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Novel small molecule inhibitors of TLR7 and TLR9: mechanism of action and efficacy *in vivo*

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Non-standard abbreviations:

| ANA | anti-nuclear antibodies |
|-------|---|
| BMDCs | Mouse bone marrow-derived dendritic cells |
| dsDNA | double-stranded DNA |
| FITC | Fluorescein isothiocyanate |
| IL-6 | Interleukin-6 |
| LPS | lipopolysaccharide endotoxin |
| PAMPA | Parallel Artificial Membrane Assay |
| PBMCs | peripheral blood mononuclear cells |
| PE | phycoerythrin |
| pIC | poly inosine-cytosine |
| SLE | Systemic Lupus Erythematosus |
| TLR | Toll-like receptor |

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Abstract

The discovery that circulating nucleic acid-containing complexes in the serum of autoimmune lupus patients can stimulate B cells and plasmacytoid dendritic cells via Toll-like receptors 7 and 9 suggested that agents that block these receptors might be useful therapeutics. We identified two compounds, AT791 and E6446, that inhibit TLR7 and 9 signaling in a variety of human and mouse cell types, and inhibit DNA - TLR9 interaction in vitro. When administered to mice, these compounds suppress responses to challenge doses of CpG-containing DNA, which stimulates TLR9. When given chronically in spontaneous mouse lupus models, E6446 slowed development of circulating anti-nuclear antibodies and had a modest effect on anti-double stranded DNA (dsDNA) titers, but showed no observable impact on proteinuria or mortality. We discovered that the ability of AT791 and E6446 to inhibit TLR7 and 9 signaling depends on two properties: weak interaction with nucleic acids and high accumulation in the intracellular acidic compartments where TLR7 and 9 reside. Binding of the compounds to DNA prevents DNA - TLR9 interaction in vitro and modulates signaling *in vivo*. Our data also confirms an earlier report that this same mechanism may explain inhibition of TLR7 and 9 signaling by hydroxychloroquine (Plaquenil), a drug commonly prescribed to treat lupus. Thus, very different structural classes of molecules can inhibit endosomal TLRs by essentially identical mechanisms of action, suggesting a general mechanism for targeting this group of TLRs.

Introduction

The Toll-like Receptors (TLRs) recognize a wide array of pathogen-associated and endogenous molecular patterns that trigger innate immune responses (reviewed in Sasai and Yamamoto, 2013). Certain types of nucleic acids can provoke a robust innate immune response, and this recognition is mediated by cytoplasmic receptors such as RIG-I and AIM2 and by TLRs localized inside endosomes and lysosomes (Barbalat et al, 2011). The nucleic acid-recognizing TLRs include TLR3, which is activated by double-stranded RNAs, TLRs 7 and 8, which are activated by single-stranded RNAs and TLR9, which mediates responses to single-stranded DNAs. The intracellular localization of these TLRs appears to prevent their spontaneous activation by circulating nucleic acids (Barton et al, 2006), however under certain pathological conditions endogenous nucleic acids can overcome this barrier. The immune complexes found in sera of patients suffering from systemic lupus erythematosus (SLE) typically contain nucleic acids associated with various proteins such as antibodies, the chromatin-associated protein HMGB1, the antimicrobial peptide LL39, ribonuclear proteins and others. These associated proteins may protect the bound nucleic acid from degradation and/or facilitate their entry into the cell, as is the case for Fc receptor-mediated uptake of antibody-nucleic acid complexes (Leadbetter et al., 2002, Means et al, 2005). Once inside the endolysosomal compartments, the nucleic acid cargo can then stimulate the intracellular TLRs, priming the immune system for further generation of anti-self antibodies. This cycle of innate immune recognition, generation of self-antibodies, and enhanced immune complex formation is believed to contribute to the pathogenesis of SLE and possibly Sjogren's syndrome (Marshak-Rothstein et al., 2006), a finding confirmed in animal models treated with TLR7 and TLR9-competitive antagonist oligonucleotides (Barrat et al., 2007; Christensen et al., 2005). In addition, TLR-mediated pathological responses to nucleic acids may contribute to other pathologies, such as damage due to liver injury or lung infection,

pancreatitis, and graft-versus-host disease (Bamboat et al., 2010, Calcaterra et al., 2008, Hoque et al., 2011, Itagaki, 2011). Recent clinical data show that an injectable, synthetic, competitive oligonucleotide inhibitor of TLR9 has efficacy in psoriasis (Kimball et al., 2013).

The purpose of our work was to develop an orally available, non-oligonucleotide small molecule inhibitor of TLR9. We describe two small molecules, AT791 and E6446, that can potently inhibit not only TLR9 stimulation by DNA, but also block TLR7 stimulation by RNA in mouse cell lines and inhibit DNA-TLR9 interaction *in vitro*. These compounds are orally bioavailable in mice, and can inhibit short-term induction of inflammatory cytokines by DNA. In a mouse MRL/lpr spontaneous model of lupus, E6446 slowed the development of circulating anti-nuclear antibodies and modestly suppressed anti-dsDNA titers, although it showed no observable impact on proteinuria or mortality. E6446 has also recently been shown to be effective in preventing hyper-inflammation and lethality caused by the parasite *Plasmodium berghei* in a mouse model of cerebral malaria (Franklin et al, 2011).

As described in an earlier preliminary report (Ishizaka, 2008), we show here that these compounds utilize an unusual mechanism of action: they interact weakly with nucleic acids but accumulate to a sufficiently high concentration in acidic compartments in cells that this interaction becomes significant. We also observed that the antimalarials hydroxychloroquine and chloroquine utilize a similar mechanism to suppress TLR7 and 9, consistent with a recent report by Kuznik et al (2011). Thus, very different structural classes of molecules can inhibit endosomal TLRs by essentially identical mechanisms of action, suggesting a general mechanism for targeting this group of TLRs.

Materials and Methods

Animals. Female BALB/c, were obtained from Charles River Laboratories or Jackson Laboratories and DO11.10 and MRL/lpr-MpJ mice from Jackson Laboratories, and housed under standard conditions. All animal experimental work was performed under protocols approved by the Eisai Andover IACUC.

Reagents and Compounds. AT791 (3-(4-(6-(3-(dimethylamino)propoxy)benzo[d]oxazol -2-yl)phenoxy)-N,N-dimethylpropan-1-amine) and E6446 (6-(3-(pyrrolidin-1-yl)propoxy) -2-(4-(3-(pyrrolidin-1-yl)propoxy)phenyl)benzo[d]oxazole) were synthesized at Eisai Inc. and their structures are shown in Figure 1A. Hydroxychloroquine and chloroquine were purchased from Sigma (St. Louis, MO). Soluble TLR9-Fc was cloned, expressed in HEK cells, and purified as previously described (Latz et al., 2004). LPS was purchased from List Biological Laboratories or Sigma. R-848, CL-097 and Cytoxan was from Sigma. Monoclonal antibodies to dsDNA (clone BV 16-13) were from Millipore.

Oligonucleotides. Phosphothioate-modified DNA or RNA oligonucleotides were obtained from Sigma Genosys or Dharmacon. Sequences (5' to 3'): **CpG2006** (TCG TCG TTT TGT CGT TTT GTC GTT), **3X-CpG2006** (a 3x concatamer of CpG2006), **CpG2216** (GGG GGA CGA TCG TCG GGG GG), **GpC2216** (GGG GGA GCA TGC TGC GGG GG), **CpG1668** (TCC ATG ACG TTC CTG ATG CT), **CpG1417** (TCG TCG TTT TGT CG), **RNA40** (GCC CGU CUG UUG UGU GAC UC), **SL4 RNA** (GGG GGA CUG CGU UCG CGC UUU CCC CU). In some cases, RNA oligos were complexed with the cationic lipid DOTAP (Roche) to facilitate uptake by cells (Hemmi et al., 2004)

In Vitro Cell-Based Assessment. HEK293 fibroblast cells (American Type Culture Collection, Manassas, VA) containing an NF-kB-luciferase reporter were stably transfected with pcDNA3.1D/V5-His-TOPO plasmid (Life Technologies) expressing human TLR9 (directly inserted as a *Taq* polymerase-amplified PCR product) or TLR7 (vector pCMV6-XL5 expressing human TLR7 cDNA from Origene). RAW 264.7 cells were stably transfected with a lentivirus containing an NF-kB-luciferase reporter (SA Biosciences). Compounds were added to cells 30 min. before stimulation with phosphothioate-modified CpG DNA or RNA oligonucleotides, the small-molecule imidazoquinoline TLR7 agonists R-848 or CL-097, or the TLR4 agonist lipopolysaccharide (LPS). Luciferase reporter activity was assayed using Steadylight (Perkin-Elmer). HEK:TLR7 respond to the imidazoquinoline TLR7 agonists, but not to RNA/DOTAP complexes. RAW cells respond to DNA, RNA (with or without DOTAP), R-848, CL-097 and LPS. For oligonucleotide uptake experiments, RAW 264.7 cells were incubated for 15 minutes with biotinylated CpG2006 complexed to phycoerythrin-streptavidin (BD Biosciences), washed and then fluorescence was visualized by confocal microscopy (Leica SP5).

Primary Cell Assays. Compounds were assayed for the suppression of BALB/c mouse spleen IL-6 production in response to stimulation by oligonucleotide CpG1668. Each compound was added to dissociated splenocytes (5×10^5 per well in complete RPMI/10% FBS in a 96 well plate) before addition of TLR agonists. Cells were stimulated for 72 hrs and supernatants were removed for ELISA analysis of IL-6 (R&D Systems). Mouse bone marrow-derived dendritic cells (BMDCs) were generated by culturing BALB/c marrow cells in RPMI containing 100ng/ml Flt3 ligand for 7 days. 1 x 10⁵ cells in 50ul were assayed for IL-6 production after overnight or 24 hour stimulation with various TLR ligands. For studies using human peripheral blood mononuclear cells (PBMCs), Ficoll-separated mononuclear

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cells were isolated from healthy volunteer donors, washed, and plated with stimulatory oligonucleotide CpG2216 in complete RPMI for 72 hrs. Interferon in supernatant was quantified by ELISA (Pestka Biomedical Laboratories).

Antigen Presentation Assay: Splenocytes were isolated from DO11 mice, washed twice after RBC lysis and re- suspended with complete RPMI. $5x10^5$ cells/well were seeded in a 96-well plate, with 10 ng/ml OVA323-339 peptide (ISQAVHAAHAEINEAGR, MW 1773.9) or 300 µg/ml OVA protein (Sigma, MW 42.7 kDa) and serial dilutions of compound. The cells were cultured at 37°C, 5% CO2 for 48 hours. 150 µl/well supernatant was harvested and stored at -80°C for IL-2 ELISA. 100 µl lysis/substrate solution of ATPLite (PerkinElmer) was added into each well. The plate was incubated at dark for 10 min. at room temperature and luminescence measured with an Envision Plate Reader (PerkinElmer).

Microarray analysis E6446 (250nM or 1250nM) or media were added to wells containing 4 x 10^{6} BDMCs. Cells were stimulated with 250nM CpG1668 or left untreated. After 4 hours, cells were harvested and total RNA was isolated using Qiagen RNeasy Mini Kit. GeneChip assay was performed using the Affymetrix Mouse Genome 430A 2.0 Array following the Affymetrix standard eukaryotic target preparation protocol using 1 µg of total RNA. Array data was normalized using standard RMA GeneData Refiner workflow. All statistical analyses were calculated in GeneData Analyst. All probes were filtered based on arithmetic mean with a threshold at a signal of 100 across all samples. A two-group sample comparison test using a standard t-test was performed between CpG stimulated samples vs. medium control. All genes that were significantly regulated by CpG (uncorrected p-value <= 0.05 and fold change >=2) were reported, which included a total of 616 probe sets. Eight probe sets did not map to any known gene with the remaining mapping to a total of 461 known gene symbols. Comparisons between all treatments with medium control were performed. Relative

normalization method was applied to all the samples relative to the reference group (medium control). Two-dimensional hierarchical clustering using the 616 probe set signature was performed using GeneData Analyst using Manhattan distance and complete linkage.

Antibody-DNA complexes. Plasmid DNA (pcDNA3.1) was linearized with DdeI restriction enzyme and incubated with anti-DNA monoclonal antibody (Chemicon MAB030; clone BV 16-13) for 30 minutes in media before adding to wells containing 50,000 BMDCs. Cells were incubated overnight, and IL-6 was assayed the next day. Anti-biotin antibody (Jackson Labs) was used as a control antibody.

DNA uptake assay. RAW 264.7 cells (1 x 10^5 cells) were added to wells of a 96-well plate with glass cover slip bottoms (Mattek) and cultured overnight. One hour prior to stimulation, plates were pre-incubated at 4 °C, 37 °C, or 37 °C in the presence of 1 µM AT791 or E6446. Biotinylated CpG2006 and streptavidin-linked phycoerythrin (PE) were mixed at a molar ratio of 8:1 (DNA:PE), and added to a final concentration of 200nM CpG2006/25nM PE and plates were further incubated at 4 °C or 37 °C. After 30 minutes, wells were washed with cold PBS and cells visualized by confocal microscopy.

Intracellular pH assay RAW 264.7 cells were incubated for 6 hours with 10 mg/ml of a mixture of fluorescein- and pHrodoRed- labelled ~ 10,000 MW dextrans (Life Technologies). Cells were washed 3X in Hank's buffer and AT791 (200nM), E6446 (200nM) or bafilomycin (10nM) were added for one hour. Cells were next visualized by confocal microscopy (Leica SP5). Fluorescein isothiocyanate (FITC; ex488/em525) and pHrodoRed (em563/ex585) fluorescence within intracellular vesicles were quantitated by intensities across line profiles.

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After background subtraction, FITC:pHrodo intensity ratios of individual peaks (n>20) were calculated and averaged.

TLR9 – DNA interaction assay. Interaction between 20nM biotinylated CpG2006 oligonucleotide and 5 μg/ml Fc-tagged ectodomain of TLR9 was assayed using an Amplified Luminescent Proximity Homogeneous Assay system (ALPHA-Screen, Perkin-Elmer), as described in Latz et al. (2007). Assays were performed in pH5.5 acetate buffer, 150mM NaCl. Oligo CpG1417 is a 14-nucleotide DNA oligomer that does not detectably interact with Fc-TLR9 in this assay (data not shown).

Compound-DNA interaction. Fluorescence spectroscopy (Hitachi F-2000) was used to monitor the intrinsic fluorescence of 100nM AT791 or E6446 in 50mM NaAce buffer (pH5.5), 150mM NaCl at 310nm excitation / 380nm emission. 400nM of 2-aminopurine was used as a control, as this compound has a very similar fluorescence spectra. Hydroxychloroquine and chloroquine (5 μM each) fluorescence were monitored in 50mM phosphate buffer (pH 7.2), 150mM NaCl at 330nm excitation / 375nm emission. pH7.2 was used as these compounds fluoresce poorly at lower pH. Various concentrations of CpG2006 DNA or RNA40 oligonucleotides were added to compound solutions, and the change in compound fluorescence as a function of DNA or RNA concentration was analyzed by non-linear regression analysis for fit to a one-site binding curve (GraphPad Prism). DNA interaction with AT791 and E6446 was also quantified using a plate-based equilibrium dialysis system (RED system; Pierce). Compounds (200nM) were added to two chambers separated by an 8kDa cutoff membrane and DNA (3X-CpG2006; 22kDa) was added at various concentrations to one of the chambers. After incubation overnight, the concentrations of compounds in each chamber were quantified by mass spectroscopic analysis, and this data

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was analyzed by non-linear regression analysis similar to above.

Intracellular localization of compounds

For the visualization of intracellular AT791 and E6446, HEK293 cells were incubated with 1µM of each compound for 5-15 min at 37 °C. The cells were then imaged using a Prairie Ultima IV multiphoton microscope system equipped with an Olympus 60x/1.15 numerical aperture water-immersion lens, and with a MaiTai HP and a MaiTai DeepSee laser (Spectra-Physics/Newport) providing excitation light at 920 nm and 707 nm, respectively. The HEK cells used in these experiments had been retrovirally transduced to stably express either Smad2-EGFP as a cytosplamic marker or LAMP-1 fused to EGFP as a lysosomal marker. AT791 was also visualized in cervical carcinoma C33A and CV-1 fibroblast cells by conventional confocal microscopy using a UV 351 nm laser ((Leica LSM SP2, courtesy of Owen Schwartz, NIH). Intracellular compound concentration was estimated by comparison to fluorescence obtained with known concentrations of AT791 spotted on microscope slides in pH5.5 buffer.

Parallel Artificial Membrane Permeation Assay (PAMPA). Five μ l of a solution of 2% *L*- α -phosphatidylcholine in dodecane was deposited per well on membranes of a 96-well MultiScreen Permeability plate (Millipore; MAIPN4510). AT791 (10 μ M), E6446 (10 μ M), hydroxychloroquine (40 μ M) or chloroquine (40 μ M) were added to one of the two compartments in pH 5.5 buffer (50 mM NaAce, 150mM NaCl) or pH 7.4 buffer (50mM KPO4, 150mM NaCl), and the plate was incubated at 37 °C. The next day, compound concentrations in both chambers were quantitated. In one variation of this experiment, 5 μ M AT791 or E6446 was added to both chambers, one of which contained pH5.5 buffer and the other pH7.4 buffer. The redistribution of compound between the two chambers was

monitored for 8 hours.

Drug Treatment in Oligo Challenge. Drug was dissolved in acidified water and administered orally (20mg/kg) 18 hours prior to subcutaneous challenge with CpG1668 (60 μ g/head). Two hours after oligo challenge, blood was collected for measurement of IL-6 in serum. IL-6 ELISA kits from BD Bioscience were used according to manufacturer's instructions.

Drug Treatment in Spontaneous Lupus Models. MRL/lpr mice were dosed orally five times a week with 20mg/kg or 60mg/kg E6446 or 60 mg/kg hydroxychloroquine beginning at 5 weeks of age. Cytoxan was administered at 50 mg/kg i.p. every 10 days. A serum sample was taken immediately before the beginning of treatment to monitor changes in autoreactive antibodies. Subsequently serum samples were collected approximately monthly and analyzed for anti-dsDNA by ELISA after 1:500 dilution (Alpha Diagnostics) Body weights and urine samples were taken at the same interval, and proteinuria assessed by ChemStrips (Roche Diagnostics). Anti-nuclear antibodies (ANA) were assessed using commercially available HEp2 slide kits (Antibodies, Inc., Davis, CA), with serum diluted to 1:100 in kit buffer. ANA scores were read blinded.

Results

Inhibition of TLR9 and TLR7signaling by small molecule ligands

HEK293 cells expressing cloned human TLR9 and an NF-kB:luciferase reporter (HEK:TLR9 cells) were used to screen a compound library for small molecules that could suppress induction of NF-kB by stimulatory DNA (CpG2006). AT791 and E6446 (Fig. 1A) potently suppressed DNA stimulation of HEK:TLR9 cells, with EC50s of 40nM and 10nM,

respectively, but were significantly less effective at suppressing lipopolysaccharide endotoxin (LPS) stimulation of HEK:TLR4 cells (Table I) or R848 stimulation of HEK:TLR7 cells.

Dendritic cells play a critical role in the initial innate immune response leading to adaptive immunity. We therefore tested the ability of AT791 and E6446 to suppress induction of IL-6 by various TLR ligands in mouse bone marrow-derived dendritic cells (BMDC). As shown in Figure 1B, AT791 and E6446 potently inhibited IL-6 production induced by CpG2216, but were ineffective against induction by the TLR3 ligand poly inosine-cytosine (pIC). Surprisingly however, the ability of these compounds to suppress TLR7 was ligand-dependent: both AT791 and E6446 were potent inhibitors of IL-6 induction by RNA, but relatively poor inhibitors of IL-6 induction by the small molecule imidazoquinoline ligand R-848. Similar results were seen in mouse splenocytes (Table I). In human PBMCs, AT791 and E6446 could suppress both IL-6 and α -interferon production induced by CpG oligo (Table I). Thus, antagonism is observed across species and output cytokine responses. E6446 showed a modest but consistent superiority over AT791, and both were significantly more potent than hydroxychloroquine (Plaquenil), which is commonly prescribed in the treatment of lupus.

To better understand this antagonism, we examined mRNA expression in BMDCs by microarray analysis. Stimulation with CpG1668 for 4 hours caused a reproducible change in a large number of genes, many of which are involved in inflammation, NF-kB signaling or the interferon response, consistent with previous reports (Klaschik et al., 2007). Significantly, 250nM and 1.25µM E6446 completely suppressed all of the CpG oligo-induced changes in gene expression (Supplemental Figure 1 & Supplemental Data I), while these concentrations of E6446 alone had no observable effect on gene expression after 4 hours.

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the compound acts at or upstream of signal initiation.

Inhibition of stimulation by immune complexes

Complexes of antibodies with DNA, RNA, chromatin and/or associated proteins are believed to be responsible for the aberrant induction of inflammatory cytokines in lupus patients, as demonstrated by the ability of immune complexes isolated from lupus patients to stimulate TLR7 and TLR9 in cell culture (Vallin et al, 1999, Means et al., 2005). We generated DNA-antibody complexes by incubating highly-purified plasmid DNA with an anti-DNA monoclonal IgG1 antibody. Neither DNA nor antibody alone significantly induced production of IL-6 in BMDCs, but when pre-incubated together, they synergistically stimulated IL-6 production (Fig. 2A). No stimulation was seen when anti-biotin antibody was substituted for anti-DNA antibody (Fig. 2A) and no stimulation was observed in BMDCs from TLR9 knockout mice (data not shown) Figure 2B shows that immune complex stimulation was inhibited by AT791. Thus, AT791 can inhibit stimulation of TLR9 by DNA-antibody complexes.

Antagonism does not involve inhibition of nucleic acid uptake or modulation of endosomal pH

Mouse RAW 264.7 cells transfected with an NF-kB-responsive luciferase reporter were stimulated by CpG2006 DNA, SL4 RNA, CL-097 or LPS. Stimulation by CpG2006 or SL4 RNA, but not by LPS or CL-097, was completely suppressed with 100nM of AT791 or E6446 (Fig. 3, left 2 panels). To visualize uptake we generated complexes of biotinylated CpG2006 and streptavidin-linked phycoerythrin (PE-DNA), incubated these with RAW cells, and washed and examined the cells by confocal microscopy. No fluorescence was observed in cells that had been incubated with PE alone (data not shown), but fluorescence appeared as

intracellular punctate spots in cells incubated PE-DNA complexes at 37 degrees (Fig. 4). When PE-DNA was incubated with cells at 4 degrees, fluorescence was confined to the cell surface. Uptake of PE-DNA could also be blocked by the GTPase inhibitor Dynasore (data not shown). Pre-treatment of cells for 3 hours with 1µM AT791 or E6446 did not cause any visible change in subsequent DNA-PE complex uptake or localization.

Since both AT791 and E6446 are weak bases, we investigated whether they inhibit TLR7 and 9 by modulating endosomal pH. First, we compared inhibition by AT791 and E6446 versus known modulators of endosomal pH, bafilomycin, monensin and methylamine. As shown in Figure 3 (center panels), these pH modulators were all effective in inhibiting TLR7 and 9 signaling, however in contrast to AT791 and E6446, they show no selectivity for nucleic acid versus imidazoquinoline ligands. Next, changes in intracellular pH were monitored with dextran (10,000 MW) labeled with fluorescein isothiocyanate (FITC) and pHrodo (Life Technologies). Both of these dyes are pH-sensitive: FITC fluorescence decreases, and pHrodo fluorescence increases as pH decreases over the range pH 7.5 to pH 5.0, and the ratio of FITC:pHrhodo fluorescence can be used to indicate pH within this range. After loading with dextran complexes, RAW cells were incubated for ~ 3 to 4 hours with a concentration of each compound that resulted in >95% inhibition in the cell-based reporter assays. Cells were imaged by confocal microscopy and intracellular fluorescence was quantitated along line profiles. The pH modulators bafilomycin, monensin and methylamine produced a clear change in intracellular pH, whereas AT791 and E6446 had no obvious effect (Fig. 5, Supplemental Figure 2). 5µM hydroxychloroquine or chloroquine also had no measurable effect on intracellular pH, even though these concentrations can inhibit TLR9 or 7 signaling induced by DNA or RNA ligands, similar to observations reported by Manzel et al. (1999) and Kuznik et al (2011). Finally, we observed that 100nM AT791 had no significant effect on

OVA peptide presentation to DO11 T cells, a process that is inhibited by changes in endosomal pH (Supplemental Figure 3). Taken together, these data indicated that these compounds do not inhibit TLR7 and 9 signaling by modulation of endosomal / lysosomal pH.

DNA – TLR9 interaction assay

We next asked if these compounds could inhibit the interaction between TLR9 and DNA *in vitro*. We used an amplified luminescent proximity homogeneous system (AlphaScreen; Perkin Elmer) to detect an interaction between biotinylated CpG2006 oligonucleotide and the extracellular domain of TLR9 fused to immunoglobulin Fc-TLR9 (Latz et al., 2007), and found that E6446 and AT791 inhibited *in vitro* DNA – TLR9 interaction (Fig.6A). In a separate experiment, these compounds did not inhibit the interaction between Fc-tagged TLR2 and the biotinylated TLR2 ligand PamCysK (data not shown). The concentrations of AT791 and E6446 required to inhibit TLR9-DNA interaction are several orders of magnitude higher than those required to inhibit TLR7 or 9 signaling in cell cultures. However, when we examined a series of analogs of AT791 and E6446, we observed a good correlation between their potencies in the TLR9-DNA interaction assay and the cell-based assay (Supplemental Figure 4), suggesting that the ability of these compounds to disrupt DNA-TLR9 interaction *in vitro* is in some way related to their inhibition of TLR9 signaling.

Identification of drug target

We next asked which of the two components in the DNA-TLR9 interaction assay is the target of the compounds: DNA or TLR9? We imagined that if these compounds interact with DNA, it might be possible to alleviate inhibition by the addition of excess free oligonucleotide, which would compete for binding to the compound. This "oligo decoy" experiment requires that the competing oligonucleotide itself does not interact with TLR9. We identified a

non-TLR9-binding, non-signaling 14-nucleotide single-stranded oligonucleotide, CpG1417, that could be used as the decoy oligo (see Methods). We started with optimal amounts of biotinylated CpG2006 oligonucleotide and Fc-TLR9, and observed the expected inhibition by 10µM AT791 (Fig. 6B). However, when we added increasing amounts of CpG1417, the assay signal increased almost to the non-suppressed level. This data suggests that AT791 inhibits DNA – TLR9 interaction in vitro via an interaction with DNA and not with TLR9.

To confirm whether the interaction of compound with DNA is relevant to its ability to inhibit DNA – TLR9 interaction in cells, we developed a live cell version of the oligo decoy experiment. We created a non-stimulatory version of the oligo CpG2216 by inverting the stimulatory CpG motifs to GpC, to generate GpC2216. As shown in Figure 6D, the stimulatory CpG2216 induced Interleukin-6 (IL-6) production in BMDCs and this was inhibited by 10µM AT791. However, when an excess of the non-stimulatory GpC2216 was also added, induction of IL-6 was restored. GpC2216 itself, either alone or in the presence of AT791, did not stimulate IL-6 production (Fig. 6D). These results are consistent with the idea that suppression of TLR9 by AT791 involves an interaction of the compound with DNA.

Analysis of compound-DNA interaction

We analyzed compound-DNA interaction using fluorescence spectrometry and equilibrium dialysis. AT791 and E6446 are intrinsically fluorescent and have similar fluorescence spectra of 312nm peak excitation and 381nm peak emission (Supplemental Figure 5). Starting with 200nM AT791 or E6446, we added increasing amounts of CpG2006 or SL4 RNA and observed that compound fluorescence decreased in a quantitative and saturable manner (Fig. 6C). The same experiment using 2-aminopurine, a compound that has a similar fluorescence (Fig. 6C).

Changes in compound fluorescence as a function of nucleic acid concentration showed an almost perfect fit to a one-site binding curve ($R^2 > 99\%$) with K_ds in the 1 ~ 4 μ M range, similar to the IC_{50s} obtained in the in vitro DNA – TLR9 interaction assay (Fig. 6A). We confirmed these results using an equilibrium dialysis method with an 8 kDa cutoff membrane. AT791 (200nM) was added to both chambers and various concentrations of DNA (3X-CpG2006; 22kDa) were added to one chamber. After overnight incubation, compound concentrations in each chamber were quantitated by mass spectrometry. We obtained an almost perfect fit to a one-site binding curve (R^2 =99.6%) and a Kd of ~ 3.4 μ M (Supplemental Figure 6). In both the fluorescence quenching and equilibrium dialysis assays, DNA and RNA were in large molar excess over compound, thus the Kds here represent the binding of one drug molecule per oligonucleotide, although when higher concentrations of AT791 were mixed with CpG2006 and injected directly into a mass spectrometer, we could detect the binding of multiple drug molecules to the oligonucleotides (data not shown). By the fluorescence spectroscopy method we also found that the affinities of AT791 for the in *vitro* decoy oligo CpG1417 was 16μ M +/- 3.2μ M and that for the *in* vivo decoy oligo GpC2216 was 0.8μ M +/- 0.1μ M (data not shown).

To further test the idea that small molecule interaction with nucleic acids might be able to inhibit TLR signaling, we tested whether known DNA-binding molecules could inhibit TLR7 and 9. We found that the dimeric cyamine DNA dye YOYO-1 could suppress DNA- or RNA-induced signaling in a concentration-dependent manner (Fig. 3). Although YOYO-1 is relatively cell-impermeant, we observed that at high concentrations YOYO-1 fluorescence appeared in a punctate pattern in the cytoplasm of RAW 264.7 cells (data not shown). As seen for AT791 and E6446, YOYO-1 inhibits DNA- and RNA-induced signaling, but not imidazoquinoline- or LPS-induced signaling. Similar to these results, Kuznik et al (2011)

have also recently observed that TLR9 activation by stimulatory DNA can be inhibited by the DNA-binding dyes Hoechst 34580 and propidium iodide.

Compound localization and accumulation

The concentrations of AT791 and E6446 required to bind to nucleic acids and inhibit DNA-TLR9 interaction in vitro are at least 100x greater than the concentrations required to inhibit TLR7 or 9 signaling in cells, suggesting these compounds might accumulate in cells. Direct visualization of AT791 and E6446 in cells by conventional fluorescence microscopy is hampered by their low excitation wavelength (~310 nm), which does not transmit well through ordinary microscope glass. We used two methods to circumvent this limitation: two-photon microscopy, which uses 2x the normal wavelength to excite the fluorescent molecule, and high-intensity off-peak excitation with a 351 nm UV laser. When HEK cells were incubated with 1µM AT791 and visualized with two-photon excitation, compound fluorescence appeared within a few minutes as a punctate pattern in the cell cytoplasm (Fig. 7), and overlapped that of the lysosomal marker Lamp-1 (Supplemental Figure 7A). We observed a similar cytoplasmic punctate pattern in C33A cells incubated with 1µM AT791 and visualized by high-intensity 351 nm excitation (Supplemental Figure 7B). Comparing the intracellular fluorescence intensities to a calibration curve generated by spotting different concentrations of AT791 on a slide, we could estimate intra-vesicle AT791 concentration to be in the 1 to 2 mM range (Supplemental Figure 7B). These results indicate that AT791 and E6446 can accumulate several orders of magnitude inside lysosomes.

AT791 and E6446 are typical of "lysosomotropic" compounds in that they are lipophilic and contain weak base amines. At neutral pH, such compounds are non-polar and can penetrate lipid membranes, but within low pH vesicles they become protonated and are trapped

(DeDuve et al., 1974). Capillary electrophoresis showed that AT791 has pKas of 7.9 and 6.1, and E6446 has pKas of 8.6 and 6.5, indicating they would be more highly protonated in endolysosomal compartments compared to cytoplasm. We examined the pH-dependent lipid permeability of these compounds using a Parallel Artificial Membrane Assay (PAMPA) assay, which consists of two aqueous chambers containing pH7.4, 6.5 or 5.5 buffers, separated by a hydrophobic layer of L- α -phosphatidylcholine. In an overnight assay, the compounds readily penetrated the L- α -phosphatidylcholine layer at pH 7.4, but were almost completely non-permeant at or below pH 6.5 (Table II). We next established a pH gradient across the PAMPA membrane, adding pH5.5 buffer to one chamber and pH7.4 buffer to the other. Pilot experiments showed that this pH gradient can be maintained at least overnight. When 5 mM AT791 or E6446 were added to both chambers, we observed a steady re-distribution of the compounds into the pH5.5 compartment over 8 hours (Fig. 8). Thus the ability of these compounds to accumulate in low-pH compartments is an intrinsic chemical property. We observed that accumulation of these compounds in living cells occurred within minutes (Fig. 7). This rapid accumulation is presumably due to the very high surface-to-volume ratio of intracellular vesicles.

If accumulation of these compounds in endolysosomal compartments is necessary for their activity, they should be ineffective at inhibiting TLR7 or 9 localized elsewhere in the cell. We tested this idea using a receptor fusion between the TLR9 ectodomain and the TLR4 cytoplasmic domain (9N4C), which localizes to the cell surface and signals in response to stimulatory DNA (Barton et al., 2006). HEK cells expressing either full-length TLR9 or the 9N4C chimera were stimulated with CpG2006 oligonucleotides. We saw the expected inhibition of reporter activity by AT791 (1 μ M) in cells expressing full-length TLR9, but not in cells expressing 9N4C (Fig 9). Similar results were obtained with E6446 (data not shown).

In vivo efficacy

AT791 and E6446 are orally bioavailable (AT791, 41%; E6446, 20%) and have high volumes of distribution in mice (AT791, 12.8 L/kg; E6446, 95.9 L/kg). To test their activity in vivo, mice were orally dosed with 20mg/kg of AT791 or E6446, and 18 hours later were challenged with 60 µg CpG1668 oligonucleotide injected subcutaneously. CpG1668-induced IL-6 production was inhibited approx. 50% by AT791 and almost completely by E6446 (Fig 10A). We took the more active compound, E6446, and tested it in a MRL/lpr mouse SLE model. MRL/lpr females were dosed orally with 20 or 60 mg/kg of E6446 per day, five days a week, starting at one month of age. Anti-nuclear antibody (ANA) development was followed by immunofluorescence staining of Hep2 cells with the mouse sera and scoring for degrees of severity. Sera from untreated mice developed ANA reactivity gradually over the observation period, culminating in 11 of the 12 animals showing some degree of ANA-positivity by 18 weeks (Fig. 10B). In contrast, development of ANA was suppressed in a dose-dependent manner in animals treated with 20 mg/kg and at 60 mg/kg E6446. Examination of anti-double stranded DNA (dsDNA) titers gave a similar result, with E6446 partially suppressing the development of circulating anti-dsDNA antibodies in a dose-dependent manner (Fig. 10C). A control immunosuppressing agent cyclophosphamide (Cytoxan) effectively blocked autoantibody development (Fig. 10D). Although E6446 suppressed ANA development, we saw no suppression of proteinuria (data not shown).

Inhibition of TLR7 and 9 by antimalarials

Hydroxychloroquine (Plaquenil) is prescribed for the treatment of lupus, and both hydroxychloroquine and its analog chloroquine inhibit TLR7 and 9 signaling (MacFarlane & Manzel, 1998), results that we confirmed in Figure 3 (right panels) and Table I. We noticed a

number of similarities between the antimalarials and our compounds. Chloroquine interacts with double-stranded DNA (Cohen & Yielding, 1965) and accumulates in acidic compartments in cells (French et al., 1987). The antimalarials also exhibit a similar pattern of inhibition to AT791 and E6446: they more potently antagonize TLR7 signaling induced by RNA than the imidazoquinolines CL-097 or R-848 (Fig. 3, right panels and Table I). We therefore asked if these compounds might utilize a mechanism of action similar to that of AT791 and E6446 to inhibit TLR7 and 9 signaling. We observed that the intrinsic fluorescence of both antimalarials is quenched in the presence of CpG2006, and the data showed an excellent fit to a one-site binding curve with virtually identical Kds of 57μ M +/- 5μ M for both compounds (R² >99%) (Supplemental Figure 8). Given that the antimalarials have IC₅₀ values in cell-based assays in the $1 \sim 5\mu M$ range, they would need to accumulate inside cells approximately $10 \sim 20$ -fold in order to achieve concentrations sufficient to interact with nucleic acids. In the PAMPA assay (Table II), both hydroxychloroquine and chloroquine were permeant at physiological pH, but non-permeant at pH 6.5 and below. Finally, neither hydroxychloroquine nor chloroquine produced any detectable change in intracellular pH at 5μ M (Fig. 5), similar to the observations of Manzel et al (1999) and Kuznik et al. (2011). These data suggest that chloroquine and hydroxychloroquine may inhibit TLR7 and 9 signaling by accumulating inside cells and binding to nucleic acids, similar to AT791 and E6446, and not by modulation of pH. A similar conclusion was recently reported by Kuznik et al (2011) based on their studies of the antimalarials chloroquine and quinacrine.

Discussion

These data indicate that the ability of AT791 and E6446 to antagonize TLR7 and TLR9 signaling depends on two intrinsic properties: (1) their affinity for DNA, and (2)

accumulation in intracellular acidic compartments. It should be noted that the Kds for the interaction of these compounds with DNA is in the μ M range, which is relatively weak. At the concentrations used to antagonize TLR7 and 9 in cells (10 ~ 50nM), there should be no significant interaction with DNA except in the intracellular vesicles where the compounds are concentrated. This localized action of the compounds may be beneficial, as it would limit potential off-target liabilities such as mutagenicity.

How does interaction of AT791 or E6446 with DNA inhibit TLR7 or TLR9 activation? As we observed *in vitro*, these compounds can interfere with DNA-TLR9 interaction. However, we found one analog of AT791 that enhanced DNA-TLR9 interaction *in vitro*, yet inhibited TLR9 activation in cell-based assays (data not shown), suggesting the involvement of other mechanisms of inhibition. DNA binding alone is not sufficient to activate TLR9, and certain DNA conformations and sequences, such as CpG motifs, are required to trigger a signaling event that is accompanied by a conformational change in TLR9 (Latz et al., 2007). Therefore, another way in which compounds such as AT791 and E6446 could inhibit TLR7 and 9 signaling is to render nucleic acids non-stimulatory by masking stimulatory sequences and/or altering their conformation.

AT791 and E6446 share several characteristics with a number of clinically approved lysosomotropic drugs such as haloperidol, levomepromazine and amantadine. All of these drugs are lipophilic, contain weak bases, exhibit high volumes of distribution *in vivo* and have long elimination half-lives. The accumulation of weak bases inside acidic vesicles has the potential to neutralize vesicle pH, and indeed chloroquine, methylamine and ammonium chloride are commonly used as biological reagents for this purpose. However, modulation of pH does not appear to explain inhibition of TLR7 and 9 signaling either by

AT791, E6446 or by the antimalarials chloroquine or hydroxychloroquine. First, we failed to see any significant effect of these compounds on endosome / lysosome pH using pH-sensitive fluorescent dyes. Strictly speaking, we do not know how the distribution of the TLR7 and 9 receptors overlaps with the dextran-containing, bright vesicles that we were able to visualize and quantitate. Furthermore, at concentrations higher than those used in the present study, AT791, E6446, chloroquine and hydroxychloroquine can all alter the fluorescence of both pH-sensitive and pH-insensitive fluorescent dyes, possibly due to direct molecular interactions between these molecules, e.g. hydrophobic ring stacking.

A stronger case is made by the distinct patterns of TLR7 antagonism caused by AT791, E6446, the antimalarials, known pH modulators and the DNA binding dye YOYO-1. These patterns of antagonism fall into two distinct groups: the known pH modulators antagonize TLR 7 activation by both RNA and imidazoquinoline ligands more or less equally, whereas AT791, E6446, the antimalarials, and YOYO-1 are highly selective for RNA versus the imidazoquinolines. Kuznik et al. (2011) also noted the selective antagonism of nucleic acid ligands by chloroquine, quinacrine and the DNA-binding dyes propidium iodide and Hoechst 34580. However, at higher concentrations, AT791, E6446, chloroquine and hydroxychloroquine can antagonize TLR7 induction by imidazoquinolines, probably because the accumulation of these weak bases is now sufficient to modulate endosomal pH. The window of selectivity between antagonizing RNA versus imidazoquinoline induction of TLR7 is 6~8-fold for chloroquine or hydroxychloroquine, and 20~40-fold for AT791 and E6446. This greater window of selectivity for AT791 and E6446 is presumably due to their higher affinity for nucleic acids. In SLE patients treated with daily doses of $200 \sim 400$ mg hydroxychloroquine, steady-state concentration of drug in the plasma has been reported to be in the range of 200 ~ 1000 ng/ml, or $0.4 \sim 2.0 \,\mu\text{M}$ (Tett et al., 1989). This is the

concentration range at which hydroxychloroquine can inhibit TLR7 and 9 in cell culture, but below the concentration required to alter endosomal pH. Indeed, hydroxychloroquine has been reported to be toxic in humans at a plasma concentration of 29 μ M (Jordan et al, 1999). Thus, AT791 and E6446 may be considered more optimized versions of Plaquenil, functioning via the same mechanism of action to suppress TLR7 and 9 signaling, but providing a greater margin of selectivity.

In the spontaneous MRL/lpr mouse model of SLE, E6446 suppressed the development of anti-nuclear and anti-DNA antibodies, but not the development of glomerular nephritis. These results resemble those obtained with a TLR9^{-/-} MRL/lpr mouse (Christensen et al., 2005). However, the role of TLR9 and TLR7 in the development of murine lupus is complex and may vary with the mouse model and experimental conditions. It has been reported that in some models TLR9 knockout can exacerbate lupus nephritis, that ablation of TLR7 is more effective at ameliorating disease, and that TLR9 modulates TLR7 activity (Wu et al., 2006, Christensen et al., 2010). A study using an oligonucleotide dual antagonist of TLR7 and TLR9 also reported efficacy in murine lupus models, showing reductions in anti-dsDNA titers in NZBxNZW and MRL models, and some positive impact on proteinuria and mortality (Barrat et al., 2007, Pawar et al., 2007).

Recently, Franklin et al (2011) have shown that E6446 is effective in preventing hyper-inflammation and lethality caused by the parasite *Plasmodium berghei* in a mouse model of cerebral malaria. Thus these compounds show efficacy in two very different animal models of disease driven in part by TLR activation. Taken together with the known efficacy of hydroxychloroquine and other antimalarials in human disease, the data presented here suggest a common mechanism of action for two structurally diverse families of endosomal Molecular Pharmacology Fast Forward. Published on December 16, 2013 as DOI: 10.1124/mol.113.089821 This article has not been copyedited and formatted. The final version may differ from this version.

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TLR inhibitors.

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Authorship contributions

Participated in research design: Lamphier, Zheng, Latz, Spyvee, Hansen, Zhao, Shen, Chow, Yu, Gusovsky, Ishizaka
Conducted experiments: Lamphier, Genest, Latz, Hansen, Rose, Yang, Zhao, Shen, C. Liu, D. Liu, Mempel, Rowbottom, Twine,
Contributed new reagents or analytic tools: Zheng, Latz, Shaffer, Shen, Mempel,
Performed data analysis: Lamphier, Latz, Hansen, Rose, Yang, Zhao, D. Liu, Mempel,
Rowbottom, Twine, Yu, Ishizaka
Wrote or contributed to the writing of the manuscript: Lamphier, Mempel, D. Liu, Twine,
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Legends for Figures

Figure 1. AT791 and E6446 structures and activities. A, Molecular structures. B, Suppression of Interleukin-6 production by mouse bone marrow-derived dendritic cells. Cells were treated with various concentrations of AT791 or E6446 and then stimulated overnight with the indicated agonists.

Figure 2. Interleukin-6 production by DNA-antibody complexes is suppressed by AT791. A, Anti-DNA antibodies and DNA synergistically stimulate production of IL-6 in mouse bone marrow-derived dendritic cells Anti-biotin antibody was used as a control. Data indicates that an optimal stoichiometry is required for efficient induction. B, Stimulation by DNA-antibody complexes is suppressed by AT791.

Figure 3. Selectivity of TLR inhibitors. RAW 264.7 cells containing an NF-κB:luciferase reporter were stimulated with optimal concentrations (approx. EC₉₀) of CpG1668 (DNA), RNA40 (RNA), CL-097 or LPS in the presence of a range of concentrations of the indicated inhibitors. After overnight incubation, luciferase activities were measured.

Figure 4. Uptake of OligoDNA – Phycoerythrin complexes by RAW 264.7 cells. DNAphycoerythrin complexes are taken up by RAW264.7 cells within 30 minutes when incubated at 37 °C, but remain on cell surface when incubated at 4 °C. AT791 and E6446, even at a relatively high concentration (1 μ M), have no obvious effect on complex uptake or localization

Figure 5. Effects of compounds on intracellular pH. Compound concentrations approximate the IC₉₀ for inhibition of TLR9 stimulation in RAW264.7 cells. Cells were pre-loaded with dextrans conjugated to the pH-sensitive dyes FITC and pHrodo and fluorescence in intracellular vesicles was quantitated by confocal microscopy. Bafilomycin (BAF), methylamine (MA) and Monensin (MN) cause a significant increase in the FITC:pHrodo, indicating an increase in pH. In contrast, concentrations of AT791, E6446, chloroquine (CHL) or hydroxychloroquine (HCQ) sufficient to suppress TLR9 stimulation do not cause an increase in pH.

Figure 6. In vitro and in vivo characterization of AT791 and E6446. A. AT791 and E6446 suppress TLR9 – DNA interaction in vitro, with an IC₅₀ in the 1 to 10 μ M range. B. Inhibition of TLR9-DNA interaction by AT791 can be relieved in the presence of an excess of a short competitor oligonucleotide CpG1417, which does not interact with TLR9. C. Addition of CpG2006 DNA (circles) or SL4 RNA (crosses) causes a quantitative change in the intrinsic fluorescence of AT791 and E6446, but not of a control compound 2-aminopurine. Fit to one-site binding curve (Graphpad Prism) gives Kµs in the 2 to 5 µM range (n=3), with R² goodness to fit >99%. D. Excess non-stimulatory oligoGpC2216 can relieve suppression of IL-6 production by AT791 in living cells (BMDCs).

Figure 7. Two-photon imaging of AT791 in living HEK cells. AT791 (1µM) was added to cultures of HEK cells and imaged 15 minutes later by two-photon microscopy. AT791 (red)

appears in a punctate pattern within the cytoplasm. Smad2-GFP is constitutively expressed and marks the cytoplasm.

Figure 8. pH partitioning of AT791 and E6446. AT791 and E6446 (5μ M) were evenly distributed between chambers containing two different pH buffers and separated by a hydrophobic barrier. Over the next 8 hours, compounds re-distributed to the low pH compartment.

Figure 9: AT791 does not inhibit cell surface-expressed TLR9. A chimera consisting of the TLR4 cytoplasmic and transmembrane regions and the TLR9 ectodomain is expressed on the cell surface and induces NF- κ B signaling in response to CpG2006 DNA. Whereas AT791 inhibits activation by the full-length, intracellular TLR9 (left panel), it has no effect on activation of the cell-surface expressed chimera (right panel).

Figure 10: In vivo efficacy of AT791. A. short-term induction of serum interleukin-6 in mice by CpG1668 DNA is effectively suppressed by pre-treatment with 20 mg/kg AT791 or E6446. Data are representative of two experiments. B. Anti-nuclear antibody (ANA) titers in 18-week old MRL/lpr mice are suppressed in a dose-dependent manner by E6446, given starting at week 5. Data representative of two experiments C. Development of anti-dsDNA antibodies in MRL-lpr mice is also suppressed by E6446. "pre" are serum samples taken before dosing at 5 weeks of age, "post" are samples taken after 7 weeks of E6446 dosing. Post-treatment samples are compared with vehicle control by one-way ANOVA with Newman-Keuls post-test. ** differs from vehicle with p<0.01, * differs from vehicle with p<0.05. Data representative of two experiments. D) Controls for experiments shown in panel C. Hydroxychloroquine (60 mg/kg, 5x per week) had no impact on anti-dsDNA, while cytoxan (50mg/kg, 1x per 10 days) caused a statistically significant suppression in titers. Statistical analysis as in C.

| Responding | Stimulus | Readout | IC ₅₀ (µM) | | |
|--------------|----------|--------------|-----------------------|-------|-------------------------|
| Cells | | | AT791 | E6446 | Hydroxy- chloroquine |
| HEK-TLR9 | CpG2006 | NF-kB – luc | 0.04 | 0.01 | 0.08 |
| HEK-TLR7 | R848 | NF-kB – luc | 3.33 | 1.78 | 2.78 |
| HEK-TLR4 | LPS | NF-kB – luc | >10 | 10.58 | >30 |
| Mouse spleen | CpG1668 | IL-6 | 0.04 | 0.02 | 3.1 |
| | R848 | IL-6 | 8.0 | 4.9 | >10 |
| | LPS | IL-6 | 8.9 | N.D. | >10 |
| Human PBMC | CpG2216 | IL-6 | 0.21 | 0.23 | 1.2 |
| | | α-interferon | 0.41 | 0.09 | 1.2 |
| | CpG2006 | IL-6 | N.D. | 0.28 | N.D. |

Table 1: Potency of small molecule inhibitors in engineered and primary cells

Luciferase reporter lines or primary mouse or human cells were stimulated overnight and activation assessed by NF- κ B-luciferase reporter or cytokine ELISA as described in Materials and Methods. Results are the mean of 2 to 5 separate determinations. N.D. = not determined.

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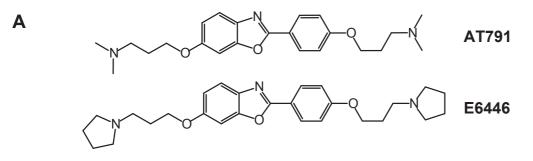
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Table 2: Effect of pH on permeability of compounds

| | Permeability (x 10 ⁻⁶ cm/s) | | | |
|--------------------|--|-------|-------|--|
| _ | pH7.4 | рН6.5 | рН5.5 | |
| AT791 | 58.5 | 0.1 | 0.2 | |
| E6446 | 67.4 | 0.3 | 0.4 | |
| Hydroxychloroquine | 1.7 | 0.2 | 0.0 | |
| Chloroquine | 19.5 | 3.7 | 1.4 | |

 10μ M AT791, 10μ M E6446, 40μ M hydroxychloroquine, or 40μ M chloroquine in were assayed in a Parallel Artificial Membrane Permeation Assay, as described in Materials and Methods. Data represent the average of three replicates. Permeability was calculated according to Wohnsland & Faller (2001).

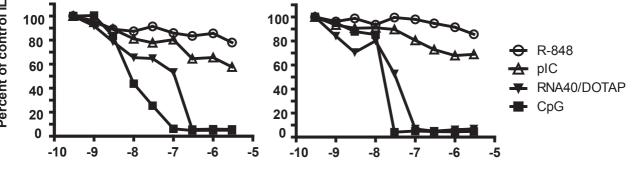
Figure 1



Percent of control IL-6 B

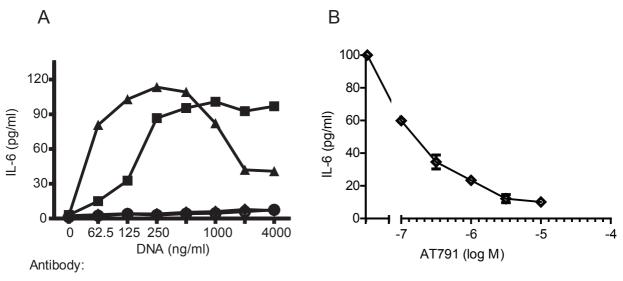






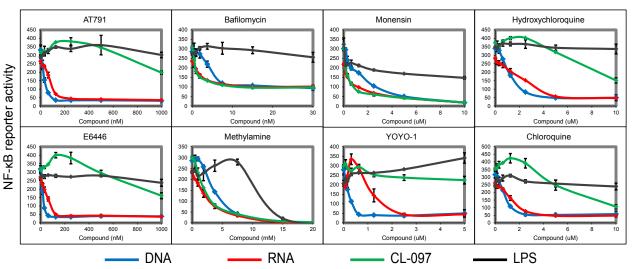
Inhibitor concentration (log M)

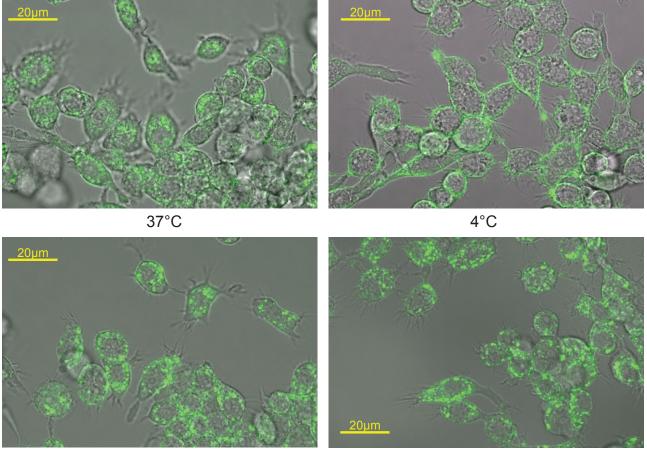
Figure 2



➡ Anti-DNA 1:25
 ➡ Anti-DNA 1:200
 ➡ None

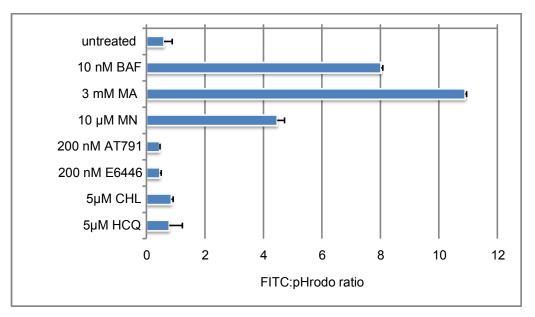
Figure 3.

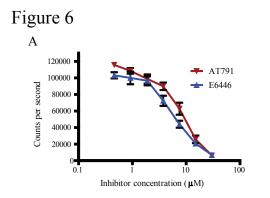


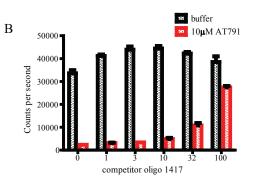


 $37^\circ C$ - 1 μM E6446

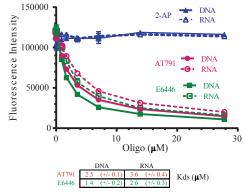
37°C - 1 μM E6446



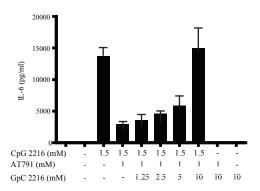


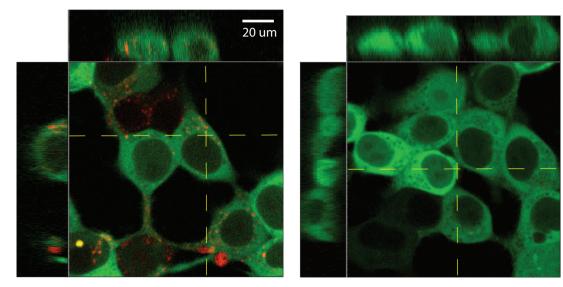






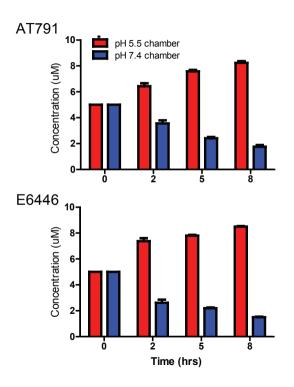
D





1µM AT791 Smad2-EGFP

(control) DMSO Smad2-EGFP



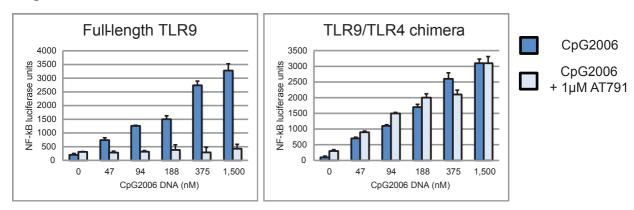
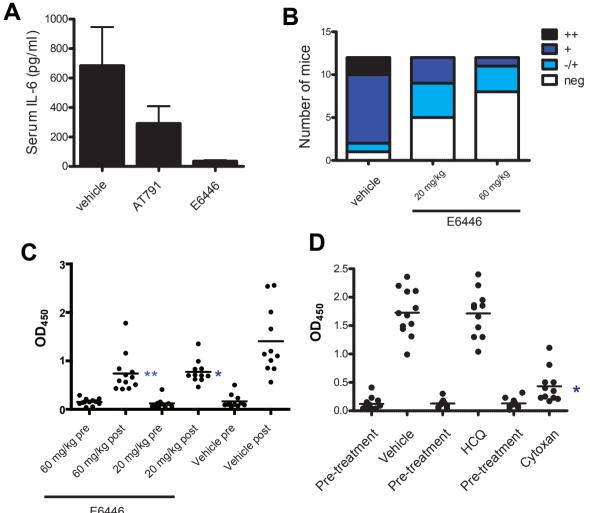
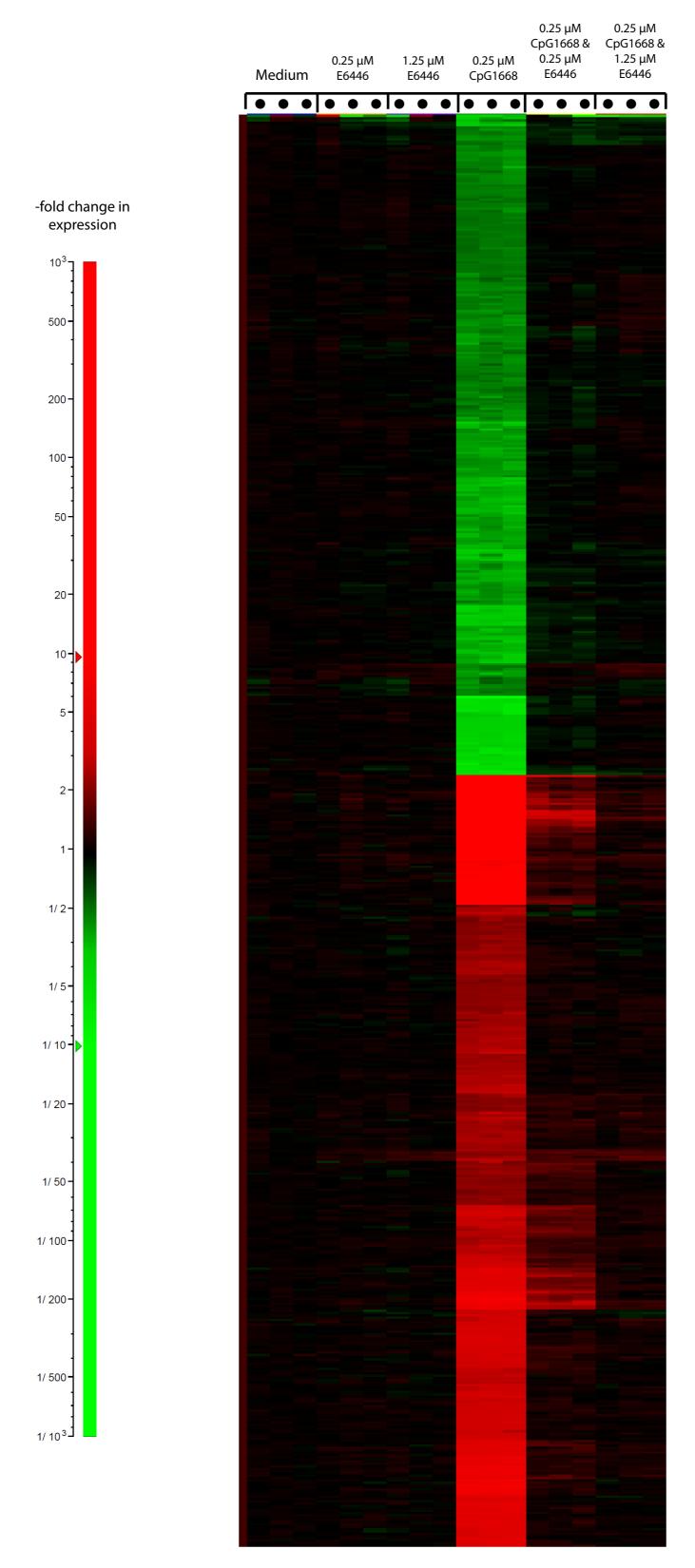


Figure 10



E6446

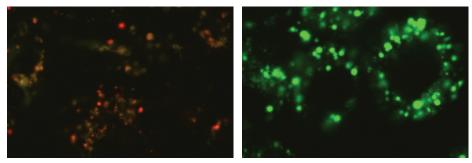
Supplementary Figure 1: Analysis of genes modulated by CpG DNA and/or E6446



Supplementary Figure 1: Heat map shows increased (red) or decreased (green) expression of genes induced in BMDCs by 250nM CpG2116 in the presence or absence of the indicated concentrations of E6446 for 4 hours. Data shows three replicates for each condition for 616 probe sets, representing 461 known genes. Gene expression was analyzed by Affymatrix gene chip. Only genes whose expression was affected by either CpG1668 or E6446 are shown. Genes are ordered by hierarchical similarity clustering (not shown). Raw data is provided in Supplementary Data 1. The scale at them left indicates the –fold change in expression.

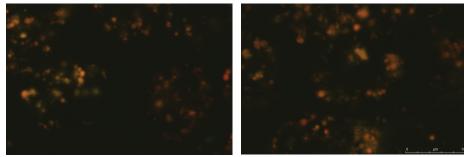
Novel small molecule inhibitors of TLR7 and TLR9: mechanism of action and efficacy in vivo D. Liu, T. Mempel, C. Rowbottom, J. Chow, N. Twine, M. Yu, F. Gusovsky, S. Ishizaka Journal: Molecular Pharmacology

Supplementary Figure 2: Effect of compounds on intracellular pH



untreated

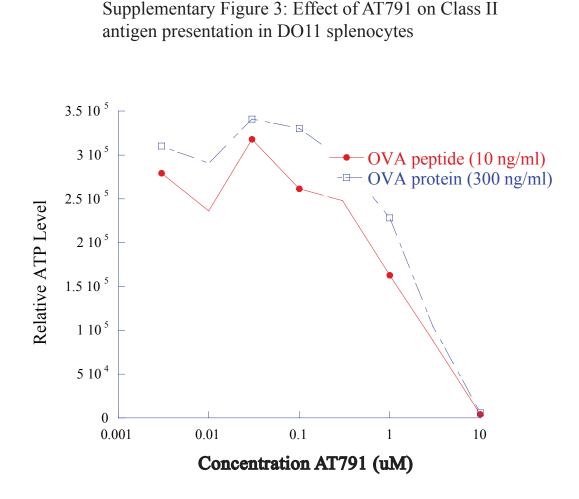
10nM bafilomycin



200nM AT791

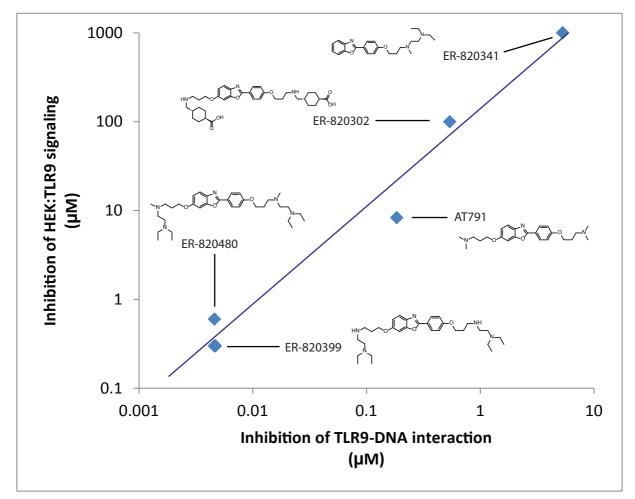
200nM E6446

Supplementary Figure 2: RAW264.7 cells were pre-loaded for 6 hours with dextrans conjugated to the pH-sensitive dyes FITC (green) and pHrodo (red). Next, cells were treated with the indicated compounds for one hour and visualized by confocal microscopy. Only bafilomycin caused an increase in pH, as indicated by a shift to green, caused by increased FITC fluorescence and decreased pHrodo fluorescence.



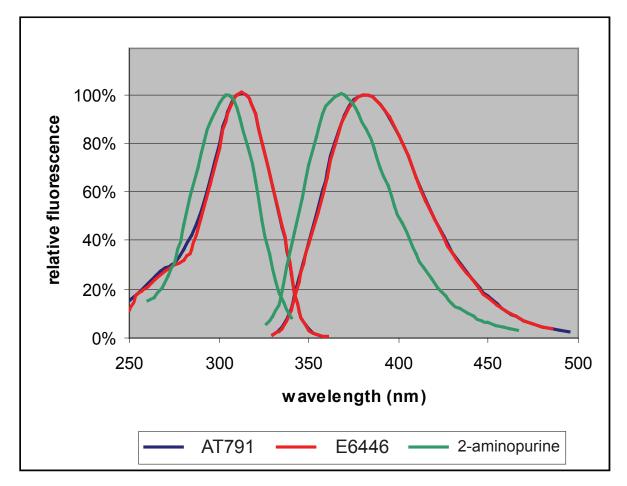
Supplementary Figure 3: DO11 mouse splenocytes were cultured with OVA peptide or protein for 2 days in the presence of the indicated concentrations of AT791. Two days later proliferation was assayed by ATP generation (ATPLite; Perkin Elmer).





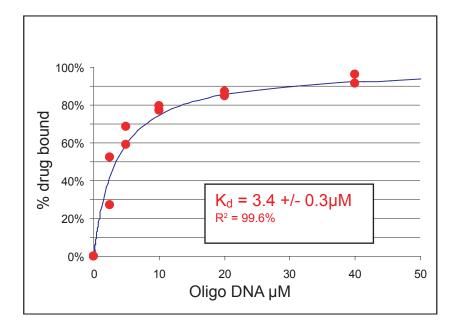
Supplementary Figure 4: AT791 and other antagonists obtained in the same high-throughput screen were assayed in the TLR9-DNA interaction assay (in vitro) and in the HEK:TLR9 NF- κ B reporter assay (cell-based). The plot shows the correlation between the in vitro and cell-based activities.

Supplementary Figure 5: Intrinsic fluorescence of AT791 and E6446



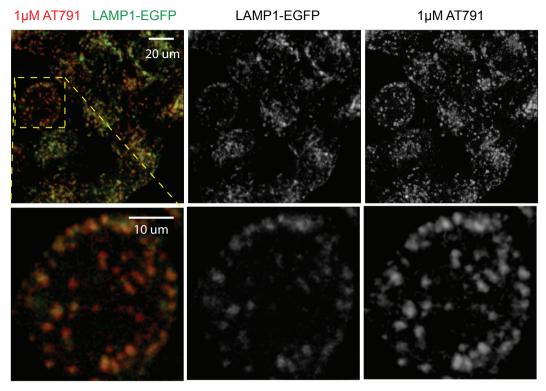
Supplementary Figure 5: Solutions of AT791, E6446 and 2-aminopurine were analyzed for fluorescence on a fluorescence spectrometer (Hitachi F-2000). The graph shows both the excitation and emission spectra. The spectra of AT791 and E6446 overlap almost completely, with peak excitation at 312nm and peak emission at 381nm. 2-aminopurine was found to have a fluorescence spectrum very similar to AT791 and E6446, and therefore used as a control in several experiments.

Supplementary Figure 6: Quantitation of AT791 - DNA interaction by equilibrium dialysis



Supplementary Figure 6: 200nM AT791 was added to both chambers of a plate-based equilibrium dialysis system (Pierce RED). 3x-2006 oligo (72nt; a 3x concatenated version of oligo CpG2006) was added at the indicated concentrations to one of the two chambers. After incubation for 4 hours at 37 °C, the amount of AT791 in each chamber was quantitated by mass spectrometry and the percentage of free versus bound compound in the DNA-containing chamber was calculated. The % bound was analyzed by non-linear regression analysis (GraphPad Prism) to fit to a one-site binding curve. Data shows results from two replicates, line represents fit to one-site binding curve as generated by Prism.

Supplementary Figure 7A: Co-localization of AT791 with the lysosomal marker Lamp-1

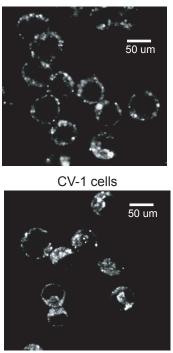


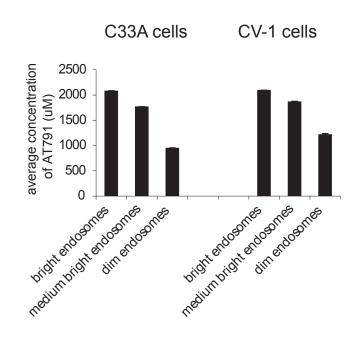
Localization of AT791 in HEK cells was visualized as shown in Figure 7, except that these HEK cells also expressed the lysosomal marker LAMP-1 fused to eGFP. Comparison of LAMP-1 and AT791 shows an overlap. AT791 on a glass slide. This analysis indicates that AT791 accumulates approximately 1,000-fold inside cells: from 1µM added to the culture media to

 $500 \sim 2000 \ \mu M$ inside vesicles.

Supplementary Figure 7B: Quantitation of AT791 accumulation in C33A and CV-1 cells

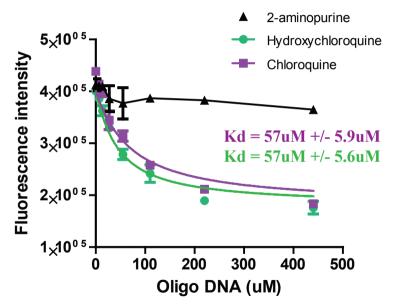
C33A cells





AT791 (1 μ M) was added to cultures of C33A and CV-1 cells and visualized by confocal microscopy using a 351nm laser. Intracellular AT791 concentrations were estimated by comparing fluorescence intensities in intracellular vesicles to a calibration curve generated by spotting different concentrations of AT791 on a glass slide. This analysis indicates that AT791 accumulates approximately 1,000-fold inside cells: from 1 μ M added to the culture media to 500 ~ 2000 μ M inside vesicles.

Supplementary Figure 8: Fluorescence spectroscopic analysis of DNA interaction with hydroxychloroquine and chloroquine



Fluorescence of hydroxychloroquine and chloroquine (5 μ M each) were quantitated at excitation 330nm and emission 375nm in pH7.2 buffer. CpG2006 oligo DNA was added at a range of concentrations as indicated and the change in intrinsic compound fluorescence was measured. As a control, 2-aminopurine was used, as it has a similar fluorescence spectrum. Non-linear regression analysis showed an excellent fit to a one-site binding curve with similar Kds of 57 μ M for both compounds.

Supplemental Data 1: detailed list of genes analyzed in Supplemental Figure 1 (see Supplemental Figure 1 for legend)

| | | e i for legend | | | | | Stimula | | | Compou | und Only | | | Stimulation an | nd Compound | |
|------------------------------|-----------------------|-----------------------|--|---------------------------------|---|--------------------------------------|----------------------|-------------------------|----------------------|------------------------------|----------------------|------------------------------|----------------------|--|----------------------|--|
| | | | Probe Set Description | | | a. () | | Medium Fold Change | | 46 vs. Medium Fold Change | 1.25 uM E64 | 46 vs. Medium Fold Change | | M E6446 vs. Medium Fold Change (Group | CpG + 1.25 t | M E6446 vs. Medium Fold Change (Group |
| Row 1418930 at | Notes | Symbol CXCL10 | Entrez Gene Name chemokine (C-X-C motif) ligand 10 | Location Extracellular Space | Type(s) | Drug(s) MDX-1100 | P-Value 6.96E-09 | (Group Means) 261.99 | P-Value 8.86E-02 | (Group Means) | P-Value 1.93E-01 | (Group Means) | P-Value 1.15E-04 | Means) 6.45 | P-Value 3.78E-03 | Means) |
| 1418930 at | | CALLIO | radical S-adenosyl methionine domain | extracential space | cytokine | MDX-1100 | 0.902-09 | 201.95 | 0.000-02 | 1.17 | 1.932-01 | 1.10 | 1.132-04 | 0.45 | 3.782.03 | 1.40 |
| 1436058 at | | RSAD2 | containing 2 chemokine (C-C motif) | Cytoplasm | enzyme | | 5.73E-06 | 60.51 | 4.81E-01 | 1.12 | 4.28E-01 | 1.13 | 2.16E-02 | 1.85 | 5.27E-01 | 1.12 |
| 1421578 at | | CCL4 CCL3L1/CCL3L3 | ligand 4 chemokine (C-C motif) ligand 3-like 1 | Extracellular Space | cytokine | | 3.47E-07 4.99E-08 | 59.21 | 6.73E-01 | 1.03 | 4.76E-01 5.69E-03 | 1.05 | 2.74E-02 5.38E-05 | 1.37 | 1.24E-01 2.49E-03 | 1.13 |
| 1419561_at | | CCL3L1/CCL3L3 | interferon-induced protein with | Extracellular space | cytokine | | 4.991-08 | 59.20 | 9.23E-01 | 1.01 | 5.69E-03 | 1.22 | 5.38E-U5 | 1.84 | 2.49E-03 | 1.36 |
| 1449025_at | | IFIT3 | tetratricopeptide repeats 3 | Cytoplasm | other | | 9.53E-07 | 47.83 | 2.02E-01 | 1.12 | 2.25E-01 | 1.11 | 2.14E-02 | 1.72 | 4.41E-02 | 1.26 |
| 1418191 at | | USP18 | ubiquitin specific peptidase 18 | Cytoplasm | peptidase | | 5.24E-07 | 44.57 | 2.51E-01 | 1.17 | 8.06E-02 | 1.14 | 1.01E-03 | 2.25 | 3.53E-02 | 1.23 |
| | | | interferon-induced protein with | | | | | | | | | | | | | |
| 1418293 at | | IFIT2 | tetratricopeptide repeats 2 nuclear factor of kappa | Cytoplasm | other | | 8.22E-07 | 43.86 | 4.24E-01 | 1.09 | 4.75E-01 | 1.09 | 4.08E-03 | 2.05 | 4.15E-02 | 1.28 |
| | | | light polypeptide gene enhancer in B-cells | | transcription | | | | | | | | | | | |
| 1448728_a_at 1431591 s at | Duplicate Gene Syr | NFKBIZ | inhibitor, zeta | Nucleus | regulator | | 1.00E-07 3.15E-07 | 38.33 38.14 | 6.55E-01 7.09E-01 | 1.03 | 9.58E-01 7.28E-01 | 1.00 | 2.51E-03 3.04E-03 | 1.55 1.85 | 3.78E-01 1.30E-01 | 0.96 |
| 1451905_a_at | | Mx1/Mx2 | myxovirus (influenza virus) resistance 1 | Nucleus | enzyme | | 8.78E-08 | 34.99 | 3.36E-01 | 1.07 | 3.60E-01 | 1.10 | 3.83E-04 | 1.89 | 3.75E-02 | 1.31 |
| | | | nuclear factor of kappa light polypeptide gene enhancer in B-cells | | transcription | | | | | | | | | | | |
| 1417483_at | Duplicate Gene Syr | NFKBIZ | inhibitor, zeta | Nucleus | regulator | | 5.88E-08 | 33.69 | 8.45E-01 | 1.01 | 7.26E-01 | 1.02 | 4.50E-05 | 2.53 | 1.57E-03 | 1.35 |
| 1419569_a_at | | ISG20 | interferon stimulated exonuclease gene 20kDa | Nucleus | enzyme | | 2.36E-08 | 33.56 | 4.90E-01 | 1.04 | 8.89E-01 | 1.00 | 2.36E-02 | 1.34 | 1.97E-01 | 1.07 |
| 1417601 at | | RGS1 | regulator of G-protein signaling 1 | Plasma Membrane | other | | 1.49E-06 | 25.95 | 8.46E-01 | 0.98 | 7.09E-01 | 1.03 | 7.88E-03 | 1.47 | 9.97E-02 | 1.16 |
| 1420549 at | | GBP2 | guanylate binding protein 2, interferon-inducible | Nucleus | other | | 4.45E-07 | 23.03 | 8.27E-01 | 1.02 | 3.79E-01 | 0.96 | 1.35E-02 | 1.49 | 9.69E-01 | 1.00 |
| 1450826 a at | | Saa3 | serum amyloid A 3 | unknown | other | | 9.97E-07 | 22.96 | 8.90E-02 | 1.09 | 6.36E-01 | 0.95 | 4.09E-05 | 3.02 | 5.52E-02 | 1.17 |
| 1449399_a_at | | IL1B | interleukin 1, beta | Extracellular Space | cytokine | IL-1 trap, canakinumab | 2.17E-07 | 21.71 | 7.98E-01 | 1.02 | 2.67E-01 | 0.95 | 1.00E-04 | 3.25 | 1.26E-02 | 1.24 |
| 1424339 at | | OASL | 2'-5'-oligoadenylate synthetase-like | Cytoplasm | enzyme | | 1.23E-06 | 20.57 | 6.76E-02 | 1.10 | 9.38E-01 | 1.00 | 3.29E-02 | 1.35 | 4.76E-01 | 1.05 |
| | | | CD40 molecule, TNF receptor superfamily | | transmembrane | SGN-40 (anti- | | | | | | | | | | |
| 1460415 a at | Duplicate Gene Syr | CD40 | member 5 | Plasma Membrane | receptor | huCD40 mAb) | 4.76E-08 | 18.35 | 9.36E-01 | 1.00 | 4.33E-01 | 0.98 | 3.50E-04 | 2.23 | 2.27E-01 | 1.05 |
| 1419004_s_at | | BCL2A1 | BCL2-related protein A1 serine (or cysteine) | Cytoplasm | other | | 2.64E-07 | 17.75 | 1.66E-01 | 1.09 | 7.42E-01 | 0.98 | 6.88E-04 | 2.41 | 1.55E-03 | 1.37 |
| 1424923_at | | Serpina3g (include | peptidase inhibitor, clade s A, member 3G | Extracellular Space | other transmembrane | | 4.86E-08 | 17.66 | 3.57E-01 | 1.03 | 4.22E-01 | 0.98 | 3.42E-04 | 1.76 | 1.39E-01 | 1.07 |
| 1416111 at | | CD83 | CD83 molecule | Plasma Membrane | receptor | | 6.16E-07 | 16.96 | 1.69E-01 | 1.09 | 7.39E-01 | 1.02 | 3.06E-05 | 3.11 | 6.58E-04 | 1.54 |
| | | | | | | | | | | | | | | | | |
| | | | | | | adalimumab, | | | | | | | | | | |
| | | | | | | etanercept, infliximab, | | | | | | | | | | |
| 1419607_at | | TNE | tumor necrosis factor | Extracellular Space | cytokine | CDP870, golimumab, thalidomide | 1.45E-06 | 16.72 | 8.54E-01 | 0.99 | 6.45E-01 | 0.97 | 1.99E-03 | 1.65 | 7.05E-01 | 1.02 |
| 1423555 a at | | IFI44 | interferon-induced protein 44 | Cytoplasm | other | chances in the | 3.70E-07 | 16.55 | 4.28E-01 | 1.08 | 5.71E-01 | 1.05 | 1.23E-02 | 1.44 | 2.16E-01 | 1.10 |
| 1418126 at | | CCL5 | chemokine (C-C motif) ligand 5 | Extracellular Space | cytokine | | 1.11E-07 | 16.07 | 6.82E-01 | 0.98 | 3.95E-01 | 0.96 | 2.26E-02 | 1.14 | 4.78E-01 | 0.98 |
| | | | CD40 molecule, TNF | | | | | | | | | | | | | |
| 1449473_s_at | Duplicate Gene Syr | CD40 | receptor superfamily member 5 interferon-induced | Plasma Membrane | transmembrane receptor | SGN-40 (anti- huCD40 mAb) | 2.64E-06 | 15.74 | 6.04E-01 | 0.97 | 8.06E-01 | 1.02 | 2.23E-04 | 2.28 | 9.88E-02 | 1.14 |
| 1421596 s at | Duplicate Gene Syr | IFI44L | protein 44-like | unknown | other | | 2.30E-07 | 15.60 | 5.26E-01 | 0.94 | 8.46E-01 | 0.99 | 1.14E-03 | 1.35 | 1.59E-01 | 1.13 |
| 1418580 at | | RTP4 | receptor (chemosensory) transporter protein 4 | Plasma Membrane | other | | 3.30E-06 | 15.56 | 4.65E-02 | 1.13 | 1.56E-01 | 1.11 | 2.78E-03 | 1.76 | 7.09E-02 | 1.12 |
| 1434380 at | | GBP7 | guanylate binding protein 7 | Cytoplasm | enzyme | | 4.73E-07 | 15.49 | 1.28E-01 | 1.08 | 2.85E-01 | 1.03 | 3.94E-02 | 1.23 | 9.56E-01 | 0.99 |
| 1449009 at | | Tgtp1/Tgtp2 | T cell specific GTPase 1 poly (ADP-ribose) polymerase family, | unknown | enzyme | | 1.12E-06 | 15.40 | 7.24E-01 | 1.02 | 2.60E-01 | 1.06 | 8.07E-03 | 1.38 | 2.26E-01 | 1.07 |
| 1426774 at | | PARP12 | member 12 interferon-induced | Nucleus | other | | 8.55E-06 | 15.02 | 8.07E-02 | 1.24 | 3.21E-01 | 1.13 | 6.75E-02 | 1.27 | 1.31E-01 | 1.30 |
| 1425917 at | Duplicate Gene Syr | IFI44L | protein 44-like | unknown | other | | 1.04E-06 | 14.57 | 4.12E-01 | 1.06 | 6.26E-01 | 0.98 | 2.67E-03 | 1.29 | 2.38E-01 | 1.12 |
| 1450971 at | Duplicate Gene Syr | GADD45B | growth arrest and DNA- damage-inducible, beta | Cytoplasm | other | | 3.16E-07 | 14.33 | 7.94E-01 | 0.98 | 7.57E-01 | 0.99 | 1.32E-02 | 1.37 | 2.11E-01 | 0.94 |
| 1420591_at | | GPR84 | G protein-coupled receptor 84 | Plasma Membrane | G-protein coupled receptor | | 6.10E-07 | 14.04 | 5.13E-01 | 0.95 | 9.65E-01 | 1.00 | 1.67E-03 | 3.39 | 3.88E-01 | 1.06 |
| 1449773_s_at | Duplicate Gene Syr | GADD458 | growth arrest and DNA- damage-inducible, beta | Cvtoplasm | other | | 4.04E-06 | 13.90 | 8.96E-01 | 0.99 | 3.28E-01 | 1.09 | 7.03E-03 | 1.52 | 5.22E-01 | 1.07 |
| 1417244 a at | | IRF7 | interferon regulatory factor 7 | Nucleus | transcription regulator | | 1.05E-06 | 13.59 | 3.81E-01 | 1.05 | 4.19E-01 | 1.06 | 2.78E-02 | 1.33 | 8.96E-01 | 1.01 |
| 1417185 at | | Ly6a (includes othe | lymphocyte antigen 6 e complex, locus A | Plasma Membrane | other | | 3.75E-07 | 13.14 | 3.69E-01 | 0.97 | 8.43E-01 | 1.01 | 1.46E-01 | 1.12 | 1.22E-01 | 1.05 |
| | | | immunity-related GTPase | e | | | 3.02E-06 | 10.00 | 6.83E-01 | | 9.43E-01 | | 2.86E-02 | | 6.88E-01 | |
| 1417793 at 1456212 x at | Duplicate Gene Syr | socsa | family M member 2 suppressor of cytokine signaling 3 | Cytoplasm | enzyme phosphatase | | 3.02E-06 | 13.08 | 6.83E-01 6.87E-01 | 0.96 | 9.43E-01 5.28E-01 | 0.99 | 2.86E-02 3.97E-03 | 1.26 | 6.88E-01 2.16E-01 | 1.05 |
| 1449363 at | | ATF3 | activating transcription factor 3 | Nucleus | transcription regulator | | 2.46E-06 | 12.95 | 2.45E-01 | 0.94 | 9.05E-02 | 1.13 | 4.07E-03 | 1.39 | 4.44E-03 | 1.31 |
| 1418392 a at | | GBP4 | guanylate binding protein 4 | Cytoplasm | enzyme | | 7.07E-07 | 12.55 | 3.88E-01 | 1.03 | 7.96E-01 | 1.01 | 3.88E-03 | 1.40 | 6.15E-01 | 1.07 |
| 1426276 at | | IFIH1 | interferon induced with helicase C domain 1 | Notiour | an=ma | | 2.22E-07 | 12.40 | 2.49E-01 | 1.08 | 6.73E-01 | 0.98 | 1.74E-03 | 1.31 | 2.29E-01 | 1.08 |
| 1426276 at 1421551_s_at | | IFIH1 Ifi202b | interferon activated gene 2028 | Nucleus | other | | 2.22E-07 3.93E-07 | 12.40 | 2.49E-01 1.84E-01 | 1.08 | 6.73E-01 5.64E-01 | 1.03 | 1.74E-03 3.96E-03 | 1.31 | 2.29E-01 8.52E-02 | 1.08 |
| | | | poly (ADP-ribose) polymerase family, | | | | | | | | | | | | | |
| 1451564_at | | PARP14 | member 14 interferon gamma | Cytoplasm | other | | 3.45E-06 | 11.88 | 1.95E-01 | 1.13 | 1.39E-01 | 1.16 | 4.25E-03 | 1.57 | 2.56E-02 | 1.27 |
| 1417141 at 1429947 a at | | lgtp ZBP1 | Z-DNA binding protein 1 | Cytoplasm | enzyme | | 3.61E-07 2.16E-06 | 11.84 | 9.43E-01 2.33E-01 | 0.94 | 5.95E-01 8.55E-01 | 1.02 | 6.31E-02 5.08E-02 | 1.17 | 2.46E-01 4.96E-01 | 0.95 |
| 1429947 a at 1455899 x at | Duplicate Gene Syr | | Z-DNA binding protein 1 suppressor of cytokine signaling 3 | Cytoplasm | other phosphatase | | 2.16E-06 1.51E-06 | 11.74 | 2.33E-01 9.46E-01 | 1.00 | 8.55E-01 8.59E-01 | 1.01 | 5.08E-02 9.97E-04 | 1.15 | 4.96E-01 1.28E-01 | 0.96 |
| 1455899_x_at 1416576 at | Duplicate Gene Syr | | suppressor of cytokine signaling 3 | Cytoplasm | phosphatase | | 4.22E-07 | 11.54 | 9.46E-01 6.54E-01 | 1.00 | 5.20E-01 | 1.02 | 9.97E-04 | 1.78 | 9.49E-01 | 1.12 |
| 1451426 at | | DHX58 | DEXH (Asp-Glu-X-His) box polypeptide 58 | Cytoplasm | enzyme | | 3.87E-06 | 10.64 | 5.43E-01 | 1.05 | 3.19E-01 | 1.08 | 4.53E-02 | 1.23 | 5.82E-01 | 1.04 |
| 1440501 | | CASDA | caspase 4, apoptosis- related cysteine | Complexe | | | 4.000 00 | 10.11 | 2.605.00 | 0.07 | F 1/5 04 | 0.00 | | 1.00 | 3 905 04 | |
| 1449591 at 1435331 at | Duplicate Geografica | CASP4 | peptidase interferon activated gene 204 | Cytoplasm Nucleus | peptidase transcription regulator | | 4.09E-07 1.19E-07 | 9.79 | 3.60E-01 9.33E-01 | 0.95 | 5.16E-01 2.82E-01 | 0.95 | 3.73E-04 1.04E-02 | 1.58 | 3.79E-01 3.31E-01 | 0.96 |
| | - apricance Grene Syr | | eukaryotic translation initiation factor 2-alpha | | - An a tot | | | 5.75 | 5-335-01 | 2.00 | 1.025-01 | 0.75 | | 1.10 | | 2.07 |
| 1422006_at | | EIF2AK2 | kinase 2 2'-5'-oligoadenylate | Cytoplasm | kinase | | 4.82E-07 | 9.49 | 6.53E-01 | 1.01 | 3.07E-01 | 0.95 | 1.05E-01 | 1.08 | 3.12E-01 | 1.03 |
| 1424775 at | | OAS1 | synthetase 1, 40/46kDa helicase with zinc finger | Cytoplasm | enzyme | | 3.14E-06 | 9.05 | 7.14E-01 | 1.02 | 2.37E-01 | 1.09 | 1.02E-02 | 1.22 | 3.71E-01 | 1.07 |
| 1435454 a at | | HELZ2 | 2, transcriptional coactivator | Nucleus | transcription regulator | | 3.16E-06 | 8.91 | 8.16E-01 | 1.02 | 5.23E-01 | 0.94 | 8.06E-03 | 1.37 | 1.56E-01 | 1.14 |
| 1450033 a at | Duplicate Gene Syr | STAT1 | signal transducer and activator of transcription 1, 91kDa | Nuclear | transcription regulator | | 3.45E-07 | 8.84 | 6.78E-01 | 1.03 | 1.75E-01 | 1.06 | 5.89E-03 | 1.30 | 4.63E-01 | 1.04 |
| 15 5 cculore | Supricate Gene Syr | 31A11 | 1, 91kDa signal transducer and activator of transcription | Nucleus | transcription | | 5.45E-U/ | 0.84 | 0.762-01 | 1.03 | 1.736-01 | 1.06 | 3.69E-U3 | 1.30 | 4.03E-01 | 1.04 |
| | Duplicate Gene Syr | | 1, 91kDa chemokine (C-C motif) | Nucleus | regulator G-protein coupled | | 2.78E-05 | 8.58 | 4.90E-01 | 1.05 | 4.47E-01 | 1.07 | 7.38E-03 | 1.24 | 1.44E-01 | 1.11 |
| 1427736_a_at | | CCRL2 | receptor-like 2 immunity-related GTPase | Plasma Membrane | receptor | | 2.35E-06 | 7.83 | 2.11E-01 | 1.08 | 1.33E-01 | 1.11 | 6.06E-04 | 1.93 | 1.95E-01 | 1.09 |
| 1418825 at | | IRGM | family, M tripartite motif- | Cytoplasm | other | l | 5.66E-07 | 7.77 | 1.31E-01 | 0.97 | 5.07E-02 | 1.05 | 5.12E-04 | 1.19 | 5.73E-01 | 0.98 |
| | o | ******* | | | | | 0.000.000 | | | | | | | | 0.047.07 | |
| 1451860 a at | Duplicate Gene Syr | Trim30a/Trim30d | containing 30A tripartite motif- containing 30A | Cytoplasm Cytoplasm | other | | 9.67E-07 2.04E-06 | 7.76 | 6.55E-02 7.72E-01 | 1.06 | 5.25E-02 4.08E-01 | 0.94 | 2.17E-03 5.91E-01 | 1.36 | 8.74E-03 1.64E-01 | 0.89 |

| | | | | | | | Stimulat | ion Only | | Compou | und Only | | | Stimulation a | nd Compound | |
|------------------------------|--|------------------|--|----------------------------------|---|--------------------------|----------------------|--------------|----------------------|---------------|----------------------|--------------|----------------------|---------------------|----------------------|--------------------|
| (| i | i | Probe Set Description signal transducer and | i | i | i | CpG vs. | Medium | 0.25 uM E64 | 46 vs. Medium | 1.25 uM E644 | 6 vs. Medium | CpG + 0.25 u | aM E6446 vs. Medium | CpG + 1.25 u | M E6446 vs. Medium |
| 1450034 at | Duplicate Gene Syr | STAT1 | activator of transcription 1, 91kDa | Nucleus | transcription regulator | | 1.14E-06 | 7.43 | 8.56E-01 | 1.01 | 6.71E-01 | 0.98 | 6.57E-03 | 1.21 | 7.13E-01 | 1.02 |
| 1417292 at | | lfi47 | interferon gamma inducible protein 47 | Cytoplasm | other | | 2.92E-08 | 6.87 | 8.51E-01 | 1.00 | 6.71E-02 | 1.06 | 1.21E-02 | 1.15 | 5.69E-02 | 1.04 |
| 1425065_at | | OAS2 | 2'-5'-oligoadenylate synthetase 2, 69/71kDa | Cytoplasm | enzyme C anatoin anoslad | | 4.48E-07 | 6.79 | 3.86E-01 | 1.07 | 9.94E-01 | 1.00 | 1.07E-01 | 1.13 | 8.15E-01 | 0.99 |
| 1422953 at | | FPR2 | formyl peptide receptor 2 poly (ADP-ribose) | Plasma Membrane | G-protein coupled receptor | | 4.32E-06 | 6.71 | 9.34E-01 | 1.01 | 2.14E-01 | 0.91 | 6.51E-04 | 1.94 | 7.83E-01 | 0.98 |
| 1416897 at | | PARP9 | polymerase family, member 9 | Nucleus | other | | 1.63E-06 | 6.58 | 1.66E-01 | 1.08 | 2.76E-01 | 1.07 | 8.74E-03 | 1.20 | 6.16E-02 | 1.11 |
| 1426716 at | | TDRD7 | tudor domain containing 7 | Cytoplasm | other | | 6.65E-06 | 6.56 | 8.32E-01 | 1.02 | 9.55E-01 | 1.00 | 1.19E-01 | 1.11 | 2.00E-01 | 1.09 |
| | | (1 400) 00 | sphingomyelin phosphodiesterase, acid- | | | | 1.36E-07 | | 0.005.04 | | 1.63E-02 | | 4.39E-04 | | 3.17E-01 | |
| 1417300 at 1452178 at | | SMPDL3B | like 3B zinc finger, NFX1-type | Extracellular Space | enzyme transcription | | 1.79E-05 | 6.54 6.49 | 2.70E-01 1.00E+00 | 0.97 | 6.56E-02 | 0.91 | 4.39E-04 1.13E-01 | 2.05 | 3.02E-01 | 1.08 |
| 1427091 at | | ZNFX1 | containing 1 C-type lectin domain | Nucleus | regulator | | 8.79E-06 | 6.45 | 6.89E-01 | 1.03 | 7.39E-01 | 1.03 | 5.80E-02 | 1.18 | 2.64E-01 | 1.12 |
| 1420330_at | Duplicate Gene Syr | CLEC4E | family 4, member E C-type lectin domain | Plasma Membrane | other | | 2.97E-06 | 6.34 | 6.52E-02 | 1.15 | 2.63E-01 | 1.06 | 2.28E-05 | 2.90 | 4.67E-03 | 1.26 |
| 1420331 at | Duplicate Gene Syr | CLEC4E | family 4, member E chemokine (C-X-C motif) | Plasma Membrane | other | | 1.19E-06 | 6.33 | 9.03E-01 | 0.99 | 1.98E-01 | 0.96 | 4.96E-06 | 2.42 | 6.90E-03 | 1.25 |
| 1449195 s at | Duplicate Gene Syr | CXCL16 | ligand 16 CASP8 and FADD-like | Extracellular Space | cytokine | | 9.10E-06 3.63E-06 | 6.31 | 4.00E-01 2.61E-01 | 0.92 | 8.04E-01 4.13E-02 | 0.98 | 4.69E-06 5.22E-02 | 2.38 | 5.66E-04 6.36E-01 | 0.97 |
| 1449317_at 1419026 at | Duplicate Gene Syr | DAXX | apoptosis regulator death-domain associated protein | Nucleus | transcription regulator | | 3.63E-06 | 6.19 | 7.90E-01 | 1.01 | 9.43E-02 | 1.00 | 5.22E-02 1.06E-01 | 1.17 | 6.53E-01 | 1.02 |
| 1415020 at | | DRAA | nuclear factor of kappa light polypeptide gene | Nucleus | regulator | | 1.472*07 | 0.19 | 7.502-01 | 1.01 | 5.432-01 | 1.00 | 1.062-01 | 1.11 | 0.552/01 | 1.02 |
| 1448306 at | Duplicate Gene Syr | NFKBIA | enhancer in B-cells inhibitor, alpha | Cytoplasm | transcription regulator | | 1.71E-06 | 6.05 | 8.85E-01 | 0.99 | 1.44E-01 | 0.93 | 1.14E-04 | 2.62 | 9.54E-01 | 1.00 |
| 1448757_at | | PML | promyelocytic leukemia | Nucleus | transcription regulator | arsenic trioxide | 3.52E-07 | 6.02 | 8.09E-02 | 1.07 | 2.33E-01 | 1.09 | 2.19E-01 | 1.07 | 2.54E-01 | 1.05 |
| 1436172 at | Duplicate Gene Syr | Gm20559 | predicted gene, 20559 fascin homolog 1, actin- | unknown | other | | 2.11E-06 | 5.95 | 9.19E-02 | 1.08 | 4.07E-01 | 1.05 | 3.12E-02 | 1.19 | 3.45E-02 | 1.08 |
| 1416514 a at | | FSCN1 | bundling protein (Strongylocentrotus purpuratus) | Cytoplasm | other | | 5.35E-06 | 5.84 | 9.49E-01 | 1.00 | 3.67E-01 | 0.93 | 3.60E-02 | 1.35 | 2.37E-01 | 1.16 |
| 1434484 at | | 1100001G20Rik | RIKEN cDNA 1100001G20 gene | Extracellular Space | | | 2.18E-09 | 5.81 | 3.91E-01 | 0.96 | 1.54E-01 | 1.05 | 4.23E-03 | 1.33 | 1.21E-03 | 1.10 |
| 1451655 at | | SLFN13 | schlafen family member 13 | Nucleus | enzyme | | 6.17E-07 | 5.67 | 5.81E-01 | 0.97 | 5.46E-01 | 0.97 | 1.46E-01 | 1.10 | 1.98E-01 | 0.95 |
| | | | tumor necrosis factor (ligand) superfamily, | | | | | | | | | | | | | |
| 1422924 at | | Tnfsf9 | member 9 zinc finger with UFM1- roacific paptidare | Plasma Membrane | other | | 1.12E-06 | 5.60 | 4.78E-01 | 0.97 | 6.91E-01 | 1.03 | 1.53E-03 | 1.55 | 2.42E-01 | 1.07 |
| 1436899 at | | ZUFSP | specific peptidase domain tyrosylprotein | unknown | other | | 6.93E-08 | 5.40 | 3.96E-03 | 1.09 | 1.75E-01 | 1.05 | 1.67E-03 | 1.15 | 1.13E-02 | 1.07 |
| 1421733_a_at 1416010 a at | Duplicate Gene Syr | TPST1 EHD1 | sulfotransferase 1 EH-domain containing 1 | Cytoplasm Cytoplasm | enzyme other | | 5.55E-06 1.02E-06 | 5.32 5.17 | 5.33E-01 3.04E-01 | 0.97 | 9.88E-01 8.56E-01 | 1.00 | 9.14E-01 1.51E-04 | 1.00 | 7.33E-01 2.36E-02 | 1.02 |
| 1424617_at | | IFI35 | interferon-induced protein 35 | Nucleus | other | | 3.56E-06 | 5.15 | 5.57E-01 | 1.04 | 6.64E-01 | 1.02 | 1.35E-01 | 1.12 | 5.61E-01 | 0.97 |
| 1417961_a_at | Duplicate Gene Syr | Trim30a/Trim30d | tripartite motif- containing 30A MARCKS-like 1 | Cytoplasm | other | | 2.09E-06 | 5.13 | 7.41E-01 | 1.02 | 3.34E-01 | 0.95 | 7.09E-01 | 0.98 | 2.94E-02 | 0.84 |
| 1437226 x at 1423466_at | Duplicate Gene Syr | MARCKSL1 | MARCKS-like 1 chemokine (C-C motif) receptor 7 | Cytoplasm Plasma Membrane | other G-protein coupled receptor | | 6.37E-06 3.90E-07 | 5.12 | 5.63E-01 6.52E-02 | 0.97 | 2.88E-01 2.48E-02 | 0.91 | 7.98E-04 1.46E-02 | 1.79 | 4.74E-01 8.29E-02 | 0.97 |
| 1423466_at 1454169 a at | Duplicate Gene Syr | Epsti1 | epithelial stromal interaction 1 (breast) | unknown | other | | 5.35E-06 | 5.03 | 1.46E-01 | 0.92 | 8.22E-01 | 1.01 | 7.69E-02 | 1.10 | 5.77E-01 | 0.97 |
| 1434109 a at | | SLFN12L | schlafen family member 12-like | unknown | enzyme | | 4.16E-06 | 4.99 | 3.60E-02 | 1.15 | 6.69E-01 | 1.01 | 2.58E-01 | 1.16 | 4.68E-02 | 1.17 |
| 1449858_at | Duplicate Gene Syr | CD86 | CD86 molecule | Plasma Membrane | transmembrane receptor | abatacept, belatacept | 7.42E-07 | 4.96 | 1.30E-01 | 1.07 | 8.57E-01 | 1.00 | 1.82E-01 | 1.08 | 2.99E-01 | 1.03 |
| 1448175 at | Duplicate Gene Syr | | EH-domain containing 1 CASP8 and FADD-like | Cytoplasm | other | | 9.28E-07 | 4.95 | 7.28E-01 | 1.03 | 6.47E-01 | 0.98 | 5.17E-05 | 1.73 | 6.02E-01 | 1.03 |
| 1425686 at 1422704 at | Duplicate Gene Syr | GK | apoptosis regulator glycerol kinase | Cytoplasm Cytoplasm | other kinase | | 1.22E-05 4.28E-06 | 4.92 4.91 | 7.96E-01 5.90E-01 | 1.02 | 2.88E-01 4.02E-01 | 0.93 0.96 | 2.29E-01 3.72E-03 | 1.12 1.27 | 8.18E-01 3.55E-02 | 1.01 1.18 |
| 1421285 at | | PIK3AP1 | phosphoinositide-3- kinase adaptor protein 1 | Cytoplasm | other | | 5.36E-06 | 4.90 | 6.43E-01 | 1.05 | 8.54E-01 | 1.02 | 1.42E-01 | 1.07 | 2.01E-01 | 1.07 |
| | | | tumor necrosis factor, | | | | | | | | | | | | | |
| 1438855_x_at 1415922 s at | Duplicate Gene Syn Duplicate Gene Syn | | alpha-induced protein 2 MARCKS-like 1 | Extracellular Space Cytoplasm | other other | | 2.20E-05 1.51E-04 | 4.86 4.85 | 8.46E-01 9.29E-01 | 1.01 0.99 | 9.09E-01 7.34E-01 | 1.01 0.96 | 5.13E-04 3.66E-03 | 2.07 1.87 | 7.96E-02 7.46E-01 | 1.18 0.96 |
| 1423543_at | | SWAP70 | SWAP switching B-cell complex 70kDa subunit | Cytoplasm | other | | 1.45E-07 | 4.83 | 2.63E-01 | 1.05 | 7.13E-01 | 0.97 | 4.36E-04 | 1.20 | 1.04E-01 | 1.08 |
| | | | Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy- | | transcription | | | | | | | | | | | |
| 1421267_a_at | Duplicate Gene Syr | CITED2 | terminal domain, 2 | Nucleus | regulator | | 1.12E-05 | 4.83 | 8.57E-01 | 1.01 | 7.86E-01 | 0.98 | 7.99E-01 | 0.99 | 8.16E-01 | 1.01 |
| 1417932_at | | IL18 | interleukin 18 (interferon- gamma-inducing factor) | Extracellular Space | cytokine | | 8.62E-06 | 4.82 | 8.65E-01 | 0.99 | 6.03E-01 | 0.97 | 3.03E-01 | 1.09 | 3.03E-01 | 0.97 |
| 1455581 x at | Duplicate Gene Syr | Gm20559 | predicted gene, 20559 Fc fragment of IgG, high | unknown | other | | 2.96E-05 | 4.79 | 5.89E-01 | 1.04 | 7.77E-01 | 0.98 | 1.63E-01 | 1.16 | 4.48E-01 | 1.05 |
| 1417876 at | | FCGR1A | affinity Ia, receptor (CD64) | Plasma Membrane | transmembrane receptor | | 1.16E-06 | 4.77 | 6.20E-01 | 1.01 | 9.57E-01 | 1.00 | 2.50E-01 | 0.97 | 8.19E-01 | 1.00 |
| | | | nuclear factor of kappa light polypeptide gene enhancer in B-cells | | transcription | | | | | | | | | | | |
| 1449731_s_at | Duplicate Gene Syr | NFKBIA | inhibitor, alpha intercellular adhesion | Cytoplasm | regulator transmembrane | | 2.29E-06 | 4.76 | 6.31E-01 | 0.97 | 5.66E-01 | 0.97 | 2.53E-04 | 2.43 | 4.66E-02 | 1.12 |
| 1424067 at 1416011 x at | Duplicate Gene Syr | ICAM1 EHD1 | molecule 1 EH-domain containing 1 | Plasma Membrane Cytoplasm | receptor other | | 1.91E-06 2.56E-07 | 4.76 4.74 | 6.85E-02 9.60E-01 | 1.10 | 2.25E-01 3.85E-01 | 1.07 | 4.63E-05 2.05E-05 | 2.14 1.69 | 1.62E-01 3.75E-01 | 1.07 |
| 1418718 at | Duplicate Gene Syr | CXCL16 | chemokine (C-X-C motif) ligand 16 | Extracellular Space | | | 2.73E-05 | 4.74 | 9.41E-01 | 1.00 | 5.73E-01 | 0.96 | 8.49E-04 | 1.79 | 3.56E-01 | 1.08 |
| 1420499 at | | GCH1 | GTP cyclohydrolase 1 lectin, galactoside- | Cytoplasm | enzyme | | 5.47E-06 | 4.73 | 2.91E-01 | 1.08 | 4.05E-01 | 1.06 | 1.77E-02 | 1.30 | 2.18E-01 | 1.08 |
| 1448380_at | | LGALS38P | binding, soluble, 3 binding protein | Plasma Membrane | transmembrane receptor | | 2.14E-06 | 4.72 | 6.76E-01 | 1.02 | 6.82E-01 | 0.98 | 1.13E-01 | 1.08 | 7.78E-01 | 0.99 |
| 1416273_at | Duplicate Gene Syr | TNFAIP2 | tumor necrosis factor, alpha-induced protein 2 | Extracellular Space | other | | 5.85E-07 | 4.68 | 2.94E-01 | 1.06 | 1.25E-01 | 1.06 | 1.06E-04 | 1.88 | 2.34E-03 | 1.21 |
| 1418077 at | Duplicate Gene Syr | | tripartite motif containing 21 | | enzyme | | 1.88E-07 | 4.67 | 5.02E-01 | 1.04 | 3.57E-01 | 1.03 | 1.61E-01 | 1.06 | 4.43E-04 | 1.07 |
| 1417409 at | Duplicate Gene Syr | JUN | jun proto-oncogene | Nucleus | transcription regulator | | 5.86E-06 | 4.66 | 7.07E-01 | 0.99 | 9.67E-01 | 1.00 | 2.86E-01 | 1.09 | 4.83E-01 | 1.03 |
| 1420697_at | | SLC15A3 | solute carrier family 15, member 3 DNA-damage regulated | Cytoplasm | transporter | | 2.10E-06 | 4.62 | 5.85E-01 | 0.98 | 9.96E-01 | 1.00 | 1.20E-02 | 1.37 | 4.86E-02 | 1.09 |
| 1424524 at | | DRAM1 | DNA-damage regulated autophagy modulator 1 tripartite motif containing | Cytoplasm | other | | 1.76E-06 | 4.61 | 3.09E-01 | 0.96 | 7.09E-01 | 0.96 | 6.44E-05 | 1.49 | 2.22E-01 | 1.07 |
| 1448940 at | Duplicate Gene Syr | TRIM21 | 21 Epstein-Barr virus | Nucleus | enzyme | | 1.96E-05 | 4.60 | 7.28E-01 | 0.97 | 9.42E-01 | 1.00 | 8.98E-01 | 0.99 | 9.31E-01 | 0.99 |
| 1449222_at | | EBI3 | induced 3 epithelial stromal | Extracellular Space | cytokine | | 1.79E-06 | 4.60 | 3.42E-01 | 0.98 | 2.92E-01 | 0.96 | 4.37E-03 | 1.21 | 7.21E-01 | 0.99 |
| 1452087 at 1450165 at | Duplicate Gene Syr | Epsti1 Slfn2 | interaction 1 (breast) schlafen 2 bone marrow stromal cell | unknown Cytoplasm | other other | | 4.80E-05 5.74E-07 | 4.60 4.55 | 2.33E-01 9.12E-01 | 0.91 1.00 | 5.04E-02 8.18E-01 | 0.90 | 7.55E-02 2.84E-03 | 1.09 1.36 | 5.59E-01 1.43E-01 | 0.96 0.95 |
| 1424921 at | | BST2 | bone marrow stromal cell antigen 2 5'-nucleotidase, cytosolic | Plasma Membrane | other | | 7.97E-05 | 4.41 | 4.78E-01 | 0.93 | 3.52E-01 | 0.94 | 3.14E-01 | 1.07 | 6.28E-01 | 1.03 |
| 1451050 at | | NTSC3A | IIIA TRAF-type zinc finger | Cytoplasm | phosphatase | | 5.30E-05 | 4.37 | 8.98E-01 | 0.99 | 6.12E-01 | 0.97 | 1.28E-01 | 1.07 | 1.20E-01 | 1.09 |
| 1428346_at | | TRAFD1 | domain containing 1 adenosine deaminase, | unknown | other | | 7.31E-06 | 4.20 | 4.58E-01 | 1.04 | 7.50E-01 | 1.02 | 9.77E-02 | 1.10 | 2.27E-01 | 1.06 |
| 1425405 a at | | ADAR | RNA-specific nicotinamide | Nucleus | enzyme | | 1.08E-07 | 4.20 | 5.52E-01 | 1.03 | 8.17E-01 | 1.01 | 7.81E-02 | 1.10 | 6.35E-01 | 1.02 |
| 1417190 at | | NAMPT RCI 2L1 | phosphoribosyltransferas e RCI 2-like 1 | Extracellular Space | | | 3.81E-07 1.42E-06 | 4.19 | 6.55E-01 | 1.01 | 8.54E-02 | 1.05 | 1.70E-03 | 1.13 | 1.27E-02 | 1.10 |
| 1420888 at | | BCL2L1 | BCL2-like 1 v-ets erythroblastosis virus E26 opcogene | Cytoplasm | other transcription | | 1.42E-06 | 4.13 | 6.21E-01 | 1.02 | 7.72E-01 | 0.99 | 3.23E-01 | 0.95 | 5.14E-02 | 0.91 |
| 1416268_at | | ETS2 | virus E26 oncogene homolog 2 (avian) Cbp/p300-interacting | Nucleus | transcription regulator | | 8.23E-06 | 4.08 | 3.03E-01 | 0.94 | 1.51E-01 | 0.87 | 2.73E-02 | 1.19 | 6.02E-01 | 1.03 |
| | | | transactivator, with Glu/Asp-rich carboxy- | | transcription | | | | | | | | | | | |
| 1452207 at | Duplicate Gene Syr | | terminal domain, 2 | Nucleus | regulator transmembrane | abatacept, | 3.78E-07 | 4.05 | 5.72E-01 | 0.98 | 2.31E-01 | 0.97 | 2.16E-01 | 0.97 | 8.47E-01 | 1.01 |
| 1420404 at | Duplicate Gene Syr | CD86 | CD86 molecule | Plasma Membrane | receptor transcription | belatacept | 1.49E-05 | 4.05 | 1.99E-01 | 1.08 | 5.69E-01 | 0.97 | 1.63E-01 | 1.12 | 8.83E-01 | 1.01 |
| 1418635_at | Duplicate Gene Syr | ETV3 DUSP16 | ets variant 3 dual specificity | Nucleus | regulator | | 2.92E-07 | 3.97 | 2.94E-02 | 1.09 | 1.05E-01 | 1.10 | 3.22E-04 5.43E-03 | 1.26 | 5.23E-03 | 1.11 |
| 1418401 a at 1448694 at | Duplicate Gene Syr | JUSP16 | phosphatase 16 jun proto-oncogene | Nucleus Nucleus | phosphatase transcription regulator | | 8.67E-06 6.44E-07 | 3.96 | 9.48E-01 3.76E-01 | 0.96 | 7.18E-01 9.31E-01 | 1.03 | 5.43E-03 8.57E-01 | 0.99 | 8.12E-02 5.94E-02 | 1.13 |
| 1448094 at | Duplicate Gene Syr | TOR1AIP2 | torsin A interacting protein 2 | Cytoplasm | other | | 1.19E-06 | 3.87 | 9.07E-01 | 1.00 | 7.50E-02 | 0.92 | 1.85E-01 | 1.04 | 9.69E-02 | 1.09 |
| 1448958_at 1418637 at | Duplicate Gene Syr | ETV3 | ets variant 3 | Nucleus | transcription regulator | | 9.94E-06 | 3.84 | 9.07E-01 4.09E-01 | 0.96 | 4.37E-02 | 0.92 | 3.66E-02 | 1.04 | 6.73E-02 | 1.00 |
| | , and deale Syl | | polyribonucleotide | | | | | | | | | | | | | |
| 1452676 a at | | PNPT1 | nucleotidyltransferase 1 CASP8 and FADD-like | Cytoplasm | enzyme | | 3.38E-06 | 3.79 | 2.73E-01 | 0.95 | 6.19E-01 | 1.03 | 5.52E-01 | 1.04 | 8.54E-01 | 1.01 |
| 1424996 at | Duplicate Gene Syr | CFLAR | apoptosis regulator | Cytoplasm | other | | 3.19E-07 | 3.78 | 6.72E-01 | 0.96 | 3.06E-01 | 0.95 | 3.59E-02 | 1.13 | 5.26E-01 | 1.03 |
| 1421098 at | | STAP1 | signal transducing adaptor family member 1 | Cytoplasm | other transcription | | 8.60E-06 | 3.74 | 4.26E-01 | 1.04 | 7.73E-01 | 0.98 | 1.42E-02 | 1.23 | 1.92E-01 | 1.09 |
| 1418133_at 1435458 at | Duplicate Gene Syr | BCL3 PIM1 | B-cell CLL/lymphoma 3 pim-1 oncogene | Nucleus Cytoplasm | regulator kinase | | 4.77E-06 3.60E-07 | 3.70 3.70 | 5.35E-01 9.48E-01 | 1.02 | 4.20E-01 6.29E-01 | 1.03 | 4.02E-04 4.63E-04 | 1.65 | 1.12E-01 1.89E-02 | 1.11 |
| | | | nuclear factor of kappa light polypeptide gene | | | | | | | | | | | | | |
| 1425902_a_at | | NFKB2 | enhancer in B-cells 2 (p49/p100) | Nucleus | transcription regulator | | 5.87E-06 | 3.68 | 8.08E-01 | 1.01 | 7.59E-01 | 0.98 | 2.49E-04 | 1.63 | 4.77E-02 | 1.12 |
| | | | | | | | | | | | | | | | | |

| | | | | | | | Stimula | ion Only Medium | | Compos 46 vs. Medium | und Only | 46 vs. Medium | | Stimulation : aM E6446 vs. Medium | and Compound | M E6446 vs. Medium |
|---|--|---|---|--|--|--|--|--------------------------------------|--|------------------------------|--|--------------------------------------|--|--------------------------------------|--|------------------------------|
| 1435526 at | Duplicate Gene Svr | | Probe Set Description torsin A interacting protein 2 | Cytoplasm | other | İ | 1.79E-04 | 3.64 | 4.77E-01 | 1.08 | 6.44E-01 | 1.05 | 4.75E-01 | 1.09 | 3.27E-01 | 1.14 |
| 1435526 at | Duplicate Gene Syr | | C-type lectin domain family 4, member A | Plasma Membrane | transmembrane receptor | | 1.79E-04 | 3.64 | 4.77E-01 5.95E-01 | 0.97 | 2.45E-01 | 0.90 | 4.75E-01 2.18E-01 | 1.09 | 7.13E-02 | 0.87 |
| | | | complement component | | G-protein coupled | | | | | | | | | | | |
| 1419482_at | Duplicate Gene Syr | CSARI | 3a receptor 1 solute carrier family 25 (mitochondrial carrier: | Plasma Membrane | receptor | | 3.94E-04 | 3.62 | 6.26E-01 | 1.06 | 9.40E-01 | 0.99 | 1.93E-01 | 1.21 | 8.68E-01 | 1.02 |
| 1452653_at 1422141 s at | | SLC25A22 | glutamate), member 22 | Cytoplasm | transporter | | 2.63E-05 3.96E-07 | 3.60 3.59 | 4.36E-01 9.94E-01 | 1.04 | 9.65E-01 1.26E-03 | 1.00 | 5.84E-01 6.03E-01 | 1.02 0.98 | 6.09E-01 9.10E-01 | 0.98 |
| 1423954_at | | C3 | complement component 3 | Extracellular Space | peptidase | | 1.65E-08 | 3.51 | 1.41E-01 | 1.08 | 1.81E-01 | 0.97 | 4.36E-04 | 1.55 | 2.17E-02 | 1.14 |
| | | | MIT, microtubule interacting and transport, | | | | | | | | | | | | | |
| 1426133_a_at 1426112_a_at | | MITD1 CD72 | domain containing 1 CD72 molecule | unknown Plasma Membrane | other transmembrane receptor | | 1.41E-05 1.18E-06 | 3.51 | 4.33E-01 4.64E-02 | 1.07 | 2.37E-01 9.83E-01 | 1.06 | 1.88E-01 5.96E-02 | 1.08 | 7.13E-02 1.61E-01 | 1.12 |
| 1428112 a at | Duplicate Gene Syr | Ifi204 (includes oth | interferon activated gene 204 | Nucleus | transcription regulator | | 5.12E-06 | 3.45 | 9.33E-01 | 1.00 | 4.85E-01 | 1.03 | 1.61E-01 | 1.07 | 5.02E-01 | 1.04 |
| 1451567 a at | Duplicate Gene Syr | Ifi204 (includes oth | interferon activated gene 204 N-myc (and STAT) | Nucleus | transcription regulator transcription | | 1.80E-06 | 3.40 | 7.42E-01 | 0.99 | 8.04E-01 | 0.99 | 8.66E-01 | 1.01 | 6.37E-01 | 1.02 |
| 1425719 a at | | NMI | interactor membrane-spanning 4- | Cytoplasm | regulator | | 5.12E-06 | 3.39 | 2.97E-01 | 1.02 | 8.99E-01 | 1.00 | 4.12E-02 | 1.10 | 1.37E-02 | 1.11 |
| 1420671 x at | Duplicate Gene Syr | Ms4a4b (includes o | domains, subfamily A, member 48 | Plasma Membrane | other | | 1.15E-08 2.38E-07 | 3.37 | 2.37E-01 | 1.04 | 5.91E-03 | 0.97 | 2.38E-02 | 1.12 | 4.03E-02 | 1.03 |
| 1427511 at 1423006 at | Duplicate Gene Syr | PIM1 | pim-1 oncogene transporter 1, ATP- | Cytoplasm | kinase | | 2.38E-07 1.13E-05 | 3.37 3.36 | 7.90E-01 5.38E-01 | 1.02 | 3.19E-01 7.56E-01 | 1.08 0.98 | 1.67E-04 7.15E-03 | 1.37 1.23 | 6.39E-01 | 1.09 0.97 |
| 1416016_at | | TAP1 | binding cassette, sub- family B (MDR/TAP) | Cytoplasm | transporter | | 1.65E-05 | 3.36 | 3.63E-01 | 1.05 | 3.59E-01 | 1.06 | 5.80E-02 | 1.17 | 2.38E-01 | 1.07 |
| 1435792 at | | Csprs (includes oth | component of Sp100-rs | Plasma Membrane | G-protein coupled receptor | | 2.24E-06 | 3.35 | 2.01E-01 | 1.05 | 4.12E-01 | 1.04 | 4.28E-01 | 1.05 | 1.16E-01 | 1.12 |
| 1451160 s at | | Pvr | poliovirus receptor torsin A interacting | Plasma Membrane | other | | 5.09E-06 | 3.34 | 8.69E-02 | 1.06 | 5.65E-01 | 0.99 | 4.44E-03 | 1.15 | 3.88E-01 | 1.04 |
| 1418115_s_at 1452925 a at | Duplicate Gene Syr | TOR1AIP2 | protein 2 membrane-associated ring finger (C3HC4) 5 | Cytoplasm | other | | 3.35E-07 2.77E-06 | 3.34 | 7.39E-01 8.11E-01 | 0.99 | 2.38E-01 1.32E-01 | 0.97 | 2.42E-01 6.50E-02 | 1.04 | 6.36E-01 4.26E-01 | 0.99 |
| | | | cyclin-dependent kinase | сторили | chaptere. | | | | | | | | | | | |
| 1424638 at | Duplicate Gene Syr | CDKN1A TLR1 | inhibitor 1A (p21, Cip1) | Nucleus Plasma Membrane | kinase transmembrane | | 5.37E-07 6.80E-06 | 3.33 | 3.90E-01 2.46E-01 | 0.97 | 1.79E-01 1.83E-01 | 0.91 | 6.74E-03 2.55E-01 | 1.26 | 1.78E-01 | 0.95 |
| 1449049 at 1448325_at | | PPP1R15A | toll-like receptor 1 protein phosphatase 1, regulatory subunit 15A | Cytoplasm | other | | 2.77E-07 | 3.31 | 6.88E-01 | 0.94 | 5.81E-01 | 0.91 | 1.38E-02 | 1.04 | 2.97E-01 8.23E-01 | 0.99 |
| 1449455 at | Development | нск | hemopoietic cell kinase | Cytoplasm | kinase | bosutinib | 6.75E-07 | 3.25 | 8.68E-01 | 0.99 | 7.18E-02 | 0.94 | 3.30E-04 | 1.35 | 9.95E-01 | 1.00 |
| 1435415 x at 1418116 at | Duplicate Gene Syr | MARCKSL1 TOR1AIP2 | MARCKS-like 1 torsin A interacting protein 2 | Cytoplasm | other | | 5.61E-07 2.77E-06 | 3.24 | 3.92E-01 9.31E-02 | 1.04 | 9.37E-01 8.52E-01 | 0.99 | 5.20E-05 1.67E-01 | 1.67 | 1.27E-01 8.81E-01 | 1.07 |
| | | | membrane-spanning 4- domains, subfamily A, | | | | | | | | | | | | | |
| 1423467 at | Duplicate Gene Syr | Ms4a4b (includes o | member 48 myristoylated alanine- rich protein kinase C | Plasma Membrane | other | | 6.16E-06 | 3.22 | 4.94E-01 | 1.03 | 8.23E-02 | 0.92 | 9.06E-01 | 1.00 | 2.91E-01 | 0.93 |
| 1415972 at | Duplicate Gene Syr | MARCKS | substrate myristoylated alanine- | Plasma Membrane | other | | 5.50E-04 | 3.22 | 3.14E-01 | 1.12 | 9.51E-01 | 1.01 | 2.24E-01 | 1.18 | 6.54E-02 | 1.30 |
| 1415971 at | Duplicate Gene Syr | MARCKS | rich protein kinase C substrate | Plasma Membrane | other | | 9.58E-07 | 3.20 | 7.23E-01 | 1.02 | 6.12E-01 | 0.99 | 7.34E-03 | 1.08 | 3.12E-01 | 1.06 |
| 1421679 a at | Duplicate Gene Svr | CDKN1A | cyclin-dependent kinase inhibitor 1A (p21, Cip1) | Nucleus | kinase | | 7.94E-06 | 3.20 | 2.07E-01 | 0.86 | 1.06E-01 | 0.91 | 2.61E-02 | 1.18 | 1.33E-02 | 0.85 |
| 1417371 at | Duplicate Gene Syr | PELI1 | pellino E3 ubiquitin protein ligase 1 | Cytoplasm | enzyme | | 4.84E-06 | 3.19 | 3.26E-01 | 1.05 | 2.10E-01 | 1.06 | 2.19E-02 | 1.14 | 1.44E-01 | 1.06 |
| 1435627 x at 1416239 at | Duplicate Gene Syr | MARCKSL1 ASS1 | MARCKS-like 1 argininosuccinate synthase 1 | Cytoplasm | other | | 2.75E-06 9.72E-07 | 3.15 | 8.00E-01 4.33E-01 | 1.01 | 7.81E-01 7.68E-01 | 0.99 | 1.17E-03 7.85E-04 | 1.50 | 8.03E-01 | 1.01 |
| 1448830_at | | DUSP1 | dual specificity phosphatase 1 | Nucleus | phosphatase | | 1.10E-05 | 3.10 | 6.85E-03 | 0.89 | 5.02E-03 | 0.83 | 6.09E-03 | 1.24 | 7.65E-03 | 0.80 |
| | | | | | | fludarabine phosphate. | | | | | | | | | | |
| 1428838 a at | Duplicate Gene Syr | DCK | deoxycytidine kinase | Nucleus | kinase | cladribine | 8.56E-05 | 3.07 | 6.82E-01 | 0.96 | 3.95E-01 | 0.91 | 4.51E-01 | 0.95 | 2.83E-01 | 0.90 |
| 1419315 at | | SLAMF9 | SLAM family member 9 | Extracellular Space | other | | 1.53E-05 | 3.06 | 2.34E-01 | 1.04 | 3.43E-01 | 0.96 | 1.03E-03 | 1.31 | 5.21E-01 | 1.03 |
| 1419483 at | Duplicate Gene Syr | C3AR1 | complement component 3a receptor 1 nuclear factor of kappa | Plasma Membrane | G-protein coupled receptor | | 2.32E-05 | 3.05 | 5.33E-01 | 1.05 | 9.32E-01 | 1.01 | 2.95E-01 | 1.10 | 8.17E-01 | 0.99 |
| | | | light polypeptide gene enhancer in B-cells | | transcription | | | | | | | | | | | |
| 1431843 a at 1419212 at | | NFKBIE | inhibitor, epsilon inducible T-cell co- stimulator ligand | Nucleus Plasma Membrane | other | | 1.89E-05 | 3.05 | 7.93E-01 3.89E-01 | 1.02 | 2.88E-01 4.75E-01 | 0.94 | 5.44E-04 2.04E-03 | 1.95 | 1.30E-01 1.72E-01 | 1.12 |
| 1450698 at | | DUSP2 | dual specificity phosphatase 2 | Nucleus | phosphatase | | 3.65E-08 | 3.04 | 1.66E-02 | 0.95 | 9.54E-01 | 1.00 | 8.71E-04 | 1.46 | 3.26E-03 | 1.09 |
| 1410125 | | 170 | lymphotoxin beta (TNF | Cutero en Huder Censor | . toking | | 8.63E-05 | 3.02 | 5.80E-01 | 1.06 | 2.18E-01 | 1.10 | 8.86E-04 | 1.75 | 1.20E-01 | |
| 1419135 at | | LIB | superfamily, member 3) membrane-spanning 4- domains, subfamily A, | Extracellular Space | cytokine | | 8.63E-05 | 3.02 | 5.80E-01 | 1.06 | 2.18E-01 | 1.10 | 8.865-04 | 1.75 | 1.20E-01 | 1.13 |
| 1424754 at 1432478 a at | Duplicate Gene Syr | MS4A7 RNF19B | member 7 ring finger protein 198 | unknown unknown | other other | | 3.80E-05 4.43E-06 | 2.99 2.99 | 4.71E-01 5.98E-01 | 1.07 0.98 | 3.52E-01 2.72E-01 | 1.06 0.95 | 5.83E-01 7.78E-04 | 1.05 1.62 | 3.03E-01 1.04E-01 | 1.07 1.15 |
| 1416505 at | | NR4A1 | nuclear receptor subfamily 4, group A, member 1 | Nucleus | ligand-dependent nuclear receptor | | 3.70E-05 | 2.97 | 1.10E-01 | 1.10 | 4.43E-02 | 1.06 | 1.16E-03 | 1.31 | 7.05E-04 | 1.19 |
| | | | membrane-spanning 4- domains, subfamily A, | | | | | | | | | | | | | |
| 1450291_s_at | Duplicate Gene Syr | Ms4a4b (includes o | member 48 baculoviral IAP repeat | Plasma Membrane | other | | 6.68E-06 | 2.96 | 9.08E-01 8.47E-01 | 0.99 | 4.81E-01 9.84E-01 | 0.97 | 3.02E-02 7.87E-04 | 1.11 | 5.27E-01 1.38E-01 | 1.02 |
| 1421392 a at 1417372_a_at | Duplicate Gene Syr | | containing 3 pellino E3 ubiquitin protein ligase 1 | Cytoplasm | enzyme enzyme | | 2.31E-05 | 2.95 | 9.84E-01 | 1.00 | 1.07E-01 | 0.92 | 1.41E-01 | 1.49 | 7.89E-01 | 1.07 |
| 1426971_at | Duplicate Gene Syr | | ubiquitin-like modifier activating enzyme 7 | Cytoplasm | enzyme | | 1.75E-06 | 2.93 | 3.40E-01 | 0.93 | 3.71E-01 | 0.93 | 6.55E-01 | 1.04 | 1.28E-01 | 1.04 |
| 1454633 at | Duplicate Gene Syr | | killer cell lectin-like receptor subfamily K, | Cytoplasm | kinase transmembrane | | 1.15E-04 | 2.93 | 8.45E-01 | 0.99 | 6.92E-01 | 0.98 | 9.13E-01 | 0.99 | 3.29E-01 | 1.05 |
| 1450495_a_at | | KLRC4-KLRK1/KLRK | member 1 | Plasma Membrane | receptor | | 1.42E-04 | 2.89 | 5.75E-01 | 0.97 | 5.29E-01 | 1.03 | 4.24E-01 | 1.04 | 8.94E-01 | 0.99 |
| | | | | | | forodesine, 9- deaza-9-(3- | | | | | | | | | | |
| 1453299 a at | Duplicate Gene Syr | PNP | purine nucleoside phosphorylase | Nucleus | enzyme | deaza-9-(3- thienylmethyl) guanine | 4.82E-07 | 2.89 | 4.15E-01 | 0.99 | 9.22E-01 | 1.00 | 9.92E-02 | 1.02 | 6.51E-02 | 1.04 |
| 1421854 at | Duplicate Gene Syr | FGL2 | fibrinogen-like 2 C-type lectin domain | Extracellular Space | peptidase transmembrane | | 1.29E-05 | 2.88 | 9.23E-01 | 1.00 | 6.00E-01 | 0.98 | 1.72E-02 | 0.77 | 3.13E-01 | 0.94 |
| 1422013_at | Duplicate Gene Syr | CLEC4A | family 4, member A siah E3 ubiquitin protein | Plasma Membrane | receptor transcription | | 1.92E-05 | 2.86 | 5.17E-01 | 1.03 | 4.98E-01 | 0.97 | 1.63E-02 | 1.16 | 8.07E-01 | 0.99 |
| 1448171 at | Developerty Correct | SIAH2 MARCH5 | ligase 2 membrane-associated | Nucleus | regulator | | 6.18E-06 | 2.82 | 8.59E-02 | 0.91 | 4.36E-01 | 0.97 | 5.78E-03 4.13E-03 | 1.26 | 1.41E-01 | 0.94 |
| 1428843 at 1425603_at | Duplicate Gene Syr | MARCH5 TMEM176A | ring finger (C3HC4) 5 transmembrane protein 176A | Cytoplasm | enzyme other | | 1.66E-07 2.22E-05 | 2.82 | 4.22E-01 1.03E-01 | 0.98 | 6.61E-01 7.05E-01 | 0.99 | 4.13E-03 5.93E-04 | 1.06 | 8.05E-01 1.86E-01 | 1.01 |
| | | | | | | | | | | | | | | | | |
| 1422512 a at 1417523 at | Duplicate Gene Syr Duplicate Gene Syr | OGFR | opioid growth factor receptor pleckstrin | Plasma Membrane Cytoplasm | other | enkephalin, methionine | 3.47E-05 | 2.80 | 8.14E-01 8.31E-01 | 0.98 | 8.00E-01 2.33E-01 | 1.03 | 3.33E-01 2.76E-03 | 1.07 | 5.35E-01 4.20E-02 | 1.04 |
| 1453181 x at | Duplicate Gene Syr | | phospholipid scramblase | Plasma Membrane | enzyme | | 3.69E-06 | 2.78 | 7.37E-01 | 1.02 | 2.37E-02 | 1.06 | 5.54E-02 | 1.11 | 2.26E-02 | 1.15 |
| 1415899 at 1433514 at | Duplicate Gene Syr | JUNB | jun B proto-oncogene ethanolamine kinase 1 | Nucleus Cytoplasm | transcription regulator | | 1.35E-05 6.07E-06 | 2.77 | 2.43E-01 9.12E-01 | 0.93 | 3.67E-01 5.12E-01 | 0.93 | 9.39E-05 4.20E-01 | 1.65 | 7.61E-01 3.75E-02 | 1.01 |
| 1433514 at 1450672 a at | Sapincate Gene Syr | TREX1 | ethanolamine kinase 1 three prime repair exonuclease 1 | Cytoplasm Nucleus | kinase enzyme | | 6.07E-06 2.12E-05 | 2.77 | 9.12E-01 7.09E-01 | 0.98 | 5.12E-01 9.40E-01 | 1.00 | 4.20E-01 1.26E-02 | 1.04 | 3.75E-02 3.42E-01 | 0.95 |
| 1451122 at | Dealizate Comm | | isopentenyl-diphosphate | Constant - | | | 2.40E-05 | | 6.21E-02 | 1.14 | 3.77E-03 | 1.31 | 1.50E-03 | | 1.67E-03 | 1.51 |
| 1451122 at 1451082 at | Duplicate Gene Syr | | delta isomerase 1 FtsJ methyltransferase domain containing 2 | Cytoplasm | enzyme | | 2.40E-05 1.01E-05 | 2.76 | 6.21E-02 8.63E-01 | 1.14 | 3.77E-03 5.72E-01 | 0.96 | 1.50E-03 4.01E-01 | 1.44 | 1.67E-03 7.00E-01 | 1.51 |
| | Duplicate Gene Syr | FISIDZ | | 1 | | | 1.16E-05 | 2.74 | 1.14E-01 | 0.96 | 3.41E-01 | 0.96 | 6.22E-01 | 0.98 | 2.36E-01 | 1.03 |
| 1426970 a at | Duplicate Gene Syr | | ubiquitin-like modifier activating enzyme 7 | Cytoplasm | enzyme | | | | | | 1 | | | | | |
| | | | activating enzyme 7 nuclear factor of kappa light polypeptide gene | Cytoplasm | | | | | | | | | | | | |
| 1426970 a at 1420088 at | Duplicate Gene Syr Duplicate Gene Syr | UBA7 NFKBIA | activating enzyme 7 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha | Cytoplasm | transcription regulator | | 9.21E-07 | 2.74 | 8.84E-01 | 1.00 | 2.668-01 | 0.97 | 5.57E-05 | 1.88 | 7.09E-02 | 1.07 |
| 1426970 a at 1420088 at 1422959_5_at | Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr | UBA7 NFKBIA RNF114 | activating enzyme 7 nuclear factor of kappa light polypeptide gene enhancer in B-cells | Cytoplasm Extracellular Space | transcription regulator other | | 1.83E-05 | 2.73 | 9.85E-01 | 1.00 | 7.74E-01 | 0.98 | 1.71E-01 | 1.09 | 7.37E-01 | 0.98 |
| 1426970 a at 1420088 at | Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr | UBA7 NFKBIA RNF114 PLSCR1 RNF198 | activating enzyme 7 nuclear factor of kappa light polypeptide gene enhancer in 8-cells inhibitor, alpha ring finger protein 114 phospholipid scramblase 1 ring finger protein 198 | Cytoplasm | transcription regulator | | | | | | 7.74E-01 5.51E-01 1.19E-01 | | | 1.00 | | |
| 1426970 a at 1420088 at 1422959 s_at 1422957 a at | Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr | UBA7 NFKBIA RNF114 PLSCR1 RNF198 | activating enzyme 7 nuclear factor of kappa light polypeptide gene enhancer in 8-cells inhibitor, alpha ring finger protein 114 phospholipid scramblase 1 ring finger protein 198 superoxide dismutase 2, mitochondrial | Cytoplasm Extracellular Space Plasma Membrane | transcription regulator other enzyme | | 1.83E-05 | 2.73 | 9.85E-01 3.73E-01 | 1.00 | 7.74E-01 5.51E-01 | 0.98 | 1.71E-01 5.05E-01 | 1.09 | 7.37E-01 6.29E-01 | 0.98 |
| 1426970 a at 1420088 at 1422959 s at 1429527 a at 1435226 at 1417193 at | Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr | UBA7 NFKBIA RNF114 PLSCR1 RNF198 SOD2 | activating enzyme 7 nuclear factor of kappa light polypeptide gene enhancer in 8-cells inhibitor, alpha ring finger protein 114 ring finger protein 198 superoxide dismutase 2, mitochondrial cytoplasmic polyademylation element | Cytoplasm Extracellular Space Plasma Membrane unknown Cytoplasm | transcription regulator other enzyme other enzyme | | 1.83E-05 1.29E-05 1.42E-05 2.72E-06 | 2.73 2.69 2.69 | 9.85E-01 3.73E-01 7.96E-01 8.61E-01 | 1.00 1.04 0.99 1.01 | 7.74E-01 5.51E-01 1.19E-01 3.78E-01 | 0.98 1.02 1.04 1.02 | 1.71E-01 5.05E-01 4.62E-05 5.84E-03 | 1.09 1.05 1.53 1.25 | 7.37E-01 6.29E-01 2.01E-02 7.81E-02 | 0.98 1.04 1.14 1.07 |
| 1426970 a at 1420088 at 1422959_5_at 1429527 a at 1435226 at | Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr | UBA7 NFKBIA RNF114 PLSCR1 RNF198 SOD2 CPEB4 | activating ensyme 7 nuclear factor of kappa light polypoptide gene enhancer in B-cells inhibitor, ajsha ring finger protein 114 phospholipid scramblase 1 ring finger protein 198 superoxide dis mutase 2, mitchchondral cytoplasmic | Cytoplasm Extracellular Space Plasma Membrane unknown | transcription regulator other enzyme other enzyme | | 1.83E-05 1.29E-05 1.42E-05 | 2.73 2.72 2.69 | 9.85E-01 3.73E-01 7.96E-01 | 1.00 1.04 0.99 | 7.74E-01 5.51E-01 1.19E-01 | 0.98 1.02 1.04 | 1.71E-01 5.05E-01 4.62E-05 | 1.09 1.05 1.53 | 7.37E-01 6.29E-01 2.01E-02 | 0.98 1.04 1.14 |
| 1426970 a at 1420088 at 1422959 s at 14229527 a at 1435226 at 1417193 at 1420618 at | Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr | UBA7 NFKBIA RNF114 PLSCR1 RNF198 SOD2 CPEB4 | activating enzyme 7 nuclear factor of kappa light polypeptide gene enhancer in 8-cells inhibitor, alpha ring finger protein 114 ring finger protein 198 superoxide dismutase 2, mitochondrial cytoplasmic polyademylasion element binding protein 4 superoxide dismutase 3, | Cytoplasm Extracellular Space Plasma Membrane unknown Cytoplasm Plasma Membrane | transcription regulator other enzyme other other | | 1.83E-05 1.29E-05 1.42E-05 2.72E-06 5.71E-04 | 2.73 2.72 2.69 2.69 2.68 | 9.85E-01 3.73E-01 7.96E-01 8.61E-01 5.64E-01 | 1.00 1.04 0.99 1.01 | 7.74E-01 5.51E-01 1.19E-01 3.78E-01 8.21E-01 | 0.98 1.02 1.04 1.02 0.98 | 1.71E-01 5.05E-01 4.62E-05 5.84E-03 1.69E-01 | 1.09 1.05 1.53 1.25 1.20 | 7.37E-01 6.29E-01 2.01E-02 7.81E-02 1.52E-01 | 0.98 1.04 1.14 1.07 |

| | | | | | | | Stimula | tion Only | | Compou | und Only | | | Stimulation a | nd Compound | |
|--|--|---|---|---|---|---|---|--|--|---|--|---|--|---|--|---|
| | İ | - | Probe Set Description fibronectin type III | İ | 1 | 1 | CpG vs. | Medium | | 46 vs. Medium | 1.25 uM E644 | | 40.000 | IM E6446 vs. Medium | 40.000 | M E6446 vs. Medium |
| 1426903 at | 1 | FNDC3A | domain containing 3A membrane-spanning 4- domains, subfamily A, | Cytoplasm | other | 1 | 1.10E-04 | 2.58 | 8.97E-01 | 0.99 | 4.29E-01 | 0.95 | 5.29E-01 | 1.05 | 2.90E-01 | 1.09 |
| 1419598 at | Duplicate Gene Syr | MS4A6A | domains, subtamily A, member 6A membrane-spanning 4- | unknown | other | | 1.31E-04 | 2.58 | 2.67E-01 | 1.06 | 5.76E-01 | 0.98 | 9.43E-01 | 1.00 | 9.87E-02 | 1.10 |
| 1419599 s at | Duplicate Gene Syr | M54A6A | domains, subfamily A, member 6A | unknown | other | | 7 355-06 | 2 57 | 6.20E-01 | 1.02 | 4.10E-01 | 0.97 | 6.43E-01 | 0.98 | 3.57E-01 | 1.03 |
| 1423161_s_at | Duplicate Gene Syr | SPRED1 | sprouty-related, EVH1 domain containing 1 | Plasma Membrane | other | | 7.68E-05 | 2.57 | 5.55E-01 | 0.95 | 6.28E-01 | 0.98 | 4.84E-01 | 1.08 | 7.39E-01 | 1.02 |
| 1423681 at | Duplicate Gene Svr | FTSID2 | EtsJ methyltransferase domain containing 2 | unknown | enzyme | | 8.37E-05 | 2.57 | 5.63E-01 | 0.96 | 8.48E-01 | 0.98 | 2.78E-01 | 1.08 | 4.20E-01 | 1.06 |
| 1425193 at | Duplicate Gene Syr | SPPL2A | signal peptide peptidase like 2A | Plasma Membrane | peptidase | | 5.03E-05 | 2.56 | 7.46E-01 | 1.02 | 5.06E-01 | 0.96 | 6.19E-02 | 1.11 | 8.51E-01 | 1.01 |
| | | | CCAAT/enhancer binding | | transcription | | | | | | | | | | | |
| 1418901 at | | CEBPB | protein (C/EBP), beta ubiquitin specific | Nucleus | regulator | | 1.94E-04 | 2.56 | 8.30E-01 | 0.99 | 9.50E-01 | 0.99 | 3.13E-04 | 1.71 | 5.93E-01 | 0.98 |
| 1448939_at | | USP25 | peptidase 25 interferon regulatory | unknown | peptidase transcription | | 3.66E-05 | 2.56 | 3.84E-01 | 0.94 | 1.04E-01 | 0.90 | 8.20E-01 | 0.97 | 5.68E-01 | 0.93 |
| 1448436 a at | Duplicate Gene Svr | IRF1 | factor 1 phosphatidylglycerophos | Nucleus | regulator | | 6.65E-07 | 2.55 | 8.87E-01 2.68E-01 | 0.94 | 1.36E-02 | 1.09 | 5.89E-02 | 1.08 | 3.71E-02 | 1.04 |
| 1455229 x at 1421685_at | Duplicate Gene Syr | PGS1 Clec4b1 | phate synthase 1 C-type lectin domain family 4, member b1 | Plasma Membrane | other | | 3.67E-05 | 2.55 | 5.43E-01 | 1.04 | 9.42E-01 2.24E-01 | 0.91 | 1.13E-02 | 1.06 | 6.21E-01 7.78E-02 | 1.02 |
| 1427874 at | Duplicate Gene Svr | RNF114 | | Extracellular Space | other | | 1.32E-07 | 2.54 | 9.21E-01 | 1.00 | 2.27E-01 | 0.97 | 1.47E-01 | 1.09 | 9.22E-01 | 1.03 |
| | | | ring finger protein 114 brain abundant, membrane attached | | transcription | | | | | | | | | | | |
| 1428572 at | | BASP1 | signal protein 1 | Nucleus | regulator | | 1.77E-05 | 2.54 | 2.44E-01 | 1.04 | 3.71E-02 | 1.07 | 1.11E-03 | 1.26 | 2.94E-03 | 1.14 |
| 1418536 at | Duplicate Gene Syr | HLA-B | major histocompatibility complex, class I, B | Plasma Membrane | transmembrane receptor | | 2.43E-05 | 2.54 | 8.98E-01 | 1.01 | 8.19E-01 | 0.99 | 1.64E-02 | 1.20 | 6.38E-01 | 1.02 |
| 1423401 at | | ETV6 | ets variant 6 | Nucleus | transcription regulator | | 2.72E-04 | 2.53 | 7.19E-01 | 1.04 | 9.10E-01 | 0.99 | 2.18E-01 | 1.12 | 3.95E-01 | 1.09 |
| 1423870 at | | AIDA | axin interactor, dorsalization associated | Contractions | ather | | 8 155-07 | 2.52 | 6.58E-01 | 1.01 | 7.66E-01 | 1.01 | 5.40E-01 | 1.02 | 6.15E-01 | 0.99 |
| 1423870 at | | ADA | myristoylated alanine- rich protein kinase C | Cytoplasm | oule | | 0.135-07 | 2.32 | 0.562-01 | 1.01 | 7.002-01 | 1.01 | 3.402-01 | 1.02 | 0.132/01 | 0.55 |
| 1415973 at | Duplicate Gene Syr | MARCKS | substrate C-type lectin domain | Plasma Membrane | other transmembrane | | 3.84E-05 | 2.52 | 8.03E-01 | 0.99 | 2.01E-01 | 0.96 | 5.54E-01 | 1.04 | 4.15E-01 | 1.03 |
| 1425407_s_at | Duplicate Gene Syr | | family 4, member A phosphatidylglycerophos | Plasma Membrane | receptor | | 1.08E-05 | 2.51 | 6.64E-02 | 1.09 | 4.65E-01 | 0.98 | 3.93E-02 | 1.15 | 2.73E-01 | 0.97 |
| 1454046 x at | Duplicate Gene Syr | PGS1 | phate synthase 1 | Cytoplasm | enzyme | <u> </u> | 1.06E-05 | 2.51 | 1.63E-01 | 0.95 | 8.90E-01 | 1.01 | 4.48E-01 | 1.02 | 4.91E-01 | 1.02 |
| | | 1 | | | | fludarabine phosphate, | | | | | | | | | | |
| 1449176 a at | Duplicate Gene Syr | DCK | deoxycytidine kinase myristoylated alanine- | Nucleus | kinase | cladribine | 1.65E-05 | 2.51 | 1.15E-01 | 1.06 | 4.02E-01 | 0.96 | 5.08E-01 | 0.95 | 5.35E-01 | 1.03 |
| 1456028 x at | Duplicate Gene Syr | MARCKS | rich protein kinase C substrate | Plasma Membrane | other | | 4.15E-04 | 2.51 | 3.13E-01 | 1.09 | 7.77E-01 | 1.03 | 1.86E-01 | 1.14 | 3.88E-01 | 1.14 |
| | | | | | | forodesine, 9- | | | | | | | | | | |
| | | | purine nucleoside | | | torodesine, 9- deaza-9-(3- thienylmethyl) | | | | | | | | | | |
| 1416530_a_at | Duplicate Gene Syr | | phosphorylase interferon regulatory | Nucleus | enzyme transcription | guanine | 1.96E-06 | 2.51 | 3.62E-01 | 1.02 | 3.79E-01 | 1.02 | 2.38E-01 | 1.03 | 1.12E-01 | 1.07 |
| 1421322 a at | | IRF9 | factor 9 basic leucine zipper | Nucleus | regulator | | 2.21E-06 | 2.49 | 1.15E-01 | 1.05 | 2.81E-01 | 1.02 | 4.29E-03 | 1.09 | 2.19E-02 | 0.95 |
| 1419410 at | | BATF | transcription factor, ATF- like | Nucleus | transcription regulator | L | 8.24E-06 | 2.46 | 4.39E-01 | 0.97 | 8.81E-01 | 1.01 | 2.70E-02 | 1.12 | 3.23E-01 | 1.03 |
| 1418154_at | | N4BP1 | NEDD4 binding protein 1 | Cytoplasm | other | | 2.72E-05 | 2.45 | 7.36E-01 | 0.99 | 5.57E-01 | 0.97 | 1.13E-02 | 1.22 | 2.39E-01 | 1.06 |
| 1451593_at | Duplicate Gene Syr | HLA-B | major histocompatibility complex, class I, B | Plasma Membrane | transmembrane receptor | | 4.26E-06 | 2.45 | 1.89E-02 | 1.07 | 2.41E-02 | 1.07 | 3.43E-03 | 1.31 | 7.29E-03 | 1.11 |
| | | | leukocyte immunoglobulin-like | | | | | | | | | | | | | |
| 1420394_s_at | | Gp49a/Lilrb4 | receptor, subfamily B, member 4 | unknown | other | | 1.67E-06 | 2.45 | 2.86E-02 | 1.14 | 8.99E-03 | 1.11 | 4.54E-05 | 1.44 | 4.01E-04 | 1.31 |
| 1454045 a at | Duplicate Gene Syr | PGS1 | phosphatidylglycerophos phate synthase 1 | Cytoplasm | enzyme | | 1.76E-06 | 2.44 | 1.02E-01 | 0.96 | 4.79E-02 | 0.96 | 3.58E-01 | 1.04 | 9.48E-01 | 1.00 |
| 1426084 a at | | Tor1aip1 | torsin A interacting protein 1 | Nucleus | other | | 6.21E-07 | 2.44 | 9.15E-02 | 0.94 | 2.69E-02 | 0.98 | 2.63E-01 | 1.01 | 1.01E-01 | 0.95 |
| 1424929_a_at | | TRIM26 | tripartite motif containing 26 | Cytoplasm | other | | 4.76E-05 | 2.44 | 6.06E-01 | 0.97 | 9.50E-01 1.58E-01 | 0.99 | 5.55E-01 | 1.04 | 3.97E-01 | 1.06 |
| 1448749 at | Duplicate Gene Syr | PLEK | pleckstrin | Cytoplasm | other | | 5.42E-05 | | | | | 1.08 | 1 29E-03 | 1 35 | 1.69E-02 | 1.16 |
| 1451821 a at | | Sn100 | puclear aptigen Sp100 | Nucleus | transcription regulator | | | 2.44 | 5.20E-01 8.67E-02 | 1.04 | | | | 0.98 | 1.095-01 | |
| 1451821_a_at 1448106 at | | Sp100 NECAP1 | nuclear antigen Sp100 NECAP endocytosis associated 1 | Nucleus Plasma Membrane | transcription regulator other | | 4.98E-06 | 2.43 | 8.67E-02 | 1.06 | 1.41E-01 | 1.05 | 4.00E-01 2.63E-02 | 0.98 | 1.09E-01 3.03E-01 | 1.05 |
| 1451821_a_at 1448106 at 1450459 at | Duplicate Gene Syr | Sp100 NECAP1 SPPL2A | nuclear antigen Sp100 NECAP endocytosis associated 1 signal peptide peptidase like 2A | | | | 4.98E-06 | | | | | 1.05 | 4.00E-01 | 0.98 | 1.09E-01 3.03E-01 2.67E-01 | |
| 1448106 at | Duplicate Gene Syr | NECAP1 | NECAP endocytosis associated 1 signal peptide peptidase like 2A fibrinogen-like 2 | | other peptidase | | 4.98E-06 9.21E-06 | 2.43 | 8.67E-02 3.51E-01 | 1.06 | 1.41E-01 6.88E-01 | 1.05 | 4.00E-01 2.63E-02 | 1.10 | 3.03E-01 | 1.05 |
| 1448106 at 1450459 at 1421855_at 1423160 at | | NECAP1 SPPL2A | NECAP endocytosis associated 1 signal peptide peptidase like 2A | Plasma Membrane Plasma Membrane Extracellular Space | other peptidase | | 4.98E-06 9.21E-06 9.48E-05 3.65E-05 5.00E-05 | 2.43 2.43 2.43 | 8.67E-02 3.51E-01 5.80E-01 | 1.06 1.03 0.95 | 1.41E-01 6.88E-01 7.34E-01 | 1.05 0.98 0.96 | 4.00E-01 2.63E-02 3.90E-01 4.43E-02 4.31E-01 | 1.10 | 3.03E-01 2.67E-01 | 1.05 1.04 0.91 |
| 1448106 at 1450459 at 1421855_at | Duplicate Gene Syr | NECAP1 SPPL2A FGL2 | NECAP endocytosis associated 1 signal peptide peptidase like 2A fibrinogen-like 2 sprouty-related, EVH1 domain containing 1 | Plasma Membrane Plasma Membrane Extracellular Space | regulator other peptidase peptidase | | 4.98E-06 9.21E-06 9.48E-05 3.65E-05 | 2.43 2.43 2.43 2.41 | 8.67E-02 3.51E-01 5.80E-01 5.53E-01 | 1.06 1.03 0.95 1.03 | 1.41E-01 6.88E-01 7.34E-01 3.76E-01 | 1.05 0.98 0.96 0.96 | 4.00E-01 2.63E-02 3.90E-01 4.43E-02 | 1.10 1.07 0.79 | 3.03E-01 2.67E-01 8.77E-01 | 1.05 1.04 0.91 0.99 |
| 1448106 at 1450459 at 1421855_at 1423160 at | Duplicate Gene Syr | NECAP1 SPPL2A FGL2 SPRED1 | NECAP endocytosis associated 1 signal peptide peptidase like 2A fibrinogen-like 2 sprouty-related, EVH1 domain containing 1 colled-coll domain | Plasma Membrane Plasma Membrane Extracellular Space Plasma Membrane | regulator other peptidase peptidase other | N | 4.98E-06 9.21E-06 9.48E-05 3.65E-05 5.00E-05 | 2.43 2.43 2.43 2.41 2.40 | 8.67E-02 3.51E-01 5.80E-01 5.53E-01 7.19E-01 | 1.06 1.03 0.95 1.03 0.98 | 1.41E-01 6.88E-01 7.34E-01 3.76E-01 5.46E-01 | 1.05 0.98 0.96 0.96 0.96 | 4.00E-01 2.63E-02 3.90E-01 4.43E-02 4.31E-01 | 1.10 1.07 0.79 1.06 | 3.03E-01 2.67E-01 8.77E-01 8.57E-01 | 1.05 1.04 0.91 0.99 0.99 |
| 1448106 at 1450459 at 1421855_at 1423160 at | Duplicate Gene Syr | NECAP1 SPPL2A FGL2 SPRED1 | NECAP endocytosis associated 1 signal peptide peptidase like 2A fibrinogen-like 2 sprouty-related, EVH1 domain containing 1 colled-coll domain | Plasma Membrane Plasma Membrane Extracellular Space Plasma Membrane | regulator other peptidase peptidase other | N- butyldecxygala ctonojirimycin, | 4.98E-06 9.21E-06 9.48E-05 3.65E-05 5.00E-05 | 2.43 2.43 2.43 2.41 2.40 | 8.67E-02 3.51E-01 5.80E-01 5.53E-01 7.19E-01 | 1.06 1.03 0.95 1.03 0.98 | 1.41E-01 6.88E-01 7.34E-01 3.76E-01 5.46E-01 | 1.05 0.98 0.96 0.96 0.96 | 4.00E-01 2.63E-02 3.90E-01 4.43E-02 4.31E-01 | 1.10 1.07 0.79 1.06 | 3.03E-01 2.67E-01 8.77E-01 8.57E-01 | 1.05 1.04 0.91 0.99 0.99 |
| 1448106 at 1450459 at 1421855 at 1423160 at 1452414 s at | Duplicate Gene Syr | NECAP1 SPPL2A FGL2 SPRED1 CCDC86 | NECAP endocytosis associated 1 signal peptide peptidase like 2A fibringen-like 2 sprouty-related, EVH1 domain containing 1 containing 86 UDP-glucose ceramide | Hasma Membrane Hasma Membrane Extracellular Space Hasma Membrane Nucleus | regulator other peptidase peptidase other other | ctonojirimycin, N- butyldeaxynaji | 4.98E-06 9.21E-06 9.48E-05 3.65E-05 5.00E-05 7.40E-05 | 2.43 2.43 2.43 2.41 2.40 2.40 | 8.67E-02 3.51E-01 5.80E-01 5.53E-01 7.19E-01 3.88E-01 | 1.06 1.03 0.95 1.03 0.98 0.94 | 1.41E-01 6.88E-01 7.34E-01 3.76E-01 5.46E-01 4.70E-01 | 1.05 0.98 0.96 0.96 0.96 0.96 | 4.00E-01 2.63E-02 3.90E-01 4.43E-02 4.31E-01 1.22E-01 | 1.10 1.07 0.79 1.06 1.13 | 3.03E-01 2.67E-01 8.77E-01 8.57E-01 3.09E-01 | 1.05 1.04 0.91 0.99 0.99 1.07 |
| 1448106 at 1450459 at 1421855 at 1423160 at 1452414 s at 1452414 s at | Duplicate Gene Syr | NECAP1 SPPL2A FGL2 SPRED1 CCDC86 | NECAP endocytosis associated 1 signal peptide peptidase like 2A fibrinogen-like 2 sprouty-related, EVH1 domain containing 1 colled coll domain containing 86 UDP-glucose ceramide <u>plucosytransferase</u> SUT-ROBO Rho GTase | Hasma Membrane Hasma Membrane Extracellular Space Hasma Membrane Nucleus | regulator other peptidase peptidase other other enzyme | ctonojirimycin, N- | 4.98E-06 9.21E-06 9.48E-05 3.65E-05 5.00E-05 7.40E-05 3.17E-05 | 2.43 2.43 2.43 2.41 2.40 2.40 2.40 2.39 | 8.67E-02 3.51E-01 5.80E-01 5.53E-01 7.19E-01 3.88E-01 5.09E-01 | 1.06 1.03 0.95 1.03 0.98 0.94 | 1.41E-01 6.88E-01 7.34E-01 3.76E-01 5.46E-01 4.70E-01 3.41E-01 | 1.05 0.98 0.96 0.96 0.96 0.96 | 4.00E-01 2.63E-02 3.90E-01 4.43E-02 4.31E-01 1.22E-01 2.61E-01 | 1.10 1.07 0.79 1.06 1.13 | 3.03E-01 2.67E-01 8.77E-01 8.57E-01 3.09E-01 2.45E-02 | 1.05 1.04 0.91 0.99 1.07 1.22 |
| 1448106 at 1450459 at 1421855 at 1423160 at 1452414 s at | Duplicate Gene Syr | NECAP1 SPPL2A FGL2 SPRED1 CCDC86 | NECAP endosytosis signal peptide peptides lite 2 A fibrinagen like 2 sproaty-related, EVH1 contact of the second second containing 1 colled-coil domain containing 86 UUDP-glucose ceramide alucosytranoferase sufficient for GPase activating protein 2 serma glutam/ | Hasma Membrane Hasma Membrane Extracellular Space Hasma Membrane Nucleus | regulator other peptidase peptidase other other | ctonojirimycin, N- butyldeaxynaji | 4.98E-06 9.21E-06 9.48E-05 3.65E-05 5.00E-05 7.40E-05 | 2.43 2.43 2.43 2.41 2.40 2.40 | 8.67E-02 3.51E-01 5.80E-01 5.53E-01 7.19E-01 3.88E-01 | 1.06 1.03 0.95 1.03 0.98 0.94 | 1.41E-01 6.88E-01 7.34E-01 3.76E-01 5.46E-01 4.70E-01 | 1.05 0.98 0.96 0.96 0.96 0.96 | 4.00E-01 2.63E-02 3.90E-01 4.43E-02 4.31E-01 1.22E-01 | 1.10 1.07 0.79 1.06 1.13 | 3.03E-01 2.67E-01 8.77E-01 8.57E-01 3.09E-01 | 1.05 1.04 0.91 0.99 0.99 1.07 |
| 1448106 at 1450459 at 1421855 at 1423160 at 1452414 s at 1452414 s at | Duplicate Gene Syr | NECAP1 SPPL2A FGL2 SPRED1 CCDC86 | NECAP endosytosis associated 1 signal peptide peptidase like 2A fibrinogen-like 2 sprosty-related, EVH1 colled-coll domain containing 86 UDP-glucose cenamide glucosytramfense SUT-ROB 0Rho GTPase activating protein | Hasma Membrane Hasma Membrane Extracellular Space Hasma Membrane Nucleus | regulator other peptidase peptidase other other enzyme | ctonojirimycin, N- butyldeaxynaji | 4.98E-06 9.21E-06 9.48E-05 3.65E-05 5.00E-05 7.40E-05 3.17E-05 | 2.43 2.43 2.43 2.41 2.40 2.40 2.40 2.39 | 8.67E-02 3.51E-01 5.80E-01 5.53E-01 7.19E-01 3.88E-01 5.09E-01 | 1.06 1.03 0.95 1.03 0.98 0.94 | 1.41E-01 6.88E-01 7.34E-01 3.76E-01 5.46E-01 4.70E-01 3.41E-01 | 1.05 0.98 0.96 0.96 0.96 0.96 | 4.00E-01 2.63E-02 3.90E-01 4.43E-02 4.31E-01 1.22E-01 2.61E-01 | 1.10 1.07 0.79 1.06 1.13 | 3.03E-01 2.67E-01 8.77E-01 8.57E-01 3.09E-01 2.45E-02 | 1.05 1.04 0.91 0.99 1.07 1.22 |
| 1448106 at 1450459 at 1421855 at 1423160 at 1452414 s at 1435133 at 1435133 at | Duplicate Gene Syr | NECAP1 SPPL2A FGL2 SPRED1 CCDC86 UGCG SRGAP2 | NECAP endocytosis associated 1 lige 12 periode peptidase lite 2A fibringen sike 2 spody-related. EVH1 domain containing 1 containing 86 UDP-glucose ceramide glucosytham ferase activating profile 2 aprima glucam) hydrolase (conjegac, | Plasma Membrane Plasma Membrane Extracellular Space Plasma Membrane Nucleus Cytoplasm Cytoplasm | regulator other peptidase peptidase other other other other | ctonojirimycin, N- butyldeaxynaji | 4.98E-06 9.21E-06 9.48E-05 3.65E-05 5.00E-05 7.40E-05 3.17E-05 1.98E-06 | 2.43 2.43 2.41 2.40 2.40 2.40 2.39 2.39 | 8.67E-02 2.51E-01 5.80E-01 5.53E-01 7.19E-01 3.88E-01 5.09E-01 4.50E-01 | 1.06 1.03 0.95 1.03 0.98 0.94 1.06 0.97 | 1.41E-01 6.88E-01 7.34E-01 2.74E-01 5.44E-01 4.70E-01 3.41E-01 7.34E-01 | 1.05 0.98 0.96 0.96 0.96 0.96 0.96 1.06 0.98 | 4.00E-01 2.61E-02 3.90E-01 4.43E-02 4.31E-01 1.22E-01 2.61E-01 8.89E-01 | 1.10 1.07 0.79 1.06 1.13 1.09 0.99 | 3.03E-01 2.67E-01 8.77E-01 8.57E-01 3.09E-01 2.45E-02 6.30E-01 | 1.05 1.04 0.91 0.99 1.07 1.22 1.02 |
| 1448106 at 1450459 at 1421855 at 1423160 at 1452414 s at 1455133 at 1429884 at 1419595 a at | Duplicate Gene Syr | NECAP1 SPP.2A FG12 SPRED1 CCDC86 SEGAP2 GGH | NECAP endocytosis ausociated I upus perfolos pepilolas Usus J Ristinggen like 2 grondy related. (VM1 colles coll domain contactional domain contactional domain auxonutorantificas subconutorantificas auxo | Plasma Membrane Plasma Membrane Extracellular Space Plasma Membrane Nucleus Cytoplasm Cytoplasm | regulator other peptidase peptidase other other other other | ctonojirimycin, N- butyldeoxynoji rimycin | 4.98E-06 9.21E-06 9.48E-05 3.65E-05 5.00E-05 7.40E-05 3.17E-05 1.98E-06 | 2.43 2.43 2.41 2.40 2.40 2.40 2.39 2.39 | 8.67E-02 2.51E-01 5.80E-01 5.53E-01 7.19E-01 3.88E-01 5.09E-01 4.50E-01 | 1.06 1.03 0.95 1.03 0.98 0.94 1.06 0.97 | 1.41E-01 6.88E-01 7.34E-01 2.74E-01 5.44E-01 4.70E-01 3.41E-01 7.34E-01 | 1.05 0.98 0.96 0.96 0.96 0.96 0.96 1.06 0.98 | 4.00E-01 2.61E-02 3.90E-01 4.43E-02 4.31E-01 1.22E-01 2.61E-01 8.89E-01 | 1.10 1.07 0.79 1.06 1.13 1.09 0.99 | 3.03E-01 2.67E-01 8.77E-01 8.57E-01 3.09E-01 2.45E-02 6.30E-01 | 1.05 1.04 0.91 0.99 1.07 1.22 1.22 1.02 |
| 144306 at 145069 at 1421855 at 142285 at 142310 at 1452114 s at 1452113 at 147905 a at 143905 a at 143905 a at 143905 a at 143905 a at | Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr | NECAP1 SPP.2A FGL2 SPED1 CCDC86 SGGAP2 GGH DCK SGBP2 | NECAP endocytosis associated I gova profilo profiloso Iling 2 Rithrogene Biel Sprody related EVH1 docted scoreshing associated association containing 86 UD-bylaceae committee Containing 86 UD-bylaceae committee Sulf-Boldo Bits GTPses activation profilos parma gluamy flyndralse (conjease, forlybolg amonglutamy) bedrasen SH3 domain brading protein 2 | Pasma Membrane Pasma Membrane Estracellular Soace Hanna Membrane Nacteus Cytoplasm Cytoplasm Nacteus Cytoplasm | regulator other oppfidase enzyme other other birgse birgse birgse birgse birgse birgse birgse other other birgse other other birgse other other birgse birgse other othe | ctonojirimycin, N- butyldecxynoji rimycin fludarabine phosphate, | 4.98E-66 9.21E-06 9.48E-05 3.65E-05 5.00E-05 7.40E-05 1.98E-06 6.68E-05 6.68E-05 6.20E-04 1.84E-04 | 2.43 2.43 2.41 2.40 2.40 2.40 2.40 2.40 2.20 2.39 2.39 2.39 2.39 2.39 2.39 2.39 2.39 | 8.67E-02 3.51E-01 5.80E-01 5.53E-01 7.19E-01 3.88E-01 5.09E-01 7.32E-01 6.28E-01 5.24E-01 | 1.06 1.03 0.95 1.03 0.98 0.94 1.06 0.97 1.02 1.02 | 1.41E-01 6.88E-01 7.34E-01 3.76E-01 5.46E-01 4.70E-01 7.36E-01 8.42E-02 1.37E-01 6.72E-01 | 1.05 0.98 0.96 0.96 0.96 0.96 0.96 0.96 0.96 0.98 0.92 0.92 | 4.005-01 2.685-02 3.905-01 4.485-02 4.315-01 1.225-01 2.665-01 8.895-01 5.485-03 7.425-01 1.015-01 | 1.10 1.07 0.79 1.06 1.13 1.09 0.99 1.21 0.97 1.17 | 2 03E 01 2 67E 01 8 77E 01 8 57E 01 3 09E 01 2 45E 02 6 30E 01 1 52E 02 4 31E 01 1 67E 01 | 1.05 1.04 0.91 0.99 0.99 1.07 1.27 1.02 1.09 1.07 1.16 |
| 1445106 at 1450459 at 1471855 at 1472185 at 1473160 at 1452144 s at 1479884 at 1479984 at 1479995 a at | Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr | NECAP1 SPE2A F612 SPEED1 CCDC86 SEGAP2 GGH DCK | NECAP endocytosis associated 1 logia profile profiles logia profile profiles logia 2. fibringen skie 2 synody-riskled EVH1 demits containing 4 synody-riskled EVH1 demits containing 6 ubox/files glacosyltematers scitcating sectors parma glacasyl fordicals (conjaste, folybolygemenglutamyl bedralse) decocyclifice kinase Stat domits binding PM binding protein | Rasma Membrane Rasma Membrane Estracellular Space Rasma Membrane Nacleus Cetoplasm Cetoplasm Nacleus | regulator other poptidase other other other other poptidase | ctonojirimycin, N- butyldecxynoji rimycin fludarabine phosphate, | 4.98E-66 9.21E-66 9.48E-65 2.65E-05 5.00E-05 7.40E-05 1.98E-06 6.68E-05 6.20E-04 | 2.43 2.43 2.43 2.40 2.40 2.40 2.40 2.40 2.39 2.39 2.39 | 8.67E-02 3.51E-01 5.80E-01 5.53E-01 7.19E-01 3.88E-01 5.09E-01 4.50E-01 7.32E-01 6.28E-01 | 1.06 1.03 0.95 1.03 0.98 0.94 1.06 0.97 1.02 1.02 | 1.41E-01 6.88E-01 7.34E-01 2.76E-01 5.46E-01 4.70E-01 7.36E-01 8.43E-01 8.43E-02 3.37E-01 | 1.05 0.98 0.96 0.96 0.96 0.96 0.96 0.96 0.96 0.98 | 2.68-02 2.68-02 3.90E-01 4.43E-02 4.31E-01 1.22E-01 2.68E-01 5.48E-03 7.42E-01 | 1.10 1.07 0.79 1.06 1.13 1.09 0.99 1.23 0.97 | 3 03E-01 2 67E-01 8 57E-01 3 09E-01 2 245E-02 6 30E-01 1 52E-02 4 31E-01 | 1.05 1.04 0.99 0.99 1.07 1.22 1.02 1.09 1.07 |
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| | | | | Probe Set Description | | | | Stimulat CpG vs. | tion Only Medium | 0.25 uM F64 | Compou 46 vs. Medium | nd Only 1.25 uM E644 | lő vs. Medium | CnG + 0.25 # | Stimulation a M E6446 vs. Medium | nd Compound | M E6446 vs. Medium | |
|--|--|--|--|---|--|--|--|---|--|--|---|--|---|--|---|---|---|--|
| | | İ | | Probe Set Description | İ | Ť 👘 | İ | cpa vs. | Medidin | 0.25 UM 204 | 40 VS. INICUIUIII | 1.25 UNI 2044 | o vs. mediam | Q14 0.25 | IN EG440 VS. MEDIUM | CpG + 1.25 0 | IN E0440 VS. MEDIDIN | |
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| | | | | | | | dipyridamole. | | | | | | | | | | | |
| | | | | | | | ketotifen, | | | | | | | | | | | |
| Name Name <t< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td>tolbutamide,</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></t<> | | | | | | | tolbutamide, | | | | | | | | | | | |
| Outer Other Desc | | | | phosphodiesterase 48 | | | theophylline, | | | | | | | | | | | |
| MALE MALE <thmale< th=""> MALE MALE <th< td=""><td>1422473 at</td><td>Duplicate Gene Syn</td><td>PDE4B</td><td>cAMP-specific</td><td>Cytoplasm</td><td>enzyme</td><td>caffeine</td><td>1.46E-05</td><td>2.24</td><td>9.31E-01</td><td>1.01</td><td>6.32E-01</td><td>0.99</td><td>1.74E-03</td><td>1.49</td><td>1.62E-01</td><td>1.05</td></th<></thmale<> | 1422473 at | Duplicate Gene Syn | PDE4B | cAMP-specific | Cytoplasm | enzyme | caffeine | 1.46E-05 | 2.24 | 9.31E-01 | 1.01 | 6.32E-01 | 0.99 | 1.74E-03 | 1.49 | 1.62E-01 | 1.05 | |
| Normal Normal </td <td>1427893_a_at</td> <td></td> <td>PMVK</td> <td>kinase</td> <td>Cytoplasm</td> <td>kinase</td> <td></td> <td>2.16E-04</td> <td>2.21</td> <td>5.58E-01</td> <td>1.03</td> <td>9.22E-02</td> <td>1.07</td> <td>1.50E-04</td> <td>1.25</td> <td>7.25E-02</td> <td>1.12</td> | 1427893_a_at | | PMVK | kinase | Cytoplasm | kinase | | 2.16E-04 | 2.21 | 5.58E-01 | 1.03 | 9.22E-02 | 1.07 | 1.50E-04 | 1.25 | 7.25E-02 | 1.12 | |
| Band A Add B < | | | | e dehydrogenase (NADP+ | | | | | | | | | | | | | | |
| Number Number Number <td>1419254_at</td> <td></td> <td>MTHFD2</td> <td>methenyltetrahydrofol ate</td> <td>Cytoplasm</td> <td>enzyme</td> <td></td> <td>1.05E-05</td> <td>2.21</td> <td>7.64E-01</td> <td>1.02</td> <td>8.47E-02</td> <td>0.93</td> <td>1.58E-01</td> <td>1.09</td> <td>1.47E-01</td> <td>0.91</td> | 1419254_at | | MTHFD2 | methenyltetrahydrofol ate | Cytoplasm | enzyme | | 1.05E-05 | 2.21 | 7.64E-01 | 1.02 | 8.47E-02 | 0.93 | 1.58E-01 | 1.09 | 1.47E-01 | 0.91 | |
| Matrix Matrix Matrix <td></td> <td></td> <td></td> <td>C-type lectin domain</td> <td></td> <td>transmembrane</td> <td></td> <td>5.31E-03</td> <td></td> <td>2.79E-01</td> <td>0.85</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>1.05</td> | | | | C-type lectin domain | | transmembrane | | 5.31E-03 | | 2.79E-01 | 0.85 | | | | | | 1.05 | |
| Mark Barlow Mar | 14154// at | | cittib | | riusina mentarane | i copiu | | 3.312 03 | | 1.750 01 | 0.05 | 0.140 01 | 0.57 | 1.130.03 | 1.71 | 4.570.01 | 1.03 | |
| BACK Marter Model Marter | 1422567 at | | | similarity 129, member A | Cytoplasm | other transcription | | | | | | | | | | | | |
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| Diable Original Original Diable Original Diable Di | 1417268_at | | | transmembrane protein | Plasma Membrane | receptor | | | | | | | | | | | | |
| Bit A Diameter A | 1425025 at | | TMEM106A | 106A | unknown | other | | 1.54E-04 | 2.18 | 4.04E-01 | 1.07 | 4.63E-01 | 1.05 | 8.46E-01 | 1.01 | 8.25E-01 | 1.01 | |
| And and any and any any any any any any any any any any | 1449645 s at | | CCT3 | | Cytoplasm | other | | 4.12E-05 | 2.17 | 9.44E-01 | 1.00 | 6.49E-01 | 0.98 | 1.44E-01 | 1.08 | 7.44E-01 | 1.02 | |
| | | | | testis derived transcript | | | | | | | | | | | | | | |
| CAD CAD <thcad< th=""> <thcad< th=""> <thcad< th=""></thcad<></thcad<></thcad<> | 1460378 a at 1422621 at | Duplicate Gene Syn Duplicate Gene Syn | TES RANBP2 | RAN binding protein 2 | Plasma Membrane Nucleus | other enzyme | | 4.14E-04 8.37E-05 | 2.17 2.17 | 5.79E-01 8.67E-01 | 0.96 | 5.92E-01 7.99E-01 | 0.95 | 2.89E-01 4.40E-01 | 1.09 | 6.37E-01 1.37E-01 | 0.96 | |
| CDA J CDA J <th< td=""><td></td><td></td><td></td><td>thymocyte selection associated family</td><td>l</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></th<> | | | | thymocyte selection associated family | l | | | | | | | | | | | | | |
| CHILA CHILA <th< td=""><td>1427041_at</td><td></td><td>THEMIS2</td><td>member 2 translation machinery</td><td>unknown</td><td>other</td><td>1</td><td>7.90E-06</td><td>2.17</td><td>4.12E-01</td><td>0.97</td><td>3.48E-01</td><td>0.95</td><td>2.49E-02</td><td>1.12</td><td>5.53E-01</td><td>1.02</td></th<> | 1427041_at | | THEMIS2 | member 2 translation machinery | unknown | other | 1 | 7.90E-06 | 2.17 | 4.12E-01 | 0.97 | 3.48E-01 | 0.95 | 2.49E-02 | 1.12 | 5.53E-01 | 1.02 | |
| Note Note <th< td=""><td>1423289_a_at</td><td></td><td>TMA16</td><td>associated 16 homolog (S. cerevisiae)</td><td>unknown</td><td>other</td><td> </td><td>1.89E-05</td><td>2.16</td><td>1.38E-01</td><td>1.06</td><td>3.52E-01</td><td>0.97</td><td>5.34E-02</td><td>1.13</td><td>9.28E-01</td><td>1.00</td></th<> | 1423289_a_at | | TMA16 | associated 16 homolog (S. cerevisiae) | unknown | other | | 1.89E-05 | 2.16 | 1.38E-01 | 1.06 | 3.52E-01 | 0.97 | 5.34E-02 | 1.13 | 9.28E-01 | 1.00 | |
| Note Note <th< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></th<> | | | | | | | | | | | | | | | | | | |
| Note Note <th< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></th<> | | | | | | | | | | | | | | | | | | |
| Note Note <th< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></th<> | | | | | | | | | | | | | | | | | | |
| No. No. <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>ethoxyzolamid e,</td> <td></td> | | | | | | | ethoxyzolamid e, | | | | | | | | | | | |
| Ale of the sector of | | | | | | | dichlorphenam ide, | | | | | | | | | | | |
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| | | | | | | | hydrochlorothi azide, | | | | | | | | | | | |
| | | | | | | | acetazolamide, trichloromethi | | | | | | | | | | | |
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| | | | | | | | chlorothiazide, dorzolamide/ti | | | | | | | | | | | |
| | | | | | | | molol, | | | | | | | | | | | |
| And And </td <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>brinzolamide,</td> <td></td> | | | | | | | brinzolamide, | | | | | | | | | | | |
| | | | | | | | brinzolamide, quinethazone, chlorthalidone, | | | | | | | | | | | |
| 1337 4 Mode Mode Machine machine<="" th=""> <th< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td>brinzolamide, quinethazone, chlorthalidone, benzthiazide,</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></th<></th> | <th< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td>brinzolamide, quinethazone, chlorthalidone, benzthiazide,</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></th<> | | | | | | | brinzolamide, quinethazone, chlorthalidone, benzthiazide, | | | | | | | | | | |
| General Barber Barb | 1448752 at | | CA2 | | Cytoplasm | еплуте | brinzolamide, quinethazone, chlorthalidone, benzthiazide, sulfacetamide, | 1.11E-05 | 2.16 | 9.55E-02 | 0.91 | 4.698-02 | 0.95 | 3.88E-03 | 1.25 | 1.73E-01 | 0.98 | |
| Lings Dirth Dirth Dirth Dirth Link 0 Link 0 <thlink 0<="" th=""></thlink> | 1436337 at | | CA2 TMEM243 | transmembrane protein 243, mitochondrial | unknown | other | brinzolamide, quinethazone, chlorthalidone, benzthiazide, sulfacetamide, | 2.60E-03 | 2.15 | 3.21E-01 | 0.87 | 7.64E-01 | 1.05 | 5.04E-01 | 1.09 | 5.79E-01 | 0.94 | |
| Shall at 0 Other And 0 N 18 0 <thn 0<="" 18="" th=""> N 18 0 <thn 0<<="" 18="" td=""><td></td><td></td><td>PLEK</td><td>transmembrane protein 243, mitochondrial pleckstrin RAN binding protein 2</td><td>unknown Cytoplasm</td><td>other other</td><td>brinzolamide, quinethazone, chlorthalidone, benzthiazide, sulfacetamide,</td><td>2.60E-03 1.60E-10</td><td>2.15 2.15</td><td>3.21E-01 8.63E-01</td><td>0.87</td><td>7.64E-01 3.61E-01</td><td>1.05 1.01</td><td>5.04E-01 1.00E-05</td><td>1.09</td><td>5.79E-01 2.20E-02</td><td>0.94</td></thn></thn> | | | PLEK | transmembrane protein 243, mitochondrial pleckstrin RAN binding protein 2 | unknown Cytoplasm | other other | brinzolamide, quinethazone, chlorthalidone, benzthiazide, sulfacetamide, | 2.60E-03 1.60E-10 | 2.15 2.15 | 3.21E-01 8.63E-01 | 0.87 | 7.64E-01 3.61E-01 | 1.05 1.01 | 5.04E-01 1.00E-05 | 1.09 | 5.79E-01 2.20E-02 | 0.94 | |
| CALC | 1436337 at 1448748 at | | PLEK RANBP2 | transmembrane protein 243, mitochondrial pleckstrin RAN binding protein 2 pyrophosphatase (inorganic) 1 | unknown Cytoplasm Nucleus | other other enzyme | brinzolamide, quinethazone, chlorthalidone, benzthiazide, sulfacetamide, | 2.60E-03 1.60E-10 6.95E-04 | 2.15 2.15 2.15 | 3.21E-01 8.63E-01 5.99E-01 | 0.87 1.00 1.04 | 7.64E-01 3.61E-01 6.18E-01 | 1.05 1.01 1.04 | 5.04E-01 1.00E-05 7.86E-02 | 1.09 1.21 1.21 | 5.79E-01 2.20E-02 7.17E-02 | 0.94 1.10 1.22 | |
| Linit a Open and bias And bias And bias Justice Justice <thjustice< th=""> Justice Justice</thjustice<> | 1436337 at 1448748 at 1450690 at | | PLEK RANBP2 PPA1 | transmembrane protein 243, mitochondrial pleckstrin RAN binding protein 2 pyrophosphatase (inorganic) 1 chromosome 19 open | unknown Cytoplasm Nucleus Cytoplasm | other other enzyme enzyme | brinzolamide, quinethazone, chlorthalidone, benzthiazide, sulfacetamide, | 2.60E-03 1.60E-10 6.95E-04 1.64E-05 | 2.15 2.15 2.15 2.15 | 3.21E-01 8.63E-01 5.99E-01 8.76E-01 | 0.87 1.00 1.04 1.01 | 7.64E-01 3.61E-01 6.18E-01 6.81E-01 | 1.05 1.01 1.04 0.99 | 5.04E-01 1.00E-05 7.86E-02 1.11E-01 | 1.09 1.21 1.21 1.06 | 5.79E-01 2.20E-02 7.17E-02 1.10E-01 | 0.94 1.10 1.22 1.06 | |
| 1177 # 1000 Monl. | 1436337 at 1448748 at 1450690 at 1416939_at | | PLEK RANBP2 PPA1 | transmembrane protein 243, mitochondrial plecktrin RAN binding protein 2 pyrophosphatase (inorganic) 1 chromosome 19 open reading frame 12 oxidative stress induced | unknown Cytoplasm Nucleus Cytoplasm | other other enzyme enzyme | brinzolamide, quinethazone, chlorthalidone, benzthiazide, sulfacetamide, | 2.60E-03 1.60E-10 6.95E-04 1.64E-05 | 2.15 2.15 2.15 2.15 | 3.21E-01 8.63E-01 5.99E-01 8.76E-01 | 0.87 1.00 1.04 1.01 | 7.64E-01 3.61E-01 6.18E-01 6.81E-01 | 1.05 1.01 1.04 0.99 | 5.04E-01 1.00E-05 7.86E-02 1.11E-01 | 1.09 1.21 1.21 1.06 | 5.79E-01 2.20E-02 7.17E-02 1.10E-01 | 0.94 1.10 1.22 1.06 | |
| | 1436337 at 1448748 at 1450690 at 1416939_at | | PLEK RANBP2 PPA1 C19orf12 | transmembrane protein 243, mitochondrial pleckstrin RAN binding protein 2 pyrophosphatase (inorganic) 1 chromosome 19 open reading frame 12 oxidative stress induced growth inhibitor family member 2 | unknown Cytoplasm Nucleus Cytoplasm unknown | other other enzyme enzyme | brinzolamide, quinethazone, chlorthalidone, benzthiazide, sulfacetamide, | 2.60E-03 1.60E-10 6.95E-04 1.64E-05 7.13E-05 | 2.15 2.15 2.15 2.15 2.15 2.14 | 3.21E-01 8.63E-01 5.99E-01 8.76E-01 2.79E-01 | 0.87 1.00 1.04 1.01 0.96 | 7.64E-01 3.61E-01 6.18E-01 6.81E-01 9.11E-01 | 1.05 1.01 1.04 0.99 1.01 | 5.04E-01 1.00E-05 7.86E-02 1.11E-01 8.21E-01 | 1.09 1.21 1.21 1.06 1.01 | 5.79E-01 2.20E-02 7.17E-02 1.10E-01 3.82E-02 | 0.94 1.10 1.22 1.06 0.91 | |
| cond cond <thcond< th=""> cond cond <thc< td=""><td>1436337 at 1448748 at 1450690 at 1450690 at 1416939_at 1424444 a at 14244289 at</td><td></td><td>PLEK RANBP2 PPA1 C19orf12 OSGIN2</td><td>transmembrane protein 243, mitochondrial peleckstrin 8AN binding protein 2 phytophorphatas (inorganic) chromosome 19 open reading frame 12 oxidative stress induced growth inhibitor family member 2 high mobility group nucleosomal binding</td><td>unknown Cytoplasm Nucleus Cytoplasm unknown unknown</td><td>other other enzyme enzyme</td><td>brinzolamide, quinethazone, chlorthalidone, benzthiazide, sulfacetamide,</td><td>2.60E-03 1.60E-10 6.95E-04 1.64E-05 7.13E-05 2.28E-05</td><td>2.15 2.15 2.15 2.15 2.14 2.14</td><td>3.21E-01 8.63E-01 5.99E-01 8.76E-01 2.79E-01 2.68E-01</td><td>0.87 1.00 1.04 1.01 0.96 0.96</td><td>7.64E-01 3.61E-01 6.18E-01 9.11E-01 8.48E-01</td><td>1.05 1.01 1.04 0.99 1.01 0.99</td><td>5.04E-01 1.00E-05 7.86E-02 1.11E-01 8.21E-01 2.95E-02</td><td>1.09 1.21 1.21 1.06 1.01</td><td>5.79E-01 2.20E-02 7.17E-02 1.10E-01 3.82E-02 3.77E-01</td><td>0.94 1.10 1.22 1.06 0.91</td></thc<></thcond<> | 1436337 at 1448748 at 1450690 at 1450690 at 1416939_at 1424444 a at 14244289 at | | PLEK RANBP2 PPA1 C19orf12 OSGIN2 | transmembrane protein 243, mitochondrial peleckstrin 8AN binding protein 2 phytophorphatas (inorganic) chromosome 19 open reading frame 12 oxidative stress induced growth inhibitor family member 2 high mobility group nucleosomal binding | unknown Cytoplasm Nucleus Cytoplasm unknown unknown | other other enzyme enzyme | brinzolamide, quinethazone, chlorthalidone, benzthiazide, sulfacetamide, | 2.60E-03 1.60E-10 6.95E-04 1.64E-05 7.13E-05 2.28E-05 | 2.15 2.15 2.15 2.15 2.14 2.14 | 3.21E-01 8.63E-01 5.99E-01 8.76E-01 2.79E-01 2.68E-01 | 0.87 1.00 1.04 1.01 0.96 0.96 | 7.64E-01 3.61E-01 6.18E-01 9.11E-01 8.48E-01 | 1.05 1.01 1.04 0.99 1.01 0.99 | 5.04E-01 1.00E-05 7.86E-02 1.11E-01 8.21E-01 2.95E-02 | 1.09 1.21 1.21 1.06 1.01 | 5.79E-01 2.20E-02 7.17E-02 1.10E-01 3.82E-02 3.77E-01 | 0.94 1.10 1.22 1.06 0.91 | |
| ADD J # Processment of the state of the sta | 1436337 at 1448748 at 1450690 at 1416939 at 1424444 a at 1424289 at 1424777 a at | Duplicate Gene Syn | PLEK RANBP2 PPA1 C19orf12 OSGIN2 Hmgn3 | transmembrane protein 243, mitochondrial pelockstrin RAN binding protein 2 prophosphatase (Inorganic) 1 chromosome 19 open reading frame 12 oxidative stress induced growth inhibitor family member 2 high mobility group nucleosomal binding domain 3 chloride intracellular channel 4 | unknown Cytoplasm Nucleus Cytoplasm unknown unknown Nucleus | other enter enzyme other other | brinzolamide, quinethazone, chlorthalidone, benzthiazide, sulfacetamide, | 2.60E-03 1.60E-10 6.95E-04 1.64E-05 7.13E-05 2.28E-05 3.95E-04 | 2.15 2.15 2.15 2.15 2.14 2.14 2.14 | 3.21E-01 8.63E-01 5.99E-01 8.76E-01 2.79E-01 2.68E-01 1.00E-01 | 0.87 1.00 1.04 1.01 0.96 0.96 | 7.64E-01 3.61E-01 6.18E-01 9.11E-01 8.48E-01 2.47E-01 | 1.05 1.01 1.04 0.99 1.01 0.99 0.94 | 5.04E-01 1.00E-05 7.86E-02 1.11E-01 8.21E-01 2.95E-02 2.46E-02 | 1.09 1.21 1.21 1.06 1.01 | 5.79E-01 2.20E-02 7.17E-02 1.10E-01 3.82E-02 3.77E-01 6.12E-02 | 0.94 1.10 1.22 1.06 0.91 1.05 1.11 | |
| 6071 a 672 b interference bases Data bases -5116 b 212 b 5126 b 108 4156 b 108 108 b 108 | 1436337 at 1448748 at 1450690 at 1416939 at 1424444 a at 1424289 at 1431777 a at 1438606 a at | Duplicate Gene Syn | PLEK RANBP2 PPA1 C19orf12 OSGIN2 Hmgn3 CLIC4 | transmembrane protein 243, mitochondrial aleckstrin RAN binding protein 2 prophosphatase (inorganic) 1 chromosome 19 open reading frame 12 onidative strass: induced prowth inhibitor family nember 2 Nigh mobility group nucleosoma binding domain 3 chloride (alamatication) histocompatibility 2, T | unknown Cytoplasm Nucleus Cytoplasm unknown unknown Nucleus | other enter enzyme other other | brinzolamide, quinethazone, chlorthalidone, benzthiazide, sulfacetamide, | 2.60E-03 1.60F-10 6.95E-04 1.64E-05 7.13E-05 2.28E-05 3.95E-04 1.24E-05 | 2.15 2.15 2.15 2.15 2.14 2.14 2.14 2.13 2.13 | 3.21E-01 8.63E-01 5.99E-01 8.76E-01 2.79E-01 2.68E-01 1.00E-01 3.71E-01 | 0.87 1.00 1.04 1.01 0.96 0.96 0.94 0.97 | 7.64E-01 3.61E-01 6.18E-01 9.11E-01 8.48E-01 2.47E-01 6.40E-01 | 1.05 1.01 1.04 0.99 1.01 0.99 0.99 0.94 0.99 | 5.04E-01 1.00E-05 7.86E-02 1.11E-01 8.21E-01 2.95E-02 2.46E-02 1.97E-01 | 1.09 1.21 1.21 1.06 1.01 1.14 1.13 1.07 | 5.79E-01 2.20E-02 7.17E-02 1.10E-01 3.82E-02 3.77E-01 6.12E-02 2.01E-02 | 0.94 1.10 1.22 1.06 0.91 1.05 1.11 1.08 | |
| Albed and stress 1 an | 1436337 at 1448748 at 1450690 at 1416939 at 1424444 a at 1424289 at 1424777 a at | Duplicate Gene Syn | PLEK RANBP2 PPA1 C19orf12 OSGIN2 Hmgn3 CLIC4 | transmembrane protein 243, michchondrial gelechtrin RAN Lindring protein gelechtrin RAN Lindring protein gelechtrin reading (trans 12 chromosome 10 spen reading (trans 12 chromosome 10 chromosome | unknown Cytoplasm Nucleus Cytoplasm unknown unknown Nucleus | other enter enzyme other other | brinzolamide, quinethazone, chlorthalidone, benzthiazide, sulfacetamide, | 2.60E-03 1.60F-10 6.95E-04 1.64E-05 7.13E-05 2.28E-05 3.95E-04 1.24E-05 | 2.15 2.15 2.15 2.15 2.14 2.14 2.14 2.13 2.13 | 3.21E-01 8.63E-01 5.99E-01 8.76E-01 2.79E-01 2.68E-01 1.00E-01 3.71E-01 | 0.87 1.00 1.04 1.01 0.96 0.96 0.94 0.97 | 7.64E-01 3.61E-01 6.18E-01 9.11E-01 8.48E-01 2.47E-01 6.40E-01 | 1.05 1.01 1.04 0.99 1.01 0.99 0.99 0.94 0.99 | 5.04E-01 1.00E-05 7.86E-02 1.11E-01 8.21E-01 2.95E-02 2.46E-02 1.97E-01 | 1.09 1.21 1.21 1.06 1.01 1.14 1.13 1.07 | 5.79E-01 2.20E-02 7.17E-02 1.10E-01 3.82E-02 3.77E-01 6.12E-02 2.01E-02 | 0.94 1.10 1.22 1.06 0.91 1.05 1.11 1.08 | |
| 13194 at 08105.0 verticate lance density 0x100 0.12 | 1436337 at 1448748 at 1450690 at 1416939 at 1424444 a at 1424289 at 1424289 at 1431777 a at 1438606 a at 143875 s at 1449875 s at | Duplicate Gene Syn | PLEK RANBP2 PPA1 C19orf12 OSGIN2 Hmgn3 CLIC4 H2-T9 RIPK2 | transmembrane protein 243, michondrala 246, michondrala 246, michondrala 246, michondrala 246, michondrala 247, michondrala 2 | unknown Cytoplasm Nucleus Cytoplasm unknown Nucleus Plasma Membrane unknown Plasma Membrane | other enzyme enzyme other other other ion channel other kinase | brinzolamide, quinethazone, chlorthalidone, benzthiazide, sulfacetamide, | 2.60E-03 1.60E-10 6.95E-04 1.64E-05 7.13E-05 2.28E-05 3.95E-04 1.24E-05 3.58E-05 9.33E-05 | 2.15 2.15 2.15 2.15 2.14 2.14 2.14 2.13 2.13 2.13 2.13 | 3.21E-01 8.63E-01 5.99E-01 8.76E-01 2.79E-01 2.68E-01 1.00E-01 3.71E-01 4.10E-01 9.72E-01 | 0.87 1.00 1.04 1.01 0.96 0.96 0.94 0.97 0.97 1.00 | 7.64E-01 3.61E-01 6.18E-01 9.11E-01 8.48E-01 2.47E-01 6.40E-01 6.12E-01 4.82E-01 | 1.05 1.01 1.04 0.99 1.01 0.99 0.94 0.99 1.03 1.04 | 5.04E-01 1.00E-05 7.86E-02 1.11E-01 8.21E-01 2.95E-02 2.46E-02 1.97E-01 3.13E-01 3.55E-01 | 1.09 1.21 1.21 1.05 1.01 1.14 1.13 1.07 0.96 | 5.79E-01 2.20E-02 7.17E-02 1.10E-01 3.82E-02 3.77E-01 6.12E-02 2.01E-02 8.30E-01 6.19E-01 | 0.94 1.10 1.22 1.06 0.91 1.05 1.11 1.08 0.99 0.98 | |
| ALDA Marcha Zaropa arma Marcha Zaropa (arma Marcha Zaropa (arma) Marcha Zaropa (arm | 1436337 at 1448748 at 1450690 at 1416939 at 1416939 at 1424444 a at 1424289 at 1431777 a at 1438606 a at 1449875 s at 1449875 s at 1431646 a at | Duplicate Gene Syn | PLEK RANBP2 PPA1 C19orf12 OSGIN2 Hmgn3 CLIC4 H2-T9 RIPK2 STX6 | transmembrane protein 243, michowodrail 244, michowodrail 246, mic | unknown Cytoplasm Nucleus Cytoplasm unknown Nucleus Plasma Membrane unknown Plasma Membrane | other enzyme enzyme other other other ion channel other kinase | brinzolamide, quinethazone, chlorthalidone, benzthiazide, sulfacetamide, | 2.60E.03 1.60E-10 6.55E.04 1.64E-05 7.13E-05 2.28E-05 2.28E-05 2.55E-04 1.24E-05 2.58E-05 2.58E-05 2.44E-06 | 2.15 2.15 2.15 2.15 2.14 2.14 2.14 2.14 2.13 2.13 2.13 2.13 2.12 2.12 2.12 | 221E-01 8.63E-01 5.99E-01 8.76E-01 2.79E-01 2.68E-01 1.00E-01 3.71E-01 4.10E-01 9.72E-01 5.86E-01 | 0.87 1.00 1.04 1.01 0.96 0.96 0.96 0.94 0.97 0.97 1.00 1.02 | 7.646-01 3.616-01 6.186-01 9.116-01 8.486-01 2.476-01 6.126-01 6.126-01 | 1.05 1.01 1.04 0.99 1.01 0.99 0.94 0.99 1.03 1.04 0.96 | 5.04E-01 1.00E-05 7.86E-02 1.11E-01 8.21E-01 2.95E-02 2.46E-02 1.97E-01 3.13E-01 3.13E-01 3.25E-02 | 1.09 1.21 1.21 1.05 1.01 1.14 1.13 1.07 0.96 | 5.796-01 2.206-02 7.17F-02 1.106-01 3.82F-02 3.77F-01 6.12F-02 2.01F-02 8.30F-01 5.59F-01 | 0.94 1.10 1.22 1.06 0.91 1.05 1.05 1.11 1.08 0.99 0.98 1.04 | |
| choose and sequences Normal method meth | 1436337 at 1448748 at 1450690 at 1416939 at 1424444 a at 1424289 at 1424289 at 1431777 a at 1438606 a at 143875 s at 1449875 s at | Duplicate Gene Syn | PLEK RANBP2 PPA1 C19orf12 OSGIN2 Hmgn3 CLIC4 H2-T9 RIPK2 STX6 | transmembrane protein 243, michowodrail 244, michowodrail 246, mic | unknown Crtoplasm Nacleus Crtoplasm unknown unknown Nacleus Piasma Membrane unknown Piasma Membrane Crtoplasm | other enzyme enzyme other other other ion channel other kinase | brinzolamide, quinethazone, chlorthalidone, benzthiazide, sulfacetamide, | 2.60E.03 1.60E-10 6.55E.04 1.64E-05 7.13E-05 2.28E-05 2.28E-05 2.55E-04 1.24E-05 2.58E-05 2.58E-05 2.44E-06 | 2.15 2.15 2.15 2.15 2.14 2.14 2.14 2.14 2.13 2.13 2.13 2.13 2.12 2.12 2.12 | 221E-01 8.63E-01 5.99E-01 8.76E-01 2.79E-01 2.68E-01 1.00E-01 3.71E-01 4.10E-01 9.72E-01 5.86E-01 | 0.87 1.00 1.04 1.01 0.96 0.96 0.96 0.94 0.97 0.97 1.00 1.02 | 7.646-01 3.616-01 6.186-01 9.116-01 8.486-01 2.476-01 6.126-01 6.126-01 | 1.05 1.01 1.04 0.99 1.01 0.99 0.94 0.99 1.03 1.04 0.96 | 5.04E-01 1.00E-05 7.86E-02 1.11E-01 8.21E-01 2.95E-02 2.46E-02 1.97E-01 3.13E-01 3.13E-01 3.25E-02 | 1.09 1.21 1.31 1.05 1.01 1.14 1.13 1.07 0.95 1.04 1.08 | 5.796-01 2.206-02 7.17F-02 1.106-01 3.82F-02 3.77F-01 6.12F-02 2.01F-02 8.30F-01 5.59F-01 | 0.94 1.10 1.22 1.06 0.91 1.05 1.05 1.11 1.08 0.99 0.98 1.04 | |
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| 4204_st Diplotes Georgy F068 calconic resulting and service of the service of th | 1430327 at 144544 pr 1450900 at 1450900 at 1416939 at 1416939 at 1424244 p at 1432444 p at 1431466 p at 1431466 pt | Duplicate Gene Syn | PLEK PLEK RANDP2 | tanomedicane protein datastructural desktimi desktimi desktimi morphical desktimi morphical desktimi morphical prophicipatase improphicipatase improphicipatase improphical sopenit nadium stress induced growth induced argenitis induced domain 3. clonde datastress induced domain 3. clonde datastress induced domain 3. histocompatibility prou- methydicastress induced domain 3. histocompatibility 7. receptor induced argenitis feast 6. 3. hydrom- | uninown Cropilasm Molese Cropolasm writnown Nacleus Plasma Membrane uninown Plasma Membrane Plasma Membrane | other other enyme other other other other other other ion channel other ion channel other in channel transporter enyme transporter transporter | brinzdamide, quinettazone, chiertalidone, benthaaidon, soliseetamide, operanate chiertalione, chiert | 2 655 63 1 655 10 6 555 64 1 64E 65 2 25E 65 2 25E 65 2 355 64 1 24E 65 9 33E 65 2 44E 66 3 14E 65 | 2.15 2.15 2.15 2.25 2.24 2.14 2.13 2.13 2.13 2.13 2.13 2.12 2.12 2.12 | 2.316.01 8.63F.01 8.76F.01 2.79F.01 2.79F.01 2.68F.01 1.00F.01 3.771F.01 4.10F.01 9.72F.01 5.86F.01 2.51F.03 | 0.87 1.00 1.01 1.01 0.96 0.96 0.94 0.97 0.97 1.00 1.02 1.17 1.02 | 7.646.01 1.617.01 6.187.01 6.187.01 9.116.01 8.458-01 2.476.01 6.406.01 6.126.01 2.606.03 9.356.01 | 105 101 104 0.99 0.99 0.99 0.99 0.94 0.99 103 104 0.96 1.34 | 5.046-01 1.006-05 2.866-02 1.11E-01 2.956-02 2.466-02 1.976-01 3.13E-01 3.556-01 3.556-01 3.556-01 3.556-03 | 109 121 121 105 101 104 114 113 107 0.96 104 108 151 126 | 5.786.01 2.206.02 2.176.02 1.106.01 3.826.02 2.776.01 6.126.02 2.016.02 8.306.01 5.596.01 1.216.04 4.226.01 | 0.94 1.10 1.22 1.06 0.91 1.05 1.05 1.05 0.99 0.98 1.04 1.50 1.50 | |
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| Image: synthesis (5-r) (simpletrahydródiste synthesis (5-r) (simpletrahydródiste (7-c)[singet] image: synthesis (5-r) (simpletrahydródiste (7-c)[singet] image: synthesis (5-r) (7-c)[singet] | 145537 at 144528 at 146529 at 141529 at 1215292 at 123277 a at 143377 a at 1433605 at 1433605 at 1433665 at 143366 at 143366 at 143277 at 143865 at 14486 at 1448 | Duglicate Gene Syn | PLEX PAGE 2 | taonomekane potein taonomekane potein Jest Nimora Jest Nimora Jest Nimora Jest Nimora Innogane 11 Nigh molitari Nigh molitari Nigh molitari Nigh molitari Might Might | unknown Cytoglasm Vectors Cytoglasm Weltow Unknown Nacleus Plasma Membrane Unknown Plasma Membrane Cytoglasm Plasma Membrane Cytoglasm Unknown Unknown | other other enzyme enzyme other other other is in channel is in channel | brinsdamide, guinethazone, usinethazone, benchhazde, souffactamide, topizamate souffactamide, souffactamide, souffactamide, souffactamide, develeukin, | 2 60E 43 1 60E 40 6 59E 64 2 28E 65 2 28E 65 2 28E 65 2 39E 64 1 24E 65 0 31E 65 0 31E 65 3 59E 66 3 14E 66 5 8PE 65 3 88E 66 1 48E 63 | 2.35 2.35 2.35 2.34 2.34 2.33 2.13 2.13 2.12 2.12 2.12 2.12 2.12 | 221E-01 261E-01 259E-01 279E-01 268E-01 100E-01 3.71E-01 4.10E-01 9.77E-01 5.84E-01 2.51E-03 5.95E-01 7.54E-01 7.54E-01 7.54E-01 2.51E-01 2.51E-01 | 0.87 1.00 1.04 1.01 0.95 0.95 0.95 0.97 1.00 1.02 1.01 1.02 1.01 0.99 0.99 0.99 0.99 0.99 0.99 | 7.6% 01 3.6% 01 6.1% 01 6.1% 01 9.1% 01 2.4% 01 6.4% 01 6.4% 01 6.4% 01 6.1% 01 2.6% 03 9.3% 01 5.7% 01 4.0% 01 3.8% 01 | 105 101 101 0.99 0.99 0.99 103 104 0.96 1.04 0.96 1.04 0.96 1.04 0.96 1.04 0.96 1.03 0.98 0.99 | 5 046 01 1 006 05 2 986 02 2 986 02 2 996 02 2 466 02 1 976 01 3 1976 01 3 1976 01 3 1976 01 3 1976 01 3 1976 01 3 496 02 2 786 03 3 856 02 2 786 03 1 006 03 1 466 01 | 109 123 123 124 106 101 114 113 107 0.96 104 108 1.08 1.51 1.22 1.54 0.85 | 579E-01 2206-02 217E-02 110E-01 3.87E-02 2.01E-0 | 0.94 1.10 1.02 1.05 0.91 1.05 1.11 1.08 0.99 0.98 1.04 1.09 1.04 1.09 1.04 1.05 1.05 1.05 1.01 1.05 0.99 0.99 0.98 1.04 0.99 0.98 1.05 0.99 0.99 0.99 0.98 1.05 0.99 0.09 0.99 0.99 0.99 0.99 0.09 0.09 0.99 0.09 | |
| MMP#5 Optimizer Op | 14/5/37 at 14/6/29 at 14/6/290 at 14/6/290 at 14/6/290 at 14/2/200 at | Duplicate Gene Syn | PECK PRAT PPAT C19er12 OSGIN2 Hmgr3 CuC4 H273 PM PPAT PM PPAT PM PPAT PM PPAT PM PPAT PM PPAT PPAT | taonomenhane protein Januarian (Januarian) Januarian (Januarian) | unknown Cytoglasm Skelosi Cytoglasm Indenoun Ind | other other enzyme enzyme other other other ion channel other enzyme enzyme other other other other other other other other | brinsdamide, quinethazone, quinethazone, benchhaide, suffactamide, topiramate suffactamide, topiramate suffactamide, topiramate suffactamide, | 2 60E 63 1 60E 40 6 59E 64 2 28E 65 2 28E 65 2 28E 65 2 39E 64 1 24E 65 2 39E 64 1 24E 65 2 39E 64 3 39E 65 3 39E | 2.35 2.35 2.35 2.25 2.14 2.33 2.33 2.13 2.13 2.12 2.12 2.12 2.12 | 221E-01 261E-01 259E-01 277E-01 268E-01 107E-01 3.77E-01 4.10E-01 0.77E-01 3.77E-01 3.77E-01 3.77E-01 2.51E-03 5.95E-01 2.51E-03 7.54E-01 7.54E-01 2.54E-01 2.54E-01 2.54E-01 | 0.87 1.00 1.04 1.01 0.95 0.95 0.95 0.95 1.00 1.02 1.02 1.01 0.99 0.99 0.99 0.99 0.99 0.98 0.99 0.98 | 7.6% 01 3.616 01 6.1% 01 9.116 01 2.47% 01 4.42% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 1.106 01 1.106 01 | 105 101 101 0.99 0.99 0.99 103 104 0.99 103 104 0.96 0.99 103 0.99 103 0.99 103 0.99 103 0.99 103 0.99 103 0.99 103 104 0.99 103 104 0.99 103 104 0.99 103 104 0.99 103 104 104 0.99 103 104 104 0.99 103 104 104 0.99 103 104 104 0.99 103 104 104 0.99 103 104 104 0.99 103 104 104 0.99 103 104 104 0.99 103 104 104 0.99 103 104 104 105 104 105 104 105 104 105 104 105 105 104 105 105 105 105 105 105 105 105 | 6 086 01 1 006 05 7 866 02 2 866 02 2 996 02 2 466 02 1 976 01 3 1976 01 3 1976 01 3 1976 01 3 1976 01 3 1976 01 3 1976 01 3 1976 01 3 4 566 02 2 786 03 8 866 02 2 786 03 1 466 01 1 4066 02 | 109 121 121 121 123 106 101 131 107 0.96 104 108 155 122 133 122 154 0.85 154 | 5 79E-01 2 20E-02 7 17F-02 3 77E-01 6 12E-02 2 01E-02 8 30E-01 6 12E-02 2 01E-02 8 30E-01 6 12E-02 2 01E-02 8 30E-01 1 3 59E-01 1 10E-01 5 30E-02 5 30E-02 3 30E-02 9 09E-02 | 0.94 1.10 1.02 1.05 0.91 1.05 0.93 1.05 0.99 0.98 1.04 1.05 1 | |
| 427314 s.at RAA3551 DAA3551 arknown other 3121 65 207 8.86E-01 0.99 991E-01 100 9.81E-03 138 8.66E-02 108 | 145237 at 146245 at 146256 at 211299 at 121299 at 122444 a at 132050 at 132050 at 132050 at 132050 at 133050 at 145050 at 1430500 at 1430500 at 1430500 at 1430500 at 1430500 at 1430500 at 145 | Duplicate Gene Syn | PECK PRAT PPAT C19er12 OSGIN2 Hmgr3 CuC4 H273 PM PPAT PM PPAT PM PPAT PM PPAT PM PPAT PM PPAT PPAT | tanomediane protein Jaskstmin Jaskstmin Rohl andre green 2. pryrophosphatase (mogranic) 1. mogranic) 1. mogranic) 1. mogranic) 1. mogranic | unknown Cytoglasm Skelosi Cytoglasm Indenoun Ind | other other enzyme enzyme other other other ion channel other enzyme enzyme other other other other other other other other | brinsdamide, quinethazone, quinethazone, benchhaide, suffactamide, topiramate suffactamide, topiramate suffactamide, topiramate suffactamide, | 2 60E 63 1 60E 40 6 59E 64 2 28E 65 2 28E 65 2 28E 65 2 39E 64 1 24E 65 2 39E 64 1 24E 65 2 39E 64 3 39E 65 3 39E | 2.35 2.35 2.35 2.25 2.14 2.33 2.33 2.13 2.13 2.12 2.12 2.12 2.12 | 221E-01 261E-01 259E-01 277E-01 268E-01 107E-01 3.77E-01 4.10E-01 0.77E-01 3.77E-01 3.77E-01 3.77E-01 2.51E-03 5.95E-01 2.51E-03 7.54E-01 7.54E-01 2.54E-01 2.54E-01 2.54E-01 | 0.87 1.00 1.04 1.01 0.95 0.95 0.95 0.95 1.00 1.02 1.02 1.01 0.99 0.99 0.99 0.99 0.99 0.98 0.99 0.98 | 7.6% 01 3.616 01 6.1% 01 9.116 01 2.47% 01 4.42% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 4.224% 01 1.106 01 1.106 01 | 105 101 101 0.99 0.99 0.99 103 104 0.99 103 104 0.96 0.99 103 0.99 103 0.99 103 0.99 103 0.99 103 0.99 103 0.99 103 104 0.99 103 104 0.99 103 104 0.99 103 104 105 0.99 103 104 105 104 105 105 105 105 105 105 105 105 | 6 086 01 1 006 05 7 866 02 2 866 02 2 996 02 2 466 02 1 976 01 3 1976 01 3 1976 01 3 1976 01 3 1976 01 3 1976 01 3 1976 01 3 1976 01 3 4 566 02 2 786 03 8 866 02 2 786 03 1 466 01 1 4066 02 | 109 121 121 121 123 106 101 131 107 0.96 104 108 155 122 133 122 154 0.85 154 | 5 79E-01 2 20E-02 7 17F-02 3 77E-01 6 12E-02 2 01E-02 8 30E-01 6 12E-02 2 01E-02 8 30E-01 6 12E-02 2 01E-02 8 30E-01 1 3 59E-01 1 10E-01 5 30E-02 5 30E-02 3 30E-02 9 09E-02 | 0.94 1.10 1.02 1.05 0.91 1.05 0.93 1.05 0.99 0.98 1.04 1.05 1 | |
| 448898_at Cc9 igard 5 tenace/lular.5pace prekine 1.56F-03 2.07 2.14E-01 0.98 9.40E-01 0.99 1.20E-01 1.19 5.00-01 1.04 | 145237 at 146245 at 146256 at 211299 at 121299 at 122444 a at 132050 at 132050 at 132050 at 132050 at 133050 at 145050 at 1430500 at 1430500 at 1430500 at 1430500 at 1430500 at 1430500 at 145 | Duplicate Gene Syn | PLOS 000000000000000000000000000000000000 | sanomenicane protein Jaka missichardina jelektivit Jelektivit | unknown Cytoglasm Nectors Cytoglasm Inform I | other other enzyme enzyme other other other iner channel other iner channel other enzyme other other other other other other other other | brinsdamide, quinethazone, quinethazone, benchhaide, suffactamide, topiramate suffactamide, topiramate suffactamide, topiramate suffactamide, | 2 60E 43 1 60E 40 6 59E 64 2 28E 65 2 28E 65 3 39E 64 1 24E 65 3 39E 64 1 24E 65 3 39E 64 3 39E 65 3 34E 65 5 82E 65 5 84E 66 3 34E 65 1 49E 63 1 49E 63 1 49E 63 1 49E 65 1 49E 65 7 39E 65 7 39E 65 7 32E 65 7 32E 65 7 32E 65 | 2.35 2.35 2.35 2.35 2.34 2.33 2.33 2.33 2.33 2.33 2.32 2.32 | 221E-01 261E-01 259E-01 278E-01 278E-01 278E-01 278E-01 278E-01 278E-01 278E-01 251E-03 595E-01 251E-03 595E-01 251E-03 754E-01 754E-01 248 | 0.87 1.00 1.04 1.01 0.95 0.95 0.95 0.95 1.00 1.02 1.00 1.02 1.02 1.01 0.99 0 | 265 01 3616 01 618 01 618 01 2475 01 6486 01 2475 01 6124 01 6124 01 6124 01 6124 01 2475 01 4275 0 | 105 101 101 0.99 0.99 103 103 104 0.99 103 104 0.99 103 104 0.99 103 104 0.99 103 104 104 105 105 105 105 105 105 105 105 | 6 086 01 1 006 05 2 864 02 2 864 02 2 956 02 2 466 02 3 186 01 3 186 01 3 556 | 109 121 121 121 123 124 124 124 126 133 107 0.96 104 108 109 109 109 109 109 109 109 109 | 5786-01 2206-02 7175-02 1106-01 3.826-02 6.126-02 8.306-01 5.598-01 1.216-04 4.226-01 1.216-04 4.226-01 1.216-04 5.396-02 3.306-02 3.416-01 9.096-02 4.336-01 9.096-02 4.336-01 | 0.94 1.10 1.05 0.91 1.05 1.11 1.06 0.99 0.98 1.04 1.30 1.03 1.03 1.03 1.03 1.03 1.03 1.04 1.05 1.05 1.05 1.09 1.05 1 | |
| | 146537 at 146784 at 146794 at 146793 at 1416939 at 1416939 at 142645 a at 1426289 at 142695 a at 143846 at 1416276 at 1418292 at 1418292 at 1418292 at 1418292 at 1418292 at 1418292 at 1418292 at 1418292 at 1418292 at 1418292 at 1418292 at 1418292 at 1418292 at 1418292 at 1418292 at 1418293 a | Duplicate Gene Syn | PLEX PLEX PLEX PLEX PLEX PLEX PLEX PLEX | sammenbare protein set and the set of the s | unknown Cytoplasm Skeinen Cytoplasm Naclous Plasma Membrane Cytoplasm Plasma Membrane Cytoplasm Unknown Cytoplasm Cytoplasm Cytoplasm Cytoplasm Cytoplasm Cytoplasm Cytoplasm | other other enzyme enzyme enzyme other other other unanomer enzyme other other other other other other other other other other other other other | brinsdamide, quinethazone, quinethazone, benchhaide, suffactamide, topiramate suffactamide, topiramate suffactamide, topiramate suffactamide, | 2 60E 63 1 60E 40 6 59E 64 2 28E 65 2 28E 65 2 28E 65 3 39E 64 1 24E 66 3 39E 64 3 39E 64 3 39E 66 3 39E 66 3 34E 66 5 58E 65 5 58E 66 5 58E 66 3 34E 66 1 49E 63 7 29E 65 1 49E 63 7 12E 65 1 05E 65 1 05E 65 1 12E 65 1 05E 65 1 05E 65 1 12E 65 1 05E 65 1 05E 65 1 12E 65 1 05E 65 1 05E 65 1 12E 65 1 05E 65 1 05E 65 1 12E 65 1 05E 65 1 12E 65 1 05E 65 1 12E | 2.35 2.35 2.35 2.14 2.34 2.33 2.33 2.13 2.13 2.12 2.12 2.12 2.12 | 221E-01 2401E-01 2597E-01 277E-01 267E-01 277E-01 267E-01 277E-01 277E-01 377E-01 377E-01 251E-03 2 | 0.87 1.00 1.04 1.01 0.95 0.95 0.95 0.95 1.00 1.02 1.01 1.02 1.01 0.99 0 | 265 01 3614 01 618 01 9 114 01 8 487 01 2 477 01 4 497 01 4 497 01 4 574 01 0 396 01 5 746 01 4 034 01 1 106 01 3 395 01 1 106 01 8 395 01 8 545 01 9 107 01 8 395 01 8 545 01 9 107 01 8 395 01 8 545 01 9 107 01 8 395 01 8 545 01 9 107 01 8 395 01 8 545 01 9 107 01 8 395 01 8 | 105 101 101 0.99 0.99 0.99 103 104 0.99 103 104 0.99 0.99 103 104 0.99 0.99 103 104 0.99 103 104 0.99 103 104 0.99 103 104 0.99 103 104 0.99 103 104 105 0.99 103 104 105 105 105 105 105 105 105 105 | 5 086 01 1 006 05 7 864 02 2 864 02 2 956 02 2 466 02 1 976 01 1 3 116 01 3 556 01 3 556 03 3 55 | 109 121 121 121 121 121 121 121 12 | 5786-01 2206-02 2176-02 1106-01 3276-02 0.126-02 0.126-02 0.126-02 0.126-02 0.126-02 0.126-02 0.126-02 0.096-02 0 | 0.94 1.10 1.05 0.91 1.05 1.05 1.11 1.06 0.99 0.98 1.04 1.05 1 | |

| | | | | | | | Stimulat | | | Сотрок | nd Only | | | Stimulation a | nd Compound | |
|---|--|---|--|--|---|--|--|--|--|--|--|---|--|--|--|--|
| | ĺ | | Probe Set Description regulatory factor X, 5 | i | i | i – | CpG vs. | Medium | 0.25 uM E644 | 16 vs. Medium | 1.25 uM E644 | 6 vs. Medium | CpG + 0.25 u | M E6446 vs. Medium | CpG + 1.25 u | M E6446 vs. Medium |
| 1423103 at | | RFX5 | (influences HLA class II expression) | Nucleus | transcription regulator | | 6.23E-06 | 2.06 | 2.35E-01 | 0.97 | 7.30E-01 | 0.98 | 3.43E-03 | 1.13 | 7.10E-01 | 1.01 |
| 1426324 at Duplic | icate Gene Syn | HLA-B | major histocompatibility complex, class I, B | Plasma Membrane | transmembrane receptor | | 1.07E-05 | 2.06 | 4.76E-01 | 1.03 | 9.79E-01 | 1.00 | 3.18E-03 | 1.27 | 8.47E-02 | 1.07 |
| 1419132 at | | TLR2 | toll-like receptor 2 | Plasma Membrane | transmembrane receptor | | 5.44E-05 | 2.06 | 1.98E-01 | 1.06 | 9.84E-01 | 1.00 | 8.68E-05 | 1.77 | 9.47E-02 | 1.07 |
| 1452225_at Duplic | icate Gene Syn | SPPL2A | signal peptide peptidase like 2A N(alpha)- | Plasma Membrane | peptidase | | 6.51E-06 | 2.05 | 8.45E-01 | 1.00 | 3.13E-01 | 1.03 | 2.31E-01 | 1.06 | 3.18E-02 | 1.11 |
| 1418244_at | | NAA20 | acetyltransferase 20, NatB catalytic subunit | Cytoplasm | enzyme transcription | | 4.23E-05 | 2.05 | 7.44E-01 | 0.99 | 4.62E-01 | 1.01 | 6.18E-01 | 0.98 | 1.04E-01 | 1.03 |
| 1419111 at | | ING2 | inhibitor of growth family, member 2 | Nucleus | regulator | | 8.91E-05 | 2.05 | 3.77E-01 | 1.02 | 4.71E-01 | 1.03 | 8.44E-01 | 0.99 | 3.08E-01 | 1.04 |
| 1434547 at | | CPD | carboxypeptidase D chemokine (C-C motif) | Extracellular Space | peptidase | maraviroc, | 1.07E-05 | 2.04 | 6.49E-01 | 0.98 | 7.60E-02 | 0.91 | 4.08E-01 | 0.96 | 8.34E-01 | 1.01 |
| 1424727 at Duplic | icate Gene Syn | CCR5 | receptor 5 (gene/pseudogene) cytochrome P450, family | Plasma Membrane | G-protein coupled receptor | vicriviroc, SCH 351125 | 8.35E-05 | 2.04 | 5.41E-01 | 0.98 | 4.62E-02 | 0.94 | 4.79E-01 | 0.98 | 4.30E-01 | 0.97 |
| 1450646 at | | CYP51A1 | 51, subfamily A, polypeptide 1 | Cytoplasm | enzyme | itraconazole | 8.63E-05 | 2.04 | 3.71E-01 | 1.05 | 1.44E-02 | 1.23 | 1.47E-03 | 1.38 | 1.34E-03 | 1.40 |
| 1416401_at | | CD82 | CD82 molecule | Plasma Membrane | other transcription | | 7.68E-06 | 2.03 | 5.76E-01 | 0.98 | 8.09E-01 | 0.99 | 5.18E-03 | 1.22 | 5.54E-01 | 0.99 |
| 1419537 at | | TFEC | transcription factor EC SAM domain and HD | Nucleus | regulator | | 1.07E-05 | 2.03 | 5.65E-01 | 0.97 | 4.09E-02 | 0.90 | 4.25E-04 | 1.33 | 1.10E-01 | 1.09 |
| 1418131 at | | SAMHD1 | domain 1 | Nucleus | enzyme | | 2.50E-06 | 2.03 | 3.59E-01 | 0.98 | 4.10E-01 | 0.98 | 1.13E-02 | 0.93 | 5.00E-01 | 0.98 |
| 1416407 at | | PEA15 | phosphoprotein enriched in astrocytes 15 | Cytoplasm | transporter | | 2.42E-05 | 2.02 | 6.65E-01 | 1.02 | 9.65E-01 | 1.00 | 5.95E-03 | 1.23 | 4.48E-02 | 1.13 |
| 1424246 a at Duplic | icate Gene Syn | TES | testis derived transcript (3 LIM domains) | Plasma Membrane | other | | 2.33E-05 | 2.02 | 9.32E-01 | 1.00 | 8.72E-01 | 1.00 | 6.14E-03 | 1.13 | 7.04E-01 | 1.01 |
| 1417333_at | | RASA4 | RAS p21 protein activator 4 homocysteine-inducible, | Cytoplasm | other | | 1.88E-04 | 2.02 | 7.00E-01 | 1.02 | 3.70E-01 | 1.06 | 4.44E-02 | 1.19 | 1.43E-01 | 1.10 |
| | | | endoplasmic reticulum stress-inducible, | | | | | | | | | | | | | |
| 1435626_a_at | | HERPUD1 | ubiquitin-like domain member 1 | Cytoplasm | other | | 5.43E-06 | 2.02 | 7.89E-01 | 1.01 | 2.75E-01 | 0.95 | 1.82E-04 | 1.31 | 1.43E-01 | 1.03 |
| 1425412 at | | NLRP3 | NLR family, pyrin domain containing 3 YTH domain family, | Cytoplasm | other | | 2.59E-04 | 2.01 | 3.27E-01 | 1.06 | 4.52E-01 | 1.06 | 1.79E-02 | 1.22 | 2.12E-01 | 1.08 |
| 1437102 at | | YTHDF1 | member 1 expressed sequence | unknown | other | | 1.72E-05 | 2.01 | 2.79E-01 | 0.94 | 7.21E-01 | 0.99 | 3.46E-01 | 1.05 | 2.73E-01 | 0.97 |
| 1434372_at 1452214 at | | AW112010 SKIL | AW112010 Ski-like oncogene | unknown Nucleus | other transcription regulator | - | 1.90E-04 2.17E-05 | 2.01 | 8.90E-02 7.35E-01 | 0.96 | 9.44E-01 2.93E-01 | 0.96 | 6.56E-02 3.45E-02 | 1.11 | 7.13E-02 1.43E-01 | 1.05 |
| 1451780 at | | BLNK | B-cell linker makorin ring finger | Cytoplasm | other | | 1.40E-05 | 2.00 | 2.30E-01 | 0.96 | 6.46E-01 | 0.97 | 2.66E-01 | 1.04 | 3.07E-01 | 1.03 |
| 1434853 x at | | MKRN1 | protein 1 | unknown | other | - | 9.34E-05 | 0.50 | 4.80E-01 | 0.97 | 8.65E-01 | 1.01 | 9.19E-02 | 0.93 | 5.82E-01 | 1.03 |
| 1425503 at | | GCNT2 | glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group) | Cytoplasm | enzyme | L | 1.00E-03 | 0.50 | 8.72E-01 | 1.01 | 5.93E-01 | 0.96 | 8.50E-01 | 1.02 | 5.55E-01 | 1.05 |
| | icate Gene Syn | ARHGAP9 | Rho GTPase activating protein 9 | Cytoplasm | other | | 4.76E-05 | 0.50 | 4.35E-01 | 0.97 | 8.39E-01 | 0.99 | 2.01E-01 | 0.93 | 2.27E-01 | 0.92 |
| 1449043 at | Ţ | NAGA | N- acetylgalactosaminidase, alpha- | Cytoplasm | enzyme | | 1.20E-04 | 0.50 | 3.82E-01 | 0.97 | 1.52E-01 | 0.94 | 8.14E-02 | 0.92 | 1.44E-02 | 0.90 |
| 1416683_at | | PLXNB2 | plexin B2 | Plasma Membrane | transmembrane receptor | | 2.86E-04 | 0.50 | 8.93E-01 | 0.99 | 8.16E-01 | 0.98 | 6.05E-01 | 0.92 | 9.26E-01 | 1.01 |
| | | | cytochrome c oxidase subunit VIIa polypeptide | | | | 1.13E-06 | 0.50 | | | 0.005.01 | | | 0.96 | | |
| 1421772_a_at Duplic | icate Gene Syn | LUX/AZL | 2 like | Cytoplasm | enzyme | | 1.131-06 | 0.50 | 1.80E-01 | 1.02 | 3.33E-01 | 1.02 | 3.71E-01 | 0.96 | 8.51E-01 | 1.00 |
| 1453596 at | | ID2 | 2, dominant negative helix-loop-helix protein | Nucleus | transcription regulator | | 4.41E-03 | 0.50 | 9.60E-01 | 0.99 | 7.68E-01 | 1.05 | 1.79E-01 | 1.17 | 6.02E-01 | 1.06 |
| | | SIPA1 | signal-induced | | | | 2.05E-04 | 0.50 | 7.40E-01 | 1.01 | | 0.98 | | 0.93 | 9.57E-01 | |
| 1416206 at 1417840 at | | CEP19 | proliferation-associated 1 centrosomal protein 19kDa | Cytoplasm | other | | 2.05E-04 | 0.50 | 2.17E-01 | 0.95 | 7.60E-01 3.68E-01 | 0.98 | 1.48E-01 1.22E-01 | 0.93 | 5.19E-01 | 1.00 |
| | | | sphingosine-1-phosphate | | | | | | | | | | | | | |
| 1450015 x at Duplic | icate Gene Syn | SGPP1 | phosphatase 1 phosphatidylinositol-5- phosphate 4-kinase, type | Cytoplasm | phosphatase | | 5.04E-05 | 0.50 | 4.07E-01 | 0.94 | 1.47E-01 | 0.94 | 4.45E-02 | 0.90 | 9.53E-01 | 1.00 |
| 1449404 at | | PIP4K2A | II, alpha suppressor of variegation | Cytoplasm | kinase | | 7.50E-05 | 0.50 | 7.29E-02 | 0.96 | 1.67E-01 | 0.93 | 1.62E-02 | 0.92 | 3.38E-01 | 0.97 |
| 1424059 at | | SUV420H2 | 4-20 homolog 2 (Drosophila) | Nucleus | enzyme | | 1.40E-04 | 0.50 | 9.57E-01 | 1.00 | 8.42E-01 | 1.01 | 2.96E-01 | 0.95 | 3.34E-01 | 1.04 |
| 1451421_a_at 1433756 at | | ROGDI S100PBP | rogdi homolog (Drosophila) S100P binding protein | unknown Nucleus | other | | 4.78E-05 5.26E-04 | 0.49 | 1.26E-01 7.54E-01 | 0.93 | 5.95E-01 9.85E-01 | 0.98 | 7.79E-01 4.27E-01 | 1.01 | 3.23E-01 5.46E-02 | 0.94 |
| | icate Gene Syn | MTA3 | metastasis associated 1 family, member 3 | Nucleus | other | | 2.91E-05 | 0.49 | 9.70E-01 | 1.00 | 1.43E-01 | 0.95 | 2.53E-03 | 0.87 | 3.20E-02 | 0.92 |
| 1451353 at Duplic | icate Gene Syn | TM6SF1 | transmembrane 6 superfamily member 1 | Plasma Membrane | other | | 5.76E-06 | 0.49 | 1.05E-01 | 0.96 | 9.83E-01 | 1.00 | 1.82E-02 | 0.94 | 2.90E-01 | 0.97 |
| 1427368 x at | | FES | feline sarcoma oncogene serine/threonine kinase | Cytoplasm | kinase | | | | | | | | | | | |
| 1417751_at | | STK10 | | | | | 1.14E-05 | 0.49 | 9.40E-01 | 1.00 | 6.05E-01 | 1.02 | 2.96E-01 | 0.97 | 1.82E-01 | 1.04 |
| | | | 10 | Cytoplasm | kinase | 4. 51.15 | 1.14E-05 3.24E-05 | 0.49 | 9.40E-01 4.17E-01 | 1.00 0.98 | 6.05E-01 1.71E-01 | 0.97 | 2.96E-01 2.79E-02 | 0.97 | | 1.04 |
| | | | 10 | Cytoplasm | kinase | dovitinib, tandutinib, XI 184 | | | | | | | | | 1.82E-01 | |
| 1 | | | 10 | Cytoplasm | kinase | XL184, ponatinib, sorafenib, | | | | | | | | | 1.82E-01 | |
| 1419538_at | | FLT3 | fms-related tyrosine kinase 3 | Cytoplasm Plasma Membrane | | XL184, ponatinib, | | | | | | | | | 1.82E-01 | |
| 1419538_at | | FLT3 | 10 fms-related tyrosine | | | XL184, ponatinib, sorafenib, lestaurtinib, | 3.24E-05 | 0.49 | 4.17E-01 | 0.98 | 1.71E-01 | 0.97 | 2.79E-02 | 0.94 | 1.82E-01 2.17E-02 | 0.92 |
| 1419538_at | | RLT3 | 10 fms-related tyrosine | | | XL184, ponatinib, sorafenib, lestaurtinib, CGP 41251 interferon | 3.24E-05 | 0.49 | 4.17E-01 | 0.98 | 1.71E-01 | 0.97 | 2.79E-02 | 0.94 | 1.82E-01 2.17E-02 | 0.92 |
| 1419538_at | | RLT3 | 10 fms-related tyrosine | | | XL184, ponatinib, sorafenib, lestaurtinib, CGP 41251 | 3.24E-05 | 0.49 | 4.17E-01 | 0.98 | 1.71E-01 | 0.97 | 2.79E-02 | 0.94 | 1.82E-01 2.17E-02 | 0.92 |
| 1419538_at | | RT3 | 10 fms-related tyrosine | | | XL184, ponatinib, sorafenib, lestaurtinib, CGP 41251 interferon alfacon-1, PEG- interferon alfa- 2a, interferon beta-1a, IFNA2, | 3.24E-05 | 0.49 | 4.17E-01 | 0.98 | 1.71E-01 | 0.97 | 2.79E-02 | 0.94 | 1.82E-01 2.17E-02 | 0.92 |
| 1419538_at | | RT3 | 10 fms-related tyrosine | | | XL184, ponatinib, sorafenib, lestaurtinib, CGP 41251 interferon alfacon-1, PEG- interferon alfa- 2a, interferon beta-1a, IFNA2, interferon alfa- 2b/ribavirin, | 3.24E-05 | 0.49 | 4.17E-01 | 0.98 | 1.71E-01 | 0.97 | 2.79E-02 | 0.94 | 1.82E-01 2.17E-02 | 0.92 |
| 1419538_at | | FLT3 | 10 fms-related tyrosine binase 3 interferon (alpha, beta and omeja) receptor 2 | | kinase | XL184, ponatinib, sorafenib, lestaurtinib, CGP 41251 interferon alfacon-1, PEG- interferon alfa- 2a, interferon beta-1a, IFNA2, interferon alfa- interferon alfa- | 3.24E-05 | 0.49 | 4.17E-01 | 0.98 | 1.71E-01 | 0.97 | 2.79E-02 | 0.94 | 1.82E-01 2.17E-02 | 0.92 |
| | | | 10 fms-related tyrosine kinase 3 | Plasma Membrane | kinase transmembrane receptor enzyme | XL184, ponatinib, sorafenib, lestaurtinib, CGP 41251 interferon alfacon-1, PEG- interferon alfa- 2a, interferon alfa- 2b/ribavrin, pegintron, | 3.24E-05 3.28E-05 | 0.49 | 4.17E-01 6.35E-01 | 0.98 | 1.71E-01 7.12E-01 | 0.97 | 2.79E-02 3.61E-01 | 0.94 | 1.82E-01 2.17E-02 4.01E-01 | 0.92 |
| 1427691 a at 1422476 at 1422444 at | | IFNAR2 IF130 ITGA6 | 10 fms-related tyrosine binace 3 interferon (alpha, beta and ornega) receptor 2 interferon, gamma- index(be protein 30 interferon, gamma- index(be protein 30 interferon gamma- | Plasma Membrane Plasma Membrane | kinase transmembrane receptor | XL184, ponatinib, sorafenib, lestaurtinib, CGP 41251 interferon alfacon-1, PEG- interferon alfa- 2a, interferon alfa- 2b/ribavrin, pegintron, | 3.24E-05 2.22E-05 1.09E-05 6.61E-05 8.22E-04 | 0.49 | 4.17E-01 6.35E-01 4.09E-01 7.16E-01 6.14E-01 | 0.98 0.99 1.04 0.99 0.99 | 1.71E-01 7.12E-01 4.85E-01 8.22E-01 2.50E-01 | 0.97 0.98 1.02 1.00 0.90 | 2.79E-02 2.61E-01 1.88E-01 2.24E-01 1.11E-01 | 0.94 0.97 1.04 1.02 0.85 | 1.82E-01 2.17E-02 4.01E-01 7.17E-02 3.06E-01 3.62E-01 | 0.92 1.02 1.06 0.97 0.93 |
| 1427091 a at 1422476 at 1422444 at 1422444 at | | IFNAR2 IFI30 ITGA6 TOR4A | 10 fmt-related tyrosine kmase 3 interferon (alpha, beta and omega) receptor 2 interferon (alpha, beta and omega) receptor 2 interferon (alpha José Cite and Comercial interferon (alpha) receptor 2 interferon (alpha) r | Plasma Membrane Plasma Membrane Çytoplasm | kinase transmembrane receptor enzyme transmembrane | XL184, ponatinib, sorafenib, lestaurtinib, CGP 41251 interferon alfacon-1, PEG- interferon alfa- 2a, interferon alfa- 2b/ribavrin, pegintron, | 1.09E-05 6.61E-05 6.28E-04 6.28E-04 6.28E-05 | 0.49 | 4.17E-01 6.35E-01 4.09E-01 7.16E-01 6.14E-01 9.22E-02 | 0.99 0.99 1.04 0.99 0.96 0.93 | 1.71E-01 7.12E-01 4.85E-01 8.22E-01 2.50E-01 9.27E-01 | 0.97 0.98 1.02 1.00 0.90 1.00 | 2.794-02 3.614-01 1.884-01 3.244-01 1.114-01 6.414-01 | 0.94 0.97 1.04 1.02 0.85 0.98 | 1.82E-01 2.17E-02 4.01E-01 7.17E-02 3.06E-01 3.62E-01 9.21E-01 | 0.92 1.02 1.05 0.97 0.93 1.00 |
| 1427691 a at 1422476 at 1422444 at | | IFNAR2 IF130 ITGA6 | 10 fms-related tyrosine kinase 3 interferon (alpha, beta and omega) receptor 2 indicitie protein 30 torosin family 4, member A SAM and 93; domain 76a4 (barnen F-cell | Plasma Membrane Plasma Membrane Cytoplasm Plasma Membrane | kinase varumembane receptor transmembane receptor other other | XL184, ponatinib, sorafenib, lestaurtinib, CGP 41251 interferon alfacon-1, PEG- interferon alfa- 2a, interferon alfa- 2b/ribavrin, pegintron, | 3.24E-05 2.22E-05 1.09E-05 6.61E-05 8.22E-04 | 0.49 | 4.17E-01 6.35E-01 4.09E-01 7.16E-01 6.14E-01 | 0.98 0.99 1.04 0.99 0.99 | 1.71E-01 7.12E-01 4.85E-01 8.22E-01 2.50E-01 | 0.97 0.98 1.02 1.00 0.90 | 2.79E-02 2.61E-01 1.88E-01 2.24E-01 1.11E-01 | 0.94 0.97 1.04 1.02 0.85 | 1.82E-01 2.17E-02 4.01E-01 7.17E-02 3.06E-01 3.62E-01 | 0.92 1.02 1.06 0.97 0.93 |
| 1427091 a at 1422476 at 1422444 at 1422444 at | | IFNAR2 IFI30 ITGA6 TOR4A | 10 fms-related tyrosine kmase 3 interferon (alpha, beta and ornega) recepto 2 imperferon, gama- imperferon, gama- imperferon, gama- imperferon (alpha 6 thread a content 10 thread of the content containing 3 Tack (buman T-cell leadernia vino, tripe 1) 9.5 and CRA: homology | Plasma Membrane Plasma Membrane Cytoplasm Plasma Membrane | kinase transmembrane receptor transmembrane receptor defer defer defer defer defer | XL184, ponatinib, sorafenib, lestaurtinib, CGP 41251 interferon alfacon-1, PEG- interferon alfa- 2a, interferon alfa- 2b/ribavrin, pegintron, | 1.09E-05 6.61E-05 6.28E-04 6.28E-04 6.28E-05 | 0.49 | 4.17E-01 6.35E-01 4.09E-01 7.16E-01 6.14E-01 9.22E-02 | 0.99 0.99 1.04 0.99 0.96 0.93 | 1.71E-01 7.12E-01 4.85E-01 8.22E-01 2.50E-01 9.27E-01 | 0.97 0.98 1.02 1.00 0.90 1.00 | 2.794-02 3.614-01 1.884-01 3.244-01 1.114-01 6.414-01 | 0.94 0.97 1.04 1.02 0.85 0.98 | 1.82E-01 2.17E-02 4.01E-01 7.17E-02 3.06E-01 3.62E-01 9.21E-01 | 0.92 1.02 1.05 0.97 0.93 1.00 |
| 1427091 a at 1422476 at 1422446 at 1424429 at 142429 at 1427007 at | | IFNAR2 IF30 ITGA5 TOR4A SASH3 | 10 fms-related tyrosine kinase 3 interferon (alpha, beta and onreag) receptor 2 indexide protein 30 treagen, alpha 6 tessin family 4, member A Sold and 93; domain indexide protein 30 tessin family 4, member A tessin family 4, member A | Pisma Membrane Pisma Membrane Cetoolasm Pisma Membrane usinown Cetoolasm | knase transmembrane receptor receptor differ other transcription | XL184, ponatinib, sorafenib, lestaurtinib, CGP 41251 interferon alfacon-1, PEG- interferon alfa- 2a, interferon alfa- 2b/ribavrin, pegintron, | 1,244-05 2,286-05 2,286-05 6,616-05 8,286-04 6,266-05 1,866-05 1,866-05 | 0.49 0.49 0.49 0.49 0.49 0.49 0.49 0.49 | 4.17E-01 6.35E-01 4.09E-01 7.16E-01 6.14E-01 9.22E-02 5.62E-01 | 0.98 0.99 1.04 0.99 0.96 0.93 1.02 | 1.718-01 7.128-01 4.858-01 8.228-01 2.508-01 9.278-01 2.428-01 | 0.97 0.98 1.02 1.00 0.90 1.00 1.00 | 2.794-02 2.616-01 1.886-01 3.246-01 1.116-01 6.416-01 9.536-01 | 0.94 0.97 1.04 1.02 0.85 0.98 1.00 | 1 & 2F- 01 2.17E-02 4.01E-01 7.17E-02 3.06E-01 3.62E-01 9.21E-01 2.80E-01 | 0.92 1.02 0.97 0.93 1.00 1.04 |
| 1427091 a at 1422076 at 142244 at 142244 at 1422007 at 1427007 at 1420169 at 1449311 at | icate Genera Ser | IFNAR2 IF30 IFG66 SASH3 TAX18P3 BACH1 | 10 fms-related tyrosine kinase 3 interferon (alpta, beta and omega) neceptor 2 indecisie genetics 30 indecisie genetics 30 integrin alpha 6 trast, fuman T-cell lackma vince type 1 blocking contents 3 30 fms of 10 domain T-cell lackma vince signer 3. basic kicene signer | Pasma Membrane Pasma Membrane Cytoplasm Pasma Membrane unitnown Cytoplasm Nacleus | transmembrane receptor estyme tonsmembrane entropy other other transcription resolutor | XL184, ponatinib, sorafenib, lestaurtinib, CGP 41251 interferon alfacon-1, PEG- interferon alfa- 2a, interferon alfa- 2b/ribavrin, pegintron, | 2,24E-05 3,28E-05 1,09E-05 6,61E-05 8,28E-04 6,24E-05 1,72E-05 9,46E-04 | 0.49 0.49 0.49 0.49 0.49 0.49 0.49 0.49 | 4.17E-01 6.35E-01 7.16E-01 6.14E-01 9.22E-02 5.62E-01 9.92E-01 | 0.99 0.99 0.99 0.99 0.99 0.99 0.93 1.02 1.04 1.00 | 1.716-01 7.126-01 4.856-01 8.226-01 9.276-01 2.426-01 1.376-01 2.036-01 | 0.97 0.98 1.02 1.00 0.99 1.00 1.00 1.00 1.06 0.88 | 2.796-02 3.616-01 1.886-01 3.246-01 1.116-01 6.416-01 7.606-01 7.606-01 7.266-02 | 0.94 0.97 1.04 1.02 0.85 0.98 1.00 0.99 | 187F-01 2.17F-02 4.01F-01 7.17F-02 3.06F-01 9.21F-01 2.269F-01 2.12F-01 3.27F-02 | 0.92 1.02 1.06 0.97 0.93 1.00 1.00 1.04 1.04 0.76 |
| 1427091 a at 1422476 at 1422469 at 142449 at 142409 at 142409 at 1429311 at 1449331 at 1412633 a at Duple | icate Gene Syr | IFNAR2 IF30 ITGA6 TOR4A SAGH3 TAX18P3 BACH1 COX7A2L | 10 fms-related tyrosine kinase 3 interferon (alpha, beta and omega) receptor 3 indicitie protein 10 indicitie protein 10 torsin family 4, nember A SAM and 934 domain indicitie protein 10 torsin family 4, nember A 10 at Daman Fell Ileakemia vins type 1) binding protein 3 Bit 3 and CK: henologic Bit 3 and CK: henologic Bit 3 and CK: henologic binding protein 3 Bit 3 and CK: henologic binding protein 3 binding | Pisma Membrane Pisma Membrane Cetoolasm Pisma Membrane usinown Cetoolasm | kinase transmembrane receptor engrine receptor other other transmitten transmi | XL184, ponatinib, sorafenib, lestaurtinib, CGP 41251 interferon alfacon-1, PEG- interferon alfa- 2a, interferon alfa- 2b/ribavrin, pegintron, | 2,24E-05 3,28E-05 6,61E-05 6,24E-05 1,86E-05 1,72E-05 9,44E-04 2,81E-05 | 0.49 0.49 0.49 0.49 0.49 0.49 0.49 0.49 | 4.17E-01 6.35E-01 7.16E-01 7.16E-01 9.22E-02 5.62E-01 5.62E-01 5.64E-01 | 0.99 0.99 0.99 0.96 0.99 0.99 0.93 1.02 1.04 1.00 1.02 | 1.716-01 7.126-01 4.856-01 8.226-01 9.276-01 1.376-01 2.428-01 1.376-01 3.696-01 | 0.97 0.98 1.02 1.00 1.00 1.06 1.06 0.98 1.02 | 2,7% 02 3,611-01 1,8% 01 3,246-01 1,111-01 6,416-01 9,536-01 7,266-02 2,7% 01 | 0.94 0.97 1.04 1.02 0.85 0.99 1.00 0.99 0.79 0.95 | 1 82F-01 2.17E-02 4.01E-01 7.17E-02 3.06E-01 3.02E-01 2.20E-01 2.12E-01 3.32E-02 4.41E-01 | 0.92 1.02 1.05 0.97 0.93 1.00 1.04 1.04 0.75 0.98 |
| 1427091 a at 1422076 at 142244 at 142244 at 1422007 at 1427007 at 1420169 at 1449311 at | icate Gene Sut | IFNAR2 IF30 IFG66 SASH3 TAX18P3 BACH1 | 10 Interferen (olden, beda and enreal) Interferen Inderferen (olden, beda and enreal) Interferen general Inderferen general- inderferen general- g | Pasma Membrane Pasma Membrane Cytoplasm Pasma Membrane unitnown Cytoplasm Nacleus | transmembrane receptor estyme tonsmembrane entropy other other transcription resolutor | XL184, ponatinib, sorafenib, lestaurtinib, CGP 41251 interferon alfacon-1, PEG- interferon alfa- 2a, interferon alfa- 2b/ribavrin, pegintron, | 2,24E-05 3,28E-05 1,09E-05 6,61E-05 8,28E-04 6,24E-05 1,72E-05 9,46E-04 | 0.49 0.49 0.49 0.49 0.49 0.49 0.49 0.49 | 4.17E-01 6.35E-01 7.16E-01 6.14E-01 9.22E-02 5.62E-01 9.92E-01 | 0.99 0.99 0.99 0.99 0.99 0.99 0.93 1.02 1.04 1.00 | 1.716-01 7.126-01 4.856-01 8.226-01 9.276-01 2.426-01 1.376-01 2.036-01 | 0.97 0.98 1.02 1.00 0.99 1.00 1.00 1.00 1.06 0.88 | 2.796-02 3.616-01 1.886-01 3.246-01 1.116-01 6.416-01 7.606-01 7.606-01 7.266-02 | 0.94 0.97 1.04 1.02 0.95 0.95 0.99 0.79 | 187F-01 2.17F-02 4.01F-01 7.17F-02 3.06F-01 9.21F-01 2.269F-01 2.12F-01 3.27F-02 | 0.92 1.02 1.06 0.97 0.93 1.00 1.00 1.04 1.04 0.76 |
| 1427091 a st 1422476 at 1422476 at 142449 at 142449 at 1424933 at 1449311 at 142910 at 142910 at 142910 at 142910 at 1429200 at 1429200 | Licate Gene Spr | IFNAR2 IF30 ITGA6 TGA6 SA9H3 BACH1 COVTA21 COVTA21 Ceacam1/Ceacam3 | 10 Interferon (alpha, beta and omega) receptor 2 Interferon (alpha, beta and omega) receptor 2 Interferon, gama- indeclife protein 10 Integrin, alpha 6 toxin family, 4, member A SAM and 934 domain Integrin, alpha 6 toxin family, 4, member A Integrin alpha 6 toxin family, 4, member A Integrin alpha 6 toxin family, 4, member A integrin alpha 6 toxin family, 40 toxin family, 40 carinoembryonic antigen existence and a second carinoembryonic antigen existence and a second to alpha 6 toxin antigen alpha 6 toxin family 40 carinoembryonic antigen relation alpha 6 toxin antigen alpha 6 toxin alpha 6 toxin antigen alpha 6 toxin antigen alpha 6 toxin antigen alpha 6 toxin alpha 6 toxin alpha 6 toxin alpha 6 toxin alpha 6 toxin alpha 6 toxin alpha 6 toxin alpha 6 toxin alpha 7 toxin alpha 6 toxin alpha 6 toxin alpha 6 toxin alpha 6 toxin alpha 7 toxin alpha 6 toxin alpha 6 toxin alpha 7 toxin alpha 6 toxin alpha 7 toxin alpha 7 | Pasma Membrane Pasma Membrane Cetoglasm Nacleus Cetoglasm Nacleus Cetoglasm Nacleus Cetoglasm Nacleus Cetoglasm | transmembrane receptor estyme tonsmembrane entropy other other transcription resolutor | XL184, ponatinib, sorafenib, lestaurtinib, CGP 41251 interferon alfacon-1, PEG- interferon alfa- 2a, interferon alfa- 2b/ribavrin, pegintron, | 2,246-05 2,286-05 2,286-05 2,286-04 6,266-05 1,286-05 2,288-04 0,466-04 2,888-05 1,286-05 1,386- | 0.49 0.49 0.49 0.49 0.49 0.49 0.49 0.49 | 4.17E-01 6.35E-01 7.16E-01 6.14E-01 9.22E-02 5.62E-01 9.92E-01 5.68E-01 8.12E-01 5.81E-02 | 0.99 0.99 0.99 0.96 0.93 1.02 1.02 1.02 1.01 1.02 1.01 1.05 | 1.716-01 7.126-01 4.856-01 8.226-01 9.276-01 2.426-01 2.426-01 3.666-01 3.666-01 5.306-01 5.306-01 | 0.97 0.98 1.02 1.00 0.90 1.00 0.93 1.02 0.98 1.02 0.98 0.98 | 2,7% 02 3,616 01 1,886 01 3,246 01 1,116 01 6,416 01 7,266 02 2,776 01 1,646 01 4,686 02 | 0.94 0.97 1.04 1.02 0.85 0.98 0.99 0.99 0.79 0.95 0.94 0.93 | 1876-01 2.17E-02 4.01E-01 4.01E-01 7.17E-02 3.06E-01 3.02E-01 2.80E-01 2.12E-01 3.32E-02 4.41E-01 6.57E-01 4.45E-03 | 0.92 1.02 1.05 0.97 0.93 1.06 1.06 0.97 0.93 0.93 0.93 0.95 0.98 0.98 0.91 |
| 1427091, a, at 1422456 at 1422446 at 1424409 at 142409 at 1427007 at 14269 at 14269 at 14269 at 1426812 a at 1426812 a at 1426812 a at 1426812 a at 1426812 a at | icate Gene Syn | IPNAR2 IF30 ITGA6 SASH3 TAX18P3 BACH1 COX7A2L | 10 Interferon (Joha, beta and omega) interferon Interferon, gampa indextRe parties 3 Interferon, gampa Interferon, gampa | Pasma Membrane Pasma Membrane Cetoglasm Ectoglasm Cetoglasm Secton Ectoglasm Secton Ectoglasm Cetoglasm Cetoglasm | Vinase Vinase receptor receptor receptor receptor vancipation receptor vancipation receptor vancipation receptor vancipation receptor vancipation receptor vancipation receptor vancipation receptor vancipation receptor vancipation receptor vancipation receptor vancipation receptor vancipation receptor vancipation vanc | X1184, X154, | 2,246-05 3,286-05 6,6516-05 8,286-05 8,286-05 1,286 | 0.49 0.49 0.49 0.49 0.49 0.49 0.49 0.49 | 4.17E-01 6.35E-01 7.16E-01 7.16E-01 6.14E-01 9.27E-02 5.62E-01 9.92F-02 5.68E-01 8.12E-01 5.81E-02 7.13E-03 | 0.99 0.99 0.99 0.99 0.99 0.96 0.93 1.02 1.02 1.02 1.02 1.02 1.02 0.93 1.02 0.93 1.02 0.93 0.93 0.93 | 1.716-01 7.126-01 8.226-01 8.226-01 9.276-01 1.376-01 2.046-01 3.666-01 6.926-01 5.366-01 8.126-01 8.126-01 | 0.97 0.98 1.02 1.00 0.99 1.00 1.00 1.00 1.05 1.05 1.05 0.98 0.98 0.98 0.95 | 2.7% 02 3.616 01 1.886 01 1.116 01 2.246 01 1.116 01 7.666 01 7.266 02 2.776 01 1.666 01 1.666 01 4.686 02 8.496 01 | 0.94 0.97 1.04 1.02 0.95 0.99 0.79 0.95 0.95 0.94 0.93 0.97 | 1 82F 01 2.17F 02 4.01F 01 4.01F 01 7.17F 02 3.06F 01 3.66F 01 2.286F 01 2.286F 01 3.12F 02 4.41E 01 6.57F 01 4.55F 01 4.55F 03 | 0.92 1.02 1.05 0.97 0.93 1.00 1.04 0.76 0.98 0.98 0.98 0.91 0.87 |
| 1427091 o at 1422476 at 1422446 at 1424429 at 1424409 at 1424109 at 1424109 at 1429313 at 1429313 at 1429313 at 1429313 at 142931400 at 142931400 at 142931400 at 142931400 at 142931400 at 142931400 at 142931400 at 142931400 at 142931400 at 142931400 at 142931400 at 142931400 at 142931400 at 142931400 at 142931400 at 142931400 at 1429414000000000000000000000000000000000 | icate Gene Syn icate Gene Syn | IFNAR2 IF130 IFG&6 TOR&A TAX18P3 ACH1 TAX18P3 Central | 10 Interferon (alpha, beta and omego) receitor 2 Interferon (alpha, beta Interferon (alpha, beta | Pasma Membrane Plasma Membrane Cytoglasm Plasma Membrane Cytoglasm Cytoglasm Necleus Cytoglasm Plasma Membrane Cytoglasm Plasma Membrane | kinase transmembrane receptor coher other coher | X1384, X154, | 2,246-05 2,286-05 2,286-05 2,286-04 6,266-05 1,286-05 2,288-04 0,466-04 2,888-05 1,286-05 1,386- | 0.49 0.49 0.49 0.49 0.49 0.49 0.49 0.49 | 4.17E-01 6.33E-01 7.16E-01 6.14E-01 9.22E-01 9.92E-01 5.69E-01 8.12E-01 5.81E-02 7.13E-01 9.22E-01 | 0.99 0.99 0.99 0.99 0.96 0.93 1.04 1.04 1.00 1.02 1.04 1.02 1.01 1.05 0.93 1.01 | 1.716-01 7.126-01 8.226-01 8.226-01 9.276-01 1.376-01 1.376-01 3.696-01 8.126-01 8.126-01 8.126-01 | 0.97 0.98 1.02 1.00 0.90 1.00 1.06 0.88 1.02 0.98 0.98 0.95 0.95 | 2.796-02 3.616-01 1.886-01 1.116-01 9.536-01 7.666-01 7.266-02 2.776-01 1.646-01 1.646-01 4.686-02 8.498-01 9.226-01 | 0.94 0.97 1.04 1.02 0.85 0.98 1.00 0.99 0.79 0.79 0.95 0.94 0.93 0.97 1.00 | 1 82F-03 2.176-02 4.01E-01 4.01E-01 3.06E-01 3.62F-03 3.62F-03 2.22E-03 2.22E-03 3.62F-03 3.22E-03 3.22E-03 3.22E-03 4.45E-03 4.45E-03 4.55E-03 | 0.92 1.02 1.02 0.97 0.93 1.00 1.04 1.04 0.76 0.98 0.98 0.98 0.98 0.98 0.91 0.91 0.97 1.00 |
| 1427091, a at 1422495 at 1422445 at 142448 at 1424829 at 142409 at 142609 at 142609 at 142609 at 1426012 a at 1426012 | icate Gene Syn icate Gene Syn icate Gene Syn | IPNAR2 IF100 IF004 SSGH1 TAX18P3 BACH1 C037A2L | 10 Indiaferon (alpha, beta kinase 3 Indiaferon (alpha, beta indiaferon (alpha, beta Indiaferon (alpha, beta Indiaferon (alpha, beta Indiaferon (alpha, beta Indiaferon (alpha 6 toxin family 4, member A Sold and SH3 domain containing 1 Indiageno (alpha 6 toxin family 4, member A Sold and SH3 domain containing 1 Indiageno(alpha 6 Indiageno(alpha 6 Indiageno | Pasma Membrane Pasma Membrane Pasma Membrane Cytoglasm Cytoglasm Cytoglasm Cytoglasm Cytoglasm Pasma Membrane Cytoglasm Pasma Membrane Cytoglasm Pasma Membrane Cytoglasm Pasma Membrane Cytoglasm Pasma Membrane Cytoglasm Pasma Membrane Cytoglasm Pasma Membrane Cytoglasm Pasma Membrane Cytoglasm Pasma Membrane Pasma Membr | Vinase Vinase receptor ecopor bonomenbane receptor other adher vanscription readator vanscription ecopor ecolor ecolor other ecolor eco | X1184, X154, | 1.09E-05 3.28E-05 6.61E-05 8.28E-04 6.26E-05 1.8EE-05 1.8EE-05 1.8EE-05 1.8EE-05 1.9EE-05 1.5EE-03 1.5EE-03 1.4EE-02 8.32E-05 3.2EE-05 | 0.49 0.49 0.49 0.49 0.49 0.49 0.49 0.49 | 4.17E-01 6.35E-01 7.16E-01 7.16E-01 6.14E-01 9.22E-02 5.62E-01 9.22E-02 5.68E-01 8.12E-01 5.88E-02 7.13E-03 9.28E-01 9.28E- | 0.99 0.99 0.99 0.99 0.96 0.93 1.02 1.04 1.00 1.02 1.02 1.01 1.02 1.05 0.93 1.01 0.93 1.01 | 1.716-01 7.126-01 8.226-01 8.226-01 9.276-01 1.376-01 2.046-01 3.696-01 5.306-01 5.306-01 5.306-01 5.306-01 5.306-01 5.306-01 | 0.97 0.98 1.02 1.00 0.90 1.00 1.00 1.06 1.06 0.88 1.02 0.98 0.98 0.98 0.95 1.04 1.01 | 2.7% 42 3.616-01 1.886-01 1.116-01 2.246-01 1.116-01 7.266-01 7.266-02 2.776-01 1.666-01 4.686-02 8.496-01 9.286-01 9.286-01 | 0.94 0.97 1.04 1.02 0.85 0.98 1.00 0.99 0.79 0.95 0.94 0.93 0.94 0.93 0.93 | 1 82F 01 2.17F 02 4.01F 01 4.01F 01 7.17F 02 3.06F 01 3.26F 01 3.26F 01 3.12F 02 4.11F 01 6.57F 01 4.55F 01 4.55F 01 3.55F | 0.92 1.02 1.05 0.97 0.93 1.00 1.04 0.76 0.98 0.98 0.98 0.91 0.93 1.00 1.04 0.55 0.98 |
| 1427091, a at 1422495 at 1422445 at 142448 at 1424829 at 142409 at 142609 at 142609 at 142609 at 1426012 a at 1426012 | icate Gene Syn icate Gene Syn | IFNAR2 IF130 IFG&6 TOR&A TAX18P3 ACH1 TAX18P3 Central | 10 Interferon (alpha, beta and ornega) receptor 2 Interferon (alpha, beta and ornega) receptor 2 Interferon (alpha, beta and ornega) receptor 2 Interferon (alpha) Interferon (alpha) | Pasma Membrane Plasma Membrane Cytoglasm Plasma Membrane Cytoglasm Cytoglasm Necleus Cytoglasm Plasma Membrane Cytoglasm Plasma Membrane | Virase vansmembrane mocolifo engyme transmembrane receitor other other unscription regidetor unscription regidetor engyme other other other other other other | X1184, X154, | 1.09E 05 1.09E 05 6.61E 05 8.28E 04 6.24E 05 1.28E 05 1.28E 05 1.28E 05 1.58E 03 1.48E 05 1.58E 03 1.48E 05 1.58E 03 1.48E 05 1.58E | 0.49 0.49 0.49 0.49 0.49 0.49 0.49 0.49 | 4.17E-01 6.33E-01 7.16E-01 6.14E-01 9.22E-01 9.92E-01 5.69E-01 8.12E-01 5.81E-02 7.13E-01 9.22E-01 | 0.99 0.99 0.99 0.99 0.96 0.93 1.04 1.04 1.00 1.02 1.04 1.02 1.01 1.05 0.93 1.01 | 1.716-01 7.126-01 8.226-01 8.226-01 9.276-01 1.376-01 2.036-01 8.096-01 8.126-01 8.126-01 8.126-01 | 0.97 0.98 1.02 1.00 0.90 1.00 1.06 0.88 1.02 0.98 0.98 0.95 0.95 | 2.796-02 3.616-01 1.886-01 1.116-01 9.536-01 7.666-01 7.266-02 2.776-01 1.646-01 1.646-01 4.686-02 8.498-01 9.226-01 | 0.94 0.97 1.04 1.02 0.85 0.98 1.00 0.99 0.79 0.79 0.95 0.94 0.93 0.97 1.00 | 1 82F-03 2.176-02 4.01E-01 4.01E-01 3.06E-01 3.62F-03 3.62F-03 2.22E-03 2.22E-03 3.62F-03 3.22E-03 3.22E-03 3.22E-03 4.45E-03 4.45E-03 4.55E-03 | 0.92 1.02 1.02 0.97 0.93 1.00 1.04 1.04 0.76 0.98 0.98 0.98 0.98 0.98 0.91 0.91 0.97 1.00 |
| 1427091, a at 1422495 at 1422445 at 142448 at 1424829 at 142409 at 142609 at 142609 at 142609 at 1426012 a at 1426012 | icate Gene Syn icate Gene Syn icate Gene Syn | IPNAR2 IF100 IF004 SSGH1 TAX18P3 BACH1 C037A2L | 10 Interferon (alpha, beta and omego) receitor 2 Interferon (alpha, beta Interferon (alpha, beta In | Pasma Membrane Pasma Membrane Pasma Membrane Cytoglasm Cytoglasm Cytoglasm Cytoglasm Cytoglasm Pasma Membrane Cytoglasm Pasma Membrane Cytoglasm Pasma Membrane Cytoglasm Pasma Membrane Cytoglasm Pasma Membrane Cytoglasm Pasma Membrane Cytoglasm Pasma Membrane Cytoglasm Pasma Membrane Cytoglasm Pasma Membrane Pasma Membr | Vinase Vinase receptor ecopor bonomenbane receptor other adher vanscription readator vanscription ecopor ecolor ecolor other ecolor eco | X1184, X154, | 1.09E-05 3.28E-05 6.61E-05 8.28E-04 6.26E-05 1.8EE-05 1.8EE-05 1.8EE-05 1.8EE-05 1.9EE-05 1.5EE-03 1.5EE-03 1.4EE-02 8.32E-05 3.2EE-05 | 0.49 0.49 0.49 0.49 0.49 0.49 0.49 0.49 | 4.17E-01 6.35E-01 7.16E-01 7.16E-01 6.14E-01 9.22E-02 5.62E-01 9.22E-02 5.68E-01 8.12E-01 5.88E-02 7.13E-03 9.28E-01 9.28E- | 0.99 0.99 0.99 0.99 0.96 0.93 1.02 1.04 1.00 1.02 1.02 1.01 1.02 1.05 0.93 1.01 0.93 1.01 | 1.716-01 7.126-01 8.226-01 8.226-01 9.276-01 1.376-01 2.046-01 3.696-01 5.306-01 5.306-01 5.306-01 5.306-01 5.306-01 5.306-01 | 0.97 0.98 1.02 1.00 0.90 1.00 1.00 1.06 1.06 0.88 1.02 0.98 0.98 0.98 0.95 1.04 1.01 | 2.7% 42 3.616-01 1.886-01 1.116-01 2.246-01 1.116-01 7.266-01 7.266-02 2.776-01 1.666-01 4.686-02 8.496-01 9.286-01 9.286-01 | 0.94 0.97 1.04 1.02 0.85 0.98 1.00 0.99 0.79 0.95 0.95 0.94 0.93 0.93 0.93 0.99 1.00 0.99 | 1 82F 01 2.17F 02 4.01F 01 4.01F 01 7.17F 02 3.06F 01 3.26F 01 3.26F 01 3.12F 02 4.11F 01 6.57F 01 4.55F 01 4.55F 01 3.55F | 0.92 1.02 1.05 0.97 0.93 1.00 1.04 0.76 0.98 0.98 0.98 0.91 0.93 1.00 1.04 0.58 0.98 |
| 1427091 a at 1422476 at 1422476 at 1422489 at 1422489 at 1424893 at 142859 at 142 | icate Gene Syn icate Gene Syn icate Gene Syn | IFNAR2 IF30 | 10 Interferon (alpha, beta and orreap) receptor 2 Interferon (alpha, beta and orreap) receptor 2 Interferon, gama- Indexide another 1 Interferon, gama- Indexide another 1 Interferon, gama- Indexide another 1 Interferon, gama- Indexide another 1 Interferon, gama- Indexide another 1 Interferon (alpha 6 Interferon | Pisma Membrane Pisma Membrane Cetoglisam Cetoglisam Cetoglisam Cetoglisam Cetoglisam Cetoglisam Cetoglisam Pisma Membrane Cetoglisam Pisma Membrane Cetoglisam Pisma Membrane Cetoglisam Nacleu | Vinase Vinase receptor receptor vanomenbane receptor vanomenbane v | X1184, X154, | 1.0%E-05 3.28E-05 6.61E-05 8.28E-04 6.24E-05 1.28E-05 1.28E-05 1.28E-05 1.28E-05 1.28E-05 1.28E-05 1.51E-03 1.48E-02 8.32E-05 1.37E-05 1.37E-05 1.37E-05 1.37E-05 1.37E-05 1.37E-05 | 0.49 0.49 0.49 0.49 0.49 0.49 0.49 0.49 | 4.17E-01 6.35E-01 7.16E-01 6.14E-01 9.22E-02 5.62E-01 5.62E-01 5.62E-01 5.62E-01 5.63E-01 5.81E-02 7.13E-01 9.24E- | 0.99 0.99 0.99 0.99 0.99 0.99 0.99 0.99 | 1.716-01 7.126-01 8.226-01 8.226-01 9.276-01 2.426-01 3.696-01 5.306-01 8.126-01 8.126-01 8.126-01 8.126-01 8.126-01 8.126-01 8.126-01 | 0.97 0.98 1.02 1.00 0.90 1.00 0.08 1.02 0.98 0.98 0.98 0.98 0.98 0.98 1.04 0.98 | 2.7% 02 3.616-01 1.8% 01 3.246-01 1.116-01 6.416-01 7.606-02 2.776-01 1.646-01 4.666-02 8.4% 01 6.586-01 6.686-02 | 0.94 0.97 1.04 1.02 0.95 0.95 0.95 0.94 0.93 0.93 0.93 0.93 0.93 0.93 0.93 0.93 | 1 8/F 01 2.17E 02 4.01E 01 4.01E 01 7.17E 02 3.06E 01 3.07E 01 2.80E 01 2.12E 01 3.32E 02 4.41E 01 6.57E 01 4.45E 01 9.50E 01 2.36E 01 2.36E 01 2.36E 01 2.36E 01 2.36E 01 | 0.92 1.02 1.02 0.97 0.93 1.00 1.04 0.76 0.98 0.98 0.98 0.91 0.91 0.47 1.00 1.04 1.02 |
| 1422091 p.at 1422076 at 1422409 at 1424209 at 1424209 at 1424209 at 1424209 at 1424209 at 1424209 at 142400 at 142409 at 142400 at 142400 at 142400 at 142400 at 142400 at 142400 at 142400 at | icate Gene Syn icate Gene Syn icate Gene Syn icate Gene Syn | IFNAR2 IF30 IF30 IF30 IF34A S4913 IF3418P3 BACH1 C0X7A2L C0X7A | 10 Instructional and synapsic Instruction (alpha, beta and ormoga) receptor 2 Instruction (alpha) Instruction | Pasma Membrane Plasma Membrane Cotoglasm Cotoglasm Cotoglasm Plasma Membrane Cotoglasm Plasma Membrane Cotoglasm Plasma Membrane Cotoglasm Plasma Membrane Cotoglasm Plasma Membrane Cotoglasm Plasma Membrane Cotoglasm Naclens Cotoglasm Naclens Cotoglasm Naclens Cotoglasm Naclens Cotoglasm Naclens Cotoglasm Naclens | Virase transmembrane receptor encyptie transmembrane receptor other other coller unscription reculator unscription reculator unscription reculator coller other other insue other coller insue other insue insue insue other insue other insue insue insue other insue i | X1184, X154, | 2,24E-05 3,28E-05 6,6EE-05 6,26E-05 6,26E-05 6,26E-05 1,27E-05 1,27E- | 0.49 0.49 0.49 0.49 0.49 0.49 0.49 0.49 | 4.17E-01 6.35E-01 7.16E-01 6.16E-01 9.22E-02 5.62E-01 9.92E-02 5.68E-03 8.12E-03 8.12E-03 8.12E-03 9.22E- | 0.99 0.99 0.99 0.96 0.93 1.02 1.04 1.02 1.04 1.02 1.01 1.05 0.93 1.02 1.01 0.93 0.95 0.95 | 1.716-01 7.126-01 8.226-01 2.596-01 2.426-01 1.376-01 8.126-01 5.366-01 8.126-01 5.366-01 8.126-01 6.936-01 8.126-01 6.936-01 8.126-01 6.946-01 6.946-01 6.946-01 6.486-01 8.177-02 4.276-01 | 0.97 0.98 1.02 1.00 0.90 1.00 1.00 0.00 1.00 0.98 0.99 0 | 2,7% 02 3,611-01 1,885-01 3,245-01 1,111E-01 6,411-01 7,265-02 2,776-01 1,645-01 2,276-01 1,645-01 6,586-01 9,296-01 6,586- | 0.94 0.97 1.05 0.99 0.79 0.79 0.79 0.95 0.99 0.79 0.95 0.99 0.99 0.99 0.99 0.99 0.99 0.9 | 1 82F-01 2.176-02 4.01E-01 4.01E-01 3.06E-01 3.06E-01 3.06E-01 2.12E-01 2.12E-01 4.32E-02 4.43E-03 4.55E-01 2.36E-01 2.36E-01 2.36E-01 4.87E-01 4.87E-01 | 0.92 1.02 1.05 0.97 0.93 1.06 0.93 1.00 1.04 0.76 0.98 0.98 0.91 0.98 0.91 0.92 1.02 0.98 0.93 |
| 1427091 a at 1422476 at 1422476 at 1424429 at 142400 at 14240 | icate Gene Syn icate Gene Syn icate Gene Syn icate Gene Syn | IFNAR2 IF30 IF30 IF30 IF30 IF30 IF30 IF30 IF30 | 10 Interferon (alpha, beta and omega) receptor 2 Interferon (alpha, beta and omega) receptor 2 Interferon (alpha) Interferon | Piarna Membrane Piarna Membrane Cotoglasm Rasma Membrane Cotoglasm Naclens Cotoglasm Piarna Membrane Cotoglasm Piarna Membrane Cotoglasm Piarna Membrane Cotoglasm Naclens Cotoglasm | Vinase Vinase receptor receptor vanomenbane receptor vanomenbane v | X1184, X154, | 2,24E-05 2,28E-05 2,28E-05 2,28E-05 2,28E-05 1,28E- | 0.49 0.49 0.49 0.49 0.49 0.49 0.49 0.49 | 4.17E-01 6.35E-01 7.16E-01 7.16E-01 6.14E-01 9.22E-02 5.62E-01 9.92E- | 0.98 0.99 0.99 0.99 0.99 0.99 1.02 1.02 1.02 1.02 1.02 1.02 1.03 1.02 1.03 1.03 1.03 1.03 1.03 1.03 1.03 1.04 1.04 1.04 1.04 1.04 1.04 1.04 1.04 | 1.716-01 7.126-01 8.226-01 2.556-01 2.556-01 3.696-01 3.696-01 5.366-01 5.366-01 5.366-01 6.936-01 5.366-01 6.936-01 8.126-01 8.126-01 8.126-01 8.126-01 8.126-01 8.126-01 8.126-02 9.366-01 | 0.97 0.98 1.02 1.00 0.99 0.99 1.00 1.05 0.98 0.99 0.98 0.99 0 | 2,796-02 3,616-01 1,886-01 3,246-01 1,116-01 3,246-01 1,116-01 4,247-01 1,646-01 4,646-02 4,646-02 1,486-01 6,586-01 1,646- | 0.94 0.97 1.04 1.02 0.99 0.99 0.99 0.99 0.99 0.99 0.93 0.94 0.93 0.94 0.93 0.94 0.93 0.94 0.93 0.94 0.93 0.94 0.93 0.94 | 1 82F-03 2.176-02 4.01E-01 3.06F-03 3.06F-03 3.62F-03 3.62F-03 3.12F-02 4.41E-03 3.12F-02 4.41E-03 3.12F-03 4.56F-03 2.36E-03 2.36E-03 4.57E- | 0.92 1.02 1.02 0.93 0.93 1.00 1.04 0.75 0.98 0.98 0.91 1.02 0.93 0.93 1.00 1.04 0.93 |
| 1422091 p.at 1422076 at 1422409 at 1424209 at 1424209 at 1424209 at 1424209 at 1424209 at 1424209 at 142400 at 142409 at 142400 at 142400 at 142400 at 142400 at 142400 at 142400 at 142400 at | icate Gene Syn icate Gene Syn icate Gene Syn icate Gene Syn | IFNAR2 IF30 IF30 IF30 IF34A S4913 IF3418P3 BACH1 C0X7A2L C0X7A | 10 Instructional and synosice kinase 3 instruction (alpha, beta and onequi) receptor 2 indicitie protein 30 indicitie protein | Pasma Membrane Plasma Membrane Cotoglasm Cotoglasm Cotoglasm Plasma Membrane Cotoglasm Plasma Membrane Cotoglasm Plasma Membrane Cotoglasm Plasma Membrane Cotoglasm Plasma Membrane Cotoglasm Plasma Membrane Cotoglasm Naclens Cotoglasm Naclens Cotoglasm Naclens Cotoglasm Naclens Cotoglasm Naclens Cotoglasm Naclens | Virase transmembrane receptor encyptie transmembrane receptor other other coller unscription reculator unscription reculator unscription reculator coller other other insue other coller insue other insue insue insue other insue other insue insue insue other insue i | X1184, X154, | 2,24E-05 3,28E-05 6,6EE-05 6,26E-05 6,26E-05 6,26E-05 1,27E-05 1,27E- | 0.49 0.49 0.49 0.49 0.49 0.49 0.49 0.49 | 4.17E-01 6.35E-01 7.16E-01 6.16E-01 9.22E-02 5.62E-01 9.92E-02 5.68E-03 8.12E-03 8.12E-03 8.12E-03 9.22E- | 0.99 0.99 0.99 0.96 0.93 1.02 1.04 1.02 1.04 1.02 1.01 1.05 0.93 1.02 1.01 0.93 0.95 0.95 | 1.716-01 7.126-01 8.226-01 2.596-01 2.426-01 1.376-01 8.126-01 5.366-01 8.126-01 5.366-01 8.126-01 6.936-01 8.126-01 6.936-01 8.126-01 6.946-01 6.946-01 6.946-01 6.486-01 8.177-02 4.276-01 | 0.97 0.98 1.02 1.00 0.90 1.00 1.00 0.00 1.00 0.98 0.99 0 | 2,7% 02 3,611-01 1,885-01 3,245-01 1,111E-01 6,411-01 7,265-02 2,776-01 1,645-01 2,276-01 1,645-01 6,586-01 9,296-01 6,586- | 0.94 0.97 1.05 0.99 0.79 0.79 0.79 0.95 0.99 0.79 0.95 0.99 0.99 0.99 0.99 0.99 0.99 0.9 | 1 82F-01 2.176-02 4.01E-01 4.01E-01 3.06E-01 3.06E-01 3.06E-01 2.12E-01 2.12E-01 4.32E-02 4.43E-03 4.55E-01 2.36E-01 2.36E-01 2.36E-01 4.87E-01 4.87E-01 | 0.92 1.02 1.05 0.97 0.93 1.06 0.93 1.00 1.04 0.76 0.98 0.98 0.91 0.98 0.91 0.92 1.02 0.98 0.93 |
| 1427091, a at 1422495 at 142244 at 1424429 at 1424429 at 142450 at 142450 at 142450 at 142523 a at 1429313 at 1429313 at 142932 a at 142939 at 142939 a at 14293 | icate Gene Syn icate Gene Syn icate Gene Syn icate Gene Syn | IFNAR2 IF30 IF30 IF30 IF30 IF30 IF30 IF30 IF30 | 10 Indications (alpha, beta Indications (alpha, beta) Indications (alpha, beta) | Pasma Membrane Plasma Membrane Cotoglasm Cotoglasm Cotoglasm Plasma Membrane Cotoglasm Plasma Membrane Cotoglasm Plasma Membrane Cotoglasm Plasma Membrane Cotoglasm Plasma Membrane Cotoglasm Plasma Membrane Cotoglasm Naclens Cotoglasm Naclens Cotoglasm Naclens Cotoglasm Naclens Cotoglasm Naclens Cotoglasm Naclens | Virase transmembrane receptor encyptie transmembrane receptor other other coller unscription reculator unscription reculator unscription reculator coller other other insue other coller insue other insue insue insue other insue other insue insue insue other insue i | X1184, X154, | 2,24E-05 2,28E-05 2,28E-05 2,28E-05 2,28E-05 1,28E- | 0.49 0.49 0.49 0.49 0.49 0.49 0.49 0.49 | 4.17E-01 6.35E-01 7.16E-01 7.16E-01 6.14E-01 9.22E-02 5.62E-01 9.92E- | 0.98 0.99 0.99 0.99 0.99 0.99 1.02 1.02 1.02 1.02 1.02 1.02 1.03 1.02 1.03 1.03 1.03 1.03 1.03 1.03 1.03 1.04 1.04 1.04 1.04 1.04 1.04 1.04 1.04 | 1.716-01 7.126-01 8.226-01 2.556-01 2.556-01 3.696-01 3.696-01 5.366-01 5.366-01 5.366-01 6.936-01 5.366-01 6.936-01 8.126-01 8.126-01 8.126-01 8.126-01 8.126-01 8.126-01 8.126-02 9.366-01 | 0.97 0.98 1.02 1.00 0.99 0.99 1.00 1.05 0.98 0.99 0.98 0.99 0 | 2,796-02 3,616-01 1,886-01 3,246-01 1,116-01 3,246-01 1,116-01 4,247-01 1,646-01 4,646-02 4,646-02 1,486-01 6,586-01 1,646- | 0.94 0.97 1.04 1.02 0.99 0.99 0.99 0.99 0.99 0.99 0.93 0.94 0.93 0.94 0.93 0.94 0.93 0.94 0.93 0.94 0.93 0.94 0.93 0.94 | 1 82F-03 2.176-02 4.01E-01 3.06F-03 3.06F-03 3.62F-03 3.62F-03 3.12F-02 4.41E-03 3.12F-02 4.41E-03 3.12F-03 4.56F-03 2.36E-03 2.36E-03 4.57E- | 0.92 1.02 1.02 0.93 0.93 1.00 1.04 0.75 0.98 0.98 0.91 1.02 0.93 0.93 1.00 1.04 0.93 |

| | | | | | | | Stimulat | tion Only | | Сотрон | ind Only | | | Stimulation a | nd Compound | |
|--|--|--|---|--|---|--|---|--|--|---|--|--|---|---|--|---|
| | i | | Probe Set Description branched chain keto acid dehydrogenase E1, alpha | İ | i | İ | CpG vs. | Medium | 0.25 uM E64 | l6 vs. Medium | 1.25 uM E644 | 6 vs. Medium | CpG + 0.25 t | IM E6446 vs. Medium | CpG + 1.25 u | M E6446 vs. Medium |
| 1416647 at 1416914 s at | | BCKDHA | polypeptide | Cytoplasm | enzyme | | 6.03E-05 8.18E-06 | 0.48 | 5.84E-01 5.88E-01 | 0.97 | 9.00E-01 6.93E-01 | 1.01 | 2.34E-01 7.98E-01 | 0.95 | 9.65E-01 1.64E-01 | 1.00 |
| 1421188 at | | CCR2 | chemokine (C-C motif) receptor 2 | Plasma Membrane | G-protein coupled receptor | | 2.53E-05 | 0.48 | 1.99E-01 | 1.03 | 1.10E-01 | 0.97 | 4.50E-02 | 0.90 | 1.38E-01 | 1.06 |
| 1415823 at | Duplicate Gene Syr | Scd2 | stearoyl-Coenzyme A desaturase 2 | Cytoplasm | enzyme | | 1.39E-04 | 0.48 | 1.79E-01 | 1.11 | 2.43E-02 | 1.17 | 1.64E-02 | 1.15 | 1.69E-03 | 1.30 |
| 1423182 at | | TNFRSF13B | tumor necrosis factor receptor superfamily, member 138 | Plasma Membrane | transmembrane receptor | | 5.90E-06 | 0.48 | 1.42E-01 | 0.96 | 2.42E-01 | 0.96 | 3.75E-02 | 0.91 | 6.85E-02 | 0.93 |
| 1423102 at | | THERAFIAR | caspase 6, apoptosis- related cysteine | Plasma interiorarie | receptor | | | 0.46 | 1.422-01 | 0.96 | | 0.96 | | 0.51 | 0.832-02 | 0.53 |
| 1415995 at | | CASP6 | peptidase | Cytoplasm | peptidase | | 7.77E-05 | 0.48 | 5.20E-01 | 0.99 | 4.67E-01 | 0.98 | 2.88E-02 | 0.90 | 3.72E-01 | 0.97 |
| 1417534_at | Duplicate Gene Syr | ITGB5 | integrin, beta 5 | Plasma Membrane | other | EMD121974 | 3.49E-06 1.30E-03 | 0.48 | 9.00E-01 | 1.00 | 3.11E-01 | 1.06 | 1.59E-02 | 0.90 | 7.10E-01 | 1.00 |
| 1453748 a at 1417038 at | Duplicate Gene Syr | KIF23 Sept9 | kinesin family member 23 septin 9 glutamate-ammonia | Cytoplasm Cytoplasm | other enzyme | | 9.00E-04 | 0.48 | 9.03E-01 6.61E-01 | 0.99 0.96 | 8.56E-01 8.88E-01 | 0.98 | 7.70E-01 6.06E-01 | 0.98 | 1.89E-01 2.32E-01 | 0.91 |
| 1426236 a at | | GLUL | ligase | Cytoplasm | enzyme | | 5.63E-05 | 0.48 | 3.99E-01 | 0.94 | 3.51E-01 | 0.89 | 3.88E-01 | 0.95 | 1.49E-02 | 0.87 |
| 1434856 at | | ANKRD44 | ankyrin repeat domain 44 | unknown | other transmembrane | | 1.37E-05 | 0.48 | 1.67E-01 | 1.04 | 4.30E-01 | 1.04 | 6.07E-02 | 0.90 | 2.08E-01 | 1.06 |
| 1428018_a_at | | CD300C | CD300c molecule multivesicular body | Plasma Membrane | receptor | | 5.90E-04 | 0.47 | 2.73E-01 | 1.03 | 4.19E-02 | 1.05 | 6.60E-01 | 0.98 | 1.38E-01 | 1.06 |
| 1428122 s at 1428242 at | | MVB12B HMHA1 | subunit 12B histocompatibility (minor) HA-1 | Cytoplasm | other transporter | | 7.05E-05 2.25E-05 | 0.47 | 3.34E-01 2.52E-01 | 0.96 | 5.79E-01 6.36E-01 | 0.96 | 3.98E-02 1.82E-01 | 0.87 | 3.12E-01 5.40E-02 | 0.96 |
| 1420905 at | | IL17RA | interleukin 17 receptor A | Plasma Membrane | transmembrane | | 7.03E-05 | 0.47 | 6.44E-01 | 1.01 | 8.97E-01 | 1.01 | 4.23E-01 | 0.94 | 4.38E-01 | 1.03 |
| | | | carcinoembryonic antigen related cell adhesion | | | | | | | | | | | | | |
| | Duplicate Gene Syr | Ceacam1/Ceacam2 | molecule 1 | Plasma Membrane | other | | 6.13E-04 3.19E-04 | 0.47 | 8.30E-01 1.04E-01 | 0.98 | 3.87E-01 7.53E-01 | 0.94 | 3.03E-02 | 0.83 | 1.04E-01 | 0.86 |
| 1433725 at 1425263 a at | | ACVR1B MBP | activin A receptor, type IB myelin basic protein | Plasma Membrane Extracellular Space | | | 3.19E-04 4.33E-04 | 0.47 | 1.04E-01 6.24E-01 | 0.90 | 7.53E-01 4.58E-02 | 0.99 | 1.72E-01 3.04E-02 | 0.92 | 1.01E-01 7.19E-02 | 0.95 |
| 1423203 8 81 | | | WAS/WASL interacting | extracementar space | ounci | | 4.332.04 | 0.47 | 014001 | 0.00 | 4.562.62 | 0.04 | 3.042.02 | 0.05 | 7.150.02 | 0.04 |
| 1436954 at 1417135 at | Duplicate Gene Syr | WIPF1 SRPK2 | protein family, member 1 SRSF protein kinase 2 | Cytoplasm Nucleus | other kinase | | 4.29E-06 1.07E-04 | 0.47 | 3.11E-01 8.52E-01 | 0.96 | 2.39E-01 1.11E-01 | 0.94 | 3.95E-03 3.69E-03 | 0.79 0.78 | 1.97E-01 2.49E-02 | 0.92 |
| | Duplicate Gene Syr | | zinc and ring finger 2 epithelial membrane | unknown | other | | 1.51E-06 | 0.47 | 4.10E-01 | 0.97 | 5.16E-01 | 0.99 | 8.08E-02 | 0.93 | 6.43E-01 | 1.01 |
| 1416529 at | | EMP1 | protein 1 EP300 interacting inhibitor of | Plasma Membrane | other transcription | | 3.02E-05 | 0.47 | 1.64E-01 | 0.97 | 6.59E-01 | 0.99 | 1.64E-02 | 0.80 | 9.74E-01 | 1.00 |
| 1448406 at | | EID1 | inhibitor of differentiation 1 | Nucleus | transcription regulator | | 3.54E-05 | 0.47 | 7.98E-01 | 0.98 | 2.29E-02 | 0.88 | 2.10E-02 | 0.76 | 3.09E-02 | 0.79 |
| 1415897 a at | | MGST1 | microsomal glutathione S- transferase 1 | Cytoplasm | enzyme | | 2.20E-05 | 0.47 | 9.18E-01 | 1.00 | 5.76E-01 | 0.98 | 1.46E-01 | 0.94 | 2.10E-01 | 1.06 |
| 1452067 at | | NAAA | N-acylethanolamine acid amidase | Cytoplasm | enzyme | | 3.68E-04 | 0.47 | 8.86E-01 | 0.99 | 1.59E-01 | 0.93 | 3.81E-03 | 0.87 | 5.97E-02 | 0.91 |
| 1448878_at | | MKD3 | MAX dimerization protein 3 | Nucleus | transcription regulator | | 2.87E-04 | 0.46 | 2.76E-01 | 0.96 | 7.13E-01 | 0.99 | 1.27E-02 | 0.86 | 1.84E-01 | 0.95 |
| | | | core-binding factor, runt domain, alpha subunit 2; | | transcription | | | | | | | | | | | |
| 1440964 s at | Duplicate Gene Syr | CBFA2T3 | translocated to, 3 | Nucleus | regulator | | 1.77E-04 | 0.46 | 6.72E-01 | 0.98 | 4.33E-01 | 0.97 | 1.21E-01 | 0.92 | 3.66E-02 | 0.91 |
| 1420822 s at | Duplicate Gene Syr | SGPP1 | sphingosine-1-phosphate phosphatase 1 | Cytoplasm | phosphatase | | 5.46E-04 | 0.46 | 8.92E-01 | 1.01 | 9.25E-01 | 1.01 | 2.99E-01 | 0.87 | 8.13E-01 | 1.03 |
| 1449127 at 1455291 s at | Duplicate Gene Syr | SELPLG | selectin P ligand zinc and ring finger 2 | Plasma Membrane | other | | 2.54E-06 1.05E-04 | 0.46 | 9.79E-01 5.66E-01 | 1.00 | 7.73E-01 8.93E-01 | 1.01 | 2.77E-02 1.50E-01 | 0.93 | 1.66E-01 2.64E-01 | 0.96 |
| 1455291 s at 1434831 a at | Duplicate Gene Syr | FOXO3 | zinc and ring finger 2 forkhead box 03 | unknown Nucleus | other transcription regulator | | 1.05E-04 7.08E-05 | 0.46 | 5.66E-01 6.71E-01 | 0.97 | 9.76E-01 | 1.00 | 1.50E-01 4.88E-01 | 0.86 | 2.64E-01 3.57E-01 | 1.07 |
| 1454031 a at | Duplicate Gene syn | S1PR4 | sphingosine-1-phosphate receptor 4 | Plasma Membrane | G-protein coupled receptor | fingolimod | 4.35E-04 | 0.46 | 6.86E-01 | 0.99 | 1.47E-01 | 1.04 | 1.43E-02 | 0.86 | 1.29E-01 | 0.97 |
| | | | CD79b molecule, immunoglobulin- | | transmembrane | | | | | | | | | | | |
| 1417640_at | | CD79B | associated beta potassium | Plasma Membrane | receptor | | 1.19E-04 | 0.46 | 3.33E-01 | 0.95 | 6.41E-01 | 0.98 | 1.80E-01 | 0.92 | 2.30E-01 | 0.93 |
| | | | intermediate/small conductance calcium- | | | | | | | | | | | | | |
| 1435945_a_at | | KCNN4 | activated channel, subfamily N, member 4 | Plasma Membrane | ion channel | clotrimazole, ICA 17043 | 4.75E-05 | 0.46 | 8.25E-01 | 0.99 | 9.30E-01 | 1.00 | 1.62E-01 | 0.93 | 9.04E-02 | 0.92 |
| 1418643 at | | TSPAN13 | tetraspanin 13 MNT, MAX dimerization | Plasma Membrane | other transcription | | 1.16E-06 | 0.46 | 4.12E-01 | 0.98 | 3.72E-01 | 0.97 | 9.23E-03 | 0.87 | 1.44E-02 | 0.92 |
| 1418192 at | | MNT | protein mitogen-activated | Nucleus | regulator | | 2.84E-05 | 0.46 | 2.28E-01 | 0.96 | 8.62E-01 | 1.01 | 4.37E-01 | 0.96 | 8.38E-01 | 1.01 |
| | | | protein kinase kinase kinase 1, E3 ubiquitin | | | | | | | | | | | | | |
| 1424850 at 1434832 at | Duplicate Gene Syr | MAP3K1 FOXO3 | protein ligase forkhead box O3 | Cytoplasm | kinase transcription | | 6.11E-05 2.24E-03 | 0.46 | 8.35E-01 6.16E-01 | 0.99 | 6.26E-01 4.18E-01 | 1.03 | 5.70E-02 3.57E-01 | 0.92 | 5.43E-01 7.49E-01 | 1.02 |
| 1434632_at | Duplicate Gene Syr | SATB1 | SATB homeobox 1 | Nucleus | regulator transcription regulator | | 4 30E-04 | 0.46 | 2.35E-01 | 0.90 | 9.83E-01 | 1.00 | 2.80E-01 | 0.94 | 3.37E-01 | 1.03 |
| 1434487 at | bupicate dene sy | MEF2D | myocyte enhancer factor 2D | Nucleus | transcription regulator | | 7.61E-05 | 0.46 | 3.16E-02 | 0.93 | 4.00E-01 | 0.98 | 3.08E-01 | 0.97 | 2.80E-02 | 1.09 |
| 1448167_at | | IFNGR1 | interferon gamma receptor 1 | Plasma Membrane | transmembrane receptor | interferon gamma-1b | 3.87E-03 | 0.46 | 7.94E-01 | 0.96 | 9.84E-01 | 1.00 | 7.35E-01 | 0.95 | 4.82E-01 | 0.90 |
| | | | ST8 alpha-N-acetyl- neuraminide alpha-2,8- | | | | 2.27E-05 | | 3.76E-01 | 0.96 | 4.65E-02 | 0.90 | 3.77E-02 | 0.89 | 4.32E-03 | 0.89 |
| 1430391_a_at | Duplicate Gene Syr | ST8SIA4 | sialyltransferase 4 | Cytoplasm | enzyme | | | | | | 4.65E-02 | 0.90 | 3.77E-02 | 0.89 | 4.32E-03 | 0.89 |
| | Duplicate Gene Syr | | Rho GTPase activating | Commission | ather | | | 0.45 | | | 4.075.01 | 0.06 | 6 335 03 | 0.07 | 1.545.01 | |
| 1450626 at | | ARHGAP9 SESN1 | protein 9 sestrin 1 | Cytoplasm Nucleus | other other | | 6.42E-05 4.86E-05 | 0.45 0.45 0.45 | 1.63E-01 8.43E-01 | 0.92 | 4.97E-01 6.16E-01 | 0.96 | 6.32E-02 2.53E-01 | 0.87 | 1.54E-01 9.25E-01 | 1.00 |
| 1419872_at 1421618_at | | SESN1 MANBA | protein 9 | Nucleus Cytoplasm | other other enzyme | sunitinib, | 6.42E-05 4.86E-05 4.19E-05 | 0.45 0.45 0.45 | 1.63E-01 8.43E-01 8.60E-01 | 0.92 1.00 | 6.16E-01 4.17E-01 | 1.01 | 2.53E-01 1.35E-01 | 0.91 | 9.25E-01 2.29E-01 | 1.00 |
| | Duplicate Gene Syr | SESN1 | protein 9 sestrin 1 mannosidase, beta A, lysosomal colony stimulating factor 1 receptor myosin IF | | | sunitinib, pazopanib | 6.42E-05 4.86E-05 | 0.45 0.45 | 1.63E-01 8.43E-01 | 0.92 | 6.16E-01 | 1.01 | 2.53E-01 | 1.04 | 9.25E-01 | 1.00 |
| 1421618 at | Duplicate Gene Syr | SESN1 MANBA CSF1R | protein 9 sestrin 1 mannosidase, beta A, lysosomal colony stimulating factor 1 receptor | Nucleus Cytoplasm Plasma Membrane | enzyme kinase | | 6.42E-05 4.86E-05 4.19E-05 1.09E-04 | 0.45 0.45 0.45 0.45 | 1.63E-01 8.43E-01 8.60E-01 4.89E-01 | 0.92 1.00 1.01 0.98 | 6.16E-01 4.17E-01 1.27E-01 | 1.01 1.04 0.96 | 2.53E-01 1.35E-01 6.86E-02 | 1.04 0.91 0.92 | 9.25E-01 2.29E-01 1.30E-01 | 1.00 1.06 0.96 |
| | Duplicate Gene Syr | SESN1 MANBA CSF1R MYO1F | protein 9 sestrin 1 mannosidase, beta A, hysosomal colony stimulating factor 1 receptor myosin IF hydrogen voltage-gated channel 1 programmed cell death 4 | Nucleus Cytoplasm Plasma Membrane Cytoplasm | enzyme kinase other | | 6.42E-05 4.86E-05 4.19E-05 1.09E-04 3.08E-05 | 0.45 0.45 0.45 0.45 0.45 | 1.63E-01 8.43E-01 8.60E-01 4.89E-01 7.72E-01 | 0.92 1.00 1.01 0.98 0.99 | 6.16E-01 4.17E-01 1.27E-01 8.67E-01 | 1.01 1.04 0.96 0.99 | 2.53E-01 1.35E-01 6.86E-02 5.49E-01 | 1.04 0.91 0.92 0.97 | 9.25E-01 2.29E-01 1.30E-01 7.69E-01 | 1.00 1.06 0.96 1.01 |
| | Duplicate Gene Syr | SESN1 MANBA CSF1R MYO1F | protein 9 sestrin 1 mannosidase, beta A, lysosomal colony stimulating factor 1 receptor myosin IF hydrogen voltage-gated channel 1 | Nucleus Cytoplasm Plasma Membrane Cytoplasm | enzyme kinase other | | 6.42E-05 4.86E-05 4.19E-05 1.09E-04 3.08E-05 | 0.45 0.45 0.45 0.45 0.45 | 1.63E-01 8.43E-01 8.60E-01 4.89E-01 7.72E-01 | 0.92 1.00 1.01 0.98 0.99 | 6.16E-01 4.17E-01 1.27E-01 8.67E-01 | 1.01 1.04 0.96 0.99 | 2.53E-01 1.35E-01 6.86E-02 5.49E-01 | 1.04 0.91 0.92 0.97 | 9.25E-01 2.29E-01 1.30E-01 7.69E-01 | 1.00 1.06 0.96 1.01 |
| 1424032_at | Duplicate Gene Syr | SESN1 MANBA CSF1R MYO1F HVCN1 | protein 9 sextrin 1 mannosidase, beta A, iyrosomal colony stimulating factor 1 receptor myosin IF hydrogen voltage-gated channel 1 programmed cell death 4 (neoplastic transformation inhibitor) ST6 beta-galactosamide alpha-2,6-sialyltranferase 1 | Nucleus Cytoplasm Plasma Membrane Cytoplasm unknown | enzyme kinase other | | 6.42E-05 4.86E-05 4.19E-05 1.09E-04 3.08E-05 3.24E-04 | 0.45 0.45 0.45 0.45 0.45 0.45 | 1.63E-01 8.43E-01 8.60E-01 4.89E-01 7.72E-01 6.11E-01 | 0.92 1.00 1.01 0.98 0.99 1.03 | 6.16E-01 4.17E-01 1.27E-01 8.67E-01 1.79E-01 | 1.01 1.04 0.96 0.99 1.09 | 2.53E-01 1.35E-01 6.86E-02 5.49E-01 4.22E-01 | 1.04 0.91 0.92 0.97 0.94 | 9.25E-01 2.29E-01 1.30E-01 7.69E-01 4.77E-02 | 1.00 1.06 0.96 1.01 1.14 |
| 1424032_at 1418840_at | Duplicate Gene Syr | SESN1 MANBA CSF1R MYO1F HVCN1 PDCD4 | protein 9 sestrin 1 mannosidase, beta A, hysosomal colony stimulating factor i receptor myosin IF hydrogen voltage-gated channel 1 programmed cell death 4 (neoplastic transformation inhibitor) 576 beta-galactosamide alpha-2,6-sialyltranferase 1 protein-Lisoaspartate (D- sapartate) O- | Nucleus Cytoplasm Plasma Membrane Cytoplasm unknown Nucleus | enzyme kinase other ion channel other | | 6.42E-05 4.86E-05 4.19E-05 1.09E-04 3.08E-05 3.24E-04 3.03E-05 | 0.45 0.45 0.45 0.45 0.45 0.45 0.45 | 1.63E-01 8.43E-01 8.60E-01 4.89E-01 7.72E-01 6.11E-01 4.68E-01 | 0.92 1.00 1.01 0.98 0.99 1.03 0.94 | 6.16E-01 4.17E-01 1.27E-01 8.67E-01 1.79E-01 7.27E-01 | 1.01 1.04 0.96 0.99 1.09 0.97 | 2.53E-01 1.35E-01 6.86E-02 5.49E-01 4.22E-01 2.39E-01 | 1.04 0.91 0.92 0.97 0.94 | 9.25E-01 2.29E-01 1.30E-01 7.69E-01 4.77E-02 7.45E-01 | 1.00 1.06 0.96 1.01 1.14 |
| 1424032_at 1418840_at | Duplicate Gene Syr | SESN1 MANBA CSF1R MYO1F HVCN1 PDCD4 ST6GAL1 | protein 9 settin 1 manasidas, beta A, lycosomal colony stimulating factor 1 receptor mosin IF hydrogen voltage-gated channel 1 hydrogen voltage-gated channel cell death 4 (nepolastic transformation inhibitor) 576 beta-gatactoaamide ajpha 2,6-ishiptranferase 1 protein-i-ciasapartate j0- methyturansferase dowanic containing 2 | Nucleus Cytoplasm Plasma Membrane Cytoplasm unknown Nucleus | enzyme kinase other other enzyme enzyme | | 6.42E-05 4.86E-05 4.19E-05 1.09E-04 3.08E-05 3.24E-04 3.03E-05 | 0.45 0.45 0.45 0.45 0.45 0.45 0.45 | 1.63E-01 8.43E-01 8.60E-01 4.89E-01 7.72E-01 6.11E-01 4.68E-01 | 0.92 1.00 1.01 0.98 0.99 1.03 0.94 | 6.16E-01 4.17E-01 1.27E-01 8.67E-01 1.79E-01 7.27E-01 | 1.01 1.04 0.96 0.99 1.09 0.97 | 2.53E-01 1.35E-01 6.86E-02 5.49E-01 4.22E-01 2.39E-01 | 1.04 0.91 0.92 0.97 0.94 | 9.25E-01 2.29E-01 1.30E-01 7.69E-01 4.77E-02 7.45E-01 | 1.00 1.06 0.96 1.01 1.14 |
| 1424032_at 1418840_at 1420928_at 1427074_at 1419156_at | | SESNI MANBA CSF1R MY01F HVCN1 PDCD4 ST6GAL1 ST6GAL1 ST6GAL1 ST6GAL1 | protein 9 section 1 manonosiase, beta A, incoronal J receptor I receptor More and the section of the section programmed cell death 4 programmed cell death 4 (receptor) Protection on babbies apparate () - section of the section of the section approximate () - in section of the section of the protein-i-isosparate () - asparate () - deanain containing 2 protein-i-isosparate () - asparate () - | Nucleus Cytoplasm Plasma Membrane Cytoplasm unknown Nucleus Cytoplasm | enzyme kinase other ion channel other enzyme | | 6.42E-05 4.86E-05 4.19E-05 1.09E-04 3.08E-05 3.24E-04 3.03E-05 9.02E-05 1.82E-04 2.44E-05 | 0.45 0.45 0.45 0.45 0.45 0.45 0.45 0.45 | 1.63E-01 8.43E-01 8.66E-01 4.89E-01 7.72E-01 6.11E-01 9.43E-01 7.50E-01 7.50E-01 | 0.92 1.00 1.01 0.98 0.99 1.03 0.94 1.00 0.99 0.99 0.98 | 6.16E-01 4.17E-01 1.27E-01 8.67E-01 1.79E-01 7.27E-01 6.38E-02 4.30E-01 4.85E-01 | 1.01 1.04 0.96 0.99 1.09 0.97 1.04 0.98 0.98 | 2.53E-01 1.35E-01 6.86E-02 5.49E-01 4.22E-01 2.39E-01 2.41E-01 1.59E-01 2.36E-01 | 1.04 0.91 0.92 0.97 0.94 0.91 0.91 0.97 0.93 0.93 1.05 | 925E-01 229E-01 130E-01 7.69E-01 4.77E-02 7.45E-01 1.92E-01 3.36E-01 9.24E-01 | 1.00 1.06 0.96 1.01 1.14 0.99 0.96 1.04 1.04 1.00 |
| 1424032_at 1418840_at 1420928_at 1427074_at 1419156_at 1451196_at | | SESNI MANBA CSF1R MY01F HVCNI POCD4 ST6GAL1 PCMTD2 | protein 9 section 1 manosoliske, beta A, phonomit J receptor and participation programmed cell death 4 programmed cell death 4 (receptation appha 2, established and a appha 2, established and appha 3, established and appha 3, established and appha 4, established and apph | Nucleus Cytoplasm Plasma Membrane Cytoplasm Nucleus Cytoplasm | enzyme kinase other other enzyme enzyme transcription | | 6.42E-05 4.86E-05 4.19E-05 1.09E-04 3.08E-05 3.24E-04 3.03E-05 9.02E-05 1.82E-04 | 0.45 0.45 0.45 0.45 0.45 0.45 0.45 0.45 | 1.63E-01 8.43E-01 8.60E-01 4.89E-01 7.72E-01 6.11E-01 4.68E-01 9.43E-01 7.50E-01 | 0.92 1.00 1.01 0.98 0.99 1.03 0.94 1.00 0.99 | 6.16E-01 4.17E-01 1.27E-01 8.67E-01 1.79E-01 7.27E-01 6.38E-02 4.30E-01 | 1.01 1.04 0.96 0.99 1.09 0.97 1.04 0.98 | 2.53E-01 1.35E-01 6.86E-02 5.49E-01 4.22E-01 2.39E-01 2.41E-01 1.59E-01 | 1.04 0.91 0.92 0.97 0.94 0.94 0.91 0.97 0.97 | 925E-01 229E-01 1.30E-01 7.69E-01 4.77E-02 7.45E-01 1.92E-01 3.36E-01 | 1.00 1.06 0.96 1.01 1.14 0.99 0.96 1.04 |
| 1424032_at 1418840_at 1420928_at 1427074_at 1419156_at 1451196_at 1451196_at | Duplicate Gene Syr | SESH1 MANBA CSF1R MYO1F HVCN1 PDCD4 ST6GAL1 ST6GAL1 ST6GAL1 ST6GAL1 ST6GAL1 ST6GAL1 ST6GAL1 ST6GAL1 | protein 9 settin 1 mannoolus, beta A, mannoolus, beta A, mannoolus, beta A, and A, and A, and A, and A, mannoolus, and A, mannoolus, and A, mannoolus, and A, mannoolus, and A, mannoolus, and A, an | Nucleus <u>Cytoplasm</u> Plasm Membrane <u>Cytoplasm</u> unknown Nucleus Cytoplasm <u>Cytoplasm</u> Nucleus unknown | enyme kinase other ion channel other enyme enyme transcription regulator other | | 6.42E-05 4.86E-05 4.19E-05 1.09E-04 3.08E-05 3.24E-04 3.03E-05 9.02E-05 1.82E-04 2.44E-05 | 0.45 0.45 0.45 0.45 0.45 0.45 0.45 0.45 | 1.63E-01 8.43E-01 8.60E-01 4.49E-01 7.72E-01 6.11E-01 4.68E-01 9.43E-01 7.50E-01 7.50E-01 7.50E-01 7.50E-01 7.11E-01 | 0.92 1.00 1.01 0.98 0.99 1.03 0.94 1.00 0.94 1.00 0.99 0.99 0.99 0.99 | 6.16E-01 4.17E-01 1.27E-01 8.67E-01 1.79E-01 7.27E-01 6.38E-02 4.30E-01 4.85E-01 4.15E-01 | 1.01 1.04 0.96 0.99 1.09 0.97 1.04 0.98 0.98 0.98 | 2.53E-01 1.35E-01 6.86E-02 5.49E-01 4.22E-01 2.39E-01 2.41E-01 1.59E-01 2.36E-01 | 1.04 0.91 0.92 0.97 0.94 0.91 0.91 0.93 1.05 0.91 | 925E-01 229E-01 130E-01 7.69E-01 4.77E-02 7.45E-01 1.92E-01 3.36E-01 9.24E-01 | 1.00 1.05 0.95 1.01 1.14 0.99 0.96 1.04 1.04 1.00 0.95 |
| 1424032_at 1418840_at 1420928_at 1427074_at 1439156_at 1419156_at 1417136_s_t 1419736_s_t 1439389_5_at | Duplicate Gene Syr | SENI MANBA CS18 MPOJF HWCN1 PDCD4 ST6GAL1 PCMTD2 S0X4 YPELS S0X4 MMADM | protein 9 settin 1 manarati massin 1 massin br>m m m m m m m m m m m | Nocleus Cytoglasm Plasma Membrane Cytoglasm Nocleus Cytoglasm Cytoglasm Nocleus Nocleus Nocleus Nocleus Nocleus | enyme kinase other ion channel other enzyme teasorietion regulator other kinase other | | 642E 65 486E 65 419E 65 109E 65 124E 64 301E 65 9.02E 65 182E 64 244E 65 207E 64 1.54E 64 | 0.45 0.45 0.45 0.45 0.45 0.45 0.45 0.45 | 1.63E-01 8.43E-01 8.60E-01 4.89E-01 6.11E-01 9.43E-01 7.50E-01 7.50E-01 7.50E-01 7.50E-01 7.11E-01 5.77E-01 4.86E-01 | 0.92 1.00 1.01 0.99 1.03 0.94 1.00 0.94 0.99 0.99 0.99 1.02 1.03 | 6.145-01 4.177-01 1.277-01 1.797-01 7.277-01 6.385-02 4.305-01 4.305-01 4.305-01 4.305-01 6.255-02 | 1.01 1.04 0.96 0.99 1.09 0.97 1.04 0.98 0.98 0.98 0.98 0.94 0.94 | 2 53E-01 1 35E-01 6 56E-02 5 .64E-01 2 .39E-01 2 .39E-01 2 .41E-01 1 .59E-01 2 .36E-01 1 .21E-01 3 .31E-02 9 .88E-02 | 1.04 0.91 0.92 0.97 0.94 0.91 0.97 0.93 1.05 0.93 0.93 0.93 0.93 0.93 0.93 0.93 0.94 | 9 25F-01 2 29E-01 1.30E-01 7.69E-01 1.92E-01 1.92E-01 9.24E-01 9.24E-01 2.03E-02 2.65E-01 | 1.00 1.06 0.96 1.01 1.14 0.99 0.96 1.04 1.00 0.95 0.87 0.87 |
| 1424032_at 1418840_at 1420928_at 1427074_at 1429156_at 1451196_at 145136_s_s_at | Duplicate Gene Syr | SESH1 MANBA CSF1R MYO1F HVCN1 PDCD4 ST6GAL1 ST6GAL1 ST6GAL1 ST6GAL1 ST6GAL1 ST6GAL1 ST6GAL1 ST6GAL1 | protein 9 jantin 1 dans, het A, hysosonal Lacadra Standard Standard Lacadra Standard Standard Lacadra Standard Standard programmad cell death 4 programmad cell deat | Nacleus Cytoglasm Planna Monthrane Cytoglasm Uninown Nacleus Cytoglasm Nacleus Nacleus Uninown Nacleus Uninown Nacleus Uninown Nacleus Uninown | enyme kinase other ion channel other enzyme enzyme transcription regulator other kinase | | 6.42E-05 4.86E-05 1.09E-04 3.08E-05 3.24E-04 2.03E-05 9.02E-05 1.82E-04 2.44E-05 2.07E-04 8.79E-06 | 0.45 0.45 0.45 0.45 0.45 0.45 0.45 0.45 | 1.63E-01 8.43E-01 8.63E-01 7.72E-01 6.11E-01 9.43E-01 7.50E-01 7.50E-01 7.50E-01 7.57E-01 5.77E-01 5.77E-01 6.31E-01 | 0.92 1.00 1.01 0.98 0.99 1.03 0.94 1.00 0.99 0.99 1.02 0.99 1.02 1.03 0.99 1.02 0.99 1.02 0.99 0.99 0.09 0 | 6.14E-01 4.17E-01 1.27F-01 8.67F-01 1.79E-01 7.27F-01 6.38E-02 4.30E-01 4.85E-01 4.15E-01 3.70E-01 | 1.01 1.04 0.96 0.99 1.09 0.97 1.04 0.98 0.98 0.98 0.98 0.95 0.34 | 2 53E-01 1 35E-01 6 56E-02 5 49E-01 2 39E-01 2 43E-01 2 43E-01 1 59E-01 2 36E-01 3 31E-02 9 88E-02 3 79E-02 | 1.04 0.91 0.92 0.97 0.94 0.91 0.91 0.97 0.93 1.05 0.93 0.93 0.93 | 9 25F-01 2 29E-01 1.30E-01 7.6FE-01 1.92E-01 1.92E-01 9.24E-01 9.24E-01 2.04E-02 2.65E-01 3.84E-01 | 1.00 1.06 0.95 1.01 1.14 0.99 0.95 1.04 1.00 0.95 0.87 0.94 0.95 |
| 1424032_st 1418840_st 1420928_st 1427074_st 1419156_st 1451366_st 1439389_s_st 1439389_s_st 1439389_s_st 1439389_s_st | Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr | SESNI MANBA CSF38 MYD1F POCD4 POCD4 ST6GAL1 PCMTD2 S004 YPELS MYADM FAMGIA ABHGAP | protein 9 jenten 9 jennin 10, ktor A. hnocornal codowy stimulating factor 1 months hydrogen voltage pasted channel 1 months hydrogen voltage pasted hydrogen voltage pasted hydrogen voltage pasted hydrogen ktor hydrogen voltage pasted hydrogen ktor hydrogen ktor hydrogen ktor Str for adversion hydrogen ktor hydrogen ktor Str for adversion hydrogen ktor Str for adversion hydrogen ktor Str for adversion hydrogen ktor hydrogen hydrogen hydrogen hydrogen hydrogen hydrogen hydrog | Nacleus Cytoplasm Planna Morhan Cytoplasm Nacleus Cytoplasm Nacleus Nacleus Indexes Nacleus Uninown Cytoplasm | engme kinase diter diter len channel other engme engme engme engme diter diter other other other | | 6.42E-05 4.84E-05 4.19E-05 1.09E-04 2.04E-05 2.24E-04 2.04E-05 9.02E-05 1.82E-04 2.24E-05 2.07E-04 8.77E-06 1.54E-04 1.24E-04 1.24E-04 1.22E-04 | 0.45 0.45 0.45 0.45 0.45 0.45 0.45 0.45 | 1.63E-01 8.63E-01 8.63E-01 7.72E-03 6.11E-01 4.68E-01 7.50E-01 7.50E-01 7.50E-01 7.50E-01 7.50E-01 5.77E-03 4.86E-01 6.31E-01 1.91E-01 | 0.92 1.00 1.01 0.98 0.99 1.03 0.94 1.00 0.99 0.99 0.99 1.02 1.03 0.97 0.91 | 6.167-01 4.177-01 1.277-01 1.277-01 1.786-01 7.277-01 6.387-02 4.367-01 4.367-01 4.367-01 4.367-01 1.376-01 2.256-02 2.256-01 2.056-01 | 1.01 1.04 0.96 0.99 1.09 1.09 1.04 0.97 1.04 0.98 0.98 0.98 0.98 0.94 0.94 0.94 0.93 0.92 | 2 53E-01 1 38E-01 1 48E-01 5 48E-02 2 39E-01 2 39E-01 2 39E-01 2 39E-01 1 21E-01 3 31E-02 9 38E-02 1 39E-02 1 39E-01 | 1.04 0.91 0.92 0.97 0.94 0.91 0.97 0.93 1.05 0.93 0.83 0.87 0.87 0.89 | 9 25E 61 2 26F 61 2 26F 61 2 26F 61 2 26F 61 4 77E 62 7 45E 61 1 92E 61 3 36E 61 9 24E 61 2 26E 61 3 26E 61 3 84E 61 1 15E 61 | 1.00 1.05 0.96 1.01 1.14 0.99 0.96 1.04 1.00 0.95 0.87 0.94 0.96 0.87 |
| 1424002_st 1418840_st 1418940_st 1420928_st 14292074_st 1419156_st 1419156_st 1419136_st 1419136_st 1419289_s_st 1438221_s_st 1449619_s_st 1438221_st | Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr | SSN1 MANBA CSF8 MOTE MOTE MOTE MOTE MOTE POCD4 STIGALI PCMTD2 SOVA VPLS SOVA FAME3A ABHGAP9 SGP1 | protein 9 protein 9 protein 1 programmal Cell and 1 programmal C | Nacleus Cytoplasm Planna Monhome Cytoplasm Nacleus Cytoplasm Nacleus Nacleus Uninown Nacleus Uninown Cytoplasm Cytoplasm Cytoplasm Cytoplasm | enyme kinsze other other enyme enyme transcription transcription other binsze other | | 6.421-65 4.846-65 4.196-65 1.086-64 1.086-65 1.246-64 1.016-65 9.021-65 9.021-65 1.876-64 1.576-66 1.546-64 1.246-64 1.246-64 1.246-64 1.246-64 1.246-64 1.246-64 | 0.45 0.45 0.45 0.45 0.45 0.45 0.45 0.45 | 1.63E-03 8.61E-03 8.60E-03 4.89E-03 7.72E-03 6.11E-03 9.43E-03 9.43E-03 7.50E-03 7.50E-03 7.50E-03 7.71E-03 8.77E-03 6.31E-03 1.91E-03 8.96E-03 | 0.92 100 101 0.98 0.99 103 0.94 100 0.99 0.99 0.99 102 103 0.97 0.91 102 | 6.166-01 4.177-01 1.277-01 1.276-01 7.2276-01 6.388-02 4.306-01 4.306-01 4.306-01 4.306-01 3.256-02 3.256-01 2.056-01 6.346-01 | 1.01 1.04 0.95 0.99 1.09 0.97 1.04 0.98 0.98 0.98 0.98 0.94 0.94 | 2.586-01 1.866-01 6.866-02 5.496-01 2.396-01 2.396-01 2.396-01 1.596-01 2.366-01 1.216-01 3.116-02 9.886-02 1.396-01 3.316-02 3.396-01 | 1.04 0.91 0.92 0.97 0.94 0.91 0.91 0.93 1.05 0.93 0.93 0.93 0.93 0.83 0.87 0.87 0.87 0.87 0.87 0.87 0.87 0.87 0.93 0.94 0.94 0.94 0.94 0.94 0.95 | 9 255 61 2 264 61 2 264 61 1 266 61 1 266 61 2 666 61 1 274 56 61 1 274 56 61 1 274 56 61 2 265 56 61 2 265 56 61 2 265 56 61 1 154 61 5 778 61 | 1.00 1.06 0.95 1.01 1.14 0.99 0.95 1.04 1.00 0.95 0.87 0.94 0.95 0.87 0.95 0.87 0.95 0.87 0.95 |
| 1424032_st 1418840_st 1420928_st 1427074_st 1419156_st 1451366_st 1439389_s_st 1439389_s_st 1439389_s_st 1439389_s_st | Duplicate Gene Syr Duplicate Gene Syr Duplicate Gene Syr | SESNI MANBA CSF38 MYD1F POCD4 POCD4 ST6GAL1 PCMTD2 S004 YPELS MYADM FAMGIA ABHGAP | protein 9 settin 1 dans, het A, hosoand, 1 neceptor moreal II programmed cell death 4 programmed | Nacleus Cytoplasm Planna Morhan Cytoplasm Nacleus Cytoplasm Nacleus Nacleus Indexes Nacleus Uninown Cytoplasm | engroe kinase other other engroe engroe engroe inascription regulator other | | 6.42E-05 4.84E-05 4.19E-05 1.09E-04 2.04E-05 2.24E-04 2.04E-05 9.02E-05 1.82E-04 2.24E-05 2.07E-04 8.77E-06 1.54E-04 1.24E-04 1.24E-04 1.22E-04 | 0.45 0.45 0.45 0.45 0.45 0.45 0.45 0.45 | 1.63E-01 8.63E-01 8.63E-01 7.72E-03 6.11E-01 4.68E-01 7.50E-01 7.50E-01 7.50E-01 7.50E-01 7.50E-01 5.77E-03 4.86E-01 6.31E-01 1.91E-01 | 0.92 1.00 1.01 0.98 0.99 1.03 0.94 1.00 0.99 0.99 0.99 1.02 1.03 0.97 0.91 | 6.167-01 4.177-01 1.277-01 1.277-01 1.786-01 7.277-01 6.387-02 4.367-01 4.367-01 4.367-01 4.367-01 1.376-01 2.256-02 2.256-01 2.056-01 | 1.01 1.04 0.96 0.99 1.09 1.09 1.04 0.97 1.04 0.98 0.98 0.98 0.98 0.94 0.94 0.94 0.93 0.92 | 2 53E-01 1 38E-01 1 48E-01 5 48E-02 2 39E-01 2 39E-01 2 39E-01 2 39E-01 1 21E-01 3 31E-02 9 38E-02 1 39E-02 1 39E-01 | 1.04 0.91 0.92 0.97 0.94 0.91 0.97 0.93 1.05 0.93 0.83 0.87 0.87 0.89 | 9 25E 61 2 26F 61 2 26F 61 2 26F 61 2 26F 61 4 77E 62 7 45E 61 1 92E 61 3 36E 61 9 24E 61 2 26E 61 3 26E 61 3 84E 61 1 15E 61 | 1.00 1.05 0.96 1.01 1.14 0.99 0.96 1.04 1.00 0.95 0.87 0.94 0.96 0.87 |
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| | | | | | | | Stimula | tion Only | | | und Only | | | | nd Compound | |
|--|--|--|---|--|--|---|--|--------------------------------------|--|--------------------------------------|--|--------------------------------------|--|--|--|--|
| 1452141 a at | İ | SEPP1 | Probe Set Description selenoprotein P, plasma, | Extracellular Space | ather | İ | CpG vs. | Medium 0.43 | 0.25 uM E64 5.07E-01 | 46 vs. Medium | 1.25 uM E644 | 6 vs. Medium | CpG + 0.25 | aM E6446 vs. Medium 0.91 | CpG + 1.25 u 3.92E-01 | M E6446 vs. Medium |
| 1452141 a at 1418396_at | | GPSM3 | 1 G-protein signaling modulator 3 | Extracellular Space | other | | 1.79E-05 2.50E-05 | 0.43 | 5.07E-01 8.96E-01 | 1.02 | 2.21E-01 2.05E-01 | 0.97 | 7.68E-02 1.36E-01 | 0.91 | 3.92E-01 5.44E-02 | 0.94 |
| 1434010 at | | FAM117B | family with sequence similarity 117, member B | unknown | other | | 3.47E-05 | 0.43 | 4.70E-01 | 0.97 | 6.23E-01 | 0.97 | 1.73E-01 | 0.92 | 9.60E-01 | 1.00 |
| 1434010_at 1415834 at | | DUSP6 | dual specificity phosphatase 6 | Cytoplasm | phosphatase | | 1.77E-03 | 0.43 | 2.76E-01 | 0.86 | 7.12E-01 | 0.95 | 3.36E-01 | 0.89 | 3.18E-01 | 0.88 |
| 1450194 a at | Duplicate Gene Syn | | v-myb myeloblastosis viral oncogene homolog (avian) | Nucleus | transcription regulator | | 1.99E-03 | 0.43 | 6.97E-01 | 0.97 | 3.49E-01 | 0.93 | 9.71E-01 | 1.00 | 8.57E-01 | 1.01 |
| 1421402 at | Duplicate Gene Syn | | metastasis associated 1 family, member 3 | Nucleus | other | | 7.62E-05 | 0.43 | 1.41E-01 | 0.97 | 1.66E-01 | 0.93 | 4.63E-03 | 0.86 | 6.44E-03 | 0.93 |
| | | | | | | n/pentazocine, acetaminophe | | | | | | | | | | |
| | | | | | | n/clemastine/ pseudoephedri pe | | | | | | | | | | |
| | | | | | | aspirin/butalbi tal/caffeine, | | | | | | | | | | |
| | | | | | | acetaminophe n/caffeine/dih ydrocodeine, | | | | | | | | | | |
| | | | | | | aspirin/hydroc odone, aspirin/oxycod | | | | | | | | | | |
| | | | | | | one, acetaminophe | | | | | | | | | | |
| | | | | | | n/aspirin/caffe ine, aspirin/pravast | | | | | | | | | | |
| | | | | | | atin, acetaminophe | | | | | | | | | | |
| | | | prostaglandin- | | | n/dexbromphe niramine/pseu doephedrine, | | | | | | | | | | |
| | | | endoperoxide synthase 1 (prostaglandin G/H | | | aspirin/mepro bamate, | | | | | | | | | | |
| 1423414_at | Duplicate Gene Syn | | synthase and cyclooxygenase) | Cytoplasm | enzyme transmembrane | aspirin/caffein e/propoxyphen | 6.97E-04 | 0.43 | 2.16E-01 | 0.93 | 1.42E-01 | 0.92 | 3.41E-02 | 0.87 | 3.47E-02 | 0.84 |
| 1426708 at | | ANTXR2 | anthrax toxin receptor 2 p21 protein (Cdc42/Rac)- | Plasma Membrane | receptor | | 1.06E-05 | 0.43 | 7.68E-01 | 1.01 | 9.00E-01 | 1.01 | 1.23E-01 | 0.89 | 3.62E-01 | 1.05 |
| 1420979 at | Duplicate Gene Syn | PAK1 | activated kinase 1 | Cytoplasm | kinase | | 2.80E-06 | 0.43 | 2.07E-01 | 0.97 | 1.41E-02 | 0.92 | 1.46E-01 | 0.96 | 5.24E-01 | 0.99 |
| 1435666 at | | MAST3 | microtubule associated serine/threonine kinase 3 | unknown | kinase | | 2.99E-05 | 0.43 | 4.76E-01 | 0.96 | 2.86E-01 | 1.04 | 5.77E-01 | 0.98 | 2.74E-01 | 1.05 |
| | | | | | | zeneca ZD 3523, | | | | | | | | | | |
| 1418944_at | | CYSLTR1 | cysteinyl leukotriene receptor 1 | Plasma Membrane | G-protein coupled receptor | montelukast, zafirlukast, pranlukast | 4.80E-05 | 0.43 | 5.09E-01 | 0.95 | 4.36E-01 | 0.93 | 1.91E-02 | 0.75 | 3.82E-03 | 0.78 |
| 1431804 a at | | SP3 | Sp3 transcription factor transmembrane 6 | Nucleus | transcription regulator | | 1.82E-02 | 0.43 | 5.01E-01 | 0.81 | 7.75E-01 | 0.91 | 5.73E-01 | 0.88 | 2.10E-01 | 0.77 |
| 1424443 at | Duplicate Gene Syn | TM6SF1 | superfamily member 1 Ras association | Plasma Membrane | other | | 6.82E-05 | 0.43 | 9.58E-01 | 1.00 | 5.34E-01 | 0.97 | 1.83E-01 | 0.88 | 3.74E-01 | 1.06 |
| 1448547 at | Duplicate Gene Syn | RASSF3 | (RalGDS/AF-6) domain family member 3 runt-related transcription | unknown | other transcription | | 2.29E-04 | 0.42 | 5.03E-01 | 0.96 | 2.16E-01 | 0.94 | 4.26E-03 | 0.75 | 1.23E-03 | 0.81 |
| 1424704_at | - | RUNK2 | factor 2 | Nucleus | regulator | acetaninoprie n/pentazocine, | 3.25E-04 | 0.42 | 3.80E-01 | 0.94 | 9.16E-01 | 0.99 | 7.03E-01 | 0.97 | 4.76E-01 | 1.07 |
| | | | | | | acetaminophe n/clemastine/ | | | | | | | | | | |
| | | | | | | pseudoephedri ne, aspirin/butalbi | | | | | | | | | | |
| | | | | | | tal/caffeine, acetaminophe n/caffeine/dih | | | | | | | | | | |
| | | | | | | ydrocodeine, aspirin/hydroc | | | | | | | | | | |
| | | | | | | odone, aspirin/oxycod one | | | | | | | | | | |
| | | | | | | acetaminophe n/aspirin/caffe | | | | | | | | | | |
| | | | | | | ine, aspirin/pravast atin, | | | | | | | | | | |
| | | | | | | acetaminophe n/dexbromphe | | | | | | | | | | |
| | | | prostaglandin- endoperoxide synthase 1 | | | niramine/pseu doephedrine, aspirin/mepro | | | | | | | | | | |
| 1436448 a at | Duplicate Gene Syn | PTGS1 | (prostaglandin G/H synthase and cyclooxygenase) | Cytoplasm | enzyme | bamate, aspirin/caffein e/propoxyphen | 3.93E-05 | 0.42 | 9.21E-01 | 1.01 | 1.51E-01 | 1.09 | 2.07E-01 | 0.88 | 9.28E-01 | 1.01 |
| 1452217 at | bopileate delle syn | AHNAK | AHNAK nucleoprotein ecotropic viral integration | Nucleus | other | er propoxyphen | 1.87E-03 | 0.42 | 8.36E-01 | 1.03 | 7.63E-01 | 0.96 | 9.20E-01 | 0.99 | 6.11E-01 | 1.07 |
| 1417513 at | | EVI5 | site 5 epidermal growth factor receptor pathway | unknown | other | | 2.16E-05 | 0.42 | 4.56E-01 | 1.03 | 2.65E-01 | 0.96 | 5.00E-02 | 0.89 | 1.95E-01 | 0.95 |
| 1422824 s at 1423632 at | | EPS8 GPR146 | substrate 8 G protein-coupled | Plasma Membrane | peptidase G-protein coupled | | 3.64E-04 | 0.42 | 8.64E-01 7.76E-01 | 0.99 | 8.42E-01 9.07E-02 | 0.99 | 1.97E-02 | 0.76 | 9.72E-01 3.79E-01 | 1.00 |
| 1423632 at 1420970_at | Duplicate Gene Syn | ADCY7 | receptor 146 ademylate cyclase 7 | Plasma Membrane | enzyme | | 4.08E-07 | 0.42 | 4.03E-01 | 1.04 | 9.07E-02 8.54E-01 | 0.99 | 7.47E-01 | 1.02 | 2.84E-03 | 1.13 |
| 1448318 at 1438931 s at | Duplicate Gene Syn | PLIN2 SESN1 | perilipin 2 sestrin 1 | Plasma Membrane Nucleus | other | | 4.17E-05 6.19E-05 | 0.42 | 6.86E-01 8.08E-01 | 1.03 | 2.45E-01 1.72E-01 | 1.05 | 1.67E-02 5.53E-01 | 0.84 | 9.90E-01 4.82E-01 | 1.00 |
| 1429775 a at | Dopinante Gene Syn | | regulator of G-protein | indicus. | ounci | | 4.99E-04 | 0.41 | 5.35E-01 | 1.04 | 3.28E-01 | 1.04 | 1.15E-01 | 0.89 | 2.86E-01 | 1.06 |
| 1416882_at | | RGS10 | signaling 10 carbohydrate (chondroitin | Cytoplasm | other | | 2.57E-05 | 0.41 | 5.02E-01 | 0.98 | 1.17E-01 | 1.05 | 5.56E-02 | 0.94 | 6.34E-01 | 0.99 |
| 1448477_at 1450718 at | | CHST12 SH2B2 | 4) sulfotransferase 12 SH2B adaptor protein 2 | Cytoplasm Cytoplasm | enzyme other | | 1.47E-05 9.28E-06 | 0.41 | 5.13E-01 5.57E-01 | 0.98 | 8.69E-01 8.16E-01 | 1.01 | 1.15E-02 7.94E-01 | 0.89 | 7.97E-01 2.76E-01 | 0.99 |
| 1415822_at | Duplicate Gene Syn | | stearoyl-Coenzyme A desaturase 2 erythrocyte membrane | Cytoplasm | enzyme | | 1.37E-05 | 0.41 | 3.21E-02 | 1.12 | 3.76E-03 | 1.25 | 2.17E-02 | 1.15 | 2.40E-03 | 1.37 |
| 1418294 at | | EPB41L4B | protein band 4.1 like 4B killer cell lectin-like receptor subfamily D, | unknown | transporter transmembrane | | 8.41E-05 | 0.41 | 3.51E-01 | 0.94 | 2.54E-01 | 0.93 | 7.32E-01 | 0.98 | 5.93E-01 | 0.98 |
| 1460245 at | | KLRD1 | member 1 hairy and enhancer of | Plasma Membrane | receptor transcription | | 6.95E-05 | 0.41 | 9.05E-01 | 1.00 | 6.99E-01 | 0.99 | 4.82E-01 | 1.06 | 3.49E-03 | 1.10 |
| 1436050 x at | | HES6 | split 6 (Drosophila) patatin-like phospholipase domain | Nucleus | regulator | | | 0.41 | | 0.93 | 1.32E-01 | 0.98 | 4.80E-01 | 0.97 | 8.04E-01 | 0.99 |
| 1451361 a at | | PNPLA7 | containing 7 | unknown | enzyme | | 7.21E-05 | 0.41 | 3.14E-01 | 1.08 | 2.24E-01 | 1.11 | 8.43E-01 | 0.99 | 2.52E-02 | 1.18 |
| 1422751_at | | TLE1 | transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) | Nucleus | transcription regulator | | 5.09E-05 | 0.41 | 9.34E-01 | 0.99 | 3.51E-01 | 0.89 | 4.90E-02 | 0.79 | 1.46E-02 | 0.76 |
| 1417266 at | Duplicate Gene Syn | Ccl6 | chemokine (C-C motif) ligand 6 | Extracellular Space | cytokine transcription | | 4.33E-04 | 0.41 | 2.08E-01 | 0.94 | 2.01E-01 | 0.92 | 3.22E-02 | 0.86 | 3.30E-02 | 0.86 |
| 1432543 a at | | KLF13 | Kruppel-like factor 13 fucosyltransferase 7 | Nucleus | regulator | | 7.14E-05 | 0.41 | 1.79E-01 | 0.87 | 2.22E-01 | 0.93 | 1.42E-02 | 0.80 | 2.06E-02 | 0.87 |
| 1420756 at | | FUT7 | (alpha (1,3) fucosyltransferase) deoxyribonuclease I-like | Cytoplasm | enzyme | | 4.48E-04 | 0.40 | 4.10E-01 | 0.96 | 8.94E-01 | 1.01 | 1.28E-01 | 0.92 | 1.23E-01 | 0.92 |
| 1429173_at 1455871 s at | 1 | DNASE1L1 RPL13 | 1 ribosomal protein L13 | Cytoplasm Cytoplasm | enzyme other | | 5.66E-05 2.24E-05 | 0.40 | 7.64E-01 2.91E-01 | 0.99 | 4.17E-01 9.83E-01 | 1.02 | 1.03E-02 7.04E-01 | 0.90 | 7.39E-01 8.23E-01 | 1.02 0.99 |
| 1451731 at | | | ATP-binding cassette, | 1 | | | 2.46E-04 | 0.40 | 5.49E-01 | 0.96 | 3.36E-01 | 0.94 | 2.47E-01 | 0.92 | 9.14E-01 | 0.99 |
| | | ABCA3 | sub-family A (ABC1), member 3 | Plasma Membrane | | | | 0.40 | 2.38E-01 | 0.93 | 6.98E-02 | 0.89 | 6.98E-01 | 0.98 | 1.26E-01 | 0.94 |
| 1452389_at | | ABCA3 CD27 | sub-family A (ABC1), | Plasma Membrane Plasma Membrane | transmembrane receptor | | 1.47E-04 | | | | | | | | 1.26E-01 | |
| | | CD27 | sub-family A (ABC1), member 3 CD27 molecule xeroderma pigmentosum, | Plasma Membrane | transmembrane receptor | | | | | | | | | | | |
| 1422532 at | | CD27 XPC | sub-family A (ABC1), member 3 CD27 molecule xeroderma pigmentosum, complementation group C Rho GTPase activating | Plasma Membrane Nucleus | transmembrane | | 1.47E-04 3.40E-04 1.08E-04 | 0.40 | 7.60E-01 8.64E-03 | 0.98 | 5.40E-01 1.36E-01 | 0.96 | 2.23E-01 6.42E-02 | 0.91 | 1.26E-01 5.20E-01 4.35E-02 | 0.96 |
| 1422532 at 1419810 x at 1416008_at | Duplicate Gene Syn | CD27 XPC ARHGAP9 SATB1 | sub-family A (ABC1), member 3 CD27 molecule xeroderma pigmentosum, complementation group C Rho GTPase activating protein 9 SATB homeobox 1 | Plasma Membrane Nucleus Cytoplasm Nucleus | transmembrane receptor other other regulator | | 3.40E-04 1.08E-04 8.66E-06 | 0.40 | 8.64E-03 5.70E-01 | 0.89 | 1.36E-01 9.73E-01 | 0.97 | 6.42E-02 8.41E-02 | 0.91 0.89 0.90 | 5.20E-01 4.35E-02 8.35E-01 | 0.96 0.94 0.99 |
| 1422532 at 1419810 x at 1416008 at 1454699 at | Duplicate Gene Syn Duplicate Gene Syn Duplicate Gene Syn | CD27 XPC ARHGAP9 SATB1 SESN1 | sub-family A (ABC1), member 3 CD27 molecule 2027 molecule 2027 molecule 2027 molecule xeroderma pigmentosum, complementation group C AFB homeobox 1 settrin 1 ST8 alpha-W-acetyl- neuraminide alpha-2.8- | Plasma Membrane Nucleus Cytoplasm Nucleus Nucleus | transmembrane receptor other other transcription | | 3.40E-04 1.08E-04 8.66E-06 4.54E-05 | 0.40 0.40 0.40 0.40 | 8.64E-03 5.70E-01 8.66E-01 | 0.89 0.96 0.99 | 1.36E-01 9.73E-01 6.15E-01 | 0.97 1.00 0.97 | 6.42E-02 8.41E-02 9.33E-01 | 0.91 0.89 0.90 1.01 | 5.20E-01 4.35E-02 8.35E-01 4.62E-01 | 0.96 0.94 0.99 1.05 |
| 1422532 at 1419810 x at 1416008 at 1454699 at 1419186 a at | Duplicate Gene Syn | CD27 XPC ARHGAP9 SATB1 SESN1 ST85IA4 | sub-family A (ABC1), member 3 CD27 molecule 2027 molecule | Plasma Membrane Nucleus Cytoplasm Nucleus Nucleus Cytoplasm | transmembrane receptor other cother transcription regulator other transcription | | 3.40E-04 1.08E-04 8.66E-06 4.54E-05 7.43E-06 | 0.40 0.40 0.40 0.40 | 8.64E-03 5.70E-01 8.66E-01 1.93E-01 | 0.89 0.96 0.99 | 1.36E-01 9.73E-01 6.15E-01 2.16E-01 | 0.97 | 6.42E-02 8.41E-02 9.33E-01 4.07E-02 | 0.91 0.89 0.90 1.01 0.85 | 5.20E-01 4.35E-02 8.35E-01 4.62E-01 1.34E-01 | 0.96 0.94 0.99 1.05 0.93 |
| 1422532 at 1419810 x at 1416008 at 1454699 at 1419186 a at 1448890 at | Duplicate Gene Syn Duplicate Gene Syn Duplicate Gene Syn | CD27 XPC ARHGAP9 SAT81 SESN1 SESN1 ST8SIA4 KLF2 | sub-family A (ABC1), member 3 CD27 molecule 2027 molecule | Plasma Membrane Nucleus Cytoplasm Nucleus Cytoplasm Nucleus | transmembrane receptor other transcription regulator other enzyme | | 3.40E-04 1.08E-04 8.66E-06 4.54E-05 7.43E-06 2.06E-05 | 0.40 0.40 0.40 0.40 0.40 | 8.64E-03 5.70E-01 8.66E-01 1.93E-01 6.59E-02 | 0.89 0.96 0.99 0.95 0.92 | 1.36E-01 9.73E-01 6.15E-01 2.16E-01 1.27E-01 | 0.97 1.00 0.97 0.95 0.93 | 6.42E-02 8.41E-02 9.33E-01 4.07E-02 3.04E-03 | 0.91 0.89 0.90 1.01 0.85 0.79 | 5.20E-01 4.35E-02 8.35E-01 4.62E-01 1.34E-01 1.66E-02 | 0.96 0.94 0.99 1.05 0.93 0.88 |
| 1422532 at 1419810 x at 1416008 at 1454699 at 1419186 a at | Duplicate Gene Syn Duplicate Gene Syn Duplicate Gene Syn | CD27 XPC ARHGAP9 SATB1 SESN1 ST85IA4 | sub-framily A (ABC1), member 3 CD27 molecule 2002 molecule 2002 molecule 2003 molecule 2004 molecule | Plasma Membrane Nucleus Cytoplasm Nucleus Nucleus Cytoplasm | transmembrane receptor other cother transcription regulator other transcription | | 3.40E-04 1.08E-04 8.66E-06 4.54E-05 7.43E-06 | 0.40 0.40 0.40 0.40 | 8.64E-03 5.70E-01 8.66E-01 1.93E-01 | 0.89 0.96 0.99 | 1.36E-01 9.73E-01 6.15E-01 2.16E-01 | 0.97 | 6.42E-02 8.41E-02 9.33E-01 4.07E-02 | 0.91 0.89 0.90 1.01 0.85 | 5.20E-01 4.35E-02 8.35E-01 4.62E-01 1.34E-01 | 0.96 0.94 0.99 1.05 0.93 |
| 1422532 at 1419810 x at 1416008 at 1454699 at 1419186 a at 1448890 at | Duplicate Gene Syn Duplicate Gene Syn Duplicate Gene Syn | CD27 XPC ARHGAP9 SAT81 ST85IA4 KLF2 ALOXSAP | sub-family A (ABC1), member 3 CD27 molecule 2027 molecule | Plasma Membrane Nucleus Cytoplasm Nucleus Cytoplasm Nucleus | transmembrane receptor other transcription regulator regulator | | 3.40E-04 1.08E-04 8.66E-06 4.54E-05 7.43E-06 2.06E-05 | 0.40 0.40 0.40 0.40 0.40 | 8.64E-03 5.70E-01 8.66E-01 1.93E-01 6.59E-02 | 0.89 0.96 0.99 0.95 0.92 | 1.36E-01 9.73E-01 6.15E-01 2.16E-01 1.27E-01 | 0.97 1.00 0.97 0.95 0.93 | 6.42E-02 8.41E-02 9.33E-01 4.07E-02 3.04E-03 | 0.91 0.89 0.90 1.01 0.85 0.79 | 5.20E-01 4.35E-02 8.35E-01 4.62E-01 1.34E-01 1.66E-02 | 0.96 0.94 0.99 1.05 0.93 0.88 |

| | | | | | | | | Stimulat | | | Compou | und Only | | | Stimulation a | nd Compound | |
|---|----------------------------|--|------------------|--|---------------------|---------------------------|-------------|----------------------|--------|----------------------|---------------|----------------------|---------------|----------------------|---------------------|----------------------|--------------------|
| BALL BAL ></td> <td>i</td> <td>i</td> <td>Probe Set Description</td> <td>i</td> <td>i</td> <td>i –</td> <td>CpG vs.</td> <td>Medium</td> <td>0.25 uM E64</td> <td>46 vs. Medium</td> <td>1.25 uM E644</td> <td>16 vs. Medium</td> <td>CpG + 0.25 u</td> <td>aM E6446 vs. Medium</td> <td>CpG + 1.25 u</td> <td>M E6446 vs. Medium</td> | | i | i | Probe Set Description | i | i | i – | CpG vs. | Medium | 0.25 uM E64 | 46 vs. Medium | 1.25 uM E644 | 16 vs. Medium | CpG + 0.25 u | aM E6446 vs. Medium | CpG + 1.25 u | M E6446 vs. Medium |
| Name | 1420980 at | Duplicate Gene Sys | PAK1 | | Cytoplasm | kinase transcription | | 2.72E-05 | 0.39 | 3.57E-01 | 1.03 | 9.39E-01 | 1.00 | 2.96E-01 | 0.96 | 3.05E-01 | 1.04 |
| Mart al and be also be also as a proper and a proper proper and a proper and a p | | | | cyclin G2 | | regulator | | | | | | | | | | | 1.03 |
| | | | | 1 (platelet) | | | ridogrel | | | | | | | | | | 0.95 |
| | | | | C-type lectin domain | | transmembrane | | | | | | | | | | | 0.94 |
| BANDY BANDY <thb< td=""><td></td><td></td><td></td><td>microtubule associated monooxygenase,</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></thb<> | | | | microtubule associated monooxygenase, | | | | | | | | | | | | | |
| | | Duplicate Gene Sys | | containing 1 | | | | | | 4.49E-01 | | 5.57E-01 | | | | | 1.03 |
| No. | | Duplicate Gene Sys | | thioredoxin interacting protein | | | | | | | | | | | | | 0.99 |
| Mar Matrix Mar Matrix </td <td></td> <td></td> <td></td> <td>polymerase II complex</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> | | | | polymerase II complex | | | | | | | | | | | | | |
| Norm | 1448076_at | | CTR9 | | Nucleus | other | | 5.77E-05 | 0.38 | 4.18E-01 | 1.08 | 3.39E-01 | 1.06 | | 0.98 | 3.26E-02 | 1.30 |
| Alt i Alt i Alt i < | 1417533 a at | Duplicate Gene Sys | ITGB5 | Ras association | Plasma Membrane | other | EMD121974 | 4.31E-05 | 0.38 | 7.24E-01 | 0.99 | 4.75E-01 | 0.95 | 4.69E-03 | 0.84 | 1.32E-01 | 0.94 |
| Name Name <th< td=""><td>1448546 at</td><td>Duplicate Gene Sys</td><td>RASSF3</td><td>family member 3</td><td>unknown</td><td>other</td><td></td><td>2.01E-04</td><td>0.38</td><td>1.91E-01</td><td>1.02</td><td>2.86E-03</td><td>0.96</td><td>4.03E-02</td><td>0.92</td><td>7.34E-01</td><td>0.99</td></th<> | 1448546 at | Duplicate Gene Sys | RASSF3 | family member 3 | unknown | other | | 2.01E-04 | 0.38 | 1.91E-01 | 1.02 | 2.86E-03 | 0.96 | 4.03E-02 | 0.92 | 7.34E-01 | 0.99 |
| Normal | | | | monooxygenase, | | | | | | | | | | | | | |
| BAT BAT <td>1456439 x at</td> <td>Duplicate Gene Sys</td> <td>MICAL1</td> <td></td> <td>Cytoplasm</td> <td>enzyme</td> <td></td> <td>6.87E-05</td> <td>0.38</td> <td>1.96E-01</td> <td>0.96</td> <td>8.60E-01</td> <td>1.01</td> <td>6.99E-01</td> <td>0.99</td> <td>7.08E-01</td> <td>1.01</td> | 1456439 x at | Duplicate Gene Sys | MICAL1 | | Cytoplasm | enzyme | | 6.87E-05 | 0.38 | 1.96E-01 | 0.96 | 8.60E-01 | 1.01 | 6.99E-01 | 0.99 | 7.08E-01 | 1.01 |
| NAME NAME NAME N | 1420498 a at | | DAB2 | phosphoprotein, homolog | Plasma Membrane | other | | 1.51E-05 | 0.38 | 6.96E-01 | 0.98 | 4.84E-01 | 0.96 | 2.27E-01 | 0.93 | 8.64E-01 | 1.01 |
| Norm Norm <t< td=""><td></td><td>Duplicate Gene Sys</td><td></td><td>HMG-box transcription</td><td></td><td>transcription</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td>1.00</td></t<> | | Duplicate Gene Sys | | HMG-box transcription | | transcription | | | | | | | | | | | 1.00 |
| Diard Jong <thjong< th=""> Jong Jong <thj< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></thj<></thjong<> | | | | | | | | | | | | | | | | | |
| Diard Diard Diard < | 1422527 at | | HLA-DMA | alpha | Plasma Membrane | | | | 0.38 | | | | | | | | 0.93 |
| No. No. <td></td> <td>Duplicate Gene Syn Duplicate Gene Syn</td> <td>Ccl6 OLFM1</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>0.90</td> | | Duplicate Gene Syn Duplicate Gene Syn | Ccl6 OLFM1 | | | | | | | | | | | | | | 0.90 |
| Differ Differ Differ <td>1419711 at</td> <td></td> <td>CD7</td> <td>CD7 molecule</td> <td>Plasma Membrane</td> <td></td> <td></td> <td>1.04E-04</td> <td>0.38</td> <td>7.74E-01</td> <td>0.99</td> <td>8.13E-01</td> <td>1.01</td> <td>5.35E-01</td> <td>0.97</td> <td>4.73E-01</td> <td>0.97</td> | 1419711 at | | CD7 | CD7 molecule | Plasma Membrane | | | 1.04E-04 | 0.38 | 7.74E-01 | 0.99 | 8.13E-01 | 1.01 | 5.35E-01 | 0.97 | 4.73E-01 | 0.97 |
| Dark A Dark A <thdark a<="" th=""> <thdark a<="" th=""> <thdark a<="" t<="" td=""><td></td><td></td><td></td><td>thioredoxin interacting</td><td></td><td>regulator</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td>1.00</td></thdark></thdark></thdark> | | | | thioredoxin interacting | | regulator | | | | | | | | | | | 1.00 |
| No. No. <td></td> <td></td> <td></td> <td>interferon regulatory</td> <td></td> <td>transcription</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>0.90</td> | | | | interferon regulatory | | transcription | | | | | | | | | | | 0.90 |
| | | - opincate Gene Syr | | chemokine (C-C motif) | | G-protein coupled | | | | | | | | | | | 1.09 |
| Norm Norm <t< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></t<> | | | | | | | | | | | | | | | | | |
| PATI A PATI A PATI A PATI A PATI A PATI A PATI A <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>belinostat,</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> | | | | | | | belinostat, | | | | | | | | | | |
| BADEM BADEM PADEM "><td>1415743 at</td><td></td><td>HDACS</td><td></td><td>Nucleus</td><td></td><td>vorinostat,</td><td>2.02E-04</td><td>0.37</td><td>4.39E-01</td><td>0.95</td><td>4.59E-01</td><td>0.95</td><td>1.47E-01</td><td>0.90</td><td>9.41E-01</td><td>1.00</td></t<> | 1415743 at | | HDACS | | Nucleus | | vorinostat, | 2.02E-04 | 0.37 | 4.39E-01 | 0.95 | 4.59E-01 | 0.95 | 1.47E-01 | 0.90 | 9.41E-01 | 1.00 |
| Differe < | | Duplicate Gene Sys | GPR137B | G protein-coupled receptor 1378 | Plasma Membrane | | | 1.38E-04 | 0.37 | 4.41E-05 | 1.15 | 2.03E-03 | 1.17 | 1.76E-01 | 0.95 | | 1.16 |
| Date Partial | 1448407_at | Duplicate Gene Sys | C10orf54 | reading frame 54 | unknown | other | | 3.71E-04 | 0.37 | 3.84E-01 | 0.96 | 6.39E-01 | 0.98 | 1.07E-03 | 0.80 | 1.87E-01 | 0.93 |
| Deck Deck <thdeck< th=""> Deck Deck <th< td=""><td>1416635_at</td><td></td><td>SMPDL3A</td><td>phosphodiesterase, acid-</td><td>Extracellular Space</td><td>enzyme</td><td></td><td>1.74E-04</td><td>0.37</td><td>3.88E-01</td><td>0.96</td><td>8.21E-01</td><td>0.99</td><td>2.32E-03</td><td>0.77</td><td>3.83E-01</td><td>0.96</td></th<></thdeck<> | 1416635_at | | SMPDL3A | phosphodiesterase, acid- | Extracellular Space | enzyme | | 1.74E-04 | 0.37 | 3.88E-01 | 0.96 | 8.21E-01 | 0.99 | 2.32E-03 | 0.77 | 3.83E-01 | 0.96 |
| Subs Junc <thjunc< th=""> Junc Junc <th< td=""><td></td><td></td><td></td><td>core-binding factor, runt</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></th<></thjunc<> | | | | core-binding factor, runt | | | | | | | | | | | | | |
| Dittor Dittor <thdittor< th=""> <thdittor< th=""> <thdittor< t<="" td=""><td>1438705 at</td><td>Duplicate Gene Sys</td><td>CBFA2T3</td><td>translocated to. 3</td><td>Nucleus</td><td></td><td></td><td>5.36E-05</td><td>0.37</td><td>3.35E-01</td><td>0.96</td><td>1.73E-01</td><td>0.96</td><td>1.84E-02</td><td>0.90</td><td>1.60E-01</td><td>0.94</td></thdittor<></thdittor<></thdittor<> | 1438705 at | Duplicate Gene Sys | CBFA2T3 | translocated to. 3 | Nucleus | | | 5.36E-05 | 0.37 | 3.35E-01 | 0.96 | 1.73E-01 | 0.96 | 1.84E-02 | 0.90 | 1.60E-01 | 0.94 |
| Disp. a Description <thdescription< th=""> <thdescription< th=""> <t< td=""><td>1426567 a at</td><td>Duplicate Gene Syn</td><td>PQLC1</td><td>containing 1 G protein-coupled</td><td>unknown</td><td>other</td><td></td><td>7.29E-05</td><td>0.37</td><td>4.29E-01</td><td>0.96</td><td>4.68E-01</td><td>0.97</td><td>5.70E-02</td><td>0.89</td><td>6.53E-01</td><td>0.98</td></t<></thdescription<></thdescription<> | 1426567 a at | Duplicate Gene Syn | PQLC1 | containing 1 G protein-coupled | unknown | other | | 7.29E-05 | 0.37 | 4.29E-01 | 0.96 | 4.68E-01 | 0.97 | 5.70E-02 | 0.89 | 6.53E-01 | 0.98 |
| Disple Open Open Open <t< td=""><td>1439256 x at</td><td></td><td>Gpr137b-ps</td><td>pseudogene</td><td>unknown</td><td>other</td><td></td><td>3.66E-05</td><td>0.36</td><td>2.17E-01</td><td>1.05</td><td>1.46E-01</td><td>1.07</td><td>2.16E-02</td><td>0.87</td><td>3.43E-01</td><td>1.05</td></t<> | 1439256 x at | | Gpr137b-ps | pseudogene | unknown | other | | 3.66E-05 | 0.36 | 2.17E-01 | 1.05 | 1.46E-01 | 1.07 | 2.16E-02 | 0.87 | 3.43E-01 | 1.05 |
| DispleyNote <t< td=""><td>1450966_at</td><td></td><td>CROT</td><td>octanoyltransferase</td><td>Cytoplasm</td><td>enzyme</td><td></td><td>3.13E-05</td><td>0.36</td><td>1.19E-01</td><td>0.92</td><td>3.57E-01</td><td>0.95</td><td>3.03E-02</td><td>0.82</td><td>7.96E-01</td><td>0.98</td></t<> | 1450966_at | | CROT | octanoyltransferase | Cytoplasm | enzyme | | 3.13E-05 | 0.36 | 1.19E-01 | 0.92 | 3.57E-01 | 0.95 | 3.03E-02 | 0.82 | 7.96E-01 | 0.98 |
| NUMBA Indepair <thindepair< th=""> Indepair <t< td=""><td>1428669_at</td><td></td><td>Bmyc</td><td>oncogene</td><td>Nucleus</td><td>other</td><td></td><td>5.36E-06</td><td>0.36</td><td>5.76E-01</td><td>0.98</td><td>3.69E-01</td><td>0.96</td><td>1.83E-02</td><td>0.89</td><td>2.83E-01</td><td>0.96</td></t<></thindepair<> | 1428669_at | | Bmyc | oncogene | Nucleus | other | | 5.36E-06 | 0.36 | 5.76E-01 | 0.98 | 3.69E-01 | 0.96 | 1.83E-02 | 0.89 | 2.83E-01 | 0.96 |
| Diable in the state interval in the state interval in the state interval in the state interval i | 1415824 at | Duplicate Gene Sys | Scd2 | desaturase 2 | Cytoplasm | enzyme | | 9.48E-07 | 0.36 | 6.98E-01 | 1.04 | 7.26E-01 | 1.03 | 1.32E-01 | 0.87 | 2.07E-01 | 0.90 |
| | | | | family, 4 | | enzyme | | | 0.00 | | | | | | | | 1.00 |
| | | Duplicate Gene Su | | | | other | | | | | | | | | | | 0.97 |
| 10176 ar Deckang form ind MOM deckang for ind MOM deckang for ind MOM index of inde | 1430307 S at | Duplicate Gene Syn | ADCIT | calcium/calmodulin- | Plasma Memorane | enzyme | | | 0.36 | | 1.05 | | 0.35 | | 0.87 | | 1.00 |
| Lintba (Lintba (Diration (< | 1452050 at 1455796 x at | Duplicate Gene Syn Duplicate Gene Syn | CAMK1D OLFM1 | ID olfactomedin 1 | | kinase other | | 1.47E-05 9.55E-05 | 0.36 | 6.48E-01 8.05E-01 | 1.01 0.98 | 8.67E-01 3.37E-01 | 1.00 | 1.49E-01 2.03E-01 | 0.91 0.85 | 2.22E-01 3.69E-01 | 1.02 0.94 |
| Normal with any with with with with a second with | 1423704 at 1425784 a at | Duplicate Gene Svi | PLA2G15 OLFM1 | XV | | | | 1.13E-05 1.03E-05 | 0.36 | 9.68E-01 1.59E-01 | 1.00 | 6.10E-01 2.68E-01 | 0.98 | 6.93E-02 | 0.84 | | 0.99 |
| hands and </td <td></td> <td></td> <td></td> <td>microtubule-associated protein, RP/EB family,</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> | | | | microtubule-associated protein, RP/EB family, | | | | | | | | | | | | | |
| Norm Alteriarie Alteriari Alteriari | | | | interferon regulatory | | | | | | | | | | | | | 0.95 |
| Sign at a plane with the second processing with the second proces with the second processing with the seco | 1448452 at | Duplicate Gene Syl | IRF8 | | Nucleus | regulator | | 4.12E-05 | 0.35 | 3.76E-01 | 0.96 | 1.806-01 | 0.93 | 2.85E-02 | 0.85 | 4.92E-02 | 0.87 |
| LixXX and LixXXX and LixXXXX and LixXXX and LixXXX and LixXXX and LixXXX and LixXXX and LixXXX and LixXXX and LixXXX and LixXXX and | 1450070 s at | Duplicate Gene Sys | PAK1 | carcinoembryonic antigen | Cytoplasm | kinase | | 3.75E-05 | 0.35 | 7.04E-01 | 1.01 | 4.40E-01 | 0.97 | 2.99E-02 | 0.94 | 3.53E-01 | 1.02 |
| Libbit Note Add | 1425538 x at | Duplicate Gene Sys | Ceacam1/Ceacam | molecule 1 | Plasma Membrane | other | | 4.89E-04 | 0.35 | 9.78E-01 | 1.00 | 2.19E-01 | 0.90 | 2.48E-02 | 0.83 | 7.98E-02 | 0.87 |
| Linits at Med Mediation Markation Markation Jate of US | 1416926 at | | TP53INP1 | inducible nuclear protein 1 | Nucleus | other | | 4.76E-05 | 0.35 | 6.48E-01 | 0.98 | 6.90E-01 | 1.02 | 1.02E-01 | 0.92 | 4.04E-01 | 1.05 |
| Statts Instrume Manual programs Autor <td></td> <td></td> <td></td> <td>hematopoietically expressed homeobox</td> <td></td> <td>transcription</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>0.99</td> | | | | hematopoietically expressed homeobox | | transcription | | | | | | | | | | | 0.99 |
| Libble sta Charge Lippingende Al jundi Ausles | | | | | | | | | | | | | | | | | |
| 12033 al. 25056 3 a | 1451075 s at | | CTDSP2 | II, polypeptide A) small | Nucleus | phosphatase | | 4.93E-07 | 0.35 | 1.91E-01 | 0.97 | 4.43E-01 | 0.97 | 1.55E-03 | 0.87 | 4.35E-02 | 0.95 |
| Light best der Ser Survey Auffer Gener Ser Survey State Ser Survey S | 1425215_at | Duplicate Gene Sys | | | | G-protein coupled | | 1.10E-03 | 0.35 | 4.09E-01 | 0.96 | 3.92E-02 | 0.95 | 3.82E-01 | 0.97 | 5.18E-03 | 0.85 |
| Libble and buildent emerge CAUDIO D Conduct memory </td <td>1455065 x at</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>2.17E-05</td> <td>0.35</td> <td>6.32E-01</td> <td>0.98</td> <td>8.23E-01</td> <td>0.98</td> <td>1.13E-01</td> <td>0.82</td> <td>8.44E-01</td> <td>0.98</td> | 1455065 x at | | | | | | | 2.17E-05 | 0.35 | 6.32E-01 | 0.98 | 8.23E-01 | 0.98 | 1.13E-01 | 0.82 | 8.44E-01 | 0.98 |
| 150055 at LLCM Index.de Finance mediance Particle constraints Parti | 1426389 at 1448960 at | Duplicate Gene Sys Duplicate Gene Sys | CAMK1D CXXC5 | ID CXXC finger protein 5 | | | | 8.81E-05 8.82E-05 | 0.35 | 1.68E-01 6.35E-01 | 0.94 | 1.67E-01 7.86E-01 | 0.94 | 1.81E-01 3.95E-01 | 0.90 | 9.36E-01 6.87E-01 | 1.00 |
| 150967 at PFLAD2 protein register autonom othor 1 446 05 0.34 7.06 cl 1.02 8.66 cl 1.01 1.86 cl 0.87 0.87 125087 at BANC03 monain containing 2 untooun othor 1.446 05 0.34 7.06 cl 1.02 8.66 cl 1.01 1.86 cl 0.87 0.87 124153 at BANC03 Marcia Containing 2 untooun other 2.916 cl 0.34 7.04 cl 0.88 8.13 cl 0.09 1.66 cl 0.84 2.264 cl 12555 t a .0 SA Cl Marcia Dalation other 8.265 cl 0.34 7.216 cl 0.99 1.66 cl 0.84 2.264 cl 120838 at Deglotet Gen SG SA Sci las - dalation periodica Marcia Dalation periodica Marcia Dalation periodica Dalation periodica Dalation periodica Dalation periodica Dalation periodica Dalation periodica Dalation periodica Dalation periodica Dalation periodica Dalation periodica Dalation periodica Dalation periodica Dalation periodica Dalation | | | L1CAM | L1 cell adhesion | | | | 2.56E-04 | 0.34 | | 1.01 | | 0.95 | | 0.97 | | 1.03 |
| 15057 at PTRAD2 PTRAD2 Propulsate-site A denote containing 2 matrix metal-solution is nuclear discussion is matrix discussi matrix dis matrix discussion is matrix discussion is matrix dis | 1450065_at | Duplicate Gene Sys | ADCY7 | protein tyrosine | Plasma Membrane | enzyme | <u> </u> | 2.87E-06 | 0.34 | 5.47E-01 | 1.02 | 6.39E-01 | 1.02 | 1.86E-01 | 0.97 | 9.23E-02 | 1.10 |
| 124183 at 84003 moder distants univer distants <thuniver distants<="" th=""></thuniver> | 1450967_at | | PTPLAD2 | phosphatase-like A | unknown | other | | 1.44E-05 | 0.34 | 7.09E-01 | 1.02 | 8.69E-01 | 1.01 | 1.88E-02 | 0.87 | 8.53E-01 | 0.99 |
| | | | | | | | | | | _ | | | | | | | |
| 145556 a.r 0.84C1 mayme h Corport 0 endiate | | | | homolog B (S. cerevisiae) | unknown | other | | | | | | | | | | | 0.95 |
| LitBld J, at C07 C07 molecule Plana Membere enception 2.346.05 6.34 5.416.01 0.97 4.166.01 0.95 1.216.02 0.79 3.800.01 133353 1.1 Deploted eme Sr 69.179 Sprote-roughed Plana Membere enception 1776.04 0.84 1.266.01 0.95 1.216.01 0.96 1.816.01 0.90 7.816.02 1202357 1.1 Deploted eme Sr 64.01 0.81 1.766.04 0.84 1.766.01 1.08 1.516.01 1.08 1.816.01 0.90 7.816.02 1202357 1.1 Deploted eme Sr 64.01 0.08 1.767.01 1.08 1.68 0.84 0.91 1.056.01 0.90 7.816.02 1202357 1.1 Deploted eme Sr 64.01 1.09 2.066.01 1.09 2.066.01 1.01 0.046.02 0.91 1.056.01 1.01 1.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 | | | | enzyme 1 | | | | | | | | | | | | | 0.93 |
| Hass Budicate Gene Set M311 G protein couplet Hana Memberse ether 1.711.64 0.04 1.246.7 1.08 1.511.01 1.08 1.811.01 0.80 7.811.01 142325 1 at Deplicate Gene Set AGD #down 1 (general) Cenglum other 8.246.01 0.83 1.511.01 1.08 1.881.01 0.80 7.811.01 142327 at Deplicate Gene Set AGD #down 1 (general) Cengentum other 8.246.01 0.83 1.511.01 1.08 1.881.01 0.80 7.811.01 148350 at Spectore Set AGD1 #down 1 (general) Cengentum cengentum | | Supricate Gene Syr | | | Plasma Membrane | G-protein coupled | | | | | | | | | | | 0.96 |
| Lid2297 at Diglicate Gene Set ADO adducts 1 (gamma) Complaint other 8.346 (7) 0.33 1.747 (3) 1.04 8.646 (1) 1.01 4.011 (2) 0.91 1.066 (1) 145326 at Mem Math Table Autor 0.91 1.066 (1) 0.91 1.066 (1) 0.91 1.066 (1) 0.91 1.061 (1) 0.91 (1) | 1439255 s at | | GPR137B | G protein-coupled receptor 1378 | | other | | 1.71E-04 | 0.34 | 3.26E-01 | 1.08 | 1.51E-01 | 1.08 | 1.83E-01 | 0.90 | 7.81E-02 | 1.11 |
| Interview B (perception) B (perceptio | 1423297 at | | | | Cytoplasm | other | <u> </u> | 8.34E-07 | 0.33 | 1.47E-01 | 1.04 | 8.64E-01 | 1.01 | 4.04E-02 | 0.91 | 1.06E-01 | 1.03 |
| LifeOID at Depicted energie HSTUIC Nutore cluter 1, 11c, Nutore 1, 11c, Nutore 1, 11c, Nutore 1, 11c, Nutore 1, 11c, Nutore 1, 11c, Nutore 1, 11c, Nutore 1, 11c, Nutore 1, 11c, Nutore 1, 11c, Nutore 1, 11c, Nutore 1, 11c, Nutore 1, 11c, Nutore 1, 11c, Nutore 1, 11c, Nutore 1, 11c, Nutore 1, 11c, Nutore 1, 11c, </td <td>1449366 at</td> <td></td> <td>MMP8</td> <td>8 (neutrophil</td> <td>Extracellular Snare</td> <td>peptidase</td> <td>marimastat</td> <td>6.32E-05</td> <td>0.33</td> <td>6.93E-01</td> <td>1.02</td> <td>7.69E-01</td> <td>1.03</td> <td>4.11E-01</td> <td>0.95</td> <td>3.72E-02</td> <td>1.08</td> | 1449366 at | | MMP8 | 8 (neutrophil | Extracellular Snare | peptidase | marimastat | 6.32E-05 | 0.33 | 6.93E-01 | 1.02 | 7.69E-01 | 1.03 | 4.11E-01 | 0.95 | 3.72E-02 | 1.08 |
| Jability at 142306 at 142326 at Life Mode for transcription (mode for transcription) Image for transcription (mode for transcription) Image for transcription (mode for transcription) Image for transcription Image for transcrit and transcription Image for transcrip | 1416101 a at | Duplicate Gene Sys | HIST1H1C | histone cluster 1, H1c | Nucleus | other | insidt | 5.06E-05 | 0.33 | 5.05E-03 | 0.85 | 3.94E-03 | 0.81 | 6.29E-03 | 0.86 | 5.50E-04 | 0.80 |
| 1523-06 LEA Internation 6 meansplan 6 meansplan Plana Membrane percention 0.08L 05 0.33 9.17-01 1.01 8.70K 01 1.01 5.51K 01 0.695 5.57K 01 122370 at Deploted ceres by RAM1 MATTRANTIC (DMM) Plana Membrane percention 5.77K 01 0.33 9.17K 01 1.01 2.26K 01 0.94 1.05K 04 0.90 7.77K 01 122370 at Deploted ceres by RAM1 MATTRANTIC (DMM) Plana Membrane percention 5.17K 05 0.33 7.07K 01 0.94 1.05K 04 0.90 7.77K 01 1218902 at Deploted ceres by RAM1 MATTRANTIC (DMM) manufer (DMM) 9.77K 05 0.32 4.65K 01 0.99 6.25K 01 0.94 1.02 2.96K 01 0.96K 7 7.77K 01 111982 at Deploted ceres by RAM1 MATTRANTIC (DMM) manufer (DTMM) 9.77K 05 0.32 5.55K 01 0.99 6.25K 01 1.01 6.25K 01 0.88 1.95K 01 111982 at CMATPHANCES Deploted ceres by RAM1 MATTRANTINE (DEPLONE) 0.97K 05 0.32 | | Duplicate Com C | | | | transcription | | | | | | | | | | | 0.98 |
| NAT activating portion 1316980 at 1316988 at 1316983 at 1316983 at 1316983 at 1316983 at 1316983 at NAT activating portion with months in Hyperbarce Parameters in Hyperbarce Paramet | | - opincate Gene Syr | | interleukin 6 receptor | | transmembrane | tocilizumab | | | | | | | | | | 0.97 |
| Liste88 at Duplicate Gene Spd CCN2 Cyclin C2 Nucleus other 6.376 05 0.32 8.456 01 0.99 6.226 01 1.02 2.985 01 0.955 7.556 01 List882 at CEPA protein (CFR) abox Imanoxidate, alpha, imanoxidate, imanoxidate, imanoxidate, alpha, imanoxidate, imanoxidate, alp | 1428790 at | Duplicate Gene Sys | NFAM1 | NFAT activating protein with ITAM motif 1 | Plasma Membrane | transmembrane receptor | | 5.17E-05 | 0.33 | 7.09E-01 | 1.01 | 2.36E-01 | 0.94 | 1.05E-04 | 0.90 | 7.70E-03 | 0.94 |
| 1413882_at CEBPA grotein (CEBP, John Nucles regulator 9,726-05 0.32 5566-01 1.03 8.836-01 1.01 6.026-03 0.83 1.956-01 manoxidase jalba, manoxidase jalba, de service s | 1416488 at | Duplicate Gene Sys | CCNG2 | cyclin G2 | Nucleus | | | 6.37E-06 | 0.32 | 8.45E-01 | 0.99 | 6.23E-01 | 1.02 | 2.58E-01 | 0.95 | 7.65E-01 | 1.01 |
| 1436781 at MAN281 class 28, member 1 Cytoplasm engme 4.14E-05 0.32 7.51E-01 1.02 7.76E-01 0.98 2.53E-01 0.90 4.31E-01 | | | | protein (C/EBP), alpha mannosidase, alpha, | | regulator | | | | | | | | | | | 0.95 |
| | | i . | MAN2B1 | | Cotoniasm | | 1 | 1 1 1 1 1 1 1 | 0.00 | | | 3 345 04 | | | 0.00 | 1.015.01 | 1.05 |
| Usibility as Displate/energy Conductor Subscience Subscinter Subscinter S | 1416701 at | | RND3 | Rho family GTPase 3 | Cytoplasm | enzyme | | 2.60E-03 | 0.32 | 6.25E-01 | 0.92 | 7.00E-01 | 0.91 | 6.32E-01 | 0.92 | 2.60E-01 | 0.80 |

| | | | | | | | Stimulat | | | | und Only | | | | ind Compound | |
|----------------------------------|--------------------|-------------------|---|--------------------------------|--|---|----------------------|----------------|-------------------------|-----------------------|----------------------|----------------------|----------------------|-----------|--------------------------|--------------------|
| 1456195 x at | Duplicate Gene Svr | ITGBS | Probe Set Description | Plasma Membrane | | EMD121974 | CpG vs. 5.75E-05 | Medium 0.31 | 0.25 uM E64 3.94E-01 | 46 vs. Medium 0.98 | 1.25 uM E644 | 6 vs. Medium 0.95 | CpG + 0.25 | 0.82 | CpG + 1.25 u 8.74E-01 | M E6446 vs. Medium |
| 1456195 x at 1417218 at | Duplicate Gene Syr | CALHM2 | calcium homeostasis modulator 2 | Plasma Membrane | other | EMD121974 | 5.75E-05 7.89E-07 | 0.31 | 3.94E-01 6.11E-01 | 1.01 | 1.02E-01 2.32E-01 | 0.95 | 1.06E-03 | 0.82 | 8.74E-01 1.90E-01 | 0.97 |
| | Duplicate Gene Syr | | adducin 3 (gamma) Fc fragment of IgG, | Cytoplasm | other | | 9.24E-06 | 0.31 | 7.31E-01 | 1.02 | 3.09E-01 | 0.94 | 9.15E-03 | 0.82 | 1.24E-01 | 0.91 |
| 1416978 at | | FCGRT | receptor, transporter, alpha | Plasma Membrane | transmembrane receptor G-protein coupled | | 2.29E-05 | 0.31 | 2.41E-01 | 0.93 | 1.26E-01 | 0.91 | 6.44E-02 | 0.87 | 4.30E-02 | 0.85 |
| 1425216_at | Duplicate Gene Syr | FFAR2 | free fatty acid receptor 2 | Plasma Membrane | receptor transmembrane | | 5.30E-06 | 0.31 | 2.04E-02 | 0.92 | 8.51E-03 | 0.95 | 1.17E-04 | 0.95 | 9.56E-04 | 0.89 |
| 1422645 at | | HFE | hemochromatosis Fc fragment of IgG, low | Plasma Membrane | receptor | | 1.48E-05 | 0.31 | 4.84E-01 | 0.96 | 6.80E-02 | 0.91 | 6.38E-03 | 0.83 | 2.57E-01 | 0.95 |
| 1448620 at | | FCGR2A | affinity IIa, receptor (CD32) | Plasma Membrane | transmembrane receptor | | 2.14E-05 | 0.31 | 5.04E-02 | 1.12 | 8.31E-02 | 1.08 | 1.05E-02 | 0.83 | 4.15E-01 | 1.04 |
| 1417391 a at | | IL16 | interleukin 16 ADP-ribosylation factor- | Extracellular Space | cytokine | | 4.18E-05 | 0.30 | 6.78E-02 | 0.95 | 1.21E-01 | 0.95 | 3.79E-02 | 0.94 | 6.39E-02 | 0.95 |
| 1436512_at 1436994 a at | Duplicate Gene Syr | ARL4C HIST1H1C | like 4C histone cluster 1, H1c | Nucleus Nucleus | enzyme other | | 5.33E-05 2.43E-05 | 0.30 | 3.53E-01 7.57E-02 | 1.05 | 7.69E-01 7.05E-03 | 0.98 | 5.97E-03 3.62E-02 | 0.85 | 3.71E-02 3.57E-02 | 0.91 0.85 |
| | | | | | | epothilone 8, isabepilone, colchicine/pro benecid, XXP9881, ABT. 751, eribulin, MST-997, AJ. MST-997, | | | | | | | | | |
| 1427347_s_at AFFX-18SRNAMur/X | , | TUBB2A Rn18s | | Cytoplasm unknown | other | n, colchicine | 2.87E-07 3.47E-02 | 0.30 | 5.45E-02 6.55E-01 | 0.96 | 8.63E-02 8.15E-01 | 0.95 | 9.25E-03 3.53E-01 | 0.73 0.47 | 1.37E-02 2.34E-02 | 0.90 |
| 1416700 at | Duplicate Gene Syr | | Rho family GTPase 3 | Cytoplasm | enzyme | | 7.14E-05 | 0.29 | 4.42E-01 | 0.93 | 5.75E-01 | 0.94 | 1.46E-01 | 0.86 | 6.84E-02 | 0.85 |
| 1420819 at 1419247 at | Duplicate Gene Syr | SLA RGS2 | Src-like-adaptor regulator of G-protein signaling 2, 24kDa | Plasma Membrane | other | | 2.93E-05 2.55E-05 | 0.29 | 2.97E-01 9.28E-01 | 1.05 | 8.36E-01 2.95E-01 | 0.99 | 6.42E-02 | 0.91 | 5.24E-01 | 0.93 |
| 1419247_at 1426624 a at | Gapincate Gene Syr | YPEL3 | yippee-like 3 (Drosophila) | unknown | other | | 2.55E-05 5.92E-05 | 0.29 | 9.28E-01 5.41E-01 | 0.96 | 2.95E-01 5.67E-01 | 0.94 | 1.40E-02 2.04E-02 | 0.82 | 1.34E-01 1.77E-01 | 0.93 |
| 1434034 at | | CERK | ceramide kinase | Plasma Membrane | kinase | | 7.85E-06 | 0.28 | 5.50E-01 | 0.97 | 8.01E-01 | 0.99 | 2.67E-04 | 0.82 | 4.03E-02 | 0.95 |
| 1419248_at | Duplicate Gene Syr | RGS2 | regulator of G-protein signaling 2, 24kDa | Nucleus | other | | 7.30E-06 | 0.28 | 5.02E-01 | 1.01 | 2.42E-01 | 0.96 | 2.27E-02 | 0.85 | 5.25E-01 | 0.98 |
| 1425714 a at | Duplicate Gene Syr | NFAM1 | NFAT activating protein with ITAM motif 1 MAX dimerization protein | Plasma Membrane | transmembrane receptor transcription | | 1.69E-05 | 0.28 | 3.78E-01 | 1.06 | 8.70E-01 | 1.01 | 7.79E-01 | 0.97 | 5.28E-01 | 1.04 |
| 1434378 a at | | MKD4 | 4 pleckstrin homology | Nucleus | regulator | | 6.86E-05 | 0.27 | 9.96E-01 | 1.00 | 4.66E-01 | 1.05 | 1.97E-02 | 0.84 | 6.13E-01 | 0.97 |
| 1417128 at | | PLEKHO1 | domain containing, family O member 1 | Plasma Membrane | other | | 3.82E-06 | 0.27 | 3.63E-01 | 0.96 | 5.36E-01 | 1.02 | 9.04E-01 | 0.99 | 1.21E-01 | 1.08 |
| 1448710_at | | CXCR4 | chemokine (C-X-C motif) receptor 4 | Plasma Membrane | G-protein coupled receptor | plerixafor | 3.53E-06 | 0.27 | 4.95E-01 | 1.03 | 6.99E-01 | 0.98 | 2.87E-02 | 0.86 | 6.43E-02 | 1.02 |
| 1418553 at | | ARHGEF18 | Rho/Rac guanine nucleotide exchange factor (GEF) 18 | Cytoplasm | other | | 1.29E-06 | 0.27 | 2.40E-01 | 1.04 | 4.62E-01 | 1.06 | 3.93E-01 | 0.97 | 1.59E-01 | 1.06 |
| 1430125 s at | Duplicate Gene Syr | | PQ loop repeat containing 1 | unknown | other | | 7.51E-06 | 0.26 | 9.30E-01 | 1.00 | 8.79E-01 | 0.99 | 2.07E-02 | 0.84 | 3.23E-01 | 0.95 |
| | | | transforming growth factor, beta-induced, | | | | | | | | | | | | | |
| 1437463 x at | Duplicate Gene Syr | | 68kDa protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting | Extracellular Space | | | 3.53E-05 | 0.26 | 5.40E-01 | 1.03 | 9.38E-01 | 1.00 | 3.23E-02 | 0.86 | 1.15E-01 | 0.92 |
| 1428578 s at 1437626 at | | Ppfia4 ZFP36L2 | protein (liprin), alpha 4 ZFP36 ring finger protein- like 2 | Notleur | other transcription regulator | | 5.05E-08 | 0.26 | 1.43E-02 3.95E-01 | 0.94 | 7.89E-03 2.60E-01 | 0.94 | 7.31E-03 | 0.86 | 1.77E-02 5.62E-02 | 0.92 |
| | | | transforming growth factor, beta-induced, | | | | | | | | | | | | | |
| 1415871 at | Duplicate Gene Syr | TGFBI | 68kDa transforming growth | Extracellular Space | other | | 8.39E-06 | 0.26 | 6.94E-01 | 0.99 | 1.73E-01 | 0.98 | 3.09E-03 | 0.84 | 5.08E-04 | 0.90 |
| 1448123 s at | Duplicate Gene Syr | TGFBI | factor, beta-induced, 68kDa transforming growth | Extracellular Space | other | | 3.68E-06 | 0.25 | 8.06E-01 | 0.99 | 4.71E-01 | 0.96 | 1.16E-02 | 0.84 | 1.75E-01 | 0.94 |
| 1456250 x at | Duplicate Gene Syr | TGFBI | factor, beta-induced, 68kDa | Extracellular Space | other | | 1.73E-05 | 0.25 | 8.05E-01 | 1.01 | 8.52E-01 | 0.99 | 6.67E-02 | 0.84 | 6.14E-01 | 0.97 |
| 1451344_at | | TMEM119 | transmembrane protein 119 | Cytoplasm | other | | 2.11E-05 | 0.24 | 5.74E-01 | 0.98 | 7.92E-01 | 0.99 | 8.12E-03 | 0.89 | 2.38E-01 | 0.97 |
| 1425275 | | 54543054 | family with sequence | | athar | | 1.95E-08 | 0.24 | 4.29E-01 | 1.04 | 1.13E-01 | 1.02 | 1.77E-01 | 0.96 | 6.06E-01 | 0.00 |
| 1435375_at 1420895 at | | FAM105A TGFBR1 | similarity 105, member A transforming growth factor, beta receptor 1 | Plasma Membrane | other kinase | | 1.95E-08 2.66E-05 | 0.24 | 4.29E-01 3.15E-01 | 0.96 | 1.13E-01 1.46E-01 | 1.03 | 1.77E-01 1.08E-01 | 0.96 | 6.06E-01 4.48E-01 | 0.99 |
| 1454858 x at | Duplicate Gene Syr | METTL7A | methyltransferase like 7A | unknown | other | | 1.27E-04 | 0.23 | 5.76E-01 | 1.07 | 3.31E-01 | 1.12 | 7.55E-01 | 0.97 | 4.03E-01 | 1.10 |
| 1451486_at | | SLC46A3 | solute carrier family 46, member 3 cytochrome P450, family | Extracellular Space | other | | 2.26E-04 | 0.23 | 4.50E-01 | 0.98 | 2.07E-01 | 0.94 | 8.35E-01 | 1.01 | 6.11E-02 | 0.95 |
| 1417590_at | | CYP27A1 | 27, subfamily A, polypeptide 1 | Cytoplasm | enzyme | | 1.51E-03 | 0.23 | 2.88E-01 | 0.96 | 4.96E-01 | 1.06 | 1.95E-02 | 0.82 | 5.37E-02 | 1.11 |
| 1419768 at | | C022 | CD22 molecule | Plasma Membrane | transmembrane | epratuzumab, BL22 immunotoxin, inotuzumab ozogamicin, combotox, RFB4-dgRTA | 5.67E-04 | 0.23 | 3.43E-01 | 0.96 | 2.238-01 | 0.94 | 5.00E-02 | 0.91 | 7.235-01 | 0.98 |
| | | | acyl-CoA synthetase short-chain family | | | | | | | | | | | 0.86 | | 1.07 |
| 1416617 at 1425281_a_at | | ACSS1 TSC22D3 | member 1 TSC22 domain family, member 3 | Cytoplasm Nucleus | enzyme transcription regulator | | 5.88E-05 3.61E-04 | 0.22 | 4.79E-01 4.86E-01 | 0.96 | 1.75E-01 7.41E-01 | 0.91 | 4.05E-02 7.55E-02 | 0.86 | 3.12E-01 2.75E-01 | 0.87 |
| 1423281_a_at 1428306 at | | DDIT4 | DNA-damage-inducible transcript 4 | Cytoplasm | other | | 1.71E-06 | 0.21 | 4.35E-01 8.15E-01 | 0.99 | 6.89E-01 | 1.02 | 2.92E-02 | 0.82 | 4.23E-01 | 1.05 |
| 1424975 at | | Siglec5 | sialic acid binding Ig-like lectin 5 chromosoma 10 onen | Plasma Membrane | other | | 2.71E-05 | 0.20 | 7.87E-01 | 1.02 | 3.31E-01 | 0.95 | 8.69E-01 | 0.99 | 1.72E-01 | 1.08 |
| 1416619_at | Duplicate Gene Syr | C10orf54 | chromosome 10 open reading frame 54 chemokine (C-C motif) | unknown | other G-protein coupled | | 2.44E-07 | 0.20 | 2.73E-01 | 0.93 | 6.06E-01 | 0.96 | 1.15E-02 | 0.81 | 4.94E-01 | 0.97 |
| 1450357 a at | | CCR6 | receptor 6 leukemia inhibitory factor | Plasma Membrane | receptor transmembrane | | 1.26E-04 | 0.19 | 2.62E-01 | 0.97 | 9.16E-01 | 1.00 | 8.85E-01 | 0.99 | 9.09E-01 | 1.00 |
| 1454984 at | 1 | LIFR | receptor alpha | Plasma Membrane | receptor G-protein coupled | | 1.48E-05 | 0.19 | 2.90E-01 | 1.05 | 4.23E-01 | 0.97 | 5.62E-02 | 0.80 | 4.08E-01 | 1.10 |
| 1425214 at | l | P2RY6 | pyrimidinergic receptor P2Y, G-protein coupled, 6 | Plasma Membrane | G-protein coupled receptor | | 4.65E-04 | 0.19 | 9.20E-01 | 1.00 | 5.43E-01 | 0.97 | 6.92E-01 | 0.98 | 6.64E-01 | 1.03 |
| 1434151_at | Duplicate Gene Syr | | methyltransferase like 7A methyltransferase like | unknown | other | | 2.91E-05 | 0.19 | 7.41E-01 | 0.99 | 1.59E-01 | 1.05 | 1.72E-02 | 0.84 | 3.61E-01 | 0.96 |
| 1434150 a at | | Metti7a2/Metti7a | 3 7A3 transmembrane protein | unknown | other | | 6.46E-05 | 0.18 | 9.45E-01 | 0.99 | 9.27E-01 | 1.01 | 1.76E-01 | 0.85 | 7.18E-01 | 1.04 |
| 1424383 at 1453474_at | | TMEM51 ABHD15 | 51 abhydrolase domain containing 15 | unknown Extracellular Space | other | | 6.44E-07 6.30E-05 | 0.18 | 8.56E-01 9.31E-01 | 0.99 | 1.07E-01 3.62E-01 | 1.02 | 1.01E-02 3.10E-03 | 0.83 | 2.38E-02 3.74E-01 | 0.96 |
| 1417395 at | Duplicate Gene Syr | KLF4 | Kruppel-like factor 4 (gut) | | transcription regulator | | 9.59E-05 | 0.13 | 6.67E-01 | 0.97 | 1.10E-01 | 0.92 | 3.90E-03 | 0.78 | 1.42E-01 | 0.87 |
| 1448747 at 1417394 at | | FBXO32 | F-box protein 32 | Cytoplasm | enzyme transcription | | 3.39E-05 | 0.16 | 4.47E-01 | 0.95 | 5.82E-01 | 0.96 | 1.12E-02 | 0.68 | 1.76E-02 | 0.73 |
| 141/394 at | Duplicate Gene Syr | NL14 | Kruppel-like factor 4 (gut) | INUCIOUS | regulator | 1 | 6.11E-06 | 0.06 | 5.21E-01 | 0.95 | 1.94E-01 | 0.91 | 6.81E-02 | 0.79 | 9.20E-01 | U.99 |