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Differential gene expression analysis of metolachlor treated human liver cells by microarray

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DIFFERENTIAL GENE EXPRESSION ANALYSIS OF METOLACHLOR TREATED HUMAN LIVER CELLS BY MICROARRAY

An Abstract of a Thesis

Submitted

In Partial Fulfillment

Of the Requirement for the Degree

Master of Science

Navinder Paul Kaur Brar

University of Northern Iowa

December 2017

ABSTRACT

Metolachlor is one of the most common pre-emergent pesticides used by Iowa farmers. It is used to control broadleaf weeds and grasses in the fields of corn and soybean. It is a frequent contaminant of groundwater and surface water due to runoff after application. It has been shown to inhibit protein and chlorophyll synthesis in plant cells, but its effect on mammalian cells has not been consistently conclusive. As metolachlor and other herbicides have been shown to be associated with harmful health effects in non-target organisms it is very important to determine a mechanism of action on non-target cells, especially human cells. Previous work from our lab studying the effects of metolachlor on human cells demonstrated that low-level metolachlor exposure can inhibit growth in several human cell types such as fibroblasts, HepG2 liver cells and THP-1 alveolar monocytes and alter the expression level of several proteins involved in cell cycle control. While we have shown that metolachlor can have an effect on cellular macromolecules involved in cell growth, is not clearly understood is if there are other cellular processes, genes and proteins that may be altered by exposure to metolachlor.

Microarray analysis was used in this study to determine if there are groups or families of genes that participate in a biological process which may be altered after herbicide exposure, and if one or several specific cellular functions are affected or altered after this exposure. Microarray analysis was performed after isolating total RNA from HepG2 cells exposed to varying levels (200 ppb, 500 ppb, and 1000 ppb) of metolachlor for varying times (24 hours, 48 hours and 72 hours) and comparing expression to that of control (0 ppb) cells for each of the time points.

To demonstrate a significant amount of differential gene expression, cells needed 1000 ppb of metolachlor at 24 hours exposure. Whereas at 48 hours of exposure, differential gene expression between control and metolachlor treated cells was observed at all three concentrations, suggesting that 48 hours of exposure may be an important and perhaps optimal time point for altered gene expression between control and metolachlor treated cells. Very little level of differential gene expression was observed at 72 hours of exposure time.

Gene Ontology (GO) analysis, using the GOrilla tool of genes that were differentially expressed between control and metolachlor treated HepG2 cells showed significant enriched clusters in the processes of DNA replication and repair, cellular response to stimuli and cell cycle regulation. Metolachlor exposure for 48 hours at 500 ppb showed eight biological processes were enriched while 1000 ppb metolachlor resulted in thirteen biological processes that were enriched.

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This study by: NAVINDER PAUL KAUR BRAR

Entitled: DIFFERENTIAL GENE EXPRESSION ANALYSIS OF METOLACHLOR TREATED HUMAN LIVER CELLS BY MICROARRAY

has been approved as meeting the thesis requirement for the

Degree of Master of Science in Biology.

Date Dr. Kavita R. Dhanwada, Chair, Thesis Committee

Date Dr. David J. McClenahan, Thesis Committee Member

Date Dr Tilahun Abebe, Thesis Committee Member

Date Dr. Patrick Pease, Interim Dean, Graduate College

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CHAPTER 1

INTRODUCTION

Use of pesticides in agriculture has become commonplace in the United States and rest of the developed world. Pesticides are defined as a diverse group of chemicals used to control pests, insects, molds, including unwanted plants. These include insecticides, fungicides, herbicides, rodenticides and nematocides (Alavanja et al. 2013). Herbicides are chemicals used to kill unwanted plants. Metolachlor, is one of the most commonly used pre-emergent (applied before a crop emerges from the soil) herbicide by Iowa farmers. It is used to control broadleaf weeds and annual grasses such as yellow nutsedge (*Cyperus esculentus*), barnyard grass (*Echinochloa crusgalli*), crabgrass (*Digitaria Spp.),* fall panicum (*Panicum dichotomiflorum*), and foxtails (*Setaria spp.)* in fields of corn, soybean, grain sorghum, peanut and cotton (EPA. 1995) as well as for general weed control on the highway, right-of-ways and woody ornamentals (Christmas trees) (Extoxnet. 2000b).

Metolachlor, 2-chloro-N-(2-ethyl-6-methylphenyl)-N-(2-methoxy-1-methylethyl) acetamide, is a member of chloroacetanilide family, which also includes alachlor and propachlor (Stamper and Tuovinen. 1998). Metolachlor was synthesized in 1972 by Ciba-Geigy Limited and was registered in 1976 for general weed control in non-crop areas (Rivard. 2003). Syngenta (formerly Ciba-Geigy) is the main producer and primary registrant of metolachlor (EPA. 1995). This herbicide is currently marketed as

Pennant Magnum, which contains the S-isomer of metolachlor, under the name S-metolachlor as the active ingredient (Syngenta. 2000).

This herbicide is absorbed through the roots and shoots of the growing plant just above the germinating seed of these target weeds and acts as a growth inhibitor by suppressing the synthesis of some of the most essential plant components including chlorophyll, proteins, fatty acids and lipids, as well as isoprenoids (including gibberellins), and flavonoids (such as anthocyanins) (EPA. 1998).   Metolachlor is slightly toxic and classified as EPA toxicity class III. It is primarily considered a General Use Pesticide (GUP), although some products may be listed as restricted use (RUP) (Extoxnet. 1996).

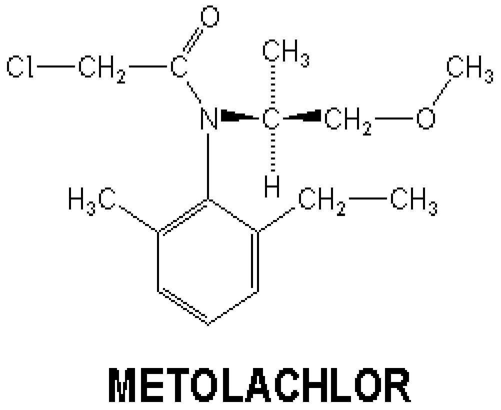

Figure 1. Chemical structure of metolachlor.

(http://passel.unl.edu/Image/siteImages/Metolachlor.gif)

Figure 1 shows the chemical structure of metolachlor, it has a six-member ring bonded to nitrogen and contains a chlorine atom. Pure metolachlor is a colorless and odorless liquid at room temperature. Trade names for products containing metolachlor include Bicep, Codal, CGA-24705, Dual, Dual 8E, and Pennant, Pennant 5G, Pimagram and Primextra. Metolachlor can be used alone or in formulations with other pesticides to control for pests but it is mostly used with herbicides that control broadleaf weeds including atrazine, cyanazine, and fluometuron (Extoxnet. 2000a).

In United States alone, the amount of pesticides used annually in 2011 and 2012 exceeded 1.1 billion pounds for both years (EPA. 2016). The largest portion of US agricultural pesticides used each year was herbicides, followed by nematocides and fumigants, insecticides, fungicides, and other pesticides. Metolachlor ranked third in the most commonly used conventional agricultural pesticides with 33-44 million pounds as the active ingredient (EPA. 2016).

Currently, there is no regulatory limit as to the maximum amount of metolachlor allowed in drinking water (maximum contamination level, MCL). The US Environmental Protection Agency (USEPA) only has a lifetime health advisory level (HAL) of 100 parts per billion (ppb) for metolachlor. The HAL is a non-regulatory, non-enforceable health based concentration of pesticide in drinking water that is *not expected* to produce any adverse non-carcinogenic effects when consumed over a given period of time (EPA. 1995).

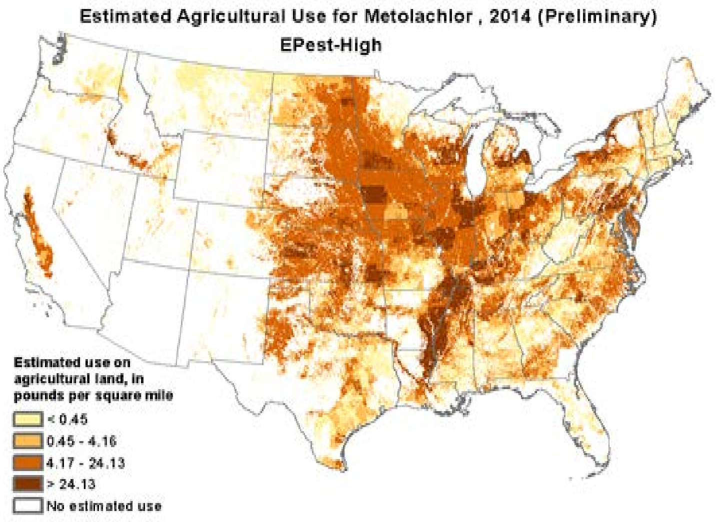

Figure 2. Estimated Agricultural Use for Metolachlor, 2014 (https://water.usgs.gov/nawqa/pnsp/usage/maps/graphics/H_METOLACHLOR_2014.png)

Mode of Exposure to General Population

Estimated usage of metolachlor in United States is 33-44 million pounds of active ingredient per year (EPA. 2016). Thus, with such a high frequency of usage, environmental contamination is becoming an increasingly common problem resulting in contamination of water, air and soil. The degree of herbicide transport in the environment depends on several factors such as rate of application, herbicide persistence in soil and water, mobility, rainfall, topography, and climate (Lin et al. 1999).

Ingestion of Contaminated Surface and Groundwater by Metolachlor

Ingestion of contaminated water is the most likely route of exposure to general population. A report by the World Health Organization (WHO) showed that 50.3% of surface water and 2% of groundwater sources in United States has measurable concentration of multiple herbicides (WHO. 1996). The concentration of metolachlor and its multiple degradates vary between 0.08-4.5 ppb in the agricultural states of Iowa, Wisconsin and Pennsylvania (Pothuluri et al. 1997), 8.6-15.4 ppb in underground water of Iowa (Kolpin et al. 2000), 28-63 ppb in Ontario streams (Frank et al. 1990), and as high as 850 ppb detected in rivers in Northern Ohio (Wolf and Moore. 2002).

In a 2003 study from the United States Geological survey (USGS), metolachlor was found in 29.11% of stream samples in underdeveloped areas, 49.74% of samples from urban areas, 71.37% of samples in mixed land use areas, and 82.74% of stream samples from agricultural land (Martin et al. 2003). Additionally, they showed that metolachlor detection frequencies in groundwater ranged from 1.49% of samples in undeveloped settings to 5.04% in mixed land use settings, 8.98% in urban settings and 17.0% in agricultural settings indicating the widespread presence of this herbicide in the environment. The 95th percentile concentrations were 0.022 μg/L or ppb in agricultural settings indicating higher contamination of freshwater and groundwater by metolachlor in agricultural settings. Similarly, the highest concentration estimated at 32.8 μg/L or ppb, was also found in an agricultural setting (Kolpin et al. 1998). This should be a very important indicator of potential contamination as 50% of the United States population is dependent on groundwater (Kolpin et al. 1998).

Metolachlor was one of the four pesticides extensively studied throughout the nation in the National Alachlor Well Water Survey project which analyzed the content of more than 6 million private and domestic wells over several years. Metolachlor was detected in over 60,000 wells (1% of the wells) at a concentration ranging from 0.1 to 1.0 ug/L or ppb (Holden and Graham. 1992). Metolachlor levels in the water have occasionally exceeded lifetime human health advisory levels of 100 ppb (EPA. 1995). In another study conducted in the five Great Lakes, geometric mean concentration of metolachlor and its stereoisomer fraction ranged from 0.00028 to 0.014 ug/L or ppb, in the 101 surface water samples collected during 2005-2006 (Kurt-Karakus et al. 2010), which is at a low level.

Exposure by Inhalation

While ingestion of contaminated water is the most likely route of exposure to general population, this pesticide can contaminate the atmosphere via drift during application and volatilization and thus can be inhaled into the body (Majewski et al. 2000). Theoretically, very little metolachlor should be lost in the atmosphere by volatilization, as predicted of its low Henry's Law Constant of 2.44 X 10^{-8} atm m^3/mol (Ciba-Geigy Corporation), and its low vapor pressure of 1.3 X 10^{-5} mm Hg (Extoxnet. 2000a). However, it has been found in the environment via dust contamination. A median concentration of 200 pg/m^3 was detected in air samples at 8 different monitoring sites across Canada in 2004 and 2005 (Yao et al. 2008). Aerosolized form of the pesticide can be carried across considerable distances depending on the direction of wind. A measurable level of metolachlor was detected in over 50% of samples collected in 39

Iowa farm and non-farm homes (Curwin et al. 2005). These studies suggest that metolachlor can enter the animal body by inhalation of small contaminated dust particles.

Dermal Exposure

Metolachlor is not readily absorbed by the skin, but repeated dermal exposures may create skin sensitization, especially among those individuals who work with metolachlor as applicators, formulators and field workers (EPA. 1998). In a study by Ross and co-workers (2001), dermal penetration was shown to vary between 2% to 20% if the pesticide is left on the skin for 8 hours or longer. Metolachlor is considered to be slightly to practically non-toxic by skin exposure, with a reported dermal LD50 of greater than 2000 mg/kg in rats (Gosselin et al. 1984). Metolachlor can act as a skin sensitizer in guinea pigs, and causes slight irritation and mild eye irritation in rabbits. This is in contrast to most formulations, as they generally do not lead to skin sensitization (Weed Science Society of America. 1994).

Environmental Fate of Metolachlor

Breakdown in Soil and Groundwater

Metolachlor is moderately persistent in the soil environment. It has a soil half-life of 7 to 292 days (EPA. 1995) and is broken down both by microbiological and photochemical degradation to at least five different products. Soils with significant soil water content may show more rapid breakdown. A very little amount of metolachlor volatilizes from the soil, whereas photo-degradation is considered a significant pathway for loss in the top few inches of soil (Zimdahl and Clark. 1982). Breakdown of metolachlor at deeper levels is mainly dependent on microbial activity as well as on temperature (Zimdahl and Clark. 1982). Microorganism metabolism can occur by both anaerobic and aerobic processes, and is affected by temperature, moisture, type of soil, amount of leaching, nitrification, oxygen concentration as well as sunlight (Zimdahl and Clark. 1982). Metolachlor and its degradates can leach from soils and have been detected in watersheds of agricultural land, in both surface and ground waters (Hladik et al. 2005; Kolpin et al. 2000; USGS. 2007; WHO. 2003). Extensive leaching is also reported to occur, especially in soils with low organic content (Zimdahl and Clark. 1982).

Breakdown in Water and Vegetation

Metolachlor is highly persistent in water over a wide range of pH. Its half-life is 97 days in highly basic waters and more than 200 days in highly acidic waters at 20℃ (EPA. 1998). Metolachlor is also considered to be relatively stable in water under natural sunlight. A slow and minimal rate of degradation by sunlight was observed, about 6.6% degraded in 30 days (EPA. 1998). Breakdown of metolachlor follows a similar pathway in corn, soybean, peanuts, and sorghum. Minimal concentration of residues and metabolites are found in grains, roots and oil, but other parts of the plants may have higher levels while cotton crops may retain higher levels of residue (EPA. 1998).

Toxicological Effects on Photosynthetic Organisms

High usage of pesticides has led to exposure of many non-target organisms including plants (aquatic and non-aquatic), bacteria, insects, and animals including humans. Metolachlor has been shown to affect several biochemical processes in plants including protein synthesis, alpha-amylase activity and gibberellin biosynthesis (Alla and Hassan. 1998). Metolachlor was shown to decrease the amount of alcohols and long chain alkanes in the wax fraction of cucumber seedling cotyledons when incubated in 5.68 ppm metolachlor, a very high dose of the herbicide (Tevini and Steinmuller. 1987).

In another study, seedlings of rice, maize and sorghum showed inhibited root and shoot growth when exposed to 2.84 ppm metolachlor in combination with Pretilachlor, another chloroacetanilide herbicide (Wu et al. 2000). *Scenedesmus vaculatus*, a green algae also showed decreased and impaired reproduction after exposure to 232 ppb of metolachlor (Junghans et al. 2003). In a similar study, this same green algae was tested for its ability to reproduce in the presence of different chloroacetanilide herbicides. When incubated in 598 ppb s-metolachlor, it showed inhibited cell growth by 50% compared to the control (Vallotton et al. 2008). Fairchild et al. (1997) tested a species of unicellular green algae (*Selenastrum capricornutum*) and a floating vascular plant (*Lemna minor*) for sensitivity. Acetanilide herbicides exhibited high toxicity to both plant species over a variable range of concentrations. In a study, a mixture of three herbicides, atrazine (54 ppb), diuron (15 ppb) and metolachlor (56 ppb), temporarily disturbed photosynthesis in phytoplanktons (Hartgers et al. 1998).

Non-Target Toxicological Effects on Aquatic Organisms

Metolachlor can cause toxicity to aquatic organisms through non-point source pollution; however, it does not pose significant cytotoxicity in these organisms (Lin et al. 1999). Metolachlor is considered to be moderately toxic to cold and warm water fish as rainbow trout, carp and bluegill sunfish. LC50 values for metolachlor were quite high at 96 hours with 3 mg/L or ppm needed in rainbow trout, 5 mg/L in carp and channel catfish, and 15.0 mg/L in bluegill sunfish. Additionally, the herbicide was rapidly excreted when the fish were placed in clean water, indicating very little accumulation. Since the residues found in fish are quite low, it is not considered to pose a threat to human health by eating these fish (Extoxnet. 2000a). Rainbow trout, carp and bluegill exposed to 2-15 ppm metolachlor for 96 hours had approximately 50% mortality (Arkhipchuk and Garanko. 2002). A crayfish (*Orconectes rusticus*), uses its chemosensory abilities and neuromuscular controls to respond to external stimuli and to locate food. When exposed to a much lower level of 50-75 ppb metolachlor, there was altered chemosensory ability causing impaired response in locating food (Wolf and Moore. 2002). In another study, water fleas (*Ceriodaphnia dubia*), which are found in littoral (shore) areas of lakes, ponds and marshes throughout the world, were exposed to 8.84 ppm Bicep, a commercial formulation of metolachlor resulting in reduced reproduction in the organism (Ort et al. 1994). Exposure of another type of water flea (*Daphnia magna*) to 1000 ppm rac-metolachlor also led to reduced brood numbers per female and survivability (Liu et al. 2006). Thus, while high levels of the herbicide are required to cause death, much reduced levels of metolachlor can lead to altered functions and abilities in these aquatic organisms.

Non-Target Toxicological Effects on Other Organisms

The increased frequency of metolachlor use has also led to increased exposure of the non-target organisms that come in contact with this chemical. Metolachlor is generally considered to be non-toxic to birds, insects and mammals (Weed Science Society of America. 1994). In a study on birds, metolachlor is found to be slightly non-toxic, oral LD50 is greater than 2000 mg/kg in mallard ducks and is greater than 4500 mg/kg in bobwhite quail. Both the mallard and the bobwhite quail show 5-day dietary LC50 values of greater than 10,000 ppm, also indicating very low toxicity to upland game birds and waterfowl (EPA. 1995). However, in another study, metolachlor is considered acutely toxic to *Collembola*, a soil dwelling arthropod which plays a role in recycling organic matter. A concentration of 12.4 ppm metolachlor increased the mortality rate by 50% (Park and Lees. 2005). Metolachlor at these high levels was also found to be toxic to bacteria *Salmonella typhimurium* (Plewa et al. 1984).

Studies have shown that metolachlor exposure can also lead to decreased body size. Pregnant adult female rats treated with metolachlor, from the 6th to 15th gestational day, showed reduction in the weight gain for the rats treated with 300 and 1000 mg/kg body weight/day compared to the control group (Katia et al. 2016**)**. A study on *Rana catesbeiana* frogs from the Yamaska river drainage basin in Southern Quebec, Canada, demonstrated reduced growth in association with higher concentrations of metolachlor from agricultural runoff (Berube et al. 2005).

A study by Hayes and colleagues (2006) on leopard frogs showed that had a mixture of 9 pesticides including 0.1 ppb of metolachlor was associated with decreased thymus size. In a study with beagle dogs, a one-year long study of metolachlor exposure (3.5 mg/kg metolachlor of body weight) showed decrease in kidney weight (Hazelette and Arthur 1989). In a similar study, two years of metolachlor exposure of different concentrations of metolachlor in the diet of albino mice resulted in a decrease in body weight gain and a decrease in the survival of female mice exposed to 1000 mg/kg (World Health Organization. 1996).

Non-target Effects of Metolachlor at the Cellular level

So far, no specific and consistent mechanism of action for metolachlor on non-target organisms has been put forth. In some cases, metolachlor exposure has resulted in the alteration of the activity of specific cellular enzymes involved in metabolism. In one study, silkworms, *Bombyx mori,* when exposed to rac-metolachlor had a significantly reduced activity of hemolymph lactate dehydrogenase, catalase and alkaline phosphatase (Zhan et al. 2006). Similarly, earthworms, *Eisenia fetida*, exposed to rac-metolachlor had increased toxic effects of cellulase and catalase activities, compared to S-metolachlor (Xu et al. 2010). In a study by Greenlee and colleagues (2004), 100 ppb of metolachlor exposure for 96 hours significantly increased the percentage of apoptosis or programmed cell death in mouse embryos.

Metolachlor is usually applied as a mixture with other herbicides in the environment. Several studies using Pacific oysters, *Crassostrea gigas,* have been performed that evaluated parameters after exposure to herbicides. In one study, Pacific oysters were exposed to a mixture of eight pesticides: atrazine (0.7 ppb), glyphosate (0.7 ppg), alachlor (0.6 ppb), metolachlor (0.6 ppb), fosetyl-aluminium 0.6 ppb), terbuthylazine (0.6 ppb), diuron (0.5 ppb) and carbaryl (0.05 ppb) at environmentally relevant concentrations over a 7-day period and then analyzed by RT-PCR. The organisms were evaluated for altered gene expression in 19 genes involved in hemocyte functional areas (cell mortality, enzyme activities and phagocytosis). It was found that phagocytosis was significantly reduced after 7 days of exposure and the 19 genes were all down-regulated in treated animals (Gagnaire et al. 2007).

In another study with Pacific oysters, oyster gametes and embryos were exposed to varying levels of S-metolachlor resulting in deleterious effects on these organisms (Mai et al. 2014). Exposure resulted in altering the fertilizing capacity of spermatozoa after 0.1 ppb exposure to metolachlor with the offspring from these gametes having dose-dependent developmental abnormalities; this was not seen with the oocyte or its offspring. The exposure of this concentration to oyster embryos resulted in embryotoxicity (Mai et al. 2014) suggesting coastal areas that have pesticide exposure may have long-term problems to oyster populations. To evaluate endocrine disruption effects of metolachlor on zebrafish embryos, genes involved in the HPT (hypothalamic-pituitary-thyroid) and the HPA (hypothalamic-pituitary-adrenal) axes were assayed. A high level of metolachlor (9.66 ppm) was used to expose embryos for 96 hours and resulted in upregulating catalase activity (256%), inhibiting cholinesterase (61%) and lactate dehydrogenase (60%) activities as well as reducing lipid peroxidase (63%) function. The results showed that S-metolachlor affected steroidogenesis as well as the HPT and HPA-axes, the endocrine systems of the organism, as it has inhibited P450 aromatase (cyp 19a2), thyroid stimulating hormone β (TSHβ) and corticotrophin releasing hormone (CRH) gene expression, genes all involved in endocrine pathways (Quintaneiro et al. 2017).

Previous studies from our lab have shown a variety of cellular effects associated with cell growth. It was shown that a very low level exposure (1.6 ppb) of metolachlor for 72 hours to normal fibroblasts resulted in a statistically significant decrease in cell proliferation (Dhanwada et al. 2003). In another study, metolachlor exposure to HepG2 cells, a human liver cell line, required a higher amount of herbicide, 50 ppb for 72 hours, to significantly inhibit cell growth, whereas a decrease in the rate of cell division required exposure to 500 ppb metolachlor with 48 hour exposure (Hartnett et al. 2013).

Thus, these results suggested that inhibition of cell growth required a lower level of metolachlor exposure compared with the more complex pathway of cell division that required a higher concentration of metolachlor. At these concentrations of metolachlor, an increased level of apoptosis and necrosis (types of cell death) was not seen, thus, we wanted to determine if the decrease we saw in cell growth was due to the expression of proteins involved in growth regulation, p53 and retinoblastoma (Rb) protein. Our results demonstrated that the levels of the retinoblastoma protein including two of its hyper-phosphorylated forms are decreased in metolachlor-exposed cells possibly leading to cell cycle arrest (Lowry et al. 2013). p53, a mediator in the DNA damage response of cells, was not significantly altered except at the highest level of metolachlor (1,000 ppb) and after a 72-hour exposure. Thus, results suggest that a mechanism of action of metolachlor is by affecting cell growth most likely due to an alteration in the cell cycle (Lowry et al. 2013).

Hypothesis and Objectives

The current research project was undertaken in order to broadly determine if there are genes, which regulate specific cellular activities, which are altered after metolachlor exposure. Our past experiences were to individually assay specific genes or proteins involved in cell growth. To broaden the scope of the genes that may be affected, we isolated total RNA from HepG2 cells exposed to varying levels of metolachlor for varying time periods and subjected the samples to microarray analysis to determine which group or family of genes were altered after herbicide exposure. Our hypothesis is that if HepG2 cells are exposed to varying concentrations of metolachlor and for different time points, then there will be differential gene expression.

We have two objectives to test this hypothesis. The first objective was to determine if there was an altered gene expression profile between metolachlor treated and non-treated (control) cells. The second objective was to determine if there in fact was a "family" of genes that participated in a biological process or function. By understanding if a specific cellular process or function is altered due to herbicide exposure, it will allow us to dig deeper into the specific mechanism of action or actions for metolachlor in human cells.

CHAPTER 2

MATERIALS AND METHODS

Cell Line

The human liver cell line, HepG2, is used for this experiment. HepG2 cells are an immortalized, non-tumorigenic liver cells derived from a 15 year-old Caucasian male with a well-differentiated hepatocellular carcinoma. HepG2 cells have a hyper diploid karyotype, having 55 chromosome pairs. These are adherent, epithelial-like cells growing in monolayer and small aggregates and can be passed indefinitely in culture (American Type Culture Collection, Manassas, VA).

Maintenance of HepG2 Cells

HepG2 cells are grown in Eagle's Minimum Essential Medium (Invitrogen), pH 7.3, containing 10% fetal bovine serum (FBS, Atlanta Biologicals), and 1% penicillin-streptomycin. This is called complete growth medium. Cells are maintained in a 100 mm petri dishes at 37°C with 5% CO_2 and are subcultured when they are 80-85% confluent. To pass or subculture cells, old growth medium is aspirated and cells are briefly rinsed with 1X PBS (phosphate buffered saline). The HepG2 cell line is adherent and requires trypsinization to dislodge the cells from the plate. To trypsinize cells, a solution of 0.25% Trypsin-0.53 mM EDTA is added to cells and kept at room temperature for 5-6 minutes. As cells begin to lose their adherence, the plate is tapped vigorously to dislodge all remaining attached cells into the trypsin solution. To inactivate the action of trypsin, 3-4 volumes of complete growth medium is added and cells are suspended in growth medium. Cells are subcultured 1:4 and growth medium is added to bring the total volume to 10 ml. The growth medium is changed every 3–4 days or as required.

Metolachlor Quantification

Metolachlor (99.5% purity, Chem Service, Inc.) is dissolved in an antibiotic and serum free medium. This stock solution is quantified by liquid chromatography-mass spectroscopy (LC-MS; Agilent 1100 Series). Known concentrations of metolachlor are dissolved in acetonitrile (solvent for metolachlor) and quantified on the LC-MS using a MOS-1 Hypersil column (Thermo Scientific) with an 80:20 acetonitrile: water mixture. Metolachlor standards of 5, 7.5, 10, 15, 20, 40, and 100 parts per million (ppm) are used to develop a standard curve to correlate area under the peak from the LC-MS to metolachlor concentrations. A linear regression line is generated, to determine the exact concentration of the experimental/stock metolachlor solution in cell culture medium. Further dilutions are made using this metolachlor solution to treat the cells. The metolachlor stock medium is stored in the dark at 4℃ and is quantified every 8-10 weeks.

Metolachlor Exposure to Cells

On day 1, 2 million (2 x 10^6) HepG2 cells are added to 100 mm petri dish and incubated overnight at 37℃ and 5% CO_2 to allow for attachment. On day 2, the growth medium is aspirated and replaced with metolachlor containing complete growth medium for the treatment groups and control cells are replaced with herbicide-free complete growth medium. Concentrations of metolachlor used are 200, 500 and 1000 parts per billion (ppb) and grown at 37 C with 5% CO_2 for 24, 48 or 72 hours (Figure 3) prior to RNA isolation.

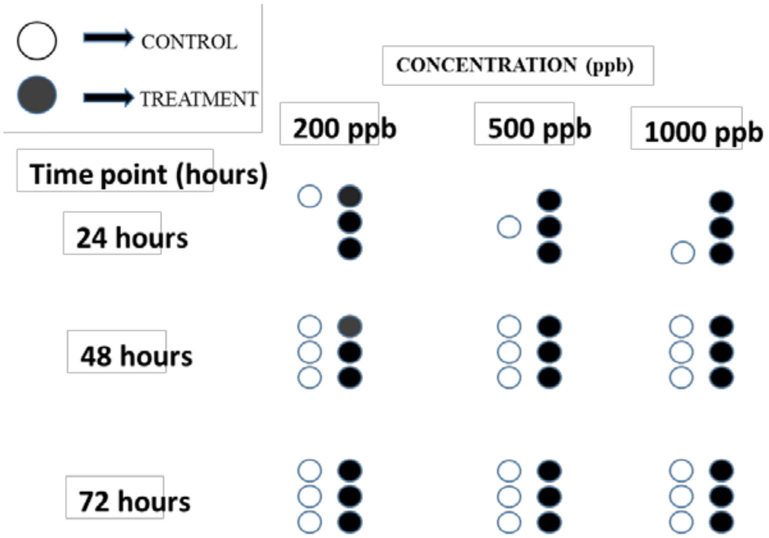

Figure 3. Schematic figure of experimental set-up.

Isolation of Total RNA

Total RNA is extracted from the samples using Trizol reagent (Gibco BRL, Carlsbad, CA) according to the manufacturer's instructions, with some modifications. Cells are lysed on the plate by adding 1 ml Trizol per plate, incubated for 4-5 minutes, removed from plate with a cell scraper and transferred into a microfuge tube before being centrifuged at 12,000 X g at 4℃ for 10 minutes. After this centrifugation, 0.2 ml of chloroform per ml of Trizol is added and the suspension is centrifuged again at 12,000 X g at 4℃ for 15 minutes and the aqueous phase is collected and transferred to new tube. To precipitate the RNA, 100% isopropanol (0.5 ml) is added and the solution is centrifuged for 10 minutes at 4°C at 14,000 X g. The supernatant is removed and pellet is washed with 75% ethyl alcohol and pellet is dissolved in 25-50 µl RNase free water. RNA is quantified on the Biotek Synergy H4 microplate spectrophotometer. The relative purity of nucleic acid, RNA and DNA, is determined by taking the ratio of the absorbance at 260 and 280. A ratio of ~2.0 is generally accepted as “pure” for RNA while a ratio of ~1.8 is generally accepted as “pure” for DNA. Samples that were used had ratios in the range of 2.0. The RNA is stored long-term in DEPC water at -80℃.

RNA Purification and Quantification

Quality of RNA is the single most important determinant of success of a microarray analysis. To remove DNA contamination, RNA samples are treated with DNase (Promega, Madison, WI). DNase treatment was performed per Promega instructions. DNase digestion reaction mixture was prepared by adding 1-8µl of RNA in water to 1µl of RNase-Free DNase 10x reaction buffer and 1µl/µg RNA of RNAse free DNase. A final volume of 10µl is achieved by adding nuclease -free water; the reaction was incubated at 37℃ for 30 minutes. To end the reaction, 1µl of DNase stop solution was added to the reaction and the mixture was incubated at 65℃ for 10 minutes to inactivate the DNase. Further purification was done by RNeasy® Mini Kit (Qiagen, Germantown, MD) to remove any remaining contamination. RNA was stored in -80℃ until use. RNA was re-quantified after purification by Biotek Synergy H4 microplate spectrophotometer. The relative purity of RNA was again determined by taking the ratio of the absorbance at 260 and 280.

DNA Microarray Sample Processing

RNA sample preparation for hybridization and the subsequent hybridization to the Illumina bead chips (HumanHT-12 v4) was performed at the Genomics Division of the Iowa Institute of Human Genetics, University of Iowa, using the manufacturer's recommended protocol. The HumanHT-12 v4 expression bead chip provides genome-wide transcriptional coverage of well-characterized genes, delivering high-throughput processing of 12 samples per bead chip. Each array on the HumanHT-12 v4 expression bead chip targets more than 47,000 probes derived from the National Center for Biotechnology Information Reference Sequence (Pruitt et al. 2012). Briefly, 100 ng total RNA was converted to amplify Biotin-aRNA using the Epicentre Target Amp-Nano Labeling Kit for Illumina Expression Bead Chip (Illumina, Inc., San Diego, CA). The amplified Biotin-aRNA product is purified through a QIAGEN RNeasy MinElute Cleanup column with modifications from Epicentre followed by mixing 750 ng of this product with Illumina hybridization buffer, placed onto Illumina-Human H12 v4 Bead Chips (BD-103-0204), and incubated at 58º C for 17 hours, with rocking, in an Illumina hybridization oven. Following hybridization, the arrays were washed, blocked, and then stained with streptavidin-Cy3 (Amersham/GE Healthcare, Piscataway, NJ). This process was done according to the Illumina Whole-Genome Gene Expression Direct Hybridization Assay protocol. Beadchips were then scanned with the Illumina iScan System (ID #N0534) and data was collected using the Genome Studio software v2011.1.

Data Pre-processing

Microarray data is an array of expression values derived from the hybridization of cDNA probes with the target. The matrix gives hybridization values as a measure of intensity of emitted fluorescence of the dyes. Experimentally, there are many sources of systematic variation, including overall intensity of light used in scanning, the dye and background emission along with the intensity of hybridization, all of which can affect measurements of gene expression levels. Thus, pre-processing of the data is done to eliminate the experimental bias and errors. The images are converted into numbers and saved as intensity data files (IDAT files). These bead summary data (IDAT file) were exported from Genome Studio.

Normalization, background correction and log2 transformation was performed using the *Limma* (Ritchie et al. 2015) package (version 3.34.0). . This process involved invoking the *neqc* function for background correction, quantile normalization and log2 transformation followed by replicate summarization. It is also used to eliminate variations and allow appropriate comparison of data obtained from the samples. We used quantile normalization, a commonly suggested method for Illumina bead chip data. Background correction is done to filter non-specific hybridization, that is, hybridization of sample transcripts whose sequences are not a perfect match to those of the probes on the array. To avoid distortion of the results by noise, we removed probes returning signals that were highly likely to be due to nonspecific background signal rather than specific probe-target hybridization. Log2 transformation of the data is done to improve the characteristics of the data distribution and allows the use of classical parametric statistics for analysis.

Differential Gene Expression Analysis

Differential gene expression analysis was performed on the preprocessed data in the *Limma package version 3.34.0*, using pipelines recommended by the tool creators. The differential expression analysis was performed by fitting the following linear model:

Intensity ~ 0 + Metolachlor concentration x Time of exposure

Where, 0 indicates no intercept in the model. This allows pairwise comparison between treatment combinations using the contrast statement. Significant differential gene expression was determined using a moderated t-statistics with empirical Bayes' shrinkage of the sample variances. *P* values were adjusted with Benjamini-Hochberg false discovery rate (FDR) correction, whereby differentially expressed genes were identified by FDR <0.05 and log2 fold change as well as FDR <0.01 and log2 fold change.

Data Analysis using GOrilla Tool to Determine Gene Ontology (GO)

The differentially expressed genes were imported to Gorilla (Eden et al. 2009), a tool for identifying and visualizing enriched GO terms in a filtered list of genes. This was done to determine if there was enrichment of specific genes that are involved in a particular cellular process or function in the samples compared to control. Enrichment was calculated by taking the frequency of genes of particular function in sample/frequency of genes of the organism.

CHAPTER 3

RESULTS

The current research project was undertaken to broadly determine if cells exposed to metolachlor have a gene expression profile that is altered after exposure. We have previously shown that human cell growth is inhibited after herbicide exposure (Dhanwada et al. 2003; Hartnett et al. 2013; Lowry et al. 2013). For previous analyses, we evaluated genes that were associated with regulating cell growth to determine if herbicide exposure altered the levels of these genes or proteins (Lowry et al. 2013). In this project, there is an attempt to broaden the scope of inquiry; we carried out microarray analysis to determine which group or family of genes was altered after herbicide exposure. After isolating total RNA from HepG2 cells exposed to varying levels of metolachlor for varying time periods, microarray analysis was performed. The goal was to understand if one or several specific cellular functions are affected/altered due to herbicide exposure.

Quantification of Metolachlor

To determine the concentration of metolachlor used for treatment, a standard curve was used to correlate the peak area of metolachlor specific peak readings from the LC-MS to the known prepared metolachlor concentrations. Using the standard curve, we could determine the concentration of our unknown stock herbicide medium. New metolachlor stock solutions were prepared every 6-8 weeks, as metolachlor tends to degrade.

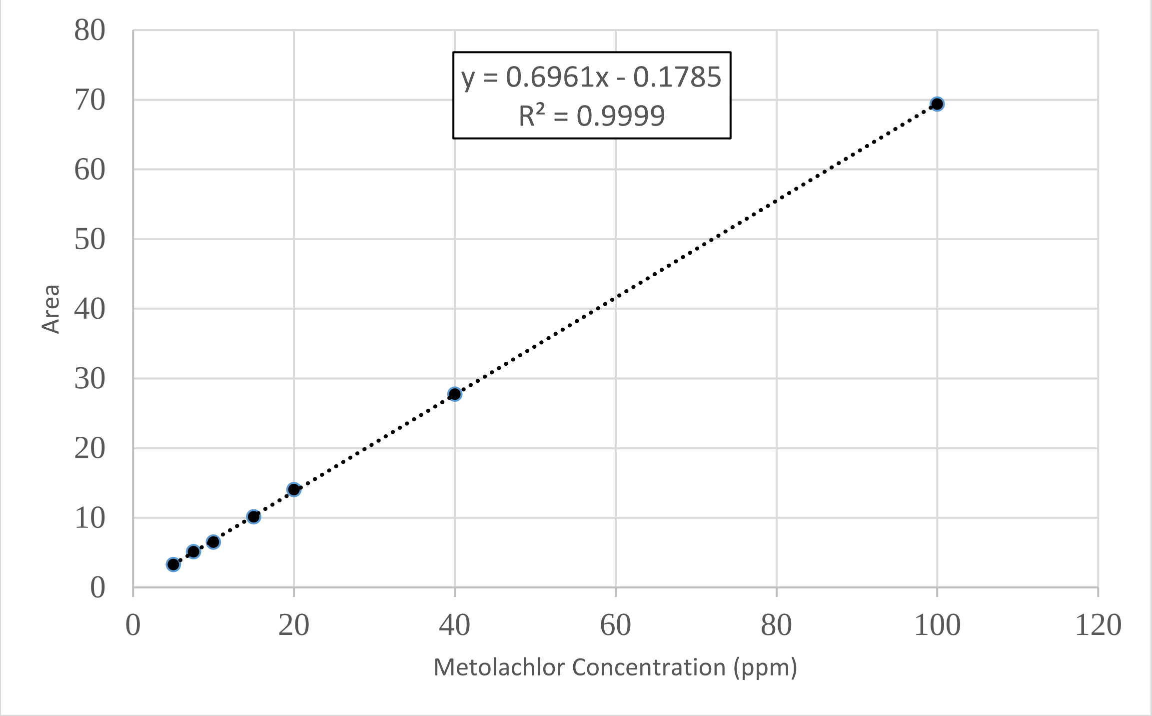

Figure 4. An example standard curve of metolachlor. The unknown concentration was determined by using the equation of the generated line regression line.

Microarray Data Analysis

In order to perform microarray data analysis, several general steps are carried out: a) quality control and data visualization (pre-processing), b) statistical analysis and c) gene ontology (GO) analysis using the GOrilla tool to visualize related genes via ontology. Below, each step is articulated.

Data Pre-processing, Quality Control and Data Visualization

In order to check the quality of the data before and after normalization, simple graphical exploration methods were used. This was done using an open source software based on R and Bioconductor (Eijssen et al. 2015). There were originally 47,000 probes that underwent quality control and normalization. To visualize the level of similarity in samples, multidimensional scaling or MDS plots (Figure 5) were used.

There were three time points in our samples: 24, 48 and 72-hour samples. From this analysis, both the 24 hour and 72 hour samples clustered rather tightly as separate groups which were similar, indicating not only were the three replicates similar in nature but the samples exposed to various metolachlor concentrations were also not very distinct. However, while the 48-hour samples also formed a cluster, it was a bit more spread out indicating that while the replicates (with same concentrations) were similar (close in distance), the samples with various concentrations were different from one another (Figure 5).

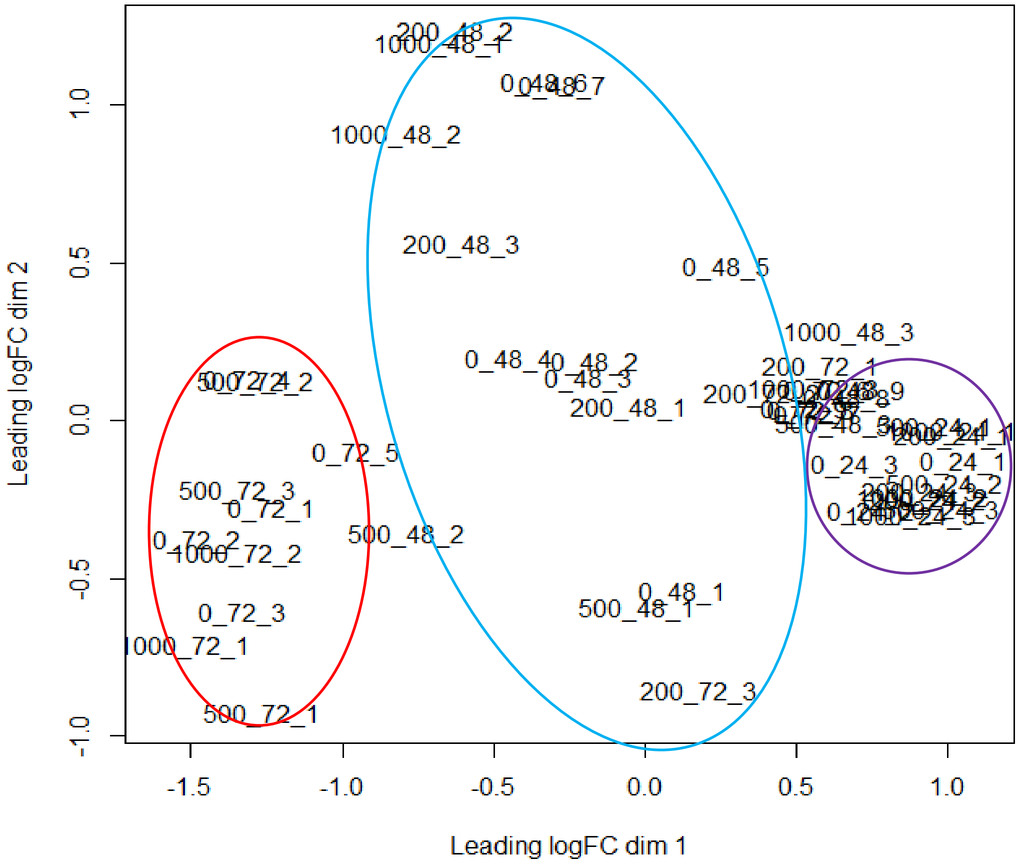

Figure 5. The software program R was used to develop multidimensional scaling (MDS) plots of samples from the various time points to show distinct clusters of the samples. A shape has been drawn around the various time points to give a sense of location: 72 hours (left oval), 48 hours (middle oval) and 24 hours (right circle).

Appendix B shows log-intensity distribution plotted for all 48 arrays. Boxplots are used to determine if all arrays have a similar distribution of expression values. After normalization of the raw data, all of the medians, marked with the horizontal bars inside the boxes, are on the same level indicating all arrays seem to have exactly the same distribution of expression values. Box plot data can be converted to histogram of the density distribution of the raw log intensities (Appendix C). Histograms are used to visually check the normalized data. The use of these plots before and after normalization is a check on the normalization step and allows for elimination of any systematic biases in the data. Correlation coefficients are computed for each pair of arrays in the dataset and a qualitative visual of the matrix is seen in Appendix D. The minimal value of this coefficient gives a good idea of the dataset homogeneity; a low coefficient indicates important difference between array intensities.

Differential Gene Expression Statistical Analysis

As mentioned, an objective of our study was to determine how the differential expression of genes between control and treated HepG2 liver cells exposed to varying concentrations of metolachlor (0, 200 ppb, 500 ppb and 1000 ppb) would vary over three different time points: 24, 48, and 72 hours. After the quality control and normalization steps, 27,482 probes were retained for further analysis. Using the moderated T test and Bayes statistical analysis, *P* values were adjusted by filtering with the Benjamini-Hochberg false discovery rate (FDR) correction equation to quantify the number of differentially expressed genes (DEGs) between control and treated cells. The conditions we used was to set either an FDR<0.05 (5%) with a log2 fold change or an FDR < 0.01(1%) and a log2 fold change. Results of these analyses are in Table 1 and Table 2.

Table 1 shows the data of differentially expressed genes (DEG) at various conditions listed.

		Differential expression of genes		
Time	**Samples (comparison of 2 treatments)**	**# Down-regulated ($p < 0.05$)**	**# Up-regulated ($p < 0.05$)**	**# Unchanged ($p < 0.05$)**
24 hours	0 ppb vs 200 ppb	0	0	27,482
	0 ppb vs 500 ppb	3	0	27,479
	0 ppb vs 1000 ppb	214	109	27,159
	200 ppb vs 500 ppb	0	0	27,482
	200 ppb vs 1000 ppb	117	88	27,277
	500 ppb vs 1000 ppb	136	245	26,868
48 hours	0 ppb vs 200 ppb	176	57	27,249
	0 ppb vs 500 ppb	739	650	26,093
	0 ppb vs 1000 ppb	688	551	26,243
	200 ppb vs 500 ppb	889	848	25,745
	200 ppb vs 1000 ppb	878	815	25,789
	500 ppb vs 1000 ppb	0	0	27,482
72 hours	0 ppb vs 200 ppb	4	2	27,476
	0 ppb vs 500 ppb	3	2	27,477
	0 ppb vs 1000 ppb	0	0	27,482
	200 ppb vs 500 ppb	0	0	27,482
	200 ppb vs 1000 ppb	0	0	27,482
	500 ppb vs 1000 ppb	0	0	27,482

Table 1. A summary list of differentially expressed genes between control and cells treated with varying concentrations of metolachlor. Data was filtered based on Benjamini Hochberg FDR < 0.05 with a log2 fold change = 1.

At the 24-hour time point, there were no genes that were differentially expressed at lowest concentration of 200 ppb of metolachlor. At 500 ppb, only three genes were down-regulated while no genes were up-regulated. However, at the highest concentration of 1000 ppb, a total of 323 genes were differentially expressed with 214 genes being downregulated and 109 genes being upregulated. A similar pattern of significantly differentiated gene expression was observed among treatment groups with the three concentrations at 24 hours. No differentially expressed genes were observed between lowest concentration of 200 ppb and 500 ppb, however, there was significant differential gene expression between 200 ppb and 1000 ppb, 117 genes being downregulated and 88 genes being upregulated. As well as between 500 ppb and 1000 ppb, 136 genes were significantly downregulated and 245 genes were upregulated.

Interestingly, a very little level of differential gene expression was observed at the maximum exposure time of 72 hours. Only the lower levels of metolachlor (200 and 500 ppb) had any genes that were affected. With 200 ppb, four genes were downregulated and two genes were upregulated while only three genes were downregulated and two genes were upregulated at 500 ppb at this longer time point. Additionally, there were no significantly differentiated genes expressed at a high concentration of 1000 ppb for maximum exposure time of 72 hours. A similar pattern was followed among the treatment group concentrations, there were no significantly differentiated genes expressed between different concentrations 200 ppb, 500 ppb and 1000 ppb.

It was very different for the samples that were exposed to varying concentrations of metolachlor for 48 hours. At a low concentration of 200 ppb of metolachlor, 176 genes were downregulated and 57 genes were upregulated. This number of differentially expressed genes significantly increased with increasing concentration with 500 ppb metolachlor, 739 and 650 genes were downregulated and upregulated respectively. At highest concentration of 1000 ppb, the number of DEGs went down slightly with 688 genes being downregulated and 551 genes being upregulated (Table 1). Again, a similar pattern was observed among samples of the various treatment groups at 48 hours of metolachlor exposure. The highest number of differentially expressed genes was between 200 ppb and 500 ppb, where 889 genes being downregulated and 848 genes being upregulated. Between 200 ppb and 1000 ppb, 878 genes were downregulated and 815 genes were upregulated. Interestingly, there were no significantly differentiated genes either downregulated or upregulated in between 500 ppb and 1000 ppb.

To determine if there was any change in differential gene expression at more stringent conditions, differentially expressed genes (DEGs) were also identified at FDR < 0.01(1%) and log2 fold. Table 2 shows the data of differentially expressed genes (DEG) at various conditions listed.

		Differential expression of genes		
Time	**Samples comparison of 2 treatments)**	**# Down-regulated (p < 0.01)**	**# Up-regulated (p < 0.01)**	**# Unchanged (p < 0.01)**
24 hours	0 ppb vs 200 ppb	0	0	27,482
	0 ppb vs 500 ppb	2	0	27,480
	0 ppb vs 1000 ppb	100	32	27,350
	200 ppb vs 500 ppb	0	0	27,482
	200 ppb vs 1000 ppb	36	14	27,432
	500 ppb vs 1000 ppb	188	125	27,169
48 hours	0 ppb vs 200 ppb	104	22	27,356
	0 ppb vs 500 ppb	676	584	26,222
	0 ppb vs 1000 ppb	629	493	26,360
	200 ppb vs 500 ppb	677	654	26,151
	200 ppb vs 1000 ppb	688	629	26,165
	500 ppb vs 1000 ppb	0	0	27,482
72 hours	0 ppb vs 200 ppb	0	0	27,482
	0 ppb vs 500 ppb	0	0	27,482
	0 ppb vs 1000 ppb	0	0	27,482
	200 ppb vs 500 ppb	0	0	27,482
	200 ppb vs 1000 ppb	0	0	27,482
	500 ppb vs 1000 ppb	0	0	27,482

Table 2. A summary list of differentially expressed genes between control and cells treated with varying concentrations of metolachlor. Data was filtered based on Benjamini Hochberg FDR < 0.01 with log2 fold change = 1.

With a FDR < 0.01, the pattern was very similar to what was seen with the less stringent conditions as the data shows. Only two genes were downregulated at 500 ppb at 24 hours and a total of 132 genes were differentially expressed at maximum concentration of 1000 ppb with 100 genes being downregulated and 32 genes being upregulated. This was a lower number of genes differentially expressed than at the FDR < 0.05.

The pattern was very similar to what was seen previously (Table 2) at 48 hours, however, there were fewer genes differentially expressed with all three concentrations (200, 500 and 1000 ppb) of metolachlor. There were 104 and 22 genes were downregulated and upregulated respectively at low concentration of 200 ppb, 676 genes downregulated and 584 genes upregulated at 500 ppb and 629 genes downregulated and 493 genes upregulated at the high concentration of 1000 ppb. There was no differential gene expression observed for metolachlor concentrations at 72 hours for any of the concentrations (Table 2).

Comparisons were also noted between various metolachlor concentrations at both 24 hours and 48 hours, with it being very significant at 48 hours of metolachlor exposure. In Table 1 and Table 2, it is to be noted that there is a significant increase in the number of differentially expressed genes when comparing 200 ppb samples with either 500 ppb or 1000 ppb, more so than is seen when comparing 0 ppb to 200 ppb indicating that the number of differentially expressed genes occurs at the higher concentrations. It also can be seen that there is not as much of an increase when comparing samples 500 ppb to 1000 ppb.

GO Analysis Using the GOrilla Tool

Differentially expressed genes were incorporated into the GOrilla (gene ontology) enrichment analysis and visualization tool. This tool is used to provide a functional analysis using the ontology of genes that were differentially expressed between control and metolachlor treated HepG2 cells.

Using data, we obtained by filtering using the Benjamini Hochberg FDR < 0.05 with log2 fold change = 1 and inputting it into the GOrilla tool, we were able to determine possible cellular process and function generated through this enrichment analysis and visualization tool. Samples with less than 5 DEGs were not used. Thus, no GO analysis was performed for 0 ppb - 200 ppb or 0 ppb – 500 ppb at 24 hours nor any of the samples at 72 hours of metolachlor treatment. GO analysis was also not performed on sample that compared two treatment groups, as current study's focus is on differential gene expression between control and treated human liver cells. GO analysis was performed on GOrilla, to retrieve the ontology of genes that were differentially expressed between control and metolachlor treated HepG2 cells for 0 ppb - 1000 ppb for 24 hours and 48 hours at 0 ppb versus 200 ppb, 500 ppb and 1000 ppb (Table 1).

Gene Enrichment: 0 ppb vs 1000 ppb Metolachlor at 24 Hours

Out of the downregulated 214 DEGs (Appendix I) of control versus 1000 ppb at 24 hours of exposure, the GOrilla database recognized only 193 genes and after removing 28 duplicate genes left a total of 165 genes in the analysis. Out of these 165, only 152 were associated with a GO term. GO terms are linked with a list of associated genes based on biological process, molecular function and cellular component. Of the 152 genes, none had gene enrichment for any biological, molecular and cellular process. Similarly, with the 109 upregulated DEGs of control versus 1000 ppb, the GOrilla database recognized only 94 genes, 9 duplicate genes and were removed leaving a total of 85 genes. Out of these 85, only 78 were associated with a GO term and none of these genes were enriched for any biological, molecular and cellular process.

Gene Enrichment: 0 ppb vs 200 ppb Metolachlor at 48 Hours

Of the downregulated 176 DEGs (Table 1) of control versus 200 ppb at 48 hours of metolachlor exposure (Appendix J), the GOrilla database recognized 167 genes with 31 duplicate genes removed, a total of 136 genes remained. Only 125 were associated with a GO term. These genes also did not show any enrichment for biological and molecular process, but showed enrichment of cellular component termed “cell surface”. Four genes enriched in cellular component “cell surface” are PLAU - plasminogen activator, urokinase, ROR1 - receptor tyrosine kinase-like orphan receptor 1, PLG - plasminogen and TSPAN8 - tetraspanin 8. Of the upregulated 57 DEGs of control versus 200 ppb, the GOrilla database recognized only 53 genes, 4 duplicate genes were removed leaving a total of 49 genes. Out of these 49, only 48 were associated with a GO term. Once again, no gene enrichment was observed out of these 48 upregulated DEGs.

Gene Enrichment: 0 ppb vs 500 ppb Metolachlor at 48 Hours

Of the downregulated 739 DEGs (Appendix M) of control versus 500 ppb entered into the GOrilla database, 696 genes were recognized with 109 duplicate genes being removed, it left a total of 587 genes. Out of these 587, only 566 were associated with a GO term. These downregulated genes were enriched in eight biological processes (Table 3).

Cellular process	**P-value**	**Genes involved**	**Sample frequency**	**Background frequency**	**Enrichment**	**GO term**
DNA metabolic process	2.78E-05	see appendix E1	58/178	114/566	1.62	GO:0006259
DNA replication	7.64E-05	see appendix E2	33/178	55/566	1.91	GO:0006260
DNA replication initiation	8.47E-04	see appendix E3	21/299	23/266	1.73	GO:0006281
DNA repair	2.09E-04	see appendix E4	39/178	71/566	1.75	GO:0010043
Cellular response to stimulus	5.69E-04	see appendix E5	68/178	150/566	1.44	GO:0051716
Cellular response to acid chemical	6.27E-04	see appendix E6	2/2	7/566	80.86	GO:0071229
Response to acid chemical	9.93E-04	see appendix E6	4/10	17/566	13.32	GO:0006270
Response to zinc ion	5.65E-04	see appendix E6	7/83	10/566	4.77	GO:0001101

Table 3. A summary of differentially expressed genes between 0 ppb and 500 ppb for 48 hours with regard to biological process. Specific genes that were associated with each process are listed in the listed appendix. Enrichment of a process is calculated by comparing the sample frequency {number of genes in the intersection(b)/number of genes

in sample set (n)} over the background frequency {number of genes associated with the process (B)/total number of genes in organism (N)}. The GO term refers to the Gene Ontology term.

Four different molecular functions were determined when looking at the same sample and the functions are shown in Table 4. There was no observed gene enrichment out of the 650 upregulated DEGs (Appendix M) entered for control versus 500 ppb at 48 hours.

Cellular function	**P-value**	**Sample frequency**	**Background frequency**	**Enrichment**	**GO term**
Chromatin binding	8.45E-05	20/151	31/566	2.42	GO:0003682
Catalytic activity, acting on DNA	1.11E-04	21/149	34/566	2.35	GO:0140097
Helicase activity	7.68E-04	13/171	17/566	2.53	GO:0004386
DNA helicase activity	8.99E-04	7/77	11/566	4.68	GO:0003678

Table 4. A summary of differentially expressed genes between 0 ppb and 500 ppb for 48 hours with regard to molecular function. Enrichment is calculated by comparing the sample frequency {number of genes in the intersection(b)/number of genes in sample set (n)} over the background frequency {number of genes associated with the process

(B)/total number of genes in organism (N)}. The GO term refers to the Gene Ontology term. Specific genes associated with function found in Appendix F1, F2.

Gene Enrichment: 0 ppb vs 1000 ppb Metolachlor at 48 Hours

Of the downregulated 688 DEGs (Appendix L) of control versus 1000 ppb at 48 hours entered, the GOrilla database recognized 646 genes. Out of which 94 duplicate genes were removed, leaving a total of 552 genes. Out of these 552, only 528 were associated with a GO term. These genes were enriched in thirteen biological processes such as: “ DNA metabolic process”, “DNA replication”, “DNA repair”, “cell cycle G1/S phase transition”, “DNA replication initiation”, “G1/S transition of mitotic cell cycle”, “response to radiation”, “cellular response to stimulus”, “DNA duplex unwinding”, “DNA duplex unwinding”,” cellular response to DNA damage stimulus”, “DNA geometric change, DNA biosynthetic process” and “cellular response to stress”. Table 5 shows the various biological processes that these samples were enriched with enrichment calculated as the sample frequency over the background frequency.

Cellular process	**P-value**	**Genes involved**	**Sample frequency**	**Background frequency**	**Enrichment**	**GO term**
DNA metabolic process	1.73 E-06	see appendix G1	62/192	104/528	1.64	GO:0006259
DNA replication	4.02 E-06	see appendix G2	38/207	52/528	1.86	GO:0006260
DNA replication initiation	1.15 E-04	see appendix G3	8/31	22/528	6.19	GO:0006281
DNA biosynthetic process	9.36 E-04	see appendix G3	22/203	30/528	1.91	GO:0044843
DNA repair	5.50 E-05	see appendix G4	42/207	63/528	1.7	GO:0006270
Cell response to DNA damage stimulus	3.47 E-04	see appendix G5	60/269	83/528	1.42	GO:0000082
DNA geometric change	7.68 E-04	see appendix G6	7/62	12/528	4.97	GO:0009314
DNA duplex unwinding	3.23 E-04	see appendix G6	7/62	11/528	5.42	GO:0051716
Cell cycle G1/S phase transition	1.01 E-04	see appendix G7	29/356	29/528	1.48	GO:0032508
G1/S transition of mitotic cell cycle	1.49 E-04	see appendix G7	28/356	28/528	1.48	GO:0006974

(Table Continues)

Cellular process	**P-value**	**Genes involved**	**Sample frequency**	**Background frequency**	**Enrichment**	**GO term**
Cellular response to stimulus	2.81 E-04	see appendix G8	74/207	134/528	1.41	GO:0032392
Cellular response to stress	9.85 E-04	see appendix G9	56/197	102/528	1.47	GO:0071897
Response to radiation	1.67 E-04	see appendix G10	21/197	27/528	2.08	GO:0033554

Table 5. A summary of differentially expressed genes between 0 ppb and 1000 ppb for 48 hours with regard to biological process. Specific genes that were associated with each process are listed in the listed appendix. Enrichment of a process is calculated by comparing the sample frequency {number of genes in the intersection(b)/number of genes in sample set (n)} over the background frequency {number of genes associated with the process (B)/total number of genes in organism (N)}. The GO term refers to the Gene Ontology term.

Three different molecular functions such as “DNA helicase activity”, “helicase activity” and “catalytic activity on DNA was found. Data is shown in Table 6.

Cellular function	**P-value**	**Sample frequency**	**Background frequency**	**Enrichment**	**GO term**
DNA helicase activity	1.24E-04	7/62	10/528	5.96	GO:0003678
Helicase activity	3.24E-04	10/97	15/528	3.63	GO:0004386
Catalytic activity, acting on DNA	5.17E-04	16/96	33/528	2.67	GO:0140097

Table 6. A summary of differentially expressed genes between 0 ppb and 1000 ppb for 48 hours with regard to molecular function. Enrichment is calculated by comparing the sample frequency {number of genes in the intersection(b)/number of genes in sample set (n)} over the background frequency {number of genes associated with the process (B)/total number of genes in organism (N)}. The GO term refers to the Gene Ontology term. Specific genes associated with each function shown in Appendix H.

CHAPTER 4

DISCUSSION

In our study, DNA microarray analysis was used to screen for altered gene expression after exposure of increasing concentrations of metolachlor to immortalized human liver (HepG2) cells. We wanted to determine the groups of genes or gene families may be involved in a possible cellular mechanism of action of the herbicide. Current studies do not show a consistent mechanism of action for this herbicide on non-target organisms, specifically humans.

Previous work from our lab has demonstrated increasing metolachlor concentration and increasing the time of exposure resulted in decreased cell growth in human cells (Dhanwada et al. 2003; Hartnett et al. 2012; Lowry et al. 2013). Exposure to 500 ppb metolachlor for 48 hours resulted in a decrease in cell division (Hartnett et al. 2013) and flow cytometry analysis of cell cycle distribution revealed that 500 ppb metolachlor treatment also resulted in fewer HepG2 cells in the G2/M phase after 72 hours (Hartnett et al. 2013). We also showed metolachlor may affect other phases of the cell cycle. In our study looking at growth suppressor proteins, we showed that the level of hyper-phosphorylated form of the retinoblastoma (Rb) protein was decreased in metolachlor exposed cells (Lowry et al. 2013). This protein is a regulator of cell growth and alternates between a hypo-phosphorylated (found in G1 phase) and hyper-phosphorylated form (found in S phase). It is involved in regulating the cell cycle at the G1/S transition. The decreased levels of the hyper-phosphorylated forms of Rb after metolachlor exposure suggested that cells are arrested or slowing down in the G1 phase of the cell cycle. The slow down or arrest at G1 or the alteration at the G2/M transition would then lengthen the remaining phases of the cell cycle so that there would be fewer cells produced in a particular time (Hartnett et al. 2013; Lowry et al. 2013).

Performing expression analysis in a low-throughput fashion, one protein at a time, as we have done in our previous work is a slow and expensive process. In the current study, DNA microarray analysis was used. This is a high throughput technology that can provide a quantitative measurement for the expression of thousands of genes. Thus, the aim of the current project was to determine which group or family of genes that participate in a biological process may be altered after herbicide exposure, and if one or several specific cellular functions are affected or altered after this exposure. Microarray analysis was performed after isolating total RNA from HepG2 cells exposed to varying levels (200 ppb, 500 ppb, and 1000 ppb) of metolachlor for varying times (24 hours, 48 hours and 72 hours) and comparing expression to that of control (0 ppb) cells for each of the time points.

Results from our analysis for the 24-hour time point with FDR < 0.05 (Table 1) showed that there were no significantly differentially expressed genes present between control and 200 ppb of metolachlor treated cells. At 500 ppb metolachlor, only three genes were downregulated. To demonstrate a significant amount of differential gene expression, cells needed 1000 ppb of metolachlor at 24 hour exposure. Under this condition, 214 genes were downregulated compared to control and 109 genes were upregulated compared to control. This suggests that quite a high level of herbicide is needed at this relatively short time point to observe a significant level of differential gene expression after metolachlor exposure (Table 1).

At 48 hours of exposure, differential gene expression between control and metolachlor treated cells was observed at all three concentrations. At the lower concentration of 200 ppb metolachlor, 176 genes were downregulated and 57 genes were upregulated. This number of differentially expressed genes significantly increased with increasing concentration of 500 ppb of metolachlor, 739 genes were downregulated and 650 genes upregulated and at 1000 ppb, the number of differentially expressed genes went slightly down with 688 genes being downregulated and 551 being upregulated (Table 1) suggesting that 48 hours of exposure may be an important and perhaps optimal time point for altered gene expression between control and metolachlor treated cells. It is interesting to see that if cells were exposed to 72 hours of exposure, very little level of differential gene expression was observed. While we don't understand with the current data why this is specifically happening, it may be the cells have compensated for the effects of metolachlor by 72 hours of exposure and are able to maintain expression similar to non-metolachlor conditions. We can speculate that this may be possibly occurring through hormesis when cells are exposed to many chemicals including pesticides (Calabrese and Baldwin, 2003). Hormesis is a biological phenomenon where lower doses of a particular agent/chemical can stimulate a beneficial effect while higher doses result in a perhaps toxic or harmful response. In this case, the "dose" would be the length of exposure and the beneficial response at 48 hours is that cells "ready" themselves by altering expression of particular genes and starting translation of particular proteins which can help reduce toxicity while by 72 hours, cells are unable to do so and thus a “toxic” environment may result.

In order to understand cellular processes affected, GO analysis was performed. This analysis uses the differentially expressed genes that were found and determines if these genes align with a particular biological process or function (GO term). This was done using GOrilla program. Analysis was done to retrieve the ontology of genes that were differentially expressed between control and metolachlor treated HepG2 cells for 0 ppb - 1000 ppb for 24 hours and 48 hours at 0 ppb versus 200 ppb, 500 ppb and 1000 ppb (Table 1).

When the analysis was performed of the DEGs of 0-1000 ppm at 24 hours (214 downregulated DEGS, 109 upregulated genes) no GO enrichment was observed using this analysis. This suggests that while these genes were recognized as being differentially expressed, they could not be clustered based on a specific biological, molecular and cellular function. So, there was some change in gene expression but not enough to affect a biological process or function.

Similarly, when analyzing the 0-200 ppb samples with 48 hours of exposure, while there were a number of genes where transcription was affected (Table 1), these genes also did not show any enrichment for biological and molecular process. However, there was of enrichment of down-regulated genes associated with a cellular component at the cell surface (*PLAU, ROR1, PLG and TSPAN8*). It could be suggested that proteins at the cell surface were being down regulated to prevent the chemical from entering the cell. There was no gene enrichment observed for the 53 upregulated genes.

The highest level of gene enrichment was observed at the 48-hour time point at 500 ppb and 1000 ppb metolachlor (Table 3 and Table 5). Additionally, the enrichment was only seen in DEGs that were downregulated DEGs; there was no enrichment seen in genes involved in a particular process, function or component in DEGs that were upregulated. Table 3 (0-500 ppb, 48 hours) and Table 5 (0-1000 ppb, 48 hours) show the various biological processes that were affected. We see that a number of genes that contribute to the processes of DNA replication and repair are affected as well as genes involved in how the cells respond to chemical stimuli, including the metal ions is seen at the 0-500 ppb condition (Table 3). This suggests that metolachlor exposure is affecting the DNA replication/repair process and as the genes are being down-regulated, the cells lack the ability to respond to this xenobiotic agent. When looking at the 0-1000 ppb condition (Table 5), 13 different biological processes were affected. These not only include the processes seen with 0-500 ppb samples (DNA replication, DNA repair and cellular response to stimuli, we see additional specificity with regard to the specific process of replication such as the geometric change of DNA, the unwinding of the DNA duplex and the cellular response to DNA damage and cellular response to stress (Table 5). Additionally, at this dose of metolachlor, there appears to be significant gene enrichment observed for many biological processes and molecular functions involved in cell cycle. Genes involved at the G1/S transition of the cell cycle were downregulated (Table 5). These results align with what we had previously shown in our results affecting the G1/S transition (Lowry et al. 2013). DNA replication occurs in the S phase of the cell cycle and if genes are being down-regulated in this process and the cell is trying to compensate for the presence of the chemical, the cell cycle would slow down in the S phase prior to entering into the G2 phase, this is consistent with our previous work (Hartnett et al. 2013).

If we look at the specific functions associated with the enrichment of genes at 48 hours of exposure at both the 0-500 ppb and 0-1000 ppb conditions, we see similar functions that are affected such as chromatin binding, helicase activity, and DNA helicase activity were observed in both groups (Table 4 and Table 6).

If we probe more deeply into these biological processes that are down-regulated by a 48 hour metolachlor exposure, we see that *CDC45* (cell division cycle 45) was affected in all DNA metabolic processes as well as DNA replication, DNA repair and DNA replication initiation (Appendix E, F, G). CDC45 is a member of highly conserved multi-protein complex including cdc6/cdc18 and is required to initiation of DNA replication along with the minichromosome maintenance proteins (MCMs) and DNA polymerase (Rosenblatt et al. 1992).

Another gene found in all DNA metabolic processes involved in cell cycle regulation is *CDK2* (cyclin-dependent kinase 2), a protein closely related to the cell cycle-regulatory protein kinase *CDC2*. *CDK2* activity rises in late G1 or early S phase and declines during mitosis, whereas *CDC2* activity peaks during mitosis. We observed *CCNA2* (Cyclin A2) was downregulated in “cell cycle G1/S phase” at 0-1000 ppb of metolachlor at 48 hours (Appendix G7). Cyclin A regulates the progression through the S phase. *CCNE2* (Cyclin E2, *CCNE1* (Cyclin E1) were also downregulated (Appendix G7) Cyclin E is expressed in the late G1 phase. In order for cells to move from each phase of the cell cycle, an optimal level of the phase associated cyclin needs to be present. When it reaches its optimal level, the cell is able to initiate a number of activities that allows for passage into the next phase. The expression pattern of Cyclin A seen in this analysis correlates to previous work from our lab, decreased transcript levels via RT-PCR were detected at 300 ppb of metolachlor at 12 hours (Hartnett et al. 2013). Thus, the current results align with our previous results that suggest that cells would accumulate in S-phase as the level of cyclin A protein has not reached a threshold level and thus would not progress into G2 phase.

Microarray analysis has been to evaluate gene expression with a number of pesticides on a variety of model systems. A study done in HepG2 cells treated with chlordane, an insecticide, showed significantly altered gene expression in key pathways such as cytochrome p450, cell cycle and apoptosis at very high levels (120 – 158 uM) of exposure (Choi et al. 2010). Thus, high levels of the insecticide were needed to show altered gene expression, but as with metolachlor, chlordane also affected the cell cycle. In another study on *E. albidus* (a soil invertebrate), when exposed to three pesticides, dimethoate (insecticide), atrazine (herbicide) and carbendazim (fungicide), in a range of concentrations that inhibited reproduction, significantly altered gene expression was seen in biological processes like translation, cell cycle regulation and general response to stress was observed (Novais et al. 2012). Again, showing that there were effects on the cell cycle. However, the effects of organophosporus pesticides (dichlorovos, fenamiphos, mefloquine) on *C. elegans* showed that these neurotoxicant pesticides alter gene expression in biological processesincluding lipid metabolism, cell adhesion, apoptosis and detoxification (Lewis et al. 2009). Thus suggesting that not only herbicides but a broad range of pesticides can also have effects on biological function similar to metolachlor

This project has generated considerable amount of data regarding changes in gene expression between control and metolachlor treated cells. The GO analyses performed suggest that there are several areas that metolachlor exposure is affecting the cells: DNA replication/repair, response to DNA damage, DNA structural changes, and cellular responses to stimuli including stress and radiation and finally the cell cycle. It is heartening that the effects on the cell cycle with regard to cellular processes correlate well with our previous results in looking at specific genes associated with this process. The current findings should provide a fundamental basis for further analysis of the molecular pathways and mechanisms involved in effect of metolachlor on cell cycle. We should look further into the mechanisms of DNA replication and repair.

In terms of next steps for this project, there are several. We observed maximum differential gene expression at the 48-hour time point for 0 vs 500 ppb and 0 vs 1000 ppb, we did not see this at 0 vs 200 ppb. It may be that there were not enough replicates and thus the results were not significant. Several studies have showed that differential expression detection using independent t-statistics has weak power for small-sample-size analysis (Vasiliu et al. 2015). Increasing the number of replicates would likely increase the statistical power for this study.

Since changes in mRNA level do not always correspond to changes in protein levels, changes in actual protein levels should be confirmed using Stable Isotope Labelling by Amino acids in cell culture (SILAC). We would focus on proteins involved in the processes that were described above.

Additionally, while ingestion of contaminated water is the primary route of exposure for metolachlor, inhalation is another mode of exposure to humans and is of particular importance to the non-farm workers who may be exposed while standing outside near a farm that has recently applied metolachlor. Further work should be done with another cell type, a human alveolar macrophage cell line (THP-1). These cells are involved with the cellular immune response in human alveoli. A similar experimental design can be used to provide an insight to the functional relation of the two cell lines and understand if there are similarities in the mode of action of this herbicide.

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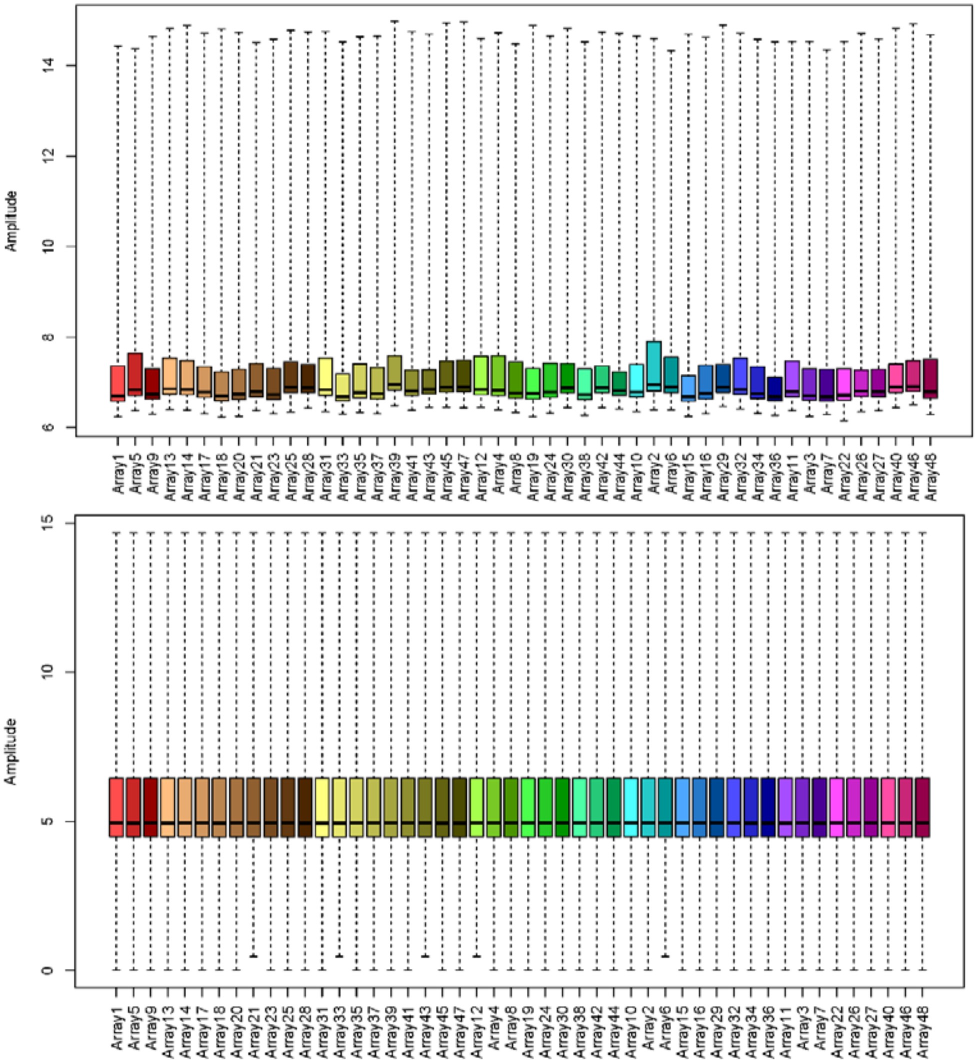
APPENDICES

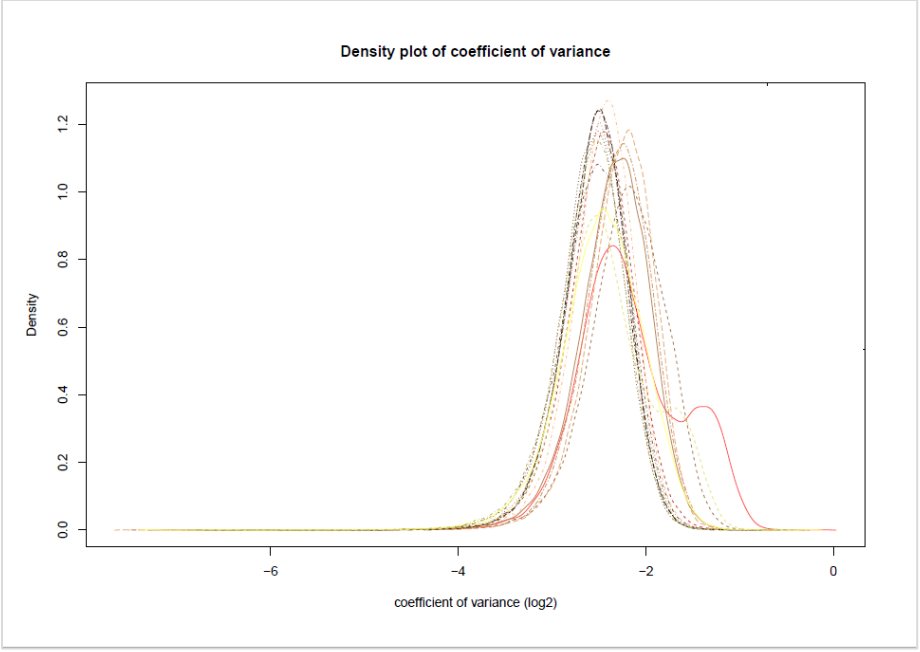
Appendix A. Sample description table: Array numbers where the particular samples were placed on the microarray chip (HumanHT-12 v4 bead chip), Illumina label on the bead chip, sample description, where lower case letter “c” and “t” indicate control and treatment, 0 ppb, 200 ppb, 500 ppb and 1000 ppb are the metolachlor concentrations, 24 hours, 48 hours and 72 hours metolachlor exposure.

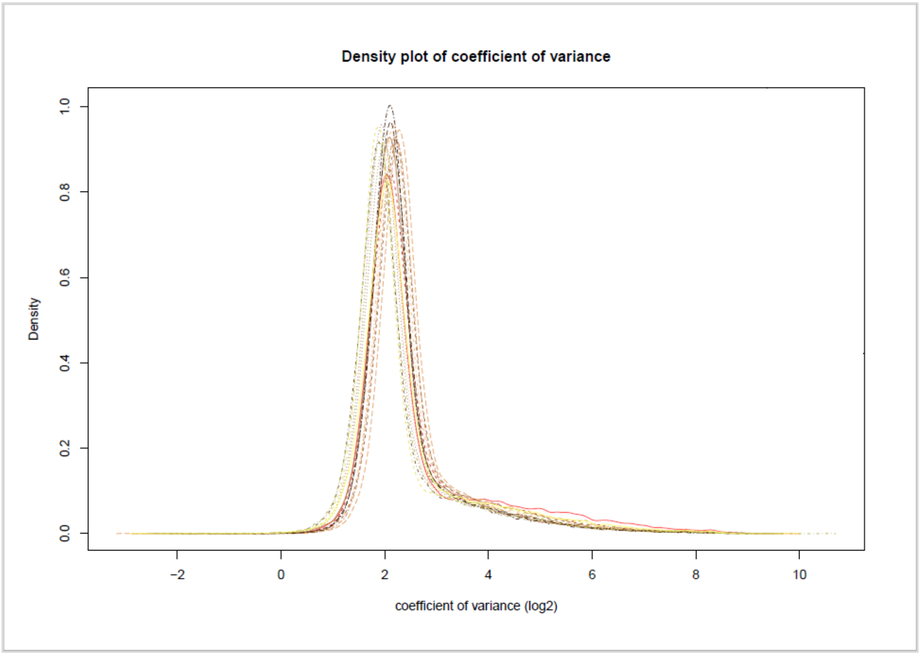
Array Number	Illumina label	Sample
1	200670660001_A	c_0_72
2	200670660001_B	t_500_72
3	200670660001_C	c_0_48
4	200670660001_D	t_500_48
5	200670660001_E	t_500_48
6	200670660001_F	c_0_72
7	200670660001_G	t_1000_72
8	200670660001_H	c_0_72
9	200670660001_I	t_1000_72
10	200670660001_J	c_0_48
11	200670660001_K	t_200_48
12	200670660001_L	t_1000_48
13	200670660069_A	c_0_72
14	200670660069_B	t_500_72
15	200670660069_C	c_0_72
16	200670660069_D	t_500_72
17	200670660069_E	c_0_48
18	200670660069_F	c_0_48
19	200670660069_G	t_200_48
20	200670660069_H	t_200_48
21	200670660069_I	c_0_48
22	200670660069_J	c_0_48
23	200670660069_K	t_1000_48
24	200670660069_L	c_0_48
25	200722200024_A	c_0_24
26	200722200024_B	t_200_24
27	200722200024_C	t_500_24
28	200722200024_D	t_1000_24
29	200722200024_E	c_0_24
30	200722200024_F	t_200_24
31	200722200024_G	t_500_24
32	200722200024_H	t_1000_24
33	200722200024_I	c_0_24
34	200722200024_J	t_200_24
35	200722200024_K	t_500_24
36	200722200024_L	t_1000_24
37	200722200030_A	c_0_72
38	200722200030_B	t_200_72
39	200722200030_C	c_0_72
40	200722200030_D	t_200_72
41	200722200030_E	c_0_72
42	200722200030_F	t_200_72
43	200722200030_G	c_0_48
44	200722200030_H	t_500_48
45	200722200030_I	c_0_48
46	200722200030_J	t_1000_48
47	200722200030_K	c_0_72
48	200722200030_L	t_1000_72

Appendix B. Boxplot analysis of log intensities of raw (top) and normalized (lower) data. A total of 48 arrays were analyzed. There were at least three replicates for each treatment (0, 200, 500 and 1000 ppb) at the three time points (24, 48, 72 hours) in addition to several additional control samples. Normalized medians (lower plot) have horizontal bars inside the boxes on the same level. This indicates, all arrays have the same distribution of expression values.

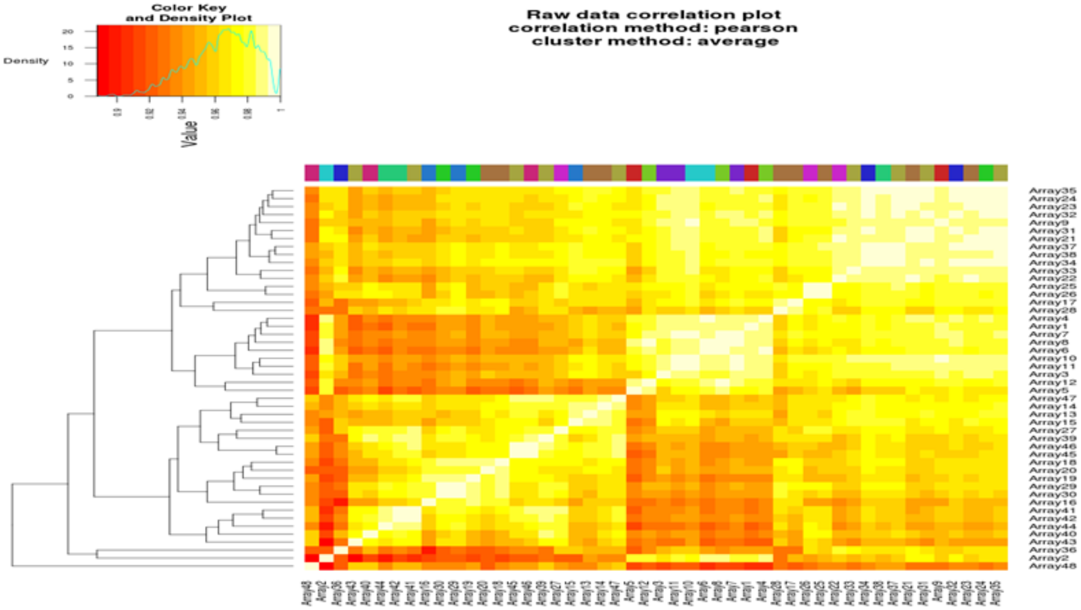


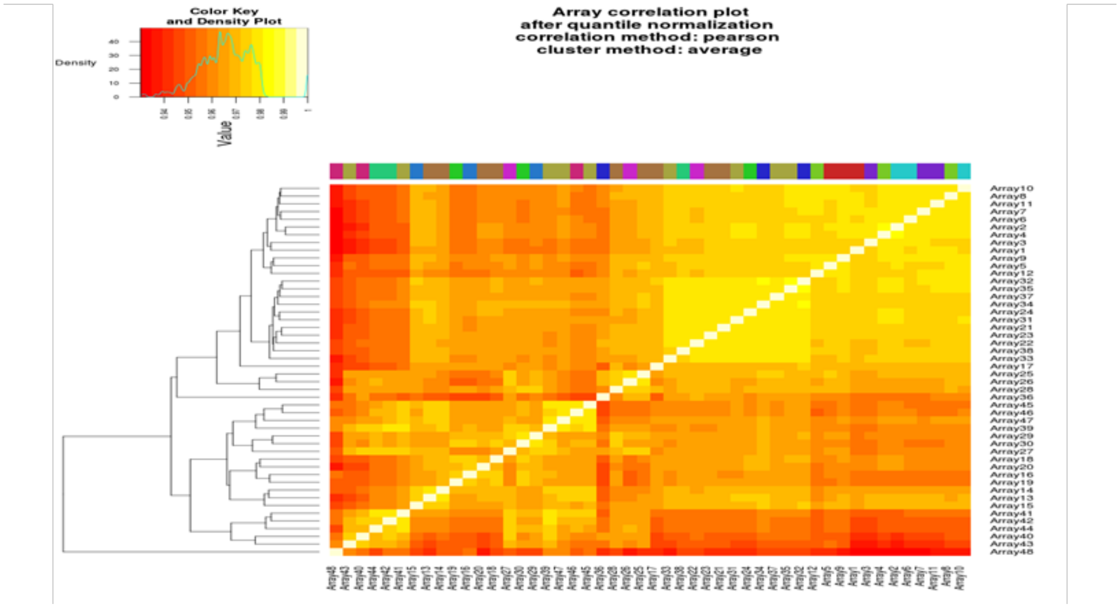
Appendix C. Density distribution of the raw log intensities for the different samples. While each array on a single histogram are not identical, the median is similar and the normalized probe set intensities are closer to identical





Appendix D. The correlation plots show correlations before (raw data, top) and after normalization of the data (lower plot). Each correlation coefficient was computed for each pair of arrays in the data set. The small plots with the color key and density plot of the normalized data has a lower coefficient which indicates differences between the arrays.





Appendix E1. Cellular process (DNA metabolic processes) enriched in DEGs between 0 ppb and 500 ppb of metolachlor exposed human liver cells for 48 hours

Cellular process	P-value	Genes involved in DNA metabolic process	sample frequency = number of genes in interesection(b)/number of genes in sample set (n)	background frequency = number of genes associated with process (B)/total number of genes in organism (N)	Enrichment (sample frequency/background frequency)
DNA metabolic process	2.78E-05		58/178	114/566	1.62
		RFC4 - replication factor c (activator 1) 4, 37kda			
		RFC5 - replication factor c (activator 1) 5, 36.5kda			
		RFC3 - replication factor c (activator 1) 3, 38kda			
		CCNE2 - cyclin e2			
		ORC1 - origin recognition complex, subunit 1			
		TK1 - thymidine kinase 1, soluble			
		BRCA1 - breast cancer 1, early onset			
		GINS3 - gins complex subunit 3 (psf3 homolog)			
		UHRF1 - ubiquitin-like with phd and ring finger domains 1			
		DTL - denticleless e3 ubiquitin protein ligase homolog (drosophila)			
		LIG1 - ligase i, dna, atp-dependent			
		PRIM2 - primase, dna, polypeptide 2 (58kda)			
		CHAF1B - chromatin assembly factor 1, subunit b (p60)			
		FANCD2 - fanconi anemia, complementation group d2			
		UNG - uracil-dna glycosylase			
		FANCG - fanconi anemia, complementation group g			
		FANCB - fanconi anemia, complementation group b			
		RPA3 - replication protein a3, 14kda			
		CDCA5 - cell division cycle associated 5			
		CHEK1 - checkpoint kinase 1			
		DUT - deoxyuridine triphosphatase			
		BLM - bloom syndrome, recq helicase-like			
		CHAF1A - chromatin assembly factor 1, subunit a (p150)			
		MCM4 - minichromosome maintenance complex component 4			
		MCM3 - minichromosome maintenance complex component 3			
		MCM6 - minichromosome maintenance complex component 6			
		MCM5 - minichromosome maintenance complex component 5			
		MCM2 - minichromosome maintenance complex component 2			
		ANKRD32 - ankyrin repeat domain 32			
		RAD51AP1 - rad51 associated protein 1			
		RMI2 - recq mediated genome instability 2			
		FANCI - fanconi anemia, complementation group i			
		APITD1 - apoptosis-inducing, taf9-like domain 1			
		BARD1 - brca1 associated ring domain 1			
		RNASEH2A - ribonuclease h2, subunit a			
		RAD54L - rad54-like (s. cerevisiae)			
		MCM10 - minichromosome maintenance complex component 10			
		KIAA0101 - kiaa0101			
		NEIL3 - nei endonuclease viii-like 3 (e. coli)			
		FEN1 - flap structure-specific endonuclease 1			
		CDC45 - cell division cycle 45			
		GINS2 - gins complex subunit 2 (psf2 homolog)			
		POLA2 - polymerase (dna directed), alpha 2, accessory subunit			
		PCNA - proliferating cell nuclear antigen			
		TRIP13 - thyroid hormone receptor interactor 13			
		UBE2T - ubiquitin-conjugating enzyme e2t (putative)			
		DNMT3L - dna (cytosine-5-)-methyltransferase 3-like			
		DNMT3B - dna (cytosine-5-)-methyltransferase 3 beta			
		GINS4 - gins complex subunit 4 (sld5 homolog)			
		HELLS - helicase, lymphoid-specific			
		POLQ - polymerase (dna directed), theta			
		POLE2 - polymerase (dna directed), epsilon 2, accessory subunit			
		POLD1 - polymerase (dna directed), delta 1, catalytic subunit			
		POLA1 - polymerase (dna directed), alpha 1, catalytic subunit			
		CDK2 - cyclin-dependent kinase 2			
		RRM1 - ribonucleotide reductase m1			
		RRM2 - ribonucleotide reductase m2			
		EXO1 - exonuclease 1			

Appendix E2. Cellular process (DNA replication) enriched in DEGs between 0 ppb and 500 ppb of metolachlor exposed human liver cells for 48 hours

Cellular process	P-value	Genes involved in DNA replication	sample frequency = number of genes in interesection(b)/number of genes in sample set (n)	background frequency = number of genes associated with process (B)/total number of genes in organism (N)	Enrichment (sample frequency/background frequency)
DNA replication	7.64E-05		33/178	55/566	1.91
		RFC4 - replication factor c (activator 1) 4, 37kda			
		RFC5 - replication factor c (activator 1) 5, 36.5kda			
		BARD1 - brca1 associated ring domain 1			
		RFC3 - replication factor c (activator 1) 3, 38kda			
		RNASEH2A - ribonuclease h2, subunit a			
		ORC1 - origin recognition complex, subunit 1			
		BRCA1 - breast cancer 1, early onset			
		DTL - denticleless e3 ubiquitin protein ligase homolog (drosophila)			
		CHAF1B - chromatin assembly factor 1, subunit b (p60)			
		MCM10 - minichromosome maintenance complex component 10			
		KIAA0101 - kiaa0101			
		FEN1 - flap structure-specific endonuclease 1			
		CDC45 - cell division cycle 45			
		RPA3 - replication protein a3, 14kda			
		POLA2 - polymerase (dna directed), alpha 2, accessory subunit			
		CHEK1 - checkpoint kinase 1			
		DUT - deoxyuridine triphosphatase			
		BLM - bloom syndrome, recq helicase-like			
		CHAF1A - chromatin assembly factor 1, subunit a (p150)			
		MCM4 - minichromosome maintenance complex component 4			
		MCM3 - minichromosome maintenance complex component 3			
		POLQ - polymerase (dna directed), theta			
		POLE2 - polymerase (dna directed), epsilon 2, accessory subunit			
		MCM6 - minichromosome maintenance complex component 6			
		MCM5 - minichromosome maintenance complex component 5			
		POLD1 - polymerase (dna directed), delta 1, catalytic subunit			
		MCM2 - minichromosome maintenance complex component 2			
		POLA1 - polymerase (dna directed), alpha 1, catalytic subunit			
		RMI2 - recq mediated genome instability 2			
		CDK2 - cyclin-dependent kinase 2			
		RRM1 - ribonucleotide reductase m1			
		RRM2 - ribonucleotide reductase m2			
		EXO1 - exonuclease 1			

Appendix E3. Cellular process (DNA replication initiation) enriched in DEGs between 0 ppb and 500 ppb of metolachlor exposed human liver cells for 48 hours

Cellular process	P-value	Genes involved in DNA replication initiation	sample frequency = number of genes in interesection(b)/number of genes in sample set (n)	background frequency = number of genes associated with process (B)/total number of genes in organism (N)	Enrichment (sample frequency/background frequency)
DNA replication initiation	8.47E-04		21/299	23/566	1.73
		POLA2 - polymerase (dna directed), alpha 2, accessory subunit			
		CDC6 - cell division cycle 6			
		CCNE2 - cyclin e2			
		ORC1 - origin recognition complex, subunit 1			
		CCNE1 - cyclin e1			
		PRIM2 - primase, dna, polypeptide 2 (58kda)			
		GINS4 - gins complex subunit 4 (sld5 homolog)			
		PRIM1 - primase, dna, polypeptide 1 (49kda)			
		MCM8 - minichromosome maintenance complex component 8			
		MCM4 - minichromosome maintenance complex component 4			
		MCM3 - minichromosome maintenance complex component 3			
		MCM10 - minichromosome maintenance complex component 10			
		POLE2 - polymerase (dna directed), epsilon 2, accessory subunit			
		MCM6 - minichromosome maintenance complex component 6			
		ORC6 - origin recognition complex, subunit 6			
		MCM5 - minichromosome maintenance complex component 5			
		MCM2 - minichromosome maintenance complex component 2			
		POLA1 - polymerase (dna directed), alpha 1, catalytic subunit			
		CDC45 - cell division cycle 45			
		GINS2 - gins complex subunit 2 (psf2 homolog)			
		CDC7 - cell division cycle 7			

Appendix E4. Cellular process (DNA repair) enriched in DEGs between 0 ppb and 500 ppb of metolachlor exposed human liver cells for 48 hours

Cellular process	P-value	Genes involved in DNA repair	sample frequency = number of genes in interesection(b)/number of genes in sample set (n)	background frequency = number of genes associated with process (B)/total number of genes in organism (N)	Enrichment (sample frequency/background frequency)
DNA repair	2.09E-04		39/178	71/566	1.75
		RFC4 - replication factor c (activator 1) 4, 37kda			
		RFC5 - replication factor c (activator 1) 5, 36.5kda			
		BARD1 - brca1 associated ring domain 1			
		RFC3 - replication factor c (activator 1) 3, 38kda			
		RNASEH2A - ribonuclease h2, subunit a			
		RAD54L - rad54-like (s. cerevisiae)			
		BRCA1 - breast cancer 1, early onset			
		DTL - denticleless e3 ubiquitin protein ligase homolog (drosophila)			
		UHRF1 - ubiquitin-like with phd and ring finger domains 1			
		LIG1 - ligase i, dna, atp-dependent			
		CHAF1B - chromatin assembly factor 1, subunit b (p60)			
		FANCD2 - fanconi anemia, complementation group d2			
		KIAA0101 - kiaa0101			
		NEIL3 - nei endonuclease viii-like 3 (e. coli)			
		CDC45 - cell division cycle 45			
		FEN1 - flap structure-specific endonuclease 1			
		UNG - uracil-dna glycosylase			
		FANCG - fanconi anemia, complementation group g			
		FANCB - fanconi anemia, complementation group b			
		RPA3 - replication protein a3, 14kda			
		GINS2 - gins complex subunit 2 (psf2 homolog)			
		CDCA5 - cell division cycle associated 5			
		PCNA - proliferating cell nuclear antigen			
		CHEK1 - checkpoint kinase 1			
		TRIP13 - thyroid hormone receptor interactor 13			
		UBE2T - ubiquitin-conjugating enzyme e2t (putative)			
		BLM - bloom syndrome, recq helicase-like			
		CHAF1A - chromatin assembly factor 1, subunit a (p150)			
		GINS4 - gins complex subunit 4 (sld5 homolog)			
		POLQ - polymerase (dna directed), theta			
		POLE2 - polymerase (dna directed), epsilon 2, accessory subunit			
		POLD1 - polymerase (dna directed), delta 1, catalytic subunit			
		POLA1 - polymerase (dna directed), alpha 1, catalytic subunit			
		ANKRD32 - ankyrin repeat domain 32			
		RAD51AP1 - rad51 associated protein 1			
		CDK2 - cyclin-dependent kinase 2			
		FANCI - fanconi anemia, complementation group i			
		EXO1 - exonuclease 1			
		APITD1 - apoptosis-inducing, taf9-like domain 1			

Appendix E5. Cellular process (cellular response to stimulus) enriched in DEGs between 0 ppb and 500 ppb of metolachlor exposed human liver cells for 48 hours

Cellular process	P-value	Genes involved in cellular response to stimulus	sample frequency = number of genes in interesection(b)/number of genes in sample set (n)	background frequency = number of genes associated with process (B)/total number of genes in organism (N)	Enrichment (sample frequency/background frequency)
cellular response to stimulus	5.69E-04	RFC4 - replication factor c (activator 1) 4, 37kda	68/178	150/566	1.44
		RFC5 - replication factor c (activator 1) 5, 36.5kda			
		RFC3 - replication factor c (activator 1) 3, 38kda			
		BRCA1 - breast cancer 1, early onset			
		AKR1C2 - aldo-keto reductase family 1, member c2			
		UHRF1 - ubiquitin-like with phd and ring finger domains 1			
		DTL - denticleless e3 ubiquitin protein ligase homolog (drosophila)			
		LIG1 - ligase i, dna, atp-dependent			
		CHAF1B - chromatin assembly factor 1, subunit b (p60)			
		PBK - pdz binding kinase			
		FANCD2 - fanconi anemia, complementation group d2			
		CASP6 - caspase 6, apoptosis-related cysteine peptidase			
		SUV39H1 - suppressor of variegation 3-9 homolog 1 (drosophila)			
		FANCG - fanconi anemia, complementation group g			
		UNG - uracil-dna glycosylase			
		FANCB - fanconi anemia, complementation group b			
		RPA3 - replication protein a3, 14kda			
		CDCA5 - cell division cycle associated 5			
		SKP2 - s-phase kinase-associated protein 2, e3 ubiquitin protein ligase			
		CHEK1 - checkpoint kinase 1			
		MT2A - metallothionein 2a			
		CD36 - cd36 molecule (thrombospondin receptor)			
		MT1A - metallothionein 1a			
		BLM - bloom syndrome, recq helicase-like			
		MT1H - metallothionein 1h			
		MT1G - metallothionein 1g			
		CHAF1A - chromatin assembly factor 1, subunit a (p150)			
		MASTL - microtubule associated serine/threonine kinase-like			
		HAMP - hepcidin antimicrobial peptide			
		MCM2 - minichromosome maintenance complex component 2			
		ANKRD32 - ankyrin repeat domain 32			
		IFIH1 - interferon induced with helicase c domain 1			
		RAD51AP1 - rad51 associated protein 1			
		FANCI - fanconi anemia, complementation group i			
		APITD1 - apoptosis-inducing, taf9-like domain 1			
		CRIP1 - cysteine-rich protein 1 (intestinal)			
		BARD1 - brca1 associated ring domain 1			
		ALOX5AP - arachidonate 5-lipoxygenase-activating protein			
		RNASEH2A - ribonuclease h2, subunit a			
		RAD54L - rad54-like (s. cerevisiae)			
		SHMT1 - serine hydroxymethyltransferase 1 (soluble)			
		MCM10 - minichromosome maintenance complex component 10			
		KIAA0101 - kiaa0101			
		ARG1 - arginase 1			
		ATAD5 - atpase family, aaa domain containing 5			
		NEIL3 - nei endonuclease viii-like 3 (e. coli)			
		CDC45 - cell division cycle 45			
		FEN1 - flap structure-specific endonuclease 1			
		RAB31 - rab31, member ras oncogene family			
		GINS2 - gins complex subunit 2 (psf2 homolog)			
		PCNA - proliferating cell nuclear antigen			
		TRIP13 - thyroid hormone receptor interactor 13			
		E2F7 - e2f transcription factor 7			
		UBE2T - ubiquitin-conjugating enzyme e2t (putative)			
		FIGNL1 - fidgetin-like 1			
		CAT - catalase			
		DNMT3B - dna (cytosine-5-)-methyltransferase 3 beta			
		UCP2 - uncoupling protein 2 (mitochondrial, proton carrier)			
		GINS4 - gins complex subunit 4 (sld5 homolog)			
		EPO - erythropoietin			
		POLQ - polymerase (dna directed), theta			
		POLE2 - polymerase (dna directed), epsilon 2, accessory subunit			
		CCNA2 - cyclin a2			
		POLD1 - polymerase (dna directed), delta 1, catalytic subunit			
		POLA1 - polymerase (dna directed), alpha 1, catalytic subunit			
		HMOX1 - heme oxygenase (decycling) 1			
		CDK2 - cyclin-dependent kinase 2			
		EXO1 - exonuclease 1			

Appendix E6. Cellular processes (cellular response to acid chemical, Zn ion) enriched in DEGs between 0 ppb and 500 ppb of metolachlor exposed human liver cells for 48 hours

Cellular process	P-value	Genes involved in cellular response to: acid chemical and Zn ion	sample frequency = number of genes in interesection(b)/number of genes in sample set (n)	background frequency = number of genes associated with process (B)/total number of genes in organism (N)	Enrichment (sample frequency/background frequency)
cellular response to acid chemical	6.27E-04	HAMP - hepcidin antimicrobial peptide	2/2	7/566	80.86
		AKR1C2 - aldo-keto reductase family 1, member c2			
cellular response to acid chemical	9.93E-04	CDO1 - cysteine dioxygenase type 1	4/10	17/566	13.32
		HAMP - hepcidin antimicrobial peptide			
		CD36 - cd36 molecule (thrombospondin receptor)			
		AKR1C2 - aldo-keto reductase family 1, member c2			
response to zinc ion	5.65E-04	HAMP - hepcidin antimicrobial peptide	7/83	10/566	4.77
		CRIP1 - cysteine-rich protein 1 (intestinal)			
		MT2A - metallothionein 2a			
		ARG1 - arginase 1			
		MT1A - metallothionein 1a			
		MT1H - metallothionein 1h			
		MT1G - metallothionein 1g			

Appendix F1. Cellular functions (chromatin binding, catalytic activity on DNA) enriched in DEGs between 0 ppb and 500 ppb of metolachlor exposed human liver cells for 48 hours.

Cellular function	P-value	Genes involved in chromatin binding function AND catalytic activity acting on DNA	sample frequency = number of genes in interesection(b)/number of genes in sample set (n)	background frequency = number of genes associated with process (B)/total number of genes in organism (N)	Enrichment (sample frequency/background frequency)
chromatin binding	8.45E-05	CDCA5 - cell division cycle associated 5	20/151	31/566	2.42
		PCNA - proliferating cell nuclear antigen			
		PLAC8 - placenta-specific 8			
		UBE2T - ubiquitin-conjugating enzyme e2t (putative)			
		ORC1 - origin recognition complex, subunit 1			
		CDT1 - chromatin licensing and dna replication factor 1			
		DNMT3B - dna (cytosine-5-)-methyltransferase 3 beta			
		UHRF1 - ubiquitin-like with phd and ring finger domains 1			
		CHAF1A - chromatin assembly factor 1, subunit a (p150)			
		CHAF1B - chromatin assembly factor 1, subunit b (p60)			
		POLQ - polymerase (dna directed), theta			
		VRK1 - vaccinia related kinase 1			
		MCM5 - minichromosome maintenance complex component 5			
		KIAA0101 - kiaa0101			
		POLD1 - polymerase (dna directed), delta 1, catalytic subunit			
		POLA1 - polymerase (dna directed), alpha 1, catalytic subunit			
		SUV39H1 - suppressor of variegation 3-9 homolog 1 (drosophila)			
		CDC45 - cell division cycle 45			
		APITD1 - apoptosis-inducing, taf9-like domain 1			
		EXO1 - exonuclease 1			
catalytic activity, acting on DNA	1.11E-04	POLA2 - polymerase (dna directed), alpha 2, accessory subu	20/151	31/566	2.35
		PCNA - proliferating cell nuclear antigen			
		RAD54L - rad54-like (s. cerevisiae)			
		BLM - bloom syndrome, recq helicase-like			
		DNMT3B - dna (cytosine-5-)-methyltransferase 3 beta			
		PRIM2 - primase, dna, polypeptide 2 (58kda)			
		LIG1 - ligase i, dna, atp-dependent			
		GINS4 - gins complex subunit 4 (sld5 homolog)			
		MCM4 - minichromosome maintenance complex component 4			
		MCM6 - minichromosome maintenance complex component 6			
		POLE2 - polymerase (dna directed), epsilon 2, accessory subunit			
		POLQ - polymerase (dna directed), theta			
		MCM5 - minichromosome maintenance complex component 5			
		POLD1 - polymerase (dna directed), delta 1, catalytic subunit			
		MCM2 - minichromosome maintenance complex component 2			
		POLA1 - polymerase (dna directed), alpha 1, catalytic subunit			
		NEIL3 - nei endonuclease viii-like 3 (e. coli)			
		UNG - uracil-dna glycosylase			
		CDC45 - cell division cycle 45			
		GINS2 - gins complex subunit 2 (psf2 homolog)			
		EXO1 - exonuclease 1			

Appendix F2. Cellular functions (Helicase activity) enriched in DEGs between 0 ppb and 500 ppb of metolachlor exposed human liver cells for 48 hours.

Cellular function	P-value	Genes involved in helicase activity	sample frequency = number of genes in interesection(b)/number of genes in sample set (n)	background frequency = number of genes associated with process (B)/total number of genes in organism (N)	Enrichment (sample frequency/background frequency)
helicase activity	7.68E-04	ERCC6L - excision repair cross-complementing rodent repair	13/171	17/566	2.53
		RAD54L - rad54-like (s. cerevisiae)			
		BLM - bloom syndrome, recq helicase-like			
		GINS4 - gins complex subunit 4 (sld5 homolog)			
		MCM4 - minichromosome maintenance complex component 4			
		HELLS - helicase, lymphoid-specific			
		MCM3 - minichromosome maintenance complex component 3			
		MCM6 - minichromosome maintenance complex component 6			
		MCM5 - minichromosome maintenance complex component 5			
		MCM2 - minichromosome maintenance complex component 2			
		IFIH1 - interferon induced with helicase c domain 1			
		CDC45 - cell division cycle 45			
		GINS2 - gins complex subunit 2 (psf2 homolog)			
DNA helicase activity	8.99E-04	MCM4 - minichromosome maintenance complex component	7/77	11/566	4.68
		MCM6 - minichromosome maintenance complex component 6			
		MCM5 - minichromosome maintenance complex component 5			
		MCM2 - minichromosome maintenance complex component 2			
		CDC45 - cell division cycle 45			
		GINS2 - gins complex subunit 2 (psf2 homolog)			
		GINS4 - gins complex subunit 4 (sld5 homolog)			

Appendix G1. Cellular process (DNA metabolic process) enriched in DEGs between 0 ppb and 1000 ppb of metolachlor exposed human liver cells for 48 hours.

Cellular process	P-value	Genes involved in DNA metabolic process	sample frequency = number of genes in interesection(b)/number of genes in sample set (n)	background frequency = number of genes associated with process (B)/total number of genes in organism (N)	Enrichment (sample frequency/background frequency)
DNA metabolic process	1.73E-06	CDC6 - cell division cycle 6	62/192	104/528	1.64
		RFC4 - replication factor c (activator 1) 4, 37kda			
		RFC5 - replication factor c (activator 1) 5, 36.5kda			
		RFC3 - replication factor c (activator 1) 3, 38kda			
		CCNE2 - cyclin e2			
		ORC1 - origin recognition complex, subunit 1			
		TK1 - thymidine kinase 1, soluble			
		BRCA1 - breast cancer 1, early onset			
		GINS3 - gins complex subunit 3 (psf3 homolog)			
		UHRF1 - ubiquitin-like with phd and ring finger domains 1			
		DTL - denticleless e3 ubiquitin protein ligase homolog (drosophila)			
		LIG1 - ligase i, dna, atp-dependent			
		PRIM2 - primase, dna, polypeptide 2 (58kda)			
		CHAF1B - chromatin assembly factor 1, subunit b (p60)			
		FANCD2 - fanconi anemia, complementation group d2			
		UNG - uracil-dna glycosylase			
		FANCG - fanconi anemia, complementation group g			
		RPA3 - replication protein a3, 14kda			
		CDCA5 - cell division cycle associated 5			
		CHEK1 - checkpoint kinase 1			
		DUT - deoxyuridine triphosphatase			
		BLM - bloom syndrome, recq helicase-like			
		CHAF1A - chromatin assembly factor 1, subunit a (p150)			
		CHEK2 - checkpoint kinase 2			
		MCM4 - minichromosome maintenance complex component 4			
		MCM3 - minichromosome maintenance complex component 3			
		MCM6 - minichromosome maintenance complex component 6			
		MCM5 - minichromosome maintenance complex component 5			
		MCM2 - minichromosome maintenance complex component 2			
		ANKRD32 - ankyrin repeat domain 32			
		RAD51AP1 - rad51 associated protein 1			
		RMI2 - recq mediated genome instability 2			
		FANCI - fanconi anemia, complementation group i			
		APITD1 - apoptosis-inducing, taf9-like domain 1			
		BARD1 - brca1 associated ring domain 1			
		RNASEH2A - ribonuclease h2, subunit a			
		RAD54L - rad54-like (s. cerevisiae)			
		CCNE1 - cyclin e1			
		MCM10 - minichromosome maintenance complex component 10			
		KIAA0101 - kiaa0101			
		TIPIN - timeless interacting protein			
		NEIL3 - nei endonuclease viii-like 3 (e. coli)			
		FEN1 - flap structure-specific endonuclease 1			
		CDC45 - cell division cycle 45			
		TICRR - topbp1-interacting checkpoint and replication regulator			
		GINS2 - gins complex subunit 2 (psf2 homolog)			
		CDC7 - cell division cycle 7			
		POLA2 - polymerase (dna directed), alpha 2, accessory subunit			
		PCNA - proliferating cell nuclear antigen			
		TRIP13 - thyroid hormone receptor interactor 13			
		UBE2T - ubiquitin-conjugating enzyme e2t (putative)			
		DNMT3L - dna (cytosine-5-)-methyltransferase 3-like			
		DNMT3B - dna (cytosine-5-)-methyltransferase 3 beta			
		GINS4 - gins complex subunit 4 (sld5 homolog)			
		HELLS - helicase, lymphoid-specific			
		POLQ - polymerase (dna directed), theta			
		WRAP53 - wd repeat containing, antisense to tp53			
		POLE2 - polymerase (dna directed), epsilon 2, accessory subunit			
		POLA1 - polymerase (dna directed), alpha 1, catalytic subunit			
		RRM1 - ribonucleotide reductase m1			
		RRM2 - ribonucleotide reductase m2			
		EXO1 - exonuclease 1			

Appendix G2. Cellular process (DNA replication) enriched in DEGs between 0 ppb and 1000 ppb of metolachlor exposed human liver cells for 48 hours.

Cellular process	P-value	Genes involved in DNA replication	sample frequency = number of genes in interesection(b)/number of genes in sample set (n)	background frequency = number of genes associated with process (B)/total number of genes in organism (N)	Enrichment (sample frequency/background frequency)
DNA replication	4.02E-06	CDC6 - cell division cycle 6	38/207	52/528	1.86
		RFC4 - replication factor c (activator 1) 4, 37kda			
		RFC5 - replication factor c (activator 1) 5, 36.5kda			
		BARD1 - brca1 associated ring domain 1			
		RFC3 - replication factor c (activator 1) 3, 38kda			
		RNASEH2A - ribonuclease h2, subunit a			
		ORC1 - origin recognition complex, subunit 1			
		BRCA1 - breast cancer 1, early onset			
		DTL - denticleless e3 ubiquitin protein ligase homolog (drosophila)			
		CHAF1B - chromatin assembly factor 1, subunit b (p60)			
		MCM10 - minichromosome maintenance complex component 10			
		KIAA0101 - kiaa0101			
		TIPIN - timeless interacting protein			
		CDC45 - cell division cycle 45			
		FEN1 - flap structure-specific endonuclease 1			
		TICRR - topbp1-interacting checkpoint and replication regulator			
		RPA3 - replication protein a3, 14kda			
		CDC7 - cell division cycle 7			
		RPA1 - replication protein a1, 70kda			
		POLA2 - polymerase (dna directed), alpha 2, accessory subunit			
		CHEK1 - checkpoint kinase 1			
		DUT - deoxyuridine triphosphatase			
		BLM - bloom syndrome, recq helicase-like			
		CHAF1A - chromatin assembly factor 1, subunit a (p150)			
		MCM4 - minichromosome maintenance complex component 4			
		MCM3 - minichromosome maintenance complex component 3			
		POLQ - polymerase (dna directed), theta			
		POLE2 - polymerase (dna directed), epsilon 2, accessory subunit			
		MCM6 - minichromosome maintenance complex component 6			
		MCM5 - minichromosome maintenance complex component 5			
		POLD1 - polymerase (dna directed), delta 1, catalytic subunit			
		MCM2 - minichromosome maintenance complex component 2			
		POLA1 - polymerase (dna directed), alpha 1, catalytic subunit			
		RMI2 - recq mediated genome instability 2			
		CDK2 - cyclin-dependent kinase 2			
		RRM1 - ribonucleotide reductase m1			
		RRM2 - ribonucleotide reductase m2			
		EXO1 - exonuclease 1			

Appendix G3. Cellular processes (DNA replication initiation, DNA biosynthetic process) enriched in DEGs between 0 ppb and 1000 ppb of metolachlor exposed human liver cells for 48 hours.

Cellular process	P-value	Genes involved in DNA replication initiation AND biosynthetic process	sample frequency = number of genes in interesection(b)/number of genes in sample set (n)	background frequency = number of genes associated with process (B)/total number of genes in organism (N)	Enrichment (sample frequency/background frequency)
DNA replication initiatio	1.15E-04	MCM4 - minichromosome maintenance complex component	8/31	22/528	6.19
		POLA2 - polymerase (dna directed), alpha 2, accessory subunit			
		MCM10 - minichromosome maintenance complex component 10			
		MCM6 - minichromosome maintenance complex component 6			
		POLE2 - polymerase (dna directed), epsilon 2, accessory subunit			
		MCM2 - minichromosome maintenance complex component 2			
		CDC45 - cell division cycle 45			
		GINS2 - gins complex subunit 2 (psf2 homolog)			
DNA biosynthetic process	9.36E-04	POLA2 - polymerase (dna directed), alpha 2, accessory subu	22/203	30/528	1.91
		PCNA - proliferating cell nuclear antigen			
		RFC4 - replication factor c (activator 1) 4, 37kda			
		RFC5 - replication factor c (activator 1) 5, 36.5kda			
		BARD1 - brca1 associated ring domain 1			
		RFC3 - replication factor c (activator 1) 3, 38kda			
		TK1 - thymidine kinase 1, soluble			
		BLM - bloom syndrome, recq helicase-like			
		BRCA1 - breast cancer 1, early onset			
		DTL - denticleless e3 ubiquitin protein ligase homolog (drosophila)			
		LIG1 - ligase i, dna, atp-dependent			
		PRIM2 - primase, dna, polypeptide 2 (58kda)			
		POLQ - polymerase (dna directed), theta			
		WRAP53 - wd repeat containing, antisense to tp53			
		POLE2 - polymerase (dna directed), epsilon 2, accessory subunit			
		KIAA0101 - kiaa0101			
		POLD1 - polymerase (dna directed), delta 1, catalytic subunit			
		RMI2 - recq mediated genome instability 2			
		RAD51AP1 - rad51 associated protein 1			
		RPA3 - replication protein a3, 14kda			
		RPA1 - replication protein a1, 70kda			
		EXO1 - exonuclease 1			

Appendix G4. Cellular process (DNA repair) enriched in DEGs between 0 ppb and 1000 ppb of metolachlor exposed human liver cells for 48 hours.

Cellular process	P-value	Genes involved in DNA repair	sample frequency = number of genes in interesection(b)/number of genes in sample set (n)	background frequency = number of genes associated with process (B)/total number of genes in organism (N)	Enrichment (sample frequency/background frequency)
DNA repair	5.50E-05	RFC4 - replication factor c (activator 1) 4, 37kda	42/207	63/528	1.7
		RFC5 - replication factor c (activator 1) 5, 36.5kda			
		BARD1 - brca1 associated ring domain 1			
		RFC3 - replication factor c (activator 1) 3, 38kda			
		RNASEH2A - ribonuclease h2, subunit a			
		RAD54L - rad54-like (s. cerevisiae)			
		BRCA1 - breast cancer 1, early onset			
		DTL - denticleless e3 ubiquitin protein ligase homolog (drosophila)			
		UHRF1 - ubiquitin-like with phd and ring finger domains 1			
		LIG1 - ligase i, dna, atp-dependent			
		CHAF1B - chromatin assembly factor 1, subunit b (p60)			
		FANCD2 - fanconi anemia, complementation group d2			
		KIAA0101 - kiaa0101			
		NEIL3 - nei endonuclease viii-like 3 (e. coli)			
		FEN1 - flap structure-specific endonuclease 1			
		CDC45 - cell division cycle 45			
		FANCG - fanconi anemia, complementation group g			
		UNG - uracil-dna glycosylase			
		TICRR - topbp1-interacting checkpoint and replication regulator			
		RPA3 - replication protein a3, 14kda			
		CDC7 - cell division cycle 7			
		GINS2 - gins complex subunit 2 (psf2 homolog)			
		RPA1 - replication protein a1, 70kda			
		CDCA5 - cell division cycle associated 5			
		PCNA - proliferating cell nuclear antigen			
		CHEK1 - checkpoint kinase 1			
		TRIP13 - thyroid hormone receptor interactor 13			
		UBE2T - ubiquitin-conjugating enzyme e2t (putative)			
		BLM - bloom syndrome, recq helicase-like			
		CHAF1A - chromatin assembly factor 1, subunit a (p150)			
		GINS4 - gins complex subunit 4 (sld5 homolog)			
		CHEK2 - checkpoint kinase 2			
		POLE2 - polymerase (dna directed), epsilon 2, accessory subunit			
		POLQ - polymerase (dna directed), theta			
		POLD1 - polymerase (dna directed), delta 1, catalytic subunit			
		POLA1 - polymerase (dna directed), alpha 1, catalytic subunit			
		ANKRD32 - ankyrin repeat domain 32			
		RAD51AP1 - rad51 associated protein 1			
		CDK2 - cyclin-dependent kinase 2			
		FANCI - fanconi anemia, complementation group i			
		EXO1 - exonuclease 1			
		APITD1 - apoptosis-inducing, taf9-like domain 1			

Appendix G5. Cellular process (response to DNA damage) enriched in DEGs between 0 ppb and 1000 ppb of metolachlor exposed human liver cells for 48 hours.

Cellular process	P-value	Genes involved in DNA cellular response to DNA damage stimulus	sample frequency = number of genes in interesection(b)/number of genes in sample set (n)	background frequency = number of genes associated with process (B)/total number of genes in organism (N)	Enrichment (sample frequency/background frequency)
cellular response to DNA damage stimulus	3.47E-04	RFC4 - replication factor c (activator 1) 4, 37kda	60/269	83/528	1.42
		VAV3 - vav 3 guanine nucleotide exchange factor			
		RFC5 - replication factor c (activator 1) 5, 36.5kda			
		RFC3 - replication factor c (activator 1) 3, 38kda			
		BRCA1 - breast cancer 1, early onset			
		DTL - denticleless e3 ubiquitin protein ligase homolog (drosophila)			
		CDC25C - cell division cycle 25c			
		UHRF1 - ubiquitin-like with phd and ring finger domains 1			
		LIG1 - ligase i, dna, atp-dependent			
		CHAF1B - chromatin assembly factor 1, subunit b (p60)			
		SFN - stratifin			
		FANCD2 - fanconi anemia, complementation group d2			
		SUV39H1 - suppressor of variegation 3-9 homolog 1 (drosophila)			
		FANCG - fanconi anemia, complementation group g			
		UNG - uracil-dna glycosylase			
		RPA3 - replication protein a3, 14kda			
		NUDT1 - nudix (nucleoside diphosphate linked moiety x)-type motif 1			
		RPA1 - replication protein a1, 70kda			
		CDCA5 - cell division cycle associated 5			
		CHEK1 - checkpoint kinase 1			
		SLX4 - slx4 structure-specific endonuclease subunit			
		BLM - bloom syndrome, recq helicase-like			
		CHAF1A - chromatin assembly factor 1, subunit a (p150)			
		MASTL - microtubule associated serine/threonine kinase-like			
		CHEK2 - checkpoint kinase 2			
		ANKRD32 - ankyrin repeat domain 32			
		RAD51AP1 - rad51 associated protein 1			
		PTTG1 - pituitary tumor-transforming 1			
		FANCI - fanconi anemia, complementation group i			
		APITD1 - apoptosis-inducing, taf9-like domain 1			
		CRIP1 - cysteine-rich protein 1 (intestinal)			
		BARD1 - brca1 associated ring domain 1			
		RNASEH2A - ribonuclease h2, subunit a			
		RAD54L - rad54-like (s. cerevisiae)			
		CETN2 - centrin, ef-hand protein, 2			
		MCM10 - minichromosome maintenance complex component 10			
		KIAA0101 - kiaa0101			
		TIPIN - timeless interacting protein			
		NEIL3 - nei endonuclease viii-like 3 (e. coli)			
		FEN1 - flap structure-specific endonuclease 1			
		CDC45 - cell division cycle 45			
		TICRR - topbp1-interacting checkpoint and replication regulator			
		CDC7 - cell division cycle 7			
		GINS2 - gins complex subunit 2 (psf2 homolog)			
		PCNA - proliferating cell nuclear antigen			
		TRIP13 - thyroid hormone receptor interactor 13			
		E2F7 - e2f transcription factor 7			
		UBE2T - ubiquitin-conjugating enzyme e2t (putative)			
		TIMELESS - timeless circadian clock			
		GINS4 - gins complex subunit 4 (sld5 homolog)			
		POLQ - polymerase (dna directed), theta			
		POLE2 - polymerase (dna directed), epsilon 2, accessory subunit			
		CCNB1 - cyclin b1			
		XRCC3 - x-ray repair complementing defective repair in chinese hamster cells 3			
		POLD1 - polymerase (dna directed), delta 1, catalytic subunit			
		POLA1 - polymerase (dna directed), alpha 1, catalytic subunit			
		HMOX1 - heme oxygenase (decycling) 1			
		EME1 - essential meiotic structure-specific endonuclease 1			
		CDK2 - cyclin-dependent kinase 2			
		EXO1 - exonuclease 1			

Appendix G6. Cellular process (DNA geometric change and DNA duplex unwinding) enriched in DEGs between 0 ppb and 1000 ppb of metolachlor exposed human liver cells for 48 hours.

Cellular process	P-value	Genes involved in DNA geometric change and duplex unwinding	sample frequency = number of genes in interesection(b)/number of genes in sample set (n)	background frequency = number of genes associated with process (B)/total number of genes in organism (N)	Enrichment (sample frequency/background frequency)
DNA geometric change	7.68E-04	MCM4 - minichromosome maintenance complex component	7/62	12/528	4.97
		MCM6 - minichromosome maintenance complex component 6			
		MCM5 - minichromosome maintenance complex component 5			
		MCM2 - minichromosome maintenance complex component 2			
		CDC45 - cell division cycle 45			
		GINS2 - gins complex subunit 2 (psf2 homolog)			
		GINS4 - gins complex subunit 4 (sld5 homolog)			
		MCM4 - minichromosome maintenance complex component	7/62	11/528	5.42
DNA duplex unwinding	3.23E-04	MCM6 - minichromosome maintenance complex component 6			
		MCM5 - minichromosome maintenance complex component 5			
		MCM2 - minichromosome maintenance complex component 2			
		CDC45 - cell division cycle 45			
		GINS2 - gins complex subunit 2 (psf2 homolog)			
		GINS4 - gins complex subunit 4 (sld5 homolog)			

Appendix G7. Cellular process (G1-S transition) enriched in DEGs between 0 ppb and 1000 ppb of metolachlor exposed human liver cells for 48 hours.

Cellular process	P-value	Genes involved in cell cycle G1/S phase transition	sample frequency = number of genes in interesection(b)/number of genes in sample set (n)	background frequency = number of genes associated with process (B)/total number of genes in organism (N)	Enrichment (sample frequency/background frequency)
cell cycle G1/S phase transition	1.01E-04	CDC6 - cell division cycle 6	29/356	29/528	1.48
		CDC25A - cell division cycle 25a			
		MCM7 - minichromosome maintenance complex component 7			
		CCNE2 - cyclin e2			
		ORC1 - origin recognition complex, subunit 1			
		CCNE1 - cyclin e1			
		CDT1 - chromatin licensing and dna replication factor 1			
		PRIM2 - primase, dna, polypeptide 2 (58kda)			
		PRIM1 - primase, dna, polypeptide 1 (49kda)			
		MCM10 - minichromosome maintenance complex component 10			
		POLE3 - polymerase (dna directed), epsilon 3, accessory subunit			
		CDC45 - cell division cycle 45			
		RPA3 - replication protein a3, 14kda			
		RPA1 - replication protein a1, 70kda			
		CDC7 - cell division cycle 7			
		RPA2 - replication protein a2, 32kda			
		SKP2 - s-phase kinase-associated protein 2, e3 ubiquitin protein ligase			
		POLA2 - polymerase (dna directed), alpha 2, accessory subunit			
		CDKN3 - cyclin-dependent kinase inhibitor 3			
		MCM4 - minichromosome maintenance complex component 4			
		MCM3 - minichromosome maintenance complex component 3			
		MCM6 - minichromosome maintenance complex component 6			
		POLE2 - polymerase (dna directed), epsilon 2, accessory subunit			
		ORC6 - origin recognition complex, subunit 6			
		CCNA2 - cyclin a2			
		MCM5 - minichromosome maintenance complex component 5			
		MCM2 - minichromosome maintenance complex component 2			
		POLA1 - polymerase (dna directed), alpha 1, catalytic subunit			
		CDK2 - cyclin-dependent kinase 2			
G1/S transition of mitotic cell cycle	1.49E-04	CDC6 - cell division cycle 6	28/356	28/528	1.48
		CDC25A - cell division cycle 25a			
		MCM7 - minichromosome maintenance complex component 7			
		CCNE2 - cyclin e2			
		ORC1 - origin recognition complex, subunit 1			
		CCNE1 - cyclin e1			
		CDT1 - chromatin licensing and dna replication factor 1			
		PRIM2 - primase, dna, polypeptide 2 (58kda)			
		PRIM1 - primase, dna, polypeptide 1 (49kda)			
		MCM10 - minichromosome maintenance complex component 10			
		POLE3 - polymerase (dna directed), epsilon 3, accessory subunit			
		CDC45 - cell division cycle 45			
		RPA3 - replication protein a3, 14kda			
		RPA1 - replication protein a1, 70kda			
		CDC7 - cell division cycle 7			
		RPA2 - replication protein a2, 32kda			
		SKP2 - s-phase kinase-associated protein 2, e3 ubiquitin protein ligase			
		POLA2 - polymerase (dna directed), alpha 2, accessory subunit			
		CDKN3 - cyclin-dependent kinase inhibitor 3			
		MCM4 - minichromosome maintenance complex component 4			
		MCM3 - minichromosome maintenance complex component 3			
		MCM6 - minichromosome maintenance complex component 6			
		POLE2 - polymerase (dna directed), epsilon 2, accessory subunit			
		MCM5 - minichromosome maintenance complex component 5			
		ORC6 - origin recognition complex, subunit 6			
		MCM2 - minichromosome maintenance complex component 2			
		POLA1 - polymerase (dna directed), alpha 1, catalytic subunit			
		CDK2 - cyclin-dependent kinase 2			

Appendix G8. Cellular process (cellular response to stimulus) enriched in DEGs between 0 ppb and 1000 ppb of metolachlor exposed human liver cells for 48 hours.

Cellular process	P-value	Genes involved in cell response to stimulus	sample frequency = number of genes in interesection(b)/number of genes in sample set (n)	background frequency = number of genes associated with process (B)/total number of genes in organism (N)	Enrichment (sample frequency/background frequency)
cellular response to stimulus	2.81E-04	RFC4 - replication factor c (activator 1) 4, 37kda	74/207	134/528	1.41
		VAV3 - vav 3 guanine nucleotide exchange factor			
		RFC5 - replication factor c (activator 1) 5, 36.5kda			
		RFC3 - replication factor c (activator 1) 3, 38kda			
		BRCA1 - breast cancer 1, early onset			
		DTL - denticleless e3 ubiquitin protein ligase homolog (drosophila)			
		CDC25C - cell division cycle 25c			
		UHRF1 - ubiquitin-like with phd and ring finger domains 1			
		LIG1 - ligase i, dna, atp-dependent			
		CHAF1B - chromatin assembly factor 1, subunit b (p60)			
		SFN - stratifin			
		FANCD2 - fanconi anemia, complementation group d2			
		SUV39H1 - suppressor of variegation 3-9 homolog 1 (drosophila)			
		FANCG - fanconi anemia, complementation group g			
		UNG - uracil-dna glycosylase			
		RPA3 - replication protein a3, 14kda			
		NUDT1 - nudix (nucleoside diphosphate linked moiety x)-type motif 1			
		RPA1 - replication protein a1, 70kda			
		CDCA5 - cell division cycle associated 5			
		CHEK1 - checkpoint kinase 1			
		SLX4 - slx4 structure-specific endonuclease subunit			
		BLM - bloom syndrome, recq helicase-like			
		CHAF1A - chromatin assembly factor 1, subunit a (p150)			
		MASTL - microtubule associated serine/threonine kinase-like			
		CHEK2 - checkpoint kinase 2			
		ANKRD32 - ankyrin repeat domain 32			
		RAD51AP1 - rad51 associated protein 1			
		PTTG1 - pituitary tumor-transforming 1			
		FANCI - fanconi anemia, complementation group i			
		APITD1 - apoptosis-inducing, taf9-like domain 1			
		CRIP1 - cysteine-rich protein 1 (intestinal)			
		BARD1 - brca1 associated ring domain 1			
		RNASEH2A - ribonuclease h2, subunit a			
		RAD54L - rad54-like (s. cerevisiae)			
		CETN2 - centrin, ef-hand protein, 2			
		MCM10 - minichromosome maintenance complex component 10			
		KIAA0101 - kiaa0101			
		TIPIN - timeless interacting protein			
		NEIL3 - nei endonuclease viii-like 3 (e. coli)			
		FEN1 - flap structure-specific endonuclease 1			
		CDC45 - cell division cycle 45			
		TICRR - topbp1-interacting checkpoint and replication regulator			
		CDC7 - cell division cycle 7			
		GINS2 - gins complex subunit 2 (psf2 homolog)			
		PCNA - proliferating cell nuclear antigen			
		TRIP13 - thyroid hormone receptor interactor 13			
		E2F7 - e2f transcription factor 7			
		UBE2T - ubiquitin-conjugating enzyme e2t (putative)			
		TIMELESS - timeless circadian clock			
		GINS4 - gins complex subunit 4 (sld5 homolog)			
		POLQ - polymerase (dna directed), theta			
		POLE2 - polymerase (dna directed), epsilon 2, accessory subunit			
		CCNB1 - cyclin b1			
		XRCC3 - x-ray repair complementing defective repair in chinese hamster cells 3			
		POLD1 - polymerase (dna directed), delta 1, catalytic subunit			
		POLA1 - polymerase (dna directed), alpha 1, catalytic subunit			
		HMOX1 - heme oxygenase (decycling) 1			
		EME1 - essential meiotic structure-specific endonuclease 1			
		CDK2 - cyclin-dependent kinase 2			
		EXO1 - exonuclease 1			

Appendix G9. Cellular process (cellular response to stress) enriched in DEGs between 0 ppb and 1000 ppb of metolachlor exposed human liver cells for 48 hours.

Cellular process	P-value	Genes involved in cellular response to stress	sample frequency = number of genes in interesection(b)/number of genes in sample set (n)	background frequency = number of genes associated with process (B)/total number of genes in organism (N)	Enrichment (sample frequency/background frequency)
cellular response to stress	9.85E-04	RFC4 - replication factor c (activator 1) 4, 37kda	56/197	102/528	1.47
		RFC5 - replication factor c (activator 1) 5, 36.5kda			
		RFC3 - replication factor c (activator 1) 3, 38kda			
		BRCA1 - breast cancer 1, early onset			
		UHRF1 - ubiquitin-like with phd and ring finger domains 1			
		DTL - denticleless e3 ubiquitin protein ligase homolog (drosophila)			
		LIG1 - ligase i, dna, atp-dependent			
		CHAF1B - chromatin assembly factor 1, subunit b (p60)			
		SFN - stratifin			
		FANCD2 - fanconi anemia, complementation group d2			
		SUV39H1 - suppressor of variegation 3-9 homolog 1 (drosophila)			
		FANCG - fanconi anemia, complementation group g			
		UNG - uracil-dna glycosylase			
		RPA3 - replication protein a3, 14kda			
		CDCA5 - cell division cycle associated 5			
		CHEK1 - checkpoint kinase 1			
		CD36 - cd36 molecule (thrombospondin receptor)			
		BLM - bloom syndrome, recq helicase-like			
		CHAF1A - chromatin assembly factor 1, subunit a (p150)			
		CHEK2 - checkpoint kinase 2			
		ANKRD32 - ankyrin repeat domain 32			
		RAD51AP1 - rad51 associated protein 1			
		FANCI - fanconi anemia, complementation group i			
		APITD1 - apoptosis-inducing, taf9-like domain 1			
		CRIP1 - cysteine-rich protein 1 (intestinal)			
		BARD1 - brca1 associated ring domain 1			
		RNASEH2A - ribonuclease h2, subunit a			
		GPX3 - glutathione peroxidase 3 (plasma)			
		RAD54L - rad54-like (s. cerevisiae)			
		MCM10 - minichromosome maintenance complex component 10			
		KIAA0101 - kiaa0101			
		ARG1 - arginase 1			
		TIPIN - timeless interacting protein			
		NEIL3 - nei endonuclease viii-like 3 (e. coli)			
		CDC45 - cell division cycle 45			
		FEN1 - flap structure-specific endonuclease 1			
		TICRR - topbp1-interacting checkpoint and replication regulator			
		CDC7 - cell division cycle 7			
		GINS2 - gins complex subunit 2 (psf2 homolog)			
		PCNA - proliferating cell nuclear antigen			
		E2F7 - e2f transcription factor 7			
		TRIP13 - thyroid hormone receptor interactor 13			
		UBE2T - ubiquitin-conjugating enzyme e2t (putative)			
		CAT - catalase			
		DNMT3B - dna (cytosine-5-)-methyltransferase 3 beta			
		UCP2 - uncoupling protein 2 (mitochondrial, proton carrier)			
		GINS4 - gins complex subunit 4 (sld5 homolog)			
		EPO - erythropoietin			
		POLQ - polymerase (dna directed), theta			
		POLE2 - polymerase (dna directed), epsilon 2, accessory subunit			
		CCNA2 - cyclin a2			
		CCNB1 - cyclin b1			
		POLD1 - polymerase (dna directed), delta 1, catalytic subunit			
		POLA1 - polymerase (dna directed), alpha 1, catalytic subunit			
		HMOX1 - heme oxygenase (decycling) 1			
		EXO1 - exonuclease 1			

Appendix G10. Cellular process (cellular response to radiation) enriched in DEGs between 0 ppb and 1000 ppb of metolachlor exposed human liver cells for 48 hours.

Cellular process	P-value	Genes involved in cellular response to radiation	sample frequency = number of genes in interesection(b)/number of genes in sample set (n)	background frequency = number of genes associated with process (B)/total number of genes in organism (N)	Enrichment (sample frequency/background frequency)
response to radiation	1.67E-04	CRIP1 - cysteine-rich protein 1 (intestinal)	21/197	27/528	2.08
		CHEK1 - checkpoint kinase 1			
		PCNA - proliferating cell nuclear antigen			
		FIGNL1 - fidgetin-like 1			
		CAT - catalase			
		RAD54L - rad54-like (s. cerevisiae)			
		BLM - bloom syndrome, recq helicase-like			
		BRCA1 - breast cancer 1, early onset			
		DNMT3B - dna (cytosine-5-)-methyltransferase 3 beta			
		DTL - denticleless e3 ubiquitin protein ligase homolog (drosophila)			
		CHEK2 - checkpoint kinase 2			
		HAMP - hepcidin antimicrobial peptide			
		PBK - pdz binding kinase			
		FANCD2 - fanconi anemia, complementation group d2			
		KIAA0101 - kiaa0101			
		POLD1 - polymerase (dna directed), delta 1, catalytic subunit			
		TIPIN - timeless interacting protein			
		FANCG - fanconi anemia, complementation group g			
		FEN1 - flap structure-specific endonuclease 1			
		RAD51AP1 - rad51 associated protein 1			
		TICRR - topbp1-interacting checkpoint and replication regulator			

Appendix H. Cellular functions (DNA helicase and catalytic activity on DNA) enriched in DEGs between 0 ppb and 1000 ppb of metolachlor exposed human liver cells for 48 hours.

Cellular function	P-value	Genes involved in DNA helicase activity and catalytic activity on DNA	sample frequency = number of genes in interesection(b)/number of genes in sample set (n)	background frequency = number of genes associated with process (B)/total number of genes in organism (N)	Enrichment (sample frequency/background frequency)
DNA helicase activity	1.24E-04	MCM4 - minichromosome maintenance complex component 4	7/62	10/528	5.96
		MCM6 - minichromosome maintenance complex component 6			
		MCM5 - minichromosome maintenance complex component 5			
		MCM2 - minichromosome maintenance complex component 2			
		CDC45 - cell division cycle 45			
		GINS2 - gins complex subunit 2 (psf2 homolog)			
		GINS4 - gins complex subunit 4 (sld5 homolog)			
helicase activity	3.24E-04	HELLS - helicase, lymphoid-specific	10/97	15/528	3.63
		MCM4 - minichromosome maintenance complex component 4			
		MCM3 - minichromosome maintenance complex component 3			
		MCM6 - minichromosome maintenance complex component 6			
		MCM5 - minichromosome maintenance complex component 5			
		ERCC6L - excision repair cross-complementing rodent repair deficiency, complementation group 6-like			
		MCM2 - minichromosome maintenance complex component 2			
		CDC45 - cell division cycle 45			
		GINS2 - gins complex subunit 2 (psf2 homolog)			
		GINS4 - gins complex subunit 4 (sld5 homolog)			
catalytic activity, acting on DNA	5.17E-04	POLA2 - polymerase (dna directed), alpha 2, accessory subunit	16/96	33/528	2.67
		PCNA - proliferating cell nuclear antigen			
		DNMT3B - dna (cytosine-5-)-methyltransferase 3 beta			
		LIG1 - ligase i, dna, atp-dependent			
		GINS4 - gins complex subunit 4 (sld5 homolog)			
		MCM4 - minichromosome maintenance complex component 4			
		POLE2 - polymerase (dna directed), epsilon 2, accessory subunit			
		MCM6 - minichromosome maintenance complex component 6			
		MCM5 - minichromosome maintenance complex component 5			
		MCM2 - minichromosome maintenance complex component 2			
		POLA1 - polymerase (dna directed), alpha 1, catalytic subunit			
		NEIL3 - nei endonuclease viii-like 3 (e. coli)			
		CDC45 - cell division cycle 45			
		UNG - uracil-dna glycosylase			
		GINS2 - gins complex subunit 2 (psf2 homolog)			
		EXO1 - exonuclease 1			

Appendix I. Gene annotated list of down-regulated genes (DEGs) when exposed to 1000 ppb of metolachlor exposed human liver cells for 24 hours compared to control.

PROBE_ID	SYMBOL	logFC	AveExpr	t	P.Value	adj.P.Val	B
ILMN_2124802	MT1H	-3.30686	7.376004	-3.94064	0.00027	0.024608	0.355485
ILMN_1729851	ODAM	-3.30651	9.537576	-5.00088	8.52E-06	0.003335	3.507496
ILMN_1655904	ROR1	-3.07058	6.856954	-5.91482	3.71E-07	0.00068	6.374454
ILMN_1770084	TACC1	-3.06064	8.010976	-6.31047	9.37E-08	0.000322	7.631076
ILMN_1685043	CYP3A7	-3.04186	6.574159	-5.17068	4.79E-06	0.002374	4.033446
ILMN_2223941	FBLN5	-3.03017	6.155538	-5.95109	3.27E-07	0.00068	6.489472
ILMN_1714446	PLG	-2.8971	5.585992	-4.63009	2.94E-05	0.006818	2.37552
ILMN_1813270	ELF5	-2.84725	6.563434	-4.95794	9.84E-06	0.003483	3.375162
ILMN_2289593	FXYD2	-2.84195	7.489644	-4.22131	0.000111	0.014627	1.161974
ILMN_3243616	LOC100127888	-2.76195	6.122736	-5.84006	4.81E-07	0.000711	6.137499
ILMN_1683263	TSPAN8	-2.74301	7.092307	-5.9201	3.64E-07	0.00068	6.391173
ILMN_1656934	REPS2	-2.55504	5.245625	-7.08595	6.29E-09	4.32E-05	10.08944
ILMN_1717381	HOXD1	-2.48926	9.325079	-5.37144	2.42E-06	0.001579	4.660135
ILMN_2398572	FXYD2	-2.47561	6.721467	-4.51536	4.29E-05	0.008237	2.030843
ILMN_1656057	PLAU	-2.43399	5.888404	-5.09649	6.16E-06	0.002823	3.803136
ILMN_1762696	FAM181A	-2.43156	5.78064	-5.05106	7.19E-06	0.003039	3.662482
ILMN_1706483	C1orf116	-2.41398	5.758243	-5.45141	1.84E-06	0.001358	4.910984
ILMN_2073446	C1orf116	-2.4136	5.063088	-7.45606	1.74E-09	0.000024	11.25208
ILMN_1780831	SLC6A12	-2.38285	8.565447	-4.26783	9.58E-05	0.013857	1.297914
ILMN_1681087	SLC7A10	-2.3743	5.206322	-6.40904	6.65E-08	0.000261	7.944399
ILMN_2052373	RAB17	-2.33516	10.631	-5.04138	7.43E-06	0.003047	3.632574
ILMN_1738414	G6PC	-2.27862	6.146442	-4.24303	0.000104	0.014116	1.225344
ILMN_1763196	WDR72	-2.27306	5.96048	-6.17432	1.51E-07	0.000414	7.198353
ILMN_1695254	FLJ46109	-2.26248	5.146751	-5.73621	6.89E-07	0.000761	5.808799
ILMN_2134801	AGXT2L1	-2.25226	6.820409	-4.59205	3.33E-05	0.007208	2.260934
ILMN_1664176	FBLN5	-2.23724	5.609963	-4.64615	2.79E-05	0.006658	2.424011
ILMN_1723358	SCARA3	-2.21097	6.198251	-4.3685	6.92E-05	0.011121	1.594108
ILMN_1810942	CYP3A5	-2.18514	5.998346	-4.29276	8.84E-05	0.013134	1.370988
ILMN_2321150	GSTTP2	-2.15258	4.962343	-5.95592	3.22E-07	0.00068	6.504791
ILMN_1652787	PIK3AP1	-2.14018	6.912868	-5.36155	2.5E-06	0.001579	4.62916
ILMN_1795484	PGC	-2.10398	11.83672	-4.26242	9.75E-05	0.013881	1.282063
ILMN_1791123	TMPRSS2	-2.09378	5.595455	-6.06214	2.22E-07	0.000556	6.841982
ILMN_2079890	G6PC	-2.05766	6.589899	-3.82574	0.000386	0.030551	0.032715
ILMN_1781745	C9orf152	-2.05167	6.022883	-5.03352	7.63E-06	0.003083	3.608263

ILMN_1805003	UGT2B4	-2.04696	5.811862	-3.92132	0.000287	0.025321	0.300894
ILMN_1766966	ACSM5	-2.04252	6.667234	-4.57352	3.54E-05	0.007324	2.205195
ILMN_1781045	FXYD2	-2.04164	6.621921	-4.43297	5.61E-05	0.010014	1.785165
ILMN_1781966	OSBP2	-1.99938	6.451602	-4.76738	1.86E-05	0.00502	2.791678
ILMN_1657235	LOC342979	-1.97953	5.419417	-5.16788	4.84E-06	0.002374	4.02474
ILMN_1752755	VWF	-1.95692	4.967932	-6.57098	3.78E-08	0.000173	8.458868
ILMN_2366654	NR5A2	-1.94402	7.563189	-5.19398	4.43E-06	0.002296	4.105931
ILMN_1799139	PLOD2	-1.92397	6.169854	-4.17636	0.000128	0.016215	1.031191
ILMN_3236858	NYNRIN	-1.91969	5.923235	-4.03276	0.000203	0.021166	0.617444
ILMN_1706813	SLC6A14	-1.89722	6.608764	-4.13902	0.000145	0.017235	0.923001
ILMN_1670807	FAM84B	-1.86513	6.597241	-5.49595	1.58E-06	0.001237	5.050959
ILMN_1789003	CPB2	-1.84866	8.025717	-4.00162	0.000223	0.022572	0.528574
ILMN_1657750	CNNM1	-1.81882	6.919607	-4.09836	0.000165	0.018391	0.805664
ILMN_1757807	AGXT2L1	-1.81774	7.166376	-3.58206	0.000811	0.045742	-0.6357
ILMN_1686291	DIO1	-1.79663	6.207823	-3.88499	0.000322	0.027531	0.198594
ILMN_1807291	CYP1A1	-1.76745	5.617474	-5.39014	2.27E-06	0.001519	4.718758
ILMN_1803673	LOC113230	-1.75457	5.862107	-5.21315	4.15E-06	0.002192	4.165623
ILMN_1812281	ARG1	-1.74776	6.173375	-3.96947	0.000247	0.023821	0.437167
ILMN_2070792	ACSM5	-1.74695	5.710034	-5.31094	2.97E-06	0.001645	4.470783
ILMN_1662932	LCP1	-1.74321	6.841837	-5.31032	2.98E-06	0.001645	4.468871
ILMN_1727200	SLCO4A1	-1.73974	7.430479	-4.38766	0.000065	0.01076	1.650768
ILMN_2193443	TRIM16L	-1.73138	5.524432	-4.95661	9.89E-06	0.003483	3.371059
ILMN_1811303	NR5A2	-1.72917	7.303482	-4.9567	9.88E-06	0.003483	3.371348
ILMN_2234187	CDO1	-1.72664	7.540783	-4.83194	0.000015	0.004486	2.988633
ILMN_2302757	FCGBP	-1.72138	10.0888	-5.17882	4.66E-06	0.002372	4.058772
ILMN_1718984	FCGBP	-1.71902	7.152559	-4.7265	2.13E-05	0.005534	2.667365
ILMN_1680507	PPP2R2C	-1.7145	6.153622	-4.96866	9.49E-06	0.003483	3.408187
ILMN_1771599	PLOD2	-1.68337	11.74409	-4.3464	7.43E-05	0.011608	1.528842
ILMN_1653042	HSD3B7	-1.64057	7.033363	-3.81141	0.000404	0.030951	-0.00719
ILMN_1788078	ACOT7	-1.6347	5.233017	-5.87815	4.21E-07	0.000711	6.258188
ILMN_1698725	FRMD3	-1.6318	7.21656	-4.57461	3.53E-05	0.007324	2.208489
ILMN_1700408	TRIM50	-1.63145	7.199426	-3.86384	0.000343	0.028553	0.139241
ILMN_2400644	SRGAP3	-1.62741	5.25564	-5.11606	5.77E-06	0.002687	3.863836
ILMN_2048478	SLC22A3	-1.62393	6.438923	-3.94611	0.000266	0.02441	0.37096
ILMN_1692535	DPP4	-1.61826	8.960929	-3.96192	0.000253	0.023821	0.415746
ILMN_2095653	AFMID	-1.61334	8.301004	-4.63745	2.87E-05	0.006793	2.397743
ILMN_1693932	LOC285733	-1.60475	10.09173	-4.79955	1.67E-05	0.004791	2.889711
ILMN_3242535	LOC100133568	-1.60417	5.676656	-5.31917	2.89E-06	0.001645	4.496531
ILMN_2372974	SIRPA	-1.59594	5.561848	-4.78974	1.73E-05	0.0048	2.859788

ILMN_1752269	ACSS1	-1.5908	8.904596	-4.28927	8.94E-05	0.01321	1.360769
ILMN_1821176		-1.57385	5.620907	-5.78498	5.82E-07	0.000761	5.963087
ILMN_1754921	FAM43B	-1.57175	7.352336	-4.30582	8.48E-05	0.012729	1.409368
ILMN_1803211	FBXO2	-1.57013	9.830126	-4.05737	0.000187	0.020279	0.68792
ILMN_2328776	MST4	-1.57005	9.082195	-4.41147	6.02E-05	0.010273	1.721322
ILMN_1748123	KLHL14	-1.5679	9.008968	-4.23748	0.000106	0.014228	1.209153
ILMN_1771261	SYNC1	-1.56563	6.822948	-4.41512	5.95E-05	0.010232	1.732156
ILMN_2384056	GPER	-1.56238	10.91006	-4.15263	0.000139	0.016866	0.962379
ILMN_2401344	PPP2R2C	-1.5621	7.565461	-4.69669	2.36E-05	0.005888	2.576934
ILMN_1812091	FAM20A	-1.5585	5.321569	-4.67533	2.53E-05	0.006207	2.51223
ILMN_1745021	SLC30A1	-1.55818	8.703737	-5.71533	7.4E-07	0.000763	5.742763
ILMN_1795298	GPER	-1.55576	10.48594	-5.65482	9.12E-07	0.000895	5.551604
ILMN_1795715	DPYD	-1.55364	5.862613	-4.07168	0.000179	0.019692	0.728961
ILMN_1764629	SLC39A14	-1.5527	11.70089	-5.75526	6.45E-07	0.000761	5.869028
ILMN_1815203	HMGCS2	-1.54441	5.557179	-3.7115	0.000548	0.037505	-0.28347
ILMN_2168564	KLHL14	-1.5344	7.422929	-4.04859	0.000193	0.020525	0.662756
ILMN_2162972	LYZ	-1.52776	10.2693	-4.99739	8.62E-06	0.003335	3.49674
ILMN_2410924	PLOD2	-1.51964	9.567461	-3.62726	0.000708	0.042644	-0.51345
ILMN_1690420	GFI1	-1.51809	8.013391	-4.8617	1.36E-05	0.004151	3.079677
ILMN_1736704	DIXDC1	-1.51351	6.493253	-3.66834	0.000625	0.04001	-0.40164
ILMN_2207988	SERPINI1	-1.51332	6.72203	-3.5933	0.000784	0.044867	-0.60536
ILMN_1760513	DYDC2	-1.50252	6.104008	-5.51623	1.47E-06	0.001213	5.11476
ILMN_3285785	LOC647307	-1.50107	11.15669	-4.32266	8.03E-05	0.012188	1.458905
ILMN_1703228	AGFG2	-1.49685	8.693002	-4.37782	6.71E-05	0.010918	1.621643
ILMN_1758146	SIRPA	-1.49666	8.276759	-4.46632	5.03E-05	0.009282	1.884426
ILMN_1701514	TRAF3IP2	-1.48837	8.273486	-4.41584	5.93E-05	0.010232	1.734308
ILMN_3289297	LOC100131277	-1.48286	4.683255	-8.98685	9.57E-12	2.63E-07	15.91612
ILMN_1781819	PAPSS1	-1.47903	10.51502	-4.66702	0.000026	0.006324	2.487101
ILMN_3249216	PDX1	-1.47719	4.841148	-6.21821	1.29E-07	0.000395	7.337828
ILMN_2375830	DIXDC1	-1.4736	6.392914	-4.01111	0.000217	0.022153	0.555629
ILMN_1799243	ANXA13	-1.46663	4.857455	-5.81876	5.18E-07	0.000711	6.070011
ILMN_2383163	DEPDC7	-1.46532	7.139951	-3.88137	0.000325	0.027584	0.188406
ILMN_1810844	RARRES2	-1.46305	9.412735	-3.79351	0.000427	0.032161	-0.05698
ILMN_1809291	TSPAN7	-1.45369	6.342504	-3.77007	0.000458	0.033257	-0.12195
ILMN_2214197	TP53INP1	-1.45002	8.294572	-3.77716	0.000449	0.032948	-0.10231
ILMN_3242315	SNORD3D	-1.44287	6.139866	-3.60722	0.000752	0.044229	-0.56775
ILMN_2277252	PPFIBP1	-1.4392	5.419289	-5.85784	4.52E-07	0.000711	6.193826
ILMN_1772446	C12orf34	-1.41874	7.129523	-3.57941	0.000817	0.045875	-0.64282
ILMN_2270299	TP53BP2	-1.41463	5.854983	-4.35672	7.19E-05	0.011421	1.559313

ILMN_1809890	IKBKAP	-1.41414	6.644846	-4.55037	3.82E-05	0.007721	2.135693
ILMN_1726114	SLC45A3	-1.40821	6.99644	-4.16502	0.000133	0.016431	0.998288
ILMN_1741159	MAP3K8	-1.40745	6.414632	-4.10096	0.000163	0.018391	0.81316
ILMN_1663092	CITED2	-1.40287	8.666946	-4.38413	6.58E-05	0.01076	1.640337
ILMN_1744806	CPB2	-1.39842	11.33722	-3.9371	0.000273	0.024718	0.345469
ILMN_2409078	SNHG10	-1.39688	6.326005	-4.86956	1.32E-05	0.004089	3.10375
ILMN_1680132	CADM1	-1.39477	10.25279	-4.41463	5.96E-05	0.010232	1.730703
ILMN_2302716	ALDH18A1	-1.39125	10.37277	-4.80868	1.62E-05	0.004696	2.917576
ILMN_1799614	PNPLA6	-1.38623	8.270318	-3.97869	0.00024	0.023479	0.463343
ILMN_1731064	CABC1	-1.37397	9.96006	-5.2397	3.79E-06	0.002042	4.248375
ILMN_1711408	ANXA4	-1.36953	8.760868	-3.57771	0.000821	0.045961	-0.64741
ILMN_1811632	FMO5	-1.35832	9.765579	-4.62876	2.95E-05	0.006818	2.371523
ILMN_1704369	LIMA1	-1.35695	8.191469	-3.95963	0.000255	0.023821	0.409257
ILMN_2391436	CPB2	-1.35393	10.53295	-3.77864	0.000447	0.032948	-0.09823
ILMN_2224103	PAPSS1	-1.35257	9.194431	-3.68745	0.00059	0.039057	-0.34941
ILMN_3252446	LOC100129543	-1.34144	7.121345	-4.17236	0.00013	0.016251	1.019572
ILMN_1682763	ALB	-1.34074	14.17602	-7.32168	2.78E-09	2.54E-05	10.8311
ILMN_2083946	TGFA	-1.33574	7.990298	-4.57016	3.58E-05	0.007337	2.195121
ILMN_2067852	SLC30A1	-1.32861	8.453924	-5.74428	6.7E-07	0.000761	5.834319
ILMN_1651705	CAT	-1.32021	10.46626	-3.56722	0.000847	0.046488	-0.67564
ILMN_2167416	MR1	-1.31443	6.694614	-4.1125	0.000157	0.01814	0.846432
ILMN_1702835	SH3BGRL	-1.31214	8.004262	-3.62226	0.000718	0.042843	-0.52701
ILMN_2148913	TMEM45A	-1.30755	8.205428	-4.14774	0.000141	0.017036	0.948221
ILMN_1745079	TRIM2	-1.30615	5.68515	-4.25866	9.87E-05	0.013906	1.271058
ILMN_1730977	SLC44A4	-1.29979	7.688902	-3.5636	0.000857	0.046893	-0.68539
ILMN_2378670	SNX15	-1.29108	6.911592	-4.60274	3.22E-05	0.00707	2.293111
ILMN_1769299	MTMR11	-1.28782	5.706991	-3.84252	0.000367	0.029999	0.079567
ILMN_1718770	FLJ36070	-1.28699	7.430948	-3.87323	0.000334	0.028116	0.165557
ILMN_1691048	SLC22A18AS	-1.28412	6.110913	-5.06516	6.85E-06	0.002956	3.706104
ILMN_1714522	CLMN	-1.28412	5.995919	-4.09941	0.000164	0.018391	0.808694
ILMN_1688089	PEBP1	-1.28314	12.49827	-4.5155	4.28E-05	0.008237	2.031245
ILMN_1730291	ATP1B1	-1.27845	10.29524	-4.88316	1.27E-05	0.004043	3.145429
ILMN_1796229	FGFR1	-1.27365	4.95166	-5.07168	6.7E-06	0.002956	3.726291
ILMN_1811758	CNP	-1.27218	5.136877	-4.60419	0.000032	0.00707	2.29747
ILMN_1805175	TGFA	-1.2661	7.432344	-4.61573	3.08E-05	0.006976	2.332242
ILMN_2174711	C21orf129	-1.25362	5.414589	-3.61817	0.000727	0.043258	-0.53809
ILMN_1717295	C6orf122	-1.25068	5.204	-5.11679	5.75E-06	0.002687	3.866101
ILMN_2082699	C8ORFK36	-1.24402	5.734667	-5.13315	5.44E-06	0.002625	3.916852
ILMN_1665092	LOC647718	-1.23702	4.921573	-5.4182	2.06E-06	0.001451	4.806753

ILMN_1749368	HIST1H3H	-1.23566	5.388403	-3.78196	0.000442	0.032739	-0.089
ILMN_3294024	LOC644990	-1.23176	5.953207	-4.45308	5.26E-05	0.009588	1.844982
ILMN_1795285	PHF15	-1.229	6.780137	-4.53126	4.07E-05	0.00793	2.078435
ILMN_1707872	RUFY2	-1.22514	5.869588	-4.16132	0.000135	0.016533	0.987577
ILMN_2092933	ADAMTS4	-1.22461	4.849561	-5.52984	1.4E-06	0.001213	5.157607
ILMN_2095597	CDH16	-1.22374	5.336534	-3.88676	0.00032	0.027465	0.203558
ILMN_3237516	SNRNP48	-1.2208	4.912968	-6.76683	1.91E-08	0.000105	9.080297
ILMN_1779882	ANKRD43	-1.2208	5.336694	-4.35883	7.14E-05	0.011409	1.565538
ILMN_3229227	LOC729629	-1.21896	4.841099	-4.82502	1.54E-05	0.004542	2.967494
ILMN_1744614	PLEKHG6	-1.20931	7.21697	-3.80981	0.000406	0.030972	-0.01165
ILMN_3240773	LOC100129445	-1.20574	5.255914	-4.99177	8.78E-06	0.003352	3.479388
ILMN_1738989	GOLSYN	-1.20573	7.42099	-3.96649	0.000249	0.023821	0.428707
ILMN_1807756	LOC651659	-1.20463	6.309761	-4.11048	0.000158	0.01814	0.840602
ILMN_1782704	CD19	-1.2034	5.534783	-4.87404	0.000013	0.004074	3.117483
ILMN_2324776	TAS1R1	-1.19447	5.37287	-4.03076	0.000204	0.021219	0.611738
ILMN_1692177	TSC22D1	-1.19083	5.958172	-3.66885	0.000624	0.04001	-0.40025
ILMN_1668910	CIDEB	-1.18712	9.686286	-3.78273	0.000441	0.032739	-0.08687
ILMN_1911484		-1.17449	6.300269	-3.54379	0.000909	0.048683	-0.73853
ILMN_1724941	CDCP1	-1.17432	5.6012	-4.01607	0.000213	0.022056	0.569797
ILMN_3244700	COX16	-1.17149	5.773971	-3.9626	0.000252	0.023821	0.417678
ILMN_1808584	FAM36A	-1.16717	8.703192	-5.7347	6.92E-07	0.000761	5.804003
ILMN_3244405	LOC100134172	-1.16438	5.728021	-4.08491	0.000172	0.01896	0.766991
ILMN_1843585		-1.16039	8.166366	-3.97994	0.000239	0.023471	0.466891
ILMN_1695135	GCM1	-1.15088	5.340239	-4.49243	4.62E-05	0.008698	1.962304
ILMN_1740466	FAM46A	-1.14726	9.615414	-4.42345	5.79E-05	0.010202	1.756882
ILMN_1658071	ATP1B1	-1.14698	10.67048	-4.70189	2.32E-05	0.00584	2.592701
ILMN_2412490	ANXA13	-1.14386	4.959173	-4.58889	3.37E-05	0.007227	2.251414
ILMN_3199483	LOC100131064	-1.1361	4.917275	-5.559	1.27E-06	0.001203	5.249432
ILMN_1802557	HEBP1	-1.13232	10.7471	-4.53186	4.06E-05	0.00793	2.080235
ILMN_1713846	PPM1H	-1.12526	9.779643	-4.20225	0.000118	0.015245	1.106428
ILMN_2045324	CCL16	-1.12523	9.393336	-3.68345	0.000597	0.03922	-0.36035
ILMN_1810560	P8	-1.11773	7.149642	-3.87429	0.000332	0.02811	0.168534
ILMN_2276688	DIXDC1	-1.11591	5.139691	-3.81313	0.000402	0.030951	-0.0024
ILMN_2219681	RBP2	-1.10197	5.317106	-4.20979	0.000115	0.014963	1.128377
ILMN_1798975	EGFR	-1.10003	7.488889	-4.00827	0.000219	0.022269	0.547542
ILMN_1699323	LOC650406	-1.09928	5.23629	-4.48412	4.75E-05	0.008817	1.937484
ILMN_1675640	OAS1	-1.09791	5.436602	-3.88354	0.000323	0.027569	0.194512
ILMN_1814305	SAMD9	-1.09292	4.938382	-4.88802	1.24E-05	0.004024	3.160323
ILMN_1708391	NR1H4	-1.0895	10.46943	-4.18988	0.000123	0.015651	1.070473

ILMN_1691747	KHDRBS3	-1.08903	9.766236	-4.23492	0.000106	0.014276	1.201666
ILMN_1725233	LOC645118	-1.08268	5.724897	-3.57035	0.000839	0.046475	-0.66722
ILMN_2288740	ZNF266	-1.08209	5.005014	-4.39513	6.35E-05	0.010712	1.672884
ILMN_1680339	PDGFRL	-1.07786	6.865025	-3.54903	0.000895	0.04821	-0.72449
ILMN_2395506	SOX6	-1.06204	4.871304	-5.71157	7.5E-07	0.000763	5.730884
ILMN_1767523	IL17RB	-1.05332	11.20929	-3.8165	0.000397	0.030767	0.006976
ILMN_2170625	LOC389286	-1.04884	5.867659	-3.75488	0.00048	0.034015	-0.16398
ILMN_1777660	RNF144	-1.04541	9.100533	-3.82166	0.000391	0.030551	0.021367
ILMN_1669781	PRLR	-1.0318	6.179672	-4.44793	5.34E-05	0.009662	1.829668
ILMN_2341254	STARD13	-1.02968	7.093917	-3.94535	0.000266	0.02441	0.368809
ILMN_1660635	LACTB2	-1.02697	7.218848	-3.56995	0.00084	0.046475	-0.6683
ILMN_2067421	PP8961	-1.02272	4.967997	-5.53801	1.36E-06	0.001213	5.183318
ILMN_1677404	RAP2A	-1.01905	9.602507	-4.09956	0.000164	0.018391	0.809136
ILMN_1814661	PHLPP1	-1.01719	7.585066	-3.7741	0.000453	0.033049	-0.1108
ILMN_1719949	LOC644019	-1.01408	5.25933	-4.17593	0.000129	0.016215	1.02993
ILMN_2229214	STOX1	-1.01318	7.294293	-4.22967	0.000108	0.014309	1.186355
ILMN_2336280	QKI	-1.01306	5.934509	-3.71407	0.000544	0.037396	-0.27641
ILMN_1654072	CX3CL1	-1.0109	10.47276	-3.9294	0.00028	0.025071	0.323706
ILMN_1727790	KHDRBS3	-1.008	7.660622	-4.14594	0.000142	0.017059	0.943012
ILMN_1745223	CDC42EP4	-1.00796	10.83722	-3.78389	0.000439	0.032723	-0.08367
ILMN_2141030	LOC641522	-1.00584	5.156292	-4.15227	0.000139	0.016866	0.961355
ILMN_1751708	ITM2B	-1.00351	11.34496	-3.75914	0.000474	0.033971	-0.1522
ILMN_1787567	TSC22D1	-1.0029	9.314914	-3.68408	0.000596	0.03922	-0.35862
ILMN_1681252	C17orf44	-1.00098	5.210076	-3.74399	0.000496	0.034896	-0.19403

Appendix. Downregulated differentially expressed genes between control and 1000 ppb at 24h

PROBE_ID	SYMBOL	logFC	AveExpr	t	P.Value	adj.P.Val	B
ILMN_1701247	LOC132241	1.002057	7.376858	3.962649	0.000252	0.023821	0.417814
ILMN_1890614		1.003072	6.567673	4.23292	0.000107	0.014298	1.195831
ILMN_1910550		1.00967	6.505661	3.825009	0.000387	0.030551	0.030689
ILMN_3299905	RNFT2	1.016361	6.282283	4.11603	0.000156	0.018049	0.856603
ILMN_2082893	LOC440157	1.016516	8.887496	3.702598	0.000563	0.038221	-0.3079
ILMN_2070052	LOC613037	1.017763	11.33307	4.065575	0.000183	0.019976	0.711443
ILMN_1651819	GALNT11	1.018522	7.412514	3.793073	0.000427	0.032161	-0.05818
ILMN_1654916	KIF7	1.01913	6.61392	3.824877	0.000387	0.030551	0.030323
ILMN_1803559	FLJ39632	1.024595	8.827253	4.6141	0.000031	0.006976	2.327318
ILMN_3235593	ZNF841	1.032033	6.00142	3.603057	0.000761	0.044405	-0.57901

ILMN_1678493	CHN1	1.032346	7.187214	4.243679	0.000104	0.014116	1.22725
ILMN_1664909	LOC729351	1.032531	5.050067	4.218293	0.000112	0.014699	1.153164
ILMN_1720604	ARSG	1.032597	5.273753	4.87724	1.29E-05	0.004074	3.127287
ILMN_2382290	KREMEN2	1.039804	5.71261	3.709988	0.000551	0.037557	-0.28762
ILMN_3210304	LOC100131139	1.047988	7.06475	4.136747	0.000146	0.017235	0.916434
ILMN_3304111	LOC729978	1.049216	11.51247	4.243127	0.000104	0.014116	1.225639
ILMN_3248781	SDHAP2	1.053974	7.897764	4.857988	1.38E-05	0.004157	3.068315
ILMN_1802550	PCSK6	1.060966	5.559368	4.761816	0.000019	0.005064	2.774738
ILMN_1707337	MSTO1	1.066574	7.32498	4.712589	2.24E-05	0.005689	2.625141
ILMN_2370091	NGFRAP1	1.069615	9.436111	3.715314	0.000542	0.037396	-0.27299
ILMN_1669201	ABCF2	1.071919	5.805289	3.5686	0.000844	0.046475	-0.67193
ILMN_1733538	RGS10	1.08161	5.780006	3.810929	0.000404	0.030951	-0.00854
ILMN_1695430	DDB1	1.083534	6.114916	4.167351	0.000132	0.016431	1.005048
ILMN_1678323	AASS	1.083949	6.711139	3.784133	0.000439	0.032723	-0.08299
ILMN_1750722	RPS7	1.089435	7.144033	3.860416	0.000347	0.028639	0.129645
ILMN_3286809	LOC100131139	1.090235	9.937382	3.661634	0.000638	0.040295	-0.41994
ILMN_1656868	LOC23117	1.093428	11.35237	4.418461	5.88E-05	0.010232	1.742079
ILMN_1813277	SUPT3H	1.099747	7.148582	3.603369	0.00076	0.044405	-0.57816
ILMN_1689968	PLEKHO2	1.106544	5.663596	4.087098	0.000171	0.018906	0.773268
ILMN_1661940	CAMTA1	1.114044	5.684079	4.773799	1.82E-05	0.005007	2.811223
ILMN_1713491	VAMP2	1.117983	6.297599	3.581412	0.000812	0.045742	-0.63744
ILMN_3263864	LOC100129905	1.122679	5.215788	3.584893	0.000804	0.045717	-0.62805
ILMN_1787556	NPC1L1	1.136899	8.60869	3.9926	0.00023	0.023136	0.502902
ILMN_1691290	CELSR3	1.140062	8.090979	3.889528	0.000317	0.027402	0.211338
ILMN_1723087	MDK	1.146627	5.427404	3.698562	0.00057	0.038221	-0.31897
ILMN_1769575	JAM3	1.150998	6.651121	3.591453	0.000788	0.045023	-0.61036
ILMN_3300797	LOC729090	1.152588	12.76087	3.606136	0.000754	0.044278	-0.57068
ILMN_3275275	LOC727962	1.160154	6.004646	4.100785	0.000163	0.018391	0.812659
ILMN_1797786	MAPK12	1.16492	6.647893	4.011437	0.000217	0.022153	0.55657
ILMN_1693317	TTC15	1.167615	8.491779	3.601477	0.000765	0.044428	-0.58328
ILMN_2363392	TNFSF14	1.167771	9.636854	3.639435	0.000682	0.041747	-0.48038
ILMN_1691376	JAG1	1.181328	8.179749	3.603266	0.000761	0.044405	-0.57844
ILMN_1671392	KCNF1	1.203029	4.981704	3.748791	0.000489	0.034565	-0.18078
ILMN_1766269	HM13	1.219398	5.544243	3.859249	0.000348	0.028657	0.126377
ILMN_1739805	NDE1	1.222507	8.635041	3.812346	0.000403	0.030951	-0.00459
ILMN_1653466	HES4	1.224177	9.630122	4.497108	4.55E-05	0.008625	1.976272
ILMN_1794707	ATHL1	1.231836	5.686385	4.391066	6.43E-05	0.010712	1.660861
ILMN_1762674	NUP43	1.231882	6.916806	3.665119	0.000631	0.040098	-0.41043
ILMN_1688070	NSUN5C	1.232069	5.885696	4.902081	1.19E-05	0.003885	3.20347

ILMN_1654398	RGL1	1.240402	7.745645	4.502261	4.47E-05	0.008539	1.991668
ILMN_1728202	TMEM22	1.241602	7.41007	3.623242	0.000716	0.042843	-0.52435
ILMN_1743205	ABCA7	1.243868	5.78892	4.247124	0.000102	0.014116	1.237318
ILMN_1719290	CRYZL1	1.246827	5.994704	4.727001	2.13E-05	0.005534	2.668889
ILMN_3205264	LOC100133312	1.26082	5.781285	4.336851	7.67E-05	0.011905	1.500689
ILMN_1736008	YRDC	1.265578	9.704618	3.862368	0.000345	0.028553	0.135113
ILMN_1688160	WDR27	1.281249	7.199472	4.957349	9.86E-06	0.003483	3.373343
ILMN_2136010	ADH4	1.294883	9.438457	3.595199	0.000779	0.044867	-0.60024
ILMN_2234697	BEX1	1.303417	9.688875	3.916097	0.000292	0.025632	0.286152
ILMN_1708858	CSNK1E	1.324828	7.993208	3.934025	0.000276	0.024874	0.336771
ILMN_3240077	LOC645993	1.325145	5.087058	4.791496	1.72E-05	0.0048	2.865156
ILMN_1663080	LFNG	1.325468	5.078129	4.265206	9.66E-05	0.013881	1.290218
ILMN_1750785	SYTL1	1.331527	5.782927	5.444973	1.88E-06	0.001358	4.890781
ILMN_1685371	SUMF2	1.334951	7.336057	3.836374	0.000374	0.030132	0.062404
ILMN_1898453		1.343828	6.327178	3.839042	0.000371	0.030132	0.069854
ILMN_2349393	MDK	1.348095	10.60424	4.931139	1.08E-05	0.003654	3.292722
ILMN_1673185	CPSF2	1.363285	7.389961	3.609908	0.000746	0.043967	-0.56048
ILMN_2060413	CD24	1.376105	9.71117	3.946533	0.000265	0.02441	0.372151
ILMN_1657701	TMEM137	1.385134	8.17683	4.03533	0.000201	0.021075	0.624807
ILMN_1907834		1.387576	5.505144	5.519637	1.45E-06	0.001213	5.125488
ILMN_1724753	NIN	1.39329	6.630643	3.921039	0.000287	0.025321	0.300093
ILMN_1767665	LOC493869	1.395429	5.158973	4.3947	6.36E-05	0.010712	1.671624
ILMN_2345142	SULF2	1.442064	7.032952	4.276187	9.33E-05	0.013706	1.322387
ILMN_1667460	SULF2	1.451478	7.87536	4.904017	1.18E-05	0.003885	3.209412
ILMN_1756784	FREQ	1.455783	5.929955	5.487944	1.62E-06	0.001237	5.025798
ILMN_3231944	LOC100130516	1.456918	10.43445	4.25888	9.86E-05	0.013906	1.271701
ILMN_1763000	ADAP2	1.45937	5.273246	5.510188	1.5E-06	0.001213	5.095758
ILMN_1769704	FLJ39632	1.465529	6.567578	4.625341	2.98E-05	0.006835	2.361206
ILMN_2377900	MAP1B	1.483625	5.944373	4.201016	0.000119	0.015245	1.102846
ILMN_1655961	C7orf54	1.493173	6.718049	4.103475	0.000162	0.018391	0.820408
ILMN_3242077	LOC648742	1.493772	5.498239	4.540122	3.95E-05	0.00787	2.10498
ILMN_1788356	C11orf17	1.502067	7.397145	3.921953	0.000287	0.025321	0.302674
ILMN_1677765	LRP8	1.508835	7.116656	4.544414	0.000039	0.007816	2.117845
ILMN_1856315		1.522988	8.1035	3.715135	0.000542	0.037396	-0.27348
ILMN_3205910	LOC100131541	1.547399	5.614667	4.323868	0.00008	0.012188	1.462449
ILMN_1812226	ICAM1	1.559549	7.062524	3.835191	0.000375	0.030148	0.059101
ILMN_1788254	PGAM5	1.560458	8.086088	3.669833	0.000622	0.04001	-0.39757
ILMN_1670926	CHST15	1.59017	8.454965	3.567167	0.000847	0.046488	-0.67579
ILMN_1731206	NKD2	1.636492	6.271759	4.384744	6.56E-05	0.01076	1.642143

ILMN_1677691	LOC648852	1.641252	8.076095	3.773666	0.000453	0.033049	-0.112
ILMN_3239343	STAG3L3	1.66556	7.468823	4.573208	3.54E-05	0.007324	2.20427
ILMN_1684554	COL16A1	1.670758	7.370581	5.328064	2.8E-06	0.001645	4.524348
ILMN_3303612	PABPC1L	1.756048	9.691457	3.711259	0.000549	0.037505	-0.28413
ILMN_1791375	STAG3L2	1.780619	7.708661	5.077937	6.56E-06	0.002956	3.745668
ILMN_1738147	NES	1.801542	6.59251	4.328845	7.87E-05	0.012122	1.477103
ILMN_1747251	LTB4R	1.813468	5.705656	3.921291	0.000287	0.025321	0.300804
ILMN_1808707	FSCN1	1.87172	10.43152	4.047373	0.000193	0.020525	0.659268
ILMN_1699867	IGF2	1.877642	6.764528	4.715338	2.22E-05	0.005689	2.633484
ILMN_2413956	IGF2	1.891462	6.326153	4.628622	2.95E-05	0.006818	2.371102
ILMN_1773952	LOC440910	1.927091	5.376174	5.063904	6.88E-06	0.002956	3.70223
ILMN_1757440	FAM69B	2.011327	5.468452	5.358296	2.53E-06	0.001579	4.618969
ILMN_1741917	OSCAR	2.022176	5.251797	3.906108	0.000301	0.026273	0.257996
ILMN_1659984	MEP1A	2.1041	8.247505	3.97112	0.000246	0.023789	0.441847
ILMN_1671263	CACNA1H	2.128506	6.321076	3.824223	0.000388	0.030551	0.028499
ILMN_1659631	LOC730024	2.207097	6.627486	4.951596	1.01E-05	0.003497	3.355637
ILMN_1705403	CYP2S1	2.24243	5.46618	5.821395	5.13E-07	0.000711	6.07837
ILMN_3239181	ITPRIP	2.258196	6.607773	4.921455	1.11E-05	0.003729	3.262962
ILMN_1757497	VGF	2.416502	5.858977	4.351442	7.31E-05	0.011485	1.543721
ILMN_1805192	ITPRIP	2.55021	6.71813	5.308873	2.99E-06	0.001645	4.464337
ILMN_1754126	SH2D5	2.677522	5.809946	4.047711	0.000193	0.020525	0.660236

Appendix. Upregulated differentially expressed genes between control and 1000 ppb at 24h

Appendix J. Gene annotated list of down-regulated genes (DEGs) when exposed to 200 ppb of metolachlor exposed human liver cells for 48 hours compared to control.

PROBE_ID	SYMBOL	logFC	AveExpr	t	P.Value	adj.P.Val	B
ILMN_1729188	HAMP	-3.99264	9.666053	-6.28688	1.02E-07	1.41E-05	7.677661
ILMN_2412336	AKR1C2	-3.98635	7.190344	-9.45199	2.06E-12	5.66E-09	18.00733
ILMN_1803862	LCN15	-3.61507	7.631751	-6.76933	1.89E-08	4.07E-06	9.289561
ILMN_1715401	MT1G	-3.41275	10.48736	-3.63603	0.000689	0.007334	-0.70935
ILMN_3251497	GSTA1	-2.99159	6.504843	-9.05418	7.65E-12	1.29E-08	16.76026
ILMN_1746720	TTC39C	-2.9138	7.586939	-7.94951	3.19E-10	1.79E-07	13.20191
ILMN_2113470	GSTA1	-2.72719	6.2465	-10.0167	3.3E-13	3.02E-09	19.74204
ILMN_1777233	E2F2	-2.7193	8.097666	-4.29397	8.81E-05	0.001646	1.223586
ILMN_1786065	UHRF1	-2.68243	10.04627	-3.96192	0.000253	0.003577	0.228726
ILMN_1806037	TK1	-2.67619	8.68445	-4.45627	0.000052	0.001139	1.722148
ILMN_2234187	CDO1	-2.6382	7.540783	-9.0422	7.96E-12	1.29E-08	16.7224
ILMN_1796094	CD36	-2.62724	6.15631	-8.21748	1.28E-10	9.25E-08	14.07662
ILMN_1713995	SCNN1A	-2.62528	8.983755	-9.26481	3.81E-12	8.73E-09	17.42303
ILMN_2124802	MT1H	-2.50262	7.376004	-3.65251	0.000656	0.007072	-0.66294
ILMN_1778543	LOC653874	-2.49627	7.55688	-5.30771	0.000003	0.000157	4.436571
ILMN_2412860	MCM4	-2.48615	8.377499	-6.46125	5.54E-08	8.86E-06	8.260113
ILMN_2353117	SLC22A7	-2.4855	7.915285	-4.23066	0.000108	0.001897	1.03119
ILMN_1809590	GINS2	-2.48398	9.82527	-4.06791	0.000181	0.002757	0.54232
ILMN_2202423	HELLS	-2.47678	7.367513	-4.47602	4.88E-05	0.001089	1.783293
ILMN_1673721	EXO1	-2.47203	6.986365	-4.75993	1.91E-05	0.000575	2.673246
ILMN_1732688	DUT	-2.46859	7.6258	-4.76986	1.85E-05	0.00056	2.704691
ILMN_2365176	ALDH8A1	-2.44632	6.788929	-7.11111	5.77E-09	1.71E-06	10.42977
ILMN_1696713	POLA2	-2.43497	7.809177	-5.07897	6.54E-06	0.000272	3.693961
ILMN_1798654	MCM6	-2.42557	9.889516	-5.33173	2.77E-06	0.000149	4.514991
ILMN_1685663	CYP24A1	-2.41816	8.819878	-4.87559	0.000013	0.000437	3.041001
ILMN_1656638	BHMT	-2.40688	6.234096	-8.64966	2.96E-11	2.77E-08	15.47248
ILMN_2413898	MCM10	-2.38587	7.748061	-4.69304	2.39E-05	0.000672	2.461863
ILMN_1682099	TNFAIP8L3	-2.37507	6.21958	-8.08502	2.01E-10	1.28E-07	13.64506
ILMN_1797391	SLC22A7	-2.35495	6.38992	-5.85067	4.63E-07	4.13E-05	6.22504
ILMN_1670238	CDC45L	-2.3497	8.922626	-4.25921	9.85E-05	0.001779	1.117808
ILMN_1779711	DTL	-2.32986	7.08112	-5.03759	7.52E-06	0.000302	3.560493
ILMN_2134801	AGXT2L1	-2.32123	6.820409	-5.79632	5.59E-07	4.76E-05	6.044782
ILMN_1784863	CD36	-2.316	5.805642	-8.78391	1.88E-11	2.25E-08	15.90195
ILMN_2249018	LOC389816	-2.31084	6.629623	-4.32862	7.87E-05	0.001525	1.329408

ILMN_3232696	LOC729816	-2.30972	9.301043	-4.53875	3.97E-05	0.000938	1.978241
ILMN_2414786	DIO1	-2.29724	8.902679	-3.88947	0.000317	0.00419	0.016654
ILMN_1678669	RRM2	-2.28617	7.152961	-4.20707	0.000116	0.002002	0.959811
ILMN_1711015	CRYAA	-2.28302	8.679583	-6.42728	6.24E-08	9.71E-06	8.146598
ILMN_2285996	KIAA0101	-2.27727	9.616738	-4.71247	2.24E-05	0.000642	2.523153
ILMN_2328972	DNMT3B	-2.26117	7.461849	-6.531	4.35E-08	7.56E-06	8.493198
ILMN_2181432	SPC24	-2.2574	8.192361	-5.39063	2.26E-06	0.000131	4.707646
ILMN_1774336	POLE2	-2.23088	7.866322	-4.37586	6.76E-05	0.001365	1.47422
ILMN_1737205	MCM4	-2.19355	9.709768	-4.96771	9.52E-06	0.000355	3.335811
ILMN_1769547	DIO1	-2.18465	9.030743	-3.69587	0.000575	0.006454	-0.54027
ILMN_1782937	LOC647169	-2.16589	5.951941	-8.21698	1.28E-10	9.25E-08	14.07502
ILMN_1808707	FSCN1	-2.15706	10.43152	-5.71268	7.47E-07	0.000059	5.767834
ILMN_1757807	AGXT2L1	-2.14348	7.166376	-5.17329	4.75E-06	0.000215	3.999196
ILMN_1814281	SPC25	-2.14315	6.868453	-4.54275	3.92E-05	0.00093	1.990699
ILMN_1659364	RFC5	-2.14248	8.989345	-6.08597	2.05E-07	2.29E-05	7.007518
ILMN_1694432	CRIP2	-2.13485	7.562975	-4.90832	1.16E-05	0.000403	3.145562
ILMN_1701831	GSTA1	-2.12516	5.677271	-8.64347	3.02E-11	2.77E-08	15.45261
ILMN_2186061	PFKFB3	-2.11896	6.216693	-6.75374	2E-08	4.22E-06	9.237489
ILMN_2413899	MCM10	-2.11823	5.994278	-6.30434	9.58E-08	1.34E-05	7.735947
ILMN_2311089	BRCA1	-2.11276	6.276748	-5.57295	1.21E-06	0.000084	5.306527
ILMN_2235137	FANCD2	-2.10813	8.504755	-6.06102	2.23E-07	2.44E-05	6.924415
ILMN_2229940	C2orf7	-2.09952	7.697343	-4.96112	9.74E-06	0.000361	3.314667
ILMN_1691156	MT1A	-2.09664	10.9377	-3.77957	0.000445	0.005374	-0.30129
ILMN_2093343	PLAC8	-2.09029	8.011637	-5.58446	1.16E-06	8.19E-05	5.344452
ILMN_2136147	BCAS1	-2.08409	5.888665	-7.43306	1.89E-09	8.24E-07	11.49954
ILMN_1774066	TMEM141	-2.06054	10.13776	-5.78886	5.74E-07	4.85E-05	6.020054
ILMN_1655642	FANCI	-2.05927	7.573273	-5.53008	1.4E-06	9.54E-05	5.165351
ILMN_1681503	MCM2	-2.05188	9.23316	-4.32679	7.92E-05	0.001531	1.323796
ILMN_2374778	DUT	-2.03507	6.442753	-4.85214	0.000014	0.000461	2.966193
ILMN_1665671	EPO	-2.03259	7.004892	-5.4813	1.66E-06	0.000106	5.004985
ILMN_1679438	MLF1IP	-2.03172	6.729059	-4.8079	1.63E-05	0.000512	2.825434
ILMN_1668055	SAA4	-2.02717	11.58747	-7.21405	4.03E-09	1.4E-06	10.77237
ILMN_1785191	TMEM14A	-2.02238	9.202155	-6.03975	2.4E-07	2.56E-05	6.853607
ILMN_1733042	BCAS1	-2.02137	6.193053	-6.09411	1.99E-07	2.25E-05	7.034647
ILMN_1804090	SLC25A10	-2.02019	8.663935	-5.31402	2.94E-06	0.000155	4.457175
ILMN_1807501	GINS4	-2.01465	6.207868	-7.11947	5.6E-09	1.71E-06	10.45762
ILMN_1798210	E2F7	-2.00804	6.32486	-5.99092	2.85E-07	2.92E-05	6.691078
ILMN_1674231	CHAF1B	-1.98837	7.856798	-5.40389	2.16E-06	0.000128	4.751052
ILMN_1712729	DKK4	-1.97315	7.299118	-5.1932	4.44E-06	0.000205	4.063837

ILMN_1670353	RAD51AP1	-1.96948	8.671042	-4.45861	5.16E-05	0.001134	1.729361
ILMN_1680757	LRRC26	-1.96711	6.244911	-4.11643	0.000155	0.002453	0.687184
ILMN_1694877	CASP6	-1.96605	6.677599	-5.74693	6.64E-07	0.000054	5.881164
ILMN_2121774	JCLN	-1.95551	5.444465	-8.47465	5.34E-11	4.31E-08	14.90957
ILMN_1746831	ZNF114	-1.95001	5.971158	-5.43991	1.91E-06	0.000118	4.869144
ILMN_1686664	MT2A	-1.94366	9.760428	-3.8674	0.00034	0.0044	-0.04756
ILMN_3251540	GSTA2	-1.93574	5.491257	-8.65266	2.93E-11	2.77E-08	15.48208
ILMN_1655261	ERP27	-1.93229	8.374345	-3.45409	0.001186	0.010993	-1.21399
ILMN_1655613	GSTA2	-1.92295	5.636318	-8.86922	1.42E-11	1.98E-08	16.17382
ILMN_2334205	ERCC6L	-1.9174	5.952169	-6.25751	1.13E-07	0.000015	7.579608
ILMN_2328977	DNMT3B	-1.91082	6.57642	-6.89107	1.24E-08	2.91E-06	9.696073
ILMN_1757697	NEIL3	-1.90977	6.087707	-5.36155	2.5E-06	0.000139	4.612459
ILMN_2151739	CAT	-1.90874	9.973881	-6.1795	1.48E-07	1.83E-05	7.319314
ILMN_1759277	OIP5	-1.8979	7.591118	-5.96317	3.14E-07	3.18E-05	6.598765
ILMN_1727466	KCNMB4	-1.89544	5.878907	-6.56428	3.87E-08	7.09E-06	8.604431
ILMN_2225537	PTGR1	-1.89326	8.124944	-8.78297	1.89E-11	2.25E-08	15.89897
ILMN_1726720	NUSAP1	-1.8812	10.11438	-5.41942	2.05E-06	0.000124	4.801934
ILMN_2368718	CENPM	-1.88014	8.519179	-4.42515	5.76E-05	0.001213	1.625975
ILMN_1681340	C1orf41	-1.87408	7.702592	-5.29452	3.14E-06	0.000162	4.393552
ILMN_1656920	CRIP1	-1.86897	9.578862	-4.13211	0.000148	0.002375	0.734153
ILMN_2168747	GSTA2	-1.86342	5.650273	-8.20302	1.34E-10	9.45E-08	14.02961
ILMN_1815169	MCM5	-1.84687	7.721421	-4.17596	0.000129	0.002142	0.865936
ILMN_1665538	SKP2	-1.84265	10.66566	-5.41883	2.05E-06	0.000124	4.800018
ILMN_1737195	CENPK	-1.84083	7.444955	-4.35081	7.33E-05	0.001443	1.397323
ILMN_2212909	MELK	-1.83303	9.121677	-4.73232	2.09E-05	0.000616	2.58585
ILMN_1753931	CDO1	-1.83172	6.353878	-7.65391	8.81E-10	4.25E-07	12.2299
ILMN_1794692	DNMT3B	-1.83046	6.582415	-6.35576	8.01E-08	1.15E-05	7.907673
ILMN_2191436	POLA1	-1.82739	8.191386	-5.88617	4.1E-07	3.84E-05	6.342875
ILMN_1740291	POLQ	-1.8269	7.424185	-4.3994	6.26E-05	0.001291	1.546606
ILMN_2196984	OIP5	-1.82213	9.661722	-5.08186	6.48E-06	0.000269	3.703276
ILMN_1812281	ARG1	-1.81886	6.173375	-5.05936	6.99E-06	0.000285	3.630661
ILMN_1796074	C18orf56	-1.81425	11.42865	-4.98128	9.1E-06	0.000346	3.379381
ILMN_1660691	RAB31	-1.81128	6.602216	-5.51985	1.45E-06	9.78E-05	5.131709
ILMN_1706779	LIG1	-1.80928	7.750503	-3.78472	0.000438	0.005325	-0.28649
ILMN_3181695	LOC100130178	-1.80232	9.333938	-6.27444	1.06E-07	1.44E-05	7.63614
ILMN_1738027	BRCA1	-1.79616	6.689855	-4.86122	1.36E-05	0.000453	2.995136
ILMN_1737728	CDCA3	-1.7949	8.107577	-4.35014	7.34E-05	0.001443	1.395281
ILMN_1673673	PBK	-1.78685	8.528968	-4.76816	1.86E-05	0.000563	2.6993
ILMN_1747911	CDC2	-1.77565	9.226916	-5.80347	5.46E-07	4.67E-05	6.068465

ILMN_1716895	RPA3	-1.77556	10.5349	-4.71994	2.18E-05	0.000632	2.546729
ILMN_1791002	SKP2	-1.77221	7.029183	-4.37411	0.000068	0.001368	1.468835
ILMN_1805828	VRK1	-1.76741	7.408146	-5.10457	0.000006	0.000254	3.776651
ILMN_1699644	42797	-1.76727	6.615575	-7.87939	4.06E-10	2.23E-07	12.97198
ILMN_1711408	ANXA4	-1.764	8.760868	-5.64389	9.47E-07	7.02E-05	5.540484
ILMN_1813043	BHMT2	-1.7583	6.337512	-8.0658	2.14E-10	1.34E-07	13.58231
ILMN_1754272	GINS3	-1.75805	7.881169	-4.96054	9.76E-06	0.000361	3.312805
ILMN_1669842	CHAF1A	-1.75747	6.149774	-4.99905	8.57E-06	0.000332	3.436482
ILMN_1783610	HELLS	-1.75659	6.585522	-4.85518	1.39E-05	0.000459	2.97588
ILMN_1715905	DSN1	-1.75433	7.533057	-4.98483	8.99E-06	0.000343	3.390784
ILMN_1796423	CLIC3	-1.75405	5.563853	-5.13285	5.45E-06	0.000238	3.868163
ILMN_2398572	FXYD2	-1.75249	6.721467	-3.91481	0.000293	0.003976	0.090619
ILMN_1699258	ALDH8A1	-1.75169	5.520045	-7.83037	4.8E-10	2.54E-07	12.811
ILMN_1753729	KNG1	-1.747	6.394949	-5.93598	3.45E-07	3.46E-05	6.50838
ILMN_1651237	CDT1	-1.73873	9.080969	-4.38626	6.53E-05	0.001333	1.506184
ILMN_1748923	SMC2	-1.73522	7.346776	-5.4246	2.01E-06	0.000123	4.818928
ILMN_1694106	GPD1L	-1.72967	8.976609	-6.79059	1.76E-08	3.87E-06	9.36058
ILMN_1695414	ASF1B	-1.72916	8.436952	-3.51551	0.000989	0.009617	-1.04528
ILMN_1781745	C9orf152	-1.72901	6.022883	-5.19527	4.41E-06	0.000205	4.070535
ILMN_1653026	PLAC8	-1.71636	6.691901	-5.02904	7.74E-06	0.000308	3.53295
ILMN_1694177	PCNA	-1.71592	11.54925	-4.54372	3.91E-05	0.000929	1.993736
ILMN_1777564	MAD2L1	-1.71568	9.242941	-5.12066	5.68E-06	0.000244	3.828704
ILMN_1805985	ANKRD32	-1.71452	5.63311	-6.09139	2.01E-07	2.26E-05	7.025601
ILMN_2389114	FIGNL1	-1.71395	5.855552	-5.75974	6.35E-07	5.21E-05	5.923599
ILMN_1797875	ALOX5AP	-1.71028	6.216303	-4.05479	0.000189	0.00285	0.503313
ILMN_3249142	JCLN	-1.7088	5.305316	-6.85378	1.41E-08	3.23E-06	9.571602
ILMN_1719032	LSM3	-1.70715	9.155878	-6.27602	1.06E-07	1.44E-05	7.641411
ILMN_2411190	SMC2	-1.69943	7.075333	-4.98557	8.97E-06	0.000342	3.393152
ILMN_1771593	RRM1	-1.69511	10.98116	-4.74864	1.98E-05	0.000592	2.637477
ILMN_2367113	CASP6	-1.69466	6.447223	-5.21372	4.14E-06	0.000196	4.130472
ILMN_1722239	TIMM8A	-1.69451	8.181685	-6.99412	8.66E-09	2.34E-06	10.03987
ILMN_1776490	C17orf53	-1.69421	7.669776	-4.95732	9.86E-06	0.000364	3.302484
ILMN_1739594	ACOT11	-1.69275	6.911635	-5.50271	1.54E-06	0.000101	5.07536
ILMN_1685625	UCP2	-1.69247	7.111294	-4.24385	0.000103	0.001848	1.071169
ILMN_1680390	GCNT2	-1.68581	8.872742	-6.63248	3.05E-08	5.99E-06	8.832324
ILMN_2289593	FXYD2	-1.68547	7.489644	-3.06618	0.003601	0.025124	-2.23746
ILMN_1810901	RNASEH2A	-1.68128	8.035717	-4.13946	0.000144	0.002334	0.756178
ILMN_2413650	STIL	-1.67988	8.940585	-4.46986	4.97E-05	0.001108	1.764195
ILMN_1660806	CSRP2	-1.66896	7.000669	-4.68871	2.42E-05	0.000676	2.448192

ILMN_1670672	TMEM37	-1.66801	6.459648	-4.71621	2.21E-05	0.000637	2.534947
ILMN_2409298	NUSAP1	-1.66591	8.51614	-4.78251	1.77E-05	0.000544	2.744795
ILMN_2355738	INCENP	-1.66196	7.073476	-5.18115	4.62E-06	0.000212	4.02472
ILMN_1751444	NCAPG	-1.65589	9.239761	-4.494	0.000046	0.001042	1.839064
ILMN_1796589	TRIP13	-1.65429	9.065836	-5.06664	6.82E-06	0.000278	3.654148
ILMN_2143155	KIF11	-1.64696	8.585071	-4.54115	3.94E-05	0.000933	1.985722
ILMN_2359945	CES1	-1.64106	10.21616	-6.03918	2.41E-07	2.56E-05	6.851696
ILMN_1715616	PPIL5	-1.6401	8.100899	-4.81356	0.000016	0.000507	2.843401
ILMN_2412384	CCNE2	-1.63924	6.026385	-5.81953	5.16E-07	0.000045	6.121739
ILMN_1731184	MELK	-1.63542	8.118863	-4.73949	2.04E-05	0.000603	2.608536
ILMN_1683120	UNG	-1.63444	10.66365	-4.10996	0.000159	0.002486	0.667823
ILMN_1778152	FIGNL1	-1.63203	6.071613	-5.62503	1.01E-06	7.37E-05	5.478228
ILMN_1668721	CCND3	-1.62452	8.027419	-5.77717	5.98E-07	4.99E-05	5.981312
ILMN_1711470	UBE2T	-1.62364	8.884332	-4.18176	0.000126	0.002112	0.883407
ILMN_1689842	SC4MOL	-1.62192	7.829762	-3.61554	0.000733	0.007662	-0.7669
ILMN_1682336	MASTL	-1.62022	6.811601	-5.48545	1.63E-06	0.000105	5.018624
ILMN_1664630	CHEK1	-1.61922	8.634158	-3.9864	0.000234	0.003361	0.300808
ILMN_2406634	DNMT3L	-1.61852	5.599879	-7.17063	4.69E-09	1.57E-06	10.62792
ILMN_1793360	APITD1	-1.6163	7.663853	-4.83866	1.47E-05	0.000478	2.92327
ILMN_1774375	LOC284422	-1.61629	9.205828	-3.26024	0.002083	0.016765	-1.73488
ILMN_1700547	CHST9	-1.61421	7.778516	-4.18813	0.000124	0.00208	0.902621
ILMN_1742922	PRIM2A	-1.61245	5.759432	-6.19147	1.42E-07	1.78E-05	7.359243
ILMN_1811933	SHMT1	-1.60862	9.3408	-5.03855	7.5E-06	0.000301	3.563576
ILMN_1801205	GPNMB	-1.60819	5.16741	-10.4489	8.34E-14	1.15E-09	21.04045
ILMN_1709484	BLM	-1.59023	5.963037	-4.9399	1.05E-05	0.000378	3.246631
ILMN_2343048	ABCB9	-1.58273	7.840741	-5.05927	6.99E-06	0.000285	3.630395
ILMN_1786125	CCNA2	-1.58117	10.27483	-4.48339	4.76E-05	0.001068	1.806131
ILMN_1695658	KIF20A	-1.58083	9.259455	-4.37292	6.82E-05	0.00137	1.465166
ILMN_1683450	CDCA5	-1.57895	10.66282	-4.09401	0.000167	0.002587	0.620156
ILMN_1751776	CKAP2L	-1.57815	7.609194	-4.21846	0.000112	0.001951	0.994246
ILMN_1781479	SUV39H1	-1.57331	8.255265	-5.30694	3.01E-06	0.000157	4.434084
ILMN_1758728	FANCG	-1.57287	8.595275	-4.67151	2.56E-05	0.000703	2.394039
ILMN_2409220	HMMR	-1.57163	9.576559	-3.53836	0.000924	0.00914	-0.98208
ILMN_1728048	LOC158160	-1.57048	9.008283	-4.25916	9.85E-05	0.001779	1.117638
ILMN_1806818	MCM3	-1.56743	10.35026	-4.34427	7.49E-05	0.001468	1.377291
ILMN_1651433	DCK	-1.56645	8.063209	-4.7403	2.04E-05	0.000603	2.611104
ILMN_1658027	RAD54L	-1.56303	8.2595	-4.07938	0.000175	0.002681	0.57649
ILMN_1678904	ENO3	-1.56035	9.493809	-4.93572	1.06E-05	0.00038	3.233232
ILMN_1727459	ORC1L	-1.55863	6.031321	-4.99125	8.8E-06	0.000338	3.411398

ILMN_1739645	ANLN	-1.55568	8.304632	-4.18078	0.000127	0.002117	0.880456
ILMN_1790537	C16orf75	-1.55516	10.27735	-3.88706	0.00032	0.004215	0.009635
ILMN_3239771	DLGAP5	-1.55506	8.540954	-4.27132	9.47E-05	0.001736	1.154599
ILMN_2229242	LSM3	-1.55445	10.15711	-5.36092	2.5E-06	0.000139	4.610397
ILMN_1666305	CDKN3	-1.55423	8.872387	-5.27993	3.3E-06	0.000168	4.345986
ILMN_3237270	LOC100133609	-1.55364	6.22844	-6.48455	5.11E-08	8.31E-06	8.337961
ILMN_2372915	P2RY2	-1.55355	6.438908	-5.50008	1.55E-06	0.000101	5.066712
ILMN_1761486	C13orf34	-1.5504	8.440198	-4.18349	0.000126	0.002104	0.88862
ILMN_1712386	C21orf45	-1.54862	7.728524	-4.68965	2.41E-05	0.000676	2.451178
ILMN_1667839	UBR7	-1.54414	9.006655	-5.54156	1.35E-06	9.19E-05	5.203156
ILMN_1794539	KIF11	-1.53679	7.951503	-4.92575	0.000011	0.00039	3.20133
ILMN_1732150	KIAA0101	-1.53009	5.717222	-7.14743	5.08E-09	1.64E-06	10.5507
ILMN_1749829	DLGAP5	-1.52903	8.800363	-4.12666	0.00015	0.002406	0.717805
ILMN_1801118	C16orf33	-1.5288	9.973505	-4.56543	3.64E-05	0.000887	2.061449
ILMN_1727553	C5orf54	-1.52804	6.515007	-5.39503	2.23E-06	0.000131	4.722023
ILMN_2139816	GPSM2	-1.5275	7.230113	-5.50386	1.53E-06	0.000101	5.079135
ILMN_1693905	HAT1	-1.52308	7.264901	-4.6933	2.38E-05	0.000672	2.462674
ILMN_2214278	ANKRD32	-1.5218	5.931362	-5.03996	7.46E-06	0.0003	3.568137
ILMN_1810844	RARRES2	-1.51691	9.412735	-4.81714	1.58E-05	0.000504	2.854791
ILMN_1796923	LOC81691	-1.51135	7.570936	-4.19223	0.000122	0.002065	0.914989
ILMN_1721495	ADAMTSL2	-1.51044	7.604732	-7.28798	3.12E-09	1.16E-06	11.01813
ILMN_1655796	42797	-1.50694	6.563464	-7.27394	3.28E-09	1.2E-06	10.97147
ILMN_2160929	FEN1	-1.50561	10.55641	-4.62031	3.03E-05	0.000787	2.23316
ILMN_2074258	BARD1	-1.50372	7.784812	-4.35901	7.14E-05	0.001419	1.422474
ILMN_2318568	HCFC1R1	-1.50344	7.07538	-5.31064	2.97E-06	0.000157	4.446144
ILMN_1724489	RFC4	-1.50341	9.420534	-4.3501	7.35E-05	0.001443	1.395153
ILMN_1781373	IFIH1	-1.50254	7.400824	-5.33083	2.78E-06	0.000149	4.512065
ILMN_2224143	MCM3	-1.50155	12.36589	-4.90885	1.16E-05	0.000403	3.147237
ILMN_1686835	C17orf41	-1.49724	5.56469	-5.51026	1.5E-06	9.97E-05	5.100175
ILMN_1698252	FANCB	-1.49696	5.566544	-5.71512	7.41E-07	5.88E-05	5.775908
ILMN_1701636	LOC647786	-1.49421	6.538817	-4.70418	0.000023	0.000655	2.496984
ILMN_2349459	BIRC5	-1.49254	9.906152	-4.66354	2.63E-05	0.000714	2.368933
ILMN_1800512	HMOX1	-1.49044	7.649133	-4.29198	8.86E-05	0.00165	1.217528
ILMN_1658143	RFC3	-1.48518	7.320607	-4.29263	8.84E-05	0.00165	1.219501
ILMN_3249240	C4orf46	-1.4784	6.771947	-4.97382	9.33E-06	0.000351	3.35542
ILMN_3275590	LOC647302	-1.4773	9.87773	-5.35506	2.56E-06	0.000139	4.591243
ILMN_1665559	CDK2	-1.47522	9.081369	-5.50027	1.55E-06	0.000101	5.067322
ILMN_1714167	CYB5A	-1.47465	11.85829	-6.08124	2.08E-07	2.31E-05	6.991762
ILMN_1710644	MARVELD3	-1.47338	7.038207	-6.15117	1.63E-07	1.96E-05	7.224838

ILMN_1719906	HADH	-1.47231	10.88901	-4.53595	4.01E-05	0.000943	1.96952
ILMN_1732516	KNTC1	-1.47142	8.65554	-3.62488	0.000713	0.007504	-0.74069
ILMN_2404906	SGOL1	-1.46988	5.910427	-6.81158	1.64E-08	3.65E-06	9.430678
ILMN_2147471	PI4K2B	-1.46931	5.80294	-5.28826	3.21E-06	0.000164	4.373124
ILMN_1685043	CYP3A7	-1.46758	6.574159	-3.05531	0.003711	0.025722	-2.26502
ILMN_1695645	CETN2	-1.46665	10.96882	-5.03063	7.7E-06	0.000308	3.538065
ILMN_1763907	C6orf173	-1.46507	9.414164	-4.62394	0.00003	0.000783	2.244542
ILMN_1756043	WDHD1	-1.4609	5.702922	-5.47685	1.68E-06	0.000107	4.990381
ILMN_1736704	DIXDC1	-1.45952	6.493253	-4.33253	7.78E-05	0.00151	1.341342
ILMN_2185339	LRTOMT	-1.45945	6.316666	-5.86583	4.4E-07	4.01E-05	6.275359
ILMN_1667564	ALDH3A2	-1.458	7.331434	-5.28657	3.23E-06	0.000165	4.367635
ILMN_1782813	DHFR	-1.45414	5.620041	-5.85091	4.63E-07	4.13E-05	6.225822
ILMN_3239785	LOC100134304	-1.45306	9.328092	-4.31869	8.13E-05	0.001559	1.299032
ILMN_2135984	MASTL	-1.45111	5.668942	-5.07693	6.59E-06	0.000273	3.687362
ILMN_1697998	FAM54A	-1.45082	6.35128	-4.95198	0.00001	0.000367	3.285361
ILMN_1709348	ALDH1A1	-1.44934	12.41048	-6.53225	4.33E-08	7.56E-06	8.497375
ILMN_1710428	CDC2	-1.44832	7.301156	-4.5555	3.76E-05	0.000909	2.030463
ILMN_1694502	PRIM1	-1.44539	8.510639	-4.55059	3.82E-05	0.000916	2.01514
ILMN_1686291	DIO1	-1.44369	6.207823	-3.8234	0.000389	0.004854	-0.17504
ILMN_1702503	ALDH3A1	-1.44335	5.118191	-5.44027	1.91E-06	0.000118	4.870323
ILMN_3241554	KANK4	-1.4415	9.568063	-4.51148	4.34E-05	0.001003	1.893378
ILMN_1727540	C1orf112	-1.43927	7.522674	-4.46234	0.000051	0.001126	1.740915
ILMN_1712803	CCNB1	-1.4382	9.027722	-5.11844	5.72E-06	0.000245	3.821524
ILMN_1789123	PLK4	-1.43682	8.423929	-4.01598	0.000214	0.003128	0.388186
ILMN_3284063	LOC341965	-1.43267	8.157408	-4.86769	1.33E-05	0.000446	3.015792
ILMN_1781943	FAM83D	-1.43239	9.782714	-4.30848	0.000084	0.001595	1.267848
ILMN_3297455	LOC729082	-1.43191	8.738763	-4.46089	5.12E-05	0.00113	1.736438
ILMN_1653292	PFKFB4	-1.42959	8.809694	-3.05662	0.003697	0.025667	-2.26169
ILMN_1777591	C10orf65	-1.42893	8.056869	-5.60967	1.07E-06	7.67E-05	5.427552
ILMN_1720114	GMNN	-1.42713	10.14332	-5.35754	2.53E-06	0.000139	4.599346
ILMN_1789096	OSTalpha	-1.42629	6.995821	-4.50549	4.43E-05	0.001015	1.874761
ILMN_1655191	CASZ1	-1.42174	7.488834	-5.77276	6.07E-07	5.04E-05	5.966715
ILMN_1756550	NUP62CL	-1.42168	5.992187	-4.98267	9.05E-06	0.000345	3.383845
ILMN_1815134	PI4K2B	-1.42046	8.879025	-6.11126	1.88E-07	2.16E-05	7.091812
ILMN_1728225	KIAA1524	-1.41809	6.177767	-4.85149	1.41E-05	0.000461	2.964122
ILMN_2066756	NCAPG2	-1.41569	6.830864	-4.04958	0.000192	0.002888	0.487816
ILMN_1712452	KIF20B	-1.41169	8.945622	-4.12132	0.000153	0.00243	0.70182
ILMN_2193315	C14orf143	-1.41053	7.67962	-4.44325	5.43E-05	0.001168	1.681868
ILMN_1686097	TOP2A	-1.40826	11.18551	-4.55351	3.78E-05	0.000909	2.024264

ILMN_2134039	ACN9	-1.40514	9.284266	-5.91435	3.72E-07	3.61E-05	6.436488
ILMN_1769299	MTMR11	-1.40378	5.706991	-5.12986	5.5E-06	0.000239	3.858464
ILMN_1754051	RMI1	-1.40351	7.213506	-4.02251	0.000209	0.003083	0.407508
ILMN_1652333	FN3KRP	-1.40049	10.2921	-5.63608	9.73E-07	7.15E-05	5.514702
ILMN_3265365	CEP78	-1.40039	6.472042	-4.50645	4.41E-05	0.001013	1.877718
ILMN_1790100	C11orf82	-1.39887	8.061855	-4.74482	2.01E-05	0.000597	2.625405
ILMN_2171183	C21orf45	-1.39828	6.854551	-3.70582	0.000558	0.006342	-0.512
ILMN_1712075	SYNM	-1.39603	6.581963	-5.50045	1.55E-06	0.000101	5.067919
ILMN_1694268	HES6	-1.39576	10.29517	-4.17655	0.000128	0.002141	0.867701
ILMN_2148150	CHAC2	-1.39443	5.833601	-4.78009	1.79E-05	0.000547	2.737123
ILMN_1730825	SGOL1	-1.39403	6.482791	-5.91661	3.69E-07	3.61E-05	6.443998
ILMN_2203896	SMAD7	-1.39019	7.508251	-4.43896	0.000055	0.001174	1.668623
ILMN_1674662	C15orf42	-1.38965	5.671594	-4.33307	7.76E-05	0.00151	1.343014
ILMN_2334204	ERCC6L	-1.38798	5.455496	-5.41879	2.05E-06	0.000124	4.799888
ILMN_1726666	GPX3	-1.38488	10.15509	-3.69461	0.000577	0.006473	-0.54383
ILMN_1693766	CEP135	-1.38021	6.699839	-4.889	1.24E-05	0.000421	3.083802
ILMN_1785095	ATP6V0E2	-1.37998	11.54702	-4.22959	0.000108	0.001901	1.027925
ILMN_3307921	PGLYRP2	-1.37851	6.468616	-3.26987	0.002026	0.016439	-1.70944
ILMN_2399463	VAV3	-1.37839	9.329338	-3.62706	0.000708	0.007466	-0.73456
ILMN_1757552	PTRF	-1.3779	9.519856	-3.97943	0.00024	0.00342	0.280258
ILMN_1785756	LOC731314	-1.37748	10.55532	-4.35287	7.28E-05	0.001438	1.403643
ILMN_1666057	REEP2	-1.37683	5.837883	-4.74985	1.98E-05	0.000591	2.641313
ILMN_1694589	PAQR8	-1.37516	9.999703	-3.8044	0.000413	0.005082	-0.22986
ILMN_3231820	SIVA1	-1.37503	9.146937	-5.34691	2.63E-06	0.000142	4.564603
ILMN_1705861	AP1M2	-1.37308	7.130809	-3.89594	0.000311	0.004133	0.035518
ILMN_2077550	RACGAP1	-1.37199	7.954921	-4.55455	3.77E-05	0.000909	2.027493
ILMN_2096372	ALDH1A1	-1.37197	12.37252	-7.16428	4.79E-09	1.59E-06	10.60677
ILMN_3272500	IFI27L1	-1.36884	7.856249	-4.50767	0.000044	0.00101	1.881523
ILMN_1705676	MRAP	-1.36603	5.074047	-6.30504	9.55E-08	1.34E-05	7.738283
ILMN_1704531	PTGR1	-1.36589	6.920656	-6.10987	1.88E-07	2.16E-05	7.087162
ILMN_1808487	PLA2G12B	-1.36455	9.191411	-4.93673	1.06E-05	0.00038	3.236492
ILMN_1745034	SLC11A2	-1.36125	10.07193	-5.34958	2.6E-06	0.000141	4.573337
ILMN_1695357	CCDC99	-1.36097	8.084316	-4.10675	0.00016	0.002507	0.658199
ILMN_1803647	FAM162A	-1.36043	8.509578	-4.62582	2.98E-05	0.000781	2.25045
ILMN_2202948	BUB1	-1.3595	8.976728	-5.24297	3.75E-06	0.000184	4.225591
ILMN_3238712	SNRNP25	-1.35923	7.277256	-3.61225	0.00074	0.007724	-0.77612
ILMN_1695386	RAD51C	-1.35865	9.4548	-4.82183	1.55E-05	0.000498	2.869723
ILMN_1741801	CDC7	-1.35836	6.827291	-3.88538	0.000321	0.004229	0.004727
ILMN_1776936	ANKRD38	-1.35578	10.29349	-4.35699	7.18E-05	0.001423	1.416272

ILMN_2362549	ZWINT	-1.3557	8.002877	-3.23704	0.002225	0.01763	-1.79597
ILMN_1731745	NINJ2	-1.35541	5.698533	-5.73741	6.86E-07	5.53E-05	5.849663
ILMN_1666208	C14orf106	-1.35501	8.494336	-4.58056	3.46E-05	0.000854	2.108733
ILMN_1711087	LOC648526	-1.35363	7.124731	-5.09788	6.14E-06	0.00026	3.75503
ILMN_1729816	VDAC3	-1.35322	11.85312	-5.99673	2.79E-07	2.88E-05	6.710409
ILMN_1706238	CSE1L	-1.35098	11.30855	-5.16681	4.86E-06	0.000219	3.97819
ILMN_1776582	PDK3	-1.34671	6.327602	-4.61077	3.13E-05	0.000801	2.203282
ILMN_1786041	ASB9	-1.34433	7.606281	-2.78586	0.007693	0.044368	-2.92691
ILMN_3273229	LOC100129781	-1.34383	5.518205	-6.17876	1.48E-07	1.83E-05	7.316875
ILMN_1776181	BIRC3	-1.33929	5.956913	-4.1016	0.000163	0.002541	0.64282
ILMN_2365383	ENO3	-1.33844	7.094956	-3.82749	0.000384	0.004821	-0.16323
ILMN_2132161	KIF18A	-1.33784	6.545876	-3.8815	0.000325	0.004275	-0.00657
ILMN_2157240	MNS1	-1.33687	5.962788	-4.65814	2.68E-05	0.000722	2.351973
ILMN_1714730	UBE2C	-1.33478	9.263373	-5.37532	2.38E-06	0.000135	4.657505
ILMN_1698185	WDR90	-1.33332	7.341004	-4.72866	2.12E-05	0.00062	2.574288
ILMN_1688299	RCAN3	-1.32717	6.285824	-5.96985	3.07E-07	3.13E-05	6.620993
ILMN_1777797	AFM	-1.32556	5.024594	-6.52172	4.49E-08	7.63E-06	8.46219
ILMN_2210837	CDC26	-1.32449	10.0279	-5.6723	8.59E-07	0.000065	5.634335
ILMN_1723709	C9orf116	-1.32372	7.12631	-4.9954	8.67E-06	0.000334	3.424737
ILMN_2219466	APOBEC3B	-1.3224	5.103355	-5.67844	8.41E-07	6.38E-05	5.65461
ILMN_1720526	CENPN	-1.32194	9.478019	-5.46794	1.74E-06	0.00011	4.961128
ILMN_1787526	MGC13057	-1.32182	6.409619	-6.10827	1.89E-07	2.16E-05	7.08183
ILMN_1658010	CENPI	-1.32024	5.338095	-5.69319	7.99E-07	6.15E-05	5.703369
ILMN_1806040	TYMS	-1.32003	10.62574	-4.28401	9.09E-05	0.001682	1.193235
ILMN_2395236	CHEK2	-1.31789	7.696364	-4.58207	3.44E-05	0.000852	2.113454
ILMN_1693221	CENPH	-1.31773	6.512788	-5.19758	4.37E-06	0.000204	4.078061
ILMN_1785914	CDC6	-1.31744	5.642259	-6.21232	1.32E-07	1.68E-05	7.428817
ILMN_3247438	C19orf69	-1.31734	5.923363	-4.54696	3.86E-05	0.000925	2.003825
ILMN_1691264	NAT8B	-1.31564	6.059194	-4.64366	2.81E-05	0.000749	2.306448
ILMN_2351916	EXO1	-1.31253	5.310077	-5.85268	4.6E-07	4.13E-05	6.231713
ILMN_2301083	UBE2C	-1.31227	9.572666	-5.08577	6.39E-06	0.000268	3.715919
ILMN_1762407	CABLES2	-1.31217	7.231956	-5.15608	5.04E-06	0.000224	3.943389
ILMN_1674411	CKAP2	-1.30795	8.05372	-3.88168	0.000325	0.004275	-0.00603
ILMN_2362545	ZWINT	-1.30756	7.169648	-3.31359	0.001786	0.014931	-1.59334
ILMN_1732509	LRRC40	-1.30743	6.373133	-4.42365	5.78E-05	0.001217	1.621354
ILMN_1731070	ORC6L	-1.30667	7.067833	-4.16668	0.000132	0.002187	0.838005
ILMN_2169089	C18orf54	-1.30656	5.823079	-4.48339	4.76E-05	0.001068	1.806137
ILMN_1673521	KISS1R	-1.30643	9.344051	-4.12384	0.000152	0.002421	0.709348
ILMN_2384056	GPER	-1.30431	10.91006	-4.24584	0.000103	0.00184	1.077201

ILMN_2293902	ABCC6	-1.30147	6.666171	-5.32272	2.85E-06	0.000152	4.485566
ILMN_1778890	PPIL5	-1.30067	6.810519	-5.49069	1.61E-06	0.000105	5.035835
ILMN_1781952	MGST1	-1.29932	6.564437	-5.46996	1.72E-06	0.00011	4.967736
ILMN_1726114	SLC45A3	-1.2986	6.99644	-4.70404	0.000023	0.000655	2.496538
ILMN_1723092	CRB3	-1.29845	8.274256	-5.8782	4.21E-07	3.91E-05	6.316428
ILMN_1742145	ESPL1	-1.29799	6.815632	-4.61202	3.12E-05	0.0008	2.207198
ILMN_3176989	HAUS8	-1.2975	6.405627	-4.25785	9.89E-05	0.001785	1.113676
ILMN_2310296	C21orf58	-1.29433	5.846452	-4.89233	1.23E-05	0.000417	3.094432
ILMN_1768293	NUP155	-1.29282	8.925634	-5.2966	3.12E-06	0.000161	4.400347
ILMN_1660654	CDCA2	-1.29133	6.699081	-4.46633	5.03E-05	0.001118	1.753266
ILMN_1718152	DEPDC7	-1.29131	7.331655	-3.77263	0.000455	0.005439	-0.3212
ILMN_1768020	HAUS8	-1.29	6.589788	-4.76777	1.86E-05	0.000563	2.698083
ILMN_2230892	IL10RB	-1.28876	8.8532	-8.86431	1.44E-11	1.98E-08	16.15818
ILMN_1785646	PMP22	-1.28747	7.207327	-3.89584	0.000311	0.004133	0.035213
ILMN_1660793	PAQR4	-1.28655	8.890741	-4.96858	9.49E-06	0.000355	3.338604
ILMN_2347592	NMB	-1.28565	6.947374	-4.69273	2.39E-05	0.000672	2.460891
ILMN_1807277	IFI30	-1.28563	6.81959	-3.64435	0.000672	0.007211	-0.68592
ILMN_1802780	M160	-1.28485	7.180029	-4.40755	0.000061	0.001267	1.5717
ILMN_2370365	RFC4	-1.28267	8.98324	-3.74233	0.000499	0.005826	-0.40795
ILMN_1732885	BTBD12	-1.27892	7.375547	-5.1881	4.52E-06	0.000208	4.047266
ILMN_1762606	AQP11	-1.27717	9.471232	-3.71182	0.000548	0.006245	-0.49493
ILMN_3201115	LOC440043	-1.27675	12.62267	-5.89738	3.94E-07	3.74E-05	6.380101
ILMN_1757210	CALML4	-1.27602	7.249484	-4.75037	1.97E-05	0.000591	2.642973
ILMN_1703326	GPR44	-1.27523	7.018752	-3.84594	0.000363	0.00463	-0.10985
ILMN_1671933	CLCC1	-1.27454	6.853751	-5.27452	3.37E-06	0.000169	4.328343
ILMN_2407124	MCM8	-1.27256	7.514888	-4.18806	0.000124	0.00208	0.902411
ILMN_1670769	CENPQ	-1.2718	7.103883	-3.73853	0.000505	0.005869	-0.41882
ILMN_1677637	BDH1	-1.26794	6.84335	-4.65103	2.74E-05	0.000736	2.329597
ILMN_2383163	DEPDC7	-1.26714	7.139951	-4.11079	0.000158	0.002483	0.67029
ILMN_2210129	PRIM1	-1.26709	9.128049	-3.67268	0.000617	0.006778	-0.60595
ILMN_1773119	CCNF	-1.26542	9.109074	-4.68865	2.42E-05	0.000676	2.448012
ILMN_1657950	RPS26P10	-1.26537	6.159242	-5.70772	7.6E-07	5.93E-05	5.751423
ILMN_2137084	LIN9	-1.26244	6.291211	-3.99696	0.000227	0.003274	0.331958
ILMN_1668814	CENPM	-1.26014	6.120106	-4.07104	0.000179	0.002735	0.551662
ILMN_3190972	LOC100130291	-1.25695	7.662373	-5.96571	3.11E-07	3.17E-05	6.60721
ILMN_2374425	CCNE1	-1.25581	7.753254	-3.32902	0.001708	0.014406	-1.55213
ILMN_1753063	KIF15	-1.25435	7.283051	-3.48433	0.001084	0.0103	-1.13114
ILMN_1687757	AKR1C4	-1.25356	11.80971	-3.96537	0.00025	0.003542	0.238858
ILMN_1753183	CDCA4	-1.25336	7.694979	-4.5668	3.62E-05	0.000884	2.065716

ILMN_1874530	DIAPH3	-1.25116	7.025489	-3.01855	0.004108	0.027777	-2.35773
ILMN_1724407	TACC3	-1.24955	8.789626	-4.59462	0.000033	0.000834	2.152681
ILMN_2149400	SPC25	-1.24938	5.899767	-3.90095	0.000306	0.004088	0.05012
ILMN_2330243	NUDT1	-1.24808	7.240407	-3.09981	0.003279	0.023479	-2.15179
ILMN_1696046	SIVA	-1.24761	10.41589	-5.37859	2.36E-06	0.000135	4.66823
ILMN_1799106	MOSC1	-1.2472	10.22573	-4.29968	8.65E-05	0.001626	1.241007
ILMN_1801307	TNFSF10	-1.24463	7.017186	-3.55954	0.000867	0.008706	-0.92328
ILMN_2090105	TAGLN2	-1.24288	6.516564	-3.23609	0.002232	0.017668	-1.79847
ILMN_3239861	C10orf140	-1.24283	6.587184	-4.54376	0.000039	0.000929	1.993856
ILMN_1771411	ALG6	-1.24281	7.146731	-4.04063	0.000198	0.002946	0.461243
ILMN_1771348	ACN9	-1.24127	7.626382	-4.44763	5.35E-05	0.001157	1.695395
ILMN_1655733	RFC2	-1.24113	5.877546	-5.27768	3.33E-06	0.000168	4.338649
ILMN_1708798	EAF2	-1.23898	5.875123	-4.18888	0.000123	0.002079	0.904879
ILMN_1734096	DCLRE1A	-1.23885	7.138553	-4.62959	2.94E-05	0.000774	2.262289
ILMN_2049642	RPA1	-1.23846	10.16978	-5.11445	5.8E-06	0.000248	3.808624
ILMN_1750102	EME1	-1.23579	6.261553	-3.8323	0.000379	0.004775	-0.14931
ILMN_1685928	WDR34	-1.23554	6.521201	-3.93096	0.000279	0.003837	0.137857
ILMN_1725260	CDC25C	-1.234	7.980853	-4.66961	2.58E-05	0.000705	2.388035
ILMN_2238928	RAD51C	-1.23212	8.137016	-5.2135	4.14E-06	0.000196	4.12976
ILMN_3277209	LOC285943	-1.23163	7.361128	-4.65133	2.74E-05	0.000736	2.33057
ILMN_1815184	ASPM	-1.2309	9.432988	-3.0951	0.003322	0.023688	-2.16382
ILMN_3215759	LOC441484	-1.22984	7.362404	-4.75495	1.94E-05	0.000583	2.657474
ILMN_2380561	PKLR	-1.22874	6.026655	-3.59316	0.000784	0.008073	-0.82957
ILMN_1765417	RBBP9	-1.2274	6.756324	-4.30364	8.54E-05	0.001612	1.25307
ILMN_1670801	MTR	-1.22684	7.513983	-6.90784	1.17E-08	2.8E-06	9.752031
ILMN_1761463	EFHD2	-1.22679	9.195373	-4.40865	6.07E-05	0.001265	1.575085
ILMN_1772292	LOC653752	-1.22654	7.118416	-3.87865	0.000328	0.004294	-0.01486
ILMN_2205032	MAGEE1	-1.22522	6.769108	-4.37518	6.77E-05	0.001366	1.472114
ILMN_1746699	SGOL2	-1.22415	7.104901	-3.57674	0.000824	0.008355	-0.8754
ILMN_3236244	C1orf174	-1.22335	9.13509	-6.5773	3.7E-08	6.87E-06	8.647942
ILMN_1662587	PNPLA7	-1.2204	7.020578	-3.28094	0.001962	0.016018	-1.68011
ILMN_1718771	CCDC24	-1.21999	6.236806	-3.23485	0.002239	0.017698	-1.80172
ILMN_2124361	LEAP2	-1.2185	9.620157	-2.74996	0.008454	0.047512	-3.01189
ILMN_1761314	NFS1	-1.21671	6.085111	-4.82756	1.52E-05	0.000493	2.88794
ILMN_1659350	CASP6	-1.2155	5.133048	-7.30159	2.98E-09	1.12E-06	11.06334
ILMN_1781045	FXYD2	-1.2153	6.621921	-3.23179	0.002259	0.01782	-1.80977
ILMN_2201580	GSTM2	-1.2145	8.348228	-3.40172	0.001383	0.012301	-1.35648
ILMN_1781966	OSBP2	-1.21444	6.451602	-3.54654	0.000901	0.008981	-0.95939
ILMN_1755834	FEN1	-1.21431	7.924053	-4.12114	0.000153	0.00243	0.701272

ILMN_1658607	DLEU2	-1.21346	6.235867	-3.63308	0.000695	0.007383	-0.71765
ILMN_3305735	LOC730101	-1.21232	8.125095	-4.03175	0.000203	0.003009	0.434901
ILMN_2203891	SMAD7	-1.21212	7.770548	-6.19691	1.39E-07	1.76E-05	7.377408
ILMN_1731343	LDLRAD1	-1.21197	5.288334	-5.92434	3.59E-07	3.56E-05	6.469695
ILMN_2343563	ANAPC11	-1.21132	8.927138	-5.64089	9.57E-07	7.07E-05	5.53058
ILMN_1795852	CCNE1	-1.2104	7.032832	-3.93024	0.000279	0.003843	0.135742
ILMN_1808071	KIF14	-1.21021	7.317113	-3.74416	0.000496	0.005808	-0.40274
ILMN_1780667	WDR51A	-1.20787	9.44498	-4.46295	5.09E-05	0.001126	1.742815
ILMN_3277332	LOC441453	-1.20687	8.736666	-5.27769	3.33E-06	0.000168	4.338694
ILMN_3236112	TP53TG1	-1.2058	6.003672	-4.4852	4.73E-05	0.001065	1.811758
ILMN_1684563	SPIN4	-1.20539	7.268288	-3.67481	0.000613	0.006756	-0.59995
ILMN_1736176	PLK1	-1.20444	9.070092	-4.91497	1.14E-05	0.000399	3.166821
ILMN_1735093	TIMELESS	-1.20413	8.665014	-3.92663	0.000282	0.00387	0.125196
ILMN_1694126	KIF24	-1.20396	5.008364	-6.52921	4.37E-08	7.56E-06	8.4872
ILMN_1737184	CDCA7	-1.20387	10.8434	-3.34058	0.001652	0.01407	-1.52118
ILMN_1781942	HMMR	-1.20255	9.366598	-3.6665	0.000628	0.006859	-0.62343
ILMN_1714861	CD68	-1.20134	9.739647	-4.27365	0.000094	0.001725	1.161685
ILMN_1709634	CMBL	-1.2012	9.621142	-4.92333	1.11E-05	0.000391	3.193564
ILMN_2407619	CDC25C	-1.20084	7.075145	-4.27508	9.36E-05	0.00172	1.166048
ILMN_1685916	KIF2C	-1.2007	7.896196	-3.82772	0.000384	0.00482	-0.16257
ILMN_1667022	PASK	-1.20004	6.739669	-3.901	0.000306	0.004088	0.050274
ILMN_1806607	SFN	-1.20001	6.846684	-3.15281	0.002826	0.021047	-2.01553
ILMN_1657087	ZNF533	-1.19812	7.60556	-4.35776	7.17E-05	0.001422	1.41864
ILMN_1692511	TMEM106C	-1.19691	9.633532	-4.11919	0.000154	0.002441	0.695425
ILMN_3241046	MYBL1	-1.19662	5.385874	-4.61747	3.06E-05	0.000792	2.224265
ILMN_1731612	UCHL5	-1.19577	9.398869	-4.85704	1.38E-05	0.000457	2.981818
ILMN_1768816	TMPO	-1.19554	7.144682	-3.19332	0.00252	0.01932	-1.9104
ILMN_1681221	C9orf100	-1.19314	6.434537	-4.75422	1.95E-05	0.000584	2.655166
ILMN_1761247	PIR	-1.19312	8.978125	-5.3821	2.33E-06	0.000134	4.679721
ILMN_1656452	C16orf59	-1.19206	7.618598	-4.29316	8.83E-05	0.001648	1.221114
ILMN_1792712	LOC201725	-1.19148	7.065163	-4.27863	9.25E-05	0.001707	1.176849
ILMN_1739032	TMEM70	-1.19147	6.493446	-5.86006	4.49E-07	4.06E-05	6.256205
ILMN_1674924	PRR17	-1.19125	7.289142	-3.98603	0.000235	0.003363	0.299715
ILMN_1737110	LOC651957	-1.19054	5.50198	-6.1401	1.7E-07	0.00002	7.187937
ILMN_1788166	TTK	-1.18976	8.328562	-3.83106	0.00038	0.004789	-0.15291
ILMN_3247163	TET1	-1.18847	7.735962	-3.57901	0.000818	0.00832	-0.86908
ILMN_1693090	CROT	-1.1856	6.12423	-4.26679	9.61E-05	0.001751	1.140848
ILMN_1722127	RAD54B	-1.18449	6.42395	-4.28661	9.02E-05	0.001673	1.201162
ILMN_1704656	PPP2R1B	-1.18437	7.347484	-5.38113	2.34E-06	0.000134	4.676543

ILMN_2103024	RBP5	-1.18199	7.590571	-4.01658	0.000213	0.003124	0.389957
ILMN_2222008	KIFC1	-1.18198	9.31171	-4.27053	0.000095	0.001739	1.152206
ILMN_1755974	ALDOC	-1.18149	8.277319	-3.23009	0.00227	0.017886	-1.81424
ILMN_1659255	RP2	-1.18137	6.003446	-4.63025	2.94E-05	0.000773	2.26436
ILMN_2230683	CDCA7L	-1.17995	5.873839	-4.99705	8.63E-06	0.000334	3.430031
ILMN_3240003	LOC100133012	-1.17948	8.418768	-3.58442	0.000805	0.008225	-0.85397
ILMN_1785198	POLE3	-1.17836	10.84926	-4.92627	1.09E-05	0.00039	3.202987
ILMN_1783676	CCDC15	-1.17783	6.338946	-3.47923	0.001101	0.010404	-1.14514
ILMN_1698546	HNF4A	-1.17767	6.462191	-5.40808	2.13E-06	0.000127	4.764791
ILMN_1767260	CCDC138	-1.17654	7.509252	-3.79878	0.00042	0.005149	-0.24604
ILMN_1697729	MAP2K6	-1.17583	4.801553	-8.64298	3.02E-11	2.77E-08	15.45105
ILMN_1691949	LOC728554	-1.17482	10.71868	-4.44143	5.46E-05	0.001172	1.676254
ILMN_1651705	CAT	-1.17473	10.46626	-3.88751	0.000319	0.004212	0.010943
ILMN_1665797	CSE1L	-1.17466	11.01453	-4.5587	3.72E-05	0.000903	2.040451
ILMN_1729051	MSH6	-1.17414	10.69507	-4.40285	6.19E-05	0.001283	1.557214
ILMN_1653042	HSD3B7	-1.17372	7.033363	-3.33966	0.001657	0.014094	-1.52366
ILMN_1683250	LOC440731	-1.17161	7.343744	-5.25073	3.65E-06	0.000179	4.250857
ILMN_1678619	DAK	-1.17116	9.413387	-3.4828	0.001089	0.01034	-1.13535
ILMN_1723625	MAP4K2	-1.17106	9.108967	-5.39574	2.22E-06	0.000131	4.72435
ILMN_2288784	CCDC34	-1.1699	9.688094	-3.24453	0.002178	0.017347	-1.77628
ILMN_1708375	IRF1	-1.16893	6.356497	-4.64549	2.79E-05	0.000746	2.312188
ILMN_1755075	IDI1	-1.16661	9.130175	-3.07964	0.003468	0.024472	-2.20322
ILMN_1683305	COMMD2	-1.16586	8.878772	-4.86514	1.34E-05	0.000448	3.007636
ILMN_1685258	TMEM14B	-1.16564	10.9595	-4.69575	2.36E-05	0.00067	2.470406
ILMN_1801391	SKP2	-1.16431	5.517885	-5.18141	4.62E-06	0.000212	4.025551
ILMN_1753582	RPA2	-1.16431	9.608117	-4.64506	0.000028	0.000746	2.310858
ILMN_2371700	UCHL5IP	-1.16074	7.797528	-4.74076	2.04E-05	0.000603	2.612543
ILMN_1660222	MTBP	-1.16042	5.470608	-5.79618	5.6E-07	4.76E-05	6.044331
ILMN_1811472	KIF23	-1.16029	7.73677	-4.31218	0.000083	0.001581	1.279163
ILMN_1681679	TSPO	-1.15958	6.885939	-4.12641	0.000151	0.002406	0.71706
ILMN_1753353	SLBP	-1.15929	9.35235	-5.12509	5.59E-06	0.000242	3.843039
ILMN_1686458	CEP152	-1.15865	5.783108	-3.63106	0.0007	0.007404	-0.72333
ILMN_2355168	MGST1	-1.1571	11.24504	-5.40993	2.12E-06	0.000126	4.770842
ILMN_2125010	SKAP2	-1.15649	7.210078	-4.67795	2.51E-05	0.000693	2.414301
ILMN_1716445	LOC727761	-1.15613	8.264883	-4.20615	0.000117	0.002006	0.95701
ILMN_1712389	CKLF	-1.15578	10.38156	-4.91533	1.14E-05	0.000399	3.167968
ILMN_1736015	PHF17	-1.15491	7.277542	-5.3214	2.87E-06	0.000152	4.481282
ILMN_1772686	FGD3	-1.15402	6.173425	-4.08319	0.000173	0.002658	0.587852
ILMN_1671905	C10orf78	-1.15385	5.670538	-4.74257	2.02E-05	0.0006	2.618283

ILMN_3234884	KIF22	-1.15349	10.15217	-4.12314	0.000152	0.002424	0.707263
ILMN_2041046	CKS1B	-1.15246	10.07838	-5.15045	5.13E-06	0.000227	3.925156
ILMN_1786050	RBBP9	-1.15137	9.289227	-5.4473	1.86E-06	0.000117	4.893374
ILMN_2391861	GSTM1	-1.15096	9.548321	-3.62532	0.000712	0.0075	-0.73947
ILMN_3234081	LOC100129076	-1.15066	5.501345	-4.87092	1.32E-05	0.000442	3.026089
ILMN_1725244	HAT1	-1.14917	9.810398	-4.02651	0.000207	0.003051	0.419359
ILMN_1758293	UBR7	-1.14825	5.943899	-4.48648	4.71E-05	0.001061	1.81573
ILMN_2216918	SHPK	-1.14785	10.41571	-5.06942	6.76E-06	0.000276	3.663131
ILMN_1718336	C7orf50	-1.14778	10.61371	-4.94103	1.04E-05	0.000377	3.250249
ILMN_1898692		-1.1463	5.213247	-5.31721	2.91E-06	0.000154	4.467603
ILMN_3185161	CEP78	-1.14613	6.059606	-4.06349	0.000184	0.00279	0.529168
ILMN_1684802	TAF5	-1.14574	6.998915	-5.14648	5.2E-06	0.00023	3.912303
ILMN_1683441	NCAPD3	-1.14492	8.593678	-4.5024	4.47E-05	0.001022	1.865137
ILMN_1727055	C12orf48	-1.14491	8.333801	-4.31648	8.19E-05	0.001567	1.292276
ILMN_1788135	APITD1	-1.14408	6.028777	-4.53932	3.96E-05	0.000938	1.98001
ILMN_1667825	MLKL	-1.14202	8.692438	-4.62067	3.03E-05	0.000787	2.234296
ILMN_1748241	CENPP	-1.14193	5.37328	-5.27748	3.33E-06	0.000168	4.338003
ILMN_2075476	GIPC2	-1.14179	6.533372	-3.78069	0.000444	0.005363	-0.29806
ILMN_1693669	WDR79	-1.14081	7.133172	-3.7045	0.00056	0.006357	-0.51575
ILMN_2338038	AK3L1	-1.14044	10.43446	-5.301	3.07E-06	0.000159	4.414699
ILMN_1762622	FAM111B	-1.13943	5.085276	-6.42651	6.26E-08	9.71E-06	8.14402
ILMN_2087629	NOL4	-1.13903	5.161867	-5.19475	4.42E-06	0.000205	4.068844
ILMN_1659990	C7orf68	-1.13878	6.450364	-4.44597	5.38E-05	0.001161	1.690265
ILMN_1732468	HSPA4L	-1.13833	7.615032	-4.23214	0.000107	0.00189	1.035676
ILMN_1776577	DSCC1	-1.13507	7.105764	-4.24339	0.000104	0.001848	1.069783
ILMN_1696266	XRCC3	-1.13388	6.632516	-3.59091	0.000789	0.008113	-0.83585
ILMN_1806502	ZNF165	-1.13372	7.450774	-7.15199	5E-09	1.64E-06	10.56589
ILMN_1725121	XPO1	-1.13366	10.89141	-3.42704	0.001284	0.011617	-1.28775
ILMN_1715991	SDPR	-1.13298	8.156017	-4.32783	7.89E-05	0.001528	1.326963
ILMN_1692517	LOC653381	-1.1328	12.03789	-4.9608	9.75E-06	0.000361	3.313622
ILMN_1715173	RPS6KA1	-1.13271	7.282787	-5.35632	2.54E-06	0.000139	4.595371
ILMN_2086095	ID2	-1.13207	10.74762	-5.35974	2.51E-06	0.000139	4.606568
ILMN_1753613	HOXA5	-1.13086	8.009951	-5.89438	3.98E-07	3.76E-05	6.370142
ILMN_1726893	EPN3	-1.13056	5.098012	-5.51135	1.5E-06	9.97E-05	5.103746
ILMN_2148796	MND1	-1.12962	7.400511	-4.13233	0.000148	0.002375	0.734812
ILMN_2366388	PRDX1	-1.12957	12.9458	-7.36012	2.43E-09	9.68E-07	11.25764
ILMN_1657796	STMN1	-1.12611	8.850204	-3.47167	0.001126	0.010576	-1.16588
ILMN_1703906	HJURP	-1.12566	8.770089	-3.501	0.001032	0.009921	-1.08529
ILMN_1787248	SIVA	-1.12495	9.21531	-4.42646	5.73E-05	0.001209	1.630019

ILMN_1775016	MPZL2	-1.1244	6.205631	-3.20609	0.002431	0.018858	-1.87707
ILMN_1745223	CDC42EP4	-1.12344	10.83722	-5.16525	4.88E-06	0.000219	3.973134
ILMN_2199676	CEP152	-1.12253	6.316478	-3.31124	0.001798	0.015019	-1.5996
ILMN_1769810	ARL6IP5	-1.12133	9.542029	-3.9506	0.000262	0.003674	0.195459
ILMN_1797307	BUB1B	-1.12033	7.239325	-4.43567	5.56E-05	0.001184	1.658449
ILMN_1801257	CENPA	-1.12023	8.754036	-4.14908	0.00014	0.002284	0.785085
ILMN_2384785	CCNE1	-1.11992	6.27555	-3.34535	0.001629	0.013932	-1.50841
ILMN_1683927	ITGAE	-1.11847	8.158213	-5.39826	2.2E-06	0.00013	4.732622
ILMN_1743747	RUSC1	-1.11829	9.631151	-5.48408	1.64E-06	0.000106	5.014128
ILMN_1665331	AMT	-1.11801	9.263654	-3.88601	0.000321	0.004225	0.006587
ILMN_1669394	EI24	-1.11793	10.40217	-7.67552	8.17E-10	4.08E-07	12.3012
ILMN_1711005	CDC25A	-1.11723	8.492509	-4.31195	8.31E-05	0.001582	1.278435
ILMN_1684289	PNPO	-1.11555	10.6104	-6.15503	1.61E-07	1.95E-05	7.237713
ILMN_2376108	PSMB9	-1.11476	5.459559	-4.48903	4.67E-05	0.001054	1.823654
ILMN_1684306	S100A4	-1.11456	5.200733	-3.48064	0.001096	0.010384	-1.14127
ILMN_1716583	NME7	-1.11448	7.439282	-5.44577	1.87E-06	0.000117	4.888353
ILMN_1703279	CXorf57	-1.11421	6.211239	-5.07588	6.61E-06	0.000273	3.683973
ILMN_1716089	KANK2	-1.1133	5.307365	-5.73517	6.91E-07	5.55E-05	5.842239
ILMN_2338963	SLC29A1	-1.1131	8.827661	-3.77544	0.000451	0.005411	-0.31315
ILMN_1654737	TRIM32	-1.11285	6.574603	-5.21423	4.13E-06	0.000196	4.13215
ILMN_1712718	BPNT1	-1.11229	6.730215	-3.4624	0.001157	0.010792	-1.19126
ILMN_1761939	TIPIN	-1.11142	6.926379	-4.81602	1.58E-05	0.000505	2.851235
ILMN_1745397	OAS3	-1.11136	6.855262	-4.97902	9.17E-06	0.000348	3.372117
ILMN_1736238	GNMT	-1.1111	5.650955	-4.07479	0.000177	0.00271	0.562821
ILMN_1707783	CCDC72	-1.1105	10.7244	-4.78479	1.76E-05	0.000541	2.75204
ILMN_2414027	CKLF	-1.11041	9.906204	-4.5591	3.71E-05	0.000902	2.041703
ILMN_1859127		-1.10992	5.172264	-6.74405	2.07E-08	4.28E-06	9.205127
ILMN_2207328	C18orf10	-1.10974	7.954058	-3.50861	0.001009	0.009771	-1.06432
ILMN_1770466	ATP5G3	-1.10846	7.154859	-5.78539	5.81E-07	4.88E-05	6.008541
ILMN_1776094	PPCS	-1.10723	9.494588	-4.6347	2.89E-05	0.000763	2.278318
ILMN_1768637	TNNI3	-1.10719	5.539207	-4.456	5.21E-05	0.001139	1.721294
ILMN_1749253	TUBD1	-1.10713	7.453763	-3.6943	0.000578	0.006477	-0.54471
ILMN_1676191	DARS2	-1.10684	8.503716	-4.2944	8.79E-05	0.001645	1.224907
ILMN_1731044	KCTD14	-1.10674	7.918634	-3.97634	0.000242	0.003449	0.271167
ILMN_1663195	MCM7	-1.10655	11.15852	-4.40252	0.000062	0.001283	1.556197
ILMN_1787477	CENPO	-1.10527	5.779922	-4.32514	7.96E-05	0.001535	1.318762
ILMN_1792356	DPYSL4	-1.10505	5.46472	-4.10468	0.000161	0.002521	0.652025
ILMN_1812701	C4orf33	-1.10474	5.781231	-4.25443	0.0001	0.001799	1.103274
ILMN_1732296	ID3	-1.10464	9.108786	-2.89099	0.005813	0.03589	-2.67363

ILMN_2383300	PTPRU	-1.10406	7.670457	-5.68358	8.26E-07	6.32E-05	5.671617
ILMN_1671906	MND1	-1.1037	7.738203	-3.95057	0.000262	0.003674	0.195379
ILMN_1751956	MGST3	-1.10355	9.236542	-4.5242	4.16E-05	0.000973	1.932941
ILMN_1880052		-1.10261	6.818611	-3.84203	0.000367	0.004669	-0.12115
ILMN_2221046	GM2A	-1.10095	6.110432	-4.64324	2.81E-05	0.000749	2.305123
ILMN_1847308		-1.09883	8.066258	-5.44632	1.87E-06	0.000117	4.890168
ILMN_1778357	DNMT3L	-1.09678	4.964666	-6.23443	1.22E-07	1.57E-05	7.502582
ILMN_2348975	NASP	-1.0965	8.259461	-5.41536	2.08E-06	0.000124	4.78865
ILMN_2344971	FOXM1	-1.09645	8.168044	-3.46636	0.001143	0.0107	-1.18043
ILMN_1783075	C6orf167	-1.09589	5.885583	-4.51119	4.35E-05	0.001004	1.892458
ILMN_1736816	C13orf3	-1.09507	6.294218	-4.12371	0.000152	0.002421	0.708961
ILMN_1754858	PASK	-1.09491	6.085086	-3.79694	0.000422	0.005176	-0.25135
ILMN_1790637	C11orf80	-1.09467	7.890969	-5.55397	1.29E-06	8.86E-05	5.244003
ILMN_1709085	GSG2	-1.09333	5.500857	-4.87252	1.31E-05	0.00044	3.031184
ILMN_1657547	CCDC34	-1.09297	10.18205	-3.45313	0.001189	0.011001	-1.21661
ILMN_1761844	ZCCHC17	-1.09245	8.591907	-5.38433	2.31E-06	0.000133	4.687009
ILMN_1761084	FNDC5	-1.09172	5.274395	-4.35607	0.000072	0.001426	1.413479
ILMN_1803033	MGST1	-1.09154	5.833932	-5.00241	8.47E-06	0.000331	3.447271
ILMN_2228463	DDC	-1.09094	9.578349	-4.15835	0.000136	0.002229	0.812936
ILMN_1753196	PTTG1	-1.09015	8.722842	-4.8142	1.59E-05	0.000506	2.845435
ILMN_2312194	CYB5A	-1.08922	10.46112	-4.11016	0.000159	0.002486	0.668424
ILMN_2062468	IGFBP7	-1.08912	6.348125	-4.55408	3.77E-05	0.000909	2.026028
ILMN_2252408	CNPY4	-1.08599	6.91746	-4.69707	2.35E-05	0.000669	2.474564
ILMN_1801864	LOC730455	-1.08557	9.040683	-5.51696	1.47E-06	9.81E-05	5.122207
ILMN_1698677	C4orf27	-1.08542	6.607831	-3.86186	0.000345	0.004458	-0.06367
ILMN_1776052	LOC148915	-1.08523	10.08165	-3.8903	0.000316	0.004181	0.019062
ILMN_1692790	ITGB3BP	-1.08355	7.93305	-3.49757	0.001043	0.01	-1.09472
ILMN_1664682	DNA2	-1.08349	6.399925	-4.24567	0.000103	0.00184	1.076694
ILMN_1654065	ATOH8	-1.08343	4.841012	-7.64583	9.06E-10	4.29E-07	12.20324
ILMN_1784641	NDUFA3	-1.08305	8.747267	-5.00066	8.52E-06	0.000331	3.441649
ILMN_1756826	MORN2	-1.08212	6.278185	-5.08296	6.45E-06	0.000269	3.706844
ILMN_1751773	POLD3	-1.08088	6.428369	-3.98478	0.000236	0.003371	0.296018
ILMN_2395926	MANBAL	-1.08051	8.107831	-5.83464	4.9E-07	0.000043	6.171835
ILMN_1744118	ASTN2	-1.08046	7.11776	-4.51294	4.32E-05	0.000999	1.897891
ILMN_1691731	PARP14	-1.08044	6.88799	-5.20631	4.25E-06	0.000199	4.106394
ILMN_1771264	ELL3	-1.08022	5.959917	-4.16102	0.000135	0.002216	0.820967
ILMN_1808792	ALKBH6	-1.07822	7.357031	-4.15042	0.00014	0.002278	0.789091
ILMN_1765044	CUTC	-1.07812	8.171967	-5.51009	1.5E-06	9.97E-05	5.099605
ILMN_2058512	PSMA2	-1.07794	7.47218	-4.813	0.000016	0.000507	2.841647

ILMN_1664265	EPHA1	-1.07729	7.859584	-3.53843	0.000923	0.00914	-0.98187
ILMN_1712430	ATP5G1	-1.07616	6.952577	-5.24912	3.67E-06	0.00018	4.245611
ILMN_1807044	UBAC1	-1.0754	9.687026	-4.25375	0.0001	0.001802	1.1012
ILMN_1758629	DONSON	-1.07511	9.121454	-4.20789	0.000116	0.001998	0.962266
ILMN_1702197	C9orf140	-1.07411	9.371425	-3.57949	0.000817	0.008311	-0.86773
ILMN_1800465	LOC654042	-1.07385	6.571706	-4.36511	0.00007	0.001395	1.441189
ILMN_1756326	CKS2	-1.07314	9.831056	-4.78912	1.73E-05	0.000535	2.765786
ILMN_2375830	DIXDC1	-1.07207	6.392914	-3.57398	0.00083	0.00841	-0.88309
ILMN_3237584	LOC100133489	-1.07151	7.737687	-3.55367	0.000882	0.008831	-0.93959
ILMN_1660436	HSPA1B	-1.07129	10.83694	-4.82182	1.55E-05	0.000498	2.869661
ILMN_3305849	LOC728431	-1.07126	5.804769	-5.8058	5.41E-07	4.65E-05	6.076195
ILMN_1671766	F12	-1.07114	7.626309	-4.22236	0.000111	0.001933	1.006047
ILMN_1712122	FANCD2	-1.07085	5.133837	-5.51762	1.46E-06	9.81E-05	5.124384
ILMN_3307786	L3MBTL2	-1.07074	7.814649	-5.71171	7.49E-07	0.000059	5.764634
ILMN_1806634	NNT	-1.07043	9.206016	-4.4193	5.87E-05	0.001231	1.607918
ILMN_2312719	EXOSC9	-1.07035	8.975556	-5.22118	4.04E-06	0.000194	4.154745
ILMN_1681754	GGH	-1.07005	10.49166	-3.86888	0.000338	0.004392	-0.04325
ILMN_1709953	DONSON	-1.06967	6.751128	-3.28926	0.001916	0.015733	-1.65807
ILMN_1825660	CCDC15	-1.06935	5.788984	-4.6895	2.41E-05	0.000676	2.450689
ILMN_2151488	RMI1	-1.06677	8.778144	-3.42354	0.001297	0.011702	-1.29727
ILMN_1720889	SC4MOL	-1.06674	11.39757	-3.19722	0.002493	0.019188	-1.90023
ILMN_2354237	PARP2	-1.0659	7.687872	-4.16159	0.000135	0.002213	0.822685
ILMN_1688621	C9orf80	-1.06569	8.170512	-4.31563	8.21E-05	0.00157	1.289696
ILMN_3237745	MIMT1	-1.06261	6.851644	-3.4787	0.001103	0.010416	-1.14661
ILMN_2179778	PHLDB2	-1.06124	7.421476	-3.00513	0.004262	0.028467	-2.3914
ILMN_1658469	TP53AP1	-1.06029	6.769735	-3.79015	0.000431	0.005262	-0.27089
ILMN_2073604	EBP	-1.05911	9.238397	-3.08235	0.003442	0.024325	-2.19634
ILMN_2373515	HSP90AA1	-1.05905	13.24064	-4.89346	1.22E-05	0.000416	3.09805
ILMN_1732127	RBKS	-1.05873	8.047357	-4.01501	0.000214	0.003133	0.385328
ILMN_1710758	RNF20	-1.05778	8.878688	-4.94944	1.01E-05	0.00037	3.277214
ILMN_1688089	PEBP1	-1.0572	12.49827	-4.55655	3.74E-05	0.000908	2.03373
ILMN_3225843	LOC729298	-1.05505	7.369763	-4.47733	4.85E-05	0.001086	1.787369
ILMN_1710150	EED	-1.05386	7.081485	-3.89859	0.000308	0.004105	0.043234
ILMN_1710676	FBXO5	-1.05367	9.343347	-4.09427	0.000167	0.002586	0.620926
ILMN_2396947	PSMC3IP	-1.05323	5.43148	-4.61156	3.12E-05	0.0008	2.205741
ILMN_1685781	C14orf142	-1.05283	8.581397	-4.91959	1.12E-05	0.000394	3.181611
ILMN_3251145	LDHA	-1.05144	6.550953	-4.1974	0.00012	0.002039	0.930576
ILMN_2064898	CCDC56	-1.05097	11.54209	-5.44902	1.85E-06	0.000116	4.899015
ILMN_1747016	CEP55	-1.05045	8.723896	-3.71551	0.000542	0.006186	-0.48444

ILMN_1762275	CSE1L	-1.04854	7.366581	-4.29959	8.65E-05	0.001626	1.240711
ILMN_2180866	RPS26P11	-1.04751	11.72408	-5.32541	2.83E-06	0.000151	4.494371
ILMN_2195914	GGH	-1.04744	9.365075	-3.32891	0.001709	0.014406	-1.55244
ILMN_1771224	SKA1	-1.04721	6.821079	-3.33437	0.001682	0.014263	-1.53783
ILMN_2326509	CASP1	-1.04644	6.21054	-3.22712	0.002289	0.017999	-1.82202
ILMN_1893633	LOC439949	-1.04572	5.919634	-4.13858	0.000145	0.002337	0.75356
ILMN_2154671	COX6B1	-1.04515	8.695314	-5.39113	2.26E-06	0.000131	4.709254
ILMN_1729905	GAL3ST1	-1.04478	5.900405	-3.75139	0.000485	0.00571	-0.38205
ILMN_2089458	SASS6	-1.04476	6.881332	-3.67144	0.000619	0.006793	-0.60947
ILMN_1803124	BIRC5	-1.04261	5.854132	-3.27868	0.001975	0.016103	-1.6861
ILMN_1680692	NUCKS1	-1.04175	7.732758	-3.07896	0.003475	0.0245	-2.20496
ILMN_1682034	HEY2	-1.04109	5.435026	-5.27709	3.34E-06	0.000168	4.336714
ILMN_1792947	ESCO2	-1.04095	4.841345	-6.15614	1.6E-07	1.95E-05	7.241422
ILMN_3253579	HAUS8	-1.03983	6.118204	-4.27969	9.22E-05	0.001703	1.180095
ILMN_1654722	MPV17L	-1.03876	7.557931	-5.11947	5.7E-06	0.000244	3.824838
ILMN_1770479	LMO7	-1.03868	5.81053	-3.87568	0.000331	0.004323	-0.0235
ILMN_3234116	LOC730382	-1.0386	7.069662	-4.30991	8.37E-05	0.001589	1.272203
ILMN_2112460	MAD2L1	-1.03712	6.553765	-3.26536	0.002052	0.016608	-1.72135
ILMN_2399431	PRPS2	-1.03705	7.873132	-4.27698	0.000093	0.001712	1.171832
ILMN_3294024	LOC644990	-1.03665	5.953207	-4.59001	3.35E-05	0.000842	2.138276
ILMN_1691131	LSMD1	-1.03648	7.531006	-3.71787	0.000538	0.006154	-0.47771
ILMN_1727288	EVPL	-1.03555	7.848774	-3.94541	0.000266	0.003717	0.180238
ILMN_1684217	AURKB	-1.03406	9.221279	-2.94799	0.004983	0.032001	-2.53362
ILMN_1777453	LOC653419	-1.03372	5.276079	-4.60297	3.21E-05	0.000818	2.178828
ILMN_1747924	LOC644254	-1.03368	6.540956	-3.79282	0.000427	0.005226	-0.26322
ILMN_2203453	MSH2	-1.0333	6.076079	-3.77136	0.000457	0.005456	-0.32484
ILMN_1704750	LOC647000	-1.03263	13.41585	-4.2394	0.000105	0.001867	1.057658
ILMN_1728972	FAM64A	-1.02977	7.574601	-3.27173	0.002015	0.016384	-1.7045
ILMN_2410540	CASP2	-1.02934	9.615122	-6.17047	1.53E-07	1.87E-05	7.289225
ILMN_1701512	KIAA0391	-1.02927	10.04311	-5.85881	4.51E-07	4.06E-05	6.252029
ILMN_2194828	C16orf53	-1.02906	10.28159	-6.42254	6.34E-08	9.74E-06	8.130768
ILMN_1801443	TSKU	-1.02839	10.24279	-6.8788	1.29E-08	2.99E-06	9.655104
ILMN_1689327	LOC730534	-1.02798	11.09621	-3.92486	0.000284	0.003886	0.120017
ILMN_1672149	CHCHD1	-1.02647	7.518725	-4.09688	0.000165	0.002568	0.628714
ILMN_1655819	LOC728919	-1.02554	5.930168	-3.45711	0.001175	0.010925	-1.20575
ILMN_1842582		-1.02505	7.110595	-4.89798	0.000012	0.000411	3.112497
ILMN_2326512	CASP1	-1.02476	6.128407	-3.12974	0.003015	0.022062	-2.07501
ILMN_2117987	TFDP1	-1.0245	10.23149	-4.99079	8.81E-06	0.000338	3.409934
ILMN_1748751	NLF2	-1.02437	5.187557	-3.93322	0.000277	0.00382	0.144482

ILMN_1741017	PIP4K2B	-1.02387	5.748891	-3.25267	0.002128	0.017052	-1.75484
ILMN_1693410	BRI3BP	-1.02124	8.843339	-5.7539	6.48E-07	5.28E-05	5.90426
ILMN_2050790	C11orf52	-1.02059	5.940035	-4.07937	0.000175	0.002681	0.576457
ILMN_1728934	PRC1	-1.01745	10.24422	-4.22754	0.000109	0.001907	1.02173
ILMN_3242540	CD163L1	-1.01645	5.909903	-3.83007	0.000381	0.004798	-0.15576
ILMN_1782389	LAD1	-1.01597	11.07513	-6.39491	6.99E-08	1.04E-05	8.038448
ILMN_1773154	NFKBIA	-1.01593	11.423	-5.2555	3.59E-06	0.000177	4.266405
ILMN_1795719	RPA1	-1.01516	8.429233	-3.70699	0.000556	0.006325	-0.50869
ILMN_2101885	TUBB	-1.01499	11.78615	-3.58936	0.000793	0.008141	-0.84017
ILMN_1771964	GSTA4	-1.01464	8.778516	-4.00247	0.000223	0.003226	0.348229
ILMN_1779841	PPP2R1B	-1.01448	6.265667	-4.39594	6.33E-05	0.001302	1.535968
ILMN_2207988	SERPINI1	-1.01431	6.72203	-2.94971	0.004959	0.031903	-2.52937
ILMN_1760635	RAD51C	-1.01409	7.809981	-3.90602	0.000301	0.004054	0.064915
ILMN_1728517	FNTB	-1.01197	8.522548	-5.15719	5.02E-06	0.000224	3.946997
ILMN_1666553	SLC25A19	-1.01177	8.995093	-4.94415	1.03E-05	0.000374	3.260248
ILMN_2357438	AURKA	-1.01148	10.9893	-4.39198	6.41E-05	0.001315	1.523765
ILMN_2145518	TMEM126B	-1.01109	10.97103	-3.57879	0.000819	0.00832	-0.86968
ILMN_2115991	TNNT1	-1.01061	4.939523	-4.24779	0.000102	0.001832	1.083124
ILMN_3228822	TMEM194A	-1.01049	8.225075	-3.39343	0.001417	0.012514	-1.37892
ILMN_2401641	ALDH3A2	-1.00883	9.297494	-6.59312	3.5E-08	6.64E-06	8.70079
ILMN_1709294	CDCA8	-1.0085	8.957603	-3.53194	0.000941	0.009275	-0.99984
ILMN_1682494	RSRC1	-1.00836	7.246741	-3.52719	0.000955	0.009373	-1.01299
ILMN_1670609	ATOX1	-1.00802	10.62136	-4.22876	0.000109	0.001902	1.025421
ILMN_1800619	BRI3BP	-1.00786	8.353472	-3.59272	0.000785	0.00808	-0.83079
ILMN_1811050	CCDC88A	-1.00721	7.007464	-3.17795	0.002632	0.019978	-1.95037
ILMN_1812489	CCDC21	-1.00627	6.837972	-4.9554	9.93E-06	0.000365	3.296315
ILMN_2174189	DKK1	-1.00622	6.834475	-3.21565	0.002365	0.018473	-1.85209
ILMN_1652846	PCYT2	-1.00541	9.542442	-3.99521	0.000228	0.00329	0.326788
ILMN_1730260	N6AMT2	-1.00529	7.651037	-4.57088	3.57E-05	0.000874	2.078456
ILMN_2343047	ABCB9	-1.0049	6.833295	-3.85358	0.000354	0.004541	-0.08768
ILMN_2359029	C11orf17	-1.00449	7.914849	-4.1329	0.000148	0.002374	0.736519
ILMN_1659437	TXNDC17	-1.00404	11.68402	-5.35817	2.53E-06	0.000139	4.601416
ILMN_2415926	THOC3	-1.00359	8.273582	-3.48531	0.001081	0.010279	-1.12846
ILMN_1763852	ACACB	-1.00351	7.185809	-3.66584	0.00063	0.006865	-0.6253
ILMN_1707695	IFIT1	-1.00285	5.772479	-3.94171	0.00027	0.003752	0.169384
ILMN_1678423	SPA17	-1.00227	7.256887	-4.38122	6.64E-05	0.001345	1.490676
ILMN_1798952	KDELR3	-1.0021	6.984459	-2.76893	0.008044	0.045854	-2.96708
ILMN_2126706	LMNB1	-1.00182	8.081677	-3.60816	0.000749	0.007796	-0.78759
ILMN_2340065	UBL5	-1.0015	10.1218	-5.27817	3.32E-06	0.000168	4.340227

ILMN_1730454	FOLR3	-1.00149	4.893275	-4.24681	0.000103	0.001836	1.080138
ILMN_1706690	KHK	-1.00011	8.274146	-5.20157	4.31E-06	0.000202	4.091016
ILMN_1662846	GPR160	-1.00003	7.117608	-3.2441	0.002181	0.017359	-1.77741

Appendix K. Gene annotated list of up-regulated genes (DEGs) when exposed to 500 ppb of metolachlor exposed human liver cells for 48 hours compared to control.

PROBE_ID	SYMBOL	logFC	AveExpr	t	P.Value	adj.P.Val	B
ILMN_1772521	MTHFD1L	1.00027	10.25262	4.342753	7.52E-05	0.001473	1.372651
ILMN_1758087	TAOK1	1.000782	7.36158	3.752453	0.000484	0.005699	-0.37902
ILMN_1755462	UGCGL1	1.001927	7.114538	4.144222	0.000142	0.002309	0.770484
ILMN_1703284	SPIRE2	1.002084	8.308868	4.445656	5.38E-05	0.001161	1.689307
ILMN_1796508	TOP1MT	1.002733	6.02332	4.263137	9.73E-05	0.001767	1.129729
ILMN_1766125	LONP1	1.005146	9.632397	4.097331	0.000165	0.002567	0.630063
ILMN_1742431	LOC651309	1.005576	5.265253	2.960313	0.004818	0.031274	-2.50311
ILMN_1798256	UPP1	1.006158	7.662561	3.11924	0.003105	0.022512	-2.102
ILMN_1699265	TNFRSF10B	1.00633	11.31079	5.808516	5.36E-07	4.65E-05	6.08521
ILMN_1746578	SLC23A2	1.006627	9.609974	4.822786	1.55E-05	0.000498	2.87275
ILMN_1751789	HNMT	1.006877	9.2645	3.881021	0.000326	0.004275	-0.00795
ILMN_1754562	ARHGEF17	1.009544	7.445561	5.409056	2.12E-06	0.000126	4.767983
ILMN_1809859	PCGF2	1.009779	9.421167	5.48813	1.62E-06	0.000105	5.027434
ILMN_1696339	ZIC2	1.01154	5.234189	3.359378	0.001564	0.013507	-1.47074
ILMN_1659099	ROCK2	1.01156	9.255951	4.399262	6.26E-05	0.001291	1.54618
ILMN_1705922	BAIAP2	1.011704	7.260503	4.623119	3.01E-05	0.000784	2.241979
ILMN_1749396	LSR	1.012515	8.29672	4.364581	7.01E-05	0.001397	1.439574
ILMN_1656837	RBP1	1.012805	6.149766	2.729072	0.008928	0.049449	-3.06096
ILMN_2234697	BEX1	1.013315	9.688875	3.728721	0.00052	0.006004	-0.4468
ILMN_2344298	STEAP2	1.014294	5.893716	3.138576	0.002941	0.021713	-2.05227
ILMN_1796106	MGAT4B	1.014978	7.912868	3.945156	0.000267	0.003718	0.179483
ILMN_1807873	SNX6	1.015075	9.740075	6.240143	1.20E-07	1.56E-05	7.521658
ILMN_1656904	SLC1A4	1.015179	7.717673	4.576327	3.51E-05	0.000862	2.095487
ILMN_1718646	MMP15	1.015394	7.640419	5.469554	1.73E-06	0.00011	4.966419
ILMN_1808095	RNF41	1.015722	7.147075	4.324819	7.97E-05	0.001535	1.31777
ILMN_1721046	PTMS	1.015979	8.2028	4.240092	0.000105	0.001864	1.059768
ILMN_1746788	TRIM10	1.016284	8.584566	4.903737	1.18E-05	0.000406	3.130899
ILMN_1756006	ATG2A	1.016701	8.347945	3.156317	0.002798	0.020862	-2.00646
ILMN_2411963	RBM39	1.018776	9.772899	4.021291	0.00021	0.003087	0.403912
ILMN_1712046	CPXM1	1.019565	5.706717	3.710541	0.00055	0.006262	-0.49858
ILMN_1756501	ST6GAL1	1.020434	10.99613	5.221928	4.03E-06	0.000194	4.15716
ILMN_3242174	LOC652900	1.020989	7.541725	3.515924	0.000987	0.009612	-1.04413
ILMN_3251620	JMY	1.021856	7.067977	3.240236	0.002205	0.017521	-1.78758

ILMN_2041222	FLJ40504	1.022366	12.21878	5.611578	1.06E-06	7.65E-05	5.43386
ILMN_1685580	CBLB	1.02408	7.824427	4.326805	7.92E-05	0.001531	1.323843
ILMN_1682081	RNF19B	1.024314	8.097368	6.124663	1.79E-07	2.09E-05	7.136478
ILMN_1730639	SLC22A15	1.024518	4.697496	3.691532	0.000583	0.006515	-0.55257
ILMN_1700257	C4orf32	1.024873	6.25694	3.409103	0.001353	0.012116	-1.33647
ILMN_2048633	LRRC8E	1.02498	6.021926	4.301039	8.61E-05	0.001621	1.245144
ILMN_2065773	SCG5	1.025672	5.639627	3.249519	0.002148	0.017161	-1.76314
ILMN_1767514	LOC441155	1.026536	7.475302	4.305005	8.50E-05	0.001606	1.257244
ILMN_1802523	HS3ST5	1.027309	4.975528	4.569635	3.59E-05	0.000877	2.074581
ILMN_1669617	GRB10	1.02819	6.968446	4.117527	0.000155	0.002448	0.690453
ILMN_3306730	RBM47	1.028319	6.278	3.179229	0.002623	0.019923	-1.94706
ILMN_1653432	HNRPDL	1.029856	9.295205	4.647834	2.77E-05	0.000742	2.319568
ILMN_1732291	LOC653125	1.032215	5.591424	4.21307	0.000114	0.001975	0.977938
ILMN_1712469	GOLGA8A	1.033047	6.21355	3.020701	0.004083	0.027674	-2.35233
ILMN_1794017	SERTAD1	1.035874	7.416582	3.635698	0.00069	0.007336	-0.71029
ILMN_1766528	SLC25A36	1.036532	7.376325	3.657818	0.000645	0.006994	-0.64796
ILMN_1805395	LTBP3	1.036784	7.267342	4.301458	8.60E-05	0.00162	1.246422
ILMN_3238435	SNORA12	1.036875	7.826151	2.888988	0.005845	0.036062	-2.67852
ILMN_1792384	HABP4	1.036885	7.371268	6.514725	4.60E-08	7.76E-06	8.438809
ILMN_1695025	CD2	1.03734	5.729731	4.061896	0.000185	0.002799	0.52443
ILMN_1661888	MEF2A	1.037795	5.345672	4.376568	6.74E-05	0.001363	1.476381
ILMN_1797594	NFAT5	1.03862	7.673531	3.77935	0.000446	0.005375	-0.30192
ILMN_1693004	C20orf117	1.038752	7.201629	5.262977	3.50E-06	0.000174	4.290741
ILMN_1730907	ZFAND1	1.03909	9.128902	3.824215	0.000388	0.004854	-0.17269
ILMN_1740900	BMP4	1.039431	10.63749	5.682474	8.29E-07	6.33E-05	5.667956
ILMN_3274226	LOC642546	1.041045	5.239925	4.879116	1.28E-05	0.000432	3.052244
ILMN_1696419	STOM	1.041188	6.774798	3.890289	0.000316	0.004181	0.019039
ILMN_1782543	EEF1D	1.041201	9.45058	3.868517	0.000338	0.004393	-0.04432
ILMN_3262454	LOC100128056	1.041388	5.17256	3.293372	0.001894	0.015618	-1.64714
ILMN_1718831	TMEM57	1.04367	7.864983	5.380616	2.34E-06	0.000134	4.674852
ILMN_2214790	LAMB1	1.044014	9.014164	5.646607	9.38E-07	6.97E-05	5.549467
ILMN_2413956	IGF2	1.045594	6.326153	3.133738	0.002982	0.021886	-2.06473
ILMN_2400512	PRKCSH	1.046828	6.602017	3.166689	0.002717	0.020427	-1.9796
ILMN_2318638	TGIF1	1.051249	9.64104	5.134087	5.43E-06	0.000238	3.872158
ILMN_1769704	FLJ39632	1.052223	6.567578	4.067267	0.000182	0.002761	0.540414
ILMN_1676728	DLK2	1.052636	7.613084	4.487531	4.70E-05	0.001059	1.818991
ILMN_2140700	CRIPAK	1.053711	7.741554	4.121928	0.000153	0.00243	0.703632
ILMN_1673509	RPL28	1.055834	8.101201	3.509663	0.001006	0.009754	-1.06141
ILMN_1807972	MICAL1	1.057061	6.099968	4.339291	7.61E-05	0.001487	1.362049

ILMN_1785405	SLC17A9	1.058403	9.134476	5.126941	5.56E-06	0.000241	3.849026
ILMN_1706813	SLC6A14	1.059302	6.608764	2.830379	0.006837	0.040744	-2.82046
ILMN_2351269	TTYH1	1.060554	5.405334	3.891146	0.000315	0.004176	0.021536
ILMN_1689400	CLK1	1.061008	9.367644	3.395437	0.001408	0.012464	-1.37349
ILMN_2352574	ZNF274	1.062529	6.873908	4.10005	0.000164	0.00255	0.638187
ILMN_2406873	ARFGAP1	1.062556	6.233658	2.965195	0.004755	0.030949	-2.49099
ILMN_1713369	RPL13A	1.062725	12.5103	6.321866	9.01E-08	1.28E-05	7.794485
ILMN_2188374	XPOT	1.062812	7.366496	2.845481	0.006567	0.039451	-2.78408
ILMN_1674560	GBA2	1.063037	7.95236	4.416707	5.92E-05	0.001238	1.599928
ILMN_2126957	NOMO1	1.065688	9.863633	4.130712	0.000149	0.002383	0.729952
ILMN_1788107	IL11	1.066056	5.067416	3.078448	0.00348	0.024529	-2.20627
ILMN_1789094	NINL	1.067029	7.906459	4.911087	1.15E-05	0.000402	3.1544
ILMN_1739751	SLC26A11	1.067135	7.697181	4.560091	3.70E-05	0.0009	2.044783
ILMN_1749792	SORBS1	1.071815	7.811702	3.857299	0.00035	0.00451	-0.07689
ILMN_2385178	MIB2	1.071882	7.471443	4.112234	0.000158	0.002479	0.674612
ILMN_3247578	FAT1	1.072146	10.43315	6.149301	1.64E-07	1.96E-05	7.218619
ILMN_2401964	CDC42EP1	1.073324	5.680641	3.79663	0.000423	0.005179	-0.25224
ILMN_3263694	LOC100128771	1.073744	9.754062	5.365657	2.46E-06	0.000139	4.625904
ILMN_1669722	LRRC61	1.075364	7.127656	3.758829	0.000474	0.005625	-0.36077
ILMN_1697227	USP36	1.075489	7.146152	4.439584	5.49E-05	0.001174	1.67054
ILMN_1718128	PABPC3	1.075523	6.86241	5.260429	3.53E-06	0.000175	4.282442
ILMN_1815745	SOX4	1.076806	7.134648	3.440555	0.001234	0.011295	-1.25094
ILMN_1652677	FAM89A	1.076941	5.338785	4.074144	0.000178	0.002711	0.560894
ILMN_2363498	LSR	1.077243	6.04789	3.650972	0.000659	0.007102	-0.66727
ILMN_2339691	SYVN1	1.077383	5.619117	3.709368	0.000552	0.006282	-0.50191
ILMN_1659947	FGA	1.078012	8.017875	4.148391	0.00014	0.002288	0.783003
ILMN_1753340	LOC728226	1.079486	6.952203	3.352503	0.001596	0.013697	-1.48921
ILMN_3236825	RAPGEF5	1.080031	8.376342	4.723197	2.16E-05	0.000628	2.557029
ILMN_1695020	NEK3	1.080128	8.389134	5.920787	3.63E-07	3.59E-05	6.457871
ILMN_1773952	LOC440910	1.080553	5.376174	3.477563	0.001106	0.010429	-1.14971
ILMN_3304049	LOC729500	1.080921	8.780535	5.589951	1.14E-06	8.10E-05	5.362547
ILMN_1652975	DLK1	1.081878	9.133103	4.030324	0.000204	0.003019	0.430671
ILMN_2117508	CTHRC1	1.082881	6.375809	2.893879	0.005768	0.035672	-2.66659
ILMN_1808860	STX5	1.08354	8.341988	4.674218	2.54E-05	0.0007	2.402553
ILMN_1651799	SLC38A2	1.083623	12.01234	3.993539	0.000229	0.003301	0.321868
ILMN_1736575	TRIM28	1.085628	9.431225	4.612759	3.11E-05	0.000799	2.209502
ILMN_2190051	CCDC91	1.085842	5.659421	3.48147	0.001094	0.010363	-1.13899
ILMN_3294222	LOC100132673	1.086699	11.95772	5.828484	5.00E-07	4.38E-05	6.151427
ILMN_2361807	OS9	1.08701	7.788484	4.7856	1.75E-05	0.00054	2.754613

ILMN_1703558	FHL3	1.087298	6.464148	3.488494	0.001071	0.01022	-1.11969
ILMN_1757129	TMEM88	1.087436	5.099833	3.477671	0.001106	0.010429	-1.14942
ILMN_1744455	NOTUM	1.088103	7.56545	5.319615	2.88E-06	0.000153	4.475443
ILMN_1782050	CEBPD	1.088139	9.727931	6.101112	1.94E-07	2.21E-05	7.057988
ILMN_2145250	NACAP1	1.090152	8.772737	4.661296	2.65E-05	0.000719	2.361891
ILMN_1723978	LGALS1	1.090281	8.465399	3.14011	0.002929	0.021648	-2.04831
ILMN_1653718	ZFAND2B	1.091212	9.403325	5.354834	2.56E-06	0.000139	4.590513
ILMN_1778064	FICD	1.092835	5.889606	3.128447	0.003026	0.022119	-2.07834
ILMN_1659913	ISG20	1.093086	8.62524	4.158451	0.000136	0.002229	0.813234
ILMN_1753370	ABTB2	1.094018	7.561791	4.859918	1.37E-05	0.000453	2.990997
ILMN_2323087	RBPMS	1.094785	7.949989	4.013991	0.000215	0.00314	0.382304
ILMN_1744665	EP300	1.095743	6.893081	4.497366	4.55E-05	0.001033	1.849517
ILMN_3234963	LOC730153	1.096002	6.310896	5.026962	7.80E-06	0.000309	3.52627
ILMN_1672486	TCF7L2	1.097383	6.996928	5.166228	4.87E-06	0.000219	3.976303
ILMN_2337655	WARS	1.098697	9.8312	3.804061	0.000413	0.005082	-0.23084
ILMN_1770610	MERTK	1.098716	8.706912	5.669299	8.68E-07	6.53E-05	5.624416
ILMN_1714444	KLF12	1.100101	5.090613	4.731374	2.10E-05	0.000617	2.58287
ILMN_1729831	LOC388814	1.100325	6.215764	3.555511	0.000878	0.008792	-0.93448
ILMN_2128795	LRIG1	1.10083	10.21542	5.227049	3.96E-06	0.000191	4.173813
ILMN_2401618	MLX	1.103076	7.105636	4.535643	4.01E-05	0.000944	1.968557
ILMN_2282077	MIB2	1.103244	8.287838	4.404071	6.16E-05	0.001279	1.560988
ILMN_1776088	NAT9	1.1038	9.362233	4.873228	1.31E-05	0.00044	3.033451
ILMN_1716014	LOC653232	1.104049	11.29034	7.202582	4.20E-09	1.44E-06	10.73423
ILMN_3244196	LOC729088	1.104314	7.419621	4.67081	2.57E-05	0.000704	2.391826
ILMN_1666444	RBMS1	1.104403	9.394926	5.393068	2.24E-06	0.000131	4.715616
ILMN_1671885	MLF2	1.104606	8.904766	4.812777	1.60E-05	0.000507	2.840924
ILMN_1753026	LPPR1	1.104889	8.488551	4.412909	5.99E-05	0.001251	1.588218
ILMN_1777759	LOC401720	1.107467	8.047926	3.597079	0.000775	0.008016	-0.81861
ILMN_2207562	C4orf16	1.108537	6.913335	3.723498	0.000529	0.006072	-0.46169
ILMN_1800276	RCN1	1.108868	11.0389	5.719767	7.29E-07	5.81E-05	5.791275
ILMN_1838320	ONECUT2	1.109632	7.956925	3.793742	0.000426	0.005218	-0.26055
ILMN_1878019		1.11172	6.718549	3.546993	0.0009	0.008973	-0.95814
ILMN_1798224	JARID1C	1.112156	5.350642	4.728228	2.12E-05	0.00062	2.572928
ILMN_1771841	FOSL1	1.114424	6.308508	3.586057	0.000801	0.008197	-0.8494
ILMN_1808238	RBPMS2	1.116645	5.59113	4.286223	9.03E-05	0.001673	1.199978
ILMN_1710264	LOC728226	1.116905	5.469496	4.241832	0.000104	0.001856	1.065043
ILMN_3251672	DSG2	1.116981	11.09782	5.207964	4.22E-06	0.000199	4.111776
ILMN_2231985	HSPA13	1.117774	7.55012	2.950678	0.004946	0.031863	-2.52697
ILMN_1813206	CP	1.118713	7.225892	3.140244	0.002928	0.021646	-2.04797

ILMN_1746819	C5	1.119405	11.26502	4.150688	0.000139	0.002278	0.789903
ILMN_1656670	HLA-G	1.119751	8.001622	4.956353	9.89E-06	0.000364	3.299374
ILMN_1762260	C3	1.119992	10.12609	3.292418	0.001899	0.015633	-1.64967
ILMN_1718303	PVRL2	1.120064	8.913997	4.773335	1.83E-05	0.000556	2.715714
ILMN_1736863	TMEM140	1.121052	7.298624	3.20641	0.002428	0.018852	-1.87624
ILMN_1766010	YARS	1.121681	11.32771	5.872643	4.29E-07	3.96E-05	6.297961
ILMN_2376723	CDKN2B	1.122212	5.065489	3.195767	0.002503	0.019232	-1.90402
ILMN_3283449	LOC440991	1.122827	10.60755	4.326297	7.93E-05	0.001531	1.322291
ILMN_2370208	CMTM3	1.122831	7.826556	4.449646	5.31E-05	0.001153	1.701643
ILMN_3271098	FAM176A	1.123722	9.275777	6.083525	2.07E-07	2.30E-05	6.999386
ILMN_2368617	FKRP	1.123862	6.439153	3.487758	0.001073	0.010232	-1.12172
ILMN_2383484	C19orf48	1.123932	7.338062	3.826356	0.000386	0.004836	-0.1665
ILMN_1813277	SUPT3H	1.125346	7.148582	4.515933	4.28E-05	0.000994	1.907213
ILMN_1790985	dJ341D10.1	1.125511	6.038059	3.091629	0.003355	0.023859	-2.17267
ILMN_2344650	N4BP2L1	1.127106	6.661976	3.273747	0.002003	0.016304	-1.69917
ILMN_3246247	LOC399491	1.128339	8.519703	4.770721	1.84E-05	0.00056	2.707427
ILMN_1668983	ACVR2B	1.128444	5.461069	4.413691	5.97E-05	0.001249	1.590631
ILMN_1800096	MPST	1.129503	8.368968	4.689015	2.42E-05	0.000676	2.449165
ILMN_2134888	TUBE1	1.130672	6.505598	3.994418	0.000229	0.003296	0.324463
ILMN_1701243	C10orf2	1.130759	8.485654	5.266513	3.46E-06	0.000172	4.302258
ILMN_1668683	MLL	1.132337	6.31882	4.960053	9.77E-06	0.000361	3.311243
ILMN_1751034	ITPRIPL2	1.132903	9.506942	5.388144	2.28E-06	0.000132	4.699494
ILMN_3251550	PHLDA1	1.133578	6.404685	5.647576	9.35E-07	6.97E-05	5.552667
ILMN_2114972	FGB	1.137884	8.830775	5.360031	2.51E-06	0.000139	4.607505
ILMN_3292008	LOC401676	1.138567	7.586616	4.233164	0.000107	0.001888	1.038766
ILMN_3279877	LOC645430	1.139852	6.251178	4.04818	0.000193	0.002899	0.483658
ILMN_1664960	KIAA0284	1.141181	6.183103	3.837641	0.000372	0.004722	-0.13387
ILMN_1757467	H1F0	1.141443	12.55389	7.083112	6.36E-09	1.82E-06	10.3365
ILMN_1740426	RASD1	1.141651	6.88782	2.742588	0.008619	0.048181	-3.02923
ILMN_1676986	NPIP	1.142196	9.044973	4.61893	3.05E-05	0.00079	2.228845
ILMN_3243664	LOC440353	1.143101	11.43449	5.896778	3.95E-07	3.74E-05	6.378107
ILMN_3237368	LOC644132	1.144152	8.702579	4.920846	1.11E-05	0.000394	3.185622
ILMN_2232339	SLC22A9	1.144271	7.056029	3.663052	0.000635	0.006911	-0.63318
ILMN_1682928	CPVL	1.144309	9.747629	5.903831	3.85E-07	3.73E-05	6.401535
ILMN_1728202	TMEM22	1.144387	7.41007	4.090097	0.000169	0.002614	0.608463
ILMN_1774659	LOC652388	1.145388	7.293809	4.046282	0.000194	0.002913	0.47802
ILMN_1774272	ESRRA	1.145694	8.111831	4.501019	4.49E-05	0.001025	1.860861
ILMN_1679299	IGSF1	1.146814	11.12284	4.96917	9.48E-06	0.000355	3.340494
ILMN_2188264	CYR61	1.147569	7.781492	3.39042	0.001429	0.012612	-1.38706

ILMN_2316955	SERPINA11	1.148739	8.910489	4.335041	7.71E-05	0.001504	1.349041
ILMN_1907095	ONECUT2	1.148838	7.519668	4.354544	7.24E-05	0.001432	1.408784
ILMN_1781859	UGT2B28	1.150129	7.063044	3.42315	0.001298	0.011712	-1.29833
ILMN_3296943	LOC100131096	1.152476	5.453644	3.006645	0.004244	0.028443	-2.38761
ILMN_3239181	ITPRIP	1.153608	6.607773	3.079185	0.003473	0.024491	-2.20439
ILMN_2412761	MAFG	1.154485	5.811034	3.643921	0.000673	0.007215	-0.68714
ILMN_2358265	F7	1.155732	5.747301	4.165829	0.000133	0.002191	0.83543
ILMN_1669972	DKFZp686O24166	1.155859	9.801503	4.961622	9.72E-06	0.000361	3.316274
ILMN_1658015	MBNL2	1.155895	8.86631	3.9941	0.000229	0.003296	0.323525
ILMN_1776047	LOC646197	1.15739	10.49313	5.578209	1.19E-06	8.33E-05	5.323846
ILMN_2186806	HLA-F	1.157493	9.846136	5.177527	4.68E-06	0.000213	4.012953
ILMN_1705364	BAT3	1.159999	9.934907	4.190247	0.000123	0.002072	0.909003
ILMN_1690621	GPR98	1.160231	5.939145	4.465001	5.05E-05	0.001121	1.74916
ILMN_1792182	RDH12	1.160352	6.087879	3.656934	0.000647	0.007004	-0.65045
ILMN_1735367	HSD17B11	1.160527	10.50784	4.532307	4.05E-05	0.000951	1.958167
ILMN_1812926	ANTXR2	1.16073	8.18574	3.445621	0.001216	0.011191	-1.23712
ILMN_2337336	PVRL2	1.16125	6.883052	4.260389	9.81E-05	0.001774	1.121378
ILMN_2166275	NOTUM	1.164968	8.862876	6.133155	1.74E-07	2.04E-05	7.164789
ILMN_2364272	MBNL2	1.165117	9.468817	3.701555	0.000565	0.006387	-0.52412
ILMN_1704196	DSG2	1.166708	6.695972	4.898412	1.20E-05	0.000411	3.113877
ILMN_1752046	SH2B3	1.167127	9.312919	4.575132	3.52E-05	0.000863	2.091753
ILMN_1673232	LASS1	1.169221	6.071669	3.545297	0.000905	0.009008	-0.96284
ILMN_1748124	TSC22D3	1.17138	5.402697	4.45119	5.29E-05	0.001151	1.70642
ILMN_3235326	LOC388796	1.171628	8.489847	5.279177	3.31E-06	0.000168	4.343525
ILMN_1680507	PPP2R2C	1.172032	6.153622	4.159953	0.000135	0.002221	0.817751
ILMN_1751328	FAM83H	1.173982	7.917149	5.083105	6.45E-06	0.000269	3.707307
ILMN_2380605	MTMR3	1.177324	5.975019	5.045029	7.34E-06	0.000296	3.584468
ILMN_1666096	ACSL3	1.179355	7.433813	4.202955	0.000118	0.002016	0.947365
ILMN_1722713	FBLN1	1.180175	6.944679	4.167606	0.000132	0.002183	0.840776
ILMN_1688775	METRNL	1.180366	5.352624	2.895317	0.005746	0.035567	-2.66308
ILMN_1656042	KIAA0319L	1.180836	5.911469	4.269943	9.52E-05	0.001741	1.150424
ILMN_1717809	RNF24	1.181761	6.198538	4.657703	2.68E-05	0.000722	2.350591
ILMN_2298818	RPS29	1.1819	7.890655	3.9591	0.000255	0.003603	0.220433
ILMN_2314080	CTAGE5	1.182849	6.925502	3.926377	0.000283	0.003871	0.124443
ILMN_1800225	PPARG	1.183088	9.508413	5.439869	1.91E-06	0.000118	4.868994
ILMN_1732071	HIST2H2BE	1.183721	8.035651	4.848051	1.42E-05	0.000465	2.953177
ILMN_3216336	LOC285741	1.183879	11.35895	4.712618	2.24E-05	0.000642	2.523618
ILMN_1672596	BCAR1	1.185464	7.692238	5.351336	2.59E-06	0.000141	4.579075
ILMN_1714352	DMWD	1.185921	6.457733	4.473954	4.91E-05	0.001096	1.776892

ILMN_1661197	CLCF1	1.186117	5.299399	2.882287	0.005951	0.036539	-2.69486
ILMN_1731353	CHPF	1.186901	9.457245	5.502001	1.54E-06	0.000101	5.073018
ILMN_1702310	LGR5	1.187868	6.468507	4.126652	0.00015	0.002406	0.717785
ILMN_1714820	ITGB1	1.189124	9.171258	3.928688	0.000281	0.003849	0.13121
ILMN_1749868	FAM171A1	1.189984	10.06429	6.14949	1.64E-07	1.96E-05	7.219248
ILMN_1737157	GRAMD1A	1.190609	9.217612	5.586147	1.16E-06	8.17E-05	5.350007
ILMN_1676336	AADACL1	1.192251	8.12154	4.847535	1.43E-05	0.000465	2.951532
ILMN_1812070	ABCB1	1.192767	9.396898	4.999764	8.55E-06	0.000332	3.438764
ILMN_1792689	HIST1H2AC	1.192784	5.112248	4.017921	0.000212	0.003114	0.393933
ILMN_1687235	HPN	1.193745	9.194848	4.418957	5.87E-05	0.001231	1.606867
ILMN_1796755	ITGB5	1.193941	8.404528	4.692779	2.39E-05	0.000672	2.46103
ILMN_1768311	LOC728888	1.195382	11.73831	6.587835	3.57E-08	6.71E-06	8.683137
ILMN_1769288	LOC402560	1.198136	6.917658	7.110967	5.77E-09	1.71E-06	10.42929
ILMN_2408572	RNASE4	1.198248	9.481287	4.907932	1.16E-05	0.000403	3.144312
ILMN_2087989	ZFAND1	1.19841	7.719036	4.126171	0.000151	0.002407	0.716344
ILMN_1741632	RAB3IL1	1.199517	6.962567	4.778246	1.80E-05	0.000549	2.731285
ILMN_2371053	EFNA1	1.199898	8.782836	4.216905	0.000113	0.00196	0.989538
ILMN_1873620		1.19994	6.193381	3.877655	0.000329	0.004305	-0.01775
ILMN_1757644	UBE2H	1.200022	7.835904	5.812309	5.29E-07	4.60E-05	6.097785
ILMN_1654060	MKNK2	1.200403	5.978373	4.546059	3.88E-05	0.000925	2.001013
ILMN_1714228	SPTBN1	1.202321	5.304406	4.458715	5.16E-05	0.001134	1.729699
ILMN_1677487	ANKZF1	1.20497	7.628426	5.269827	3.42E-06	0.000171	4.313057
ILMN_2318643	TGIF1	1.205676	8.387988	4.773099	1.83E-05	0.000556	2.714964
ILMN_1724738	TFR2	1.205732	6.49652	3.263324	0.002064	0.016671	-1.72673
ILMN_1728218	RBPMS	1.206339	7.346989	3.822291	0.00039	0.004862	-0.17825
ILMN_1713182	LOC653879	1.206826	11.01666	3.93392	0.000276	0.003817	0.146536
ILMN_1695946	TRNP1	1.208652	10.65458	5.218103	4.08E-06	0.000194	4.144725
ILMN_1664233	LOC644590	1.209401	6.64635	4.205828	0.000117	0.002007	0.956047
ILMN_2082865	PLLP	1.211314	10.4039	7.578496	1.14E-09	5.32E-07	11.98088
ILMN_1752226	P2RY11	1.211561	6.72761	3.783246	0.00044	0.005339	-0.29073
ILMN_1735014	KLF6	1.213452	9.286334	5.04627	7.31E-06	0.000295	3.588468
ILMN_1743711	LOC650215	1.213839	10.21949	4.394406	6.36E-05	0.001307	1.531232
ILMN_1654392	KHNYN	1.215989	9.545793	5.087285	6.36E-06	0.000267	3.720808
ILMN_1678730	NOMO1	1.21649	9.924609	4.653557	2.72E-05	0.000731	2.337555
ILMN_3240173	MTSS1L	1.216853	7.215633	5.468122	1.73E-06	0.00011	4.961716
ILMN_1696974	ANG	1.217001	9.559406	6.141493	1.69E-07	2.00E-05	7.192585
ILMN_1774733	SOCS1	1.218018	7.064432	5.073684	6.66E-06	0.000274	3.676892
ILMN_1777444	STX5	1.220141	6.891706	3.854813	0.000353	0.004532	-0.08411
ILMN_3246273	RNU1-3	1.223033	7.875202	3.841693	0.000368	0.004672	-0.12213

ILMN_1727271	WARS	1.223034	8.674801	4.167452	0.000132	0.002183	0.840314
ILMN_1737255	C22orf36	1.225387	7.950391	4.616854	3.07E-05	0.000792	2.222337
ILMN_1783771	UBE2Z	1.229171	7.384294	5.775768	6.01E-07	5.00E-05	5.976678
ILMN_1652185	IL4R	1.232154	8.051157	3.477785	0.001106	0.010429	-1.1491
ILMN_1746706	LOC653103	1.232782	9.507402	5.565273	1.24E-06	8.60E-05	5.281227
ILMN_3199955	LOC645430	1.233036	7.83103	5.88249	4.15E-07	3.87E-05	6.330659
ILMN_1783350	PCNXL3	1.233524	8.745693	4.670419	2.57E-05	0.000704	2.390596
ILMN_1855278		1.233876	6.025839	3.851688	0.000357	0.004566	-0.09317
ILMN_1706571	SLC35D2	1.234125	9.912218	6.183285	1.46E-07	1.82E-05	7.331954
ILMN_3233442	LOC387825	1.23429	10.40174	5.917428	3.68E-07	3.61E-05	6.44671
ILMN_1652434	MTHFD2L	1.235099	6.252689	3.874176	0.000333	0.004337	-0.02787
ILMN_1705750	TGM2	1.236179	8.156841	5.179915	4.64E-06	0.000212	4.0207
ILMN_1661335	SPTBN1	1.236217	10.35871	4.835888	1.48E-05	0.000481	2.914441
ILMN_1789809	LOC644511	1.236559	11.2328	5.257552	3.57E-06	0.000176	4.273072
ILMN_1754476	TRIM15	1.237029	10.47979	5.502877	1.54E-06	0.000101	5.0759
ILMN_2061732	YRDC	1.237111	9.700314	4.520944	4.21E-05	0.000981	1.922798
ILMN_1712896	FST	1.23717	9.079729	2.828119	0.006878	0.04088	-2.82589
ILMN_1691736	ST6GALNAC6	1.237351	8.029592	5.391143	2.26E-06	0.000131	4.70931
ILMN_1728478	CXCL16	1.239234	10.84067	5.86077	4.47E-07	4.06E-05	6.258551
ILMN_2294978	RNASE4	1.239325	9.174172	5.635661	9.75E-07	7.15E-05	5.513329
ILMN_1699226	UBR4	1.240814	9.304722	4.582042	3.44E-05	0.000852	2.113351
ILMN_1756982	CLIC1	1.241637	12.13027	7.421779	1.96E-09	8.39E-07	11.46216
ILMN_1785660	SRPR	1.242104	9.245287	4.492496	4.62E-05	0.001045	1.834398
ILMN_1663032	FNDC4	1.243957	7.010247	5.120457	5.68E-06	0.000244	3.828043
ILMN_3307982	MGC11082	1.244134	5.671902	3.584676	0.000804	0.008225	-0.85326
ILMN_2401344	PPP2R2C	1.244379	7.565461	4.582284	3.44E-05	0.000852	2.114108
ILMN_3235027	TAF1D	1.247053	8.151787	4.640702	2.84E-05	0.000752	2.297164
ILMN_1713491	VAMP2	1.247642	6.297599	4.895023	1.22E-05	0.000414	3.103046
ILMN_1667561	IFRD1	1.247885	9.557512	4.543861	3.90E-05	0.000929	1.994162
ILMN_1751886	REC8	1.250489	6.465083	4.706336	2.28E-05	0.000652	2.503791
ILMN_1721651	LOC646463	1.250829	6.874878	5.219134	4.06E-06	0.000194	4.148079
ILMN_1658709	LAMB1	1.251715	9.807998	6.546688	4.12E-08	7.39E-06	8.545623
ILMN_1796490	GRINA	1.253375	7.413559	5.84546	4.72E-07	4.18E-05	6.207743
ILMN_3178307	KRT18P28	1.253502	7.696399	4.190884	0.000123	0.00207	0.910925
ILMN_1677032	DSP	1.257753	5.326232	4.589032	3.36E-05	0.000842	2.135211
ILMN_3252936	KRT18P17	1.260399	8.357173	5.5268	1.42E-06	9.62E-05	5.154574
ILMN_1757872	DKFZp761P0423	1.264048	8.914457	5.707571	7.60E-07	5.93E-05	5.750932
ILMN_2294976	RNASE4	1.264741	9.448674	6.24251	1.19E-07	1.56E-05	7.529559
ILMN_1710740	C2	1.269847	10.15531	4.578033	3.49E-05	0.000859	2.100821

ILMN_1743714	CARD10	1.270775	9.032494	6.686689	2.53E-08	5.11E-06	9.013478
ILMN_1815057	PDGFRB	1.271747	7.996981	4.695753	2.36E-05	0.00067	2.470406
ILMN_2391765	C6orf48	1.271756	11.91823	6.739619	2.10E-08	4.31E-06	9.190321
ILMN_1751028	SERPINH1	1.273497	8.738285	4.490516	4.65E-05	0.001051	1.828252
ILMN_1740169	TYRO3	1.275145	8.623787	5.215013	4.12E-06	0.000196	4.134682
ILMN_1658519	SLC13A3	1.275656	5.714595	3.808796	0.000407	0.005022	-0.21719
ILMN_1775743	BTG1	1.278748	10.19602	5.263989	3.49E-06	0.000174	4.294039
ILMN_1765670	LOC285216	1.279097	5.370127	4.86477	1.35E-05	0.000448	3.006471
ILMN_2115669	SEMA4C	1.27961	6.844638	4.745202	2.01E-05	0.000597	2.626606
ILMN_1657983	TERF2IP	1.279756	10.00076	6.120659	1.81E-07	2.10E-05	7.123134
ILMN_1756806	MCL1	1.280857	7.001017	4.695667	2.36E-05	0.00067	2.470134
ILMN_1811049	POU2AF1	1.281779	5.602575	4.686434	2.44E-05	0.000679	2.441031
ILMN_1701877	AXL	1.284803	5.565722	3.089839	0.003371	0.023953	-2.17724
ILMN_1791232	SPRED2	1.286762	9.191777	6.95812	9.82E-09	2.52E-06	9.919804
ILMN_1815937	TMEM184A	1.287139	5.771147	4.245525	0.000103	0.00184	1.076248
ILMN_1766221	B4GALT1	1.290716	7.605198	4.857708	1.38E-05	0.000456	2.983953
ILMN_1723843	CSNK2A2	1.291238	9.368552	5.036631	7.55E-06	0.000302	3.55741
ILMN_1784287	TGFBR3	1.291806	11.4615	5.228754	3.93E-06	0.000191	4.179357
ILMN_1805750	IFITM3	1.292482	11.06352	5.885561	4.11E-07	3.84E-05	6.340856
ILMN_1786843	KCTD13	1.294815	6.712812	4.115679	0.000156	0.002457	0.684924
ILMN_1791483	PDE4D	1.297334	5.253625	4.936426	1.06E-05	0.00038	3.235507
ILMN_2360705	ACSL3	1.297747	11.85655	6.374363	7.50E-08	1.10E-05	7.969821
ILMN_3238221	FLJ42627	1.297824	6.146468	3.086799	0.0034	0.024095	-2.185
ILMN_2396571	GPR108	1.298038	7.155756	4.235389	0.000106	0.001879	1.045511
ILMN_2359456	ERGIC3	1.299357	10.15807	4.930221	1.08E-05	0.000387	3.215635
ILMN_1771026	GARS	1.299522	11.35548	6.409638	6.64E-08	1.01E-05	8.087661
ILMN_1769911	SLC38A1	1.300188	9.733023	5.394076	2.24E-06	0.000131	4.718916
ILMN_1807833	HM13	1.301725	7.569326	4.164627	0.000133	0.002198	0.83181
ILMN_3188984	C20orf199	1.302643	10.84515	4.906377	1.17E-05	0.000405	3.139337
ILMN_1670272	LRP10	1.305086	9.67885	3.953999	0.000259	0.003648	0.205445
ILMN_1732808	TNRC9	1.305978	8.59156	4.250539	0.000101	0.001818	1.091463
ILMN_1721087	SHC2	1.306102	5.92378	4.168747	0.000132	0.002179	0.844209
ILMN_3236653	RNU1-5	1.30633	8.32575	4.07559	0.000177	0.002704	0.565201
ILMN_1738773	HRC	1.306903	6.805876	5.330079	2.78E-06	0.000149	4.509614
ILMN_2165753	HLA-A29.1	1.309409	9.589015	4.907708	1.17E-05	0.000403	3.143595
ILMN_2406313	RBCK1	1.311111	9.630669	4.898296	1.20E-05	0.000411	3.113505
ILMN_2384241	TGFBR2	1.312864	11.65152	7.138945	5.24E-09	1.67E-06	10.52245
ILMN_2156172	HK2	1.319846	9.188308	5.467169	1.74E-06	0.00011	4.958588
ILMN_1763104	TRAF4	1.319961	6.328147	4.790814	1.72E-05	0.000533	2.77116

ILMN_3238369	JHDM1D	1.320604	6.687375	5.235014	3.85E-06	0.000188	4.19972
ILMN_1673352	IFITM2	1.322038	11.28191	6.273093	1.07E-07	1.44E-05	7.631638
ILMN_1660904	TRIM15	1.322208	10.04785	5.834709	4.90E-07	4.30E-05	6.172073
ILMN_3249435	UBASH3B	1.324162	6.048904	3.697592	0.000572	0.006439	-0.53537
ILMN_1746888	PCOLCE2	1.325648	6.421563	3.929379	0.00028	0.003846	0.133234
ILMN_1655614	DSP	1.32593	10.39094	6.537771	4.25E-08	7.55E-06	8.515825
ILMN_1810584	IL1R1	1.326596	7.912603	4.883636	1.26E-05	0.000427	3.066675
ILMN_2310685	FOXK2	1.327271	6.172294	4.647195	2.78E-05	0.000743	2.31756
ILMN_1658677	DTX3	1.328537	5.992187	6.05842	2.25E-07	2.44E-05	6.915762
ILMN_2364384	PPARG	1.328587	8.087167	5.697148	7.88E-07	6.10E-05	5.716463
ILMN_1809208	KIAA1543	1.329063	6.574035	4.820191	1.56E-05	0.0005	2.864494
ILMN_1746704	TRIM8	1.331747	10.49243	6.473852	5.31E-08	8.53E-06	8.302221
ILMN_1692260	MAFG	1.332216	6.479339	4.80977	1.62E-05	0.00051	2.831366
ILMN_3263974	KRT18P13	1.333497	10.31155	4.861449	1.36E-05	0.000453	2.995881
ILMN_1740407	CHSY3	1.336303	6.024633	5.665238	8.80E-07	6.61E-05	5.610999
ILMN_1747251	LTB4R	1.337871	5.705656	3.543063	0.000911	0.009049	-0.96903
ILMN_3199755	LOC646821	1.338969	7.300348	4.929455	1.08E-05	0.000387	3.213182
ILMN_1655595	SERPINE2	1.339299	9.938894	3.299725	0.001859	0.015423	-1.63025
ILMN_1726460	RPL14	1.340051	10.99368	4.531233	4.07E-05	0.000953	1.954821
ILMN_3303612	PABPC1L	1.344672	9.691457	3.480542	0.001097	0.010384	-1.14154
ILMN_1690826	TNKS1BP1	1.344953	6.473187	5.553656	1.29E-06	8.86E-05	5.242966
ILMN_1758497	TTYH1	1.346951	7.224928	5.179674	4.65E-06	0.000212	4.019919
ILMN_1656501	DUSP5	1.347595	6.58391	3.403266	0.001376	0.012259	-1.35229
ILMN_2374164	HERPUD1	1.349766	10.20629	5.695269	7.93E-07	6.12E-05	5.710253
ILMN_1772370	ARHGEF1	1.351625	6.685508	5.710775	7.52E-07	5.90E-05	5.76153
ILMN_1881081		1.354874	5.693294	4.234916	0.000106	0.001881	1.044076
ILMN_1790891	CKAP4	1.356005	9.715534	6.704229	2.38E-08	4.84E-06	9.072083
ILMN_1661264	SHMT2	1.356293	11.98044	5.766161	6.21E-07	5.12E-05	5.944854
ILMN_1774287	CFB	1.357877	11.58653	6.672021	2.66E-08	5.30E-06	8.964466
ILMN_1674719	NID1	1.364401	6.57102	3.891375	0.000315	0.004175	0.022202
ILMN_2268381	RRBP1	1.364684	9.580022	5.075037	6.63E-06	0.000274	3.681257
ILMN_1653856	STS-1	1.365675	8.088521	4.170856	0.000131	0.002168	0.85056
ILMN_1659749	DSP	1.365998	6.773371	5.21483	4.12E-06	0.000196	4.134087
ILMN_1770084	TACC1	1.36721	8.010976	3.452472	0.001191	0.011019	-1.21841
ILMN_1677768	POR	1.368397	9.061743	6.117359	1.84E-07	2.12E-05	7.112133
ILMN_2220978	NR0B2	1.373452	8.874454	4.321421	8.06E-05	0.00155	1.307381
ILMN_1801077	PLIN2	1.373579	10.52231	6.042847	2.38E-07	2.54E-05	6.863902
ILMN_1756146	WDR45	1.374275	7.040432	4.580766	3.46E-05	0.000854	2.109362
ILMN_1683859	SLC7A1	1.375357	11.10195	6.244725	1.18E-07	1.56E-05	7.53695

ILMN_2331010	TNFRSF10B	1.375415	7.582136	6.241805	1.19E-07	1.56E-05	7.527204
ILMN_2414826	VPS13A	1.37628	6.695927	5.36473	2.47E-06	0.000139	4.622875
ILMN_2098446	PMAIP1	1.376702	5.871476	4.62727	2.97E-05	0.000779	2.255003
ILMN_1753139	LOC124220	1.377878	5.465778	5.308041	3.00E-06	0.000157	4.437661
ILMN_1658337	AKIRIN1	1.377895	7.938143	6.23378	1.22E-07	1.57E-05	7.500424
ILMN_1655229	SLC7A11	1.379245	5.209846	5.520303	1.45E-06	9.78E-05	5.133201
ILMN_1798327	PAQR9	1.380898	8.801484	5.232152	3.89E-06	0.000189	4.190407
ILMN_1696843	LOC613037	1.381551	9.102195	5.860042	4.49E-07	4.06E-05	6.256135
ILMN_1791095	SERPINA11	1.385064	10.10639	4.831088	1.51E-05	0.000488	2.899163
ILMN_1703244	MAP1LC3B	1.385089	9.636183	5.25225	3.63E-06	0.000179	4.25581
ILMN_2155480	RAB43	1.390417	7.788738	5.714645	7.42E-07	5.88E-05	5.774332
ILMN_2366463	FN1	1.391297	6.274813	4.358706	7.14E-05	0.001419	1.42155
ILMN_1779147	ENC1	1.392092	9.347831	7.708903	7.29E-10	3.71E-07	12.41126
ILMN_2317658	SLC3A2	1.392374	7.083965	4.896369	1.21E-05	0.000413	3.107348
ILMN_1698732	PALLD	1.393948	5.841685	2.955955	0.004876	0.031522	-2.51391
ILMN_2147105	LOC440348	1.394899	9.130654	6.682681	2.56E-08	5.14E-06	9.000085
ILMN_1726456	SLC3A2	1.395234	10.72286	5.158018	5.00E-06	0.000224	3.949685
ILMN_3246766	LOC100132247	1.396727	9.684529	5.919345	3.65E-07	3.60E-05	6.45308
ILMN_3191922	KRT8P9	1.397643	6.844915	2.996819	0.004361	0.028953	-2.41221
ILMN_1771084	ACSM3	1.40017	7.836601	4.792186	1.72E-05	0.000531	2.775515
ILMN_1802799	AKIRIN1	1.401551	9.569408	6.958409	9.81E-09	2.52E-06	9.920768
ILMN_1709026	C6orf145	1.401736	5.958734	4.235337	0.000106	0.001879	1.045353
ILMN_2358560	TIAM2	1.401846	6.414379	6.816675	1.61E-08	3.62E-06	9.447693
ILMN_1675677	TMPRSS3	1.402028	5.61101	5.120599	5.68E-06	0.000244	3.828503
ILMN_2391900	SLC26A6	1.402106	6.600874	4.799074	1.68E-05	0.000522	2.797386
ILMN_2195821	C5orf41	1.405436	6.616747	3.383069	0.00146	0.012791	-1.40691
ILMN_1737387	LOC728441	1.405583	5.903614	4.223336	0.000111	0.001928	1.008999
ILMN_1706015	FAM43A	1.408913	6.490753	3.507718	0.001012	0.009783	-1.06677
ILMN_1775498	FAM100B	1.409594	6.607736	4.170541	0.000131	0.002169	0.849611
ILMN_1673529	AGXT2L2	1.411482	6.366397	5.196441	4.39E-06	0.000205	4.074345
ILMN_2368585	GGT1	1.411803	5.82905	4.383211	6.60E-05	0.00134	1.4968
ILMN_1728844	PTPRN2	1.413751	5.616797	4.473338	4.92E-05	0.001097	1.774983
ILMN_1803988	MCL1	1.416871	9.482834	5.421751	2.03E-06	0.000123	4.809585
ILMN_3244646	RNU1G2	1.418676	7.702058	4.602407	3.22E-05	0.000818	2.177071
ILMN_1669645	PKD1	1.418889	5.639306	4.718205	2.19E-05	0.000635	2.54126
ILMN_1675117	HSD17B11	1.422253	9.381591	4.388967	6.48E-05	0.001323	1.514497
ILMN_1697548	LPHN2	1.422907	8.3105	6.490353	5.01E-08	8.19E-06	8.357362
ILMN_1699829	CTGF	1.423637	12.63702	5.925897	3.57E-07	3.55E-05	6.474853
ILMN_2118663	ERV3	1.428016	6.044819	4.551914	3.80E-05	0.000913	2.019273

ILMN_1710075	FAM89A	1.432825	6.012632	4.454528	5.23E-05	0.001143	1.716744
ILMN_1794677	TMC6	1.432904	8.823885	5.374099	2.39E-06	0.000136	4.653525
ILMN_1746968	PHF1	1.435365	7.489333	7.025778	7.76E-09	2.15E-06	10.14543
ILMN_1694475	GTPBP2	1.439826	5.774917	3.187175	0.002565	0.019588	-1.9264
ILMN_3188106	CYTH2	1.441379	8.193471	4.973493	9.34E-06	0.000351	3.35437
ILMN_1686116	THBS1	1.443535	7.767025	4.2305	0.000108	0.001897	1.030696
ILMN_1752478	DHRS3	1.448726	9.488353	4.236054	0.000106	0.001879	1.047525
ILMN_3241034	SNORD3C	1.450277	6.127042	3.354338	0.001587	0.013659	-1.48428
ILMN_1736539	ALDH1L2	1.454619	5.452369	5.156443	5.03E-06	0.000224	3.944581
ILMN_2363165	TACC2	1.4556	7.143712	5.296156	3.13E-06	0.000161	4.398886
ILMN_1766359	GATAD2B	1.455669	6.918302	6.536886	4.26E-08	7.55E-06	8.512866
ILMN_1724145	CBX4	1.455974	9.750239	6.329858	8.76E-08	1.25E-05	7.821172
ILMN_2413331	TMEM107	1.456337	7.561845	3.426907	0.001284	0.011617	-1.28811
ILMN_1811238	ALPK2	1.459576	8.646852	4.854075	1.39E-05	0.00046	2.972373
ILMN_1666078	HLA-H	1.467132	9.750661	4.954302	9.96E-06	0.000366	3.292798
ILMN_3236694	LOC100132139	1.470931	8.20638	4.918065	1.13E-05	0.000395	3.176725
ILMN_1757604	TPM2	1.473492	5.760343	4.371761	6.85E-05	0.001375	1.461616
ILMN_1787673	PLLP	1.473859	9.239169	6.99326	8.69E-09	2.34E-06	10.03701
ILMN_1719988	HAL	1.47523	5.753255	3.587244	0.000798	0.00818	-0.84609
ILMN_1700081	FST	1.479114	11.28889	3.946428	0.000266	0.003709	0.183215
ILMN_1786720	PROM1	1.479971	8.649983	6.978783	9.14E-09	2.41E-06	9.988726
ILMN_1663640	MAOA	1.483955	8.434453	4.532268	4.05E-05	0.000951	1.958046
ILMN_1707123	DDX19B	1.486408	5.819684	4.320032	8.10E-05	0.001555	1.303138
ILMN_1673941	RBM24	1.487208	5.266734	3.955153	0.000258	0.003637	0.208833
ILMN_1786197	NR2F1	1.488783	8.609058	4.8141	1.59E-05	0.000506	2.84513
ILMN_1716507	EPB41L1	1.494074	6.561456	6.021044	2.57E-07	2.70E-05	6.791317
ILMN_1805665	FLRT3	1.495027	5.771142	3.125124	0.003055	0.022265	-2.08689
ILMN_3227023	SNHG7	1.497142	9.321404	6.122528	1.80E-07	2.10E-05	7.129364
ILMN_1699695	TNFRSF21	1.497232	11.00083	8.023554	2.47E-10	1.42E-07	13.44426
ILMN_1713985	MAF1	1.497584	7.335514	4.49322	4.61E-05	0.001043	1.836645
ILMN_2208802	NPIP	1.500759	8.71578	5.573272	1.21E-06	8.40E-05	5.307576
ILMN_1726245	TGFBR2	1.501265	11.26538	7.569077	1.18E-09	5.40E-07	11.94975
ILMN_2141790	HYOU1	1.501447	9.158871	4.995959	8.66E-06	0.000334	3.426534
ILMN_1698404	ERN1	1.502104	8.314402	4.601146	3.23E-05	0.000821	2.173123
ILMN_1803811	TRIB1	1.502416	10.46397	5.21902	4.07E-06	0.000194	4.147708
ILMN_2413833	TOX3	1.503688	9.199645	5.094424	6.21E-06	0.000262	3.743871
ILMN_1717639	SIK1	1.5046	9.005205	5.340841	2.68E-06	0.000145	4.544772
ILMN_3240308	LOC100133511	1.507723	8.960599	4.36631	6.97E-05	0.001392	1.444882
ILMN_1666731	C3orf32	1.511547	9.745227	6.932939	1.07E-08	2.65E-06	9.835793

ILMN_2392189	CTDSPL	1.514326	9.347562	7.09588	6.08E-09	1.78E-06	10.37904
ILMN_1651610	LOC730525	1.514959	6.545408	5.173352	4.75E-06	0.000215	3.999409
ILMN_3308138	RNU4-2	1.515087	7.777587	3.532806	0.000939	0.009256	-0.99746
ILMN_2124386	RGL2	1.517133	7.100442	6.002625	2.74E-07	2.85E-05	6.730015
ILMN_2339028	PKD1	1.517161	5.625421	4.621103	3.03E-05	0.000786	2.235658
ILMN_1709257	DSCR6	1.517224	5.735233	2.941805	0.005067	0.0324	-2.54891
ILMN_2393296	GK	1.518353	9.598436	5.729897	7.04E-07	5.62E-05	5.824792
ILMN_1804735	CBS	1.518364	10.34944	7.11591	5.67E-09	1.71E-06	10.44575
ILMN_3233229	SNHG7	1.518682	8.421681	5.440008	1.91E-06	0.000118	4.869451
ILMN_1811767	INHBE	1.528896	9.754692	4.058812	0.000187	0.002823	0.515259
ILMN_2058270	SOAT2	1.529102	7.857075	4.925121	1.10E-05	0.00039	3.199306
ILMN_1700888	ENPP1	1.529809	9.764005	5.001077	8.51E-06	0.000331	3.442988
ILMN_1679093	ZNF581	1.53104	10.25565	5.147761	5.18E-06	0.000229	3.916447
ILMN_2167808	TM4SF5	1.532999	11.79583	6.191479	1.42E-07	1.78E-05	7.359285
ILMN_1766446	C6orf48	1.535471	7.526632	6.14257	1.68E-07	2.00E-05	7.196175
ILMN_1654414	ACSL3	1.535824	6.668668	5.992155	2.84E-07	2.92E-05	6.695178
ILMN_1673649	HYOU1	1.537197	8.39254	5.097261	6.15E-06	0.00026	3.753038
ILMN_1776788	C5orf41	1.543878	6.165423	3.832594	0.000378	0.004774	-0.14847
ILMN_2347193	GSDMB	1.545542	5.756193	5.74358	6.71E-07	5.44E-05	5.870083
ILMN_1686531	GGT1	1.548457	5.878204	5.323671	2.85E-06	0.000152	4.488684
ILMN_1803846	EIF1	1.555872	12.23278	7.304532	2.95E-09	1.12E-06	11.07311
ILMN_1789196	TPM2	1.556535	6.444984	4.782331	1.77E-05	0.000544	2.744241
ILMN_2162972	LYZ	1.557457	10.2693	6.239507	1.20E-07	1.56E-05	7.519535
ILMN_2377900	MAP1B	1.558252	5.944373	5.403976	2.16E-06	0.000128	4.751338
ILMN_1690708	SPTBN1	1.560353	7.631696	4.385119	6.56E-05	0.001335	1.502665
ILMN_1660810	TTC17	1.574919	8.13524	5.376087	2.38E-06	0.000135	4.660028
ILMN_1741768	TMPRSS3	1.579749	6.903718	6.075801	2.12E-07	2.34E-05	6.973656
ILMN_1781386	WIPI1	1.585125	8.179527	5.20688	4.24E-06	0.000199	4.108252
ILMN_2150654	ZSWIM4	1.586539	6.481661	5.069732	6.75E-06	0.000276	3.664135
ILMN_1651496	HIST1H2BD	1.588528	5.891656	4.284524	9.08E-05	0.00168	1.194801
ILMN_1671005	IRF2BP2	1.588824	8.468867	5.416365	2.07E-06	0.000124	4.791931
ILMN_3235647	SIK1	1.591689	7.273008	4.838093	1.47E-05	0.000479	2.92146
ILMN_3244583	NCRNA00219	1.594441	10.19459	5.635395	9.75E-07	7.15E-05	5.51245
ILMN_1758798	LOC728734	1.594587	10.05776	6.269489	1.08E-07	1.45E-05	7.61961
ILMN_1737683	FGG	1.597046	10.37204	8.74887	2.12E-11	2.25E-08	15.79005
ILMN_1795582	CHRD	1.604484	7.239119	6.791063	1.76E-08	3.87E-06	9.362158
ILMN_1801703	CPLX1	1.605544	5.470666	3.263487	0.002063	0.016671	-1.7263
ILMN_1787923	PNPLA2	1.611465	9.652567	7.414151	2.02E-09	8.39E-07	11.43687
ILMN_2121408	HBEGF	1.61187	5.770787	3.939875	0.000271	0.003764	0.163992

ILMN_1808047	PHC2	1.614769	7.147382	6.285168	1.02E-07	1.41E-05	7.671949
ILMN_1815023	PIM1	1.62168	8.750129	3.83225	0.000379	0.004775	-0.14946
ILMN_1710482	APLP2	1.621702	9.924484	6.632381	3.05E-08	5.99E-06	8.832002
ILMN_2162799	AHR	1.624037	7.097382	6.186604	1.44E-07	1.80E-05	7.343024
ILMN_1725773	DNAJC12	1.627427	6.985032	4.021503	0.00021	0.003087	0.40454
ILMN_1803810	RRBP1	1.629408	8.896375	5.805563	5.42E-07	4.65E-05	6.075419
ILMN_1773809	FOXP4	1.631708	6.032714	4.787205	1.74E-05	0.000538	2.759707
ILMN_1710284	HES1	1.632811	6.944184	5.480335	1.66E-06	0.000107	5.001823
ILMN_1812226	ICAM1	1.633175	7.062524	4.918882	1.12E-05	0.000395	3.179338
ILMN_1778237	FN1	1.633277	6.500482	5.294368	3.14E-06	0.000162	4.393053
ILMN_1725471	GK	1.635328	9.103442	5.952342	3.26E-07	3.28E-05	6.562759
ILMN_3309349	SNHG8	1.636706	10.46313	6.363788	7.79E-08	1.13E-05	7.934497
ILMN_2329914	SPRY1	1.647772	10.55645	8.037742	2.36E-10	1.41E-07	13.49064
ILMN_3239574	SNORD3A	1.647883	8.179776	3.321685	0.001745	0.01467	-1.57173
ILMN_1655296	UTRN	1.662423	6.625507	5.914712	3.71E-07	3.61E-05	6.437685
ILMN_1712197	KCNMB3	1.662713	7.8784	4.410438	6.04E-05	0.001259	1.580605
ILMN_1746465	FJX1	1.663345	6.287374	4.419563	5.86E-05	0.001231	1.608735
ILMN_1754126	SH2D5	1.665144	5.809946	3.083002	0.003436	0.024295	-2.19467
ILMN_2089875	TNFSF4	1.668742	7.819721	6.058268	2.25E-07	2.44E-05	6.915256
ILMN_1680139	MAFF	1.67658	6.370089	4.623528	3.00E-05	0.000784	2.243262
ILMN_1729987	SRC	1.677794	9.163396	6.569378	3.80E-08	7.01E-06	8.621455
ILMN_3209399	LOC399965	1.678081	7.710526	5.782018	5.88E-07	4.92E-05	5.997385
ILMN_3236249	LOC727877	1.678147	6.203565	5.867377	4.37E-07	4.01E-05	6.280482
ILMN_1737406	KLF6	1.681715	7.259223	5.014467	8.13E-06	0.00032	3.486054
ILMN_1657234	CCL20	1.69009	11.26734	6.07004	2.16E-07	2.38E-05	6.954466
ILMN_1716815	CEACAM1	1.693302	11.05792	8.617593	3.29E-11	2.86E-08	15.36958
ILMN_1707720	SLC1A5	1.695233	9.884699	6.743993	2.07E-08	4.28E-06	9.204933
ILMN_1703477	ARHGEF2	1.696256	10.39926	5.219705	4.06E-06	0.000194	4.149935
ILMN_1753830	ETV4	1.699778	10.07547	7.117557	5.64E-09	1.71E-06	10.45123
ILMN_1773742	DNAJB9	1.702029	8.826509	4.973595	9.34E-06	0.000351	3.354698
ILMN_1734445	LOC91461	1.702282	5.96495	6.503659	4.78E-08	7.96E-06	8.401828
ILMN_1803882	VEGFA	1.705314	6.737519	6.844174	1.46E-08	3.32E-06	9.539518
ILMN_1825249		1.709849	6.086498	4.554905	3.76E-05	0.000909	2.0286
ILMN_1736742	GLT25D2	1.711502	5.37586	6.562244	3.90E-08	7.10E-06	8.597614
ILMN_1819608		1.715042	8.279237	4.678227	2.51E-05	0.000693	2.415176
ILMN_1756595	SH3TC1	1.719221	7.158128	5.119449	5.70E-06	0.000244	3.824783
ILMN_1797596	SPRY4	1.720179	5.335656	5.400833	2.18E-06	0.000129	4.741043
ILMN_1678671	KLHL24	1.728049	7.487356	4.505147	4.43E-05	0.001015	1.873686
ILMN_2341661	ETV4	1.732014	9.830773	6.290486	1.01E-07	1.40E-05	7.689705

ILMN_1780861	LOC653506	1.734968	5.931647	3.779076	0.000446	0.005377	-0.30271
ILMN_1673113	F2RL1	1.739811	7.664741	3.48809	0.001072	0.010225	-1.12081
ILMN_1788377	COL27A1	1.752404	6.051092	6.404509	6.76E-08	1.01E-05	8.070528
ILMN_2041190	F2RL1	1.754039	8.405214	4.097407	0.000165	0.002567	0.630289
ILMN_2305116	CTH	1.759705	6.529212	6.390961	7.08E-08	1.05E-05	8.025268
ILMN_1693014	CEBPB	1.761456	12.13235	6.917843	1.13E-08	2.75E-06	9.785423
ILMN_1751598	SESN2	1.77748	6.617689	5.126679	5.56E-06	0.000241	3.848178
ILMN_1740559	F7	1.778737	8.054437	5.587109	1.15E-06	8.16E-05	5.353176
ILMN_1791678	TAT	1.785179	6.796641	3.776318	0.00045	0.005404	-0.31062
ILMN_1673933	LOC440341	1.785291	9.854232	7.052773	7.06E-09	1.98E-06	10.23541
ILMN_1659027	SLC2A1	1.789375	10.77361	9.488051	1.83E-12	5.59E-09	18.11937
ILMN_1770673	AKNA	1.794982	6.227932	3.690596	0.000584	0.006523	-0.55522
ILMN_1731941	APOM	1.805021	11.77507	9.136298	5.83E-12	1.14E-08	17.01931
ILMN_1781400	SLC7A2	1.806557	10.93851	6.264022	1.10E-07	1.47E-05	7.601359
ILMN_2285817	FAM89A	1.819314	6.073706	5.807581	5.38E-07	4.65E-05	6.082109
ILMN_1689004	TNFRSF12A	1.820586	8.815333	4.79981	1.67E-05	0.000522	2.799723
ILMN_2269256	DNAJC12	1.824137	9.070196	5.071298	6.71E-06	0.000275	3.669191
ILMN_1777060	CTH	1.832045	5.827141	6.511161	4.66E-08	7.81E-06	8.426897
ILMN_1786429	P2RY5	1.835728	7.448349	6.353286	8.08E-08	1.16E-05	7.899418
ILMN_1654609	TIGA1	1.836383	10.28649	6.358638	7.93E-08	1.15E-05	7.917295
ILMN_1763887	SFI1	1.837182	6.690311	6.595868	3.47E-08	6.62E-06	8.709981
ILMN_1773586	SLC17A2	1.842968	9.042135	4.657704	2.68E-05	0.000722	2.350594
ILMN_1663401	LARP6	1.84933	7.231756	4.885926	1.25E-05	0.000425	3.073989
ILMN_1757338	PLSCR4	1.864019	6.141297	4.990061	8.83E-06	0.000338	3.407581
ILMN_1744381	SERPINE1	1.865632	8.188479	4.478615	4.83E-05	0.001082	1.791341
ILMN_2375879	VEGFA	1.86673	7.915044	8.765612	2.00E-11	2.25E-08	15.84354
ILMN_2384496	ST6GAL1	1.869271	7.623431	6.456998	5.63E-08	8.94E-06	8.245902
ILMN_1679041	SLC3A2	1.876752	5.823742	4.739717	2.04E-05	0.000603	2.609253
ILMN_1760649	PCK2	1.877859	9.026261	6.168249	1.54E-07	1.88E-05	7.281805
ILMN_1803073	DNAJC12	1.885763	9.001682	5.159468	4.98E-06	0.000223	3.954385
ILMN_1769290	TTC39B	1.896425	5.787998	9.731574	8.28E-13	4.55E-09	18.87156
ILMN_2375557	SCMH1	1.897413	7.049744	7.119981	5.59E-09	1.71E-06	10.45931
ILMN_1746175	TNFSF4	1.90484	6.343405	7.233708	3.77E-09	1.34E-06	10.83774
ILMN_2115125	CTGF	1.906451	11.09757	6.907817	1.17E-08	2.80E-06	9.751963
ILMN_2232712	MYO10	1.9077	8.583376	6.616174	3.23E-08	6.21E-06	8.777841
ILMN_2305112	CTH	1.908913	8.479815	5.661806	8.90E-07	6.67E-05	5.599662
ILMN_1691884	STC2	1.910966	10.41196	6.626212	3.12E-08	6.08E-06	8.811387
ILMN_1856480		1.922871	7.199651	5.867791	4.37E-07	4.01E-05	6.281856
ILMN_1682717	IER3	1.92307	11.18917	6.495839	4.91E-08	8.09E-06	8.375694

ILMN_1788874	SERPINA3	1.923365	12.99773	8.177544	1.46E-10	9.81E-08	13.94669
ILMN_3202591	LOC440311	1.924491	6.322049	4.497235	4.55E-05	0.001033	1.84911
ILMN_1723486	HK2	1.927839	10.16923	7.199961	4.24E-09	1.44E-06	10.72551
ILMN_1757497	VGF	1.934805	5.858977	4.267061	9.60E-05	0.00175	1.141659
ILMN_1814327	AGTR1	1.944121	6.132153	6.441026	5.95E-08	9.40E-06	8.192533
ILMN_1714445	SLC6A9	1.945431	8.500084	5.029539	7.73E-06	0.000308	3.534569
ILMN_1786972	SARS	1.948335	9.53073	6.016245	2.61E-07	2.74E-05	6.775342
ILMN_2371724	CEACAM1	1.958968	9.861435	9.07179	7.22E-12	1.29E-08	16.81588
ILMN_2361862	VLDLR	1.9621	6.054054	5.893006	4.00E-07	3.77E-05	6.365581
ILMN_1699354	EPHA2	1.966249	7.960369	6.943056	1.03E-08	2.61E-06	9.869549
ILMN_1787815	TRIB3	1.97696	11.36315	6.278603	1.05E-07	1.43E-05	7.650032
ILMN_1665792	ITGA2	1.987047	7.13923	5.6509	9.25E-07	6.90E-05	5.563643
ILMN_3307841	AGR2	2.003399	6.874941	4.453568	5.25E-05	0.001145	1.713774
ILMN_1674706	MTHFD2	2.016274	10.95131	7.219732	3.95E-09	1.39E-06	10.79127
ILMN_2341343	AGTR1	2.018424	6.15464	6.616156	3.23E-08	6.21E-06	8.777782
ILMN_2311020	DNAJC12	2.022232	8.418522	5.435714	1.94E-06	0.000119	4.855367
ILMN_1666206	GSDMB	2.024436	6.592874	5.901746	3.88E-07	3.73E-05	6.394609
ILMN_2188862	GDF15	2.035548	10.82013	5.732573	6.97E-07	5.59E-05	5.833649
ILMN_2358457	ATF4	2.043475	9.589603	7.665317	8.47E-10	4.16E-07	12.26755
ILMN_1691860	SPRY1	2.043897	10.05598	9.740713	8.03E-13	4.55E-09	18.89964
ILMN_1800540	CD55	2.052199	6.37405	5.07145	6.71E-06	0.000275	3.66968
ILMN_1658318	LOC120376	2.053308	6.883083	8.02196	2.49E-10	1.42E-07	13.43905
ILMN_1752810	LARP6	2.061859	5.6379	4.720151	2.18E-05	0.000632	2.547407
ILMN_1777556	SOAT2	2.06306	8.987973	5.84404	4.74E-07	4.19E-05	6.203032
ILMN_1669523	FOS	2.063286	5.481568	5.359828	2.51E-06	0.000139	4.60684
ILMN_2374865	ATF3	2.079166	7.38966	6.988657	8.83E-09	2.36E-06	10.02166
ILMN_2367469	CARS	2.087374	9.643049	6.948003	1.02E-08	2.59E-06	9.886054
ILMN_1715452	FREM1	2.09758	8.74687	7.445075	1.81E-09	8.03E-07	11.53936
ILMN_2367010	GPR126	2.124124	10.01283	8.244371	1.17E-10	8.90E-08	14.16404
ILMN_1696317	CACNA2D4	2.12484	8.091464	6.41373	6.54E-08	9.99E-06	8.101333
ILMN_1773082	CYP21A2	2.12831	6.504005	7.238451	3.71E-09	1.34E-06	10.85351
ILMN_1664330	CEACAM1	2.147119	6.753032	8.75125	2.10E-11	2.25E-08	15.79766
ILMN_1659984	MEP1A	2.159551	8.247505	4.991782	8.78E-06	0.000338	3.413111
ILMN_1775380	SMOX	2.163279	9.050811	6.997539	8.56E-09	2.34E-06	10.05128
ILMN_1659936	PPP1R15A	2.166471	9.286803	5.847685	4.68E-07	4.16E-05	6.215126
ILMN_1677466	DUSP6	2.205025	5.628412	8.339382	8.44E-11	6.63E-08	14.47229
ILMN_1799819	MARS	2.219646	10.16831	8.041563	2.33E-10	1.41E-07	13.50313
ILMN_1661599	DDIT4	2.228964	10.12103	7.831346	4.78E-10	2.54E-07	12.8142
ILMN_1796928	BPIL1	2.229558	9.706077	7.089413	6.22E-09	1.80E-06	10.35749

ILMN_1741465	PTPRH	2.249834	7.395738	5.564036	1.25E-06	8.61E-05	5.277151
ILMN_1680874	TUBB2B	2.255137	9.438586	9.549247	1.50E-12	5.59E-09	18.30913
ILMN_2074748	HAL	2.266848	6.836806	5.125398	5.59E-06	0.000242	3.844032
ILMN_1656369	C8orf4	2.269895	8.082855	6.930446	1.08E-08	2.65E-06	9.827476
ILMN_1667239	INPP1	2.282077	9.085398	8.614897	3.32E-11	2.86E-08	15.36092
ILMN_1669114	WNK4	2.308378	8.219533	7.402686	2.10E-09	8.60E-07	11.39886
ILMN_2405521	MTHFD2	2.317578	10.60824	7.497004	1.51E-09	6.82E-07	11.71134
ILMN_1760087	SLC26A3	2.323839	6.402623	4.816943	1.58E-05	0.000504	2.854167
ILMN_1696066	CARS	2.344893	7.918319	6.578403	3.69E-08	6.87E-06	8.651616
ILMN_1699574	NRP1	2.373921	6.551993	6.287196	1.02E-07	1.41E-05	7.678721
ILMN_2367258	SMOX	2.387797	8.805321	6.500482	4.84E-08	8.00E-06	8.39121
ILMN_1755649	SLC16A5	2.404804	6.360544	5.236598	3.83E-06	0.000187	4.204873
ILMN_1789244	SOX8	2.414592	6.366195	6.898273	1.21E-08	2.86E-06	9.72011
ILMN_1676984	DDIT3	2.416675	8.27581	5.961722	3.15E-07	3.19E-05	6.59395
ILMN_2396020	DUSP6	2.472152	10.20803	10.97882	1.59E-14	4.38E-10	22.59589
ILMN_2086105	SPRY4	2.533923	9.163	6.963102	9.65E-09	2.52E-06	9.936424
ILMN_2198912	TTR	2.561975	12.13851	9.341842	2.96E-12	7.39E-09	17.66403
ILMN_1658494	C13orf15	2.67051	6.590829	4.899409	1.20E-05	0.000411	3.117063
ILMN_3234837	PKDCC	2.6973	7.473534	9.491824	1.81E-12	5.59E-09	18.13108
ILMN_1663171	MATN3	2.710158	7.961871	8.544111	4.22E-11	3.51E-08	15.13338
ILMN_1674785	COL2A1	2.786542	7.516263	6.424933	6.29E-08	9.71E-06	8.138765
ILMN_2398107	ASNS	2.79327	9.521718	8.092601	1.95E-10	1.28E-07	13.66981
ILMN_1702933	ADM2	2.854776	7.863882	6.521143	4.50E-08	7.63E-06	8.460257
ILMN_1697220	NT5E	2.946159	7.944787	6.404726	6.75E-08	1.01E-05	8.071252
ILMN_1796417	ASNS	3.238268	10.7741	9.238476	4.16E-12	8.79E-09	17.34047
ILMN_2391150	FILIP1L	3.399903	8.074033	8.86767	1.42E-11	1.98E-08	16.16888
ILMN_1738578	FILIP1L	3.453337	9.065107	9.552737	1.48E-12	5.59E-09	18.31994
ILMN_1730906	FILIP1L	3.515759	8.048492	8.747663	2.13E-11	2.25E-08	15.7862
ILMN_1762899	EGR1	3.908202	8.401157	6.939086	1.05E-08	2.62E-06	9.856304
ILMN_1767556	C10orf10	4.08641	9.518496	6.390435	7.10E-08	1.05E-05	8.023511
ILMN_2387385	IGFBP1	4.411931	11.52883	6.551542	4.05E-08	7.32E-06	8.561846
ILMN_1728445	IGFBP1	4.721005	8.913454	5.478812	1.67E-06	0.000107	4.996823

Appendix L. Gene annotated list of down-regulated genes (DEGs) when exposed to 1000 ppb of metolachlor exposed human liver cells for 48 hours compared to control.

PROBE_ID	SYMBOL	logFC	AveExpr	t	P.Value	adj.P.Val	B
ILMN_1803862	LCN15	-3.41451	7.631751	-6.39377	7.01E-08	1.78E-05	8.036573
ILMN_1729188	HAMP	-3.33572	9.666053	-5.25248	3.63E-06	0.000241	4.286637
ILMN_1777233	E2F2	-2.99434	8.097666	-4.72826	2.12E-05	0.000776	2.614329
ILMN_1715401	MT1G	-2.89231	10.48736	-3.08154	0.00345	0.026486	-2.12933
ILMN_1786065	UHRF1	-2.84861	10.04627	-4.20737	0.000116	0.002375	1.012011
ILMN_1656638	BHMT	-2.79971	6.234096	-10.0614	2.86E-13	5.15E-09	19.75615
ILMN_2353117	SLC22A7	-2.7485	7.915285	-4.67833	2.50E-05	0.000856	2.457803
ILMN_1806037	TK1	-2.70433	8.68445	-4.50313	4.46E-05	0.001232	1.913162
ILMN_2412336	AKR1C2	-2.67796	7.190344	-6.34968	8.18E-08	1.94E-05	7.890488
ILMN_1796094	CD36	-2.64888	6.15631	-8.28514	1.01E-10	1.99E-07	14.24069
ILMN_2249018	LOC389816	-2.6336	6.629623	-4.93322	1.07E-05	0.000477	3.262274
ILMN_1696713	POLA2	-2.61368	7.809177	-5.45174	1.83E-06	0.000156	4.933479
ILMN_1732688	DUT	-2.60168	7.6258	-5.02703	7.80E-06	0.000383	3.561534
ILMN_2413898	MCM10	-2.59677	7.748061	-5.10788	5.93E-06	0.000329	3.820646
ILMN_1809590	GINS2	-2.54078	9.82527	-4.16092	0.000135	0.002634	0.872799
ILMN_1746720	TTC39C	-2.48892	7.586939	-6.79034	1.76E-08	7.44E-06	9.350696
ILMN_1670238	CDC45L	-2.4781	8.922626	-4.49197	4.63E-05	0.001258	1.878724
ILMN_2412860	MCM4	-2.46817	8.377499	-6.4145	6.52E-08	1.76E-05	8.10528
ILMN_1779711	DTL	-2.45136	7.08112	-5.30028	3.08E-06	0.000221	4.441368
ILMN_2234187	CDO1	-2.42058	7.540783	-8.29631	9.77E-11	1.99E-07	14.27656
ILMN_2328972	DNMT3B	-2.40372	7.461849	-6.94272	1.04E-08	4.80E-06	9.85498
ILMN_1713995	SCNN1A	-2.39951	8.983755	-8.46804	5.46E-11	1.66E-07	14.82624
ILMN_2093343	PLAC8	-2.39338	8.011637	-6.39421	7.00E-08	1.78E-05	8.03801
ILMN_1678669	RRM2	-2.38486	7.152961	-4.38868	6.48E-05	0.001597	1.561563
ILMN_1680757	LRRC26	-2.37501	6.244911	-4.97002	9.45E-06	0.000438	3.379476
ILMN_1673721	EXO1	-2.37004	6.986365	-4.56354	3.66E-05	0.00108	2.100131
ILMN_1797391	SLC22A7	-2.36177	6.38992	-5.86761	4.37E-07	6.00E-05	6.296797
ILMN_1681503	MCM2	-2.33197	9.23316	-4.91741	1.13E-05	0.000496	3.212007
ILMN_1798654	MCM6	-2.32231	9.889516	-5.10475	5.99E-06	0.000329	3.810614
ILMN_2365176	ALDH8A1	-2.31715	6.788929	-6.73563	2.13E-08	8.49E-06	9.169495
ILMN_1784863	CD36	-2.27214	5.805642	-8.61757	3.29E-11	1.13E-07	15.30231
ILMN_2181432	SPC24	-2.26582	8.192361	-5.41076	2.11E-06	0.000175	4.800047
ILMN_1711015	CRYAA	-2.2564	8.679583	-6.35234	8.10E-08	1.94E-05	7.8993
ILMN_1733042	BCAS1	-2.24477	6.193053	-6.76765	1.91E-08	7.82E-06	9.275532

ILMN_1774336	POLE2	-2.20181	7.866322	-4.31884	8.13E-05	0.001866	1.348736
ILMN_2413899	MCM10	-2.18001	5.994278	-6.48821	5.05E-08	1.52E-05	8.349565
ILMN_1814281	SPC25	-2.16615	6.868453	-4.59151	3.34E-05	0.001023	2.186992
ILMN_1653026	PLAC8	-2.16383	6.691901	-6.34014	8.45E-08	1.97E-05	7.858866
ILMN_2311089	BRCA1	-2.16108	6.276748	-5.70043	7.79E-07	9.01E-05	5.746979
ILMN_1778543	LOC653874	-2.14768	7.55688	-4.56652	3.62E-05	0.001076	2.109363
ILMN_2121774	JCLN	-2.12262	5.444465	-9.1989	4.74E-12	3.25E-08	17.12803
ILMN_1685663	CYP24A1	-2.11079	8.819878	-4.25586	9.96E-05	0.002149	1.15803
ILMN_2136147	BCAS1	-2.10402	5.888665	-7.50416	1.48E-09	1.23E-06	11.70469
ILMN_1737205	MCM4	-2.10362	9.709768	-4.76406	1.88E-05	0.000707	2.726874
ILMN_2414786	DIO1	-2.1018	8.902679	-3.55857	0.00087	0.009706	-0.86379
ILMN_3232696	LOC729816	-2.10169	9.301043	-4.12996	0.000149	0.002811	0.78039
ILMN_1712729	DKK4	-2.10066	7.299118	-5.52882	1.41E-06	0.000134	5.184971
ILMN_1804090	SLC25A10	-2.10063	8.663935	-5.5256	1.42E-06	0.000134	5.174443
ILMN_1737728	CDCA3	-2.0972	8.107577	-5.08281	6.46E-06	0.000343	3.740195
ILMN_1665671	EPO	-2.09495	7.004892	-5.64944	9.29E-07	9.90E-05	5.579707
ILMN_1774066	TMEM141	-2.09318	10.13776	-5.88056	4.18E-07	5.83E-05	6.33947
ILMN_3251497	GSTA1	-2.09177	6.504843	-6.33083	8.73E-08	2.02E-05	7.828038
ILMN_3249142	JCLN	-2.09149	5.305316	-8.3887	7.14E-11	1.78E-07	14.57266
ILMN_1659364	RFC5	-2.09072	8.989345	-5.93892	3.41E-07	5.04E-05	6.531896
ILMN_2374778	DUT	-2.07309	6.442753	-4.9428	1.04E-05	0.000469	3.292769
ILMN_2285996	KIAA0101	-2.07005	9.616738	-4.28367	9.10E-05	0.002005	1.242095
ILMN_2124802	MT1H	-2.06688	7.376004	-3.01655	0.00413	0.030061	-2.29283
ILMN_2229940	C2orf7	-2.06645	7.697343	-4.88297	1.27E-05	0.000536	3.102655
ILMN_1695414	ASF1B	-2.04018	8.436952	-4.14785	0.000141	0.002707	0.833733
ILMN_1796423	CLIC3	-2.03997	5.563853	-5.96955	3.07E-07	4.87E-05	6.632971
ILMN_2235137	FANCD2	-2.00736	8.504755	-5.7713	6.10E-07	7.42E-05	5.979787
ILMN_1674231	CHAF1B	-2.00641	7.856798	-5.45293	1.83E-06	0.000156	4.937357
ILMN_1807501	GINS4	-1.98468	6.207868	-7.01357	8.10E-09	4.25E-06	10.08922
ILMN_1682099	TNFAIP8L3	-1.98239	6.21958	-6.74828	2.04E-08	8.24E-06	9.211395
ILMN_2328977	DNMT3B	-1.97982	6.57642	-7.13992	5.22E-09	3.05E-06	10.50645
ILMN_1694432	CRIP2	-1.96264	7.562975	-4.51238	4.33E-05	0.00121	1.941733
ILMN_1808707	FSCN1	-1.96068	10.43152	-5.19261	4.45E-06	0.00028	4.093327
ILMN_1706779	LIG1	-1.91963	7.750503	-4.01557	0.000214	0.003639	0.441662
ILMN_2202423	HELLS	-1.91366	7.367513	-3.45837	0.001171	0.012005	-1.13859
ILMN_2113470	GSTA1	-1.90833	6.2465	-7.0091	8.22E-09	4.25E-06	10.07444
ILMN_2355738	INCENP	-1.9053	7.073476	-5.93976	3.40E-07	5.04E-05	6.534673
ILMN_3307921	PGLYRP2	-1.89668	6.468616	-4.49897	4.52E-05	0.001237	1.900323
ILMN_1791002	SKP2	-1.89628	7.029183	-4.68032	2.49E-05	0.000854	2.464037

ILMN_1797875	ALOX5AP	-1.89541	6.216303	-4.49371	4.60E-05	0.001254	1.884084
ILMN_1656920	CRIP1	-1.89426	9.578862	-4.18802	0.000124	0.002482	0.953925
ILMN_1815169	MCM5	-1.89154	7.721421	-4.27697	9.30E-05	0.00204	1.221828
ILMN_1731745	NINJ2	-1.88875	5.698533	-7.99501	2.73E-10	3.95E-07	13.30484
ILMN_2406634	DNMT3L	-1.883	5.599879	-8.3424	8.35E-11	1.91E-07	14.42438
ILMN_1665538	SKP2	-1.88267	10.66566	-5.53652	1.37E-06	0.000134	5.21012
ILMN_1754272	GINS3	-1.87684	7.881169	-5.29571	3.13E-06	0.000222	4.426543
ILMN_2196984	OIP5	-1.85436	9.661722	-5.17174	4.78E-06	0.00029	4.026075
ILMN_1651237	CDT1	-1.85063	9.080969	-4.66854	2.59E-05	0.000877	2.427182
ILMN_1683120	UNG	-1.83823	10.66365	-4.62243	3.01E-05	0.000966	2.28322
ILMN_1769547	DIO1	-1.83804	9.030743	-3.1095	0.003191	0.025044	-2.0583
ILMN_1777564	MAD2L1	-1.83511	9.242941	-5.47711	1.68E-06	0.000149	5.01617
ILMN_2368718	CENPM	-1.83415	8.519179	-4.31689	8.18E-05	0.001871	1.342824
ILMN_1798210	E2F7	-1.8291	6.32486	-5.45706	1.80E-06	0.000155	4.950829
ILMN_2134801	AGXT2L1	-1.82683	6.820409	-4.56176	3.68E-05	0.001082	2.094585
ILMN_1759277	OIP5	-1.8158	7.591118	-5.70523	7.66E-07	8.93E-05	5.762711
ILMN_2359945	CES1	-1.81367	10.21616	-6.67438	2.64E-08	9.56E-06	8.96657
ILMN_1694877	CASP6	-1.80908	6.677599	-5.2881	3.21E-06	0.000226	4.401891
ILMN_1655642	FANCI	-1.80668	7.573273	-4.85175	1.41E-05	0.000573	3.003697
ILMN_2334205	ERCC6L	-1.79004	5.952169	-5.84185	4.78E-07	6.41E-05	6.211956
ILMN_1758728	FANCG	-1.7882	8.595275	-5.31104	2.97E-06	0.000215	4.476218
ILMN_1796589	TRIP13	-1.78404	9.065836	-5.46402	1.76E-06	0.000153	4.973496
ILMN_1681340	C1orf41	-1.78395	7.702592	-5.0399	7.46E-06	0.000376	3.602708
ILMN_1796923	LOC81691	-1.77556	7.570936	-4.92511	1.10E-05	0.000487	3.236475
ILMN_2212909	MELK	-1.77536	9.121677	-4.58342	3.43E-05	0.00104	2.161834
ILMN_1653292	PFKFB4	-1.7746	8.809694	-3.79429	0.000426	0.005885	-0.20055
ILMN_1776490	C17orf53	-1.77207	7.669776	-5.18513	4.56E-06	0.000283	4.069218
ILMN_1669842	CHAF1A	-1.77078	6.149774	-5.03692	7.54E-06	0.000378	3.593154
ILMN_1810901	RNASEH2A	-1.7635	8.035717	-4.34188	7.54E-05	0.001771	1.418808
ILMN_2191436	POLA1	-1.76267	8.191386	-5.6777	8.43E-07	9.46E-05	5.672377
ILMN_2349459	BIRC5	-1.75861	9.906152	-5.49486	1.58E-06	0.000145	5.07409
ILMN_1683450	CDCA5	-1.74988	10.66282	-4.53724	3.99E-05	0.00114	2.018605
ILMN_1715616	PPIL5	-1.74947	8.100899	-5.13454	5.42E-06	0.000311	3.906336
ILMN_1813043	BHMT2	-1.74346	6.337512	-7.99772	2.70E-10	3.95E-07	13.31364
ILMN_1679438	MLF1IP	-1.73934	6.729059	-4.11599	0.000156	0.002891	0.738802
ILMN_1796074	C18orf56	-1.73861	11.42865	-4.77362	1.82E-05	0.000694	2.756985
ILMN_1789096	OSTalpha	-1.73185	6.995821	-5.47071	1.72E-06	0.000151	4.995314
ILMN_1660806	CSRP2	-1.72697	7.000669	-4.85168	1.41E-05	0.000573	3.003498
ILMN_1794692	DNMT3B	-1.72451	6.582415	-5.98786	2.88E-07	4.77E-05	6.693413

ILMN_2413650	STIL	-1.72326	8.940585	-4.58528	3.41E-05	0.001038	2.167636
ILMN_1738027	BRCA1	-1.71942	6.689855	-4.65352	2.72E-05	0.000904	2.380244
ILMN_1757697	NEIL3	-1.71328	6.087707	-4.80991	1.62E-05	0.000634	2.87143
ILMN_1694177	PCNA	-1.70316	11.54925	-4.50995	4.36E-05	0.001212	1.934231
ILMN_1806818	MCM3	-1.70281	10.35026	-4.71949	2.18E-05	0.000791	2.586797
ILMN_1722239	TIMM8A	-1.69166	8.181685	-6.98234	9.02E-09	4.43E-06	9.985999
ILMN_1702503	ALDH3A1	-1.68244	5.118191	-6.34146	8.42E-08	1.97E-05	7.863235
ILMN_1785191	TMEM14A	-1.67884	9.202155	-5.01378	8.15E-06	0.000396	3.519161
ILMN_1793360	APITD1	-1.67101	7.663853	-5.00243	8.47E-06	0.000406	3.482918
ILMN_1685625	UCP2	-1.66622	7.111294	-4.17803	0.000128	0.002541	0.923997
ILMN_1801118	C16orf33	-1.66532	9.973505	-4.97311	9.35E-06	0.000435	3.389332
ILMN_1726720	NUSAP1	-1.66518	10.11438	-4.79711	1.69E-05	0.000657	2.831041
ILMN_1673673	PBK	-1.66332	8.528968	-4.43853	5.51E-05	0.001427	1.71428
ILMN_1668721	CCND3	-1.65681	8.027419	-5.89198	4.02E-07	5.73E-05	6.377095
ILMN_1811933	SHMT1	-1.65649	9.3408	-5.18848	4.51E-06	0.000282	4.08
ILMN_1695658	KIF20A	-1.65641	9.259455	-4.58196	3.44E-05	0.001043	2.15731
ILMN_1727459	ORC1L	-1.65568	6.031321	-5.30202	3.06E-06	0.00022	4.446978
ILMN_2225537	PTGR1	-1.65109	8.124944	-7.65955	8.64E-10	8.48E-07	12.21331
ILMN_1715905	DSN1	-1.64733	7.533057	-4.6808	2.48E-05	0.000854	2.465538
ILMN_1771593	RRM1	-1.64445	10.98116	-4.60671	3.17E-05	0.000991	2.23426
ILMN_1739594	ACOT11	-1.64256	6.911635	-5.33955	2.69E-06	0.000205	4.568666
ILMN_1714730	UBE2C	-1.64255	9.263373	-6.61475	3.25E-08	1.09E-05	8.768947
ILMN_2186061	PFKFB3	-1.63911	6.216693	-5.22431	3.99E-06	0.000258	4.195632
ILMN_1737195	CENPK	-1.6373	7.444955	-3.86975	0.000337	0.00503	0.016456
ILMN_2343048	ABCB9	-1.63182	7.840741	-5.21618	4.11E-06	0.000263	4.169379
ILMN_1779448	EFHD1	-1.62941	5.161493	-7.00431	8.36E-09	4.25E-06	10.05862
ILMN_2411190	SMC2	-1.62722	7.075333	-4.77371	1.82E-05	0.000694	2.757263
ILMN_2318568	HCFC1R1	-1.60466	7.07538	-5.66818	8.71E-07	9.63E-05	5.641136
ILMN_2185339	LRTOMT	-1.60164	6.316666	-6.43732	6.03E-08	1.74E-05	8.180899
ILMN_1781943	FAM83D	-1.59484	9.782714	-4.79711	1.69E-05	0.000657	2.831025
ILMN_2367113	CASP6	-1.59433	6.447223	-4.90502	1.18E-05	0.000508	3.172642
ILMN_1749829	DLGAP5	-1.59217	8.800363	-4.29706	8.72E-05	0.001956	1.282666
ILMN_1773119	CCNF	-1.59008	9.109074	-5.89158	4.02E-07	5.73E-05	6.3758
ILMN_1727466	KCNMB4	-1.58658	5.878907	-5.49464	1.58E-06	0.000145	5.073366
ILMN_1790537	C16orf75	-1.5825	10.27735	-3.9554	0.000258	0.004148	0.265301
ILMN_2409298	NUSAP1	-1.58058	8.51614	-4.53753	3.99E-05	0.00114	2.019517
ILMN_1651433	DCK	-1.57646	8.063209	-4.77061	1.84E-05	0.000696	2.747512
ILMN_1786125	CCNA2	-1.57641	10.27483	-4.46988	4.97E-05	0.001326	1.81066
ILMN_1732150	KIAA0101	-1.57624	5.717222	-7.36301	2.41E-09	1.79E-06	11.24129

ILMN_2151739	CAT	-1.5724	9.973881	-5.0906	6.29E-06	0.000339	3.765197
ILMN_1781479	SUV39H1	-1.57062	8.255265	-5.29788	3.11E-06	0.000221	4.433594
ILMN_1812281	ARG1	-1.56414	6.173375	-4.35084	7.33E-05	0.001738	1.446079
ILMN_2171183	C21orf45	-1.56307	6.854551	-4.14255	0.000143	0.002738	0.817937
ILMN_1711470	UBE2T	-1.56173	8.884332	-4.02231	0.000209	0.00358	0.461507
ILMN_1805828	VRK1	-1.56006	7.408146	-4.50571	4.42E-05	0.001226	1.921123
ILMN_2169261	TNNI2	-1.55815	5.550003	-5.26398	3.49E-06	0.000236	4.323842
ILMN_2301083	UBE2C	-1.55453	9.572666	-6.02468	2.53E-07	4.38E-05	6.815011
ILMN_1761486	C13orf34	-1.55402	8.440198	-4.19325	0.000122	0.002448	0.969629
ILMN_1716895	RPA3	-1.55236	10.5349	-4.12659	0.000151	0.002831	0.770338
ILMN_1699258	ALDH8A1	-1.55126	5.520045	-6.9344	1.07E-08	4.80E-06	9.827477
ILMN_1774375	LOC284422	-1.5466	9.205828	-3.11966	0.003102	0.024573	-2.03238
ILMN_1780667	WDR51A	-1.54606	9.44498	-5.71252	7.47E-07	8.78E-05	5.78667
ILMN_1782937	LOC647169	-1.54273	5.951941	-5.85281	4.60E-07	6.26E-05	6.248041
ILMN_1667839	UBR7	-1.5408	9.006655	-5.52956	1.40E-06	0.000134	5.187366
ILMN_1658143	RFC3	-1.53977	7.320607	-4.45041	5.30E-05	0.001392	1.750783
ILMN_1728048	LOC158160	-1.53816	9.008283	-4.17148	0.00013	0.002576	0.904393
ILMN_1785646	PMP22	-1.53809	7.207327	-4.65421	2.71E-05	0.000904	2.382383
ILMN_2362549	ZWINT	-1.53576	8.002877	-3.66697	0.000628	0.007717	-0.56162
ILMN_1704531	PTGR1	-1.52866	6.920656	-6.83799	1.49E-08	6.51E-06	9.508444
ILMN_1703326	GPR44	-1.52791	7.018752	-4.60798	3.16E-05	0.00099	2.238235
ILMN_2372915	P2RY2	-1.52639	6.438908	-5.40394	2.16E-06	0.000177	4.777857
ILMN_1709484	BLM	-1.52101	5.963037	-4.72486	2.15E-05	0.000783	2.603639
ILMN_1712386	C21orf45	-1.52021	7.728524	-4.60361	3.21E-05	0.000998	2.224611
ILMN_1874530	DIAPH3	-1.5159	7.025489	-3.65728	0.000646	0.007873	-0.58885
ILMN_1753729	KNG1	-1.51569	6.394949	-5.15005	5.14E-06	0.000305	3.95624
ILMN_1664630	CHEK1	-1.50967	8.634158	-3.71669	0.00054	0.006933	-0.42138
ILMN_1742922	PRIM2A	-1.50429	5.759432	-5.77616	6.00E-07	7.35E-05	5.995763
ILMN_1776582	PDK3	-1.50149	6.327602	-5.1407	5.31E-06	0.000307	3.92614
ILMN_1694268	HES6	-1.49897	10.29517	-4.48536	4.73E-05	0.001274	1.858355
ILMN_1660793	PAQR4	-1.49856	8.890741	-5.78736	5.77E-07	7.15E-05	6.032625
ILMN_1712803	CCNB1	-1.4972	9.027722	-5.32842	2.80E-06	0.00021	4.532557
ILMN_1718771	CCDC24	-1.49609	6.236806	-3.96694	0.000249	0.004062	0.299028
ILMN_2205032	MAGEE1	-1.49062	6.769108	-5.32292	2.85E-06	0.000211	4.514749
ILMN_3239861	C10orf140	-1.49029	6.587184	-5.44845	1.86E-06	0.000157	4.922766
ILMN_1794539	KIF11	-1.48475	7.951503	-4.75894	1.92E-05	0.000715	2.710768
ILMN_1726666	GPX3	-1.4835	10.15509	-3.95771	0.000256	0.004128	0.272048
ILMN_3238712	SNRNP25	-1.48307	7.277256	-3.94137	0.00027	0.004286	0.224345
ILMN_1778152	FIGNL1	-1.48275	6.071613	-5.11051	5.88E-06	0.000327	3.82911

ILMN_1761463	EFHD2	-1.48178	9.195373	-5.32497	2.83E-06	0.000211	4.521384
ILMN_1805985	ANKRD32	-1.48111	5.63311	-5.26212	3.51E-06	0.000237	4.317811
ILMN_1688666	HIST1H2BH	-1.48075	5.160872	-5.60759	1.07E-06	0.000112	5.442588
ILMN_2395236	CHEK2	-1.47988	7.696364	-5.14529	5.22E-06	0.000306	3.940909
ILMN_1673521	KISS1R	-1.47855	9.344051	-4.66714	2.60E-05	0.00088	2.422795
ILMN_2160929	FEN1	-1.47825	10.55641	-4.53634	4.00E-05	0.001142	2.015822
ILMN_1719906	HADH	-1.47467	10.88901	-4.54322	3.91E-05	0.001122	2.037124
ILMN_1751444	NCAPG	-1.4738	9.239761	-3.9998	0.000225	0.003777	0.395317
ILMN_2143155	KIF11	-1.47378	8.585071	-4.06363	0.000184	0.00326	0.583442
ILMN_1717403	C9orf100	-1.47204	5.940914	-5.37484	2.39E-06	0.000188	4.683276
ILMN_1739645	ANLN	-1.46992	8.304632	-3.9503	0.000262	0.004193	0.250412
ILMN_2202948	BUB1	-1.46849	8.976728	-5.66329	8.86E-07	9.67E-05	5.625114
ILMN_2362545	ZWINT	-1.46814	7.169648	-3.72053	0.000533	0.006875	-0.41051
ILMN_1721495	ADAMTSL2	-1.46199	7.604732	-7.05422	7.03E-09	3.86E-06	10.22351
ILMN_2412384	CCNE2	-1.46174	6.026385	-5.18936	4.50E-06	0.000282	4.082856
ILMN_1662587	PNPLA7	-1.46164	7.020578	-3.92949	0.00028	0.004415	0.189738
ILMN_1658027	RAD54L	-1.46023	8.2595	-3.81109	0.000404	0.005698	-0.15242
ILMN_1806607	SFN	-1.45841	6.846684	-3.83168	0.000379	0.005463	-0.09328
ILMN_1727540	C1orf112	-1.45641	7.522674	-4.51547	4.28E-05	0.001203	1.95128
ILMN_1772686	FGD3	-1.45387	6.173425	-5.14411	5.24E-06	0.000306	3.93712
ILMN_1731184	MELK	-1.4527	8.118863	-4.20995	0.000115	0.002361	1.019751
ILMN_2224143	MCM3	-1.44911	12.36589	-4.7374	2.06E-05	0.000754	2.643017
ILMN_3239771	DLGAP5	-1.44688	8.540954	-3.97418	0.000243	0.004017	0.32021
ILMN_1693669	WDR79	-1.44566	7.133172	-4.6944	2.37E-05	0.000837	2.508108
ILMN_1724489	RFC4	-1.44367	9.420534	-4.17725	0.000128	0.002545	0.92167
ILMN_1783610	HELLS	-1.43987	6.585522	-3.97977	0.000239	0.003956	0.336593
ILMN_1740291	POLQ	-1.43833	7.424185	-3.46367	0.001153	0.011876	-1.12415
ILMN_1785756	LOC731314	-1.43804	10.55532	-4.54421	3.90E-05	0.00112	2.040209
ILMN_1712075	SYNM	-1.43658	6.581963	-5.6602	8.95E-07	9.73E-05	5.61498
ILMN_1670353	RAD51AP1	-1.43452	8.671042	-3.24755	0.00216	0.018836	-1.70155
ILMN_2374425	CCNE1	-1.43359	7.753254	-3.8003	0.000418	0.005813	-0.18333
ILMN_1710644	MARVELD3	-1.42872	7.038207	-5.96474	3.12E-07	4.93E-05	6.617081
ILMN_2074258	BARD1	-1.42863	7.784812	-4.14132	0.000144	0.002745	0.814259
ILMN_2139816	GPSM2	-1.42857	7.230113	-5.1474	5.19E-06	0.000305	3.947703
ILMN_3239785	LOC100134304	-1.42755	9.328092	-4.24287	0.000104	0.002215	1.118841
ILMN_1741801	CDC7	-1.4262	6.827291	-4.07942	0.000175	0.003148	0.630192
ILMN_1705861	AP1M2	-1.42605	7.130809	-4.04626	0.000194	0.003381	0.532105
ILMN_1697998	FAM54A	-1.42541	6.35128	-4.86528	1.34E-05	0.000557	3.046563
ILMN_1757552	PTRF	-1.4254	9.519856	-4.11662	0.000155	0.002887	0.74066

ILMN_1674662	C15orf42	-1.42418	5.671594	-4.44076	5.47E-05	0.00142	1.721122
ILMN_2334204	ERCC6L	-1.42386	5.455496	-5.55888	1.27E-06	0.000128	5.283212
ILMN_1714861	CD68	-1.42334	9.739647	-5.06341	6.89E-06	0.000359	3.677979
ILMN_1785914	CDC6	-1.42237	5.642259	-6.70714	2.35E-08	8.98E-06	9.0751
ILMN_1658289	WDR54	-1.41504	6.568023	-3.18143	0.002607	0.021622	-1.87364
ILMN_1761939	TIPIN	-1.414	6.926379	-6.12719	1.77E-07	3.34E-05	7.153846
ILMN_1800512	HMOX1	-1.40998	7.649133	-4.06026	0.000186	0.003286	0.573482
ILMN_1730454	FOLR3	-1.40944	4.893275	-5.97669	2.99E-07	4.83E-05	6.656526
ILMN_1763907	C6orf173	-1.40907	9.414164	-4.4472	5.36E-05	0.001403	1.7409
ILMN_1751776	CKAP2L	-1.40833	7.609194	-3.76454	0.000466	0.006231	-0.2855
ILMN_1747911	CDC2	-1.40704	9.226916	-4.59873	3.26E-05	0.001007	2.209429
ILMN_2389114	FIGNL1	-1.40546	5.855552	-4.72306	2.16E-05	0.000786	2.597994
ILMN_1655613	GSTA2	-1.40502	5.636318	-6.48039	5.19E-08	1.52E-05	8.323652
ILMN_1772292	LOC653752	-1.40439	7.118416	-4.44106	5.47E-05	0.00142	1.722035
ILMN_1808487	PLA2G12B	-1.40425	9.191411	-5.08036	6.51E-06	0.000345	3.73234
ILMN_1656452	C16orf59	-1.40416	7.618598	-5.05703	7.04E-06	0.000363	3.657565
ILMN_1800619	BRI3BP	-1.40268	8.353472	-5.00011	8.54E-06	0.000408	3.475494
ILMN_2066756	NCAPG2	-1.40245	6.830864	-4.0117	0.000216	0.003669	0.4303
ILMN_2049642	RPA1	-1.40196	10.16978	-5.78964	5.72E-07	7.15E-05	6.040107
ILMN_1719032	LSM3	-1.40063	9.155878	-5.14915	5.16E-06	0.000305	3.953329
ILMN_2216918	SHPK	-1.40038	10.41571	-6.18472	1.45E-07	2.87E-05	7.344196
ILMN_2201580	GSTM2	-1.39848	8.348228	-3.91702	0.000291	0.004527	0.153465
ILMN_1665559	CDK2	-1.39785	9.081369	-5.21182	4.17E-06	0.000266	4.155291
ILMN_1699644	3-Mar	-1.39619	6.615575	-6.22493	1.26E-07	2.61E-05	7.477303
ILMN_1684563	SPIN4	-1.39382	7.268288	-4.24926	0.000102	0.002183	1.138122
ILMN_1753183	CDCA4	-1.39349	7.694979	-5.07737	6.58E-06	0.000348	3.72274
ILMN_1691264	NAT8B	-1.39021	6.059194	-4.90683	1.17E-05	0.000506	3.178373
ILMN_2134039	ACN9	-1.38954	9.284266	-5.84866	4.67E-07	6.29E-05	6.23439
ILMN_1686664	MT2A	-1.38942	9.760428	-2.76459	0.008136	0.049194	-2.90425
ILMN_3240003	LOC100133012	-1.3887	8.418768	-4.22024	0.000112	0.00231	1.050705
ILMN_1753931	CDO1	-1.38737	6.353878	-5.79717	5.58E-07	7.08E-05	6.064886
ILMN_1667564	ALDH3A2	-1.38697	7.331434	-5.02901	7.74E-06	0.000382	3.567868
ILMN_3201115	LOC440043	-1.38674	12.62267	-6.40539	6.73E-08	1.77E-05	8.075082
ILMN_2343047	ABCB9	-1.38543	6.833295	-5.31282	2.95E-06	0.000215	4.481995
ILMN_3265365	CEP78	-1.38342	6.472042	-4.45185	5.28E-05	0.001388	1.755211
ILMN_1655796	3-Mar	-1.38262	6.563464	-6.67385	2.64E-08	9.56E-06	8.964814
ILMN_1716445	LOC727761	-1.38233	8.264883	-5.02908	7.74E-06	0.000382	3.568085
ILMN_1803124	BIRC5	-1.38139	5.854132	-4.34403	7.49E-05	0.001764	1.425341
ILMN_1781745	C9orf152	-1.38128	6.022883	-4.1504	0.00014	0.002691	0.841373

ILMN_1671766	F12	-1.38038	7.626309	-5.44138	1.90E-06	0.00016	4.89974
ILMN_1666305	CDKN3	-1.37816	8.872387	-4.68179	2.48E-05	0.000854	2.46863
ILMN_3181695	LOC100130178	-1.37773	9.333938	-4.79629	1.69E-05	0.000658	2.828454
ILMN_1684217	AURKB	-1.37682	9.221279	-3.92517	0.000284	0.004444	0.177147
ILMN_1702197	C9orf140	-1.3685	9.371425	-4.56053	3.70E-05	0.001083	2.09079
ILMN_1701831	GSTA1	-1.36817	5.677271	-5.56462	1.24E-06	0.000127	5.301985
ILMN_1732516	KNTC1	-1.36376	8.65554	-3.35966	0.001563	0.014874	-1.40483
ILMN_2090105	TAGLN2	-1.36194	6.516564	-3.54609	0.000903	0.009937	-0.89826
ILMN_3275590	LOC647302	-1.36123	9.87773	-4.93429	1.07E-05	0.000477	3.265678
ILMN_1689842	SC4MOL	-1.36023	7.829762	-3.03217	0.003956	0.029071	-2.25374
ILMN_1776052	LOC148915	-1.35976	10.08165	-4.87444	1.30E-05	0.000547	3.075598
ILMN_1678619	DAK	-1.35799	9.413387	-4.0384	0.000199	0.003446	0.508912
ILMN_1753196	PTTG1	-1.35637	8.722842	-5.98984	2.86E-07	4.76E-05	6.699943
ILMN_2330243	NUDT1	-1.35562	7.240407	-3.36691	0.00153	0.014614	-1.38541
ILMN_2124361	LEAP2	-1.35517	9.620157	-3.05838	0.00368	0.027659	-2.18787
ILMN_2135984	MASTL	-1.35498	5.668942	-4.7406	2.04E-05	0.000747	2.653082
ILMN_3297455	LOC729082	-1.35132	8.738763	-4.20985	0.000115	0.002361	1.019454
ILMN_1685928	WDR34	-1.35104	6.521201	-4.29841	8.68E-05	0.001954	1.286763
ILMN_1756043	WDHD1	-1.34791	5.702922	-5.05326	7.14E-06	0.000364	3.645485
ILMN_1802780	M160	-1.34731	7.180029	-4.62182	3.02E-05	0.000966	2.28132
ILMN_1785095	ATP6V0E2	-1.34532	11.54702	-4.12335	0.000152	0.002851	0.760706
ILMN_2077550	RACGAP1	-1.34519	7.954921	-4.46557	5.05E-05	0.00134	1.797381
ILMN_1652333	FN3KRP	-1.34425	10.2921	-5.40974	2.12E-06	0.000175	4.796736
ILMN_1727553	C5orf54	-1.34393	6.515007	-4.74499	2.01E-05	0.000739	2.666885
ILMN_1729905	GAL3ST1	-1.34376	5.900405	-4.82494	1.54E-05	0.000612	2.918916
ILMN_1757807	AGXT2L1	-1.3437	7.166376	-3.243	0.002188	0.018998	-1.71346
ILMN_1782813	DHFR	-1.33735	5.620041	-5.38098	2.34E-06	0.000187	4.703232
ILMN_2395240	CHEK2	-1.33685	6.452484	-4.77423	1.82E-05	0.000694	2.758902
ILMN_2149400	SPC25	-1.33287	5.899767	-4.16163	0.000135	0.00263	0.874905
ILMN_1762606	AQP11	-1.33126	9.471232	-3.86902	0.000338	0.005039	0.014342
ILMN_1737184	CDCA7	-1.33113	10.8434	-3.69371	0.000579	0.007275	-0.48633
ILMN_1728972	FAM64A	-1.32974	7.574601	-4.22477	0.00011	0.002296	1.064309
ILMN_1753063	KIF15	-1.32668	7.283051	-3.68524	0.000594	0.007417	-0.51021
ILMN_1724407	TACC3	-1.32663	8.789626	-4.87802	1.29E-05	0.000543	3.086954
ILMN_1723709	C9orf116	-1.32061	7.12631	-4.98367	9.02E-06	0.000424	3.423023
ILMN_3249240	C4orf46	-1.31994	6.771947	-4.44072	5.47E-05	0.00142	1.721013
ILMN_1659990	C7orf68	-1.31753	6.450364	-5.14385	5.25E-06	0.000306	3.936288
ILMN_3237270	LOC100133609	-1.31479	6.22844	-5.48764	1.62E-06	0.000147	5.050528
ILMN_2125869	ACTA1	-1.3144	9.137073	-3.6109	0.000743	0.008756	-0.71855

ILMN_3247163	TET1	-1.31319	7.735962	-3.9546	0.000259	0.004154	0.262966
ILMN_1696266	XRCC3	-1.30701	6.632516	-4.13919	0.000145	0.002756	0.807894
ILMN_2221046	GM2A	-1.30377	6.110432	-5.49865	1.56E-06	0.000145	5.086446
ILMN_2399463	VAV3	-1.29974	9.329338	-3.4201	0.00131	0.013045	-1.24233
ILMN_1735093	TIMELESS	-1.29947	8.665014	-4.23752	0.000106	0.002236	1.102725
ILMN_2391861	GSTM1	-1.29875	9.548321	-4.09083	0.000169	0.003071	0.66403
ILMN_1682336	MASTL	-1.29797	6.811601	-4.39443	6.36E-05	0.001582	1.579131
ILMN_1768020	HAUS8	-1.29659	6.589788	-4.79212	1.72E-05	0.000665	2.8153
ILMN_1695645	CETN2	-1.29551	10.96882	-4.44363	5.42E-05	0.00141	1.729945
ILMN_3277209	LOC285943	-1.29491	7.361128	-4.89029	1.24E-05	0.000526	3.125879
ILMN_3231820	SIVA1	-1.29416	9.146937	-5.03243	7.66E-06	0.000382	3.578811
ILMN_2409220	HMMR	-1.29195	9.576559	-2.90871	0.005542	0.037332	-2.55901
ILMN_1681679	TSPO	-1.28979	6.885939	-4.58976	3.36E-05	0.001025	2.181539
ILMN_1674924	PRR17	-1.28917	7.289142	-4.31368	8.26E-05	0.001883	1.333066
ILMN_3241554	KANK4	-1.28888	9.568063	-4.03383	0.000202	0.00348	0.495447
ILMN_2351916	EXO1	-1.2888	5.310077	-5.74689	6.64E-07	8.00E-05	5.899564
ILMN_1701636	LOC647786	-1.28875	6.538817	-4.05733	0.000187	0.0033	0.564807
ILMN_1668055	SAA4	-1.28711	11.58747	-4.58042	3.46E-05	0.001048	2.152514
ILMN_1775708	SLC2A3	-1.28645	12.1239	-3.83685	0.000373	0.005398	-0.07843
ILMN_2407619	CDC25C	-1.28627	7.075145	-4.57922	3.47E-05	0.001049	2.148783
ILMN_2210129	PRIM1	-1.28625	9.128049	-3.7282	0.000521	0.006782	-0.38878
ILMN_1810844	RARRES2	-1.28585	9.412735	-4.08338	0.000173	0.003115	0.64194
ILMN_1762407	CABLES2	-1.28486	7.231956	-5.04874	7.24E-06	0.000369	3.631
ILMN_1723092	CRB3	-1.28398	8.274256	-5.81266	5.29E-07	6.85E-05	6.115857
ILMN_1750102	EME1	-1.28279	6.261553	-3.97806	0.000241	0.003975	0.331561
ILMN_2167922	TRMT5	-1.28228	10.59038	-4.78692	1.75E-05	0.000676	2.798905
ILMN_2396948	PSMC3IP	-1.27824	5.304857	-7.16052	4.86E-09	2.92E-06	10.57441
ILMN_1666057	REEP2	-1.27669	5.837883	-4.40439	6.16E-05	0.001546	1.609601
ILMN_1694106	GPD1L	-1.27545	8.976609	-5.00735	8.33E-06	0.000401	3.498625
ILMN_1732885	BTBD12	-1.2753	7.375547	-5.17341	4.75E-06	0.00029	4.031458
ILMN_1657087	ZNF533	-1.27451	7.60556	-4.6356	2.89E-05	0.000941	2.324292
ILMN_2229242	LSM3	-1.27444	10.15711	-4.39523	6.34E-05	0.00158	1.581591
ILMN_2230683	CDCA7L	-1.27206	5.873839	-5.38712	2.29E-06	0.000185	4.723182
ILMN_1685916	KIF2C	-1.27152	7.896196	-4.05349	0.00019	0.003325	0.553482
ILMN_1742145	ESPL1	-1.27063	6.815632	-4.51478	4.29E-05	0.001204	1.949154
ILMN_2230117	AVP	-1.26993	5.474926	-4.98572	8.96E-06	0.000422	3.429576
ILMN_1806040	TYMS	-1.26867	10.62574	-4.11733	0.000155	0.002886	0.742764
ILMN_1678904	ENO3	-1.26554	9.493809	-4.00317	0.000222	0.003753	0.405231
ILMN_1790100	C11orf82	-1.26426	8.061855	-4.28823	8.97E-05	0.001995	1.255893

ILMN_1711005	CDC25A	-1.26295	8.492509	-4.87437	1.30E-05	0.000547	3.075363
ILMN_1725260	CDC25C	-1.25795	7.980853	-4.76022	1.91E-05	0.000714	2.714781
ILMN_2041046	CKS1B	-1.25755	10.07838	-5.6201	1.03E-06	0.000108	5.483559
ILMN_2371700	UCHL5IP	-1.25549	7.797528	-5.12773	5.54E-06	0.000315	3.884444
ILMN_1807277	IFI30	-1.25388	6.81959	-3.55434	0.000881	0.009754	-0.87549
ILMN_1801391	SKP2	-1.25326	5.517885	-5.57728	1.19E-06	0.000123	5.343377
ILMN_1765417	RBBP9	-1.25297	6.756324	-4.39329	6.38E-05	0.001583	1.575638
ILMN_1787280	C1orf135	-1.25267	7.149328	-3.9268	0.000282	0.004435	0.18191
ILMN_1693221	CENPH	-1.251	6.512788	-4.9344	1.07E-05	0.000477	3.266027
ILMN_1720114	GMNN	-1.24774	10.14332	-4.68411	2.46E-05	0.00085	2.475889
ILMN_1745034	SLC11A2	-1.24717	10.07193	-4.90123	1.19E-05	0.000512	3.160598
ILMN_1748923	SMC2	-1.24682	7.346776	-3.89778	0.000309	0.004716	0.097588
ILMN_2348975	NASP	-1.24248	8.259461	-6.13635	1.72E-07	3.26E-05	7.184158
ILMN_1777591	C10orf65	-1.24235	8.056869	-4.87717	1.29E-05	0.000544	3.084264
ILMN_1776936	ANKRD38	-1.24158	10.29349	-3.98998	0.000232	0.003859	0.366504
ILMN_1768293	NUP155	-1.24094	8.925634	-5.08404	6.43E-06	0.000342	3.74415
ILMN_1698185	WDR90	-1.24052	7.341004	-4.39952	6.26E-05	0.001567	1.594703
ILMN_1682034	HEY2	-1.23976	5.435026	-6.28406	1.03E-07	2.28E-05	7.673084
ILMN_1711087	LOC648526	-1.2391	7.124731	-4.66657	2.60E-05	0.00088	2.421013
ILMN_1736176	PLK1	-1.23847	9.070092	-5.05386	7.12E-06	0.000364	3.647391
ILMN_1777031	PKLR	-1.23406	6.715434	-3.09292	0.003342	0.025868	-2.10047
ILMN_1768637	TNNI3	-1.23211	5.539207	-4.95876	9.81E-06	0.000451	3.343603
ILMN_2049021	PTTG3P	-1.23177	9.64644	-4.51324	4.32E-05	0.001208	1.944394
ILMN_1758104	PRPS2	-1.23124	7.696124	-4.92249	1.11E-05	0.000491	3.228159
ILMN_1660691	RAB31	-1.23092	6.602216	-3.75121	0.000486	0.006417	-0.32343
ILMN_1786050	RBBP9	-1.23043	9.289227	-5.82136	5.13E-07	6.71E-05	6.144476
ILMN_1665331	AMT	-1.22958	9.263654	-4.27384	9.40E-05	0.002056	1.212355
ILMN_1722127	RAD54B	-1.22829	6.42395	-4.44511	5.39E-05	0.001408	1.734489
ILMN_1689327	LOC730534	-1.22574	11.09621	-4.67992	2.49E-05	0.000854	2.462766
ILMN_1692517	LOC653381	-1.22447	12.03789	-5.36223	2.49E-06	0.000194	4.642312
ILMN_1728517	FNTB	-1.22383	8.522548	-6.23689	1.21E-07	2.58E-05	7.516907
ILMN_1703079	NFS1	-1.22347	5.305621	-7.43914	1.85E-09	1.49E-06	11.49138
ILMN_2380561	PKLR	-1.22299	6.026655	-3.57636	0.000824	0.009398	-0.81456
ILMN_1683250	LOC440731	-1.22229	7.343744	-5.47782	1.68E-06	0.000149	5.018503
ILMN_1801205	GPNMB	-1.22151	5.16741	-7.93654	3.33E-10	4.36E-07	13.11531
ILMN_1737110	LOC651957	-1.22141	5.50198	-6.29929	9.75E-08	2.21E-05	7.723539
ILMN_1775016	MPZL2	-1.22097	6.205631	-3.48145	0.001094	0.01144	-1.07568
ILMN_1696046	SIVA	-1.22009	10.41589	-5.25994	3.54E-06	0.000237	4.310758
ILMN_1658010	CENPI	-1.21966	5.338095	-5.25946	3.54E-06	0.000237	4.309219

ILMN_1692511	TMEM106C	-1.21948	9.633532	-4.19685	0.00012	0.002427	0.980413
ILMN_2285375	SORD	-1.21231	9.327208	-4.45775	5.18E-05	0.001364	1.77333
ILMN_1787248	SIVA	-1.21157	9.21531	-4.76733	1.86E-05	0.000701	2.737158
ILMN_1714167	CYB5A	-1.21081	11.85829	-4.99319	8.74E-06	0.000416	3.453412
ILMN_1771411	ALG6	-1.20998	7.146731	-3.9339	0.000276	0.004372	0.202567
ILMN_1657796	STMN1	-1.20739	8.850204	-3.72227	0.000531	0.006863	-0.4056
ILMN_3190972	LOC100130291	-1.2069	7.662373	-5.72819	7.08E-07	8.35E-05	5.838103
ILMN_1676393	ATP5G1	-1.20675	10.85128	-5.27534	3.36E-06	0.00023	4.360599
ILMN_1736015	PHF17	-1.20475	7.277542	-5.55103	1.30E-06	0.00013	5.257544
ILMN_3304200	ZNF385B	-1.20451	7.473165	-3.8909	0.000316	0.004788	0.077654
ILMN_1731070	ORC6L	-1.20396	7.067833	-3.83916	0.000371	0.005377	-0.07177
ILMN_2370365	RFC4	-1.20362	8.98324	-3.5117	0.001	0.010712	-0.99289
ILMN_2148150	CHAC2	-1.20361	5.833601	-4.12595	0.000151	0.002832	0.768453
ILMN_1785198	POLE3	-1.20355	10.84926	-5.03162	7.68E-06	0.000382	3.576202
ILMN_3225843	LOC729298	-1.20298	7.369763	-5.10509	5.99E-06	0.000329	3.811696
ILMN_2384785	CCNE1	-1.20097	6.27555	-3.58746	0.000798	0.009174	-0.78374
ILMN_1668814	CENPM	-1.20039	6.120106	-3.878	0.000329	0.00494	0.040308
ILMN_1709634	CMBL	-1.1991	9.621142	-4.91473	1.14E-05	0.000497	3.203488
ILMN_1800465	LOC654042	-1.1979	6.571706	-4.86937	1.33E-05	0.000552	3.059524
ILMN_2148796	MND1	-1.1977	7.400511	-4.38139	6.64E-05	0.001625	1.539289
ILMN_1664265	EPHA1	-1.19676	7.859584	-3.93086	0.000279	0.004401	0.193716
ILMN_1784641	NDUFA3	-1.19619	8.747267	-5.52301	1.44E-06	0.000135	5.165971
ILMN_1755834	FEN1	-1.1959	7.924053	-4.05868	0.000187	0.003299	0.568803
ILMN_1767260	CCDC138	-1.19568	7.509252	-3.86056	0.000347	0.005117	-0.0101
ILMN_3247438	C19orf69	-1.19563	5.923363	-4.12685	0.00015	0.002831	0.771134
ILMN_1670672	TMEM37	-1.19473	6.459648	-3.37802	0.001482	0.014308	-1.35564
ILMN_1753353	SLBP	-1.19405	9.35235	-5.27878	3.32E-06	0.000228	4.371734
ILMN_1718336	C7orf50	-1.19305	10.61371	-5.13588	5.39E-06	0.00031	3.91065
ILMN_1777453	LOC653419	-1.19292	5.276079	-5.31184	2.96E-06	0.000215	4.478801
ILMN_1667825	MLKL	-1.19199	8.692438	-4.82286	1.55E-05	0.000614	2.912335
ILMN_1694502	PRIM1	-1.19174	8.510639	-3.75201	0.000484	0.006407	-0.32115
ILMN_2207328	C18orf10	-1.19032	7.954058	-3.76337	0.000468	0.006236	-0.28883
ILMN_2222008	KIFC1	-1.18908	9.31171	-4.29616	8.74E-05	0.00196	1.279924
ILMN_1710428	CDC2	-1.18747	7.301156	-3.73502	0.00051	0.006677	-0.36943
ILMN_3251592	C9orf140	-1.18741	8.024459	-3.77989	0.000445	0.006045	-0.24169
ILMN_2384056	GPER	-1.18711	10.91006	-3.8643	0.000343	0.005077	0.00071
ILMN_1893633	LOC439949	-1.18593	5.919634	-4.69348	2.38E-05	0.000837	2.505229
ILMN_1732296	ID3	-1.18561	9.108786	-3.10291	0.003251	0.025378	-2.07507
ILMN_1657950	RPS26P10	-1.1853	6.159242	-5.34654	2.63E-06	0.000203	4.591359

ILMN_3234884	KIF22	-1.18459	10.15217	-4.2343	0.000107	0.002251	1.093013
ILMN_2365383	ENO3	-1.18369	7.094956	-3.38495	0.001452	0.014116	-1.33703
ILMN_1761247	PIR	-1.18336	8.978125	-5.33804	2.71E-06	0.000205	4.563764
ILMN_2075476	GIPC2	-1.18169	6.533372	-3.91284	0.000295	0.004566	0.141299
ILMN_2404906	SGOL1	-1.18162	5.910427	-5.47576	1.69E-06	0.000149	5.011797
ILMN_3272500	IFI27L1	-1.18117	7.856249	-3.88966	0.000317	0.004798	0.07406
ILMN_1755974	ALDOC	-1.17964	8.277319	-3.22502	0.002303	0.019724	-1.76045
ILMN_2101885	TUBB	-1.17817	11.78615	-4.16643	0.000133	0.002604	0.889258
ILMN_1654722	MPV17L	-1.1758	7.557931	-5.79489	5.62E-07	7.09E-05	6.057386
ILMN_2347592	NMB	-1.17528	6.947374	-4.28985	8.92E-05	0.00199	1.260826
ILMN_1768816	TMPO	-1.17218	7.144682	-3.13093	0.003005	0.024023	-2.00356
ILMN_3232156	C7orf58	-1.172	7.233206	-4.22297	0.000111	0.002302	1.058915
ILMN_1655733	RFC2	-1.17146	5.877546	-4.98139	9.09E-06	0.000426	3.415758
ILMN_1698252	FANCB	-1.17127	5.566544	-4.4717	4.94E-05	0.001319	1.81626
ILMN_1757210	CALML4	-1.1685	7.249484	-4.3501	7.35E-05	0.00174	1.443833
ILMN_1695880	LOX	-1.16778	7.430772	-3.2721	0.002013	0.017754	-1.63711
ILMN_2219466	APOBEC3B	-1.16569	5.103355	-5.00552	8.38E-06	0.000402	3.492762
ILMN_2096372	ALDH1A1	-1.16563	12.37252	-6.0868	2.04E-07	3.69E-05	7.020301
ILMN_1663195	MCM7	-1.16552	11.15852	-4.63714	2.87E-05	0.000937	2.329085
ILMN_1698766	PYCARD	-1.16508	6.850793	-3.83974	0.00037	0.005371	-0.07011
ILMN_1653042	HSD3B7	-1.16454	7.033363	-3.31353	0.001787	0.01635	-1.52766
ILMN_1781966	OSBP2	-1.16362	6.451602	-3.39814	0.001397	0.013694	-1.30157
ILMN_1783676	CCDC15	-1.16198	6.338946	-3.43243	0.001264	0.012688	-1.20899
ILMN_2343563	ANAPC11	-1.16132	8.927138	-5.40804	2.13E-06	0.000175	4.791221
ILMN_2193315	C14orf143	-1.16082	7.67962	-3.65667	0.000647	0.007884	-0.59053
ILMN_2180866	RPS26P11	-1.1607	11.72408	-5.90086	3.89E-07	5.63E-05	6.406373
ILMN_1708375	IRF1	-1.16011	6.356497	-4.61041	3.14E-05	0.000987	2.245793
ILMN_3237584	LOC100133489	-1.15913	7.737687	-3.84429	0.000365	0.00531	-0.05701
ILMN_2396947	PSMC3IP	-1.15899	5.43148	-5.07463	6.64E-06	0.000348	3.713961
ILMN_3251540	GSTA2	-1.15812	5.491257	-5.17675	4.69E-06	0.000289	4.042213
ILMN_1738093	TMEM118	-1.15798	7.552311	-4.66479	2.62E-05	0.000882	2.415443
ILMN_1711408	ANXA4	-1.1577	8.760868	-3.70405	0.000561	0.007119	-0.45715
ILMN_1665797	CSE1L	-1.15658	11.01453	-4.48853	4.68E-05	0.001266	1.868127
ILMN_2312719	EXOSC9	-1.15453	8.975556	-5.63182	9.88E-07	0.000104	5.521948
ILMN_1753582	RPA2	-1.15365	9.608117	-4.60253	3.22E-05	0.001	2.221263
ILMN_1719581	MYOM3	-1.15355	7.517695	-5.34202	2.67E-06	0.000204	4.576683
ILMN_1792712	LOC201725	-1.15258	7.065163	-4.13894	0.000145	0.002756	0.807147
ILMN_2157240	MNS1	-1.1517	5.962788	-4.01294	0.000216	0.00366	0.433925
ILMN_1801939	CCNB2	-1.14995	9.822392	-4.68567	2.44E-05	0.00085	2.480781

ILMN_1730260	N6AMT2	-1.14909	7.651037	-5.22468	3.99E-06	0.000258	4.196835
ILMN_1655191	CASZ1	-1.14784	7.488834	-4.66062	2.66E-05	0.00089	2.402417
ILMN_1795852	CCNE1	-1.14743	7.032832	-3.72577	0.000525	0.006811	-0.39566
ILMN_1726114	SLC45A3	-1.14736	6.99644	-4.15618	0.000137	0.002667	0.858621
ILMN_1686097	TOP2A	-1.14662	11.18551	-3.70751	0.000555	0.00708	-0.44734
ILMN_2214278	ANKRD32	-1.14581	5.931362	-3.79476	0.000425	0.005883	-0.19921
ILMN_1667022	PASK	-1.14526	6.739669	-3.72292	0.000529	0.006854	-0.40375
ILMN_1680390	GCNT2	-1.14424	8.872742	-4.50179	4.48E-05	0.001233	1.909043
ILMN_2228780	SLC5A11	-1.14403	5.378936	-6.70783	2.35E-08	8.98E-06	9.077383
ILMN_1678612	ANXA6	-1.14378	6.511639	-5.66764	8.73E-07	9.63E-05	5.639374
ILMN_1672149	CHCHD1	-1.14351	7.518725	-4.56403	3.65E-05	0.00108	2.101631
ILMN_3307786	L3MBTL2	-1.14276	7.814649	-6.09585	1.98E-07	3.65E-05	7.050216
ILMN_2399431	PRPS2	-1.14193	7.873132	-4.70954	2.26E-05	0.000807	2.55556
ILMN_1801257	CENPA	-1.14118	8.754036	-4.22668	0.000109	0.002283	1.070066
ILMN_1761084	FNDC5	-1.14052	5.274395	-4.55079	3.82E-05	0.001105	2.060599
ILMN_1776181	BIRC3	-1.1384	5.956913	-3.48637	0.001078	0.011318	-1.06226
ILMN_2112460	MAD2L1	-1.13576	6.553765	-3.57595	0.000826	0.009402	-0.81569
ILMN_1806502	ZNF165	-1.13478	7.450774	-7.15865	4.89E-09	2.92E-06	10.56825
ILMN_1756289	PPP1R12B	-1.13273	6.633054	-4.20683	0.000117	0.002376	1.010383
ILMN_1706690	KHK	-1.13228	8.274146	-5.88898	4.06E-07	5.73E-05	6.367213
ILMN_1698677	C4orf27	-1.13169	6.607831	-4.0265	0.000207	0.00354	0.473849
ILMN_1758293	UBR7	-1.13117	5.943899	-4.41975	5.86E-05	0.001495	1.656649
ILMN_1743747	RUSC1	-1.13036	9.631151	-5.54329	1.34E-06	0.000132	5.232226
ILMN_1670801	MTR	-1.13	7.513983	-6.36256	7.82E-08	1.91E-05	7.933156
ILMN_1749253	TUBD1	-1.12937	7.453763	-3.76851	0.000461	0.006181	-0.27419
ILMN_1750636	RPS26L	-1.12826	11.21525	-4.87613	1.30E-05	0.000545	3.080942
ILMN_1754051	RMI1	-1.12466	7.213506	-3.22332	0.002314	0.019789	-1.76488
ILMN_1774589	IQCC	-1.124	6.703395	-4.6208	3.03E-05	0.000968	2.278141
ILMN_1701289	MGC40489	-1.12384	8.089448	-4.53941	3.96E-05	0.001134	2.025323
ILMN_2174437	CIDEC	-1.12184	7.730952	-3.60121	0.000765	0.008904	-0.74553
ILMN_2383300	PTPRU	-1.12183	7.670457	-5.77506	6.02E-07	7.35E-05	5.992171
ILMN_1706238	CSE1L	-1.1212	11.30855	-4.28802	8.98E-05	0.001995	1.255284
ILMN_1676191	DARS2	-1.12068	8.503716	-4.34808	7.39E-05	0.00175	1.437673
ILMN_1781373	IFIH1	-1.11813	7.400824	-3.967	0.000249	0.004062	0.299184
ILMN_2275803	LRRC45	-1.11696	6.827554	-3.29592	0.00188	0.01697	-1.57428
ILMN_2168747	GSTA2	-1.11659	5.650273	-4.91535	1.14E-05	0.000497	3.205461
ILMN_3176989	HAUS8	-1.11623	6.405627	-3.663	0.000635	0.007779	-0.57278
ILMN_1690695	PEX11A	-1.11535	7.635844	-4.64844	2.77E-05	0.000914	2.364367
ILMN_2293902	ABCC6	-1.11486	6.666171	-4.55951	3.71E-05	0.001085	2.087612

ILMN_1671906	MND1	-1.1136	7.738203	-3.98601	0.000235	0.003896	0.354854
ILMN_1748352	CTSL2	-1.11223	7.538909	-3.33307	0.001688	0.015741	-1.47576
ILMN_2410540	CASP2	-1.11209	9.615122	-6.66652	2.71E-08	9.56E-06	8.940508
ILMN_1808792	ALKBH6	-1.11179	7.357031	-4.27964	9.22E-05	0.002025	1.2299
ILMN_1880052		-1.108	6.818611	-3.86081	0.000347	0.005116	-0.00938
ILMN_1732127	RBKS	-1.10791	8.047357	-4.20152	0.000119	0.002398	0.994447
ILMN_3236244	C1orf174	-1.10784	9.13509	-5.95628	3.21E-07	5.00E-05	6.589162
ILMN_2310296	C21orf58	-1.1075	5.846452	-4.18615	0.000124	0.002495	0.94832
ILMN_2401641	ALDH3A2	-1.10702	9.297494	-7.23483	3.75E-09	2.46E-06	10.81938
ILMN_1807044	UBAC1	-1.10458	9.687026	-4.36914	6.91E-05	0.001674	1.501883
ILMN_1651705	CAT	-1.10443	10.46626	-3.65486	0.000651	0.007913	-0.59561
ILMN_1763852	ACACB	-1.10329	7.185809	-4.03036	0.000204	0.00351	0.485219
ILMN_1746831	ZNF114	-1.10256	5.971158	-3.07578	0.003506	0.026749	-2.14392
ILMN_1698546	HNF4A	-1.10227	6.462191	-5.06184	6.93E-06	0.000359	3.672953
ILMN_1703279	CXorf57	-1.10122	6.211239	-5.01672	8.07E-06	0.000394	3.528582
ILMN_1745397	OAS3	-1.10111	6.855262	-4.9331	1.07E-05	0.000477	3.261904
ILMN_1683305	COMMD2	-1.10052	8.878772	-4.59249	3.33E-05	0.001021	2.190045
ILMN_2328378	OSBPL3	-1.09998	7.368919	-4.13397	0.000147	0.002788	0.792339
ILMN_2203896	SMAD7	-1.09988	7.508251	-3.51199	0.000999	0.010708	-0.99209
ILMN_1737635	RAD1	-1.09869	6.420312	-4.67673	2.52E-05	0.00086	2.452791
ILMN_1799667	KIF4A	-1.09802	7.720912	-3.90374	0.000303	0.004661	0.114893
ILMN_1736816	C13orf3	-1.09769	6.294218	-4.13359	0.000147	0.00279	0.791215
ILMN_1726647	LOC650646	-1.09765	11.97286	-5.88835	4.07E-07	5.73E-05	6.365133
ILMN_1781952	MGST1	-1.09723	6.564437	-4.61917	3.05E-05	0.000971	2.273081
ILMN_1686835	C17orf41	-1.09687	5.56469	-4.03678	0.0002	0.003459	0.50414
ILMN_1704925	LOC653609	-1.09679	5.073639	-5.31277	2.95E-06	0.000215	4.481823
ILMN_1660222	MTBP	-1.09677	5.470608	-5.47827	1.68E-06	0.000149	5.019983
ILMN_1685258	TMEM14B	-1.09461	10.9595	-4.40961	6.05E-05	0.001531	1.62558
ILMN_3234081	LOC100129076	-1.09411	5.501345	-4.63152	2.92E-05	0.000947	2.311559
ILMN_1727288	EVPL	-1.0934	7.848774	-4.16582	0.000133	0.002604	0.887442
ILMN_3249093	LOC100132802	-1.09287	5.072464	-4.15559	0.000137	0.002667	0.856851
ILMN_1775008	NCAPD2	-1.0923	9.496973	-3.99206	0.00023	0.003841	0.372609
ILMN_1660654	CDCA2	-1.08836	6.699081	-3.76429	0.000467	0.006231	-0.28619
ILMN_2355168	MGST1	-1.08819	11.24504	-5.08773	6.35E-06	0.00034	3.755962
ILMN_3266197	LOC100130171	-1.08751	6.014467	-4.38175	6.63E-05	0.001625	1.540372
ILMN_3251145	LDHA	-1.08638	6.550953	-4.33687	7.67E-05	0.001784	1.403564
ILMN_1670037	POLR2L	-1.08622	8.147362	-4.39602	6.33E-05	0.00158	1.584008
ILMN_1691131	LSMD1	-1.08615	7.531006	-3.89602	0.000311	0.004726	0.092497
ILMN_3284063	LOC341965	-1.08501	8.157408	-3.68649	0.000592	0.007396	-0.50669

ILMN_1776577	DSCC1	-1.0847	7.105764	-4.05509	0.000189	0.003313	0.558205
ILMN_1756550	NUP62CL	-1.08458	5.992187	-3.80122	0.000417	0.005808	-0.18072
ILMN_1695357	CCDC99	-1.08445	8.084316	-3.27235	0.002012	0.017747	-1.63645
ILMN_2103024	RBP5	-1.08384	7.590571	-3.68302	0.000598	0.007454	-0.51645
ILMN_1681221	C9orf100	-1.08367	6.434537	-4.31804	8.15E-05	0.001867	1.346312
ILMN_1703906	HJURP	-1.08318	8.770089	-3.36889	0.001522	0.01456	-1.3801
ILMN_1788356	C11orf17	-1.08273	7.397145	-3.46243	0.001157	0.011907	-1.12755
ILMN_1703692	LOC647000	-1.08272	10.11497	-3.65821	0.000644	0.007857	-0.58622
ILMN_3305735	LOC730101	-1.08254	8.125095	-3.60014	0.000768	0.008922	-0.74849
ILMN_1715991	SDPR	-1.08094	8.156017	-4.12903	0.000149	0.002817	0.777624
ILMN_2058141	HMGN2	-1.08005	11.0727	-4.39655	6.32E-05	0.001578	1.585607
ILMN_1787526	MGC13057	-1.07982	6.409619	-4.98997	8.83E-06	0.000418	3.443108
ILMN_1813350	HSD11B2	-1.07981	8.049867	-5.5607	1.26E-06	0.000127	5.289161
ILMN_1684289	PNPO	-1.07868	10.6104	-5.95162	3.27E-07	5.00E-05	6.573798
ILMN_1708151	LAGE3	-1.07847	8.626655	-4.61206	3.12E-05	0.000984	2.25092
ILMN_1748751	NLF2	-1.07838	5.187557	-4.1406	0.000144	0.002749	0.812113
ILMN_1708798	EAF2	-1.07563	5.875123	-3.63662	0.000688	0.008231	-0.64673
ILMN_1792356	DPYSL4	-1.07557	5.46472	-3.99521	0.000228	0.003815	0.381853
ILMN_2338323	CDC25B	-1.07542	9.556138	-4.66986	2.58E-05	0.000875	2.431286
ILMN_1664511	NDC80	-1.07511	7.682285	-3.54325	0.00091	0.009994	-0.90608
ILMN_1662359	HIST1H4K	-1.07479	6.613247	-3.55486	0.000879	0.009752	-0.87405
ILMN_1771264	ELL3	-1.07449	5.959917	-4.13892	0.000145	0.002756	0.807101
ILMN_2189406	C15orf38	-1.07347	5.947702	-4.91879	1.12E-05	0.000495	3.216375
ILMN_1730201	DTNA	-1.07219	7.587523	-3.88436	0.000322	0.004863	0.058696
ILMN_2376108	PSMB9	-1.07154	5.459559	-4.31502	8.23E-05	0.001878	1.337141
ILMN_1803647	FAM162A	-1.07152	8.509578	-3.64346	0.000674	0.008115	-0.62758
ILMN_1684802	TAF5	-1.07087	6.998915	-4.81018	1.62E-05	0.000634	2.872273
ILMN_1810127	ZNF789	-1.07013	8.041709	-5.20451	4.27E-06	0.000271	4.131705
ILMN_1755075	IDI1	-1.06952	9.130175	-2.82332	0.006967	0.043864	-2.76503
ILMN_1683470	TMEM139	-1.06914	5.884278	-3.08796	0.003389	0.026162	-2.11305
ILMN_1691949	LOC728554	-1.06796	10.71868	-4.03745	0.0002	0.003454	0.506131
ILMN_1800573	RPS21	-1.0678	9.548477	-4.5358	4.01E-05	0.001143	2.014161
ILMN_1747016	CEP55	-1.06771	8.723896	-3.77655	0.000449	0.006078	-0.25123
ILMN_1751773	POLD3	-1.06376	6.428369	-3.92167	0.000287	0.004477	0.166986
ILMN_1778890	PPIL5	-1.06312	6.810519	-4.48787	4.69E-05	0.001266	1.866102
ILMN_1741017	PIP4K2B	-1.06286	5.748891	-3.37656	0.001488	0.014349	-1.35956
ILMN_1729051	MSH6	-1.06259	10.69507	-3.98457	0.000236	0.003911	0.350657
ILMN_1801307	TNFSF10	-1.06174	7.017186	-3.0365	0.003909	0.028866	-2.24289
ILMN_2344971	FOXM1	-1.06169	8.168044	-3.35647	0.001578	0.01495	-1.41334

ILMN_1660436	HSPA1B	-1.06117	10.83694	-4.77628	1.81E-05	0.00069	2.765344
ILMN_2115991	TNNT1	-1.06083	4.939523	-4.45891	5.16E-05	0.001361	1.776909
ILMN_1756443	INHA	-1.06028	5.74552	-4.36158	7.08E-05	0.001705	1.478829
ILMN_2338963	SLC29A1	-1.05964	8.827661	-3.59412	0.000782	0.009042	-0.76524
ILMN_2126706	LMNB1	-1.05963	8.081677	-3.8164	0.000398	0.005626	-0.13719
ILMN_2298936	THOC3	-1.05956	7.906037	-3.79801	0.000421	0.005841	-0.1899
ILMN_2357438	AURKA	-1.0579	10.9893	-4.59353	3.31E-05	0.001021	2.193272
ILMN_1709294	CDCA8	-1.05751	8.957603	-3.70357	0.000562	0.007119	-0.45848
ILMN_1788166	TTK	-1.0575	8.328562	-3.40516	0.001369	0.013468	-1.28267
ILMN_1790637	C11orf80	-1.05738	7.890969	-5.36482	2.47E-06	0.000193	4.650713
ILMN_1704750	LOC647000	-1.0572	13.41585	-4.34028	7.58E-05	0.001778	1.413915
ILMN_1710962	TMEM97	-1.05696	12.02929	-4.40735	6.10E-05	0.001536	1.618687
ILMN_1859127		-1.05663	5.172264	-6.4202	6.40E-08	1.76E-05	8.124159
ILMN_2132161	KIF18A	-1.05595	6.545876	-3.06365	0.003626	0.027355	-2.17457
ILMN_2230892	IL10RB	-1.05579	8.8532	-7.26189	3.42E-09	2.29E-06	10.90854
ILMN_1744118	ASTN2	-1.05523	7.11776	-4.40759	6.09E-05	0.001536	1.619395
ILMN_2363668	YIF1B	-1.05499	9.193791	-5.00825	8.31E-06	0.0004	3.501503
ILMN_1688299	RCAN3	-1.05461	6.285824	-4.74384	2.01E-05	0.000741	2.663279
ILMN_1748241	CENPP	-1.05357	5.37328	-4.86911	1.33E-05	0.000552	3.058714
ILMN_1674411	CKAP2	-1.05339	8.05372	-3.12621	0.003045	0.024251	-2.01564
ILMN_1787477	CENPO	-1.05317	5.779922	-4.12127	0.000153	0.002862	0.754505
ILMN_1729816	VDAC3	-1.0528	11.85312	-4.66543	2.61E-05	0.000882	2.417459
ILMN_1728225	KIAA1524	-1.05228	6.177767	-3.59998	0.000768	0.008922	-0.74896
ILMN_1730825	SGOL1	-1.0521	6.482791	-4.46537	5.05E-05	0.00134	1.796794
ILMN_1731044	KCTD14	-1.05207	7.918634	-3.77996	0.000445	0.006045	-0.24152
ILMN_1746699	SGOL2	-1.05088	7.104901	-3.07046	0.003558	0.026998	-2.15737
ILMN_1669394	EI24	-1.05082	10.40217	-7.21473	4.02E-09	2.57E-06	10.75316
ILMN_2355665	MTP18	-1.05044	9.342882	-4.8115	1.61E-05	0.000632	2.876436
ILMN_1712389	CKLF	-1.05001	10.38156	-4.4655	5.05E-05	0.00134	1.797168
ILMN_1681754	GGH	-1.04938	10.49166	-3.79417	0.000426	0.005885	-0.20089
ILMN_1708006	MICB	-1.04852	8.378671	-3.27322	0.002007	0.017714	-1.63415
ILMN_1661432	NUP43	-1.04704	10.66829	-5.17254	4.76E-06	0.00029	4.028652
ILMN_1732336	RFC2	-1.0456	5.72035	-4.52456	4.16E-05	0.001177	1.97937
ILMN_2062468	IGFBP7	-1.04527	6.348125	-4.37071	6.87E-05	0.001671	1.50666
ILMN_1651987	C6orf129	-1.04508	8.007652	-3.81731	0.000396	0.005625	-0.13458
ILMN_3269849	ISM2	-1.04485	6.389796	-4.14465	0.000142	0.002727	0.824201
ILMN_1669070	MIPEP	-1.04453	7.276097	-4.06042	0.000186	0.003286	0.573961
ILMN_1731343	LDLRAD1	-1.04285	5.288334	-5.09768	6.14E-06	0.000334	3.787896
ILMN_1707783	CCDC72	-1.04255	10.7244	-4.492	4.63E-05	0.001258	1.878821

ILMN_1736238	GNMT	-1.03863	5.650955	-3.80898	0.000407	0.005721	-0.15846
ILMN_1709348	ALDH1A1	-1.03843	12.41048	-4.68026	2.49E-05	0.000854	2.463845
ILMN_1797693	BRI3BP	-1.03789	8.44883	-3.96915	0.000247	0.004049	0.305498
ILMN_1757877	HCFC1R1	-1.03764	8.931847	-3.70697	0.000556	0.007088	-0.44888
ILMN_1799106	MOSC1	-1.03716	10.22573	-3.57558	0.000826	0.009402	-0.81671
ILMN_2252408	CNPY4	-1.03705	6.91746	-4.48541	4.73E-05	0.001274	1.858491
ILMN_1734096	DCLRE1A	-1.03508	7.138553	-3.86811	0.000339	0.005047	0.011701
ILMN_1683441	NCAPD3	-1.03502	8.593678	-4.07024	0.00018	0.003218	0.60301
ILMN_1796949	TPX2	-1.03451	9.717618	-3.83686	0.000373	0.005398	-0.0784
ILMN_1761314	NFS1	-1.03421	6.085111	-4.10345	0.000162	0.002972	0.701519
ILMN_1696183	HBQ1	-1.03306	8.211097	-4.18212	0.000126	0.00252	0.936259
ILMN_2415926	THOC3	-1.03291	8.273582	-3.58712	0.000798	0.009176	-0.7847
ILMN_1762002	CSTF3	-1.03273	8.182912	-4.23126	0.000108	0.002264	1.083863
ILMN_3300972	SIVA1	-1.03225	11.12065	-4.56173	3.68E-05	0.001082	2.094515
ILMN_1752988	C11orf17	-1.03193	9.519869	-4.49444	4.59E-05	0.001254	1.886345
ILMN_1655068	TOM1L2	-1.03167	6.843426	-4.1644	0.000133	0.002614	0.883186
ILMN_1710758	RNF20	-1.03115	8.878688	-4.82484	1.54E-05	0.000612	2.918586
ILMN_1712452	KIF20B	-1.03072	8.945622	-3.00913	0.004216	0.030559	-2.31136
ILMN_2398926	C17orf58	-1.03072	9.956388	-4.04151	0.000197	0.003416	0.518114
ILMN_2359029	C11orf17	-1.03067	7.914849	-4.24061	0.000105	0.002224	1.112036
ILMN_1652580	POLD1	-1.0292	7.281727	-3.53611	0.00093	0.010168	-0.92577
ILMN_1695386	RAD51C	-1.0291	9.4548	-3.65226	0.000656	0.007951	-0.60292
ILMN_1898692		-1.02866	5.213247	-4.7715	1.84E-05	0.000696	2.75031
ILMN_1680955	AURKA	-1.02824	11.17709	-4.911	1.15E-05	0.000501	3.191632
ILMN_1710150	EED	-1.02762	7.081485	-3.8015	0.000416	0.005806	-0.17991
ILMN_1797793	BLVRB	-1.02706	6.634262	-4.92888	1.09E-05	0.000483	3.248478
ILMN_1745005	GGCT	-1.02649	8.332668	-3.04585	0.00381	0.028357	-2.21942
ILMN_3237645	LRTOMT	-1.02555	6.398547	-4.50338	4.46E-05	0.001232	1.913931
ILMN_1756326	CKS2	-1.02497	9.831056	-4.57416	3.53E-05	0.001059	2.133081
ILMN_2209027	RPS26	-1.02412	10.35925	-5.37651	2.37E-06	0.000188	4.688689
ILMN_1762674	NUP43	-1.0238	6.916806	-3.73061	0.000517	0.006743	-0.38196
ILMN_2154671	COX6B1	-1.02366	8.695314	-5.28025	3.30E-06	0.000227	4.376481
ILMN_1794349	XYLB	-1.02305	8.730831	-4.23053	0.000108	0.002267	1.081675
ILMN_1701512	KIAA0391	-1.02269	10.04311	-5.82136	5.13E-07	6.71E-05	6.144505
ILMN_1692163	NSDHL	-1.02242	10.0107	-4.02153	0.00021	0.003585	0.459221
ILMN_2064898	CCDC56	-1.02206	11.54209	-5.29912	3.09E-06	0.000221	4.43758
ILMN_1655819	LOC728919	-1.02088	5.930168	-3.44138	0.001231	0.012436	-1.18473
ILMN_2194828	C16orf53	-1.02036	10.28159	-6.36825	7.67E-08	1.91E-05	7.951996
ILMN_1768732	SPAG16	-1.01912	7.737249	-3.92824	0.000281	0.004424	0.186099

ILMN_1725121	XPO1	-1.01847	10.89141	-3.07881	0.003477	0.026643	-2.13626
ILMN_3246678	NPW	-1.01781	8.817778	-3.64963	0.000661	0.007997	-0.6103
ILMN_1661755	FAM129B	-1.01728	9.902563	-5.26682	3.45E-06	0.000236	4.333012
ILMN_1715715	CEBPA	-1.01585	10.85433	-3.91718	0.000291	0.004527	0.153928
ILMN_1663390	CDC20	-1.01528	11.28824	-4.37885	6.69E-05	0.001635	1.531503
ILMN_1726893	EPN3	-1.01523	5.098012	-4.94913	1.01E-05	0.000462	3.312929
ILMN_1712718	BPNT1	-1.01495	6.730215	-3.15938	0.002774	0.022656	-1.93052
ILMN_1788135	APITD1	-1.01448	6.028777	-4.02512	0.000207	0.003551	0.469782
ILMN_1749612	LOC729101	-1.01426	7.834988	-4.36176	7.07E-05	0.001705	1.479367
ILMN_1709085	GSG2	-1.01345	5.500857	-4.51649	4.27E-05	0.001202	1.954443
ILMN_1670218	EXOSC6	-1.01303	10.92987	-6.41882	6.43E-08	1.76E-05	8.119565
ILMN_1763129	DCTPP1	-1.01288	10.25154	-5.05578	7.07E-06	0.000364	3.653551
ILMN_1694589	PAQR8	-1.01177	9.999703	-2.79908	0.007429	0.046024	-2.82275
ILMN_1812489	CCDC21	-1.01131	6.837972	-4.98023	9.13E-06	0.000427	3.412031
ILMN_2395926	MANBAL	-1.0111	8.107831	-5.45981	1.78E-06	0.000154	4.959772
ILMN_2218002	LIPC	-1.01109	8.71355	-3.45121	0.001196	0.012175	-1.15805
ILMN_2142554	NENF	-1.01085	9.23355	-4.95739	9.86E-06	0.000452	3.33923
ILMN_1723625	MAP4K2	-1.01082	9.108967	-4.65742	2.68E-05	0.000899	2.392401
ILMN_1720889	SC4MOL	-1.00914	11.39757	-3.02458	0.00404	0.029544	-2.27276
ILMN_1734600	WWOX	-1.00764	5.518718	-4.22749	0.000109	0.002281	1.07252
ILMN_2325337	APOL2	-1.00535	5.934811	-4.38124	6.64E-05	0.001625	1.538822
ILMN_1722102	ANAPC11	-1.00475	9.743961	-4.32064	8.08E-05	0.00186	1.354201
ILMN_2042771	PTTG1	-1.00449	10.94071	-3.60223	0.000763	0.008892	-0.74269
ILMN_2288784	CCDC34	-1.00404	9.688094	-2.78454	0.00772	0.04744	-2.8572
ILMN_1707084	UBE2D4	-1.00381	7.809451	-5.8743	4.27E-07	5.90E-05	6.318846
ILMN_1693766	CEP135	-1.0024	6.699839	-3.55072	0.00089	0.009845	-0.8855
ILMN_1789123	PLK4	-1.00233	8.423929	-2.80156	0.00738	0.045826	-2.81686
ILMN_1671933	CLCC1	-1.00162	6.853751	-4.1451	0.000142	0.002725	0.825525
ILMN_1808071	KIF14	-1.00102	7.317113	-3.09696	0.003305	0.025702	-2.09021
ILMN_1659327	LOC283683	-1.00022	5.714683	-4.75349	1.95E-05	0.000725	2.693601

Appendix M. Gene annotated list of down-regulated genes (DEGs) when exposed to 500 ppb of metolachlor exposed human liver cells for 48 hours compared to control.

PROBE_ID	SYMBOL	logFC	AveExpr	t	P.Value	adj.P.Val	B
ILMN_2413956	IGF2	1.000749	6.326153	2.999334	0.004331	0.031163	-2.33577
ILMN_2317658	SLC3A2	1.001333	7.083965	3.52125	0.000972	0.010502	-0.96666
ILMN_1792182	RDH12	1.002379	6.087879	3.159069	0.002777	0.022656	-1.93133
ILMN_2358760	HPN	1.003722	8.583197	3.831738	0.000379	0.005463	-0.09313
ILMN_1772370	ARHGEF1	1.003743	6.685508	4.240933	0.000104	0.002224	1.113003
ILMN_1789596	ETV6	1.004403	6.968483	4.891131	1.23E-05	0.000526	3.128538
ILMN_1715069	TANK	1.004751	8.817938	4.991733	8.78E-06	0.000417	3.448752
ILMN_1810559	RHOQ	1.005137	7.983553	3.675646	0.000611	0.007561	-0.53722
ILMN_1669972	DKFZp686O24166	1.006224	9.801503	4.319301	8.12E-05	0.001865	1.350143
ILMN_1731353	CHPF	1.006322	9.457245	4.664907	2.62E-05	0.000882	2.415813
ILMN_1732291	LOC653125	1.006588	5.591424	4.108469	0.000159	0.002937	0.716421
ILMN_2074860	RN7SK	1.007097	7.166411	4.151514	0.000139	0.002683	0.844688
ILMN_1755462	UGCGL1	1.007433	7.114538	4.166996	0.000132	0.002602	0.890965
ILMN_3305273	LOC729779	1.008125	10.40749	3.42509	0.001291	0.012898	-1.22885
ILMN_1738407	ULBP1	1.009979	4.980206	4.074742	0.000177	0.003178	0.616342
ILMN_1751789	HNMT	1.011247	9.2645	3.897862	0.000309	0.004716	0.097829
ILMN_1700257	C4orf32	1.011279	6.25694	3.363887	0.001544	0.014708	-1.39351
ILMN_1661888	MEF2A	1.011369	5.345672	4.265121	9.66E-05	0.002098	1.186003
ILMN_2333440	TM9SF1	1.012103	8.436798	3.776788	0.000449	0.006078	-0.25056
ILMN_1804454	FAM135A	1.013466	6.49385	3.034591	0.00393	0.028945	-2.24768
ILMN_1753026	LPPR1	1.013474	8.488551	4.047802	0.000193	0.003369	0.53667
ILMN_2140700	CRIPAK	1.014392	7.741554	3.968119	0.000248	0.004055	0.302471
ILMN_1676986	NPIP	1.015358	9.044973	4.10601	0.000161	0.002952	0.70911
ILMN_1680223	PNPLA8	1.015888	7.353371	3.156355	0.002798	0.022764	-1.93832
ILMN_1699829	CTGF	1.015889	12.63702	4.228642	0.000109	0.002276	1.075976
ILMN_1757129	TMEM88	1.01694	5.099833	3.252219	0.002131	0.018633	-1.68932
ILMN_1687351	ANKRA2	1.017078	7.468997	4.563208	3.66E-05	0.00108	2.099091
ILMN_1754476	TRIM15	1.017217	10.47979	4.525051	4.15E-05	0.001176	1.980903
ILMN_2151281	GABARAPL1	1.017486	7.338998	3.698749	0.00057	0.007201	-0.47211
ILMN_1659923	GNAQ	1.018755	6.436635	3.668862	0.000624	0.00769	-0.5563
ILMN_2352009	ACADVL	1.019008	8.47131	4.064788	0.000183	0.003255	0.586877
ILMN_1872122		1.019114	6.190207	3.96951	0.000247	0.004049	0.306541
ILMN_1803744	SELS	1.019501	9.233934	3.847986	0.000361	0.005272	-0.04636
ILMN_1720053	ZFAND3	1.01957	6.890615	3.799505	0.000419	0.005821	-0.18561

ILMN_2331010	TNFRSF10B	1.020709	7.582136	4.632106	2.92E-05	0.000946	2.313395
ILMN_2396571	GPR108	1.020994	7.155756	3.331418	0.001697	0.015794	-1.48014
ILMN_1788107	IL11	1.021769	5.067416	2.950559	0.004948	0.034356	-2.45649
ILMN_1758497	TTYH1	1.022213	7.224928	3.930898	0.000279	0.004401	0.193835
ILMN_2408572	RNASE4	1.02403	9.481287	4.194346	0.000121	0.002442	0.972903
ILMN_1682928	CPVL	1.024305	9.747629	5.284695	3.25E-06	0.000227	4.390878
ILMN_1778560	ZNF3	1.025307	6.899942	3.721361	0.000532	0.006874	-0.40816
ILMN_1776088	NAT9	1.026949	9.362233	4.533934	4.03E-05	0.001147	2.008384
ILMN_1788160	KIF5B	1.028867	9.059416	4.590393	3.35E-05	0.001024	2.183513
ILMN_1687721	PROC	1.029178	10.00071	5.140989	5.30E-06	0.000307	3.927075
ILMN_3304049	LOC729500	1.029361	8.780535	5.323309	2.85E-06	0.000211	4.515998
ILMN_1653133	SH3D19	1.031167	9.666525	4.891144	1.23E-05	0.000526	3.12858
ILMN_1783350	PCNXL3	1.032019	8.745693	3.907471	0.0003	0.004619	0.125712
ILMN_2118832	RBM24	1.032523	4.902558	3.572307	0.000835	0.009473	-0.82578
ILMN_1774272	ESRRA	1.032699	8.111831	4.057102	0.000188	0.0033	0.564148
ILMN_1704196	DSG2	1.033226	6.695972	4.337988	7.64E-05	0.001783	1.406953
ILMN_1749868	FAM171A1	1.033698	10.06429	5.341848	2.67E-06	0.000204	4.576137
ILMN_1907095	ONECUT2	1.033713	7.519668	3.918177	0.00029	0.004521	0.156818
ILMN_1721087	SHC2	1.033881	5.92378	3.299886	0.001858	0.016848	-1.56379
ILMN_1689734	IL1RN	1.034719	4.929464	3.787389	0.000435	0.005961	-0.22028
ILMN_1658579	CDK5RAP3	1.037064	5.337937	4.415614	5.94E-05	0.001508	1.643988
ILMN_1732182	FBXO44	1.037332	5.657597	4.991796	8.78E-06	0.000417	3.448952
ILMN_1722713	FBLN1	1.037577	6.944679	3.664044	0.000633	0.007765	-0.56984
ILMN_1761275	FUT6	1.038103	5.448895	4.134297	0.000147	0.002788	0.793312
ILMN_1705116	C6orf85	1.038788	9.973763	5.245839	3.71E-06	0.000245	4.265181
ILMN_1710092	ZBTB46	1.039908	7.862701	5.105178	5.99E-06	0.000329	3.811979
ILMN_1658677	DTX3	1.040581	5.992187	4.745277	2.01E-05	0.000739	2.667784
ILMN_1785290	DOK6	1.042014	6.729859	4.47485	4.89E-05	0.00131	1.825965
ILMN_1705364	BAT3	1.042329	9.934907	3.765192	0.000465	0.006229	-0.28363
ILMN_3263974	KRT18P13	1.044102	10.31155	3.80642	0.00041	0.005742	-0.16581
ILMN_1796490	GRINA	1.04417	7.413559	4.869771	1.32E-05	0.000552	3.060796
ILMN_1653718	ZFAND2B	1.044543	9.403325	5.125819	5.58E-06	0.000317	3.878294
ILMN_1750400	C19orf66	1.044621	7.404768	5.532976	1.39E-06	0.000134	5.198539
ILMN_2124386	RGL2	1.047385	7.100442	4.144039	0.000142	0.002731	0.822371
ILMN_1765558	NPAS2	1.047471	7.518801	6.217601	1.30E-07	2.66E-05	7.453033
ILMN_1767514	LOC441155	1.048592	7.475302	4.397501	6.30E-05	0.001576	1.588528
ILMN_1735367	HSD17B11	1.048853	10.50784	4.096175	0.000166	0.003032	0.679896
ILMN_2368773	FAM3C	1.048946	6.753342	3.275731	0.001992	0.017632	-1.62754
ILMN_1659544	STX3	1.050159	8.696746	3.366066	0.001534	0.01464	-1.38768

ILMN_3303965	ZC3H11B	1.050391	10.2252	5.462762	1.77E-06	0.000154	4.969405
ILMN_1802799	AKIRIN1	1.050656	9.569408	5.216289	4.10E-06	0.000263	4.169728
ILMN_1799487	N4BP2L1	1.051273	6.514086	2.793526	0.007539	0.046578	-2.83593
ILMN_3262454	LOC100128056	1.051463	5.17256	3.325235	0.001727	0.015977	-1.49658
ILMN_2214678	MXD1	1.051557	7.596661	3.767479	0.000462	0.006197	-0.27711
ILMN_1797154	AZGP1	1.051767	8.340814	4.089679	0.000169	0.003076	0.660618
ILMN_1746578	SLC23A2	1.052818	9.609974	5.044088	7.36E-06	0.000373	3.616111
ILMN_1810941	COMT	1.052846	6.001911	4.328035	7.89E-05	0.001825	1.376682
ILMN_1791232	SPRED2	1.053004	9.191777	5.694083	7.97E-07	9.16E-05	5.72613
ILMN_2374770	TAX1BP1	1.053937	9.632211	4.474744	4.90E-05	0.00131	1.82564
ILMN_1737157	GRAMD1A	1.054264	9.217612	4.946438	1.02E-05	0.000465	3.304349
ILMN_1713369	RPL13A	1.055023	12.5103	6.276049	1.06E-07	2.32E-05	7.646566
ILMN_1778136	ZMYND15	1.055689	6.145736	4.163088	0.000134	0.002622	0.879276
ILMN_2219246	LOC162073	1.056412	5.428552	5.080167	6.51E-06	0.000345	3.731715
ILMN_2358265	F7	1.056492	5.747301	3.808118	0.000408	0.005721	-0.16094
ILMN_1743714	CARD10	1.05963	9.032494	5.575663	1.20E-06	0.000123	5.33809
ILMN_1664960	KIAA0284	1.061564	6.183103	3.569898	0.000841	0.009519	-0.83245
ILMN_1655614	DSP	1.06193	10.39094	5.236063	3.84E-06	0.000252	4.233589
ILMN_1762080	JMY	1.064074	5.939176	3.816579	0.000397	0.005626	-0.13667
ILMN_1675117	HSD17B11	1.066807	9.381591	3.292086	0.001901	0.017097	-1.58441
ILMN_1757702	LOC647673	1.069121	9.885343	5.385731	2.30E-06	0.000185	4.718661
ILMN_1663145	NOMO3	1.06956	6.556098	3.720808	0.000533	0.006875	-0.40973
ILMN_1698404	ERN1	1.069932	8.314402	3.277343	0.001983	0.017567	-1.6233
ILMN_1740155	COL9A3	1.070632	7.319927	5.136616	5.38E-06	0.00031	3.91301
ILMN_1756982	CLIC1	1.072621	12.13027	6.411502	6.59E-08	1.76E-05	8.095328
ILMN_1800225	PPARG	1.072983	9.508413	4.933605	1.07E-05	0.000477	3.263505
ILMN_3233442	LOC387825	1.073827	10.40174	5.148139	5.17E-06	0.000305	3.950077
ILMN_1753370	ABTB2	1.075232	7.561791	4.776465	1.81E-05	0.00069	2.76594
ILMN_2364272	MBNL2	1.075405	9.468817	3.416542	0.001324	0.013135	-1.25195
ILMN_1660345	NGRN	1.075776	7.756836	3.92331	0.000285	0.004461	0.171749
ILMN_3208330	LOC100132797	1.075992	8.319426	3.933134	0.000277	0.004377	0.200347
ILMN_1727633	PVRL3	1.077154	7.912563	5.954541	3.23E-07	5.00E-05	6.583438
ILMN_1698020	DLC1	1.079142	9.184358	2.769371	0.008034	0.048752	-2.893
ILMN_2385178	MIB2	1.080972	7.471443	4.147105	0.000141	0.002712	0.831521
ILMN_2371053	EFNA1	1.082048	8.782836	3.802733	0.000415	0.005787	-0.17637
ILMN_1752478	DHRS3	1.082443	9.488353	3.165047	0.00273	0.022397	-1.91593
ILMN_1777261	FAM3C	1.083069	6.571743	4.076869	0.000176	0.003164	0.62264
ILMN_1739083	SIRT1	1.084662	8.192974	4.287442	8.99E-05	0.001997	1.25352
ILMN_1673352	IFITM2	1.086014	11.28191	5.153158	5.09E-06	0.000304	3.966233

ILMN_1730639	SLC22A15	1.086915	4.697496	3.916361	0.000292	0.004531	0.15154
ILMN_1651610	LOC730525	1.088144	6.545408	3.715845	0.000541	0.006948	-0.42378
ILMN_1728478	CXCL16	1.088577	10.84067	5.148259	5.17E-06	0.000305	3.950464
ILMN_1746704	TRIM8	1.088845	10.49243	5.293064	3.16E-06	0.000223	4.417978
ILMN_2113074	UFM1	1.089407	8.318354	4.577704	3.49E-05	0.001052	2.144086
ILMN_1679268	PELI1	1.090346	7.497507	4.080964	0.000174	0.003135	0.634776
ILMN_3247578	FAT1	1.090455	10.43315	6.254312	1.14E-07	2.49E-05	7.574581
ILMN_1690826	TNKS1BP1	1.092298	6.473187	4.51038	4.36E-05	0.001212	1.935556
ILMN_2310685	FOXK2	1.093466	6.172294	3.828569	0.000383	0.005498	-0.10224
ILMN_1686116	THBS1	1.093528	7.767025	3.20475	0.00244	0.020555	-1.8132
ILMN_1714228	SPTBN1	1.094121	5.304406	4.057465	0.000187	0.0033	0.565219
ILMN_1660904	TRIM15	1.095781	10.04785	4.835522	1.48E-05	0.000595	2.952363
ILMN_1685327	SON	1.095846	5.059986	6.803252	1.68E-08	7.23E-06	9.393436
ILMN_1714444	KLF12	1.095867	5.090613	4.713168	2.23E-05	0.000802	2.566946
ILMN_1683859	SLC7A1	1.098261	11.10195	4.986585	8.94E-06	0.000422	3.43232
ILMN_1736154	ProSAPiP1	1.098328	7.437138	4.001441	0.000224	0.003768	0.400143
ILMN_2371280	CSF3R	1.099035	8.243398	4.028712	0.000205	0.003522	0.480366
ILMN_1757644	UBE2H	1.099709	7.835904	5.326441	2.82E-06	0.00021	4.526154
ILMN_1768311	LOC728888	1.099823	11.73831	6.061202	2.23E-07	3.96E-05	6.935684
ILMN_2340919	GRB10	1.099934	5.252354	4.075405	0.000177	0.003174	0.618306
ILMN_1706571	SLC35D2	1.10183	9.912218	5.520454	1.45E-06	0.000136	5.157638
ILMN_1663640	MAOA	1.1026	8.434453	3.367541	0.001528	0.014598	-1.38373
ILMN_1713182	LOC653879	1.102986	11.01666	3.595429	0.000779	0.009022	-0.76161
ILMN_1785660	SRPR	1.1042	9.245287	3.993719	0.000229	0.003827	0.377475
ILMN_1658635	CLGN	1.10468	5.367074	3.695184	0.000576	0.007249	-0.48217
ILMN_1796755	ITGB5	1.105681	8.404528	4.345872	7.45E-05	0.001758	1.43095
ILMN_1813206	CP	1.106132	7.225892	3.104927	0.003232	0.025276	-2.06994
ILMN_2411963	RBM39	1.106257	9.772899	4.366592	6.96E-05	0.001684	1.494102
ILMN_1666924	PINK1	1.108002	7.461681	3.95456	0.000259	0.004154	0.26284
ILMN_3237368	LOC644132	1.111999	8.702579	4.78256	1.77E-05	0.000682	2.785146
ILMN_3283449	LOC440991	1.114185	10.60755	4.293	8.83E-05	0.001973	1.270355
ILMN_2145250	NACAP1	1.115762	8.772737	4.770802	1.84E-05	0.000696	2.748102
ILMN_1660439	LOC651149	1.121617	9.50487	5.533633	1.38E-06	0.000134	5.200684
ILMN_1800276	RCN1	1.121937	11.0389	5.787181	5.77E-07	7.15E-05	6.032023
ILMN_3296943	LOC100131096	1.122643	5.453644	2.928813	0.005249	0.035803	-2.50988
ILMN_1721651	LOC646463	1.123109	6.874878	4.686214	2.44E-05	0.00085	2.482474
ILMN_1710740	C2	1.123175	10.15531	4.049254	0.000192	0.003362	0.540961
ILMN_3292008	LOC401676	1.123801	7.586616	4.178265	0.000128	0.002541	0.924698
ILMN_2361807	OS9	1.123832	7.788484	4.947707	1.02E-05	0.000463	3.308391

ILMN_1766359	GATAD2B	1.124195	6.918302	5.048355	7.25E-06	0.000369	3.629771
ILMN_1753005	RELN	1.1254	9.51533	3.662751	0.000636	0.007781	-0.57347
ILMN_2389273	FXR1	1.126463	8.835851	4.6393	2.85E-05	0.000935	2.335837
ILMN_1717639	SIK1	1.127224	9.005205	4.001279	0.000224	0.003768	0.399668
ILMN_1741674	PPP1R9A	1.12781	6.629968	4.261024	9.79E-05	0.002121	1.173626
ILMN_1812226	ICAM1	1.127952	7.062524	3.397225	0.001401	0.013726	-1.30403
ILMN_3236694	LOC100132139	1.131111	8.20638	3.781875	0.000442	0.006023	-0.23603
ILMN_1765547	IRF2	1.131239	6.362625	4.477617	4.85E-05	0.001302	1.834487
ILMN_1790985	dJ341D10.1	1.131648	6.038059	3.108486	0.0032	0.0251	-2.06088
ILMN_2341661	ETV4	1.132039	9.830773	4.111442	0.000158	0.002919	0.725259
ILMN_1724738	TFR2	1.135022	6.49652	3.071945	0.003544	0.026939	-2.15362
ILMN_1666731	C3orf32	1.135312	9.745227	5.207281	4.23E-06	0.000269	4.140656
ILMN_1673232	LASS1	1.135532	6.071669	3.443146	0.001224	0.012394	-1.17994
ILMN_2065299	EDEM3	1.136417	7.612588	5.632073	9.87E-07	0.000104	5.522778
ILMN_2368585	GGT1	1.137448	5.82905	3.531426	0.000943	0.010282	-0.93867
ILMN_1692260	MAFG	1.137696	6.479339	4.107484	0.00016	0.002944	0.713492
ILMN_1775743	BTG1	1.139463	10.19602	4.690617	2.40E-05	0.000842	2.49626
ILMN_3235027	TAF1D	1.139662	8.151787	4.241064	0.000104	0.002224	1.113399
ILMN_1696339	ZIC2	1.139673	5.234189	3.784914	0.000438	0.005989	-0.22735
ILMN_1762260	C3	1.141315	10.12609	3.3551	0.001584	0.014976	-1.417
ILMN_1713985	MAF1	1.142322	7.335514	3.427324	0.001283	0.012832	-1.2228
ILMN_2391765	C6orf48	1.142822	11.91823	6.05634	2.27E-07	4.00E-05	6.919614
ILMN_1676336	AADACL1	1.1432	8.12154	4.648101	2.77E-05	0.000914	2.363305
ILMN_1707123	DDX19B	1.146479	5.819684	3.332077	0.001693	0.01578	-1.47839
ILMN_1658015	MBNL2	1.148945	8.86631	3.970086	0.000247	0.004044	0.308226
ILMN_1758087	TAOK1	1.14953	7.36158	4.31019	8.36E-05	0.001896	1.322479
ILMN_1700204	ZMYND8	1.152327	5.804664	5.031423	7.68E-06	0.000382	3.575582
ILMN_1654392	KHNYN	1.152948	9.545793	4.823543	1.54E-05	0.000613	2.914493
ILMN_1661264	SHMT2	1.153063	11.98044	4.902147	1.19E-05	0.000511	3.163511
ILMN_2364384	PPARG	1.154279	8.087167	4.949694	1.01E-05	0.000462	3.314716
ILMN_1770927	KIAA1026	1.155456	6.567543	4.223528	0.00011	0.002302	1.060584
ILMN_1718128	PABPC3	1.155739	6.86241	5.652767	9.19E-07	9.86E-05	5.590603
ILMN_1770610	MERTK	1.15807	8.706912	5.975559	3.01E-07	4.83E-05	6.652804
ILMN_1746819	C5	1.16069	11.26502	4.303769	8.53E-05	0.001927	1.302999
ILMN_1677768	POR	1.162776	9.061743	5.198137	4.37E-06	0.000276	4.111157
ILMN_1717809	RNF24	1.162869	6.198538	4.583245	3.43E-05	0.00104	2.161299
ILMN_1764629	SLC39A14	1.163657	11.70089	5.282611	3.27E-06	0.000227	4.384131
ILMN_3242315	SNORD3D	1.165163	6.139866	3.56761	0.000846	0.009558	-0.83879
ILMN_2220978	NR0B2	1.165337	8.874454	3.666611	0.000628	0.007722	-0.56263

ILMN_1812070	ABCB1	1.165416	9.396898	4.885113	1.26E-05	0.000534	3.109446
ILMN_1727271	WARS	1.165508	8.674801	3.971436	0.000246	0.004037	0.312178
ILMN_1733305	EIF2A	1.165708	10.41476	5.295645	3.13E-06	0.000222	4.426341
ILMN_1656501	DUSP5	1.166268	6.58391	2.945337	0.005019	0.034721	-2.46934
ILMN_1730907	ZFAND1	1.16895	9.128902	4.302143	8.58E-05	0.001935	1.298069
ILMN_1716507	EPB41L1	1.169368	6.561456	4.712498	2.24E-05	0.000802	2.564844
ILMN_1726460	RPL14	1.170427	10.99368	3.957669	0.000256	0.004128	0.271921
ILMN_1656042	KIAA0319L	1.170617	5.911469	4.232991	0.000107	0.002255	1.089073
ILMN_1878019		1.170711	6.718549	3.735209	0.00051	0.006677	-0.3689
ILMN_2298818	RPS29	1.171186	7.890655	3.923209	0.000286	0.004461	0.171453
ILMN_2232339	SLC22A9	1.171964	7.056029	3.751701	0.000485	0.00641	-0.32204
ILMN_1679299	IGSF1	1.174316	11.12284	5.088336	6.34E-06	0.00034	3.757918
ILMN_1803846	EIF1	1.174615	12.23278	5.514602	1.48E-06	0.000137	5.138527
ILMN_1709026	C6orf145	1.179223	5.958734	3.563018	0.000858	0.009633	-0.8515
ILMN_1732808	TNRC9	1.181008	8.59156	3.843801	0.000365	0.005315	-0.05841
ILMN_2167808	TM4SF5	1.181369	11.79583	4.771317	1.84E-05	0.000696	2.749723
ILMN_3239735	WASH5P	1.181442	6.100935	4.234899	0.000106	0.00225	1.094819
ILMN_2344650	N4BP2L1	1.182065	6.661976	3.433379	0.00126	0.012673	-1.20641
ILMN_1764398	TUBE1	1.18461	7.509018	4.33642	7.68E-05	0.001785	1.402181
ILMN_1815745	SOX4	1.184804	7.134648	3.785625	0.000437	0.005984	-0.22532
ILMN_3214893	LOC100132761	1.185874	6.992144	4.684771	2.45E-05	0.00085	2.477954
ILMN_1809173	LOC729021	1.186004	7.426811	4.448976	5.33E-05	0.001397	1.746365
ILMN_1699226	UBR4	1.18795	9.304722	4.386826	6.52E-05	0.001601	1.555888
ILMN_1732071	HIST2H2BE	1.188802	8.035651	4.86886	1.33E-05	0.000552	3.05791
ILMN_1730491	FMNL2	1.190688	9.551668	5.649565	9.29E-07	9.90E-05	5.580106
ILMN_1655595	SERPINE2	1.191227	9.938894	2.934911	0.005163	0.035392	-2.49494
ILMN_1773809	FOXP4	1.193573	6.032714	3.501778	0.00103	0.010951	-1.02009
ILMN_2374164	HERPUD1	1.194477	10.20629	5.040034	7.46E-06	0.000376	3.603135
ILMN_1740407	CHSY3	1.195664	6.024633	5.069	6.77E-06	0.000354	3.695908
ILMN_1722025	CPEB4	1.195715	5.581306	3.998542	0.000226	0.003787	0.39163
ILMN_1794677	TMC6	1.196587	8.823885	4.487792	4.69E-05	0.001266	1.865848
ILMN_1785405	SLC17A9	1.197211	9.134476	5.799335	5.54E-07	7.08E-05	6.072005
ILMN_2126957	NOMO1	1.197216	9.863633	4.640526	2.84E-05	0.000932	2.339662
ILMN_1651799	SLC38A2	1.197233	12.01234	4.412234	6.00E-05	0.001521	1.633633
ILMN_1756595	SH3TC1	1.19884	7.158128	3.569874	0.000841	0.009519	-0.83252
ILMN_1671123	LOC647543	1.200522	5.859405	5.075123	6.63E-06	0.000348	3.715541
ILMN_1695946	TRNP1	1.201091	10.65458	5.185459	4.56E-06	0.000283	4.070278
ILMN_1661833	ANKRD12	1.201693	7.613573	3.856319	0.000351	0.005168	-0.02233
ILMN_2392189	CTDSPL	1.206548	9.347562	5.653682	9.16E-07	9.86E-05	5.593604

ILMN_2266948	SLC38A1	1.207899	5.461907	4.708147	2.27E-05	0.000809	2.551199
ILMN_1798224	JARID1C	1.209116	5.350642	5.140446	5.31E-06	0.000307	3.925328
ILMN_3212284	LOC645693	1.209857	7.799652	4.890213	1.24E-05	0.000526	3.125626
ILMN_1669617	GRB10	1.210459	6.968446	4.847448	1.43E-05	0.000578	2.990095
ILMN_1670272	LRP10	1.211003	9.67885	3.668959	0.000624	0.00769	-0.55603
ILMN_2339028	PKD1	1.211613	5.625421	3.69044	0.000584	0.007324	-0.49555
ILMN_1668983	ACVR2B	1.212705	5.461069	4.743264	2.02E-05	0.000742	2.661454
ILMN_1746706	LOC653103	1.212764	9.507402	5.474906	1.69E-06	0.000149	5.008997
ILMN_1661197	CLCF1	1.213627	5.299399	2.949135	0.004967	0.034452	-2.45999
ILMN_1658709	LAMB1	1.213863	9.807998	6.348715	8.21E-08	1.94E-05	7.887278
ILMN_1653856	STS-1	1.214139	8.088521	3.708057	0.000554	0.007075	-0.44581
ILMN_1706579	SHBG	1.214245	8.155579	3.917113	0.000291	0.004527	0.153726
ILMN_1653432	HNRPDL	1.214612	9.295205	5.481654	1.66E-06	0.000149	5.031006
ILMN_1740169	TYRO3	1.214695	8.623787	4.96779	9.52E-06	0.00044	3.372374
ILMN_1678730	NOMO1	1.215657	9.924609	4.650373	2.75E-05	0.000911	2.3704
ILMN_1652677	FAM89A	1.216207	5.338785	4.600999	3.23E-05	0.001003	2.216498
ILMN_3235647	SIK1	1.220893	7.273008	3.711023	0.000549	0.007021	-0.43742
ILMN_1702310	LGR5	1.221939	6.468507	4.245016	0.000103	0.002203	1.125314
ILMN_1811238	ALPK2	1.222059	8.646852	4.064171	0.000183	0.003259	0.585051
ILMN_1801077	PLIN2	1.223156	10.52231	5.381083	2.34E-06	0.000187	4.703553
ILMN_2312906	MIA3	1.223755	5.656534	5.021287	7.95E-06	0.000389	3.543165
ILMN_1666444	RBMS1	1.224501	9.394926	5.979537	2.96E-07	4.83E-05	6.665935
ILMN_1803988	MCL1	1.224863	9.482834	4.687018	2.43E-05	0.00085	2.48499
ILMN_2384241	TGFBR2	1.224899	11.65152	6.660619	2.77E-08	9.56E-06	8.920961
ILMN_1726456	SLC3A2	1.224982	10.72286	4.528616	4.10E-05	0.001165	1.99193
ILMN_2359456	ERGIC3	1.226932	10.15807	4.655418	2.70E-05	0.000901	2.386158
ILMN_3307982	MGC11082	1.228262	5.671902	3.538945	0.000922	0.010099	-0.91796
ILMN_1675677	TMPRSS3	1.23031	5.61101	4.493437	4.61E-05	0.001254	1.883255
ILMN_1815937	TMEM184A	1.230413	5.771147	4.058421	0.000187	0.003299	0.568046
ILMN_1810584	IL1R1	1.236978	7.912603	4.553722	3.78E-05	0.0011	2.069676
ILMN_1771026	GARS	1.237062	11.35548	6.101567	1.94E-07	3.60E-05	7.069121
ILMN_1703244	MAP1LC3B	1.237791	9.636183	4.693697	2.38E-05	0.000837	2.505909
ILMN_2134888	TUBE1	1.237943	6.505598	4.373382	6.81E-05	0.001659	1.514821
ILMN_2363165	TACC2	1.24012	7.143712	4.512139	4.33E-05	0.00121	1.94099
ILMN_1679727	CLK1	1.241892	9.756854	4.663459	2.63E-05	0.000884	2.411288
ILMN_1803810	RRBP1	1.244042	8.896375	4.432509	5.62E-05	0.001452	1.695795
ILMN_1752046	SH2B3	1.244892	9.312919	4.879968	1.28E-05	0.000541	3.093125
ILMN_1657983	TERF2IP	1.245962	10.00076	5.959035	3.18E-07	5.00E-05	6.598267
ILMN_2413833	TOX3	1.246244	9.199645	4.222214	0.000111	0.002304	1.056631

ILMN_1765670	LOC285216	1.248882	5.370127	4.749858	1.97E-05	0.00073	2.682187
ILMN_2406313	RBCK1	1.25228	9.630669	4.678507	2.50E-05	0.000856	2.458348
ILMN_1686531	GGT1	1.253642	5.878204	4.310082	8.36E-05	0.001896	1.322153
ILMN_1669645	PKD1	1.255495	5.639306	4.174875	0.000129	0.002555	0.914545
ILMN_2207562	C4orf16	1.258493	6.913335	4.227192	0.000109	0.002281	1.07161
ILMN_2231985	HSPA13	1.260224	7.55012	3.326713	0.00172	0.015919	-1.49265
ILMN_2318643	TGIF1	1.260565	8.387988	4.990394	8.82E-06	0.000418	3.444478
ILMN_1716815	CEACAM1	1.26157	11.05792	6.420413	6.39E-08	1.76E-05	8.124858
ILMN_1706813	SLC6A14	1.262668	6.608764	3.373758	0.0015	0.014436	-1.36707
ILMN_1682818	TTLL3	1.263345	6.140035	4.502722	4.47E-05	0.001233	1.911907
ILMN_1803811	TRIB1	1.263419	10.46397	4.388804	6.48E-05	0.001597	1.561934
ILMN_1771841	FOSL1	1.263902	6.308508	4.067055	0.000182	0.003239	0.593584
ILMN_1794707	ATHL1	1.266517	5.686385	5.529346	1.41E-06	0.000134	5.186681
ILMN_3241441	MEGF6	1.266964	7.845899	5.497694	1.57E-06	0.000145	5.083337
ILMN_1680139	MAFF	1.268754	6.370089	3.498861	0.001039	0.011034	-1.02808
ILMN_2141790	HYOU1	1.268927	9.158871	4.222265	0.000111	0.002304	1.056783
ILMN_1774287	CFB	1.27151	11.58653	6.247651	1.17E-07	2.50E-05	7.552524
ILMN_1797594	NFAT5	1.272528	7.673531	4.630498	2.93E-05	0.000948	2.308381
ILMN_2162972	LYZ	1.277443	10.2693	5.117711	5.74E-06	0.000323	3.852235
ILMN_3188984	C20orf199	1.277772	10.84515	4.812701	1.60E-05	0.000631	2.880241
ILMN_2058270	SOAT2	1.278988	7.857075	4.119523	0.000154	0.002872	0.749303
ILMN_3243664	LOC440353	1.280018	11.43449	6.603078	3.38E-08	1.11E-05	8.730275
ILMN_2412761	MAFG	1.280211	5.811034	4.040754	0.000198	0.003423	0.51587
ILMN_3233229	SNHG7	1.281738	8.421681	4.591259	3.34E-05	0.001023	2.186204
ILMN_3279877	LOC645430	1.282996	6.251178	4.556559	3.74E-05	0.001092	2.07847
ILMN_1786843	KCTD13	1.284894	6.712812	4.084145	0.000172	0.003109	0.644206
ILMN_2188374	XPOT	1.28956	7.366496	3.452555	0.001191	0.01214	-1.15439
ILMN_1679093	ZNF581	1.289632	10.25565	4.336085	7.69E-05	0.001786	1.401162
ILMN_1744381	SERPINE1	1.289951	8.188479	3.096641	0.003308	0.02571	-2.09102
ILMN_1787923	PNPLA2	1.291674	9.652567	5.942832	3.37E-07	5.03E-05	6.544805
ILMN_1682717	IER3	1.292116	11.18917	4.364572	7.01E-05	0.001694	1.487939
ILMN_1769911	SLC38A1	1.293957	9.733023	5.368223	2.44E-06	0.000192	4.66177
ILMN_1766528	SLC25A36	1.294236	7.376325	4.567232	3.61E-05	0.001075	2.111577
ILMN_1792689	HIST1H2AC	1.29449	5.112248	4.36052	7.10E-05	0.001706	1.475583
ILMN_2391900	SLC26A6	1.294549	6.600874	4.430935	5.65E-05	0.001458	1.690964
ILMN_2087989	ZFAND1	1.296044	7.719036	4.462331	5.10E-05	0.001351	1.787428
ILMN_1753830	ETV4	1.296776	10.07547	5.430049	1.98E-06	0.000165	4.862836
ILMN_1658337	AKIRIN1	1.299214	7.938143	5.87782	4.22E-07	5.85E-05	6.33044
ILMN_1707720	SLC1A5	1.300222	9.884699	5.172557	4.76E-06	0.00029	4.028699

ILMN_1743711	LOC650215	1.300536	10.21949	4.708273	2.27E-05	0.000809	2.551592
ILMN_1731941	APOM	1.305533	11.77507	6.608089	3.32E-08	1.10E-05	8.74688
ILMN_3209399	LOC399965	1.305851	7.710526	4.499458	4.52E-05	0.001237	1.901834
ILMN_1729987	SRC	1.306764	9.163396	5.116614	5.76E-06	0.000323	3.848711
ILMN_1734445	LOC91461	1.31394	5.96495	5.019977	7.98E-06	0.00039	3.538979
ILMN_1689400	CLK1	1.314078	9.367644	4.205311	0.000117	0.002378	1.005816
ILMN_1794190	CCPG1	1.315643	7.542989	2.953513	0.004908	0.034176	-2.44922
ILMN_1808047	PHC2	1.315768	7.147382	5.121368	5.67E-06	0.000321	3.863987
ILMN_1753139	LOC124220	1.32259	5.465778	5.095054	6.19E-06	0.000336	3.779476
ILMN_2404063	APP	1.326112	7.79339	4.149445	0.00014	0.002697	0.838508
ILMN_1807972	MICAL1	1.327928	6.099968	5.451218	1.84E-06	0.000156	4.931784
ILMN_1838320	ONECUT2	1.334156	7.956925	4.561371	3.69E-05	0.001082	2.093394
ILMN_2314080	CTAGE5	1.334392	6.925502	4.429412	5.68E-05	0.001462	1.686291
ILMN_1728844	PTPRN2	1.337725	5.616797	4.232779	0.000107	0.002255	1.088433
ILMN_1815057	PDGFRB	1.339046	7.996981	4.944246	1.03E-05	0.000467	3.29737
ILMN_2358560	TIAM2	1.340252	6.414379	6.517165	4.56E-08	1.41E-05	8.445528
ILMN_3249435	UBASH3B	1.34639	6.048904	3.759659	0.000473	0.006292	-0.29939
ILMN_1756146	WDR45	1.346629	7.040432	4.488613	4.68E-05	0.001266	1.868378
ILMN_1748124	TSC22D3	1.347321	5.402697	5.119758	5.70E-06	0.000321	3.858812
ILMN_2065773	SCG5	1.347591	5.639627	4.269418	9.53E-05	0.002077	1.198989
ILMN_1787673	PLLP	1.349083	9.239169	6.401217	6.83E-08	1.77E-05	8.061243
ILMN_3251550	PHLDA1	1.349752	6.404685	6.724573	2.21E-08	8.69E-06	9.132851
ILMN_1655229	SLC7A11	1.350887	5.209846	5.406802	2.14E-06	0.000176	4.787181
ILMN_2232712	MYO10	1.351015	8.583376	4.685511	2.45E-05	0.00085	2.480271
ILMN_3227023	SNHG7	1.352895	9.321404	5.532635	1.39E-06	0.000134	5.197424
ILMN_1738773	HRC	1.352897	6.805876	5.51766	1.46E-06	0.000137	5.148514
ILMN_1758798	LOC728734	1.353738	10.05776	5.322539	2.86E-06	0.000211	4.513498
ILMN_1736539	ALDH1L2	1.354005	5.452369	4.79978	1.67E-05	0.000653	2.839453
ILMN_1781386	WIPI1	1.354805	8.179527	4.450316	5.30E-05	0.001392	1.750482
ILMN_3246766	LOC100132247	1.355597	9.684529	5.745035	6.68E-07	8.01E-05	5.893461
ILMN_2360705	ACSL3	1.357597	11.85655	6.668341	2.69E-08	9.56E-06	8.946548
ILMN_1714820	ITGB1	1.359145	9.171258	4.490413	4.65E-05	0.001262	1.87393
ILMN_1735014	KLF6	1.361796	9.286334	5.663178	8.86E-07	9.67E-05	5.624741
ILMN_1694475	GTPBP2	1.363033	5.774917	3.017187	0.004123	0.030016	-2.29125
ILMN_1710482	APLP2	1.368917	9.924484	5.598547	1.11E-06	0.000115	5.412978
ILMN_2165753	HLA-A29.1	1.368936	9.589015	5.130819	5.49E-06	0.000313	3.894368
ILMN_3209070	LOC341230	1.37173	6.38417	3.910698	0.000297	0.004589	0.135085
ILMN_1790891	CKAP4	1.372191	9.715534	6.784255	1.80E-08	7.49E-06	9.33053
ILMN_3246273	RNU1-3	1.372522	7.875202	4.311253	8.33E-05	0.001895	1.325706

ILMN_1673529	AGXT2L2	1.372915	6.366397	5.054456	7.11E-06	0.000364	3.64931
ILMN_1771084	ACSM3	1.373277	7.836601	4.700141	2.33E-05	0.000824	2.5261
ILMN_2268381	RRBP1	1.375946	9.580022	5.116918	5.75E-06	0.000323	3.849689
ILMN_1674719	NID1	1.375983	6.57102	3.924408	0.000284	0.004452	0.174943
ILMN_1659749	DSP	1.376371	6.773371	5.254427	3.60E-06	0.00024	4.292946
ILMN_2208802	NPIP	1.376875	8.71578	5.113209	5.82E-06	0.000325	3.837773
ILMN_1667561	IFRD1	1.377417	9.557512	5.01552	8.11E-06	0.000394	3.524732
ILMN_1812926	ANTXR2	1.377801	8.18574	4.089995	0.000169	0.003075	0.661557
ILMN_1855278		1.377911	6.025839	4.30131	8.60E-05	0.001939	1.295542
ILMN_2115125	CTGF	1.37906	11.09757	4.996873	8.63E-06	0.000412	3.465161
ILMN_1737683	FGG	1.383442	10.37204	7.578716	1.14E-09	1.04E-06	11.94895
ILMN_1666078	HLA-H	1.388189	9.750661	4.687724	2.43E-05	0.000849	2.487202
ILMN_1723486	HK2	1.40176	10.16923	5.235196	3.85E-06	0.000252	4.230787
ILMN_1689004	TNFRSF12A	1.402668	8.815333	3.698006	0.000571	0.007214	-0.4742
ILMN_3188106	CYTH2	1.403574	8.193471	4.843046	1.45E-05	0.000583	2.976164
ILMN_3202591	LOC440311	1.404211	6.322049	3.281422	0.00196	0.017419	-1.61255
ILMN_2384496	ST6GAL1	1.404798	7.623431	4.852574	1.40E-05	0.000573	3.006322
ILMN_1770084	TACC1	1.415938	8.010976	3.57552	0.000827	0.009402	-0.81688
ILMN_1873620		1.418645	6.193381	4.584407	3.42E-05	0.00104	2.16491
ILMN_2366463	FN1	1.418871	6.274813	4.445093	5.39E-05	0.001408	1.734433
ILMN_1657234	CCL20	1.420254	11.26734	5.100911	6.07E-06	0.000333	3.798276
ILMN_1712469	GOLGA8A	1.421251	6.21355	4.155836	0.000137	0.002667	0.8576
ILMN_2098446	PMAIP1	1.421585	5.871476	4.778127	1.80E-05	0.000689	2.771178
ILMN_1729831	LOC388814	1.422646	6.215764	4.597039	3.28E-05	0.001011	2.20418
ILMN_1673941	RBM24	1.42351	5.266734	3.78575	0.000437	0.005984	-0.22496
ILMN_1673113	F2RL1	1.424081	7.664741	2.855093	0.006401	0.041337	-2.68887
ILMN_1811049	POU2AF1	1.424434	5.602575	5.208009	4.22E-06	0.000269	4.143006
ILMN_1725773	DNAJC12	1.424627	6.985032	3.520369	0.000974	0.010522	-0.96908
ILMN_3241034	SNORD3C	1.427283	6.127042	3.301156	0.001852	0.016816	-1.56043
ILMN_2150654	ZSWIM4	1.427959	6.481661	4.562996	3.67E-05	0.00108	2.098433
ILMN_3240308	LOC100133511	1.430505	8.960599	4.142689	0.000143	0.002738	0.818341
ILMN_3307841	AGR2	1.431394	6.874941	3.181997	0.002602	0.021599	-1.87217
ILMN_1712896	FST	1.436758	9.079729	3.28437	0.001943	0.017345	-1.60477
ILMN_1673649	HYOU1	1.447402	8.39254	4.799506	1.67E-05	0.000653	2.838586
ILMN_3244646	RNU1G2	1.452159	7.702058	4.711032	2.25E-05	0.000805	2.560246
ILMN_1774659	LOC652388	1.457346	7.293809	5.148326	5.17E-06	0.000305	3.950679
ILMN_2121408	HBEGF	1.461636	5.770787	3.57266	0.000834	0.009471	-0.8248
ILMN_1801703	CPLX1	1.461641	5.470666	2.970985	0.00468	0.032962	-2.4061
ILMN_1881081		1.463586	5.693294	4.574713	3.53E-05	0.001058	2.134799

ILMN_1797596	SPRY4	1.465264	5.335656	4.600477	3.24E-05	0.001003	2.214873
ILMN_1784287	TGFBR3	1.465951	11.4615	5.93363	3.48E-07	5.11E-05	6.514448
ILMN_3309349	SNHG8	1.467887	10.46313	5.70739	7.61E-07	8.90E-05	5.769812
ILMN_1751886	REC8	1.468475	6.465083	5.526749	1.42E-06	0.000134	5.178197
ILMN_1699695	TNFRSF21	1.469871	11.00083	7.876926	4.09E-10	4.89E-07	12.92171
ILMN_1712197	KCNMB3	1.472251	7.8784	3.905226	0.000302	0.004647	0.119194
ILMN_2347193	GSDMB	1.473341	5.756193	5.475265	1.69E-06	0.000149	5.010169
ILMN_1659984	MEP1A	1.474015	8.247505	3.407174	0.001361	0.013399	-1.27723
ILMN_1724145	CBX4	1.47553	9.750239	6.414877	6.52E-08	1.76E-05	8.106513
ILMN_1757604	TPM2	1.479401	5.760343	4.389293	6.47E-05	0.001597	1.563429
ILMN_1804735	CBS	1.480096	10.34944	6.936563	1.06E-08	4.80E-06	9.834623
ILMN_1780861	LOC653506	1.480106	5.931647	3.22394	0.00231	0.019766	-1.76326
ILMN_2414826	VPS13A	1.487245	6.695927	5.797271	5.58E-07	7.08E-05	6.065216
ILMN_3238369	JHDM1D	1.490687	6.687375	5.90924	3.78E-07	5.50E-05	6.434011
ILMN_1746968	PHF1	1.491439	7.489333	7.300245	2.99E-09	2.11E-06	11.03481
ILMN_1690708	SPTBN1	1.491613	7.631696	4.191936	0.000122	0.002457	0.965674
ILMN_1791483	PDE4D	1.492079	5.253625	5.677438	8.44E-07	9.46E-05	5.671514
ILMN_2413331	TMEM107	1.496749	7.561845	3.522	0.00097	0.010499	-0.9646
ILMN_2147105	LOC440348	1.497605	9.130654	7.174726	4.62E-09	2.89E-06	10.62127
ILMN_1726245	TGFBR2	1.49999	11.26538	7.562647	1.21E-09	1.04E-06	11.89634
ILMN_1786720	PROM1	1.502859	8.649983	7.08671	6.28E-09	3.58E-06	10.33083
ILMN_2393296	GK	1.504678	9.598436	5.678291	8.41E-07	9.46E-05	5.674311
ILMN_2195821	C5orf41	1.510326	6.616747	3.635553	0.00069	0.008249	-0.64971
ILMN_1737406	KLF6	1.511427	7.259223	4.506712	4.41E-05	0.001223	1.924226
ILMN_2375557	SCMH1	1.513683	7.049744	5.680047	8.36E-07	9.46E-05	5.680074
ILMN_3244583	NCRNA00219	1.517356	10.19459	5.362946	2.49E-06	0.000194	4.644628
ILMN_2329914	SPRY1	1.519475	10.55645	7.411913	2.03E-09	1.60E-06	11.40198
ILMN_1736863	TMEM140	1.519711	7.298624	4.346646	7.43E-05	0.001757	1.433305
ILMN_1760649	PCK2	1.52437	9.026261	5.007136	8.34E-06	0.000401	3.49794
ILMN_1659027	SLC2A1	1.526685	10.77361	8.095151	1.94E-10	3.18E-07	13.62878
ILMN_2374865	ATF3	1.53791	7.38966	5.169345	4.81E-06	0.000292	4.018351
ILMN_1696843	LOC613037	1.541074	9.102195	6.536681	4.26E-08	1.35E-05	8.510211
ILMN_1680874	TUBB2B	1.54433	9.438586	6.539377	4.22E-08	1.35E-05	8.519146
ILMN_1811767	INHBE	1.547598	9.754692	4.10846	0.000159	0.002937	0.716393
ILMN_2041190	F2RL1	1.557244	8.405214	3.637697	0.000686	0.008214	-0.64371
ILMN_1677032	DSP	1.573924	5.326232	5.742611	6.74E-07	8.01E-05	5.885494
ILMN_1671005	IRF2BP2	1.574542	8.468867	5.367676	2.45E-06	0.000192	4.659993
ILMN_2305116	CTH	1.581316	6.529212	5.743081	6.72E-07	8.01E-05	5.887039
ILMN_1786197	NR2F1	1.581396	8.609058	5.113571	5.82E-06	0.000325	3.838934

ILMN_1773742	DNAJB9	1.58456	8.826509	4.630333	2.94E-05	0.000948	2.307865
ILMN_1693014	CEBPB	1.586654	12.13235	6.231336	1.23E-07	2.59E-05	7.498506
ILMN_1786972	SARS	1.5867	9.53073	4.899554	1.20E-05	0.000514	3.155279
ILMN_1746175	TNFSF4	1.586765	6.343405	6.025805	2.52E-07	4.38E-05	6.818726
ILMN_1741768	TMPRSS3	1.591931	6.903718	6.122654	1.80E-07	3.37E-05	7.138856
ILMN_1725471	GK	1.594512	9.103442	5.803778	5.45E-07	7.03E-05	6.086625
ILMN_1654414	ACSL3	1.595473	6.668668	6.224881	1.26E-07	2.61E-05	7.477135
ILMN_2118663	ERV3	1.596331	6.044819	5.08843	6.33E-06	0.00034	3.75822
ILMN_1778237	FN1	1.596858	6.500482	5.176312	4.70E-06	0.000289	4.040798
ILMN_1710075	FAM89A	1.601858	6.012632	4.980038	9.14E-06	0.000427	3.41143
ILMN_1754126	SH2D5	1.603496	5.809946	2.968863	0.004707	0.033102	-2.41134
ILMN_2305112	CTH	1.604567	8.479815	4.759119	1.92E-05	0.000715	2.711323
ILMN_1736742	GLT25D2	1.607044	5.37586	6.161732	1.57E-07	3.05E-05	7.26813
ILMN_3236653	RNU1-5	1.609715	8.32575	5.022114	7.93E-06	0.000389	3.545812
ILMN_1700888	ENPP1	1.616523	9.764005	5.284552	3.25E-06	0.000227	4.390417
ILMN_2162799	AHR	1.616743	7.097382	6.158818	1.59E-07	3.05E-05	7.258489
ILMN_1770673	AKNA	1.619453	6.227932	3.329698	0.001705	0.015834	-1.48472
ILMN_1807833	HM13	1.62434	7.569326	5.196773	4.39E-06	0.000276	4.106759
ILMN_1777060	CTH	1.626593	5.827141	5.780977	5.90E-07	7.27E-05	6.011619
ILMN_1665792	ITGA2	1.632215	7.13923	4.641803	2.83E-05	0.00093	2.343648
ILMN_1703477	ARHGEF2	1.636152	10.39926	5.034753	7.60E-06	0.00038	3.586235
ILMN_1791678	TAT	1.636604	6.796641	3.462026	0.001158	0.011907	-1.12863
ILMN_1654609	TIGA1	1.637567	10.28649	5.67022	8.65E-07	9.63E-05	5.647837
ILMN_2089875	TNFSF4	1.638624	7.819721	5.948928	3.30E-07	5.00E-05	6.564916
ILMN_1740559	F7	1.640927	8.054437	5.154239	5.07E-06	0.000303	3.96971
ILMN_1651496	HIST1H2BD	1.641535	5.891656	4.42749	5.71E-05	0.001467	1.680398
ILMN_1815023	PIM1	1.648873	8.750129	3.896512	0.00031	0.004726	0.093913
ILMN_1679041	SLC3A2	1.649564	5.823742	4.165957	0.000133	0.002604	0.887858
ILMN_2377900	MAP1B	1.654567	5.944373	5.737994	6.84E-07	8.11E-05	5.870327
ILMN_1789196	TPM2	1.65683	6.444984	5.090479	6.29E-06	0.000339	3.764795
ILMN_1710284	HES1	1.65769	6.944184	5.563838	1.25E-06	0.000127	5.299414
ILMN_2371724	CEACAM1	1.662697	9.861435	7.699787	7.52E-10	8.18E-07	12.34473
ILMN_1746465	FJX1	1.664306	6.287374	4.422118	5.81E-05	0.001488	1.663922
ILMN_1766446	C6orf48	1.673929	7.526632	6.696462	2.44E-08	9.19E-06	9.039723
ILMN_1699354	EPHA2	1.683101	7.960369	5.943228	3.36E-07	5.03E-05	6.546111
ILMN_1673933	LOC440341	1.684687	9.854232	6.655341	2.82E-08	9.56E-06	8.903469
ILMN_1678671	KLHL24	1.685072	7.487356	4.393103	6.39E-05	0.001583	1.575077
ILMN_2375879	VEGFA	1.686334	7.915044	7.918528	3.55E-10	4.43E-07	13.05684
ILMN_3238435	SNORA12	1.6888	7.826151	4.705412	2.29E-05	0.000814	2.542623

ILMN_1825249		1.690013	6.086498	4.502064	4.48E-05	0.001233	1.909877
ILMN_2358457	ATF4	1.695713	9.589603	6.360821	7.87E-08	1.91E-05	7.927387
ILMN_1788377	COL27A1	1.705008	6.051092	6.23129	1.24E-07	2.59E-05	7.498354
ILMN_1751598	SESN2	1.705795	6.617689	4.919922	1.12E-05	0.000494	3.219988
ILMN_1664330	CEACAM1	1.705844	6.753032	6.952697	1.00E-08	4.74E-06	9.88798
ILMN_1787815	TRIB3	1.709626	11.36315	5.429581	1.98E-06	0.000165	4.861315
ILMN_1781400	SLC7A2	1.716259	10.93851	5.950924	3.27E-07	5.00E-05	6.571501
ILMN_3236249	LOC727877	1.7357	6.203565	6.068601	2.18E-07	3.88E-05	6.960139
ILMN_1696317	CACNA2D4	1.738434	8.091464	5.247383	3.69E-06	0.000244	4.270172
ILMN_1757497	VGF	1.73859	5.858977	3.834323	0.000376	0.005433	-0.08569
ILMN_2367469	CARS	1.750493	9.643049	5.826667	5.04E-07	6.69E-05	6.161957
ILMN_1741465	PTPRH	1.75064	7.395738	4.329485	7.85E-05	0.00182	1.381089
ILMN_1775380	SMOX	1.751442	9.050811	5.665376	8.80E-07	9.67E-05	5.631948
ILMN_1674706	MTHFD2	1.762373	10.95131	6.31058	9.37E-08	2.15E-05	7.760939
ILMN_3303612	PABPC1L	1.763168	9.691457	4.563775	3.66E-05	0.00108	2.10085
ILMN_1655296	UTRN	1.766589	6.625507	6.285323	1.02E-07	2.28E-05	7.67728
ILMN_3309453	RNU4-1	1.769574	8.223643	4.283909	9.10E-05	0.002005	1.242823
ILMN_2269256	DNAJC12	1.775409	9.070196	4.935829	1.06E-05	0.000477	3.270582
ILMN_1773082	CYP21A2	1.777063	6.504005	6.043849	2.37E-07	4.15E-05	6.878338
ILMN_1660810	TTC17	1.783064	8.13524	6.086604	2.04E-07	3.69E-05	7.019649
ILMN_1760087	SLC26A3	1.788173	6.402623	3.706594	0.000556	0.00709	-0.44994
ILMN_1788874	SERPINA3	1.790343	12.99773	7.611975	1.02E-09	9.64E-07	12.05779
ILMN_1773586	SLC17A2	1.798609	9.042135	4.545596	3.88E-05	0.001117	2.044496
ILMN_2367258	SMOX	1.802443	8.805321	4.906929	1.17E-05	0.000506	3.178698
ILMN_1656369	C8orf4	1.811846	8.082855	5.531931	1.39E-06	0.000134	5.195124
ILMN_1805665	FLRT3	1.81236	5.771142	3.78846	0.000433	0.005949	-0.21722
ILMN_1795582	CHRD	1.814643	7.239119	7.680569	8.03E-10	8.18E-07	12.28198
ILMN_2396020	DUSP6	1.821762	10.20803	8.090437	1.97E-10	3.18E-07	13.61356
ILMN_1700081	FST	1.822645	11.28889	4.863005	1.35E-05	0.000559	3.039357
ILMN_1803882	VEGFA	1.827952	6.737519	7.336373	2.64E-09	1.91E-06	11.15368
ILMN_1661599	DDIT4	1.830139	10.12103	6.430095	6.18E-08	1.76E-05	8.156946
ILMN_1677466	DUSP6	1.838458	5.628412	6.953028	9.99E-09	4.74E-06	9.889075
ILMN_1659936	PPP1R15A	1.857204	9.286803	5.01292	8.18E-06	0.000396	3.516422
ILMN_1691884	STC2	1.869043	10.41196	6.480843	5.18E-08	1.52E-05	8.32514
ILMN_1786429	P2RY5	1.879069	7.448349	6.503287	4.79E-08	1.46E-05	8.399529
ILMN_1776788	C5orf41	1.880645	6.165423	4.668599	2.59E-05	0.000877	2.427355
ILMN_2188862	GDF15	1.882945	10.82013	5.302809	3.06E-06	0.00022	4.449546
ILMN_1669523	FOS	1.892751	5.481568	4.916825	1.13E-05	0.000496	3.210145
ILMN_2341343	AGTR1	1.894574	6.15464	6.210191	1.33E-07	2.68E-05	7.428503

ILMN_3308138	RNU4-2	1.910896	7.777587	4.455734	5.21E-05	0.001371	1.767138
ILMN_1799819	MARS	1.927424	10.16831	6.98287	9.01E-09	4.43E-06	9.987747
ILMN_1763887	SFI1	1.929045	6.690311	6.925675	1.10E-08	4.87E-06	9.798608
ILMN_1691860	SPRY1	1.937508	10.05598	9.233688	4.22E-12	3.25E-08	17.23596
ILMN_1769290	TTC39B	1.944225	5.787998	9.976865	3.75E-13	5.15E-09	19.50313
ILMN_1800540	CD55	1.953165	6.37405	4.826714	1.53E-05	0.00061	2.924515
ILMN_1803073	DNAJC12	1.965763	9.001682	5.378348	2.36E-06	0.000187	4.694665
ILMN_2311020	DNAJC12	1.966301	8.418522	5.285373	3.24E-06	0.000227	4.393073
ILMN_1819608		1.979758	8.279237	5.400309	2.19E-06	0.000178	4.76606
ILMN_1715452	FREM1	1.980627	8.74687	7.029966	7.65E-09	4.12E-06	10.1434
ILMN_2367010	GPR126	1.982785	10.01283	7.695793	7.62E-10	8.18E-07	12.33169
ILMN_1714445	SLC6A9	1.985521	8.500084	5.133185	5.44E-06	0.000312	3.901977
ILMN_1757338	PLSCR4	2.001699	6.141297	5.358638	2.52E-06	0.000195	4.63064
ILMN_1666206	GSDMB	2.011141	6.592874	5.862987	4.44E-07	6.07E-05	6.281569
ILMN_1755649	SLC16A5	2.029646	6.360544	4.419671	5.86E-05	0.001495	1.656421
ILMN_1777556	SOAT2	2.032979	8.987973	5.75883	6.37E-07	7.71E-05	5.938801
ILMN_1658318	LOC120376	2.034978	6.883083	7.950345	3.18E-10	4.36E-07	13.16008
ILMN_1796928	BPIL1	2.038173	9.706077	6.480859	5.18E-08	1.52E-05	8.325192
ILMN_2285817	FAM89A	2.043788	6.073706	6.524142	4.45E-08	1.39E-05	8.468651
ILMN_2086105	SPRY4	2.048236	9.163	5.628457	9.99E-07	0.000105	5.51093
ILMN_1856480		2.048703	7.199651	6.251778	1.15E-07	2.49E-05	7.566191
ILMN_1669114	WNK4	2.051336	8.219533	6.578384	3.69E-08	1.19E-05	8.648432
ILMN_2361862	VLDLR	2.06211	6.054054	6.193378	1.41E-07	2.81E-05	7.372854
ILMN_1696066	CARS	2.11853	7.918319	5.94336	3.36E-07	5.03E-05	6.546546
ILMN_1752810	LARP6	2.128702	5.6379	4.873174	1.31E-05	0.000548	3.071585
ILMN_3239574	SNORD3A	2.158708	8.179776	4.35137	7.32E-05	0.001736	1.447694
ILMN_3234837	PKDCC	2.183913	7.473534	7.685208	7.91E-10	8.18E-07	12.29713
ILMN_2405521	MTHFD2	2.189275	10.60824	7.081964	6.38E-09	3.58E-06	10.31516
ILMN_1814327	AGTR1	2.193131	6.132153	7.266018	3.37E-09	2.29E-06	10.92213
ILMN_1789244	SOX8	2.247397	6.366195	6.420611	6.39E-08	1.76E-05	8.125516
ILMN_1663401	LARP6	2.259575	7.231756	5.969794	3.07E-07	4.87E-05	6.633775
ILMN_2398107	ASNS	2.299804	9.521718	6.662942	2.74E-08	9.56E-06	8.928656
ILMN_1667239	INPP1	2.330511	9.085398	8.797739	1.80E-11	8.24E-08	15.87249
ILMN_1663171	MATN3	2.340111	7.961871	7.377491	2.29E-09	1.75E-06	11.28888
ILMN_2198912	TTR	2.380354	12.13851	8.679589	2.67E-11	1.05E-07	15.499
ILMN_1699574	NRP1	2.418253	6.551993	6.404607	6.75E-08	1.77E-05	8.072478
ILMN_1702933	ADM2	2.44316	7.863882	5.580892	1.18E-06	0.000122	5.355197
ILMN_1658494	C13orf15	2.571964	6.590829	4.718613	2.19E-05	0.000791	2.58403
ILMN_1676984	DDIT3	2.580262	8.27581	6.365278	7.75E-08	1.91E-05	7.942154

ILMN_1796417	ASNS	2.650698	10.7741	7.562195	1.21E-09	1.04E-06	11.89486
ILMN_1674785	COL2A1	2.764928	7.516263	6.375099	7.48E-08	1.89E-05	7.974696
ILMN_1697220	NT5E	2.89139	7.944787	6.285662	1.02E-07	2.28E-05	7.678405
ILMN_1762899	EGR1	3.067246	8.401157	5.445953	1.87E-06	0.000158	4.914632
ILMN_2391150	FILIP1L	3.235136	8.074033	8.437922	6.04E-11	1.66E-07	14.73007
ILMN_1730906	FILIP1L	3.275976	8.048492	8.151051	1.60E-10	2.93E-07	13.80919
ILMN_1738578	FILIP1L	3.294418	9.065107	9.11313	6.29E-12	3.46E-08	16.86128
ILMN_2387385	IGFBP1	3.333056	11.52883	4.949456	1.01E-05	0.000462	3.313958
ILMN_1728445	IGFBP1	3.52539	8.913454	4.091279	0.000168	0.00307	0.665367
ILMN_1767556	C10orf10	3.83529	9.518496	5.997727	2.78E-07	4.72E-05	6.725991