is still unclear what is the specific role of transcriptome and proteome in determination of egg quality in Teleostei fishes. The aim of this study was to perform integrated transcriptomic-proteomic analysis of eggs of pikeperch – a commercially relevant freshwater fish species. [more...](#)

Organism: Sander lucioperca

Type: **Expression profiling by array**

Platform: [GPL27937](#) 10 Samples

[Download data: TXT](#)

Series Accession: GSE167376 ID: 200167376

[The amniotic fluid cell-free transcriptome in spontaneous preterm labor](#)

321. (Submitter supplied) The amniotic fluid (AF) cell-free (cf) RNA was shown to reflect physiological and pathological processes in pregnancy, but its value in prediction of spontaneous preterm delivery is unknown. Here we profiled cfRNA in AF samples collected from women who underwent transabdominal amniocentesis after an episode of spontaneous preterm labor and subsequently delivered within 24h (n=10) or later (n=28) in gestation. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL29735](#) 38 Samples

[Download data: CEL](#)

Series Accession: GSE166956 ID: 200166956

[Gene expression in bovine SCNT vs AI D30 foetal tissues \(whole body with no head, no tail\) in vivo developed in Holstein or Normande cows](#)

322. (Submitter supplied) Evaluate the influence of somatic cell nuclear transfer on gene expression profiles in foetal tissues (whole bodies) at D30

Organism: Bos taurus

Type: **Expression profiling by array**

Platform: [GPL6695](#) 8 Samples

[Download data: GPR](#)

Series Accession: GSE98488 ID: 200098488

[Different expression profiles of lncRNA, mRNA and circRNA in peripheral blood \(ceRNA\) of normal newborns and children with BPD.](#)

323. (Submitter supplied) Increasing evidence shows that circular RNAs (circRNAs) play a vital role in the development of various diseases. A recent sequencing analysis of peripheral blood of bronchopulmonary dysplasia (BPD) patients showed that circABCC4 expression was significantly up-regulated. However, the specific function and potential mechanism of circRNAs in BPD remain unclear.

Organism: Homo sapiens

Type: **Expression profiling by array**; Non-coding RNA profiling by array

Platform: [GPL22120](#) 2 Samples

[Download data: TXT](#)

Series Accession: GSE158423 ID: 200158423

[Lung transcriptome profile in healthy and OVA-sensitized/challenged mice fed a diet supplemented with or without Cap or ODNCap](#)

324. (Submitter supplied) CpG-oligodeoxynucleotides (CpG-ODNs) constitute an attractive alternative for asthma treatment. We found that free feeding of an ODNCap (a CpG-ODN-embedded particle) -containing feed (ODNCap-F) prophylactically attenuates allergic airway inflammation, hyperresponsiveness, and goblet cell hyperplasia in an ovalbumin (OVA) -induced asthma model. To seek the suppressive mechanism of action of ODNCap-F in OVA-induced airway insults, we analyzed the lung transcriptome using DNA microarray analysis.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: [GPL21163](#) 8 Samples

[Download data: TXT](#)

Series Accession: GSE180287 ID: 200180287

 [Differences in fetal longissimus muscle gene expression between low and high maternal nutrition](#)

325. (Submitter supplied) To investigate the impact of maternal nutrient restriction on skeletal muscle gene expression, we profiled gene expression in longissimus muscle of Japanese Black fetal calves in high and low nutrient condition of pregnant maternal cows .

Organism: Bos taurus

Type: **Expression profiling by array**

Platform: GPL11649 2 Samples

[Download data: TXT](#)

Series Accession: GSE176377 ID: 200176377

 [miRNA and mRNA expression in placental tissue from high altitude pregnant women](#)

326. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Homo sapiens; synthetic construct

Type: **Expression profiling by array**; Non-coding RNA profiling by array

Platforms: GPL15207 GPL19117 40 Samples

[Download data: CEL](#)

Series Accession: GSE168130 ID: 200168130

 [Gene expression in Placental Tissue from high altitude European and Tibetan women](#)

327. (Submitter supplied) We used in silico analyses to identify the distinct transcriptome signatures of two populations living at high altitudes and identified potential mechanisms that underlie high-altitude adaptation. Data generated in this study indicate that placentas from Tibetan women are genetically distinct from European women at high altitudes, and appear to be protected from hypoxia and stress.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL15207 20 Samples

[Download data: CEL](#)

Series Accession: GSE168021 ID: 200168021

 [AKT signaling promotes epigenetic reprogramming via upregulation of TET and its cofactor, alpha-ketoglutarate during iPSC generation](#)

- (Submitter supplied) Phosphoinositide-3 kinase (PI3K)/AKT signaling participates in cellular proliferation, survival, and tumorigenesis as well as cellular reprogramming including generation of induced pluripotent stem cells (iPSCs). In this study, we revealed that activation of AKT in somatic cells undergoing reprogramming enhances epigenetic reprogramming. Activated AKT in reprogramming cells triggers elevated anabolic glucose metabolism, and, accordingly, increases the level of α-ketoglutarate (αKG) which is an essential cofactor for the enzymatic activity of the 5-methylcytosine (5mC) dioxygenase TET. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL13912 4 Samples

[Download data: TXT](#)

Series Accession: GSE161399 ID: 200161399

 [Gene expression data from patients with pancreatic ductal adenocarcinoma](#)

329. (Submitter supplied) Pancreatic ductal adenocarcinoma (PDAC) is one of the most treatment-resistant malignancies in human. To perform transcriptomic profiling on PDAC, we collected primary PDAC tissues from surgically resected PDAC patients at the Memorial-Sloan Kettering Cancer Center (NY, USA). Morphogenesis of epithelial tissues relies on the precise developmental control of cell polarity and architecture. In the early Drosophila **embryo**, the primary epithelium forms during cellularisation, following a tightly controlled genetic programme where specific sets of genes are up-regulated. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL17586](#) 82 Samples

Download data: CEL, CHP

Series Accession: GSE184585 ID: 200184585

- [Characterizing the Human Menstrual Cycle from a gene co-expression perspective reveals the pregnant endometrium as a global transcriptionally derepressed state](#)
330.

(Submitter supplied) Background: a fundamental challenge for reproductive biology is to understand the menstrual cycle, specially the window of implantation, whose regulation and mechanistic remain incompletely understood in human reproductive physiology. Transcriptomics from a systems biology perspective provides a genomic framework to discover endometrial tissue specific regulation and behavior and its function in reproductive physiology. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL26199](#) 529 Samples

Download data: GPR

Series Accession: GSE126581 ID: 200126581

- [Transcriptome changes in Drosophila HB10 cells in response to a temperature shift from 24 to 14°C](#)

331. (Submitter supplied) Cells in ectothermic organisms often maintain homeostatic function over a considerable range of ambient temperatures. However, as temperature has pronounced effects on all biological processes, but not necessarily in a uniform manner on each of the myriad of distinct processes, cellular acclimation to distinct temperatures is predicted to involve complex regulation. Initially, to assess the effects of temperature change within the readily tolerated temperature range on the transcriptome, we have performed expression profiling with S2R+ cells, a hemocyte-like cell line derived from the ectothermic organism Drosophila melanogaster. [more...](#)

Organism: Drosophila melanogaster

Type: **Expression profiling by array**

Platform: [GPL16820](#) 6 Samples

Download data: TXT

Series Accession: GSE159173 ID: 200159173

- [Role of TGFb1 and Wnt6 in FGF2 and BMP4-driven endothelial differentiation of murine embryonic stem cells](#)

332. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: [GPL6887](#) 40 Samples

Download data

Series Accession: GSE164631 ID: 200164631

- [Role of TGFb1 and Wnt6 in FGF2 and BMP4-driven endothelial differentiation of murine embryonic stem cells](#)

333. [3h]

(Submitter supplied) In this work we investigated the molecular mechanisms that sustain the endothelial differentiation of murine embryonic stem cells (ES). When ES cells are co-cultured with the stromal PA6 cells in serum-free medium they differentiate mainly into neurons, thanks to the neural inducing activity exerted by the stroma. The addition of exogenous FGF2 allows also the differentiation of endothelial cells whereas, in presence of exogenous BMP4, ES cells differentiate exclusively into endothelium. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: [GPL6887](#) 6 Samples

Download data: TXT

Series Accession: GSE164630 ID: 200164630

- [Role of TGFb1 and Wnt6 in FGF2 and BMP4-driven endothelial differentiation of murine embryonic stem cells](#)

334. [7d]

(Submitter supplied) In this work we investigated the molecular mechanisms that sustain the endothelial differentiation of murine embryonic stem cells (ES). When ES cells are co-cultured with the stromal PA6 cells in serum-free medium they differentiate mainly into neurons, thanks to the neural inducing activity exerted by the stroma. The addition of exogenous FGF2 allows also the differentiation of endothelial cells whereas, in presence of exogenous BMP4, ES cells differentiate exclusively into endothelium. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6887 16 Samples

[Download data: TXT](#)

Series Accession: GSE164629 ID: 200164629

- [Role of TGFb1 and Wnt6 in FGF2 and BMP4-driven endothelial differentiation of murine embryonic stem cells](#)
335. [\[3d\]](#)

(Submitter supplied) In this work we investigated the molecular mechanisms that sustain the endothelial differentiation of murine embryonic stem cells (ES). When ES cells are co-cultured with the stromal PA6 cells in serum-free medium they differentiate mainly into neurons, thanks to the neural inducing activity exerted by the stroma. The addition of exogenous FGF2 allows also the differentiation of endothelial cells whereas, in presence of exogenous BMP4, ES cells differentiate exclusively into endothelium. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6887 18 Samples

[Download data: TXT](#)

Series Accession: GSE164625 ID: 200164625

- [SOCS1](#)

336. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Homo sapiens; Mus musculus

Type: Expression profiling by high throughput sequencing; **Expression profiling by array**

Platforms: GPL24676 GPL24247 GPL17400 48 Samples

[Download data: CEL](#)

Series Accession: GSE154794 ID: 200154794

- [Expression data from Arabidopsis plants overexpressing CLE 3 in roots](#)

337. (Submitter supplied) Plant hormones and small secretory peptides often function as environmental stress mediators. Some recent reports indicate that small secretory peptides, such as CLAVATA3/EMBRYO SURROUNDING REGION-RELATED (CLE), also function as mediators of environmental stimuli. CLE 3 is induced in roots by defense elicitor treatment. Plants without functional CLE3 showed compromised defense gene responses in shoots when plant roots were treated with NaSA. [more...](#)

Organism: Arabidopsis thaliana

Type: **Expression profiling by array**

Platform: GPL17416 12 Samples

[Download data: CEL, CHP](#)

Series Accession: GSE176064 ID: 200176064

- [Expression data from human hematopoietic stem cells with different culture systems](#)

338. (Submitter supplied) To date, different experimental strategies have been developed for the ex vivo expansion of human hematopoietic stem (HSCs) in clinical application. However, it is still unclear to what difference in genomic function in HSCs expansion under different culture systems. In this study, we compared gene-expression profile of ex vivo expanded serum (10% FBS, fetal bovine serum) and serum-free culture systems, and then analyze molecular function of differentially expressed gene using microarray chips.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL16686 4 Samples

[Download data: CEL](#)

Series Accession: GSE126909 ID: 200126909

[Gene expression data of mRNA from longissimus muscle sample of F2 population based German Landrace 339. \(DL\) and Pietrain \(Pi\) pig breeds](#)

(Submitter supplied) 47,845 probe-sets were screened, in the first part of this study pig embryos at 63 days post conception (dpc)

Organism: Sus scrofa

Type: **Expression profiling by array**

Platform: GPL16569 118 Samples

Download data: CEL

Series Accession: GSE162754 ID: 200162754

[Amniotic Fluid primary human keratinocyte culture](#)

340. (Submitter supplied) Fetal wounds repair by regeneration rather than wound healing and the environment is dominated by amniotic fluid. We are looking at early transcriptional regulation of keratinocytes cultured in amniotic fluid in vitro.

Keratinocytes were isolated and expanded to passage three after which they were starved in DMEM for 12h then cultured for 24h in human amniotic fluid (50%), fcs (50%) or DMEM alone for another 24h. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL570 3 Samples

Download data: CEL

Series Accession: GSE182704 ID: 200182704

[SIRT1 in mouse heart development](#)

341. (Submitter supplied) The goal of this project is to investigate the role of SIRT1, the most conserved mammalian NAD+-dependent protein deacetylase, in the regulation of heart development. SIRT1 is important for heart development and functions. However, the underlying molecular mechanisms remain undefined. In this study, we analyzed the gene expression profiles in E18.5 WT and SIRT1 KO mouse hearts.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL4134 8 Samples

Download data: TXT

Series Accession: GSE86835 ID: 200086835

[Rapid production and genetic stability of human mesenchymal progenitor cells derived from human somatic cell nuclear transfer-derived pluripotent stem cells](#)

(Submitter supplied) Pluripotent stem cell-derived mesenchymal progenitor cells (PSC-MPCs) are primarily derived through two main methods: 3-dimensional (3D) embryonic body-platform (EB formation) and 2D direct differentiation method. We recently established somatic cell nuclear transfer (SCNT)-PSC lines and showed their stemness. In the present study, we produced SCNT-PSC-MPCs using a novel direct differentiation method, and the characteristics, gene expression, and genetic stability of these MPCs were compared with those derived through the EB formation method. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL16686 8 Samples

Download data: CEL

Series Accession: GSE182415 ID: 200182415

[Expression data from Sarcoma Tumors expressing the EWSR1-CREB fusions](#)

343. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Homo sapiens

Type: **Expression profiling by array**; Expression profiling by high throughput sequencing

Platforms: GPL29829 GPL11154 16 Samples

Download data: CEL, CHP, CSV

Series Accession: GSE168562 ID: 200168562

 [Gene expression in the mouse embryo following early pregnancy exposure to ethanol or nicotine](#)

344. (Submitter supplied) The in utero environment is a critical determinant of the immediate and future health of the developing fetus. Two of the most commonly used drugs during pregnancy are alcohol and nicotine. While prolonged gestational exposure to alcohol or nicotine has been associated with a range of adverse outcomes in the offspring, the consequences of exposure during early gestation only are less well understood. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6887 36 Samples

Download data: [TXT](#)

Series Accession: GSE94347 ID: 200094347

 [Long Noncoding RNA RP11-115N4.1Promotes Inflammatory Responses by Interacting with HNRNPH3 and](#)

345. [Enhancing the Transcription of HSP70 in Unexplained Recurrent Spontaneous Abortion](#)

(Submitter supplied) RP11-115N4.1 was identified as the most differentially expressed lncRNA which was highly upregulated in peripheral blood of non-pregnant URSA patients ($P = 3.63E-07$, Fold change = 2.96), and this dysregulation was further validated in approximately 26.7% additional patients (4/15). RP11-115N4.1 expression was detected in both lymphocytes and monocytes of human peripheral blood, and in vitro overexpression of RP11-115N4.1 decreased cell proliferation in K562 cells significantly. [more...](#)

Organism: Homo sapiens

Type: Non-coding RNA profiling by array; **Expression profiling by array**

Platform: GPL21827 10 Samples

Download data: [TXT](#)

Series Accession: GSE179996 ID: 200179996

 [Cell fusion enhances energy metabolism of mesenchymal tumor hybrid cells to sustain their proliferation and](#)

346. [invasion](#)

(Submitter supplied) Cell-to-cell fusion is emerging as a key element of the metastatic process in various cancer types. We recently showed that hybrids made from the spontaneous merging of pre-malignant (IMR90 E6E7, i.e. E6E7) and malignant (IMR90 E6E7 RST, i.e. RST) mesenchymal cells recapitulate the main features of human undifferentiated pleomorphic sarcoma (UPS), with a highly rearranged genome and increased spreading capacities. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL6480 10 Samples

Download data: [TXT](#)

Series Accession: GSE171471 ID: 200171471

 [Comparison of periosteal, adipose, and dermal CD146+ human pericytes](#)

347. (Submitter supplied) Human pericytes demonstrate multilineage differentiation potential, and their descendants participate in tissue homeostasis and repair. Increasing evidence from developmental biology and tissue engineering suggest that regional specification by tissue of origin exists among human pericytes. Here, we sought to define the differentiation of CD146+ human pericytes from skeletal and soft tissue sources. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL23126 9 Samples

Download data: [CEL](#)

Series Accession: GSE118962 ID: 200118962

 [Gene expression signatures for gata4/5/6 knocking down in zebrafish](#)

348. (Submitter supplied) Zebrafish gata4/5/6 are known to lie on the apex of the regulatory hierarchy in primitive myelopoiesis. However, little is known about the roles of microRNAs in this process. Performing microarray analysis on the expression changes of microRNAs in the gata4/5/6 knockdown embryos, we found that miR-210-5p is a novel regulator in zebrafish

primitive myelopoiesis. To uncover the target genes of miR-210-5p to mediate its role in inhibiting zebrafish primitive myelopoiesis, we performed microarray analysis to identify differentially expressed genes in gata4/5/6 knockdown embryos.

Organism: Danio rerio

Type: **Expression profiling by array**

Platform: GPL14664 5 Samples

Download data: [TXT](#)

Series Accession: GSE117958 ID: 200117958

[Expression data from human blastocyst stage embryo](#)

349. (Submitter supplied) Clinical data suggest that both undisturbed culture of embryos and selection algorithms based on TL morphometric parameters can in correlation and potentially improve **embryo** survival rates and live birth rates. However, there remains a need to validate and understand the mechanisms underlying the potential benefits of this technology remains. We used microarray to obtain and analyse transcriptome data of individual human embryos grown for up to 6 days to blastocyst in a TL incubator to study associations between morphokinetic TL parameters and the human **embryo** gene expression.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL570 10 Samples

Download data: [CEL](#)

Series Accession: GSE180605 ID: 200180605

[Immunoregulatory function of peripheral blood CD71+ erythroid cells in pediatric inflammatory diseases](#)

350. (Submitter supplied) Human CD71+ erythroid cells (CECs) have been recognized to have an immunoregulatory function via direct cell-cell interaction and soluble mediators such as arginase-2 and reactive oxygen species. Circulating CECs increase in healthy newborns or patients with hemolytic, malignant and cardiopulmonary disorders. To assess the pathophysiological role of CECs in inflammatory diseases, we studied the gene expression and function focusing on systemic-onset juvenile idiopathic arthritis (SoJIA). [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL23126 6 Samples

Download data: [CEL](#)

Series Accession: GSE164120 ID: 200164120

[CHAF1A Blocks Neuronal Differentiation and Promotes Neuroblastoma Oncogenesis via Metabolic](#)

351. [Reprogramming](#)

(Submitter supplied) Neuroblastoma (NB) arises from neural crest cells (NCCs) secondary to a block in differentiation. Retinoic acid (RA) differentiation therapy has limited therapeutic efficacy, and the mechanisms preventing terminal differentiation remain elusive. We found that the chromatin modifier CHAF1A restricts neuronal differentiation and promotes NB oncogenesis. CHAF1A blocks NC differentiation into mature neurons in both human NCCs and zebrafish models. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL16686 12 Samples

Download data: [CEL](#)

Series Accession: GSE144311 ID: 200144311

[RGS5 channels intracellular signaling pathways to feature growth arrest of vascular smooth muscle cells](#)

352. (Submitter supplied) Members of the regulator of G-protein signaling (RGS) family terminate the activity of specific Ga subunits. As such, RGS5 acts as an inhibitor of Gαq/11 and Gαi/o activity in vascular smooth muscle cells (VSMCs), which regulate the arterial tone and blood pressure. While Rgs5 shows a variable expression in different types of mouse arteries, neither global nor SMC-specific genetic ablation of Rgs5 altered the blood pressure. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL21970 6 Samples

[Download data: CEL](#)

Series Accession: GSE174130 ID: 200174130

 [Ventral mesencephalic dopaminergic \(vmDA\) precursors derived from human embryonic stem cells](#)

353. (Submitter supplied) Identify gene expression patterns between LMX1A+ and LMX1A- vmDA precursors derived from human embryonic stem cells (hESCs).

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL570 6 Samples

[Download data: CEL](#)

Series Accession: GSE171769 ID: 200171769

 [Genome-wide expression profiling in Drosophila wing imaginal discs](#)

354. (Submitter supplied) The imaginal discs of *Drosophila melanogaster*, where most known Hedgehog (Hh) signaling target genes are expressed with a restricted pattern, offers an accessible model system for identifying novel targets of the Hh signaling pathway. In the wing discs, cells near the A/P compartment boundary (B: ptc+) receive the highest level of Hh stimulation, A cells (A: hh-) further from the border receive lower levels of stimulation, while P cells (P: hh+) do not respond to Hh. [more...](#)

Organism: *Drosophila melanogaster*Type: **Expression profiling by array**

Platform: GPL1322 9 Samples

[Download data: CEL](#)

Series Accession: GSE180120 ID: 200180120

 [Expression data from normal adults and fetal human thyroids](#)

355. (Submitter supplied) Transcriptomic signature of human embryonic thyroid is not described so far. The goal of this project was to evaluate what enables the transition from differentiation to functional maturation of the human developing thyroid, by performing transcriptomic analysis of human thyroids covering the period of gestation weeks 7-11 and comparing it to adult human thyroids. We defined a non TSH (thyroid stimulating hormone) dependent transition from differentiation to maturation of thyroid. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL570 21 Samples

[Download data: CEL](#)

Series Accession: GSE165706 ID: 200165706

 [Analysis of 2-cell embryos resulted from COPS3 protein inactivation in pronuclear-stage mouse oocytes](#)

356. (Submitter supplied) In metazoans, maternal factors deposited in the ooplasm during oocyte growth are largely responsible for the control of initial development of the newly formed **embryo**. The gradual handover from oocytic to embryonic control, known as oocyte-to-**embryo** or maternal-to-zygotic transition, involves de novo synthesis of new embryonic factors (embryonic genome activation) as well as the timely degradation of preexisting maternal factors deposited in oocytes as transcripts or proteins. [more...](#)

Organism: *Mus musculus*Type: **Expression profiling by array**

Platform: GPL20266 8 Samples

[Download data: CEL](#)

Series Accession: GSE155205 ID: 200155205

 [Differentially expressed genes in CSRP2BP knockdown HTR-8 cells](#)

357. (Submitter supplied) CSRP2BP plays an important role in cell cycle progression, apoptosis and mammalian development, CSRP2BP knockdown by specific shRNA (CSRP2BP-shRNA) significantly inhibited the proliferation, migration, and invasion of HTR-8 trophoblast cells, and placental explant outgrowth, while CSRP2BP overexpression did the opposite. To elucidate

the mechanisms by which CSRP2BP regulated the function of trophoblast cells, we performed microarray analysis to compare the transcription profiling between the HTR-8-shNC and HTR-8-shCSRP2BP cells

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL15207 6 Samples

Download data: CEL, CHP

Series Accession: GSE179177 ID: 200179177

[IGF2BP1 is required for hepatic outgrowth during early liver development in zebrafish](#)

358. (Submitter supplied) IGF2BPs, a subclass of RNA-binding proteins, regulate cellular differentiation, proliferation and migration during multiple organs development, but its function still remains unclear. Here, we provide the *in vivo* evidence that *Igf2bp1* is pivotal during liver development by using zebrafish as a model organism. Whole-mount *in situ* hybridization showed that *igf2bp1* was highly expressed in liver, and the morpholino knockdown had no effect on hepatoblast differentiation, but the liver size was significantly reduced. [more...](#)

Organism: Danio rerio

Type: **Expression profiling by array**

Platform: GPL14664 2 Samples

Download data: TXT

Series Accession: GSE134318 ID: 200134318

[Targeting trisomy 12 in chronic lymphocytic leukemia using molecular networks identified from pluripotent stem cells](#)

359. (Submitter supplied) Chronic lymphocytic leukemia (CLL) is the most common hematologic malignancy in adults. While B cell-targeted therapies have revolutionized treatment, the underlying molecular targets of disease have not been addressed. A quarter of CLL patients have somatic trisomy 12 (tri12) which confers intermediate risk, and is otherwise embryonically lethal. Here, we report human pluripotent stem cells (PSC) harboring tri12 uniquely genocopy and phenocopy tri12 CLL. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL6244 10 Samples

Download data: CEL

Series Accession: GSE133697 ID: 200133697

[Expression data from imbibed wheat seeds developed at different temperatures](#)

360. (Submitter supplied) Transcriptomic analysis of maintenance of dormancy induced by seed development temperature We used Affymetrix GeneChip Wheat Genome Array to detail transcriptional programs underlying maintenance of dormancy induced by seed development temperature in imbibing seeds of wheat

Organism: Triticum aestivum

Type: **Expression profiling by array**

Platform: GPL3802 6 Samples

Download data: CEL

Series Accession: GSE153527 ID: 200153527

[Molecular profiling of cumulus cells and their correlation with pregnancy outcome: away from single gene marker and toward pathways analysis](#)

(Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Homo sapiens

Type: **Expression profiling by array**; Methylation profiling by genome tiling array

Platforms: GPL13534 GPL10558 48 Samples

Download data: IDAT

Series Accession: GSE144665 ID: 200144665

- [Molecular profiling of cumulus cells and their correlation with pregnancy outcome: away from single gene marker and toward pathways analysis \[Expression data\]](#)
- 362.

(Submitter supplied) Worldwide the rate of infertility is on rise which put increasing pressure on assisted reproductive technology (ART) programs worldwide. Therefore it is important to increase the efficiency of ART. Toward this aim studies has been performed to find the best predictive biomarkers to choose the best germ cells for fertilization and the best **embryo** for transfer into uterus. However, across different studies no universal markers were found. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL10558 24 Samples

Download data: IDAT, TXT

Series Accession: GSE144516 ID: 200144516

- [Epithelial cell plasticity drives endoderm formation during gastrulation](#)

363. (Submitter supplied) It is generally accepted that epiblast cells ingress into the primitive streak by epithelial-to-mesenchymal transition (EMT) to give rise to the mesoderm; however, it is less clear how the endoderm acquires an epithelial fate. Here, we used embryonic stem cell and mouse **embryo** knock-in reporter systems to combine time-resolved lineage labelling with high-resolution single-cell transcriptomics. This allowed us to resolve the morphogenetic programs that segregate the mesoderm from the endoderm germ layer. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6246 16 Samples

Download data: CEL

Series Accession: GSE148226 ID: 200148226

- [TRAP analysis of somatic muscle populations in Drosophila embryos](#)

364. (Submitter supplied) Microarray profiling of mRNA engaged in translation from 3 populations of somatic muscle at 3 different time points. The goal is to compare within a same population at different time points and between population the translatome present in these cell types in order to define specific properties giving rise to functional muscles

Organism: Drosophila melanogaster

Type: **Expression profiling by array**

Platform: GPL27460 54 Samples

Download data: TXT, XLSX

Series Accession: GSE137443 ID: 200137443

- [Human corneal endothelial cells, iPS cells, CECSi cells, and neural crest cells](#)

365. (Submitter supplied) Transcriptional profiling of human iPS cells, CECSi cells and iPS-derived neural crest cells (NCC) comparing human corneal endothelial cells (HCE)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL21185 11 Samples

Download data: TXT

Series Accession: GSE178434 ID: 200178434

- [Effect of FGF10 on human Embryonic Stem Cells \(hESC\) and induced Pluripotent Stem Cells \(hiPSC\)](#)

366. (Submitter supplied) We wish to assess the transcriptomic regulation of FGF10 on human Embryonic Stem Cells (hESC) and human induced Pluripotent Stem Cells (hiPSC) that have been induced to express the earliest lung progenitor genetic marker, NKX2.1. Shortly after NKX2.1 was expressed in these cells, they were reseeded and FGF10 was added to the culture medium (experimental conditions) for either 12 or 24 hrs. Control samples had no FGF10 added. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL20844 8 Samples

Download data: GPR

Series Accession: GSE152597 ID: 200152597

- [Mechanistic Evaluation of Reduced Reproduction in Daphnia pulex Exposed to the Insensitive Munition, 1-methyl-3-nitro-1-nitroguanidine \(MeNQ\)](#)
- 367.

(Submitter supplied) The US Department of Defense (DOD) is developing insensitive munitions (IMs) that are resistant to unintended detonation to protect warfighters. To enable evaluation of the material life-cycle for the IM, 1-methyl-3-nitro-1-nitroguanidine (MeNQ), ecotoxicological impacts assessment was required. A previous investigation of MeNQ exposures in *Daphnia pulex* revealed concentration-responsive decreases in reproduction relative to controls (0 mg/L) across a 174, 346, 709, 1385, and 2286 mg/L exposure range. [more...](#)

Organism: *Daphnia pulex*

Type: **Expression profiling by array**

Platform: GPL29611 24 Samples

Download data: [TXT](#)

Series Accession: GSE164957 ID: 200164957

- [Maternal folic acid mild over consumption in mice leads to sex-specific transcriptional alterations in embryonic placenta](#)
- 368.

(Submitter supplied) Food fortification and increased use of multivitamins have led to concerns over high folate intake periconceptionally. We reported that diets containing 5-fold higher FA than recommended for mice (5xFASD) during pregnancy, resulted in deficiency of methylenetetrahydrofolate reductase (MTHFR) and altered choline/methyl metabolism, with neurobehavioral abnormalities in newborns. Our goal was to determine whether these changes had their origins in the placenta during embryonic development. [more...](#)

Organism: *Mus musculus*

Type: **Expression profiling by array**

Platform: GPL23038 16 Samples

Download data: [CEL](#), [XLSX](#)

Series Accession: GSE164408 ID: 200164408

- [POWV isolate from Long Island infects brain endothelial cells and pericytes.](#)

369. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: *Homo sapiens*

Type: **Expression profiling by array**

Platform: GPL23159 12 Samples

Download data: [CEL](#)

Series Accession: GSE176253 ID: 200176253

- [POWV isolate from Long Island infects brain endothelial cells and pericytes. \[hBVPs\]](#)

370. (Submitter supplied) POWV isolate from Long Island (POWV-LI-9) is released basolaterally from human brain microvascular endothelial cells (hBMECs) and infects primary human brain vascular pericytes (hBVPs).

Organism: *Homo sapiens*

Type: **Expression profiling by array**

Platform: GPL23159 6 Samples

Download data: [CEL](#)

Series Accession: GSE176252 ID: 200176252

- [POWV isolate from Long Island infects brain endothelial cells and pericytes. \[hBMECs\]](#)

371. (Submitter supplied) POWV isolate from Long Island (POWV-LI-9) is released basolaterally from human brain microvascular endothelial cells (hBMECs) and infects primary human brain vascular pericytes (hBVPs).

Organism: *Homo sapiens*

Type: **Expression profiling by array**

Platform: GPL23159 6 Samples

Download data: [CEL](#)

Series Accession: GSE176251 ID: 200176251

- [Prenatal skeletal muscle transcriptome with intrauterine growth restriction in pigs \[mRNA\]](#)

372. (Submitter supplied) 47,845 probe-sets were screened, in the first part of this study pig embryos at 63 days post conception (dpc).

Organism: Sus scrofa

Type: **Expression profiling by array**

Platform: GPL16569 24 Samples

Download data: CEL

Series Accession: GSE169092 ID: 200169092

- [Gene expression data from HEK293T cells stably expressing human TRAF7 wildtype or G536S mutant](#)

373. [isoforms](#)

(Submitter supplied) The TRAF7 gene is recurrently mutated in meningiomas, adenomatoid tumors of the genital tract, well-differentiated papillary mesotheliomas, and intraneuronal perineuriomas. However, the mechanisms by which these recurrent missense mutations contribute to tumorigenesis has not yet been described. To elucidate the transcriptional differences between HEK293T cells overexpressing wildtype vs mutant TRAF7, we used Affymetrix microarrays to identify the gene transcripts that are upregulated and downregulated dependent on TRAF7 status.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL17692 3 Samples

Download data: CEL

Series Accession: GSE136012 ID: 200136012

- [In-vivo inhibition of Fgfr2b signalling in FACS-isolated Sftpc-expressing cells in embryonic mouse lungs from](#)

374. [E14.5 to E18.5](#)

(Submitter supplied) We are interested in studying the role of FGF/FGFR2b signalling on lung alveolar epithelial bipotent progenitors. Bipotent progenitors give rise to alveolar type 1 and type 2 cells (AECI and AECII, respectively). Previous research has shown that AECII cells isolated from lungs where FGF signalling has been globally inhibited show a gene signature much closer to type 1 cells. Furthermore, the relative number of AECI in experimental lungs was increased compared to control lungs. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL21810 8 Samples

Download data: GPR

Series Accession: GSE115879 ID: 200115879

- [In-vivo inhibition of Fgfr2b signalling in FACS-isolated AECs from embryonic mouse lungs from E16.5 to E18.5](#)

375. (Submitter supplied) Rosa26rtTA;tetOsFgfr2b (C75Bl6) induced from E16.5 until E18.5, lungs were harvest at E18.5, AECI and AECII were sorted using FACS. Mice were kept on water and food ad libitum.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL21810 8 Samples

Download data: GPR

Series Accession: GSE115878 ID: 200115878

- [In-vivo inhibition of Fgfr2b signalling in embryonic whole mouse lungs at E16.5](#)

376. (Submitter supplied) In this experiment we inhibited FGF signalling in E16.5 mouse lungs by using a dominant negative mouse model. We are interested in assessing the genetic regulation by FGF signalling at this stage of lung development. Specifically, we used a tetracycline controlled transcriptional activation model (Tet(o)) to manipulate FGF signalling. Genetically modified male mice that expressed a reverse tetracycline-controlled trans activator (rtTA) on the Rosa26 locus and a soluble FGFR2b on the Tet(o) promoter (Tet(o)sFgfr2b) (B6.Cg-Gt(ROSA)26Sortm1.1(rtTA,EGFP)NagyTg(tetO-Fgfr2b/lgh)1.3Jaw/sbel), were crossed with females lacking the Tet(o)sFgfr2b allele. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL21810 8 Samples

Download data: GPR

Series Accession: GSE115877 ID: 200115877

[Implication of Repeat Insertion Domains in the Trans-Activity of the Long non-coding RNA ANRIL](#)

377. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Homo sapiens

Type: Other; **Expression profiling by array**

Platforms: [GPL24539](#) [GPL18573](#) 30 Samples

Download data: [BED](#), [BIGWIG](#), [CEL](#), [CHP](#)

Series Accession: GSE162224 ID: 200162224

[Implication of repeat insertion domains in the trans-activity of the long non-coding RNA ANRIL](#)

378. [\[ANRIL_LNA_Affy\]](#)

(Submitter supplied) To identify the genes differentially expressed upon the knockdown of the lncRNA ANRIL using LNA GapmeRs in HEK293 cells

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL24539](#) 10 Samples

Download data: [CEL](#), [CHP](#)

Series Accession: GSE162223 ID: 200162223

[Implication of Repeat Insertion Domains in the Trans-Activity of the Long non-coding RNA ANRIL](#)

379. [\[ANRIL_DEx8_Affy\]](#)

(Submitter supplied) To identify the genes differentially expressed upon removal of the Exon8 of the lncRNA ANRIL in HEK293 cells

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL24539](#) 10 Samples

Download data: [CEL](#), [CHP](#)

Series Accession: GSE162222 ID: 200162222

[Gene expression profiling for cigarette smoke \(CS\) exposed lung treated with human umbilical cord](#)

380. [mesenchymal stem cells derived extracellular vesicle \(hUCMSC-EV\) and human umbilical cord derived mesenchymal stem cells \(hUC-MSC\)](#)

(Submitter supplied) To study the genes and pathway involved in cigarette smoke induced lung inflammation, and treatment with hUC-MSC-EV and hUC-MSC we have employed microarray expression profiling to identify the differentially expressed genes

Organism: Rattus norvegicus

Type: **Expression profiling by array**

Platform: [GPL22145](#) 8 Samples

Download data: [TXT](#), [XLSX](#)

Series Accession: GSE175478 ID: 200175478

[Development of gene expression signatures for SL-13R](#)

381. (Submitter supplied) To further development of our gene expression, we have employed whole genome microarray expression profiling. Human cord blood CD34+ cells from healthy donors was cultured for 2 days with or without SL-13R.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL17077](#) 2 Samples

Download data: [TXT](#)

Series Accession: GSE167599 ID: 200167599

[Genomic profiling of spermatogonial stem cells and embryonic stem cells](#)

382.

(Submitter supplied) Through comparing the global expression profiles of SSCs and ESCs using DNA microarrays, the differences between the SSC and ESCs have been revealed , especially these pluripotency-related genes.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6887 6 Samples

Download data: [TXT](#)

Series Accession: GSE38776 ID: 200038776

- [Expression data from EML4-ALK overexpression in HEK293 cell line and EML4-ALK knockdown in H2228 lung cancer cell line.](#)

(Submitter supplied) We demonstrate that EML4-ALK siRNAs significantly reduced cell viability in EML4-ALK positive lung cancer cell lines,while overexpression of EML4-ALK increased cell viability in HEK293 cells in vitro. The aim of this study was to analyze the EML4-ALK regulated gene expression in lung cancer.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL570 4 Samples

Download data: [CEL](#)

Series Accession: GSE174772 ID: 200174772

- [Expression data from umbilical cord blood and peripheral blood stem cell-derived monocytes of human](#)

383. (Submitter supplied) To identify the differences between human umbilical cord blood and peripheral blood monocytes, we performed unsupervised bioinformatic analyses by microarrays.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL6480 6 Samples

Download data: [TXT](#)

Series Accession: GSE128562 ID: 200128562

- [Gene Expression Profile From 15 day Embryonic Mouse Eyes](#)

385. (Submitter supplied) Absence of Ocular albinism type 1 (Oa1) gene is associated with abnormal pigmentation and misrouting of retinal ganglion cell (RGC) axons at the optic chiasm of the brain. Expression of the Oa1 gene is tightly correlated with development of RGCs. In mice the Oa1 gene is expressed at embryonic day (E) 10.5. Soon afterwards the RGCs appear and at E15.5 majority of their axons pass through the optic chiasm. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL1261 6 Samples

Download data: [CEL, CHP](#)

Series Accession: GSE174287 ID: 200174287

- [RNA microarray analysis of Human Umbilical Vein Endothelial Cells in normal pregnancy and preeclampsia](#)

386. (Submitter supplied) To investigate the differentially expressed lncRNAs,CircRNAs and mRNAs in Human Umbilical Vein Endothelial Cells between normal pregnancy and preeclampsia, we performed the human lncRNA,cirRNA and mRNA microarray analysis of 8 samples from clinical patients.

Organism: Homo sapiens

Type: **Expression profiling by array**; Non-coding RNA profiling by array

Platform: GPL22120 8 Samples

Download data: [TXT](#)

Series Accession: GSE165324 ID: 200165324

- [The role of ESRG in human pluripotency II](#)

387. (Submitter supplied) Human pluripotent stem cells (PSCs) express human endogenous retroviruses type-H (HERV-Hs), which exist more than a thousand copies on the human genome and frequently produce chimeric transcripts as long-non-coding RNAs (lncRNAs) fused with downstream neighbor genes. Previous studies showed that HERV-H expression is

required for the maintenance of PSC identity, and the aberrant HERV-H expression attenuated neural differentiation potentials, but little is known what their roles are. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL14550 48 Samples

Download data: [TXT](#)

Series Accession: GSE159101 ID: 200159101

[Microarray and qPCR Analysis of Mitochondrial Metabolism Activation during Prenatal and Early Postnatal](#)

388. [Development in Rats and Humans with Emphasis on CoQ10 Biosynthesis](#)

(Submitter supplied) During the mammalian ontogenesis, a rapid switch from glycolytic metabolism to oxidative phosphorylation must proceed during postnatal adaptation to extra-uterine conditions. It was proposed that in the course of intra-uterine fetal development, expression changes proceed to cover all metabolic demands all along this critical and extremely fast period. Using microarray techniques, quantitative PCR, enzyme activities' and coenzyme Q content measurements, we describe perinatal mitochondrial metabolism acceleration in rat liver and skeletal muscle between the 16th day of gestation and the first days of life and possible correlation with results in human. [more...](#)

Organism: Rattus norvegicus

Type: **Expression profiling by array**

Platform: GPL6247 54 Samples

Download data: [CEL](#)

Series Accession: GSE131012 ID: 200131012

[PHAROH lncRNA regulates c-Myc translation in hepatocellular carcinoma via sequestering TIAR](#)

389. (Submitter supplied) Hepatocellular carcinoma, the most common type of liver malignancy, is one of the most lethal forms of cancer. We identified a long non-coding RNA, Gm19705, that is over-expressed in hepatocellular carcinoma and mouse embryonic stem cells. We named this RNA Pluripotency and Hepatocyte Associated RNA Overexpressed in HCC, or PHAROH. Depletion of PHAROH impacts cell proliferation and migration, which can be rescued by ectopic expression of PHAROH. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL19057 4 Samples

Download data: [TXT](#)

Series Accession: GSE167316 ID: 200167316

[Expression data of human endometrial stromal cells after miR-371a-3p mimic transfection](#)

390. (Submitter supplied) Members of the miR-371 cluster are of the earliest de novo synthesized by embryos and have important actions in mammalian reproduction. MiR-371a is secreted by embryos at the peri-implantation period and its release has been previously associated with poor **embryo** quality and lower implantation rates in women undergoing IVF. Here we investigated the potential biological role of miR-371a release in regards to embryonic implantation, and specifically the molecular effects that this miRNA exerts on the cells of the endometrial lining. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL23159 6 Samples

Download data: [CEL](#)

Series Accession: GSE158998 ID: 200158998

[Effect of senktide administration on the **embryo** collected from superovulated cows](#)

391. (Submitter supplied) To clarify the effect of intravenous senktide administration on the quality and developmental stage of collected **embryo** from superovulated cows, mRNA expression profiles of the **embryo** were investigated. Hierarchical cluster analysis with the expression levels of all genes was divided these cows into three clusters. First cluster was composed of control cows, second cluster contained senktide (30 nmol/min, 2h) treated cows and third cluster consisted of senktide (300 nmol/min, 2h) treated cows.

Organism: Bos taurus

Type: **Expression profiling by array**

Platform: GPL11649 10 Samples

Download data: [TXT](#)

Series Accession: GSE164925 ID: 200164925

[Integrated Genome and Transcriptome Analyses Reveal the Mechanism of Genome Instability in Ataxia with Oculomotor Apraxia 2](#)
392.

(Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus; Homo sapiens

Type: Expression profiling by high throughput sequencing; Genome binding/occupancy profiling by high throughput sequencing; **Expression profiling by array**[4 related Platforms](#) 48 SamplesDownload data: [BIGWIG](#), [BW](#), [CEL](#)

Series Accession: GSE143574 ID: 200143574

[Expression data from co- and mono-cultured human brain microvascular endothelial cells and human brain vascular pericytes treated with and without estradiol](#)
393.

(Submitter supplied) For the formation of the blood-brain barrier not only endothelial cells alone, but also their interaction with surrounding cell types, like pericytes, plays an important role, and co-culture of the two cell types increases barrier function in vitro. Furthermore, observed sex differences with regard to several cardiovascular as well as neurodegenerative disorders have led to the hypothesis that the female sex hormone estrogen might protect from endothelial barrier breakdown. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**[Platform: GPL23159](#) 24 SamplesDownload data: [CEL](#), [TXT](#)

Series Accession: GSE168514 ID: 200168514

[Hoxa10 mediates positional memory to govern stem cell function in adult skeletal muscle](#)

394. (Submitter supplied) Muscle stem cells (satellite cells) are distributed throughout the body and have heterogeneous properties among muscles. However, functional topographical genes in satellite cells of adult muscle remain unidentified. Here, we show that expression of Homeobox-A (Hox-A) cluster genes accompanied with DNA hypermethylation of the Hox-A locus was robustly maintained in both somite-derived muscles and their associated satellite cells in adult mice, which recapitulates their embryonic origin. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**[Platform: GPL16570](#) 9 SamplesDownload data: [CEL](#), [CHP](#)

Series Accession: GSE139315 ID: 200139315

[Astrocytes differentiation is modulated by the NF-KB pathway](#)

395. (Submitter supplied) We demonstrate that persistent NF-KB activation affects neural progenitor cells-derived astrocytes differentiation

Organism: Mus musculus

Type: **Expression profiling by array**[Platform: GPL6246](#) 26 SamplesDownload data: [CEL](#)

Series Accession: GSE117736 ID: 200117736

[Gene expression profiles of cultured megakaryocytes](#)

396. (Submitter supplied) Cells obtained from adipose tissue are able to differentiate into megakaryocytes. We compared the gene expression profile of human adipose tissue derived megakaryocytes with that of megakaryocytes differentiated from human CD34 positive cord blood hematopoietic stem cells.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL570 5 Samples](#)

Download data: [CEL](#), [CHP](#)

Series Accession: GSE112820 ID: 200112820

[Preeclampsia is associated with reduced ISG15 levels impairing extravillous trophoblast invasion.](#)

397. (Submitter supplied) Preeclampsia (PE), a major cause of excess maternal and perinatal morbidity and mortality, has a worldwide prevalence of 2-8%. Excess inflammation with immune maladaptation in the maternal decidua causes shallow trophoblast invasion, resulting in incomplete spiral artery transformation that are characteristic of PE. To mimic the separate and combined paracrine effects of IL-11 and IL-6 on trophoblasts in normal versus preeclamptic pregnancies, primary cytotrophoblast (CTB) cultures treated with IL-11 or IL-6 or IL-11+IL-6 were analyzed by whole genome microarray. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL10558 12 Samples](#)

Download data: [TXT](#)

Series Accession: GSE171439 ID: 200171439

[Transcripts identified by microarray analysis that were deregulated in E10.5 Pax2-cre;Tbx2\(f/f\);Tbx3\(f/f\)](#)

398. ([Tbx2/3cDKO](#)) otocysts.

(Submitter supplied) Evaluation of the transcriptional changes in E10.5 otocysts upon loss of Tbx2 and Tbx3 in the otic epithelium.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: [GPL11202 4 Samples](#)

Download data: [TXT](#)

Series Accession: GSE154305 ID: 200154305

[Impact of 6-mercaptopurine on LPS treated primary cultures of enteric nervous system](#)

399. (Submitter supplied) Enteric nervous system is involved in the regulation of intestinal inflammation. We developed mouse primary cultures of enteric nervous system to study impact of LPS, as pro-inflammatory mediator, and of the pro-drug 6-mercaptopurine on enteric inflammatory pathways. We used microarrays to detail the global programme of gene expression underlying enteric neuro-inflammation and identified classes of up-regulated genes during this process.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: [GPL23038 12 Samples](#)

Download data: [CEL](#), [CHP](#)

Series Accession: GSE171308 ID: 200171308

[Generation of caudal-type serotonin neurons and hindbrain fate organoids from hPSCs](#)

400. (Submitter supplied) Serotonin (5-HT) neurons, the major components of the raphe nuclei, arise from ventral hindbrain progenitors. Based on the anatomical location and axonal projection, 5-HT neurons are coarsely divided into rostral and caudal groups. Here, we propose a novel strategy to generate hindbrain 5-HT neurons from human pluripotent stem cells (hPSCs), which involves the formation of ventral-type neural progenitor cells (NPCs) and stimulation of the hindbrain 5-HT neural development. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: [GPL16686 9 Samples](#)

Download data: [CEL](#)

Series Accession: GSE167278 ID: 200167278

[FOXD1 Promotes Dedifferentiation and Vemurafenib-resistance in Melanoma by Regulating the Expression of](#)

401. [CTGF](#)

(Submitter supplied) Metastatic melanoma is the most aggressive skin cancer and associated with a poor prognosis. Targeted therapy is one of the most important treatments for patients with BRAFV600E-mutated advanced melanoma. However, the development of resistance to this treatment compromises its therapeutic success. Increasing evidence has indicated that NC-associated genes play important roles in tumor progress and drug resistance. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL10558 14 Samples

Download data: [TXT](#)

Series Accession: GSE162973 ID: 200162973

[Expression Data from Ets1/2 WT, Ets1KO, Ets2KO and Ets1/2 DKO endothelial cells](#)

402. (Submitter supplied) Angiogenesis is a highly orchestrated process involving complex crosstalk between several endothelial cell (EC) processes including cell cycle, cell survival and migration. Transcription factors ETS1 and ETS2 are required for EC functions necessary for embryonic angiogenesis. However owing to the lethal nature of the double mutant **embryo**, the specific gene targets of these factors are yet to be identified. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL1261 12 Samples

Download data: [CEL](#)

Series Accession: GSE140157 ID: 200140157

[HMGB1 and Alu-siRNA inhibit the growth of human lung tumor cells](#)

403. (Submitter supplied) We performed expression profiling using microarray technology. The expression profiling identified genes or mechanism potentially regulating the proliferation of human lung cancer cells by BoxA of HMGB1 and Alu-siRNA transfection. The RNAs of our experiment were hybridized with Agilent SurePrint G3 Human GE 8X60K, V3 Microarrays (Agilent®).

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL20844 24 Samples

Download data: [TXT](#)

Series Accession: GSE112429 ID: 200112429

[Effect of Notch1 on gene expression profiles of mouse decidua on E7.5 of first and subsequent pregnancies](#)

404. (Submitter supplied) Decidualization is one of the most important processes during female reproduction, decidualization was regulated differently in first and subsequent pregnancies Notch1 affects decidualization of mouse uterine stromal cells, but the mechanism under is still unclear

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL1261 10 Samples

Download data: [CEL](#)

Series Accession: GSE153964 ID: 200153964

[Expression data for the siCtrl and siHPIP treated BeWo cells](#)

405. (Submitter supplied) HPIP is an oncogenic protein and plays a major role in cancer progression, while its role in trophoblast differentiation is largely unknown. Therefore we analysed the effect of HPIP knockdown on gene expression signature in BeWo cells.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL15207 4 Samples

Download data: [CEL, TXT](#)

Series Accession: GSE159953 ID: 200159953

[Comparison of transcriptomic adjustments to availability of sugar, cellular energy, and oxygen in germinating rice embryos](#)

406. [rice embryos](#)

(Submitter supplied) During germination, the availability of sugars, oxygen, or cellular energy fluctuates under dynamic environmental conditions, and the global RNA profile of rice genes can be affected by their availabilities. In the aerobically germinating rice embryos, most sugar-regulated genes are responsive to low energy and anaerobic conditions, indicating that sugar-regulation is closely associated with energy and anaerobic signaling. [more...](#)

Organism: Oryza sativa

Type: **Expression profiling by array**

Platform: GPL25932 12 Samples

Download data: CEL, CHP

Series Accession: GSE168915 ID: 200168915

[Development of gene expression signatures for ovarian cancer stem cells](#)

407. (Submitter supplied) To understand the differentiation of ovarian cancer stem cells (CSCs), We derived two phenotypes of CSCs and identified the gene expression profiling. The CSCs were derived from Cp70 ovarian cancer cells and cultured in suspension and examined every day for sphere formation. Spheres were then dissociated and passaged at least eight times in 2 months to generate spheres, which are henceforth referred to as SR cells. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL14550 3 Samples

Download data: TXT

Series Accession: GSE111776 ID: 200111776

[Neural lineage cells derived from dental pulp stem cells generate Schwann cells via oligodendrocyte progenitor](#)

408. [cells in peripheral nerve regeneration](#)

(Submitter supplied) The current understanding is that Schwann cell transplantation is ideal strategy for peripheral nerve regeneration instead of autograft. It is difficult to obtain the required amount of Schwann cells which are best transplant condition, and central nervous cells have been gained attention in recent years, but its regenerative mechanism remain unknown. Neural stem/progenitor cells (NSPC) can generate various type of neural lineage cells (NLCs), and NSPCs derived from pluripotent stem cells are promising cells for cell therapy for neurodegenerative diseases. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL23159 6 Samples

Download data: CEL

Series Accession: GSE168399 ID: 200168399

[Comparison of skin and in vitro differentiated human Langerhans cells](#)

409. (Submitter supplied) Langerhans cells were prepared from skin or derived from cord blood CD34+ cells

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL570 8 Samples

Download data: CEL

Series Accession: GSE168167 ID: 200168167

[Transcriptome analysis of human erythroid cells differentiated from iPSCs, cord blood and adult peripheral](#)

410. [blood](#)

(Submitter supplied) The aim of the study is to develop a scalable continuous agitation suspension culture bioprocess for differentiation of hiPSCs towards erythroid cells. Using process optimization, we developed the entire process completely in agitation suspension culture condition starting from hiPSC expansion through to hematopoietic induction and erythroid differentiation. Transcriptome profiling was carried out to facilitate comparisons between erythroid cells differentiated from hiPSCs using this bioprocess, and erythroid cells differentiated from cord blood and adult CD34+ cells.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL23126 11 Samples

Download data: CEL

Series Accession: GSE137917 ID: 200137917

- [The common germline TP53-R337H mutation is hypomorphic and confers incomplete tumor penetrance and late tumor onset in a mouse model](#)
- 411.

(Submitter supplied) The TP53-R337H founder mutation exists at high frequency throughout southern Brazil and represents the most common germline TP53 mutation reported to date. It was originally identified in pediatric adrenocortical tumors in families with no reported history of cancer. The R337H mutation has since been found in association with early-onset breast cancers and Li-Fraumeni syndrome. To study this variability in tumor susceptibility we generated a knockin mutant p53 mouse model (R334H). [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL16570 14 Samples

Download data: CEL

Series Accession: GSE166819 ID: 200166819

- [HAND2 is a novel obesity-linked adipogenic transcription factor regulated by glucocorticoid signaling](#)

412. (Submitter supplied) Aims: Adipocytes are critical cornerstones of energy metabolism. While obesity-induced adipocyte dysfunction is associated with insulin resistance and systemic metabolic disturbances, adipogenesis, the formation of new adipocytes and healthy adipose tissue expansion are associated with metabolic benefits. Understanding the molecular mechanisms governing adipogenesis is of great clinical potential to efficiently restore metabolic health in obesity. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL23159 9 Samples

Download data: CEL

Series Accession: GSE148699 ID: 200148699

- [Sperm modulate uterine immune parameters relevant to embryo implantation and reproductive success](#)

413. (Submitter supplied) Seminal fluid factors modulate the female immune response at conception to facilitate **embryo** implantation and reproductive success. Whether sperm affect this response has not been clear. We evaluated global gene expression by microarray in the mouse uterus after mating with intact or vasectomized males. Intact males induced greater changes in gene transcription, prominently affecting pro-inflammatory cytokine and immune regulatory genes, with TLR4 signaling identified as a top-ranked upstream driver. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6246 12 Samples

Download data: CEL

Series Accession: GSE167485 ID: 200167485

- [An Esrrb and Nanog Cell Fate Regulatory Module Controlled by Feed Forward Loop Interactions.](#)

414. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus

Type: Genome binding/occupancy profiling by high throughput sequencing; **Expression profiling by array**; Methylation profiling by genome tiling array

Platforms: GPL9185 GPL14781 GPL6246 50 Samples

Download data: CEL, PAIR, WIG

Series Accession: GSE31842 ID: 200031842

- [An Esrrb and Nanog Cell Fate Regulatory Module Controlled by Feedback Interactions \[gene expression\]](#)

415. (Submitter supplied) Cell fate decisions during development are governed by multi-factorial regulatory mechanisms including chromatin remodelling, DNA methylation, binding of transcription factors to specific loci, RNA transcription and protein synthesis. However, the mechanisms by which such regulatory 'dimensions' coordinate cell fate decisions are currently poorly understood. Here we quantified the multi-dimensional molecular changes that occur in mouse embryonic stem cells (mESCs) upon depletion of Estrogen related receptor beta (Esrrb), a key pluripotency regulator. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6246 12 Samples

[Download data: CEL](#)

Series Accession: GSE31791 ID: 200031791

[Ki-67 promotes carcinogenesis by enabling global transcriptional programmes](#)

416. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus; Homo sapiens

Type: Expression profiling by high throughput sequencing; **Expression profiling by array**; Genome binding/occupancy profiling by high throughput sequencing

Platforms: GPL16699 GPL28038 GPL17021 52 Samples

[Download data: TAB, TXT](#)

Series Accession: GSE163114 ID: 200163114

[Exosomal RNA expression profiles in umbilical cord blood from preeclampsia patients](#)

417. (Submitter supplied) We used microarray technology to establish the differential RNA expression profiles in umbilical cord blood exosomes from preeclampsia patients compared with normal controls.

Organism: Homo sapiens

Type: **Expression profiling by array**; Non-coding RNA profiling by array

Platform: GPL22120 6 Samples

[Download data: TXT](#)

Series Accession: GSE166846 ID: 200166846

[Gene expression analysis of mouse hair follicle stem cells cultured in different conditions](#)

418. (Submitter supplied) In mammals, organ induction occurs only during embryonic development except for hair follicles (HFs). However, HF-resident epithelial stem cells (HFSCs), which are responsible for repetitive HF regeneration, are not fully characterized. We establish in vitro culture systems that are capable of controlling the ability of HFSCs to regenerate HFs and perform microarray analysis to compare gene expression profile in different culture condition.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL1261 6 Samples

[Download data: CEL, CHP](#)

Series Accession: GSE160632 ID: 200160632

[Complete absence of DNA methylation effect on histone modifications H3K4me2, H3K27me3 and H3K9me2](#)

419. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus

Type: **Expression profiling by array**; Genome binding/occupancy profiling by genome tiling array

Platforms: GPL13912 GPL4134 GPL15365 64 Samples

[Download data: TXT](#)

Series Accession: GSE36702 ID: 200036702

[Expression profiles in the complete absence of DNA methylation \[Agilent-028005\]](#)

420. (Submitter supplied) Using all three CpG DNA methyltransferases, Dnmt1, Dnmt3a and Dnmt3b deficient (TKO) mouse ES cells and TKO ntTS cells, we examined three histone modifications H3K4me2, H3K27me3 and H3K9me2, of promoter region in ES, TS and Flk1+ mesodermal cells with WT or TKO background by ChIP-chip analysis. Global profile analysis of gene expression and histone modification showed that the difference of profiles was mainly lineage dependent. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL13912 12 Samples

[Download data: TXT](#)

Series Accession: GSE36663 ID: 200036663

[Expression profiles in the complete absence of DNA methylation \[Agilent-014868\]](#)

421.

(Submitter supplied) Using all three CpG DNA methyltransferases, Dnmt1, Dnmt3a and Dnmt3b deficient (TKO) mouse ES cells and TKO ntTS cells, we examined three histone modifications H3K4me2, H3K27me3 and H3K9me2, of promoter region in ES, TS and Flk1+ mesodermal cells with WT or TKO background by ChIP-chip analysis. Global profile analysis of gene expression and histone modification showed that the difference of profiles was mainly lineage dependent. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL4134 16 Samples

Download data: [TXT](#)

Series Accession: GSE36662 ID: 200036662

[Expression data from mouse wild type, PRDM14-overexpressing and Dnmts KO embryonic stem cells \(ESCs\).](#)

422. (Submitter supplied) Germline cells reprogram extensive epigenetic modifications to ensure the cellular totipotency of the next generation and prevent accumulation of epimutations. Primordial germ cells (PGCs)1, the common source of both oocytes and sperm, erase genome-wide DNA methylation and histone H3 lysine 9 dimethylation (H3K9me2), a process called genome-wide epigenetic reprogramming^{2,3}. However, little is known about the molecular mechanism of DNA demethylation by developing PGCs. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL13912 10 Samples

Download data: [TXT](#)

Series Accession: GSE36371 ID: 200036371

[The role of mammalian DNA methyltransferases in the regulation of temporal order of DNA replication](#)

423. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus

Type: Other; **Expression profiling by array**

Platforms: GPL1261 GPL18635 20 Samples

Download data: [CEL](#)

Series Accession: GSE119479 ID: 200119479

[The role of mammalian DNA methyltransferases in the regulation of temporal order of DNA replication](#)

424. [\[microarray\]](#)

(Submitter supplied) Multiple epigenetic pathways underlie the temporal order of DNA replication (replication timing) in the context of development and disease. DNA methylation by DNA methyltransferases (DNMTs) and downstream chromatin reorganization and transcriptional changes are thought to impact DNA replication, yet this remains to be comprehensively tested. Using cell biological and genome-wide approaches to measure replication timing, we identified a number of genomic regions undergoing subtle but reproducible replication timing changes in various DNMT-mutant mouse ES cell lines that include a line with a drug-inducible DNMT3a2 expression system. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL1261 4 Samples

Download data: [CEL](#)

Series Accession: GSE119406 ID: 200119406

[Time and concentration dependent transcriptome signatures in the ZFE of a mixture consisting of diruron,](#)

425. [diclofenac and naproxen](#)

(Submitter supplied) Time and concentration dependent transcriptome signatures in the ZFE of a mixture consisting of diruron, diclofenac and naproxen. Mixture composition: diuron 11%; diclofenac 2.6%; naproxen 86.4% Keywords:

Expression profiling by array

Organism: Danio rerio

Type: **Expression profiling by array**

Platform: GPL19785 64 Samples

Download data: [TXT](#)

Series Accession: GSE109498 ID: 200109498

[Expression data \(mRNA\) from GD-9.5 \(E9.5\), Folr1+/+ \(Folr1 WT\) and Folr-/- \(Folr1 KO\) mouse embryos](#)

426. (Submitter supplied) Folic acid is a nutrient essential for embryonic development. Folate deficiency can cause embryoletality or neural tube defects and orofacial anomalies. Folate receptor 1 (Folr1), is a folate binding protein that facilitates the cellular uptake of dietary folate. Animal studies highlighted critical roles of folate in embryogenesis including orofacial development. Orofacial clefts were observed in the offspring of experimental animals on folic acid-deficient diets.
[more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL339 5 Samples

Download data: CEL, CHP

Series Accession: GSE155428 ID: 200155428

 [Integrative analysis of DNA methylation and gene expression data among preterm and/or small for gestational age infants during perinatal period](#)

427. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Homo sapiens

Type: **Expression profiling by array**; Methylation profiling by genome tiling array

Platforms: GPL13534 GPL21185 212 Samples

Download data: TXT

Series Accession: GSE110829 ID: 200110829

 [Integrative analysis of DNA methylation and gene expression data among preterm and/or small for gestational age infants during perinatal period \[expression\]](#)

428. (Submitter supplied) Preterm or small for gestational age (SGA) infants are to be at high risk of noncommunicable diseases in adolescence, because they are exposed to hypoxia and malnutrition in and ex utero during perinatal period. Epigenetics could be one of the most important mechanisms of DOHaD. In the field of premature babies, previous studies investigated the methylation alterations related to gestational age and birthweight by using cord blood samples. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL21185 55 Samples

Download data: TXT

Series Accession: GSE110822 ID: 200110822

 [Stimulation of HUVEC by BMP9/10](#)

429. (Submitter supplied) The experiment monitors the response of human umbilical vein endothelial cells to stimulation with BMP9 and BMP10

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL16686 4 Samples

Download data: CEL, TXT

Series Accession: GSE160023 ID: 200160023

 [Transcriptome profile of peritoneal lavage in response to adjuvants Alum and the polysaccharide from the roots of Actinidia eriantha \(AEPS\)](#)

(Submitter supplied) Analysis of peritoneal lavage from BALB/c mice 2 hours after intraperitoneal injection with PBS, AEPS, OVA, OVA+AEPS, or OVA+Alum. Results provide insight to explore the potential role of mRNAs and lncRNAs in adjuvant-induced innate immune response.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL10787 5 Samples

Download data: TXT

Series Accession: GSE124938 ID: 200124938

[Toxoplasma and Eimeria co-opt the host cFos expression for intracellular development in mammalian cells](#)

431. (Submitter supplied) Successful asexual reproduction of intracellular pathogens depend on their potential to exploit host resources and subvert antimicrobial defense. Here, we deployed two prevalent intracellular parasites of mammalian cells, namely *Toxoplasma gondii* and *Eimeria falciformis*, to identify the potential host determinants of infection. Expression analyses of the young adult mouse colonic (YAMC) epithelial cells showed regulation of several distinct transcripts upon infection by either parasite, indicating that closely-related pathogens program their intracellular niches in notably adaptive manner. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL4134 28 Samples

Download data: [TXT](#)

Series Accession: GSE157395 ID: 200157395

[Inceptor counteracts insulin signalling in β-cells to control glycaemia](#)

432. (Submitter supplied) Resistance to insulin and insulin-like growth factor 1 (IGF1) in pancreatic β-cells causes overt diabetes in mice; thus, therapies that sensitize β-cells to insulin may protect patients with diabetes against β-cell failure. Here we identify an inhibitor of insulin receptor (INSR) and IGF1 receptor (IGF1R) signalling in mouse β-cells, which we name the insulin inhibitory receptor (inceptor; encoded by the gene *lir*). [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL20775 20 Samples

Download data: [CEL](#)

Series Accession: GSE144519 ID: 200144519

[Genome-wide analysis of normal and high glucose condition](#)

433. (Submitter supplied) Transcriptional profiling of Mouse cavernous primary pericytes (MCPs) in comparing normal glucose condition with high glucose condition

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL10787 2 Samples

Download data: [TXT](#)

Series Accession: GSE146357 ID: 200146357

[Expression data from human venous and arterial endothelial cells](#)

434. (Submitter supplied) The vascular tree has considerable diversity, with discrete regions having different physiologic characteristics and permeability. Of note are venules that are significantly more sensitive to pro-inflammatory cytokines than arterioles. We used microarrays to identify molecular signatures that distinguish primary human venous endothelial cells from arterial endothelial cells. We used microarrays to identify genes differentially expressed by venous vs arterial human endothelial cells.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL6244 12 Samples

Download data: [CEL, CHP](#)

Series Accession: GSE137041 ID: 200137041

[Gene transcription in wild-type \(WT\) and c-abl/arg knockout MEFs](#)

435. (Submitter supplied) Abl kinases, which are required for multiple cellular processes, including proliferation, apoptosis, adhesion, cell migration, and stress responses, widely participate in the regulation of gene transcription. To illustrate the role of Abl kinase in gene expression, the transcription of approximately 22,000 genes in wild-type (WT) and c-abl/arg knockout MEFs was detected using Affymetrix GeneChips (Mouse Genome 430 2.0).

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL1261 6 Samples

Download data: [CEL](#)

Series Accession: GSE154568 ID: 200154568

 [Inhibition of cyclooxygenase activity by diclofenac inhibits varicose remodeling of mouse veins](#)

436. (Submitter supplied) BACKGROUND: As evidenced by epidemiological and etiological studies, the development of varicose veins is driven by risk-factors which support the development of venous hypertension and thus chronically augment circumferential stress of the venous wall (e.g. dysfunctional venous valves, pregnancy or obesity). We have previously verified the relevance of this biomechanical stimulus for the activation of venous endothelial as well as smooth muscle cells and the subsequent detrimental structural remodeling of the vein wall in experimental mouse models. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL21970 6 Samples

Download data: CEL

Series Accession: GSE121557 ID: 200121557

 [Peptidylarginine deiminase IV \(PADI4\) has a novel tumor cell-autonomous suppressor role in regulating breast cancer stem cells \[Array\]](#)

437. (Submitter supplied) Peptidylarginine deiminases (PADIs) catalyze post-translational modification of many target proteins and have been suggested to play a role in carcinogenesis. Since citrullination of histones by PADI4 was recently implicated in regulating embryonic stem and hematopoietic progenitor cells, here we investigated a possible role for PADI4 in regulating breast cancer stem cells. We showed by genetic and pharmacologic approaches that PADI4 activity limits the number of cancer stem cells (CSCs) in vitro and in vivo in multiple breast cancer models. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL23159 6 Samples

Download data: CEL

Series Accession: GSE138407 ID: 200138407

 [Expression data for Npac depleted E14 mES cells](#)

438. (Submitter supplied) Though chromatin modification makes great contribution to pluripotency maintenance in embryonic stem cell (ESC), it remains obscure for the mechanisms. Here, we show that one “reader” of histone H3 trimethyl lysine 36 (H3K36me3), Npac, is essential to maintain mouse ESC pluripotency. On one hand, depletion of Npac causes mESC differentiation by repressing genes associated with pluripotency while activating developmental related genes. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL1261 4 Samples

Download data: CEL

Series Accession: GSE93296 ID: 200093296

 [Expression data from rat NSCs co-cultured with green fluorescence protein \(GFP\)-ectodermal mesenchymal stem cells \(EMSCs\) versus mono-cultured rat NSCs](#)

(Submitter supplied) Rat NSCs were isolated from developing whole brain of the SD rat embryos at day 13.5. In the NSC/GFP-EMSC co-culture system, the NSCs showed significantly enhanced neuronal differentiation rather than astrocytic commitment, in comparison with the mono-cultured NSCs. In order to reveal the gene expression profiles of NSCs under these two different culture conditions, we used microarrays to examine the global programme of gene expression of NSCs under these two different culture conditions.

Organism: Rattus norvegicus

Type: **Expression profiling by array**

Platform: GPL22388 2 Samples

Download data: CEL

Series Accession: GSE108752 ID: 200108752

 [Chemical Genetics of Regeneration: Contrasting Temporal Effects of CoCl2 on Axolotl Tail Regeneration](#)

440.

(Submitter supplied) The Mexican axolotl provides a powerful model to investigate mechanisms of tissue regeneration. A recent chemical screen found that HDAC inhibitor romidepsin, administered for only 1-minute post amputation (1 MPA), blocks axolotl tail regeneration. Here, we tested the potential for cobalt chloride (CoCl₂), a chemical stabilizer of HIF1a and inducer of hypoxia, to rescue romidepsin-inhibition of tail regeneration. [more...](#)

Organism: Ambystoma mexicanum

Type: **Expression profiling by array**

Platform: GPL25286 37 Samples

[Download data: CEL, XLS](#)

Series Accession: GSE150947 ID: 200150947

[Transcriptional profile of organ fibroblasts from adult mice](#)

441. (Submitter supplied) Organ fibroblasts are essential components of homeostatic and diseased tissues, as they participate in sensing the microenvironment and communicating with other resident cells. They are also involved in pathological remodeling and fibrosis, caused by excessive deposition of connective tissue after injury, which impairs organ function. It is estimated that 45% of deaths in developed countries are linked to chronic fibrosis, yet current drugs on the market are both inefficient and non-specific to this condition [1]. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL13912 19 Samples

[Download data: TXT](#)

Series Accession: GSE98783 ID: 200098783

[Age-Related Injury Responses of Human Oligodendrocytes to Metabolic Insults: Link to BCL-2 and Autophagy](#)

442. [Pathways](#)

(Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Homo sapiens

Type: Expression profiling by high throughput sequencing; **Expression profiling by array**

Platforms: GPL16686 GPL20301 21 Samples

[Download data: CEL, RDS](#)

Series Accession: GSE160813 ID: 200160813

[Aflatoxin B1 attenuates endocrine function, protein synthesis and energy production of human primary](#)

443. [trophoblast](#)

(Submitter supplied) Aflatoxin B1 (AFB1) is a mycotoxin produced by Aspergillus flavus and A. parasiticus. AFB1 targeted gene expression profiles were determined in human primary trophoblast cells, isolated from full term placentae after delivery, and exposed to 1 µM AFB1 for 72 hours. Gene expression profiling conducted with human HT-12 expression beadchips

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL10904 8 Samples

[Download data: TXT](#)

Series Accession: GSE153590 ID: 200153590

[Expression data from Arabidopsis plants overexpressing CLE2 in roots](#)

444. (Submitter supplied) Plant hormones and small secretory peptides often function as environmental stress mediators. Some recent reports indicate that small secretory peptides, such as CLAVATA3/EMBRYO SURROUNDING REGION-RELATED (CLE), also function as mediators of environmental stimuli. CLE2 is induced in roots by light deprivation. Plants without functional CLE2 showed a chlorosis phenotype when grown under shade. Here, we identified specific genes downstream of CLE2 in roots and shoots with transformed Arabidopsis plants.

Organism: Arabidopsis thaliana

Type: **Expression profiling by array**

Platform: GPL17416 12 Samples

[Download data: CEL, CHP](#)

Series Accession: GSE149015 ID: 200149015

[Evolutionary Origin of Vertebrate Oct4/POUV Functions in Supporting Pluripotency](#)

445. (Submitter supplied) Pluripotency is the capacity of early embryonic cells to make all the future lineages of the organism, and the existence of a pluripotent population of cells is important to both germ cell function and the pool of progenitor cells that enable vertebrate development to proceed over time through the process of gastrulation. Oct4, a class V POU transcription factor, is required for maintenance of pluripotency in embryonic stem cells (ESCs) and induction of pluripotency via transcription factor reprogramming. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL13912 6 Samples

[Download data: TXT](#)

Series Accession: GSE148167 ID: 200148167

 [Neonatal T helper 17 responses are skewed towards an immunoregulatory interleukin-22 phenotype](#)

446. (Submitter supplied) We report broad developmental differences in gene expression profiles between neonatal (term) and adult naive CD4 T cells, resulting in non-stereotypic Th17 differentiation responses to TGF-beta.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL10558 24 Samples

[Download data: TXT](#)

Series Accession: GSE135467 ID: 200135467

 [Transcripts identified by microarray analysis that were deregulated in E14.5 Tbx18cre/+;Gata2fl/fl \(Gata2cKO\)](#)

447. ureters

(Submitter supplied) Evaluation of the transcriptional changes in E14.5 ureters upon loss of Gata2 in the ureteric mesenchyme.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL11202 2 Samples

[Download data: TXT](#)

Series Accession: GSE127702 ID: 200127702

 [Multiple genetic programs contribute to CD4 T cell memory differentiation and longevity by maintaining T cell](#)

448. quiescence

(Submitter supplied) While memory T-cells (Tmem) represent a hallmark of adaptive immunity, and despite extensive characterization of CD8+ Tmem, little is known about regulation of CD4+ Tmem cell survival. In this study, we analyzed antigen-specific CD4+T cell memory populations in mice and human to characterize their unique genetic and surface phenotypes. First, using microarray technology, we studied dynamic gene expression of antigen specific CD4+ T cells during infection, memory differentiation, and survival up to nearly a year. [more...](#)

Organism: Musculus; Mus musculus

Type: **Expression profiling by array**

Platform: GPL7202 18 Samples

[Download data: TXT](#)

Series Accession: GSE151583 ID: 200151583

 [Cockayne syndrome proteins CSA and CSB maintain mitochondrial homeostasis through NAD+ signaling](#)

449. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Caenorhabditis elegans; Homo sapiens

Type: **Expression profiling by array**

Platforms: GPL28098 GPL10094 44 Samples

[Download data: TXT](#)

Series Accession: GSE144558 ID: 200144558

[Cockayne syndrome proteins CSA and CSB maintain mitochondrial homeostasis through NAD⁺ signaling](#)

450. [\[Agilent-020186 array\]](#)

(Submitter supplied) Cockayne syndrome (CS) is a rare premature aging disease, which in the majority of cases is caused by mutations of the genes encoding the CSA or CSB proteins. CS patients display cachectic dwarfism and severe neurological manifestations and die by 12 years of age on average. The CS proteins are involved in transcription and DNA repair, including a specialized form of DNA repair called transcription-coupled nucleotide excision repair (TC-NER). [more...](#)

Organism: *Caenorhabditis elegans*

Type: **Expression profiling by array**

Platform: GPL10094 32 Samples

Download data: [TXT](#)

Series Accession: GSE144556 ID: 200144556

[Chorioamnion after choriodecidual Group B Streptococcal infection](#)

451. (Submitter supplied) Choriodecidual infection is associated with preterm premature rupture of membranes (pPROM) and preterm birth. MicroRNAs (miRNAs) are small, non-coding RNAs that regulate gene expression and may be involved in the pathway leading to chorioamnion weakening following infection. The study objective was to determine if a miRNA profile in the chorioamnion is associated with Group B Streptococcal infection and membrane weakening.

Organism: *Macaca nemestrina; synthetic construct*

Type: **Expression profiling by array**

Platform: GPL14613 10 Samples

Download data: [CEL](#)

Series Accession: GSE77152 ID: 200077152

[Gene expression underlying differential adult brain morphogenesis in honeybee castes](#)

452. (Submitter supplied) Learning and memory-related skills that honeybees use for navigation, foraging and other activities are associated with a central region of the brain, the mushroom bodies, which are relatively more developed in workers than in queens. During larval period, however, the differential feeding offered to prospective queens promotes faster brain development and higher expression of several neurogenic genes (ataxin-2, cryptocephal, dachshund, Eph Receptor, fax, shot, krüppel homolog-1 and tetraspanin 5D). [more...](#)

Organism: *Apis mellifera*

Type: **Expression profiling by array**

Platform: GPL14758 2 Samples

Download data: [TXT](#)

Series Accession: GSE90156 ID: 200090156

[Effect of short-term hyperglycemia on primary fetoplacental endothelial cells \(fpEC\) isolated from human](#)

453. [placenta arteries](#)

(Submitter supplied) In order to investigate the effect of in vitro hyperglycemia on gene expression of fpEC, cells were treated with hyperglycemia (25mM) for 24h.

Organism: *Homo sapiens*

Type: **Expression profiling by array**

Platform: GPL96 2 Samples

Download data: [CEL, CHP](#)

Series Accession: GSE155263 ID: 200155263

[Denuded HUVEC/HUASMC spheroids vs. HUASMC spheroids](#)

454. (Submitter supplied) Here, we investigated changes of the VSMC transcriptome by utilizing 3D human vascular organoids organized as a core of VSMCs enclosed by a monolayer of ECs. Unbiased microarray-based analyses indicated that interaction with ECs for 48 hours down-regulates the VSMC expression of genes controlling rate-limiting steps of the cholesterol biosynthesis such as HMGCR, HMGCS1, DHCR24 and DHCR7. Protein analyses revealed a decrease in the abundance of 24-dehydrocholesterol reductase and lower cholesterol levels in VSMCs co-cultured with ECs. [more...](#)

Organism: *Homo sapiens*

Type: **Expression profiling by array**

Platform: GPL24989 6 Samples

Download data: CEL

Series Accession: GSE156274 ID: 200156274

[Human heart-forming organoids recapitulate early heart and foregut development - microarray data](#)

455. (Submitter supplied) Organoid models of early tissue development have been produced for the intestine, brain, kidney and other organs, but similar approaches for the heart have been lacking. Here we generate complex, highly structured, three-dimensional heart-forming organoids (HFOs) by embedding human pluripotent stem cell aggregates in Matrigel followed by directed cardiac differentiation via biphasic WNT pathway modulation with small molecules. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL26355 18 Samples

Download data: TXT

Series Accession: GSE150051 ID: 200150051

[Gene expression profiling in neuronal cells identifies a different type of transcriptome modulated by NF-Y](#)

456. [\[Grp94\]](#)

(Submitter supplied) We knocked down NF-Y in two types of neuronal cells, neuro2a neuroblastoma cells and sorted brain striatal cells, and performed gene expression profiling. We found that the down-regulated genes preferentially contained NF-Y-binding motifs in their proximal promoters, and notably enriched genes related to ER functions rather than those for cell cycle. These are highly contrast to the profiling data of HeLa and embryonic stem cells in which distinct down-regulation of cell cycle-related genes was observed by NF-Y knockdown. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6246 8 Samples

Download data: CEL, TXT

Series Accession: GSE151146 ID: 200151146

[Gene expression profiling in neuronal cells identifies a different type of transcriptome modulated by NF-Y](#)

457. [\[YAYC_Affymetrix\]](#)

(Submitter supplied) We knocked down NF-Y in two types of neuronal cells, neuro2a neuroblastoma cells and sorted brain striatal cells, and performed gene expression profiling. We found that the down-regulated genes preferentially contained NF-Y-binding motifs in their proximal promoters, and notably enriched genes related to ER functions rather than those for cell cycle. These are highly contrast to the profiling data of HeLa and embryonic stem cells in which distinct down-regulation of cell cycle-related genes was observed by NF-Y knockdown. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6246 5 Samples

Download data: CEL

Series Accession: GSE151145 ID: 200151145

[Gene expression profiling in neuronal cells identifies a different type of transcriptome modulated by NF-Y](#)

458. [\[YAYC_Agilent\]](#)

(Submitter supplied) We knocked down NF-Y in two types of neuronal cells, neuro2a neuroblastoma cells and sorted brain striatal cells, and performed gene expression profiling. We found that the down-regulated genes preferentially contained NF-Y-binding motifs in their proximal promoters, and notably enriched genes related to ER functions rather than those for cell cycle. These are highly contrast to the profiling data of HeLa and embryonic stem cells in which distinct down-regulation of cell cycle-related genes was observed by NF-Y knockdown. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL10787 6 Samples

Download data: TXT

Series Accession: GSE151144 ID: 200151144

- [Role of Jagged1 in cochlear supporting cell differentiation and maintenance](#)
459. (Submitter supplied) Inner ear cochlear supporting cells (SCs) are highly specialized glia-like cells that structurally and functionally support neighboring mechano-sensory hair cells. Despite their importance for proper auditory function, little is known about the molecular mechanisms that control their development. In this study we investigated the function of the Notch ligand Jagged1 (Jag1) in cochlear SC differentiation and maintenance. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL20266 6 Samples

Download data: CEL

Series Accession: GSE148009 ID: 200148009

- [Mexican Ganoderma lucidum extracts decrease lipogenesis modulating transcriptional metabolic networks and gut microbiota in C57BL/6 mice fed with a high-cholesterol diet from early Drosophila embryo](#)
460. (Submitter supplied) Background: Prevention of hyperlipidemia and associated diseases is a health priority. Complementary medicine based on scientific evidence has recently recognized the potential of natural products for modulating lipid metabolism, such as the medicinal mushroom Ganoderma lucidum (Gl), which possesses hypocholesterolemic, prebiotic and antidiabetic properties. Methods: Whole-transcriptomic changes in liver and kidney from a mouse model (C57BL/6), under a high-cholesterol diet and standardized Gl extracts (Gl-1, Gl-2) or simvastatin administration, were analyzed to determine Gl hypocholesterolemic activity. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6246 45 Samples

Download data: CEL, TXT

Series Accession: GSE159656 ID: 200159656

- [Gene expression analysis of rat macrophages](#)

461. (Submitter supplied) We used microarray to compare gene expression between bone marrow-derived (BMDM), monocyte-derived (MDM), alveolar (AM), peritoneal (PM) and embryonic stem cell (ESC) derived rat macrophages. The expression of liver macrophages (Kupffer cells) were inferred by analysis of whole livers from Csfr1r deficient rats. The transcriptional response of BMDM to LPS was also examined.

Organism: Rattus norvegicus

Type: **Expression profiling by array**

Platform: GPL19271 52 Samples

Download data: CEL, TXT

Series Accession: GSE156188 ID: 200156188

- [Analysis of differentially expressed genes in endothelial cells following tumor cell adhesion and role of PRKAA2 and miR-124-3p](#)
462. (Submitter supplied) Tumor cell adhesion to endothelium is one pattern of tumor-endothelium interaction and one key step during tumor metastasis. The endothelium integrity is an important barrier to prevent tumor invasion and metastasis. Changes happened in ECs according to tumor cells adhesion provide important signaling mechanisms for the angiogenesis and metastasis of tumor cells. However, it is unclarified by now. In this present study we used Affymetrix Gene Chip Human Transcriptome Array 2.0. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL17586 6 Samples

Download data: CEL

Series Accession: GSE162957 ID: 200162957

- [Neuronal-like differentiation of A549 cells in response to PRMT1 knockdown](#)

463. (Submitter supplied) Formerly we found that cancer-promoting factors, such as some typical epigenetic modification factors, are neural specific or enriched in embryonic neural cells, and play a key role in conferring the property of neural stemness to cancer cells or in maintaining neural stemness in neural stem/progenitor cells. Our recent study demonstrated

that PRMT1, a protein arginine methyltransferase, serves also to maintain neural stemness in either neural stem/progenitor cells or cancer cells. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL15207 2 Samples

Download data: CEL

Series Accession: GSE162840 ID: 200162840

[HEK-293 cells: Control cells transfected with hRIZ2 and rRIZ1](#)

464. (Submitter supplied) In order to evaluate the effects of RIZ2 overexpression on gene expression, a pilot expression study was performed through microarrays analysis. We compared the differential gene expression between HEK-293 cells overexpressing human RIZ2 (pEGFP-hRIZ2) and rat RIZ1 (pEGFP-rRIZ1) versus control cells transfected with the E-GFP empty vector alone (pEGFP).

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL10332 12 Samples

Download data: TXT

Series Accession: GSE150031 ID: 200150031

[Effect of glutathione reductase \(Gsr\) deficiency on lung transcriptomics in embryonic mice and neonatal and](#)

465. [adult mice exposed to hyperoxia.](#)

(Submitter supplied) Gsr is an antioxidant enzyme responsible for maintaining the supply of reduced glutathiones which reduce reactive oxygen species and maintain cellular redox balance. However, the role for Gsr in the development of oxidative lung injury is not well characterized. We used microarray analysis to identify Gsr-dependent genes and pathways in embryonic, neonate, and adult lungs. We also determined Gsr-dependent lung transcriptomics in mouse neonates and adults which were neonatally exposed to hyperoxia (O₂) or air.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL1261 32 Samples

Download data: CEL, CHP

Series Accession: GSE116485 ID: 200116485

[A stem cell based in vitro model of NAFLD enables the analysis of patient specific individual metabolic](#)

466. [adaptations in response to a high fat diet and AdipoRon interference](#)

(Submitter supplied) A stem cell based in vitro model of NAFLD recapitulates regulatory networks and suggests a steatosis associated phenotype. AdipoRon treatment influences metabolism, immune system, cell stress and signalling

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL23159 9 Samples

Download data: CEL

Series Accession: GSE162797 ID: 200162797

[Expression data of lentivirus sponge Protein Arginine Methyltransferase 5 downregulated NCI-H929 cell line](#)

467. [compared with control lentivirus sponge](#)

(Submitter supplied) Multiple myeloma is characterized by frequent chromosomal alterations. Protein Arginine Methyltransferase 5 (PRMT5) catalyzes symmetric dimethylation of arginine, a post-translational modification involved in cancer and embryonic development. We sought to functionally validate the role of PRMT5 and delineate their downstream target genes in MM. Using "sponge" lentiviral vectors to knock down PRMT5 in vitro and in vivo, we have documented enhanced apoptosis and descend proliferation of MM cells compared with control lentivirus sponge . [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL15207 6 Samples

Download data: CEL

Series Accession: GSE162715 ID: 200162715

- [Grb10a knockdown in Danio rerio during early life alters growth and cardiometabolic function associated with a remodelled transcriptome](#)
468.

(Submitter supplied) Embryonic growth trajectory is a risk factor for chronic metabolic and cardiovascular disorders and influences birth weight and early post-natal weight gain in humans. Grb10 is a negative regulator of the main pathways driving embryonic growth. Grb10 knock-out in mammals increases insulin sensitivity and growth trajectory. This study has now investigated the long-term cardiometabolic consequences and associated transcriptomic profiles of morpholino induced early life disruption in grb10a expression in Danio rerio. [more...](#)

Organism: Danio rerio
 Type: **Expression profiling by array**
 Platform: GPL16933 30 Samples
 Download data: CEL
 Series Accession: GSE162474 ID: 200162474

- [Whole genome transcriptome profiling identifies TIGIT as a regulator of T cell exhaustion in liver cancer](#)

469. (Submitter supplied) PD-1 checkpoint inhibition has shown promising results in patients with hepatocellular carcinoma, inducing objective responses in approximately 20% of the treated patients. The role of other co-inhibitory molecules and their individual contribution to T cell dysfunction in liver cancer, however, remain largely elusive. Here we perform for the first time a comprehensive mRNA profiling of CD8 T cells in a murine model of autochthonous liver cancer by comparing the whole genome transcriptome of naive, functional effector and exhausted, tumor-specific CD8 T cells. [more...](#)

Organism: Mus musculus
 Type: **Expression profiling by array**
 Platform: GPL19096 11 Samples
 Download data: TXT
 Series Accession: GSE137610 ID: 200137610

- [Maternal antioxidant treatment prevents behavioural and neurological changes in offspring exposed to prenatal](#)

470. [social stress](#)

(Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Rattus norvegicus
 Type: **Expression profiling by array**; Other; Expression profiling by high throughput sequencing
 Platforms: GPL19924 GPL22396 36 Samples
 Download data: RCC
 Series Accession: GSE130574 ID: 200130574

- [Maternal antioxidant treatment prevents the adverse effects of prenatal stress on the offspring's brain and](#)

471. [behavior \[NanoString nCounter rat miRNA\]](#)

(Submitter supplied) Maternal exposure to stress during pregnancy is associated with an increased risk of psychiatric disorders in the offspring in later life. The mechanisms through which the effects of maternal stress are transmitted to the fetus are unclear, however the placenta, as the interface between mother and fetus, is likely to play a key role. Using a rat model, we investigated a role for placental oxidative stress in conveying the effects of maternal social stress to the fetus and the potential for treatment using a nanoparticle-bound antioxidant to prevent adverse outcomes in the offspring. [more...](#)

Organism: Rattus norvegicus
 Type: **Expression profiling by array**; Other
 Platform: GPL19924 24 Samples
 Download data: RCC, TXT
 Series Accession: GSE130573 ID: 200130573

- [PHF6 is a key regulator of normal human hematopoiesis by modulating NOTCH1 signaling activity](#)

472. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Homo sapiens
 Type: **Expression profiling by array**
 Platforms: GPL19197 GPL14550 27 Samples
 Download data: TXT

Series Accession: GSE85373 ID: 200085373

 [PHF6 keeps hematopoietic lineage development in check \[OP9-DLL1\]](#)

473. (Submitter supplied) Analysis of the mutational landscape of various hematological malignancies has shown that key regulators implicated in lineage commitment and differentiation are frequently implicated in leukemic transformation. In T-cell acute lymphoblastic leukemia, the role of various oncogenic and tumor suppressing transcription factors has been investigated. More recently, an exceptional high prevalence of mutations affecting epigenetic modifiers in T-ALL has also been noted. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL19197 6 Samples

Download data: [TXT](#)

Series Accession: GSE85370 ID: 200085370

 [PHF6 keeps hematopoietic lineage development in check \[OP9-GFP\]](#)

474. (Submitter supplied) Analysis of the mutational landscape of various hematological malignancies has shown that key regulators implicated in lineage commitment and differentiation are frequently implicated in leukemic transformation. In T-cell acute lymphoblastic leukemia, the role of various oncogenic and tumor suppressing transcription factors has been investigated. More recently, an exceptional high prevalence of mutations affecting epigenetic modifiers in T-ALL has also been noted. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL19197 6 Samples

Download data: [TXT](#)

Series Accession: GSE85369 ID: 200085369

 [Expression data from murine TLR5 overexpressing HEK293 cells treated with flagellins of *E. coli* Nissle \(EcN\)](#)

475. [and *Salmonella Typhimurium* SL1344 \(ST\)](#)

(Submitter supplied) The healthy gut microbiota is composed of three different functional subgroups, symbionts, commensals and pathobionts. Additionally, infection with pathogenic bacteria can occur. Microbe Associated Molecular Patterns (MAMPs) are expressed by most members of both, microbiota and pathogens and interact with Pattern Recognition Receptors (PRRs), resulting in activation of the innate immune system. It is still unclear whether the interaction of PRRs with MAMPs of different origin, leads to a differential activation of innate immunity and whether thereby, distinction can be made between symbionts, commensals, pathobionts and pathogens. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL17692 18 Samples

Download data: [CEL](#)

Series Accession: GSE71660 ID: 200071660

 [Expression profiling of immature ovule and pistil samples of sexual and apomictic *Boechera* \(Brassicaceae\)](#)

476. (Submitter supplied) Sexual reproduction (meiosis and syngamy) is the major form of reproduction in diploid *Boechera* species, but most species hybrids reproduce by apomixis (unreduced gametophyte formation followed by parthenogenesis of the unreduced egg). In this study, we used *Arabidopsis* microarrays to detail global programs of gene expression underlying sexual and apomictic modes of reproduction.

Organism: *Boechera stricta*; *Boechera microphylla*; *Arabidopsis thaliana*; *Boechera lignifera*; *Boechera formosa* x *Boechera* sp. JC-2020Type: **Expression profiling by array**

Platform: GPL198 20 Samples

Download data: [CEL, TXT](#)

Series Accession: GSE156684 ID: 200156684

 [An Investigation into the Biological Effects of Indirect Potable Reuse Water Using Zebrafish Embryos](#)

477.

(Submitter supplied) In the search for sustainable drinking water, many countries are weighing up the benefits of advanced treatment technologies as a proactive measure to assist with the transformation of treated wastewater into a source of water used for the production of potable water. We investigated the biological effects along a pilot plant with an advanced water treatment process, using zebrafish embryos at different stages of development. [more...](#)

Organism: **Danio rerio**

Type: **Expression profiling by array**

Platform: [GPL28652](#) 132 Samples

[Download data: TXT](#)

Series Accession: GSE152131 ID: 200152131

[Characterisation of human PSC-derived cardiovascular cell types](#)

478. (Submitter supplied) Vascularization and maturation options for cardiac tissue engineered structures are currently intensively investigated. Therefore, the generation and characterisation of all cardiovascular cell types from human pluripotent stem cells (hPSC; either induced -iPSC- or embryonic -hESC) are of particular interest. In our group, differentiation and selection methods were described for obtaining highly pure hPSC-derived cardiomyocytes (CM; selected for cMHC), endothelial cells (EC; selected for CD31) and PDGFR β expressing cardiac pericyte-like cells (PC). [more...](#)

Organism: **Homo sapiens**

Type: **Expression profiling by array**

Platform: [GPL26355](#) 16 Samples

[Download data: TXT](#)

Series Accession: GSE145957 ID: 200145957

[Expression data from mouse brain during development](#)

479. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: **Mus musculus**

Type: **Expression profiling by array**

Platform: [GPL6246](#) 8 Samples

[Download data: CEL](#)

Series Accession: GSE140762 ID: 200140762

[Expression data from E17.5 mouse brain regions](#)

480. (Submitter supplied) During brain development, layer 5 neurons distributed across most areas of the neocortex innervate the pontine nuclei (basilar pons) by the initiation and extension of collateral branches interstitially along their corticospinally extending axons. We used microarrays to compare gene expression profiles of brain areas that were projected (pontine nucleus, superior colliculus) and were not projected (cerebellum, olfactory bulb) by axon collaterals from the corticospinal tract in order to understand genetic programs that regulate axon collaterals formation.

Organism: **Mus musculus**

Type: **Expression profiling by array**

Platform: [GPL6246](#) 4 Samples

[Download data: CEL](#)

Series Accession: GSE140761 ID: 200140761

[Expression data from mouse pontine nucleus](#)

481. (Submitter supplied) During brain development, layer 5 neurons distributed across most areas of the neocortex innervate the pontine nuclei (basilar pons) by the initiation and extension of collateral branches interstitially along their corticospinally extending axons. We used microarrays to compare gene expression profiles of pontine nucleus when axon collaterals towards the pontine nucleus start to extend (embryonic day 17.5 (E17.5) to postnatal day 1 (P1)), and/or throughout the development (E17.5-P14) in order to understand genetic programs that regulate axon collaterals formation.

Organism: **Mus musculus**

Type: **Expression profiling by array**

Platform: [GPL6246](#) 4 Samples

[Download data: CEL](#)

Series Accession: GSE140760 ID: 200140760

[Transcriptional Changes in Rat Dorsal Root Ganglia Neurons During Stretch-Mediated Axon Growth](#)

482. (Submitter supplied) The development of meter-long axons within the nervous system is a remarkable, yet unresolved biological process. The most widely studied aspects of neuronal growth focus on the extension and chemotropism of growth cones. However, over the course of organismal development, short axons elongate up to one meter in length with the systemic expansion of mitotic tissues. The preeminent regulatory mechanism for such synchronized growth between the nervous system and the tissues it spans, is the biomechanical stretch of axons, a known stimulus of axon growth. [more...](#)

Organism: Rattus norvegicus

Type: **Expression profiling by array**

Platform: GPL6247 10 Samples

Download data: CEL, TXT

Series Accession: GSE98535 ID: 200098535

 [Biomarkers for aristolochic acid nephrotoxicity](#)

483. (Submitter supplied) Aristolochic acid (AA) is a major ingredient in several Chinese herbs that exhibits a wide range of pharmacological effects. Recently, clinical reports and experimental studies have demonstrated that AA causes renal toxicities, acute renal failure and interstitial fibrosis. However, the molecular mechanism underlying AA nephrotoxicity is not yet fully understood. Embryonic stem cells (ESCs) are pluripotent cells isolated from early embryos, which have highly undifferentiated potential and are capable of differentiating into all kinds of body tissues and organs. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL1261 6 Samples

Download data: CEL, DCP, XLSX

Series Accession: GSE162195 ID: 200162195

 [Analysis of gene expression in Sox10 Dom mutant sacral neural crest cells](#)

484. (Submitter supplied) Hirschsprung's disease (HSCR) is a congenital disease which is characterized by the reduction or absence of neurons and glial cells in the enteric nervous system (ENS). Failure of neural crest cells (NCCs) to colonize the gut during the embryonic development has been considered as one of the possible causes of the disease. In this study, the migration and gene expression of sacral NCCs from the spontaneous mouse mutant Dominant megacolon (Dom) which is a HSCR animal model expressing a mutated transcription factor Sox10, were analyzed in order to identify candidate genes which may possibly affect the NCC migration in the mutant.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6246 8 Samples

Download data: CEL

Series Accession: GSE161579 ID: 200161579

 [RNA microarray analysis of human placenta in normal pregnancy and preeclampsia](#)

485. (Submitter supplied) To investigate the differentially expressed lncRNAs and mRNAs in human placenta between normal pregnancy and preeclampsia, we performed the human LncRNA microarray analysis of 8 samples from clinical patients.

Organism: Homo sapiens

Type: **Expression profiling by array**; Non-coding RNA profiling by array

Platform: GPL16956 8 Samples

Download data: TXT

Series Accession: GSE160888 ID: 200160888

 [TET1 KO affects Sox9 function \[cell line\]](#)

486. (Submitter supplied) Ten eleven translocation 1 (Tet1) directs chondrogenic differentiation in the mouse embryonic growth plate. We have characterized the global exon array analysis upon Tet1 knockdown induced by two different shRNAs. In this dataset, we include the expression data obtained from in vitro differentiation of ATDC5 chondroprogenitor cells for 15 days in presence (non-target) and absence (Tet1 sh1 and Tet1 sh2) of Tet1. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6246 3 Samples

[Download data: CEL, TXT](#)

Series Accession: GSE61855 ID: 200061855

[Keystone genes for tooth development](#)

487. (Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus; Rattus norvegicus; Myodes glareolus

Type: **Expression profiling by array**; Expression profiling by high throughput sequencing

4 related Platforms 67 Samples

[Download data: CEL](#)

Series Accession: GSE142201 ID: 200142201

[Keystone genes for tooth development \[microarray\]](#)

488. (Submitter supplied) The expression levels of developing mouse molar transcriptome were measured. 5 samples of both E13.5 and E14.5 of mouse developing molar tooth.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL27901 10 Samples

[Download data: CEL](#)

Series Accession: GSE141907 ID: 200141907

[Targeted suppression of metastasis controlling transcription factor SOX2 in various cancers using a sequence-specific designer Pyrrole-Imidazole Polyamide](#)

(Submitter supplied) SOX2 is a well-known transcription factor that plays a central role in maintaining self renewal, pluripotency of embryonic stem cells, and cell fate determination during embryonic development. N-Methylpyrrole-N-methylimidazole polyamides (PIPs) are chemical compounds that can selectively recognize DNA sequence and achieve operative control over gene expression. In this study, the antitumor activity of a PIP targeting SOX2 binding sequence (SOX2i), which was recently shown to induce the targeted differentiation of stem cells into cardiomyocytes, was evaluated.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL20844 2 Samples

[Download data: TXT](#)

Series Accession: GSE138617 ID: 200138617

[Genome-wide expression changes induced by bisphenol A, F and S in human stem cell derived hepatocyte-like cells](#)

490. (Submitter supplied) The debate about possible adverse effects of bisphenol A (BPA) has been ongoing for decades and bisphenol-F (BPF) and -S (BPS) have been suggested as "safer" alternatives. In the present study we used hepatocyte-like cells (HLC) derived from the human embryonic stem cell lines Man12 and H9 to compare the three bisphenol derivatives. Stem cell-derived progenitors were produced using an established system, and, during their transition to HLCs, they were exposed to BPA, BPF and BPS for 8 days. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL570 47 Samples

[Download data: CEL](#)

Series Accession: GSE160360 ID: 200160360

[Kinetic modeling of stem cell transcriptome dynamics to identify regulatory modules of normal and disturbed neuroectodermal differentiation](#)

(Submitter supplied) Thousands of transcriptome data sets are available, but approaches for their use in dynamic cell response modelling are sparse, especially for processes affected simultaneously by two orthogonal influence variables. We approached this problem for neuroepithelial development of human pluripotent stem cell (differentiation variable), in the presence or absence of valproic acid (signaling variable). Using few basic assumptions (sequential differentiation states of

cells; discrete on/off states for individual genes in these states), and time-resolved transcriptome data, a comprehensive model of spontaneous and perturbed gene expression dynamics was developed. [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL570 140 Samples

Download data: CEL

Series Accession: GSE147270 ID: 200147270

- [Molecular Analysis of Fetal and Adult Primary Human Liver Sinusoidal Endothelial Cells: A Comparison to Other Endothelial Cells](#)
- 492.

(Submitter supplied) In human F8 deficiency leads to hemophilia A and is largely synthesized and secreted by the sinusoidal endothelial cells of the liver (LSECs). However, the specificity and characteristics of these cells is not well known. In this study, we performed genome wide expression and CpG methylation profiling of fetal and adult human LSECs together with other fetal endothelial cells, from lung (micro-vascular and arterial), and heart (micro-vascular). [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**; Methylation profiling by genome tiling array

4 related Platforms 60 Samples

Download data: IDAT

Series Accession: GSE140079 ID: 200140079

- [Molecular atlas of fetal and adult human liver sinusoidal endothelial cells: a F8 secreting cell \[expression array\]](#)

493. (Submitter supplied) In human F8 deficiency leads to hemophilia A and is largely synthesized and secreted by the sinusoidal endothelial cells of the liver (LSECs). However, the specificity and characteristics of these cells is not well known. In this study, we performed genome wide expression and CpG methylation profiling of fetal and adult human LSECs together with other fetal endothelial cells, from lung (micro-vascular and arterial), and heart (micro-vascular). [more...](#)

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL10558 32 Samples

Download data: IDAT, TXT

Series Accession: GSE139993 ID: 200139993

- [Expression data from BAX/BAK double knockout mouse embryonic fibroblast at baseline and following exposure to genotoxic stress.](#)

494. (Submitter supplied) The BCL-2 family proteins are central regulators of apoptosis. However, cells doubly deficient for BAX and BAK or overexpressing BCL-2 still succumb to oxidative stress upon DNA damage or loss of matrix attachment. Our studies indicate a central role for the transcription factor deltaNp63alpha (referred to as p63 from this point forward) in this form of non-apoptotic cell death. We used microarrays to investigate gene expression in apoptosis-incompetent cells expressing a control vector or p63, at baseline and following exposure to genotoxic stress, to further elucidate molecular mechanisms regulating this type of non-apoptotic death and the role of p63 in this context.

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6246 4 Samples

Download data: CEL

Series Accession: GSE106214 ID: 200106214

- [ROS amplification drives mouse spermatogonial stem cell self-renewal](#)

495. (Submitter supplied) Reactive oxygen species (ROS) play critical roles in self-renewal division for various stem cell types. However, it remains unclear how ROS signals are integrated with selfrenewal machinery. Here we report that the MAPK14/MAPK7/BCL6B pathway creates a positive feedback loop to drive spermatogonial stem cell (SSC) self-renewal via ROS amplification. The activation of MAPK14 induced MAPK7 phosphorylation in cultured SSCs, and targeted deletion of Mapk14 or Mapk7 resulted in significant SSC deficiency after spermatogonial transplantation. [more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL6246 14 Samples

[Download data: CEL](#)

Series Accession: GSE106103 ID: 200106103

- [Experimental data of ex vivo treated human cord blood \(CB\) derived hematopoietic stem and progenitor cells \(HSPCs\) with Ciclopirox ethanalamine.](#)
496.

(Submitter supplied) Ciclopirox ethanalamine (CPX), is a novel regulator of HSCs and preserve the primitive stem cell state of these cells. By treateing human CB-HSPCs with CPX we observed a substantial increas on number of stem and porgenitor cells detected by phenotypic monitoring of stem cell markers. we performed this microarray analysis to identify the differentially expressed genes upon CPX treatment.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL16686 12 Samples

[Download data: CEL](#)

Series Accession: GSE159100 ID: 200159100

- [Transcriptomic analysis of porcine blastocyst form cumulus oocyte complexes matured in coculture with porcine luteal cells](#)
497.

(Submitter supplied) The transcriptome pattern in blastocyst that developed from cumulus oocyte complexes matured in coculture with porcine luteal cells was investigated.

Organism: Sus scrofa

Type: **Expression profiling by array**

Platform: GPL17779 4 Samples

[Download data: TXT](#)

Series Accession: GSE154587 ID: 200154587

- [A complementary study pipeline unravels novel players in the pathoetiology of Hirschsprung's disease](#)

498. (Submitter supplied) Purpose: Hirschsprung's disease (HSCR, OMIM 142623) represents one of the main causes of neonatal intestinal obstruction. It is caused by dysfunction of neural crest cells (NCCs) and their progeny during development of the enteric nervous system (ENS). HSCR is considered a multifactorial disorder, however, associated risk genes only account for a minority of cases. Consequently, defining disease-relevant variants is still a demanding task.
[more...](#)

Organism: Mus musculus

Type: **Expression profiling by array**

Platform: GPL26644 9 Samples

[Download data: CEL](#)

Series Accession: GSE144442 ID: 200144442

- [Comparative gene expression of CD34+ human hematopoietic progenitor cells upon knockdown of STAT5](#)

499. (Submitter supplied) The objective of the study is to identify the genes regulated by STAT5 in very primitive human hematopoietic stem progenitor cells (HSPCs). We used Affymetrix Human Genome U133 Plus 2.0 microarrays to investigate gene expression in human CD34+CD38- HSPC upon expression of STAT5 or control luciferase shRNA-encoding vectors.

Organism: Homo sapiens

Type: **Expression profiling by array**

Platform: GPL23270 4 Samples

[Download data: CEL](#)

Series Accession: GSE97552 ID: 200097552

- [Gene expression profile of DOCK8+CD4 T cell which causes systemic lupus erythematosus](#)

500. (Submitter supplied) Systemic lupus erythematosus (SLE) is a prototypical autoimmune disease of unknown cause. We show here that a novel T follicular helper cell type expressing the guanine nucleotide exchange factor DOCK8 on the cell surface causes SLE. These cells, which we have designated autoantibody-inducing CD4 T (aiCD4 T) cells, are generated after resuscitation from anergy following strong TCR stimulation by antigen. [more...](#)

Organism: Mus musculus
Type: **Expression profiling by array**
Platform: GPL21163 6 Samples
[Download data: TXT](#)
Series Accession: GSE159240 ID: 200159240