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# GENE EXPRESSION PROFILING REVEALS NOVEL ACTIONS OF GLUCOCORTICOIDS ON IMMUNE CELLS DURING INFLAMMATION

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# 1. SUMMARY

The innate immune response is triggered by bacterial activators such as lipopolysaccharide (LPS) which, upon binding to CD14 and TLR4 receptors on responsive cells, is able to activate numerous cell signalling events. This leads to cytokine and chemokine secretion, complement activation, eicosanoides synthesis, production of reactive oxygen intermediates, nitric oxide and other mediators, which co-ordinate the body's response to inflammation. In addition to the beneficial effects of such a response to LPS, this activation also accounts for the pathophysiologic state usually observed in septic shock. To suppress the ongoing inflammation, several glucocorticoid-based drugs have been used. Their efficacy as immunosuppressive and anti-inflammatory agents is based upon their ability to activate the glucocorticoid receptor (GR) which in turns predominantly mediates transrepression of target genes.

A combination of array-based technologies and subtractive suppressive hybridisation has allowed for the identification of genes that are altered upon activation of peritoneal macrophages by LPS, and those whose expression is further modulated upon administration of glucocorticoids (GC). In total, more than 350 genes/ESTs were identified as being induced or repressed by LPS, whereas 106 (30%) of them responded to GC treatment. The molecular mechanisms of GC action on the expression of LPS induced or repressed genes have been deciphered using peritoneal macrophages (PMΦ) obtained from $GR^{dim}$ and $GR^{LysCre}$ mutant mice. $GR^{dim}$ mice carry a dimerisation-defective GR in which the receptor is no longer able to dimerise and bind to its response elements in the promoter region of target genes. In contrast, GR interactions with other

transcription factors such as AP-1 and NF-κB, which are independent of binding to DNA, are preserved. Only a small subset of all GC-regulated genes in peritoneal macrophages (12 out of 106) were identified as also being modulated by GCs in $GR^{dim}$ cells. On the other hand, the expression of 94 (89%) of GC-responsive genes/ESTs was not modulated in peritoneal macrophages from $GR^{dim}$ mice. Cell-specific $GR^{LysCre}$ mutant mice lack the GR in cells of the myeloid lineage. Survival of $GR^{LysCre}$ mutants upon LPS injection has been shown to be severely impaired compared to wild type mice. Gene expression profiling of PMΦ from $GR^{LysCre}$ mice confirmed the GR-specificity of GC action, since induction or repression of target genes by GCs was abolished in these cells.

The combination of state of the art expression profiling approaches with the use of function-selective and tissue-specific GR mouse mutants led to the conclusion that activation of macrophages by LPS evokes rapid transcription of various pro- and anti-inflammatory mediators. Furthermore, this analysis highlights the importance of both DNA-binding dependent and independent actions of the GR in modulating cell responses to inflammatory stimuli. Finally, identifying the spectrum of genes whose expression is influenced by GCs will allow development of selective GC-based drugs able to discriminate between two mechanisms of GR actions, thus contributing to better anti-inflammatory therapies.

# 2. INTRODUCTION

## 2. 1. PRIMING THE INNATE IMMUNE REPONSE

The immune system of higher vertebrates consists of two components: innate and adaptive [1]. The immediate, innate response is mediated largely by macrophages and granulocytes (e.g. neutrophils), cells that phagocyte the pathogens and concurrently co-ordinate additional host responses by synthesising a wide range of inflammatory mediators [2]. Once internalised by macrophages, the infectious agent is degraded within the maturing phagosome and the components of the pathogen are presented to T cells. This results in activation of the adaptive immune response and establishment of protective immunity [2]. While all multicellular organisms have some form of innate host defence system, adaptive immunity occurs only in vertebrates [3].

A major challenge to the innate immune system is to detect and discriminate between a large number of potential pathogens. This task has been achieved by the evolution of a variety of pattern-recognition receptors (PRRs) [4]. PRRs of the innate immune defence system, such as CD14, mannose binding protein, toll-like receptors (TLRs), and alternative complement system are expressed on membrane surfaces or in soluble forms. They function to detect microbial structures, which are foreign to and structurally distinct from host-defined structures [2,4]. They recognise conserved motifs on pathogens that are called pathogens-associated molecular patterns, PAMPs [4]. This important recognition system induces the expression of co-stimulatory molecules on antigen presenting cells and serves to alert the host to initiate a series of clearance mechanisms to eliminate the invading microbial agents [4]. PAMPs have essential roles in the biology of the invading agents and include mannans in the yeast cell wall, formylated peptides and various

bacterial cell-wall components such as lipopolysaccharide (LPS, endotoxin), lipopeptides, peptidoglycans, lipoteichoic acids, lipoarabinomannan (LAM) and bacterial DNA [4,5].

LPS is an essential structural component of the outer membrane of all Gram-negative bacteria [6]. Investigations into the structural components of LPS demonstrated that conserved lipid A region is necessary for LPS stimulation of macrophages [7-9]. Nevertheless, oligosaccharide components of LPS, and more specifically 2-keto-2-deoxyoctulosonic acid (KDO) determinants, may function to facilitate either the initial interaction, or some biochemical signal transductive mechanism [10,11]. Although CD14 is known to bind LPS, this PRR is anchored into the cell membrane by a glycosyl phosphatidylinositol linkage, which suggests that it would have little signalling capacity [6,12,13]. There is now clear evidence that mammalian Toll-like receptors, together with CD14 receptor, mediate the response to LPS [5,10,11,14-21]. TLRs contain a cytoplasmic portion that is homologous to the IL-1 receptor and hence can trigger intracellular signalling pathways [22-27]. These signals, in turn, activate transcription factors (mainly NF-κB and AP-1) which trigger a wide variety of cellular responses, including cytokine and chemokine production, release of reactive oxygen and nitrogen intermediates all of which are responsible for the pathophysiologic reaction (Figure 1) [24,28]. Despite the intense research on LPS, it is now clear that other microbial products also act as potent activators of innate immunity and that the immune system encounters a 'cocktail' of these molecules when interacting with pathogens *in vivo*. Overactivation of the inflammatory response by LPS and other pathogens can lead to irreversible destruction of organs and tissues (i.e. multiorgan dysfunction syndrome), and eventually death [5,29-31].

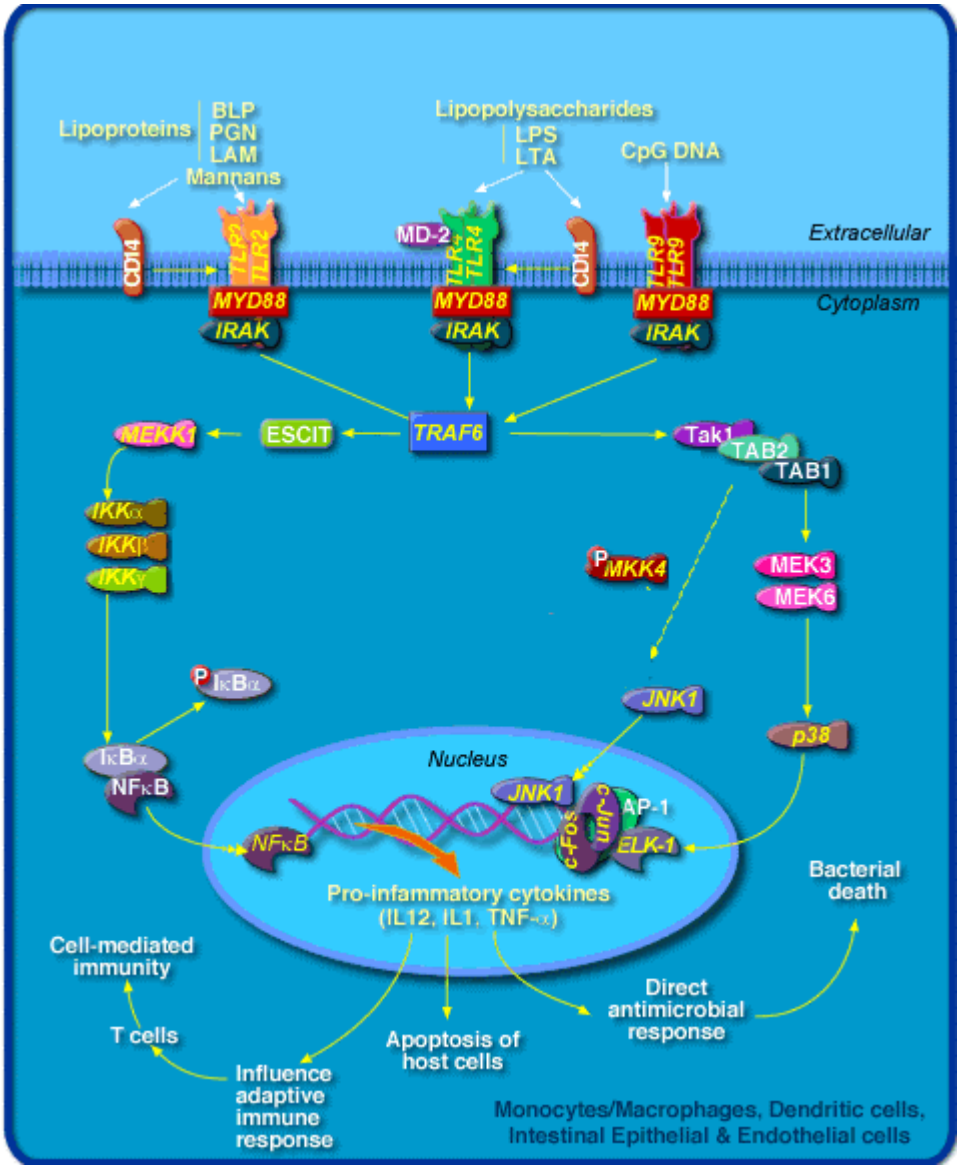



Figure 1. Signalling pathways through which LPS might activate the transcription of immune response genes

LPS is recognised by the CD14 receptor. CD14 associates with the cell surface by means of a glycolipid linkage and is not capable of generating a transmembrane signal. It is likely that the LPS alone or LPS-CD14 complex activates TLR4, which in turn signals through the adapter protein MyD88 and the serine kinase IRAK. This leads to the autophosphorylation of IRAK, which then forms a complex with TRAF6 and this, in turn, results in the activation of the MAP 3-kinase family member, and finally the I-κB kinases. Sequential phophorylation of I-κB leads to its proteolytic degradation and translocation of NF-κB to the nucleus. Concomitantly, members of the activator protein-1 (AP-1) transcription factor family (Jun and Fos) are activated, and together with NF-κB are involved in the transcription of immune response genes. Taken from *http://www.biocarta.com*

# 2. 2. ANTI-INFLAMMATORY ACTIONS OF GLUCOCORTICOIDS

The characteristics of the inflammatory response and the site of inflammation differ depending on the invading pathogenic agent, but all involve the recruitment and activation of inflammatory cells and the production of various proteins that are involved in the complex inflammatory cascades [32]. The increased expression of cytokines, chemokines, growth factors, enzymes, receptors and adhesion molecules is the result of enhanced gene transcription/translation since many of them are not expressed under normal resting conditions [32,33]. Glucocorticoids (GC) have been demonstrated to block the expression of multiple cytokines and chemokines. This inhibition has been reported to occur at the transcription level for IL-1 to IL-6, IL-11, IL-12, IL-13, TNF-$\alpha$ and M-CSF [34-38]. Most of these genes require transcription factors, such as AP-1, NF-$\kappa$B, or NF-AT, for their expression, suggesting that GCs may exert their anti-inflammatory function by interfering with the activity of some of these factors. This may explain their therapeutic efficacy in the treatments of allergic diseases (rhinitis, atopic dermatitis), asthma, rheumatoid arthritis, inflammatory bowel disease and autoimmune diseases which are marked by high expression of interleukins and other mediators [34].

### 2. 2. 1. Glucocorticoid receptor in the regulation of gene transcription

GCs exert their effects by binding to the glucocorticoid receptor (GR), which is predominantly localised in the cytoplasm of target cells [39-41]. Inactivated GR is bound to a protein complex of approximately 300 kDa that includes two molecules of heat-shock protein (hsp90), an immunophilin protein and various other inhibitory proteins [42]. The hsp90 molecules act as a molecular chaperone, preventing the unoccupied GR from translocating to the nuclear compartment, in the absence of a ligand [42]. Once the ligand binds to the GR, hsp90 dissociates, thus exposing two nuclear localisation signals on GR allowing the activated GR-ligand complex to rapidly move into the nucleus and bind to DNA.

The activated GR then directly or indirectly regulates the transcription of target genes (Figure 2) [40,43]. Transactivation by the GR requires binding of receptor homodimers to consensus glucocorticoid response elements (GREs), defined as the palindromic 15 bp sequence AGAACA*nnn*TGTTCT (where *n* is any nucleotide), in the promoter region of glucocorticoid-responsive genes [44,45]. Recent evidence suggests that the GR dimer undergoes a cycle of non-specific bindings to DNA in which it attaches and dissociates repeatedly until a high-affinity GRE site is encountered [46]. Whereas the mechanism of transactivation is well characterised, transrepression of target genes by steroid hormones is much less understood.

Most genes that are negatively regulated by the GR do not contain a classical GRE, and therefore, distinct modes of action using different classes of response elements, namely negative, composite, and tethering GREs, have been proposed to account for transrepression [47-50]. Negative GREs have been found in only a few genes and require DNA binding of the GR, as exemplified by the pro-opiomelanocortin (POMC) gene (Figure 2) [49].

GR may also inhibit protein synthesis by reducing the stability of mRNA containing constitutive AU-rich elements in the 3'-UTR, thus shortening the turnover time of the mRNA [51]. This is a mechanism whereby GCs inhibit the synthesis of the cytokine granulocyte-macrophage colony-stimulating factor (GM-CSF), which plays a key role in the survival of inflammatory cells at the site of inflammation [52]. This mechanism may also be important for the repressive effect of GCs on inducible cyclooxygenase (COX-2) expression [53,54].

Finally, at composite elements, such as in the proliferin gene promoter, the GR contacts DNA together with another transcription factor, whereas at tethering elements, repression is mediated by protein-protein interaction without direct DNA binding by the GR (e.g. collagenase type I and collagenase-3) (Figure 2) [44,55-59]. Direct protein-protein interaction between AP-1 and the liganded GR was shown to result in repression of collagenase gene expression, whereby AP-1/GR complex prevents GR interaction with respective response elements [5,60-63]. In addition to the cross talk with AP-1, GR may also interact with the p65 subunit of NF-κB in a similar manner, and this mechanism has been proposed to account for many of the immunosuppressive effects of GCs [64-66]. Direct protein-protein interactions have been demonstrated between GR and CREB, and

between signal transducers and activators of transcription (STATs) proteins, such as STAT3, STAT5 and STAT6 [67-71]. This suggests that GCs modulate either the binding or activation of these transcription factors and thus modify the expression of inflammatory genes. The repressive action of GCs may be due to competition between GR and the binding sites on CBP for other transcription factors including AP-1, NF-κB, Sp1, Ets, NF-AT and STATs [72-74]. The interactions between activated GR and transcription factors usually occur within the nucleus, but may also occur in the cytoplasm [75]. Alternatively, activated GR may bind to one of several transcriptional co-repressor molecules that have different histone deacetylase activity. This would result in the deacetylation of histones, tightening of DNA around histone residues and thus reduced access of transcription factors such as AP-1 and NF-κB to their binding sites and finally the repression of inflammatory genes [76,77].

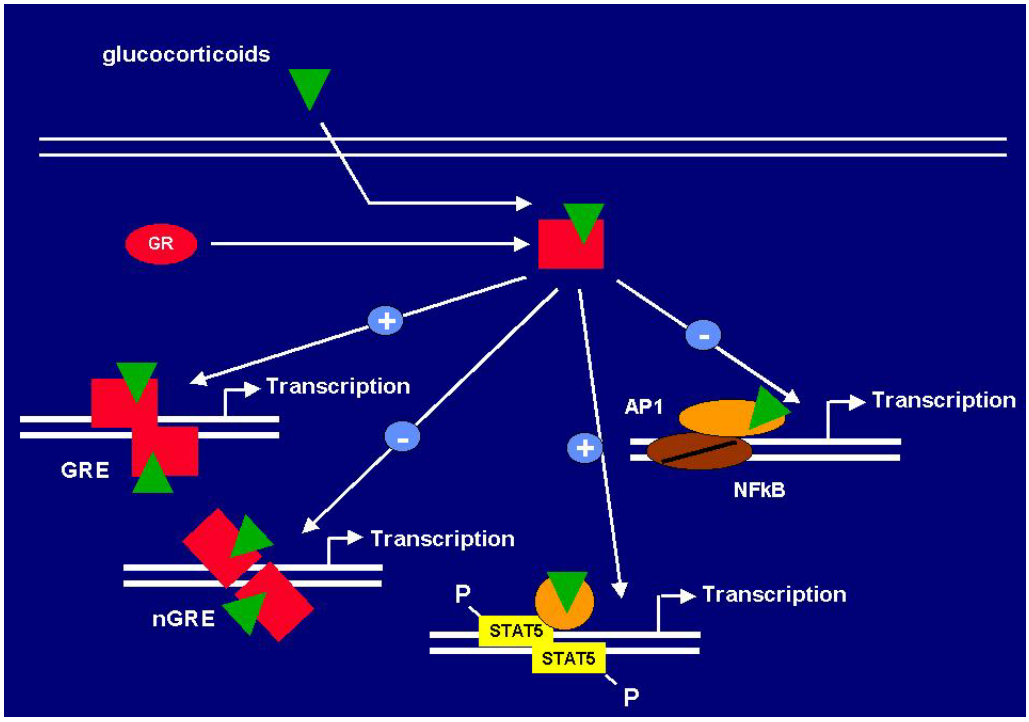



Figure 2. Classical model of glucocorticoid action

Glucocorticoids enter the cell and bind to cytoplasmic glucocorticoid receptor (GR) that is complexed with two molecules of heat shock protein (hsp90). The ligand bound receptor translocates to the nucleus where, as a dimer, it binds to glucocorticoid recognition sequences (GRE) in the 5'-upstream promoter sequence of glucocorticoid-responsive genes. GREs may increase transcription and negative (n)GREs may decrease transcription, resulting in increased or decreased mRNA synthesis. Direct interaction between the transcription factors AP-1 and NF-κB and the GR may result in mutual repression. In this way glucocorticoids may counteract the chronic inflammatory effects of cytokines which activate these transcription factors. A positive interaction between GR and STAT5 suggests that GCs may enhance the effects of certain cytokines.

### 2. 2. 2. Functional and cell-specific mutations of the glucocorticoid receptor

Separation of the transactivation and transrepressive domains of the GR has been demonstrated using reporter gene constructs in transfected cells with selective mutations of the GR [78]. The clinical relevance of these effects was demonstrated by the generation of $GR^{dim/dim}$ mice (denoted as $GR^{dim}$) [79]. The point mutation (A458T) was introduced into the second zinc finger of the GR by gene targeting using the Cre/loxP recombination system [79] (Figure 3). This resulted in impaired receptor dimerisation and thereby prevented GRE-dependent transactivation while the functions that require cross-talk with other transcription factors remained intact [79]. In contrast to

$GR^{-/-}$ mice, which die shortly after birth due to a number of severe abnormalities, $GR^{dim}$ mice are viable, showing that DNA-binding independent activities of GR are important for survival [79,80]. In $GR^{dim}$ animals, dexamethasone was able to inhibit AP-1-driven gene transcription, but the ability to facilitate GRE-mediated effects such as cortisol suppression, erythroblast proliferation and T cell apoptosis were markedly inhibited [79].

It has been previously described that cells of myeloid lineage play a major role in the maintenance of tissue homeostasis and immunological defence. In particular, the mononuclear phagocytes, including blood monocytes and resident tissue macrophages, are of key importance for the establishment of innate immunity as well as the cytokine-mediated regulation of acquired immune responses [3]. The *in vivo* contribution of GR signalling in establishing the proper innate immune response has been demonstrated by generation of a mouse mutant, which has the GR selectively inactivated in macrophages and granulocytes (F. Tronche et al., unpublished). In order to conditionally target these cells for the expression of the GR, a modified $GR^{flox/flox}$ allele was generated, using homologous recombination in embryonic stem cells, where exon 3, which encodes the first zinc-finger of the GR DNA-binding domain, was flanked by two loxP sites (Figure 3) [81]. Mice homozygous for $GR^{flox/flox}$ appeared normal and expression of the GR protein was identical to that of wild type mice. $GR^{flox/flox}$ mice were crossed with mice expressing the *Cre* recombinase under murine M lysozyme promoter (LysMcre mice) [82,83]. This resulted in generation of viable $GR^{flox/flox;LysCre}$ mutant mice, abbreviated further as $GR^{LysCre}$ (F. Tronche et al., unpublished data). Preliminary studies investigating the possible impact of the altered cytokine response in $GR^{LysCre}$ mice, conducted by determining the survival rate upon LPS injection, revealed an enhanced mortality of these mice in comparison to control littermates (F. Tronche, H. M. Reichardt, A. Bauer, unpublished data), thus underscoring the importance of GR signalling in myeloid cells for protection against an overshooting inflammatory response.

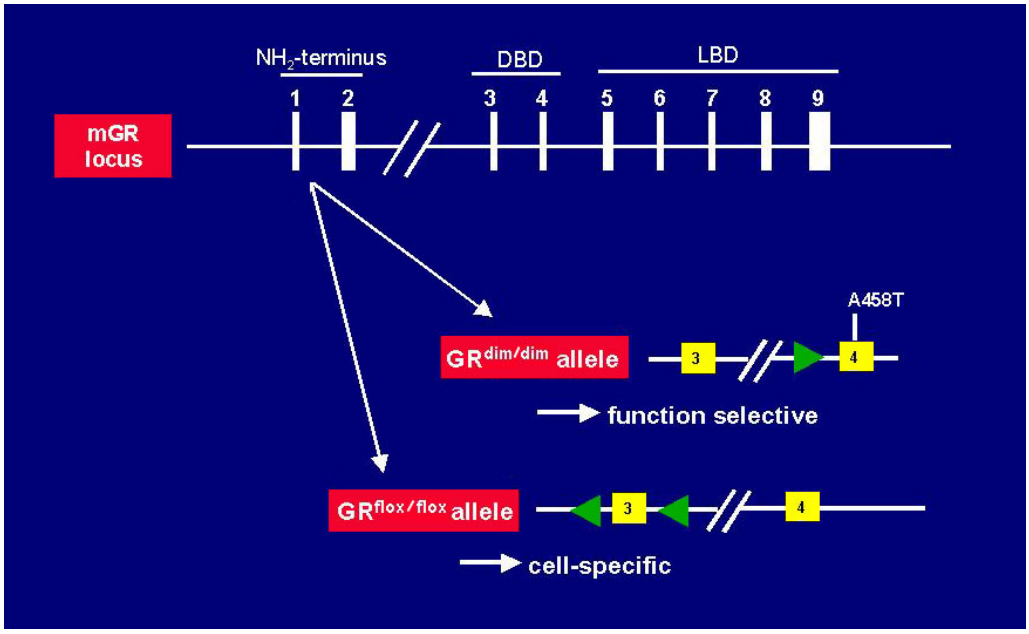



Figure 3. Targeted disruption of the GR locus

The murine GR gene and its domains are depicted at the top, with the relative position of exons 1-9 indicated. Modified GR loci are denoted as $GR^{dim}$ and $GR^{flox/flox}$. A point mutation (alanine 458 to threonine) was introduced into the second zinc finger (exon 4) in the DNA-binding domain of the $GR^{dim/dim}$ allele. The $GR^{flox/flox}$ allele was constructed to have exon 3, which encodes the first zinc finger of the GR DNA-binding domain, flanked by two loxP sites (triangles).

## 2. 3. MOLECULAR LINK BETWEEN LPS AND GR SIGNALLING IN MACROPHAGES; GENE EXPRESSION PROFILING METHODOLOGIES

LPS is thought to stimulate macrophages to respond more rapidly and effectively against invading agents. Several recent studies have supplied a wealth of data regarding molecular changes in response to LPS stimulation [6,84-88]. However, the spectrum of genes whose expression is altered by GCs during LPS stimulation of macrophages has not been extensively analysed. One way to investigate this process as well as to identify genes that contribute to LPS's critical role during inflammation, is with a general approach such as gene expression profiling.

Since the expression pattern of a gene provides putative information about its function, a number of approaches have been developed to determine the cell and tissue-specific distribution of

large numbers of genes, and/or to identify those that are differentially expressed between two or more given populations. Some of these methods are designed for *de novo* isolation of genes expressed at different levels in samples being compared. Most of these techniques are limited in that they are only capable of analysing a limited number of transcripts simultaneously and do not provide quantitative data on expression levels. Examples include differential display (DD) [89], representation difference analysis (RDA) [90,91], and suppressive subtractive hybridisation (SSH) [92]. The following methods, provide direct information about transcript abundance, as they exploit high-throughput sequencing and sequence databases either to estimate transcript abundance, e.g. EST numerical analysis and serial analysis of gene expression (SAGE) [93,94], or to construct DNA microarrays of thousands of gene sequences derived from the databases using either nylon membranes of glass slides as solid support (e.g. gene fragments arrays or oligonuclotide arrays) [95,96]. The latter allow the expression of hundreds of genes to be studied simultaneously without biasing conclusions drawn from a subset of genes presumed to be involved in a process under investigation.

### 2. 3. 1. Suppressive subtractive hybridization

Suppressive subtractive hybridisation is a powerful approach to identify and isolate cDNAs of differentially expressed genes [92,97-100]. The method is designed to selectively amplify target cDNA fragments and simultaneously suppress nontarget cDNA amplification [92,101]. It overcomes the problem of differences in mRNA abundance by incorporating a hybridisation step that normalises (equalises) sequence abundance during the course of subtraction by standard hybridisation kinetics. With a single subtractive hybridisation round, greater than 1,000-fold enrichment for differentially expressed cDNAs can be achieved [92,101]. SSH generates small cDNAs ranging from 50 to ~1,000 bp which can be from any part of the mRNA. While this methodology is more high-throughput and generates less false positives then DD-RTPCR, the short cDNA fragments need to be subcloned or extended to yield more information about the sequence of corresponding transcripts [91,92]. Apart from the characterisation of known

transcripts, SSH also permits the isolation of novel, uncharacterised genes. However, its major drawback is the inability to quantitatively measure the expression of enriched cDNAs. For this purpose, additional mRNA quantitative methods have to be included to determine the expression levels of subtracted genes/ESTs.

### 2. 3. 2. Gene arrays

Array-based technologies have made it straightforward to simultaneously monitor the expression pattern of thousands of genes across a wide variety of tissues, cell types, and conditions [95,96,102]. The technique is amenable to the analysis of a few hundred well-defined genes or family members as well as to the monitoring of 'global' expression profiles of the entire complement of an organism's expressed genes [103-107]. In addition to providing broad and in-depth information on gene expression patterns, gene microarrays are a powerful tool to dissect the mechanism of action of drug candidates and their metabolic pathways, and/or to identify potential markers to follow effect and dose of drugs in the clinical setting [104,108-110].

Microarrays of gene fragments (PCR/cDNA products) are typically constructed using sequences of characterised genes and/or ESTs [96,111,112]. Nevertheless, one can also readily array inserts from clones randomly picked from a cDNA or subtracted library [107]. The oligonucleotide gene expression chip (Affymetrix, Santa Clara, CA) is designed to contain 25-mer oligonucleotide sequences from a gene/EST of interest tiled directly on the solid glass wafer. The oligonuclotides are organised as perfect match/mismatch pairs (PM/MM) with the mismatch acting as a control for hybridisation specificity [110]. These short oligonucleotides can be designed to discriminate between splice variants and members of gene families (up to 70-80% of homology). In these cases, hybridisation patterns of inserts reveal information on gene expression (abundance). Still, a major drawback of either nylon-based cDNA arrays or oligonuclotide arrays, is the inability to identify low abundant mRNAs that usually fall within the 'noise' of the hybridisation.

Finally, although techniques for large-scale gene expression profiling have advanced considerably, some limitations remain to be addressed, such as enhanced ability to constantly identify low

abundant mRNA, improved signal-to-noise ratio, standardised software systems for the collection, quality scoring, and tracking of data, as well as extracting biological information from the immense amount of data [105,113].

# 3. AIM OF THE PROJECT

One way to decipher the molecular events of the macrophage response during inflammation caused by LPS, and the modulatory role of GCs on this process, is to determine differential changes in genes expression.

To meet this objective, suppressive subtractive hybridisation (SSH) and gene array hybridisation approaches, techniques that rely on quantitative and qualitative analysis of mRNA content, were employed. In order to confirm that GC effects are mediated specifically via the GR, and to dissect the mechanisms of GR actions on modulating the expression of LPS induced/repressed genes, gene expression profiling analysis was performed using peritoneal macrophages obtained from $GR^{LysCre}$ and $GR^{dim}$ mutant mice. Dimerisation-defective $GR^{dim}$ mice will address whether GCs-mediated induction/repression of LPS-target genes is achieved in a DNA-binding dependent or independent manner by GR interaction with other transcription factor (proteins).

The results obtained using a combination of state of the art expression profiling approaches with functional and tissue-specific mouse mutants should provide a deeper understanding of the molecular pathogenesis of LPS and the molecular mechanisms of anti-inflammatory actions of GCs.

# 4. RESULTS

## 4. 1. *In vitro* CULTURE OF PERITONEAL MACROPHAGES

Macrophages have evoked the ability to recognise bacterial products and to initiate an immune response to clear the invading agent [85]. An innate pattern of this response is triggered by LPS, which promotes rapid changes in signalling pathways within macrophages and adaptive changes in gene expression [6,85]. In order to examine how the gene expression profile in macrophages is affected upon LPS stimulation, an *in vitro* model of peritoneal macrophages was established. To obtain primary peritoneal macrophages (PMΦ), mice were injected intra-peritoneal with thioglycollate and the cells were harvested by peritoneal lavage [114]. To confirm that the isolated cells were macrophages and to determine the purity, immunohistochemical staining was performed with M3/84 macrophage monoclonal antibody, which detects Mac-3 antigen on tissue and thioglycollate-elicited PMΦ. After overnight culture, 90-95% of the adherent cells stained positively for the expression of Mac-3 as illustrated in Figure 4. The remaining 5-10% of the cells represented mostly lymphocytes and some granulocytes.

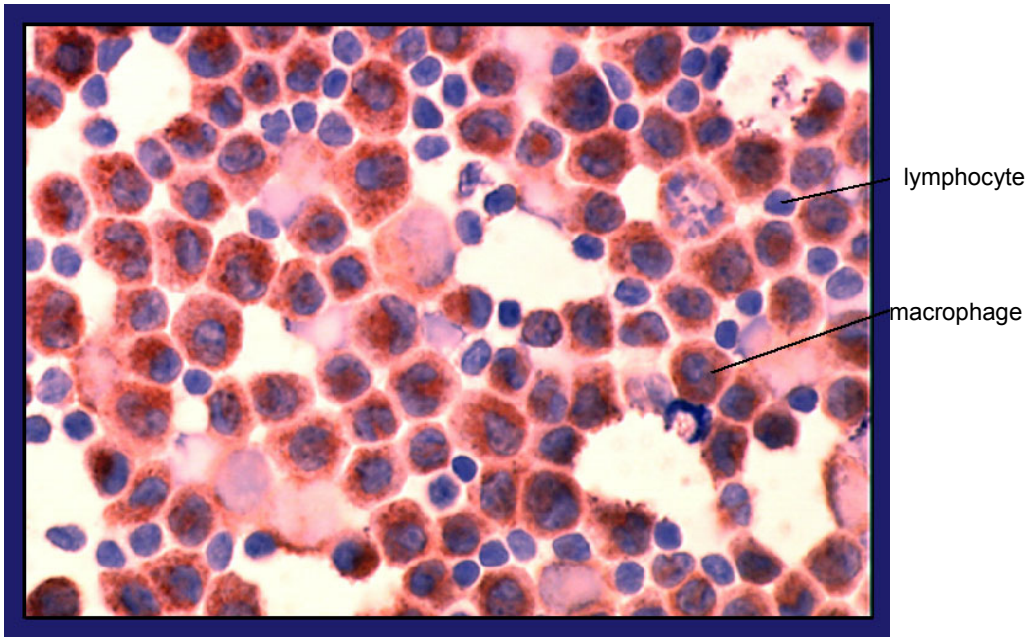



Figure 4. Staining of macrophage cytospin section using M3/84 antibody

Cytospin sections were prepared using 100,000 cells obtained by peritoneal lavage. Immunohistochemical staining was performed with the M3/84 antibody which reacts with the Mac-3 antigen expressed on mononuclear phagocytes. The analysis was performed by Prof. Dr. H-J. Gröne from the Department of Cell and Molecular Pathology, German Cancer Research Centre, Heidelberg.

In order to monitor the process of macrophage activation by LPS, isolated PMΦ were treated with LPS and the mRNA expression of two major proinflammatory cytokines known to be induced by LPS (TNF-α and IL-6) was measured using the RNase protection assay. Already after 30 min of LPS (100 ng/ml) application, the mRNA expression of both cytokines was increased and reached a maximum at 1h (42-fold increase) and 6h (16-fold increase) for TNF-α and IL-6, respectively (Figure 5). After 24h the mRNA expression of TNF-α and IL-6 was almost back to basal levels. Collectively, these results establish that prepared PMΦ cultures can be considered almost pure and respond, as expected, to inflammatory stimuli such as LPS.

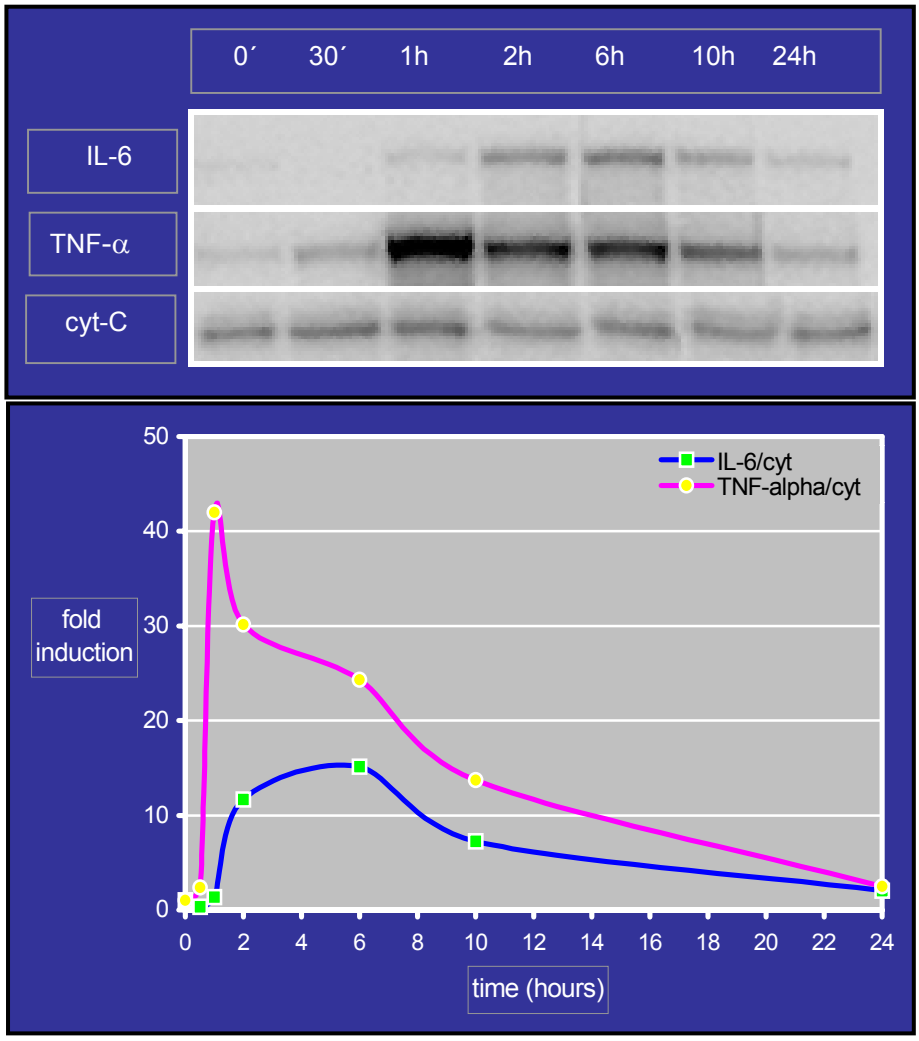



Figure 5. Time course of TNF-α and IL-6 mRNA expression upon LPS-stimulation of PMΦ

mRNA expression of TNF-α and IL-6 was analysed by RNase protection using total RNA obtained from unstimulated PMΦ and cells stimulated by LPS (100 ng/ml) for the indicated times. α-$^{32}$P-UTP antisense RNA probes for TNF-α, IL-6 and cytochrome C (cyt-C) were *in vitro* transcribed and hybridised against 5 µg of total RNA from each treatment. Cyt-C was used to normalise the data. Signal intensities were quantified by PhosphoImager and the analysis is shown in the lower panel. The data are representative of two RNase protection experiments.

# 4. 2. GENE EXPRESSION PROFILING OF PERITONEAL MACROPHAGES

As demonstrated previously, LPS promotes rapid production of TNF-α, IL-6 and other pro- and anti-inflammatory mediators, which are involved in the endotoxin signalling cascade [85]. To address experimentally early LPS-mediated activation events, PMΦ were stimulated *in vitro* by LPS (100 ng/ml) for 2h. Further more, the role of glucocorticoids (GC) in modulating the LPS elicited response at molecular level was investigated upon dexamethasone administration to PMΦ (1 μM dex added 1h prior to LPS).

In order to decipher the molecular mechanisms of GC-mediated action, mice containing two different types of mutation in the GR were used in this study. $GR^{dim}$ mutant mice were generated by gene targeting to have impaired dimerisation. However, those GR interactions, which are independent of receptor binding to DNA, are preserved in these mice [79]. The second strain of mutant mice, $GR^{LysCre}$, have been generated to selectively lack the GR in cells of the myeloid lineage and are therefore expected to be refractory to GC treatment (Dr. F. Tronche, unpublished data).

Differential gene expression of LPS-stimulated PMΦ and the modulatory role of GCs on this process was examined by exploiting the methods of suppressive subtractive hybridisation (SSH) combined with real-time quantitative PCR, and oligonucleotide gene chip arrays.

### 4. 2. 1. Identification of differentially expressed mRNAs by the SSH approach

SSH is thought to allow isolation and identification of both known and novel genes/ESTs that are differentially expressed between two cell populations [92]. The enrichment of differentially expressed cDNAs is achieved by incorporating a suppressive PCR step, whereas two hybridisation steps account for normalisation (equalisation) of low and high abundant mRNA transcripts [92]. Although SSH supports generation of genes/ESTs which are differentially expressed, it does not provide information on the quantitative expression of enriched transcripts.

In order to identify genes and ESTs differentially expressed in LPS stimulated PMΦ, a subtracted and normalised library was constructed using the SSH technology (see *Material and Methods* Section). The mRNAs prepared from LPS-stimulated PMΦ of wild type animals (*tester*) were subtracted against unstimulated mRNAs (*driver*). The resulting cDNA pool should thus be enriched for transcripts that are up regulated in LPS stimulated cells. 290 clones were picked from the SSH library and processed by automatic PCR sequencing. This analysis revealed 212 clones containing inserts of 300-500 bp in size on average, which were used in homology search in GenBank and EMBL databases using BLAST (available at *http://www.ncbi.nlm.nih.gov/BLAST/*) algorithm. An outline of the procedure is given in Figure 6. The results of the database homologies found were classified into the following categories: **known mouse genes** (for sequences with high identity over the majority of the insert) and **ESTs** (expressed sequence tags of unknown function which are either homologous to mouse ESTs or represent novel transcripts). 61 known genes were identified from the SSH library screen. They were grouped into 8 functional categories based on the information derived from the PubMed literature, as shown in Table 1. Some genes were represented by multiple SSH-fragments, which often derived from different parts of the gene. For example, the immune-responsive gene (Irg1) was represented by 10 SSH-fragments. However, most identified genes were represented by only one or two SSH-fragments. Out of 76 ESTs obtained, 63 had partial homologies to sequences in the databases whereas 13 ESTs corresponded to novel transcripts.

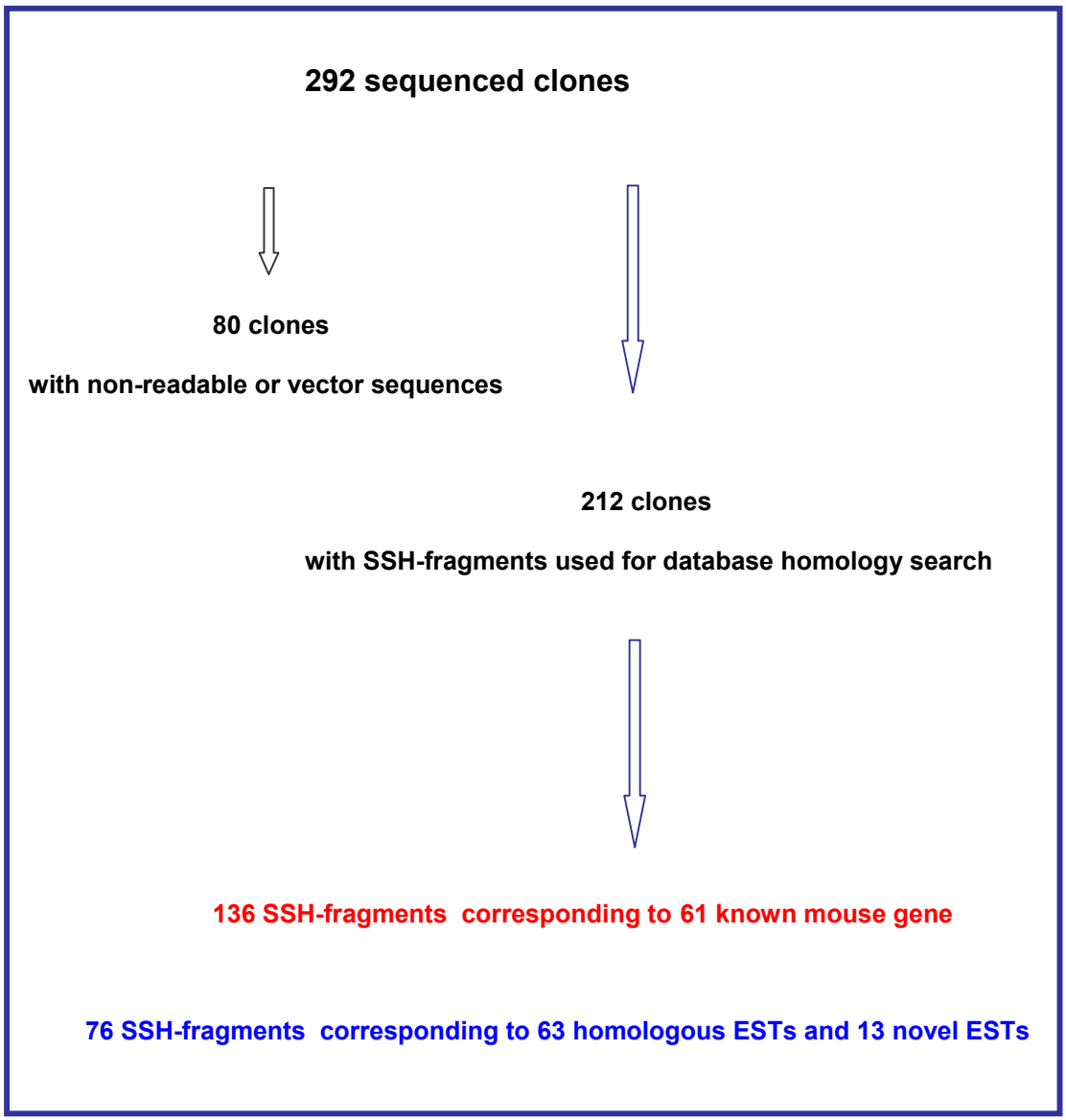



Figure 6. Generation of SSH library and database sequence homology search

The above illustration shows the types of sequences isolated and the results of a database homology search with these sequences. 136 SSH-fragments showed homology to 61 known genes. In the case of the ESTs and novel sequences, the "real" number of genes identified is unknown as the sequences so not reflect full length genes and several may correspond to the same gene.

Table 1. Functional classes of homologous genes found in the SSH library

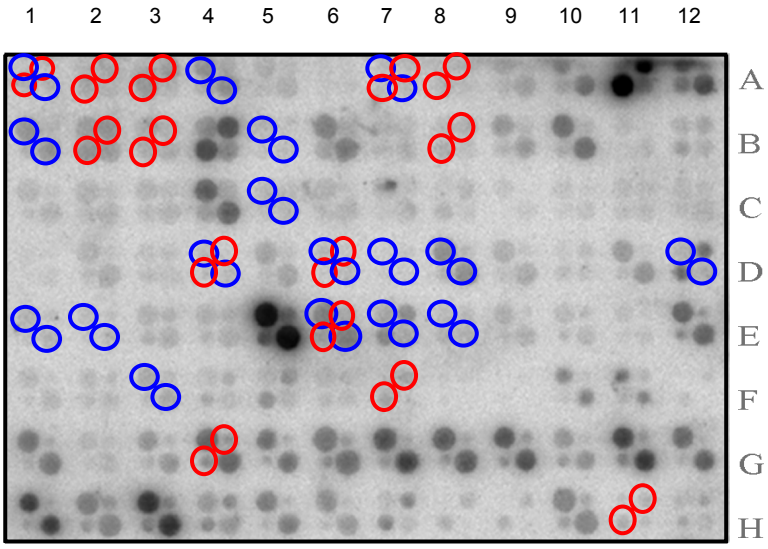
| Acc. Num. | Gene Name | Functional classes | # |
|---|---|---|---|
| X75926 | **ABC1 transporter transmembrane protein** | | **1** |
| U04672 | **BMP receptor/ BRK-1 type I receptor** | | **1** |
| X13987 | **CD14** | | **4** |
| X933278 | **F4/80 gene** | ***Cell surface antigens*** | **1** |
| X07640 | **Mac-1α cell surface glycoprotein** | ***and transmembrane proteins*** | **1** |
| U37226 | **plasma phospholipid transfer protein** | | **1** |
| AC005835 | **T-cell receptor α,β,γ** | | **1** |
| AF124741 | **Toll-like receptor 2** | | **2** |
| K02782 | **complement component C3 α,β subunit** | | **1** |
| G198293 | **IL-1β** | | **3** |
| M74294 | **IL-1R antagonist protein** | ***Cytokines,*** | **1** |
| X75337 | **IL-2Rγ** | ***chemokines*** | **1** |
| J03783 | **IL-6** | ***and their receptors*** | **2** |
| X53798 | **macrophage inflammatory protein-2 (MIP-2)** | | **2** |
| M59378 | **TNFR-I** | | **3** |
| M38296 | **tumor necrosis factor alpha (TNF-α)** | | **10** |
| D37837 | **65-kDa macrophage cytosolic protein** | | **1** |
| AF133912.1 | **ARL-6 interacting protein** | ***Cytoskeleton*** | **1** |
| M21495 | **cytoplasmic γ-actin gene** | ***and motility proteins*** | **2** |
| X93167 | **fibronectin** | | **3** |
| M87276 | **trombospondin-1** | | **15** |
| NM_023885 | **chloride intralcellular channel protein (mitochondrial), Clic4** | | **1** |
| L21768 | **eps15** | | **1** |
| U43384 | **gp91phox (Cybb)** | | **2** |
| X65026 | **GTP-binding protein** | | **1** |
| AF119038 | **Ig heavy chain VH12-JH** | ***Modulators,*** | **1** |
| L38281 | **immune-responsive gene (Irg-1)** | ***intracellular transducers*** | **10** |
| AF061260 | **immunosuperfamily protein BL2** | ***and adaptor molecules*** | **1** |
| AF072543 | **inhibitory receptor SHPS-1 long isoform** | | **2** |
| L20315 | **MPS1** | | **1** |
| AJ001616 | **myeloid associated differentiation protein** | | **1** |
| Y11550 | **p40 protein** | | **1** |
| L24118 | **primary response gene B94** | | **6** |
| AF020313 | **proline-rich protein 48** | | **1** |
| U92793 | **α-glucosidase II α subunit** | | **1** |
| D85596 | **AMP deaminase H-type** | | **1** |
| Z38015 | **DMR-N9 gene and DM-PK gene** | | **1** |
| AF046783.1 | **lysyl hydroxylase 3** | | **1** |
| M82831 | **macrophage metalloelastase** | | **1** |
| AF135185 | **MAPK38β** | | **1** |
| X16490 | **PAI-2** | ***Protein turnover*** | **1** |
| AF133125.1 | **phospholipase C δ-1** | | **1** |
| AF181829 | **Pleckstrin** | | **5** |
| M94967 | **prostaglandin synthase/cyclooxigenase (COX-2)** | | **2** |
| X78542 | **protease-6** | | **1** |
| AF062484 | **SDP8** | | **1** |
| M55154 | **transglutaminase (Tgm 2)** | | **1** |
| D10576 | **ubiquitin activation enzyme E1** | | **1** |
| AF069502 | **ubiquitin specific protease UBP43 (Usp18)** | | **1** |
| U19463 | **A20 Zfp** | | **4** |
| X13661 | **elongation factor 1-α (EF1-α)** | | **1** |
| NM_005762 | **KRAB-associated protein 1 (TIF1B)** | ***Transcription factors*** | **1** |
| AF155372 | **NF-κB p100** | ***and DNA-binding proteins*** | **1** |
| M57999 | **p70 TFp105 NF-κB precursor** | | **3** |
| AF010305 | **Stra13 basic helix-loop-helix cofactor** | | **1** |
| X14678 | **Zfp 36 (TIS11)** | | **1** |
| X03765 | **cytoplasmic β-actin** | ***House-keeping genes*** | **1** |
| M33330 | **insulinoma (rig) gene** | | **1** |
| X93035 | **BRP-protein 39** | ***Oncogenes*** | **1** |
| X06368 | **c-fms proto-oncogene** | ***and tumor suppressors*** | **1** |
| X82564 | **rRNA (45S, 28S, 18S)** | ***Ribosomal RNA*** | **18** |

The classification of the 61 known genes, represented by 136 SSH-fragments, is based on to gene information from PubMed. The numer of SSH-fragments representing each homologue gene is indicated by the simbol #. The accession Number (Acc. Num.) for each gene is given.

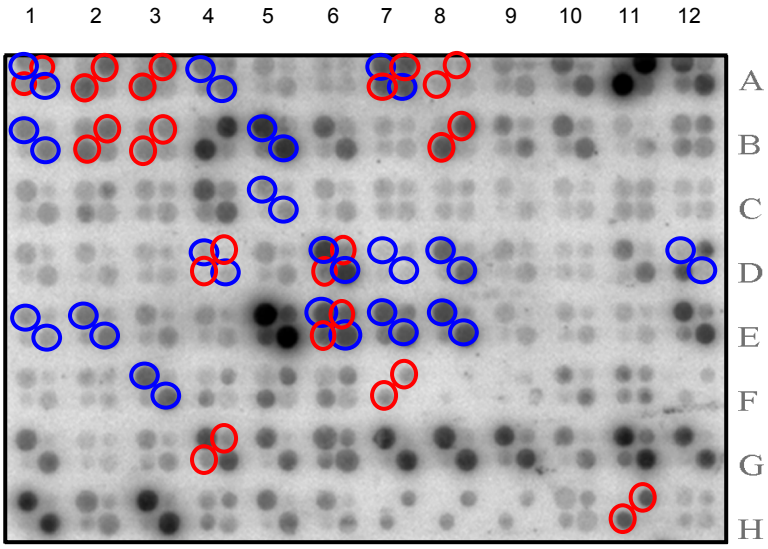
#### *4. 2. 1. 1. Quantitative expression analysis of transcripts obtained by SSH: Measuring the expression levels on nylon arrays containing transcripts from SSH-library*

In order to enable a high-throughput quantitative expression analysis of subtracted genes/ESTs, with the intent of identifying those associated with the LPS phenotype in PMΦ, gene array technology was employed [95,111]. For this purpose, inserts from SSH clones were PCR amplified and spotted on to nylon Hybond $N^+$ membranes using robotic printing. Multiple housekeeping genes and randomly selected DNAs were also spotted and served as internal/normalisation controls. The 'SSH-arrays' were then hybridised with $\alpha$-$^{32}$P dATP labelled first strand cDNA probes derived from the *tester* and *driver* samples (Figure 7). To permit comparison between multiple array experiments, the data set were normalised to each other using the average expression level of selected house-keeping genes (for details see *Material and Methods*).

**A. unstimulated (ctrl)**




**B. stimulated with LPS (LPS)**



**C. Comparison of expression levels in unstimulated and LPS-stimulated PMΦ**

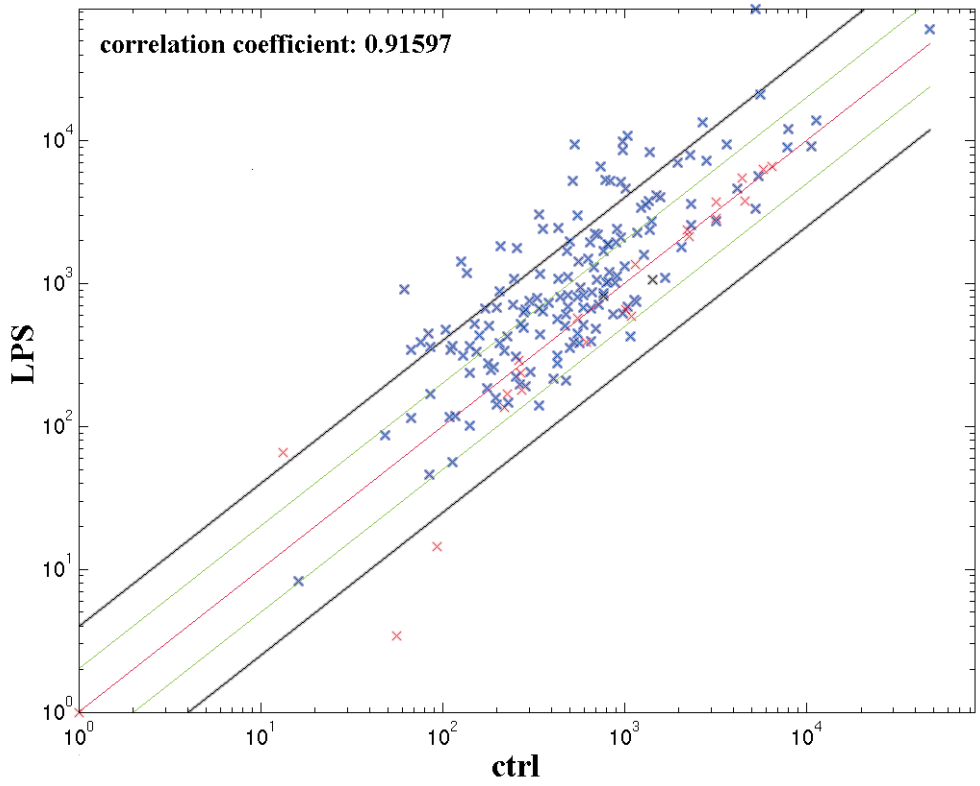



Figure 7. Expression profile of LPS-stimulated PMΦ as assessed by hybridisation of SSH-arrays

The SSH-arrays were hybridised with $\alpha$-$^{32}$P dATP-labelled first-strand cDNA probe derived from unstimulated PMΦ of wild type mice (A) and, cells stimulated with 100 ng/ml of LPS for 2h (B). The hybridisation signals were collected using a Phosphoimager. The circled pairs of cDNA spots represent the genes that are differentially expressed upon LPS stimulation of PMΦ compared to unstimulated cells. These data are representative of three hybridisation experiments. Blue and red circles indicate duplicates of differentially expressed known genes and ESTs, respectively; (C) Scatter plot of measured expression intensities. Measurements of empty spots or spotted heterologous DNA are indicated by black crosses. House-keeping genes used to standardise the median of differences to the centreline of the plot are coloured in red. Spots representing genes with differential expression are in blue. The red, green and black lines indicate 1-, 2- and 4-fold differences in expression level, respectively.

Using the criteria of differential expression by a factor of two or more, the expression level of 34, out of 140 unique SSH genes/ESTs, were found to be induced by LPS. These mRNAs correspond to 21 known genes and 13 ESTs which are listed in Table 2. The gene information provided by SSH-array analysis is available at *http://www.dkfz.de/tbi/macrophage*.

Table 2. Analysis of differential expression of subtracted genes/ESTs upon LPS stimulation of PMΦ by array hybridisation

| | | Grid | hybridisation intensities | | | Average | | hybridisation intensities | | | Average | | Fold change |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Acc. Num. | Gene / clone Name | position | ctrl #1 | ctrl #2 | ctrl #3 | ctrl | StDev | LPS #1 | LPS #2 | LPS #3 | LPS | StDev | LPS/ctrl |
| D37837 | **65-kDa protein** | D8G | 1012.80 | 486.60 | 1322.10 | **940.50** | 422.42 | 2916.00 | 1168.80 | 2861.60 | **2315.47** | 993.41 | **2.5** |
| U19463 | **A20 protein** | A2E | 3813.60 | 1243.10 | 1307.10 | **2121.27** | 1465.95 | 11212.50 | 4457.40 | 2653.60 | **6107.83** | 4511.83 | **2.9** |
| X75926 | **ABC 1 transporter** | D4G | 1536.00 | 607.90 | 1296.60 | **1146.83** | 481.83 | 10233.00 | 3198.80 | 4558.50 | **5996.77** | 3731.15 | **5.2** |
| U92793 | **α-glucosidase II α subunit** | B8G | 1148.20 | 506.80 | 1454.80 | **1036.60** | 483.75 | 2832.10 | 1387.40 | 3597.90 | **2605.80** | 1122.49 | **2.5** |
| L24118 | **B94 gene** | B3E | 457.40 | 212.70 | 694.80 | **454.97** | 241.06 | 3369.20 | 1455.10 | 3430.00 | **2751.43** | 1123.07 | **6.0** |
| K02782 | **C3 α, β subunit** | C5G | 1447.00 | 551.00 | 1197.90 | **1065.30** | 462.48 | 4355.20 | 2097.90 | 3050.80 | **3167.97** | 1133.20 | **3.0** |
| X13987 | **CD14** | A4G | 2769.00 | 1043.00 | 2316.60 | **2042.87** | 894.97 | 15942.20 | 4976.90 | 10435.70 | **10451.60** | 5482.67 | **5.1** |
| NM_013885 | **Clic4** | H11E | 521.00 | 363.40 | 541.00 | **475.13** | 97.28 | 6033.10 | 2123.20 | 1893.10 | **3349.80** | 2326.65 | **7.1** |
| M94967 | **COX-2** | B1G | 890.50 | 428.70 | 741.20 | **686.80** | 235.66 | 6327.30 | 2039.50 | 5308.10 | **4558.30** | 2240.08 | **6.6** |
| X93167 | **Fibronectin** | D7G | 1395.90 | 523.70 | 1472.70 | **1130.77** | 527.14 | 4513.80 | 1281.00 | 3258.80 | **3017.87** | 1629.81 | **2.7** |
| M21495 | **γ-actin** | E6G | 2206.10 | 1226.80 | 2319.30 | **1917.40** | 600.75 | 9139.60 | 4125.30 | 7717.60 | **6994.17** | 2584.24 | **3.6** |
| G198293 | **IL-1β** | D6G | 5450.50 | 2052.30 | 2878.50 | **3460.43** | 1772.27 | 99093.00 | 23768.00 | 29988.00 | **50949.67** | 41809.18 | **14.7** |
| J03783 | **IL-6** | E2G | 606.30 | 255.80 | 518.70 | **460.27** | 182.41 | 11264.80 | 3368.70 | 3158.10 | **5930.53** | 4620.81 | **12.9** |
| L38281 | **Irg-1** | A7G | 1057.40 | 287.30 | 574.10 | **639.60** | 389.21 | 6143.10 | 1705.90 | 2872.10 | **3573.70** | 2300.30 | **5.6** |
| X07640 | **Mac-1α** | D9G | 715.80 | 548.90 | 1210.30 | **825.00** | 343.96 | 2575.70 | 1376.60 | 2799.50 | **2250.60** | 765.13 | **2.7** |
| X53798 | **MIP-2** | F3G | 1411.50 | 677.00 | 1097.10 | **1061.87** | 368.52 | 4502.90 | 1441.00 | 4254.50 | **3399.47** | 1700.62 | **3.2** |
| X16490 | **PAI-2** | D12G | 3096.80 | 1451.20 | ~ | **2274.00** | 1163.61 | 9629.30 | 7446.40 | ~ | **8537.85** | 1543.54 | **3.8** |
| AF181829 | **Pleckstrin** | A3E | 920.20 | 476.40 | 1205.70 | **867.43** | 367.50 | 2397.70 | 2108.50 | 6970.50 | **3825.57** | 2727.43 | **4.4** |
| M38296 | **TNF-α** | B5G | 437.50 | 168.30 | 541.00 | **382.27** | 192.39 | 3650.10 | 1934.00 | 4431.60 | **3338.57** | 1277.61 | **8.7** |
| M59378 | **TNFR-I** | A1G | 700.80 | ~ | 545.20 | **623.00** | 110.03 | 2125.20 | ~ | 1151.80 | **1638.50** | 688.30 | **2.6** |
| AF069502 | **UBP43 (Usp18)** | E7G | 1007.10 | 530.90 | 860.70 | **799.57** | 243.92 | 11829.10 | 3594.30 | 7243.20 | **7555.53** | 4126.28 | **9.4** |

| Acc. Num. | Gene / clone Name | Grid position | hybridisation intensities ctrl #1 | ctrl #2 | ctrl #3 | Average ctrl | StDev | hybridisation intensities LPS #1 | LPS #2 | LPS #3 | Average LPS | StDev | *Fold change LPS/ctrl* |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **clone I 14-4** | A4E | 1029.70 | 317.10 | 1382.70 | **909.83** | 542.82 | 2970.20 | 1797.50 | 2861.80 | **2543.17** | 648.04 | ***2.8*** |
| | **clone I 15-7** | A5E | ~ | 110.30 | 344.70 | **227.50** | 165.75 | ~ | 313.20 | 1017.70 | **665.45** | 498.16 | ***2.9*** |
| | **clone I 27-4** | B1E | ~ | 131.40 | 243.00 | **187.20** | 78.91 | ~ | 495.70 | 1352.00 | **923.85** | 605.50 | ***4.9*** |
| E | **clone I 33-8** | B5E | ~ | 76.20 | 512.80 | **294.50** | 308.72 | ~ | 493.30 | 1391.90 | **942.60** | 635.41 | ***3.2*** |
| | **clone II 23-3** | C11E | ~ | 252.20 | 887.10 | **569.65** | 448.94 | ~ | 581.60 | 1812.80 | **1197.20** | 870.59 | ***2.1*** |
| S | **clone II 33-4** | D6E | 1226.60 | 577.00 | 1250.40 | **1018.00** | 382.10 | 15179.30 | 4849.20 | 6679.40 | **8902.63** | 5512.24 | ***8.7*** |
| | **clone II 34-6** | D7E | ~ | 156.10 | 544.60 | **350.35** | 274.71 | ~ | 606.90 | 1143.10 | **875.00** | 379.15 | ***2.5*** |
| T | **clone II 52-2** | E2E | 198.80 | 69.00 | ~ | **133.90** | 91.78 | 2074.40 | 1009.10 | ~ | **1541.75** | 753.28 | ***11.5*** |
| | **clone II 9-5** | C2E | ~ | 544.40 | 792.70 | **668.55** | 175.57 | ~ | 2139.90 | 3384.10 | **2762.00** | 879.78 | ***4.1*** |
| | **clone III 14-1** | F4E | ~ | 131.10 | 232.10 | **181.60** | 71.42 | ~ | 510.80 | 1222.80 | **866.80** | 503.46 | ***4.8*** |
| | **clone III 3-1** | E6E | 1827.50 | 837.00 | 988.80 | **1217.77** | 533.47 | 5698.00 | 2473.20 | 3016.70 | **3729.30** | 1726.47 | ***3.1*** |
| | **clone III 3-3** | E7E | ~ | 285.80 | 983.30 | **634.55** | 493.21 | ~ | 762.70 | 2145.00 | **1453.85** | 977.43 | ***2.3*** |
| | **clone III 6-1** | E8E | ~ | 182.30 | 397.70 | **290.00** | 152.31 | ~ | 567.60 | 1430.60 | **999.10** | 610.23 | ***3.4*** |

The table illustrates hybridisation intensities from SSH-array experiments of 21 genes and 13 ESTs, whose expression was increased by more than 2-fold upon LPS stimulation in comparison to levels in unstimulated cells. The hybridisation intensities of unstimulated (ctrl) and LPS-stimulated PMΦ (LPS) are shown as average values, calculated from two or three hybridisation experiments, indicated as #1, #2 and #3. Fold change is calculated relative to the value from unstimulated cells (LPS / ctrl). Values obtained by SSH-array hybridisation analysis are indicated in yellow. ctrl - unstimulated PMΦ from wild type mice; LPS - PMΦ from wild type mice stimulated for 2 h with LPS (100 ng/ml); StDev - Standard deviation; Acc. Num. - Accession Number; ~ - no data available

### *4. 2. 1. 2. Quantitative expression analysis of transcripts obtained by the SSH: Evaluation of SSH-array data using real-time quantitative PCR*

Quantitative real-time PCR (LightCycler, Roche) was used to confirm and more accurately measure differential expression of 21 genes, identified by SSH-array analysis. This method allows measurements to be made during the log-linear phase of a PCR, in contrast to conventional PCR, where quantification is acquired only in the plateau phase (end-point determination) [115]. For this purpose, fluorescent dsDNA SYBR Green I dye was used, which allowed on-line monitoring of product synthesis during each PCR cycle. The hypoxanthine phosphoribosyltransferase (HPRT) gene was used as an 'external standard' and normalisation reference gene. The analysis was performed using first strand cDNAs obtained from unstimulated and LPS stimulated PMΦ from wild type mice. The expression of 21 LPS-inducible genes evaluated by real-time quantitative PCR is shown in Table 3.

Table 3. Confirmation and quantification of relative gene expression by real-time quantitative PC

| Acc. Num. | Gene Name | ctrl #1 | ctrl #2 | ctrl #3 | Average ctrl | StDev | LPS #1 | LPS #2 | LPS #3 | Average LPS | StDev | *Fold change LPS/ctrl* |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| D37837 | **65-kDa protein** | 2.58 | 2.31 | 2.78 | **2.56** | 0.24 | 5.92 | 5.86 | 6.24 | **6.01** | 0.20 | ***2.3*** |
| U19463 | **A20 protein** | 11.40 | 17.90 | 10.70 | **13.33** | 3.97 | 84.50 | 73.70 | 101.60 | **86.60** | 14.07 | ***6.5*** |
| U92793 | **ABC 1 transporter** | 3.20 | 2.33 | 3.18 | **2.90** | 0.50 | 10.30 | 5.81 | 7.84 | **7.98** | 2.25 | ***2.8*** |
| X75926 | **α-glucosidase II α subunit** | 2.11 | 0.74 | ~ | **1.43** | 0.97 | 2.65 | 0.79 | ~ | **1.72** | 1.32 | ***1.2*** |
| L24118 | **B94 gene** | 35.05 | 30.99 | ~ | **33.04** | 2.89 | 533.25 | 116.79 | ~ | **325.02** | 294.48 | ***9.8*** |
| K02782 | **C3 α, β subunit** | 8.10 | 8.20 | 6.00 | **7.43** | 1.24 | 32.20 | 24.70 | 20.50 | **25.80** | 5.93 | ***3.5*** |
| X13987 | **CD14** | 11.58 | 12.17 | 10.99 | **11.58** | 0.59 | 45.51 | 44.09 | 46.92 | **45.51** | 1.42 | ***3.9*** |
| NM_013885 | **Clic4** | 0.86 | 5.84 | 2.39 | **3.03** | 2.55 | 8.90 | 14.26 | 10.31 | **11.16** | 2.78 | ***3.7*** |
| M94967 | **COX-2** | 0.02 | 0.05 | ~ | **0.03** | 0.02 | 10.32 | 19.28 | ~ | **14.80** | 6.34 | ***> 100*** |
| X93167 | **Fibronectin** | 63.79 | 51.14 | 15.94 | **43.62** | 24.79 | 67.49 | 75.24 | 18.54 | **57.09** | 25.03 | ***1.3*** |
| M21495 | **γ-actin** | 5.23 | 8.83 | 6.90 | **6.99** | 1.80 | 41.88 | 21.78 | 32.60 | **32.09** | 10.06 | ***4.6*** |
| G198293 | **IL-1β** | 5.70 | 0.02 | 0.08 | **1.93** | 3.26 | 14.90 | 5.28 | 8.49 | **9.56** | 4.90 | ***4.9*** |
| J03783 | **IL-6** | 0.06 | 0.01 | 0.01 | **0.02** | 0.03 | 13.21 | 11.41 | 6.63 | **9.84** | 3.01 | ***> 100*** |
| L38281 | **Irg-1** | 21.99 | 21.52 | 16.10 | **19.87** | 3.27 | 621.84 | 518.84 | 439.00 | **526.56** | 91.66 | ***26.5*** |
| X07640 | **Mac-1α** | 23.89 | 41.21 | ~ | **32.55** | 12.25 | 24.27 | 59.71 | ~ | **42.00** | 25.07 | ***1.3*** |
| X53798 | **MIP-2** | 1.01 | 0.95 | 1.08 | **1.01** | 0.07 | 83.93 | 60.79 | 119.07 | **87.93** | 29.35 | ***86.8*** |
| X16490 | **PAI-2** | 6.68 | 25.05 | 75.35 | **35.69** | 35.55 | 71.76 | 83.32 | 188.20 | **114.43** | 64.15 | ***3.2*** |
| AF181829 | **Pleckstrin** | 1.88 | 3.12 | 0.18 | **1.73** | 1.48 | 8.24 | 9.75 | 4.83 | **7.61** | 2.52 | ***4.4*** |
| M38296 | **TNF-α** | 0.06 | 0.04 | 0.01 | **0.04** | 0.02 | 28.80 | 13.39 | 9.80 | **17.33** | 10.09 | ***> 100*** |
| M59378 | **TNFR-I** | 9.78 | 4.39 | 1.95 | **5.36** | 3.98 | 17.21 | 33.74 | 20.65 | **23.87** | 8.72 | ***4.5*** |
| AF069502 | **UBP43 (Usp18)** | 1.43 | 3.16 | ~ | **2.30** | 1.22 | 10.78 | 8.55 | ~ | **9.67** | 1.58 | ***4.2*** |

Real-time PCR quantification of relative expression of 21 genes identified in the SSH-array analysis. The expression intensities in unstimulated (ctrl) and LPS-stimulated (LPS) cells from wild type mice were quantified and normalised to HPRT expression. The fold change was calculated relative to the value from unstimulated cells (LPS / ctrl). The average values from two or three real-time PCR experiments (indicated as #1, #2 and #3) are indicated in orange. ctrl - unstimulated PMΦ from wild type mice; LPS - PMΦ from wild type mice stimulated for 2 h with LPS (100 ng/ml); StDev - Standard deviation; Acc. Num. - Accession Number; ~ - no data available

The expression of 18 genes determined by real-time PCR correlated well with data obtained by array analysis (see also Table 2). In contrast, a differential expression of less than 2-fold was detected for Mac-1α, fibronectin and α-glucosidase II α subunit by real-time PCR analysis, which did not correlate with the SSH-array results. These genes were classified as non-differentially expressed genes and were excluded from further analysis.

### 4. 2. 2. The effects of GCs on the expression of LPS target genes in peritoneal macrophages from wild type and GR mutant mice

The SSH approach, substantiated by array and real-time PCR analysis, provided an initial set of 18 genes whose expression was up-regulated upon LPS stimulation. To investigate the role of GCs and the mechanism(s) of GR action on modulating the expression of these genes, PMΦ were treated with dexamethasone (1 μM dex) 1h prior to LPS stimulation (100 ng/ml; 2h). Differential gene expression was tested in PMΦ from wild type, $GR^{dim}$ and $GR^{LysCre}$ mice upon LPS and dex+LPS stimulation, using real-time quantitative PCR [79,115]. Table 4 summarises the expression patterns of 9, out of 18 LPS-inducible genes, which were strongly modulated by GCs in PMΦ from wild type mice. The expression levels of Irg-1, B94, A20 protein, γ-actin, TNFR-I, Pleckstrin, C3 α, β subunit, 65-kDa cytosolic protein and ABC1 transporter remained unchanged upon GCs administration (data not shown).

Table 4. Comparison of differential expression of LPS target genes upon GC-stimulation of PMΦ from wild type and GR mutant mice

| | | wild type | | | | | | Fold change | |
|---|---|---|---|---|---|---|---|---|---|
| **Acc. Num.** | **Gene Name** | **ctrl** | StDev | **LPS** | StDev | **dex+LPS** | StDev | ***LPS/ctrl*** | ***LPS/dex+LPS*** |
| X13987 | **CD14** | 11.58 | 0.59 | 45.51 | 1.42 | 15.43 | 0.55 | ***3.9*** | ***2.9*** |
| NM_013885 | **Clic4** | 3.03 | 2.55 | 11.16 | 2.78 | 4.60 | 1.55 | ***3.7*** | ***2.4*** |
| M94967 | **COX-2** | 0.03 | 0.02 | 14.80 | 6.34 | 2.22 | 0.99 | ***>100*** | ***6.7*** |
| G198293 | **IL-1β** | 1.93 | 3.26 | 9.56 | 4.91 | 1.83 | 1.43 | ***4.9*** | ***5.2*** |
| J03783 | **IL-6** | 0.02 | 0.02 | 9.84 | 3.01 | 2.03 | 1.10 | ***>100*** | ***4.8*** |
| X53798 | **MIP-2** | 1.01 | 0.07 | 87.93 | 29.35 | 23.92 | 3.95 | ***86.8*** | ***3.7*** |
| X16490 | **PAI-2** | 35.69 | 35.55 | 114.43 | 64.15 | 35.56 | 2.46 | ***3.2*** | ***3.2*** |
| M38296 | **TNF-α** | 0.04 | 0.02 | 17.33 | 10.09 | 1.48 | 0.71 | ***>100*** | ***11.7*** |
| AF069502 | **UBP43** | 2.30 | 1.22 | 9.67 | 1.58 | 3.88 | 0.58 | ***4.2*** | ***2.5*** |

| | | $GR^{dim}$ | | | | | | Fold change | |
|---|---|---|---|---|---|---|---|---|---|
| **Acc. Num.** | **Gene Name** | **ctrl** | StDev | **LPS** | StDev | **dex+LPS** | StDev | ***LPS/ctrl*** | ***LPS/dex+LPS*** |
| X13987 | **CD14** | 8.46 | 2.77 | 116.12 | 37.50 | 100.35 | 9.11 | ***13.7*** | ***1.2*** |
| NM_013885 | **Clic4** | 0.75 | 0.21 | 5.20 | 0.43 | 5.71 | 1.83 | ***6.9*** | ***0.9*** |
| M94967 | **COX-2** | 0.00 | 0.00 | 5.75 | 3.11 | 2.15 | 0.78 | ***>100*** | ***2.7*** |
| G198293 | **IL-1β** | 0.09 | 0.04 | 9.81 | 0.08 | 2.68 | 0.58 | ***>100*** | ***3.7*** |
| J03783 | **IL-6** | 1.07 | 0.75 | 7.41 | 2.34 | 1.75 | 0.93 | ***6.9*** | ***4.2*** |
| X53798 | **MIP-2** | 2.90 | 4.54 | 53.17 | 20.52 | 16.37 | 8.55 | ***18.3*** | ***3.2*** |
| X16490 | **PAI-2** | 3.36 | 1.65 | 90.80 | 38.67 | 99.94 | 21.80 | ***27.0*** | ***0.9*** |
| M38296 | **TNF-α** | 0.02 | 0.01 | 13.84 | 0.92 | 2.62 | 0.32 | ***>100*** | ***5.3*** |
| AF069502 | **UBP43** | 2.71 | ~ | 9.16 | ~ | 3.49 | ~ | ***3.4*** | ***2.6*** |

| | | $GR^{LysCre}$ | | | | | | Fold change | |
|---|---|---|---|---|---|---|---|---|---|
| **Acc. Num.** | **Gene Name** | **ctrl** | StDev | **LPS** | StDev | **dex+LPS** | StDev | ***LPS/ctrl*** | ***LPS/dex+LPS*** |
| X13987 | **CD14** | 18.04 | ~ | 182.11 | ~ | 275.58 | ~ | ***10.1*** | ***0.7*** |
| NM_013885 | **Clic4** | 9.11 | 2.61 | 27.95 | 2.02 | 29.39 | 2.79 | ***3.1*** | ***1.0*** |
| M94967 | **COX-2** | 0.72 | ~ | 15.50 | ~ | 17.80 | ~ | ***21.5*** | ***0.9*** |
| G198293 | **IL-1β** | 0.16 | ~ | 8.54 | ~ | 5.52 | ~ | ***53.4*** | ***1.5*** |
| J03783 | **IL-6** | 0.03 | 0.00 | 4.45 | 1.58 | 6.38 | 2.42 | ***>100*** | ***0.7*** |
| X53798 | **MIP-2** | 0.00 | ~ | 13.35 | ~ | 16.02 | ~ | ***>100*** | ***0.8*** |
| X16490 | **PAI-2** | 60.98 | ~ | 228.08 | ~ | 151.37 | ~ | ***3.7*** | ***1.5*** |
| M38296 | **TNF-α** | 0.57 | 0.03 | 21.74 | 5.87 | 28.20 | 1.40 | ***38.1*** | ***0.8*** |
| AF069502 | **UBP43** | 2.25 | 1.41 | 1.81 | 0.69 | 1.93 | 1.19 | ***0.8*** | ***0.9*** |

Quantification of relative gene expression upon LPS and dex+LPS stimulation of PMΦ was analysed using real-time PCR. Listed are those 9 genes whose mRNA expression levels were elevated by LPS and modulated by GCs by more than 2-fold. The expression intensities were quantified and normalised to HPRT expression. The fold change was calculated relative to the value from unstimulated cells (LPS / ctrl), and relative to cells stimulated with dex+LPS (LPS / dex+LPS). The data represent average values from two to three real-time PCR experiments. Values obtained by real-time PCR analysis are indicated in orange.
ctrl - unstimulated PMΦ; LPS - PMΦ stimulated for 2 h with LPS (100 ng/ml); StDev - Standard deviation; ~ - no data available

A comparison of differential gene expression in unstimulated, LPS and dex+LPS stimulated cells from wild type, $GR^{dim}$ and $GR^{LysCre}$ mice, demonstrated that the expression levels of 18 LPS-inducible genes identified in wild type PMΦ were also increased in PMΦ derived from GR mutant mice. Therefore, the cell response to LPS does not involve the activation of GR-dependent genes. Of these 18 genes, the expression of 6 (TNF-α, IL-6, IL-1β, MIP-2, COX-2 and UBP43) was down-modulated by GCs by more than 50% in cells of wild type and $GR^{dim}$ mice. In $GR^{dim}$ PMΦ, GCs exert their effects by binding to a dimerisation-defective glucocorticoid receptor, which is able to mediate gene repression by interacting with other proteins, such as NF-κB and AP-1, in a DNA-binding independent manner [79]. 3 genes (CD14, PAI-2 and Clic4) were found to be repressed in PMΦ from wild type but not but not $GR^{dim}$ mice, suggesting that they are regulated in a GR-DNA dependent manner. PMΦ from $GR^{LysCre}$ mice lack a functional GR and are therefore expected to be refractory to GCs. None of the 18 LPS-inducible genes was repressed by GCs in $GR^{LysCre}$ PMΦ, confirming that the observed effects are indeed GR-specific.

Collectively, these data illustrated the use of the SSH technique to obtain numerous transcripts which are differentially expressed in LPS-stimulated PMΦ. Some of the identified genes have already been described in the extensive literature on macrophage biology (e.g. TNF-α, IL-6) [116], whereas others such as ubiquitin binding protein (UBP43) [117] and chloride intracellular channel (Clic) 4 [118], are reported here for the first time as LPS-inducible transcripts. In addition, investigation of GCs modulatory roles on the expression of LPS inducible genes with the use of functional and cell-specific GR mutant mice provided insight into the mechanisms by which GR regulates the expression of target genes.

### 4. 2. 3. Identification of differentially expressed mRNAs by oligonucleotide gene chip analysis

Gene chip technology was used in addition to SSH, to provide a more global profiling of differential expression of a variety of genes and gene families encoding for proteins with a wide range of functions [96,110,112]. Although restricted to a number of selected genes and ESTs, a major advantage of this method is the simultaneous profiling and quantitative analysis of mRNA changes in a single hybridisation experiment.

The oligonucleotide gene chip station, provided by the company Affymetrix, Santa Clara, CA, was used to analyse expression patterns of a variety of genes upon LPS-stimulation and to explore the role of GCs in modulating their expression. The MuU74Av2 oligonucleotide gene chip, which contains 12488 oligonucleotide probe sets corresponding to more than 8000 murine genes and 4000 ESTs, was used to reveal patterns of gene expression in unstimulated, LPS stimulated (100 ng/ml; 2h) and dex+LPS stimulated PMΦ (1 μM dex added 1h prior to LPS). Cells were obtained from wild type and two mutant mouse strains, generated by gene targeting to have either impaired dimerisation function of the GR ($GR^{dim}$) [79], or to lack GR in cells of the myeloid lineage ($GR^{LysCre}$) (F. Tronche et al., unpublished).

The standard labelling protocol, suggested by Affymetrix, recommends the use of 1 μg of poly(A)$^+$RNA or 8-10 μg of total RNA, as starting material [106,112,119]. The RNA is subjected to one round of mRNA amplification by *in vitro* transcription (IVT) [119]. This method is believed to maintain the complexity and linearity (relative distribution) of the original mRNA population, and as such should be suitable to produce specific probes for high-throughput studies, and to detect differentially expressed genes [106,112]. A recently published report described a modified amplification protocol, which minimises the generation of template-independent products and generates the sufficient quantities of message-derived material [120]. By applying a second round of cDNA synthesis and *in vitro* transcription, the required starting material was reduced significantly such that quantities between 2 and 200 ng of total RNA were used [120]. This experiment recaptured very well the trends and salient features of the data set obtained using 10 μg of total RNA in standard Affymetrix protocol, with high correlation coefficients ($0.994 > r > 0.984$) [120].

Since on average 5-7 µg of total RNA was obtained from one mouse (corresponds to 1-3 x $10^6$ PMΦ), the hybridisation probes were therefore generated using 200 ng of total RNA as staring material and two rounds of IVT according to the modified amplification protocol (for details please refer to the *Material and Methods* Section).

cRNA probes generated from unstimulated, LPS and dex+LPS-stimulated PMΦ from wild type, $GR^{dim}$ and $GR^{LysCre}$ mice, were hybridised with the MuU74Av2 oligonucleotide gene chips. The array images were captured and reduced to intensity values [Average Differences (AD)] and absolute calls [Present (P) / Absent (A) / Marginal (M)] using GeneChip Software (MicroArray Suite version 4.0, Affymetrix, Santa Clara, CA). The expression level for each gene was derived from the 16 representative oligonucleotide pairs using a trimmed mean algorithm. Those genes/ESTs which were rated as present (P) by the GeneChip software (Affymetrix) and which fulfilled certain criteria were selected for further analysis.

After 2h of LPS treatment, the RNA expression levels of 327 transcripts, corresponding to 158 genes and 169 ESTs, were significantly and reproducibly elevated by more than 2-fold in PMΦ from wild type, $GR^{dim}$ and $GR^{LysCre}$ mice. The expression of 225 of these transcripts was not changed by treatment with GCs in PMΦ from wild type, $GR^{dim}$ or $GR^{LysCre}$ mice. On the other hand, the expression of 102 of the LPS-induced transcripts was modulated by GCs by more than 2-fold in wild type PMΦ. 11 genes/ESTs, out of these 102, were affected by GCs to similar extent in cells from both $GR^{dim}$ and wild type mice, indicating that GR-mediated regulation of these genes is independent of the receptor binding to DNA. 91 genes/ESTs were repressed by GCs in cells from wild type but not $GR^{dim}$ mice, indicating that these genes are modulated via a mechanism requiring GR binding to DNA. As expected, none of the GR regulated genes/ESTs identified was found to be modulated by GCs in $GR^{LysCre}$ PMΦ, confirming that GC-mediated gene regulation of LPS-induced genes/ESTs is mediated via the GR. Due to the extensive amount of data accumulated from the oligonucleotide array analysis, the complete data set on the expression levels of 327 target genes/ESTs is presented in the Appendix and is also available at web site *http://www.dkfz.de/tbi/macrophage*.

## 4. 3. CORRELATION BETWEEN SSH-ARRAY AND OLIGONUCLEOTIDE GENE CHIP DATA

Gene array approaches provided a cross-section of the diversity of macrophage genes, whose mRNA expression levels were altered at a given time point after LPS and/or dex+LPS stimulation. Several of the identified transcripts such as TNF-$\alpha$, IL-6, COX-2, IL-1$\beta$, TNFR-I, MIP-2 and Irg-1 were identified by both SSH and oligonucleotide array analysis confirming the validity of the generated data. In addition, these data showed that changes in patterns of gene expression agreed qualitatively but that there was certain quantitative variation. To ameliorate such discrepancies in order to define the expression pattern(s) of an identified target gene with high reliability, an independent verification using real-time PCR was performed. As illustrated in Table 5, quantitative disagreements were observed when the expression of TNF-$\alpha$, IL-6, MIP-2 and IL-1$\beta$ genes was measured by oligonucleotide gene chip arrays and by real-time PCR. In those cases where array and real-time PCR results were in disagreement, the later were taken as a more reliable measurement of gene expression [115]. This decision was based on experiments showing that real-time quantitative PCR is highly sensitive and reproducible method. The product synthesis and reliable quantification analysis of relative gene expression was observed in intra- (two repeats on one LightCycler run) and inter-assay (two independent runs), over six orders of magnitude under a satisfactory test linearity ($0.98 < r < 1.00$). Finally, expression of 2 of these questionable genes was further substantiated by RNase protection assays (data not shown).

Table 5. Correlation of mRNA expression patterns

| | | wild type | | | Fold change | | GR dim | | | Fold change | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Acc. Num. | Gene Name | ctrl | LPS | dex+LPS | LPS/ctrl | LPS/dex+LPS | ctrl | LPS | dex+LPS | LPS/ctrl | LPS/dex+LPS |
| G198293 | IL-1β | 3460.40 | 50949.70 | | 14.7 | | | | | | |
| | | 3565.65 | 86212.00 | 50256.95 | 24.2 | 1.7 | 8497.60 | 83023.03 | 73836.73 | 9.8 | 1.1 |
| | | 1.93 | 9.56 | 1.83 | 5.0 | 5.2 | 0.09 | 9.81 | 2.68 | >100 | 3.7 |
| | | | | | | | | | | | |
| J03783 | IL-6 | 460.30 | 5930.50 | | 12.9 | | | | | | |
| | | 69.10 | 27738.90 | 9667.75 | >100 | 2.9 | 65.77 | 18572.87 | 13893.30 | >100 | 1.3 |
| | | 0.02 | 9.84 | 2.03 | >100 | 4.8 | 1.07 | 7.41 | 1.75 | 6.9 | 4.2 |
| | | | | | | | | | | | |
| X53798 | MIP-2 | 1061.90 | 3399.50 | | 3.2 | | | | | | |
| | | 5567.70 | 48481.60 | 35722.00 | 8.7 | 1.4 | 5074.97 | 40017.53 | 40120.00 | 7.9 | 1.0 |
| | | 4.26 | 92.45 | 23.92 | 21.7 | 3.9 | 2.90 | 53.17 | 16.37 | 18.3 | 3.2 |
| | | | | | | | | | | | |
| M38296 | TNF-α | 382.27 | 3338.57 | | 8.7 | | | | | | |
| | | 682.05 | 67676.55 | 27160.20 | 99.2 | 2.5 | 989.43 | 63700.63 | 37811.60 | 64.4 | 1.7 |
| | | 0.04 | 17.33 | 1.48 | >100 | 11.7 | 0.02 | 13.84 | 2.62 | >100 | 5.3 |

The cDNA expression patterns of cognate mRNAs are listed in the expression columns extracted from the respective databases. Differential gene expression indicated as fold change is given as measured by SSH- (yellow), oligonucleotide gene array analysis (green) and real-time PCR (orange). Discrepancies in gene expression detected by the different methods are indicated in blue.
ctrl - unstimulated PMΦ; LPS - PMΦ stimulated for 2 h with LPS (100 ng/ml); dex+LPS - PMΦ stimulated 1h with dex (1µM) prior to LPS (100 ng/ml; 2 h); Acc. Num. - Accession Number

All together, these results suggest that the semiquantitative array techniques can reliably detect trends in altered gene expression but may over or underestimate the magnitude of these changes. This limitation may not be only due to the method used to estimate gene expression but also due to alternative splice isoforms or closely related genes that give different measurements depending on the sequences (i.e. oligonucleotide) used to represent a gene. Parameters that may contribute to disconcordance between array and real-time PCR results are summarised in Table 6.

Table 6. Potential sources of discrepancies between arrays and real-time PCR data

| | SSH-arrays | Oligonucleotide gene chip | Real-time quantitative PCR |
|---|---|---|---|
| *Gene Representation* | cDNA/PCR fagment;<br>>300 bp in size;<br>*Rsa*I fragments can derive from any part of a gene;<br>Neither 3' nor 5' biased | Oligonucleotide probe pairs;<br>16 oligonucleotide pairs (PM/MM);<br>3'-UTR biased | Gene-specific primer pairs can be designed from any selected part of a gene;<br>Usual primer length: 18-22 nt;<br>Additional primers can be included to cover other regions of a gene;<br>Gene specificity can be achieved by blasting primer sequences |
| *Starting material:* | 100 ng of mRNA | 200 ng of total RNA | first-strand cDNA<br>(RT using 0.5-2 µg of total RNA) |
| *RNA amplification:* | none | T7 RNA amplification<br>1. two rounds of IVT amplification<br>2. shortening of the 5'-region of template during IVT, due to use of random hexamers<br>3. fragments are proned to overamplification (preferential amplification of short fragments) | none |
| *Labelling method:* | radioactive<br>(reverse transcription performed using $\alpha^{32}$P-ATP) | fluorescent<br>biotin labelling during the last IVT using 11-bio-NTP) | fluorescent<br>(SYBR Green I dye) |
| *Detection method:* | hybridisation of nylon membranes;<br>correlation cofficient < 0.947 | hybridisation of glass slide arrays;<br>correlation cofficient < 0.998 | PCR amplification;<br>0.98 < correlation cofficient < 1.0 |
| | the signal might derive from a highly homologue gene or splice variant | | |
| *Background subtraction:* | AIS and MATLAB software | Microarray Suite Genechip software vs. 4.0 | none |
| *Normalisation:* | set of house-keeping genes or 'selected' NC genes | spike-in controls<br>(defined by manufacturer) | usually one house- keeping gene |
| *Data mining:* | MATLAB; Excel | Microarray Suite Genechip software; Excel | LightCycler SDM-method (Roche) |

Table illustrates some major differences between arrays (SSH- and oligounucleotide gene chip) and real-time PCR analysis. Several steps that may contribute to disagreement of data are described. For experimental details, please refer to the *Material and Methods* Section; NC - not changed; RT - reverse transcription; IVT - *in vitro* transcription; SDM - Second Derivative Maximum

## 4. 4. PATTERNS OF GENE EXPRESSION; MOLECULAR MECHANISMS OF GR ACTION

To obtain a broad range of information on the response of PMΦ to LPS stimulation and modulatory role of GCs on this process, SSH and oligonucleotide gene chip techniques were used in the current study. The results which identified differential expression of numerous genes/ESTs in response to LPS suggested that the macrophage's transcriptional machinery undergoes a massive change following this stimulation. Specifically, the expression of 350 Genes/ESTs were found to be modulated by LPS by more than 2-fold. These transcripts were classified into Group 1 (204 genes/ESTs) and Group 2 (146 genes/ESTs), according to whether LPS caused an increase or decrease of gene/EST expression, respectively (Table 7). Similar patterns of gene expressions were also observed in $GR^{dim}$ and $GR^{LysCre}$ PMΦ. Of these 350 LPS-regulated genes/ESTs, 244 (69.7 %) did not respond to GC treatment [Fold change (LPS/dex+LPS) less than 2-fold]. These genes/ESTs are classified into Group 1-A and 2-A (Table 7, Figure 8). Upon LPS-stimulation, the expression level of the 140 gene/ESTs belonging to Group 1-A, was increased by several fold by LPS and was unaffected by treatment with dex+LPS, in PMΦ from wild type, $GR^{dim}$ and $GR^{LysCre\ mice}$ (Table 7, Figure 8). Expression level of the 104 genes/ESTs belonging to Group 2-A, where decreased by LPS stimulation.

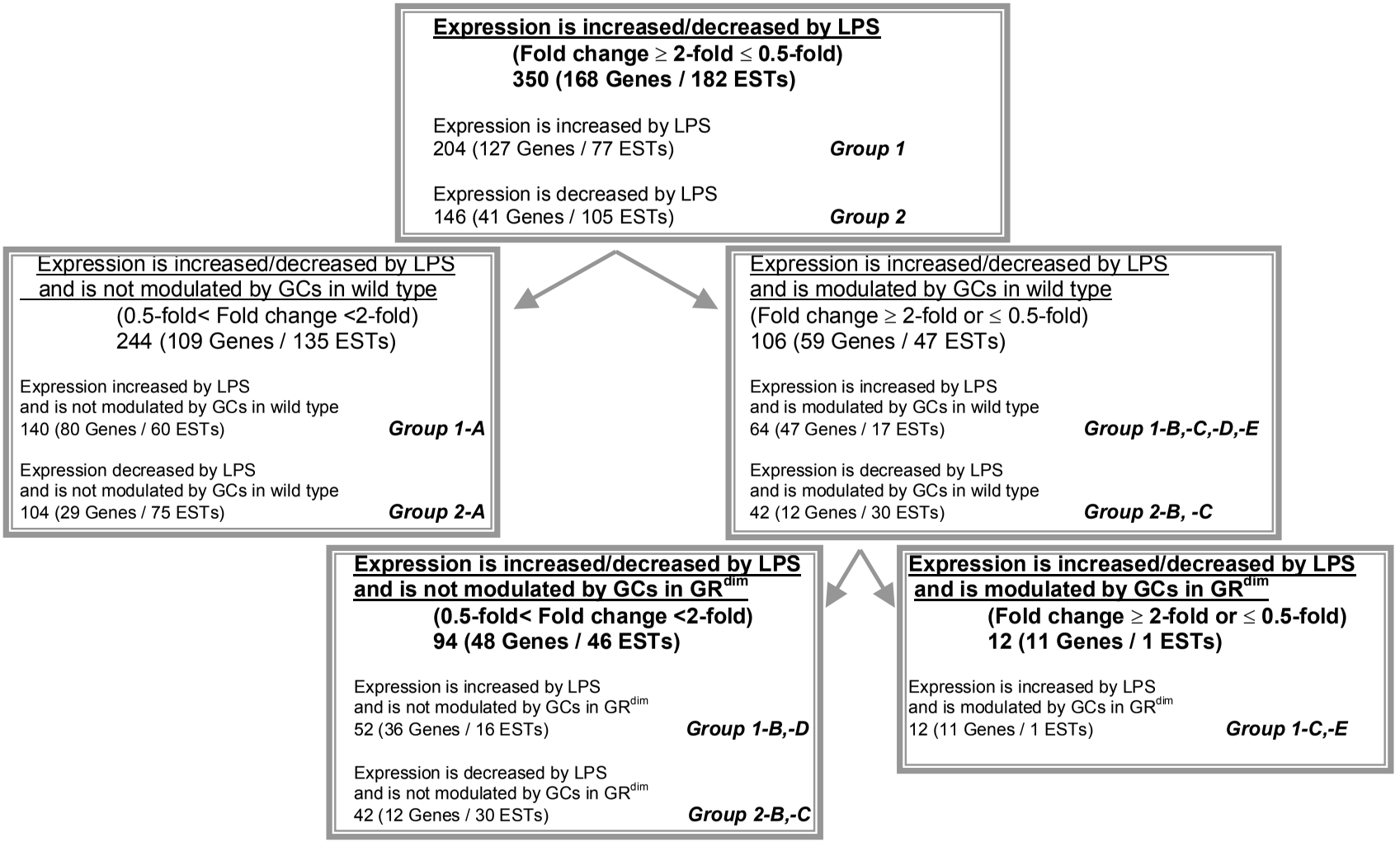
Of the identified LPS target genes/ESTs, 106 (30.3%) were regulated by GCs, since their expression levels were either down- or up-regulated by dex+LPS treatment of PMΦ obtained from wild type animals (Fold change=LPS/dex+LPS is $\geq$ 2-fold or $\leq$ 0.5-fold) (Table 7). It was expected that the expression of some genes/ESTs, upon LPS or dex+LPS stimulation, would follow similar patterns (trends) in wild type and in $GR^{dim}$ PMΦ. This would support a mechanism of GR action independent of its binding to DNA, where GR interacts with other transcription factors (or proteins) to regulate gene transcription. Some genes/ESTs while regulated by GCs in cells from wild type mice may not be regulated in PMΦ from $GR^{dim}$ mice. These genes would require an interaction of GR with DNA to be modulated by GCs.

Based on this, 6 additional subgroups can be distinguished according to the molecular mechanisms by which GR mediates repression/induction of LPS target genes/ESTs, as illustrated in Figure 8:

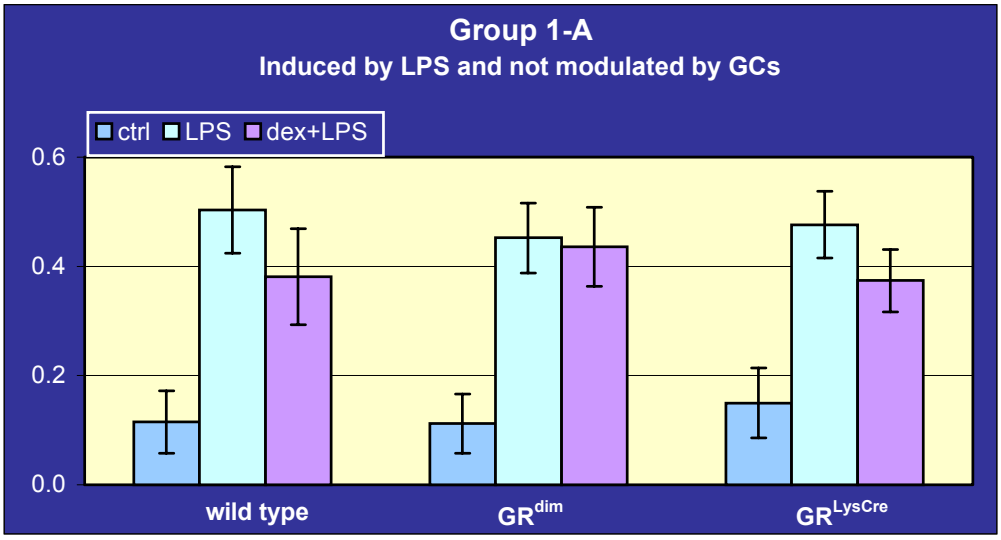
- Group 1-B and Group 2-C, consist of 47 and 4 genes/ESTs, respectively, which are repressed upon GCs in wild type but not in $GR^{dim}$ mice, indicating that GR acts in a DNA-binding dependent manner.
- Group 1-C represents 10 genes/ESTs which were repressed by the GR in cells from wild type and in $GR^{dim}$ mice. These genes thus require DNA-binding independent action of the GR for their regulation.
- Group 1-D and Group 2-B represent 5 and 38 genes/ESTs, respectively, whose expression was further increased by dex+LPS treatment compared to LPS alone. In this case, GR acts in a DNA-binding dependent fashion, since induction in gene expression was observed only in cells from wild type but not $GR^{dim}$ mice.
- Group 1-E consists of only 2 genes. The expression of these genes was increased by GCs in PMΦ from wild type and $GR^{dim}$ mice indicating that GR acts in a DNA-binding independent fashion.

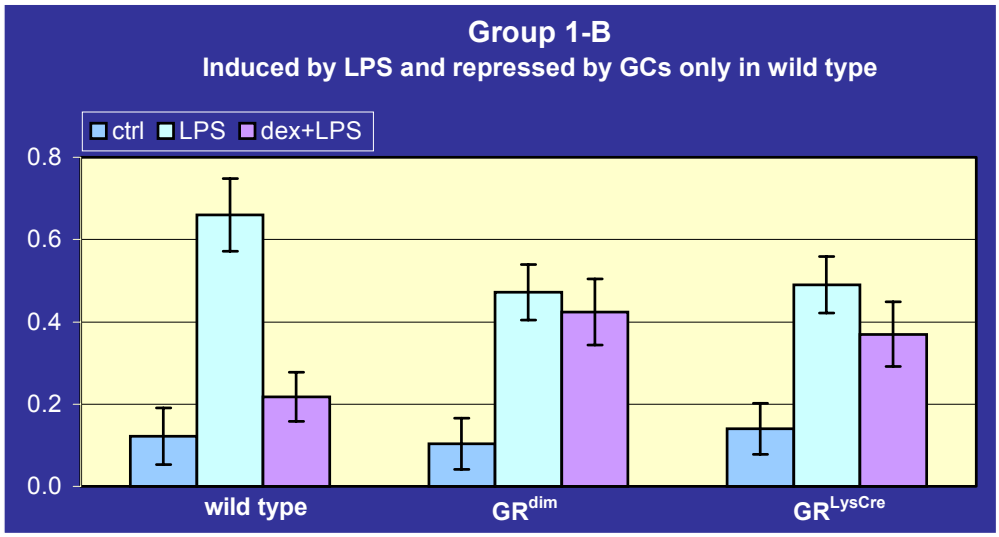
In total, 182 ESTs have been identified by SSH and oligonucleotide gene chips analysis as being significantly modulated by LPS and by GCs, which did not match any gene name in the public databases. This is only an approximate estimate of the number of novel genes found because a fraction of the mRNAs for known genes still have poor 5' representation and even uncharacterised 3' untranslated region. It could be, in some cases that those identified ESTs represent, or belong to, the same gene(s), the question that will be finally solved when more complete sequences are obtained. In any case, their presence indicates that a substantial fraction of the regulatory or functional circuitry of macrophages remains unexplored and that valuable tools for their investigation will emerge from a combination of RNA expression studies and analysis of genomic sequences.

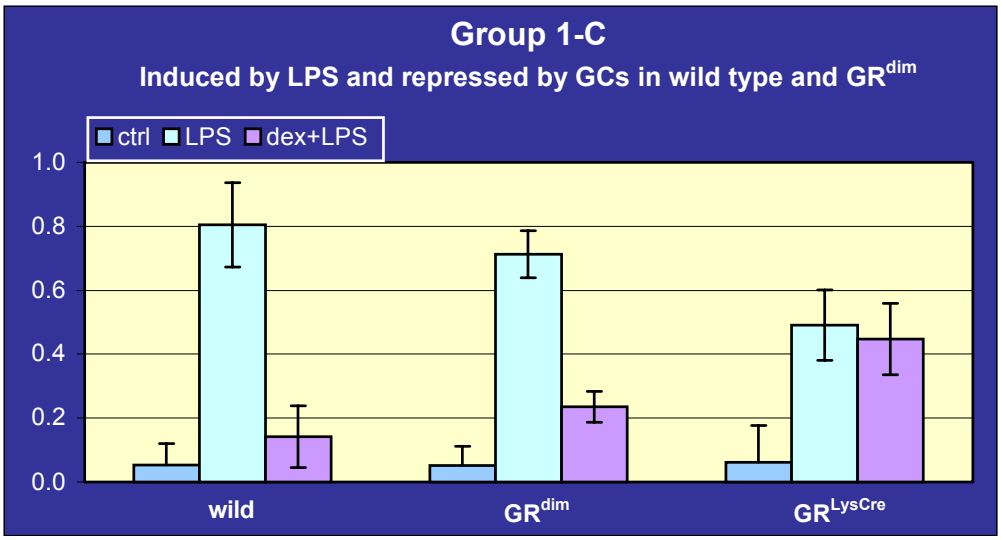
Table 7.Expression patterns of genes/ESTs identified by SSH and oligonucleotide gene chip array analysis

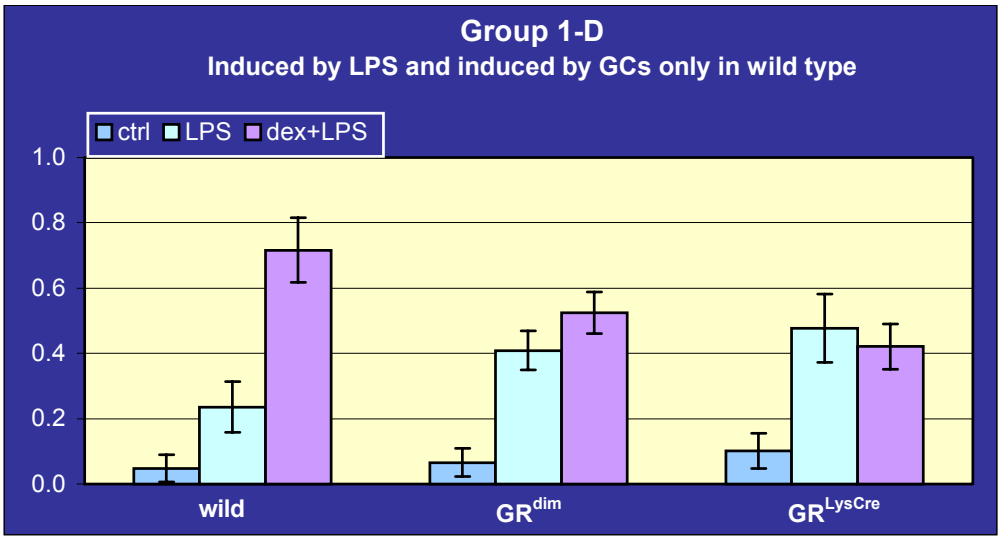


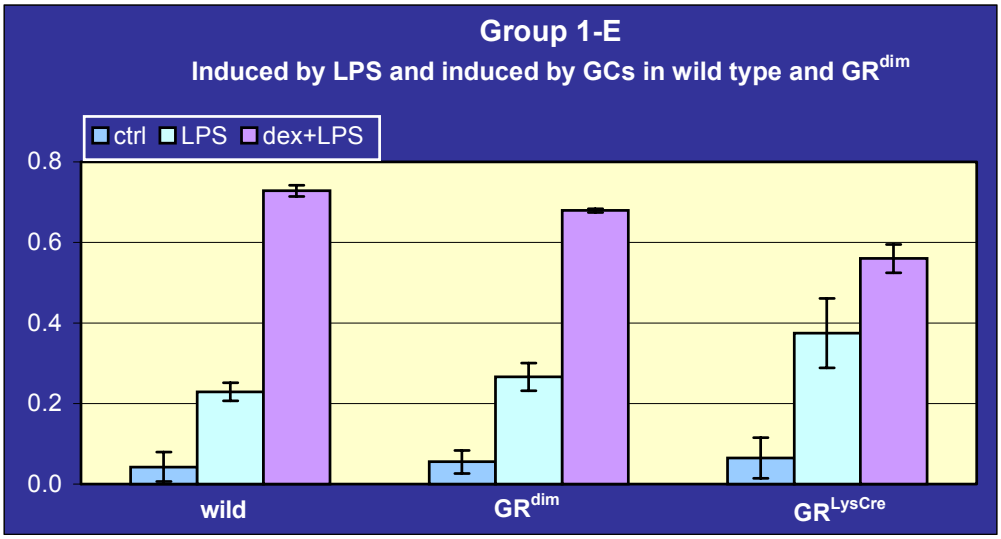

Shown is the total number of genes and ESTs, which were identified by SSH- and oligonucleotide gene chip array analysis. The expression data sets from all 350 genes/ESTs belonging to Group 1 and 2 and the respective subgroups are shown in the Appendix and are available at *http://www.dkfz.de/tbi/macrophage*

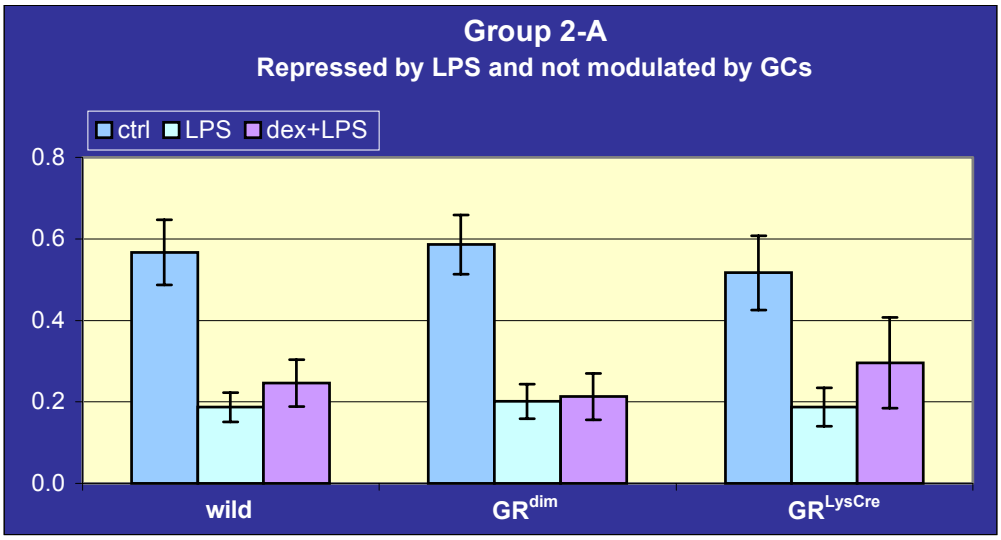

Group 1-A
Induced by LPS and not modulated by GCs
ctrl
LPS
dex+LPS
0.6
0.4
0.2
0.0
wild type
GR^dim
GR^LysCre


Group 1-B
Induced by LPS and repressed by GCs only in wild type
ctrl
LPS
dex+LPS
0.8
0.6
0.4
0.2
0.0
wild type
GR^dim
GR^LysCre


Group 1-C
Induced by LPS and repressed by GCs in wild type and GR^dim
ctrl
LPS
dex+LPS
1.0
0.8
0.6
0.4
0.2
0.0
wild
GR^dim
GR^LysCre


Group 1-D
Induced by LPS and induced by GCs only in wild type
ctrl
LPS
dex+LPS
1.0
0.8
0.6
0.4
0.2
0.0
wild
GR^dim
GR^LysCre


Group 1-E
Induced by LPS and induced by GCs in wild type and GR^dim
ctrl
LPS
dex+LPS
0.8
0.6
0.4
0.2
0.0
wild
GR^dim
GR^LysCre


Group 2-A
Repressed by LPS and not modulated by GCs
ctrl
LPS
dex+LPS
0.8
0.6
0.4
0.2
0.0
wild
GR^dim
GR^LysCre

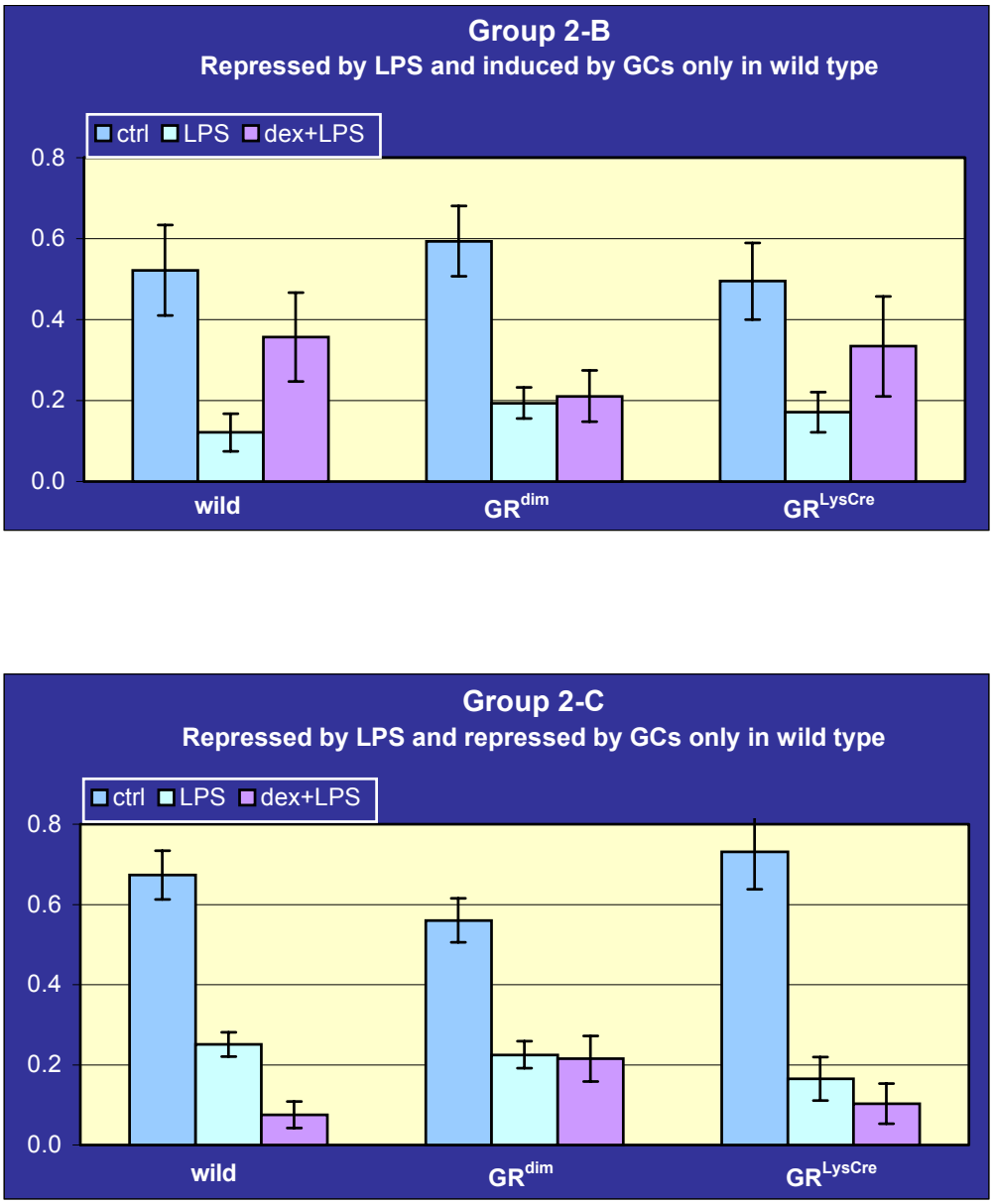



Figure 8. The mechanism of GR action in the regulation of expression of LPS target genes/ESTs in PMΦ from wild type and GR mutant mice

Genes are grouped according to the mechanism by which GR modulates their expression. A graphical illustration of expression patterns of genes/ESTs comprising Group 1-A, -B, -C, -D, -E, 2-A, -B, -C, is shown in the form of a histogram with explanation given in the text. The method used to represent the expression profile of each group and the measured expression levels of genes/ESTs are shown in detail in the Appendix and at *http://www.dkfz.de/tbi/macrophage.*

## 4. 5. CONSTRUCTING A DATABASE FOR mRNA CHANGES IN PERITONEAL MACROPHAGES DURING STIMULATION WITH LPS AND GCs

From the obtained results, an in-house database (available at *http://www.dkfz.de/tbi/macrophage*) was constructed that includes 3 interlinked subdatabases for collecting gene information from SSH, oligonucleotide gene chip arrays and real-time PCR. The linkage between subdatabases was established by GenBank accession numbers. This database was developed to provide a reference for later research on PMΦ response to LPS and GCs. It contains an in-depth pattern analysis of gene expression in PMΦ from wild type, $GR^{dim}$ and $GR^{LysCre}$ mice and includes not only genes/ESTs represented in public databases but also novel transcripts revealed by this study.

# 5. DISCUSSION

## 5. 1. CRITICAL ASPECTS ON TECHNIQUES TO MONITOR GENE EXPRESSION

The recently developed technique of SSH has allowed cloning and isolation of cDNAs that are differentially expressed between two RNA populations being compared [92,101]. The study described here showed, in accordance with others, that the SSH technique is a relatively simple and efficient method for generating differentially expressed genes/ESTs. The relative difference in gene expression apparently did not impact whether a gene is recovered by SSH. In a mixed population of differentially expressed genes, in which some differ by few-fold and others by several orders of magnitude, both low and highly expressed genes were equally amplified with no obvious preference for the later genes. For example, IL-6 [121], TNF-$\alpha$ [116] and MIP-2 [122] showed fold change in expression of more than 100, whereas CD14 [12] expression changed by just 4-fold. 2 SSH-fragments from the subtracted library were found to correspond to the IL-6 and MIP-2 genes, whereas TNF-$\alpha$ and CD14 were represented by 10 and 4 SSH-fragments, respectively. Furthermore, fragments from high (e.g. Irg1, PAI-2 gene [123,124]) and low abundant transcripts (e.g. UBP43 [117,125], MIP-2 [122]) were isolated, demonstrating that the absolute expression level was not a crucial determinant for identifying genes.

However, there are some limitations inherent to SSH. As with all subtractive approaches, only two samples can be compared at a time (e.g. LPS-stimulated versus non-stimulated cells). Furthermore, two micrograms of poly(A)$^+$ RNA from both cell populations are needed in the analysis. Depending on the source of RNA, this amount may be difficult to obtain, as with PM$\Phi$ in

which only 5-7 µg of total RNA was obtained per mouse. To circumvent this problem, a technique capable of amplifying small amounts of mRNA, without significantly distorting the information content of both *driver* and *tester* cDNAs, could be incorporated to generate sufficient quantities of both cDNA samples [126]. Finally, each SSH experiment leads to the recovery of distinct number of cDNAs, which likely represent a subset of all the differentially expressed genes.

Whereas the generation of a subtracted library can be accomplished rather quick, identification and characterisation of enriched transcripts along with their quantitative expression analysis, is much more time-consuming. In order to profile the expression of enriched genes/ESTs simultaneously, inserts from SSH clones were arrayed onto nylon membranes and their expression measured by hybridisation. Surprisingly, this analysis revealed only 25% of all processed SSH sequences as differentially expressed upon LPS stimulation of PMΦ. The remaining 75%, which showed no differential expression, were thus considered as 'false-positive' genes/ESTs.

On the other hand, nylon- and glass slide- based arrays have become the preferred tool for rapid determination of gene expression as they allow simultaneous profiling of differential expression of numerous genes in a single hybridisation experiment [95,102,105,109]. However, the array methods already faced some limitations in particular for the quantification of differential expression of low abundant mRNAs. Since, low abundant mRNAs usually give a signal close to background level, the calculated ratios for these genes tend to be high and thus not a reliable indicator of differential gene expression [127]. On the basis of this considerations, an independent method for quantification of gene expression (such as by real-time quantitative PCR) should be included in order to evaluate and more reliably quantify level(s) of differential gene(s) expression [115]. In addition to this, certain improvements in array manufacturing, hybridisation conditions, signal-to-noise ratio and refinements in statistical analysis of the data, are all expected to enhance the ability to consistently and more accurately quantify levels of gene expression and to accelerate data mining.

## 5. 2. BEYOND GENE EXPRESSION PROFILING

Following the simultaneous analysis of several hundreds or thousand genes at the mRNA level, the challenge becomes how to efficiently utilise this information to provide insights into an investigating process(es). The advantage of characterised genes for which reagents such as antibodies, cell lines, and knockout mice are available gives the possibility for testing plausible hypotheses generated from the data. Some applications of transcript profiling include, among others, gene promoter analysis, sequence and structure characterisation of novel ESTs, RNA interference (siRNA), and finally, development of certain animal models where changes in gene expression can be recorded and compounds to modulate their expression considered and tested. Information collected from combined multiple gene expression profiling approaches can be used to prepare 'custom chips' which contain selected genes/EST, that can be probed with RNAs from different tissues. Furthermore, sequences of unknown ESTs and genes identified here suffice to clone their cDNAs, and some of these gene products may be useful as pharmaceutical targets for novel intervention therapies.

Further more, the findings of this study are based on changes in mRNA expression levels which do not necessarily correspond to changes in protein levels. There are several reports in the literature where differences between mRNA and protein levels appear to be substantially larger than initially assumed [16,128,129]. Possible causes include differential expression of certain mRNAs at various stages of cell growth and differentiation *in vitro*, translation regulation, post-translation protein modification and selective degradation or excretion of proteins *in vivo*. Differences observed between gene expression and protein abundance suggest that selective post-transcriptional controls may be as important as changes in mRNA levels. At present, post-transcriptional control is less well explored than transcriptional control [16,128,129]. Therefore, novel high-throughput strategies, equipment and bioinformatical tools should be developed to make such systematic, global and quantitative analysis feasible in order to fully pursue the biological relevance of generated data.

## 5. 3. SIGNATURES OF INFLAMMATION

The combination of gene expression profiling approaches with the use of function- and tissue-specific mouse mutants, suggested that the macrophage's transcriptional program undergoes a massive change during activation by LPS and highlighted the myriad of ways in which cells attempt to control inflammation. As hypothesised here, LPS, as a structural component of all Gram-negative bacteria, should play a principal role in stimulating the early innate response of macrophages [6,85]. A few recent studies have compared changes in host gene expression caused by virulent bacteria and purified LPS [88,130]. These reports showed a remarkable degree of overlap between genes induced by virulent bacteria and purified LPS, suggesting that there is a redundancy in host response. This supports the concept that different bacterial inputs can initiate a conserved program of macrophage responses. Comparison of changes in gene expression in PMΦ activated by LPS, with those obtained using other cells of innate and/or acquired immunity, and different bacterial structural components, will likely reveal a conserved host gene expression profile that serves as a common signature of inflammation and infection.

## 5. 4. THE CONSEQUENCES OF LPS ACTIVATION OF PERITONEAL MACROPHAGES AND THE MODULATORY ROLE OF GCs

Comparison between resting and LPS-stimulated macrophages revealed comprehensive LPS-inducible gene expression profile. This data provides molecular evidence that, upon stimulation with LPS, macrophages will reprioritise their gene expression away from normal physiology towards establishing an anti-inflammatory state. In addition to the beneficial effects of such a response, the activation of host-derived inflammatory mediators can also account for the deleterious pathophysiologic state [31].

The insights gained from the current gene expression analysis suggest that upon LPS stimulation, macrophages enhance transcription of genes involved in a variety of cell processes, from cell-cell communication, immune and stress response, chemotactic migration, and controlled cell death (Table 8). The release of proinflammatory and antibacterial mediators (interleukins, macrophage inflammatory proteins, complement components, small inducible cytokines), represents only a subset of the potential stimulatory loops created when a macrophage population is stimulated with LPS [85]. Other products act back upon the macrophages themselves to regulate the late LPS response and include end products of both the cyclooxygenase and lipoxygenase pathways of arachidonic acid (COX-2, prostaglandin E synthase, cholesterol hydroxylase), growth and differentiation factors (G-CSF, M-CSF, GM-CSF), in addition to surface expression of macrophage receptors and other markers (CD14, TNFR-I, dystroglycan, R13 adenosine receptor, G-protein coupled receptor TDAG8, CCR1, CCR5) [85]. Activation of macrophages is deleterious only at the extremes and normally forms part of the protective immune response. However, the possibility that small changes in the levels or ratios of some transcription factors, receptors, cytokines and other identified genes could produce marked changes, potentially limits the significance of generated data and their relevance in certain (patho)physiological states.

Table 8. Clustering of gene expression patterns according to common involvement in biological processes

Genes for which information on protein function and role in biological processes was available from MJD, SwissProt (available at *http:// www.expasy.ch*), GeneNest (available at *http://www.dkfz.de/tbi/services/GeneNest/index*) and Gene Ontology databases were sorted by GeneOntology clustering algorhytm. This analysis was done with the use of scripts written in the Perl programming language (available at *http://www.perl.com/*) and the Sequence Retrieval System, SRS (Tim Beißbarth, personal communication).
Main biological processes are indicated with the respective clusters titled in dark blue. Genes whose expression was modulated only by LPS (increased/decreased) are shown in black (see also Group 1-A and 2-A in Figure 8). Genes modulated by LPS and further by GCs are indicated depending on the mechanism of GR action. Those which are modulated by GR in a DNA-binding dependent fashion, i.e. not regulated in $GR^{dim}$ PMΦ, are shown in blue (see also Group 1-B, 1-D, 2-B, 2-C in Figure 8), whereas those employing DNA-binding independent action of GR, i.e. genes which are affected in $GR^{dim}$ and in wild type PMΦ, are shown in red (see also Group 1-C, 1-E in Figure 8).
Due to the extensive amount of data generated, genes are represented in clusters by Gene Name and Accession Number only. A detailed gene expression analysis is available in the Appendix and at *http://www.dkfz.de/tbi/macrophage* site.

**A.**

| | Cell-to-Cell Signalling |
|---|---|
| | **Cell Communication and Cell Adhesion** |
| ***Acc. Num*** | ***Gene Name*** |
| M26071 | Coagulation factor III |
| M63801 | Connexin 43 (alpha-1 gap junction) |
| D10475 | Epimorphin |
| M90551 | Intercellular adhesion molecule |
| L07508 | Mouse Golli-mpb (alternate transcript from clone BG21) |
| M33960 | Mouse plasminogen activator inhibitor (PAI-1) |
| X62700 | muPAR1 |
| X16490 | PAI-2 |
| D89571 | Ryudocan core protein |
| M84487 | Vascular cell adhesion molecule 1 |
| | **Extracellular Signalling Receptors** |
| X13987 | CD14 gene |
| U43512 | Dystroglycan 1 |
| X69619 | Inhibin β-A |
| U14135 | Integrin α V (Cd51) |
| L32838 | Interleukin 1 receptor antagonist (IL-1rn) gene |
| M83312 | Tumor necrosis factor receptor superfamily, member 5 |
| | **G-protein Coupled Receptor Protein Signaling** |
| AI644801 | Adora2a gene, exon 1 (and joined CDS) |
| U77630 | Adrenomedullin |
| U05673 | Balb/C clone R13 adenosine receptor subtype |
| U67187 | G protein signaling regulator RGS2 (rgs2) |
| U39827 | Putative G protein-coupled receptor TDAG8 (TDAG8) |

**B.**

| | **Cell Growth and Maintenance** |
|---|---|
| ***Acc. Num*** | ***Gene Name*** |
| M13926 | Colony stimulating factor, granulocyte |
| J04103 | E26 avian leukemia oncogene 2, 3 domain |
| V00727 | FBJ osteosarcoma oncogene |
| X03020 | Granulocyte-macrophage colony stimulating factor (GM-CSF) |
| X57687 | LYL gene (clone L6) |
| AI852608 | RNA 3'-terminal phosphate cyclase-like protein (rcl1 gene) |
| U10531 | Ski/sno related |
| | **Cell Cycle** |
| U00937 | GADD45 protein (gadd45) gene |
| X61940 | Growth factor-inducible immediate early gene (3CH134) |
| | **Cytoskeleton** |
| M21495 | Cytoplasmic γ-actin gene |
| L00919 | Erythrocyte protein band 4.1 |

**C.**

| | **Cell Motility / Chemotaxis** |
|---|---|
| ***Acc. Num*** | ***Gene Name*** |
| AF022990 | CC chemokine receptor-5 (CCR5) gene |
| U29678 | Chemokine (C-C) receptor 1 |
| J04596 | GRO1 oncogene |
| J04491 | Macrophage inflammatory protein (MIP-1α) |
| X53798 | Macrophage inflammatory protein 2 (small inducible cytokine A3) |
| M35590 | Macrophage inflammatory protein (MIP-1β) |
| M19681 | Small inducible cytokine A2 ( PDGF-inducible protein) |
| U27267 | Small inducible cytokine B subfamily, member 5 |

**D.**

| Immune Resoponse | |
|---|---|
| ***Acc. Num*** | ***Gene Name*** |
| L41352 | Amphiregulin |
| K02782 | Complement component C3 α, β subunit |
| X56602 | Interferon-induced 15-KDa |
| M86672 | Interleukin 12α |
| M14639 | Interleukin 1α |
| M15131 | Interleukin 1β |
| J03783 | Interleukin 6 |
| AV152244 | ISG15 gene |

**E.**

| Cell Death - Apoptosis | |
|---|---|
| ***Acc. Num*** | ***Gene Name*** |
| U19463 | A20 zinc-finger protein |
| U75506 | BH3 interacting domain death agonist |
| U23778 | Hematopoietic-specific early-response A1-b protein (A1b) gene |
| U23778 | Hematopoietic-specific early-response A1-d protein (A1d) gene |
| M59378 | Murine tumor necrosis factor I receptor (TNFR-I) |
| X87128 | p75 TNF receptor DNA |
| U44088 | TDAG51 (TDAG51) |
| D86344 | Topoisomerase-inhibitor suppressed |
| L15435 | Tumor necrosis factor (ligand) superfamily, member 9 |
| D84196 | Tumor necrosis factor alpha (TNF-α) |

| F. | |
|---|---|
| | |
| | **Intracellular Signal Transduction** |
| ***Acc. Num*** | ***Gene Name*** |
| M28489 | (clone Mu6a) ribosomal protein S6 kinase (rsk) |
| D37837 | 65-kDa macrophage cytosolic protein |
| U20159 | 76 kDa tyrosine phosphoprotein SLP-76 |
| AJ242778 | ABINl, (A20-binding inhibitor of NF-kappa B activation, large) |
| L03290 | Amino acid transporter, cationic 2 (low affinity) |
| AJ130975 | Ariadne-2 protein |
| AI844806 | Borg4 |
| AF076156 | Catechol-O-methyltransferase |
| NM_013885 | Chloride intracellular channel 4 (mitochondrial) (Clic4) |
| U53455 | Chloride ion current inducer protein (CLCI) |
| X78445 | Cyp1-β-1 cytochrome P450 |
| X55663 | Cytoplasmic tyrosine kinase, Dscr28C related (Drosophila) |
| U78818 | Downstream of tyrosine kinase 1 |
| X70764 | ELKL motif kinase |
| X14961 | Fatty acid binding protein heart 1 |
| Z29532 | Follistatin |
| U10551 | GTP binding protein (gene overexpressed in skeletal muscle) |
| L07924 | Guanine nucleotide dissociation stimulator for a ras-related GTPase |
| M98036 | Guanine nucleotide exchange factor delta subunit (JGR1A) |
| AW122990 | Hagoromo |
| AI642048 | I-kappaB α chain |
| U19799 | I-kappaB β chain |
| AF042487 | Intermediate conductance potassium channel mIK1 |
| L16956 | Janus kinase 2 |
| X66473 | Matrix metalloproteinase 1 |
| X61399 | Mouse F52 novel protein |
| M73696 | Murine Glvr-1 |
| X54149 | Myeloid differentiation primary response gene 118 |
| AF073882 | Myotubularin related protein 7 |
| X86000 | N-glycan alpha 2,8-sialyltransferase |
| D83484 | Protein tyrosine phosphatase epsilon |
| AW047476 | Putative purine nucleotide binding protein |
| M22998 | Solute carrier family 2 (facilitated glucose transporter), member 1 |
| U88328 | Suppressor of cytokine signalling-3 (SOCS-3) |
| L35302 | Tnf receptor-associated factor 1 (TRAF-1) |
| D78141 | Tnf receptor-associated factor 5 (TRAF-5) |
| U59864 | TRAF-interacting protein (I-TRAF) |
| AF069502 | Ubiquitin specific protease UBP43 |

## G.

| Nuclear Control of Cellular Activation | |
|---|---|
| ***Acc. Num*** | ***Gene Name*** |
| M61909 | Avian reticuloendotheliosis viral (v-rel) oncogene homolog A |
| U08185 | B lymphocyte induced maturation protein |
| AF017085 | BAP-135 homolog (Diws1t) |
| M62362 | CCAAT/enhancer binding protein (C/EBP), α |
| M28845 | Early growth response 1 |
| AA182189 | Ets-protein Spi-C |
| AF017128 | Fos-like antigen 1 |
| M32489 | Interferon concensus sequence binding protein |
| D43643 | Mouse YL-1 YL-1 protein (nuclear protein with DNA-binding ability) |
| L36829 | Mus musculus a A-crystallin-binding protein I (a A-CRYBP1) gene |
| AB028921 | NAKAP95 |
| AW047899 | NF-kappa B subunit p100, alternative splice products |
| M57999 | NF-kappa B light chain gene enhancer in B-cells 1, p105 |
| U20735 | transcription factor junB (junB) gene |
| X62940 | Transforming growth factor beta 1 induced transcript 4 |
| X14678 | Zinc finger protein 36 |

**H.**

| | Cell Energetics |
|---|---|
| | **Protein Metabolism** |
| ***Acc. Num*** | ***Gene Name*** |
| L09737 | GTP cyclohydrolase 1 |
| M60474 | Myristoylated alanine rich protein kinase C substrate |
| U05245 | T-cell lymphoma invasion and metastasis 1 |
| | **Lipid Metabolism** |
| M62766 | 3-hydroxy-3-methylglutaryl-coenzyme A reductase |
| AF059213 | Cholesterol 25-hydroxylase |
| M94967 | Cyclooxygenase 2 |
| U35233 | Endothelin 1 |
| U11680 | Glycerol-3-phosphate acyltransferase gene |
| X57437 | Histidine decarboxylase cluster |
| AB033887 | mACS4 variant2 Acyl-CoA synthetase 4 variant2 |
| AI060798 | PGES prostaglandin E synthase |
| M34141 | Prostaglandin-endoperoxide synthase 1 |
| M26270 | Stearoyl-coenzyme A desaturase 2 |
| AI854821 | U8 |
| | **Carbohydrate Metabolism** |
| M96265 | Galactose-1-phosphate uridyl transferase (GALT) |
| Y11666 | Gene encoding hexokinase II, exon 1 (and joined CDS) |
| X04725 | Insulin I |
| X13586 | Murine 2,3-bisphosphoglycerate mutase |
| AI853802 | Phosphofructokinase-1 C isozyme |
| Z14132 | Sphingomyelin phosphodiesterase 1, acid lysosomal |
| | **Nucleobase, Nucleoside and Nucleotide Metabolism** |
| U22262 | Apolipoprotein B editing complex 1 |
| D44464 | Uridine phosphorylase |
| U27398 | Xeroderma pigmentosum, complementation group C |

## I.

| NON-CLASSIFIED GENES | |
|---|---|
| ***Acc. Num*** | ***Gene Name*** |
| X75926 | ABC1 transporter transmembrane protein |
| X82786 | Antigen identified by monoclonal antibody Ki 67 |
| AF02915 | Antigen identified by monoclonal antibody MRC OX-2 |
| M64292 | B-cell translocation gene 2, anti-proliferative |
| D85785 | Brain immunological-like with tyrosine-based motifs |
| D89613 | Cytokine inducible SH2-containing protein |
| U86137 | Cytokine inducible SH2-containing protein 7 |
| AB001990 | Dcra |
| D30782 | Epiregulin |
| AI845886 | eRF1 |
| X67644 | gly96 |
| U05265 | Glycoprotein 49 B |
| AI323667 | Immune-responsive gene 1 (Irg1) |
| AF077861 | Inhibitor of DNA binding 2 |
| AB024717 | Macrophage C-type lectin Mincle |
| AB012808 | mBOCT |
| M59821 | Mouse growth factor-inducible protein (pip92) |
| M73748 | Mouse OTS-8 |
| Y15163 | Mrg1 protein |
| AB026569 | MSSP |
| AF181829 | Pleckstrin |
| L24118 | Primary response gene B94 (TNF induced protein 2) |
| AF020313 | Proline-rich protein 48 |
| AF030185 | Putative beta chemokine receptor (E01) |
| U90926 | Putative TNF-resistance related protein |
| X95281 | Retinal short-chain dehydrogenase/reductase |
| AI840446 | SCHIP-1 |
| AF099973 | Schlafen2 (Slfn2) |
| D78188 | SCID complementing gene 2 |
| U86137 | Telomerase associated protein 1 |
| X70956 | TOP gene for topoisomerase I, exons 19-21 |
| AB030505 | UBE-1c1, UBE-1c2, UBE-1c3 |
| D83266 | vav-T |

Stimulation by LPS enhanced the macrophage's ability to interact with other cells through the co-ordinated expression of receptors, such as ICAM-1, VCAM-1, TNFR-I, TNFR superfamily member 5, CD14, integrin-$\alpha$ and $\beta$, and G-protein coupled receptors, which act to transmit the signal and activate intracellular transduction pathways (Table 8A). Importantly, GCs influenced the expression of the CD14 receptor [12,131], which is involved in endotoxin entry into the cell, emphasising their potency in interfering with early inflammatory events.

LPS stimulation of macrophages broadly affected the expression of chemokines such as MIP-1$\alpha$ [132], MIP-1$\beta$, MIP-2$\alpha$ [133], GRO1 and chemokine receptors (CCR1 and CCR5)[134], which are involved in the recruitment and trafficking of inflammatory leukocytes to the site of inflammation [135] (Table 8C). Whereas macrophage chemotaxis is rapidly inhibited by LPS and TNF-$\alpha$, (within 1h of treatment) [136], the repression of CCR1, CCR5, MIP1$\beta$, MIP2, and TNF-$\alpha$ by GCs, might restore this process in order to allow recruitment of macrophages to combat the inflammation. These results indicate that a wide variety of chemokines may also orchestrate under pathophysiologic conditions and play a role in inflammatory reactions. In addition, altered expression of various proteases and protease inhibitors (PAI-1, PAI-2), muPAR1 and dystroglycan may promote macrophage entry into infected tissues via remodelling the extracellular matrix [137-139](Table 8A).

Elevated transcription of the inhibitory $\kappa$B (I-$\kappa$B) $\alpha$ and $\beta$ inhibitory subunits of NF-$\kappa$B was observed upon LPS stimulation of PM$\Phi$. These proteins are known to down-regulate the transcriptional program initiated by the translocation of NF-$\kappa$B to the nucleus [140]. The levels of the mRNA encoding NF-$\kappa$B p105 and NF-$\kappa$B p100 were strongly increased upon incubation of cells with LPS (Table 8F, G) and similar observation were reported when cells were treated with TNF-$\alpha$ or PMA [141]. This indicates that for the fast responses to external signals, preformed cytosolic NF-$\kappa$B is sufficient but that longer lasting responses need the direct induction of NF-$\kappa$B mRNA [141]. The present study also identified a few participants of ubiquitination-dependent protein degradation pathway as being involved in macrophage response to LPS stimulation [142]. Specifically, the expression of UBP43 [117,125] and Ariadne-2 protein was induced upon LPS stimulation of

macrophages, whereas the expression of *Hagoromo* decreased. The role of these proteins in the LPS response is at present unclear. However, degradation of the I-κB α and β subunits is mediated by the ubiquitination system. Thus increased activity of the ubiquitination degradation system would be expected to result in increased I-κB degradation and thus increased expression of NF-κB target genes [143,144].

Immediate early genes such as junB [145], tristetraprolin (Zfp36) [146], Egr-1 [147], NF-kB [148] and Ets-protein, were up-regulated by LPS, while the expression of C/EBP α and NAKAP95 was decreased (Table 8G). Tristetraprolin, encoded by the gene Zfp36, regulates mRNA stability. Studies with knockout mice have shown that it lowers TNF-α protein levels by binding to the AU-rich elements in TNF-α mRNA [146,149,150]. This causes destabilisation of TNF-α messenger, which accounts for many anti-inflammatory responses promoted by LPS itself. Egr-1 controls both monocyte development and appears necessary for maintenance of macrophage differentiation, as the expression of many cytokines and receptors important during the inflammatory response are regulated by Egr-1 activity [147]. Expression of these transcription factors during macrophage maturation is usually coupled with an inhibition of cell proliferation. The expression level of some genes controlling transition through the G1 to S phase of the cell cycle, such as cyclin D1 and cyclin-dependent kinase (cdk) 4, were described to be down-regulated [88]. At present, the biological significance of the decreased expression of numerous genes mostly remains to be clarified.

### 5. 4. 1. LPS activates the TNF-α signalling pathway

Numerous proinflammatory cytokines and interleukins (TNF-α, IL-1α, IL-1β, IL-6, IL-12), were expressed at higher levels in LPS-stimulated macrophages than in resting cells and these mediators play a central role in the initiation of systemic response [31,85,151]. It has been recently described that autocrine production of TNF-α is sufficient to induce apoptosis of macrophages and neutrophils, in a time- and dose-dependent manner [152,153]. The potent regulatory abilities of

TNF-α are transduced by the cell-surface receptors type I, TNFR-I (55 kD), and type II, TNFR-II (75 kD) [154-159] (Figure 9). TNF-α and TNFR-I/II, along with several other components of its signalling loop (TRAF-1, TRAF-5, TRAF-interacting protein) [24,160], were identified as LPS-inducible genes (Table 8E, F). These mediators, in turn, activate downstream signal transducers, which can promote apoptosis via activation of NF-κB [148,153,161].

On the other hand, LPS-induced apoptosis may be tempered by the expression of mediators such as BID, A20 protein and Gadd45. BH3-interacting domain death agonist (BID) has been described to counter the protective anti-apoptotic effects of BCL2 and serves as a proximal substrate for activated caspase-8. Following cleavage by caspase-8, BID translocates to the mitochondria where it triggers cytochrome c release and membrane depolarisation [162,163] (Figure 9). In BID -/- cultured cells treated with TNF, this apoptotic resonse is delayed or significantly altered [164]. The mRNA expression levels of BID were decreased when PMΦ were stimulated by LPS and remained unchanged upon GCs administration. This finding would indicate that decreased expression of BID might counteract apoptosis observed when macrophages were treated with LPS [152,153], similar to the effects seen with BID -/- cells.

The expression of TNF-α primary response A20 zinc-finger protein [165,166] was elevated by LPS and, as with BID, its expression was not modulated by GCs. The role of A20 protein was demonstrated by the generation of A20-/- deficient mutant mice which showed severe inflammation and cachexia, hypersensitivity to LPS and TNF and failed to terminate TNF-induced NF-κB responses [167] (Figure 9).

The expression of the Gadd45 gene was increased several fold upon LPS stimulation of PMΦ and was efficiently repressed by GCs via a DNA-binding dependent mechanism of GR action. It has been reported that antisense inhibition of Gadd45 result in prolonged JNK activation and cytotoxicity after TNFR triggering. Therefore, during LPS stimulation, down-regulation of JNK through the transcriptional activation of Gadd45, would be beneficial for the cell [168,169] (Figure 9).

Together, the massive activation of the TNF-α pathway by LPS points to different mechanisms of gene regulation that enable proper cell response to proinflammatory stimuli such as LPS and defend macrophages from an inflammatory burst. All this suggests that there must be a balance, tightly controlled, between proinflammatory responses and negative feed back regulation during LPS stimulation of macrophages, at least in early stages.

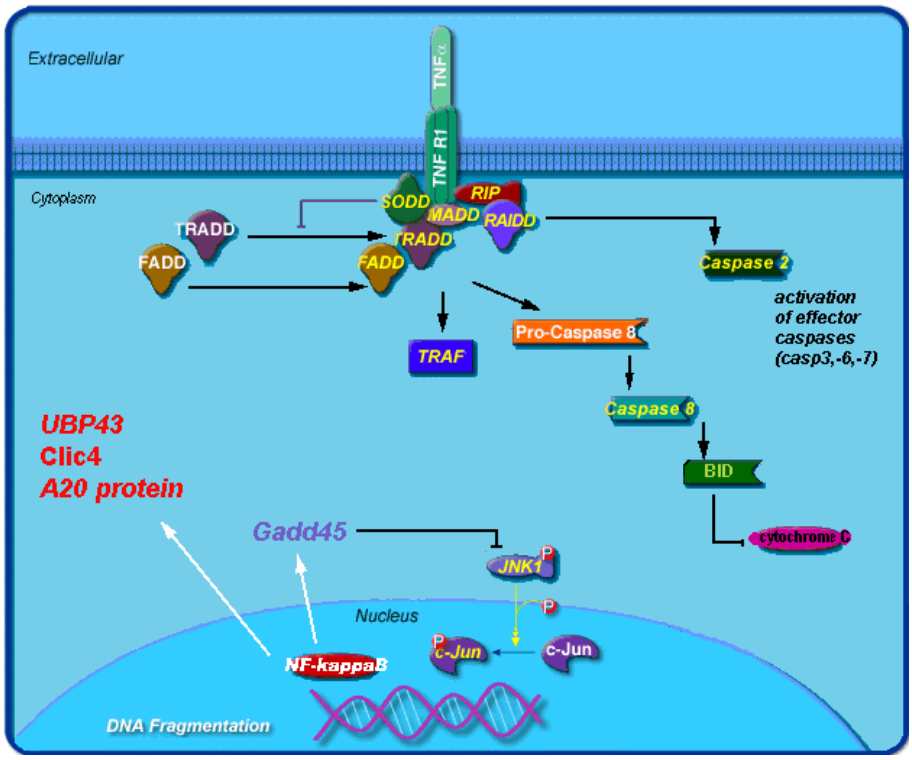



Figure 9. TNF-α signalling loop

The TNFR superfamily contains several members with homologous cytoplasmatic domains known as death domains (DD). TNF-induced receptor aggregation recruits the adapter protein TRADD-3,-5, FADD, TRAF-2 and RIP to form an active TNFR-I signalling complex. This triggers an apoptotic response mediated by the proteolytic caspase cascade that results in the degradation of many critical cellular proteins. Modified from *http://www.biocarta.com*.

## 5.5. THE PHYSIOLOGICAL RELEVANCE OF DIFFERENT MODES OF GENE REGULATION BY THE GR

Targeted mutagenesis of the GR has revealed an essential function of the receptor in survival and regulation of multiple physiological processes. Mutant mice containing a dimerisation-defective GR ($GR^{dim}$ mice) revealed that transcriptional regulation dependent on DNA binding is dispensable for survival, since in these mutants GR functions, which involve receptor binding to GRE, are no longer present [79]. Analysis of these mice under challenging conditions (i.e. upon LPS injection) demonstrated the beneficial effects of GR, since $GR^{dim}$ mice were resistant to LPS-induced endotoxic shock to an extent similar as their control littermates (H. M. Reichardt, personal communication). In contrast, mice containing a macrophage specific deletion of the GR ($GR^{LysCre}$ mutant mice) lack the beneficial effects of the glucocorticoid-regulatory circuit in this cell type. It can be speculated that the lack of the GR in macrophages from these mice impairs phagocytosis, which is normally regulated by GCs [2,170], and renders these cells unable to remove toxic and apoptotic cells. This, in turn, contributes to a persistent inflammatory environment and may account for the enhanced mortality rate observed in these mice upon LPS injection (H. M. Reichardt, F. Tronche, personal communication). Together, these results underscore the importance of GR signalling in PMΦ for the control of physiological and pathological processes.

Current gene expression profiling study supported by *in vivo* animal experiments, allowed the molecular mechanisms of GR signalling during LPS stimulation of macrophages to be deciphered. Numerous LPS responsive genes have been identified as also being regulated by GCs which are involved in a variety of biological processes (Table 8; see also Figure 8 and Table 7 in the *Results* Section). GR regulates the expression of these genes either via receptor interaction with DNA or via protein-protein interactions which are independent of DNA binding. More than 90 genes/ESTs (89% of all GC-regulated genes) have been identified as significantly modulated by GCs treatment. For these genes, the preferential mechanism of GR action involved binding of the GR to DNA (Figure 8). This clearly shows that a substantial number of genes with a wide variety of functions exist which are modulated (induced or repressed) by GR in a DNA-binding dependent manner. In contrast, 12 of the 106 GC-responsive genes/ESTs (i.e. 11%) were identified as being

modulated by GCs in $GR^{dim}$ macrophages, and are thus regulated by GR-DNA binding independent interactions. Some of these genes, such as IL-6 [121], TNF-$\alpha$ [151], IL-1$\beta$ [171], MIP-2 [122] and COX-2 [54], are among the most prominent and important proinflammatory mediators and down-regulation of their transcription by the GR could account for the beneficial, immunomodulatory, effects of GCs, at least, during early inflammatory stages. Thus interaction of GR with other proteins, which is independent of receptor binding to DNA, is an important mechanism of glucocorticoid-mediated regulation of gene expression. Interestingly, the expression of both endothelin 1 and growth factor-inducible immediate early gene was found to be increased upon GC administration to $GR^{dim}$ macrophages. Although the lack of co-operative DNA binding by $GR^{dim}$ receptor severely impedes its ability to bind conventional GREs, some DNA elements might exist that permit direct DNA binding by GR independent of dimerisation, thus resulting in gene activation by the $GR^{dim}$ [172,173]. Increased expression of endothelin 1 and growth factor-inducible immediate early gene might be due to interaction(s) between $GR^{dim}$ and other transcription factors (proteins), similarly as has been reported in the literature [69,70,174].

These data support, to certain extent, the hypothesis that most of the anti-inflammatory effects of GCs are mediated by GR actions independent of binding to DNA, thus resulting in gene repression [34,175]. The side effects, often observed during long-term GC treatment, are likely due to transactivation of genes through binding of the GR to DNA. Therefore, the potential to constitute a new class of anti-inflammatory glucocorticoid-based drugs, which would be able to separate beneficial effects of GCs from deleterious ones (transrepression from transactivation), is already under way [176,177]. The findings that more than 90 GC-responsive gene are being modulated by GR in a DNA-binding dependent manner will certainly help in the future development of novel glucocorticoid-based agents. Finally, how *in vitro* separation of transrepression from transactivation activity translates into *in vivo* models is expected to provide evidence of therapeutic usefulness of such "dissociated" drugs.

# 6. MATERIAL AND METHODS

## 6. 1. BIOLOGICAL MATERIAL

### 6. 1. 1. Mouse strain models

- C57BL/6 mice were obtained from CR Wiga, Germany.

- $GR^{dim}$ mice were generated by homologous recombination using Cre/loxP system, as previously described by H. M. Reichardt et al [79]. A point mutation (alanine 458 to threonine) in the exon 4 of the murine GR gene has been introduced by site-directed mutagenesis, that affected the structure of the second zinc-finger in the DNA-binding domain of GR.

- $GR^{flox/flox}$ mice were generated by flanking exon 3 of the GR allele by two loxP sites [81].

- LysMcre conditional mutant mice were generated by targeted insertion of the *cre* cDNA into endogenous M lysosyme locus causing Cre to be expressed in cells of myeloid lineages [82].

- $GR^{LysCre}$ mutants were generated by Dr. F. Tronche (unpublished), by crossing $GR^{flox/flox}$ and LysMcre conditional mutants.

### 6. 1. 2. Cloning vector and bacterial strain

The pT7Blue cloning vector (Novagen Inc.) with following sequence landmarks was used for cloning and sequencing: 2887 bp in size, multiple cloning region containing an *Eco*RV blunt cloning site, a T7 promoter, f1 origin of replication, *lac* Z sequences and ampicillin resistance.

NovaBlue Singles cells (Novagen Inc.) were used for heat-shock transformation reactions. The identification of recombinants was achieved through α-complementation, in which deletion mutants of the operator-proximal segment of *lac*Z gene were complemented by β-galactosidase-negative mutants that have the intact operator-proximal region. The Lac+ bacteria that resulted from the α-complementation formed blue colonies in the presence of the chromogenic substrate 5-bromo-4-chloro-3-indolyl-β-D-galactosidase (X-gal) allowing easy recognition. In contrast, insertion of DNA into the polycloning site of the plasmid resulted in production of an amino-terminal fragment that was not capable of α-complementation, therefore bacteria carrying the recombinant plasmid formed white colonies.

### 6. 1. 3. Primers used

Commercially availabe and gene-specific primers, used in this study, are listed bellow. Gene-specific primer pairs were designed using Primer3 input program (available at: *http://www-genome.wi.mit.edu/cgi-bin/primer/primer3www.cgi*).

CDS (cDNA sequence) primer (Clontech, Palo Alto, CA)

5´-AAGCAGTGGTAACAACGCAGAGTAC$(T)_{30}N_{-1}$N -3´ [N = A, C, G, or T; $N_{-1}$ = A, C, or G].

SMART II primer (Clontech, Palo Alto, CA)

5´-AAGCAGTGGTAACAACGCAGAGTACGCGGG-3´

T7 primer:

5´-AATACGACTCACTATAGGG-3´

U-19 primer:

5´-GGTTTTCCCAGTCACGACG-3´

(dT)-T7 primer:

5´-GCATTAGCGGCCGCGAAATTAATACGACTCACTATAGGGAGA$(T)_{21}$N-3´

HPRT; Accesion Number [J00423]; product size 389 bp

5´-CATTATGCCGAGGATTTG-3´ and 5´-TTGGGGCTGTACTGCTTA-3´

TNF-α; Accesion Number [M38296]; product size 379 bp

5´-CATTCCTGCTTGTGGCAGGG-3´ and 5´-GCAAATCGGCTGACGGTGTG-3´

IL-6; Accesion Number [J03783]; product size 471 bp

5´-CACAAGTCCGGAGAGGAGAC-3´ and 5´-GCCACTCCTTCTGTGACTCC-3´

IL-1β; Accesion Number [M15131]; product size 332 bp

5´-TCCTGAACTCAACTGTGA-3´ and 5´-CCAGCAGGTTATCATCAT-3´

MIP-2α; Accesion Number [X53798]; product size 440 bp

5´-GGAAGCCTGGATCGTACCTG-3´ and 5´-CTGTTCTACTCTCCTCGGTGC-3´

CD14; Accesion Number [X13987]; product size 445 bp

5´-GGACACGGAAGCAGATCTGG -3´ and 5´-GAACTTGAGGGGACAGAGGG-3´

PAI-2; Accesion Number [X16490]; product size 452 bp

5´-CTCACCCTAAAAGGGGAAGACC-3´ and 5´-CTGGGTGAATATCATGGGAAAG-3´

Clic4; Accesion Number [NM_013885]; product size 385 bp

5´-GCCTTAGTGGGTGTGAGGTG-3´ and 5´-TCCAAGGTGGAGGGCTTATAC-3´

USP43; Accesion Number [AF069502]; product size 412 bp

5´-GCTGGAGAAGATGCAGGACAG-3´ and 5´-GCTTCAGAACCTGTTTCCAAG-3´

COX-2; Accesion Number [M94967]; product size 390 bp

5´-GCAAACGCTTCTCCCTGAAG -3´ and 5´-CGCTTGCATTGATGGTGGCTG -3´

Irg1; Accesion Number [L38281]; product size 584 bp

5´-CGGTGCCTTCTATGCCAACT-3´ and 5´-CCACCGTGTCCCTGCATAGC-3´

B94; Accesion Number [L24118]; product size 394 bp

5´-GCTCCTCACACCACCACAGTC-3´ and 5´-TCATCAACAGCGGTCGTCTACA-3´

A20 protein; Accesion Number [U19463]; product size 408 bp

5´-ACAAGCAAGTGCAGGAAAGC-3´ and 5´-ACTCGTTGGCTTAGGTGCTG-3´

γ-actin; Accesion Number [M21495]; product size 492 bp

5´-CAGCAAGCAGGAGTATGATGAG-3´ and 5´-GGCAAGAAGGAGTGGTAACTGG-3´

TNFR-I; Accesion Number [M59378]; product size 399 bp

5´-GAGGTTGGCTTTGGGTGTGTT-3´ and 5´-ATGTATGGGGTGGTGGTCAG-3´

Pleckstrin; Accesion Number [AF181830]; product size 500 bp

5´-GCAAGGGATGTCCTTATTGGTC-3´ and 5´-CAGTGTTGCATCACTTACGTGC-3´

C3 α, β subunit; Accesion Number [K02782]; product size 396 bp

5´-AGAGAAGGACGATGGGATGC-3´ and 5´-CACGTGTCCTTCCCAATGATG-3´

65 kDa protein; Accesion Number [D37837]; product size 461 bp

5´-CTCTCACGCTGGCATTGGTTTG -3´ and 5´-CTCAGGCTTGTCTGTGTCGATTTC-3´

ABC1; Accesion Number [X75926]; product size 449 bp

5´-TGGTGTGGAACCAAGCAGAC-3´ and 5´-GCAACACTGAACAAGAGAACCAA-3´

Fibronectin; Accesion Number [X93167]; product size 410 bp

5´-GCCTCAATCCAAATGCCTCT-3´ and 5´-ACTGCCAAAGCCCAAGCAC-3´

Mac-1α; Accesion Number [X07640]; product size 405 bp

5´-ATCTCAACTTCACGGCTTCAGAG-3´ and 5´-GGATCTCAGTGCTGCTCACAAG-3´

α glucosidase II α subunit; Accesion Number [U92793]; product size 405 bp

5´-GCTGTAACTGGAGCACAGTCATTTG-3´ and 5´-CCTAATTGTGTGGAAGCGTCTCCC-3´

### 6. 1. 4. Oligonucleotide gene chip arrays

Mouse oligonucleotide array GeneChip U74Av2, which contain oligonucleotide probe sets corresponding to approximately 12000 genes/ESTs, were purchased from Affymetrix, Santa Clara, CA (*http://www.affymetrix.com*).

# 6. 2. METHODS

### 6. 2. 1. Isolation of peritoneal macrophages

Mice were injected intra-peritoneal with 1.5 ml of sterile 2.98% water-solubilised thioglycollate medium (Sigma) and cells were harvested after four days by peritoneal lavage using 5-7 ml of cold PBS (1.2 M NaCl, 280 mM $Na_2HPO_4x2H_2O$, 25 mM $KH_2HPO_4$). After centrifugation, supernatant was discarded and the pellet was resuspended in RPMI medium supplemented with 10 % FCS (GIBCO, BRL).

Freshly isolated peritoneal macrophages (PMΦ) were seeded at a concentration of $10^7$ cells in 100 mm dishes containing RPMI medium with 10% FCS (GIBCO, BRL). The cells were allowed to adhere to the plastic surface for approximately 3 hours and non-adherent cells were removed by exchanging the medium [114]. After overnight incubation at 37°C in 5% $CO_2$, cells were treated with vehicle, with 100 ng/ml LPS (E.coli 055:B5, Sigma) for 2h, or with 1 µM dexamethasone (Sigma) 1h prior to LPS. During treatment, cells were kept in RPMI medium without FCS.

### 6. 2. 2. Molecular cloning

For subcloning purposes, Perfectly Blunt Cloning Kit (Novagen Inc.) was used. Briefly, DNA fragments generated from PCR were first extracted with chloroform to inactivate the Taq DNA Polymerase avoiding the possible regeneration of termini heterogeneity on the PCR product. This consisted of adding chloroform:isoamyl alcohol (24:1) to the PCR reaction and vortexing vigorously for 1 min and centrifugation at 14.000 rpm for 1 min. The aqueous phase was transferred into a fresh tube and an aliquot (2 µl) was used in the end conversion reaction to generate DNA fragments with blunt ends to allow cloning into vector. The end-conversion reaction was performed in presence of 5 µl of enzyme mix, supplied in the kit, in a total reaction volume of 10 µl. After 15 min incubation at 22°C, the enzyme was heat-inactivated for 5 min, the mixture cooled briefly on

ice and then used in ligation reactions. For this purpose, 50 ng of pT7Blue vector and 10 µl of the insert prepared in the end conversion reaction was ligated with 4 U of T4 DNA Ligase for 2 hours at 22°C. A molar ratio of insert to vector of 2.5:1 was maintained under these conditions.

NovaBlue Singles cells were transformed with 1 µl of ligation reaction using the heat shock method (30 seconds in a 42°C water bath) and cooled for 2 minutes on ice. Cells were recovered by adding 80 µl of room temperature SOC medium (2 % tryptone, 0.5% Bacto yeast extract, 10 mM NaCl, 2.5 mM KCl, 10 mM $MgCl_2$, 10 mM $MgSO_4$ , 20 mM glucose), incubated for 30 minutes at 37°C with shaking. The transformation mixture, 10 µl and 90 µl, was spread on LB agar plates [LB medium (1 % Tryptone (Difco), 0.5 % Bacto yeast extract (Difco), 0.5 % NaCl, 50 µg/ml ampicillin), 1.5 – 2% (w/v) Bacto-agar (Difco), 80 µM isopropylthio-ß-D-galactosid (IPTG), 70 µg/ml X-gal].

### 6. 2. 3. Plasmid DNA isolation

Plasmid DNA was isolated according to the following procedure (Quiagen): 1.5 ml of overnight bacterial culture was centrifuged and the pellet resuspended in 0.05 ml of P1 solution (1M Tris-Cl pH 8.0, 0.5M EDTA pH 8.0) and 0.1 ml of P2 (0.2M NaOH, 1% SDS). Then, 0.075 ml of 3M K-acetate pH 4.5 was added and the mixture centrifuged for 10 min at 14.000 rpm. The supernatant was transferred to a new tube, mixed with 0.33 ml of 6 M guanidinethyocyanat and 0.45 ml of 2-butanol and centrifuged. The pellet was washed once with 70% ethanol and resuspended in 50 µl of TE buffer (10 mM Tris-Cl pH 8.0, 1 mM EDTA pH 8.0). The quality of isolated DNA was checked by gel electrophoresis.

### 6. 2. 4. DNA/RNA electrophoresis

1-2.5 % agarose gels were used for the analysis of DNA fragments of 0.2 – 5 kb size, as well as for RNA samples. The gels were prepared using 1x TBE buffer (0.09 M Tris-Cl, 0.09 M Boric acid, 2 mM EDTA pH 8.0) containing 1 µg/ml ethidium bromid; 1x TBE was used as a running

buffer. Electrophoresis was performed at constant voltage for 30-60 minutes, and the DNA/RNA bands were visualised using a UV-transilluminator.

### 6. 2. 5. Polymerase Chain Reaction

The amplification of DNA fragments of known sequence was performed using Polymerase Chain Reaction (PCR)[178]. This method consists of 30-40 cycles, each with 3 basic steps: denaturation of DNA, annealing of primer to template at the specific melting temperature of the primer, and polymerisation at 72°C [178]. For all PCR reactions, a master mix was prepared containing 1x PCR buffer (Roche), 1.5 mM $MgCl_2$, 5 µM each dATP, dTTP, dGTP, dCTP (Pharmacia), 0.5 µM 'forward' and 0.5 µM 'reverse' primer. Reactions were carried out in a 20 µl volume using 100-200 ng DNA as template and 1 U of *Taq* DNA Polymerase.

### 6. 2. 6. Quantitative real-time PCR

The real-time quantitative PCR was performed using the LightCycler – FastStart DNA Master SYBR Green I ready-to-use PCR reaction mix, which contains *Taq* DNA Polymerase and DNA double-strand specific SYBR Green I dye (Roche Diagnostics, Mannheim, Germany). The FastStart *Taq* DNA Polymerase is held inactive at room temperature due to the heat-labile blocking groups on some of the amino acid residues of the enzyme. SYBR Green I is a fluorescence dye, which binds to the amplified PCR products during each phase of DNA synthesis allowing the amplicon to be detected by fluorescence. The mRNA/cDNA abundance was calculated relative to the expression of a house-keeping gene HPRT, which was also used as 'external standard' for creating a calibration curve.

LightCycler PCR reactions were performed in a 10 µl volume using 2 µl of 1:10 diluted first strand cDNA, 1 µl of “a+b” pre-mix (FastStart enzyme and SYBR Green I dye), 2 mM $MgCl_2$, and 0.5 µM primer mix, with amplification conditions as follows:

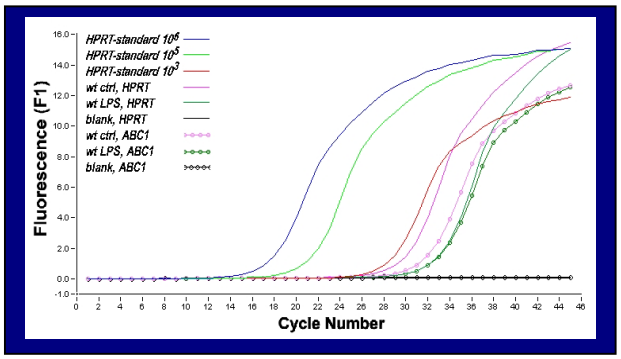
Step 1: pre-incubation and denaturation of the template DNA: 95°C for 10 min;

Step 2: Amplification of target DNA: 45 cycles (95°C for 15 sec, 60°C for 5 sec, 72°C for 15 sec);

Step 3: Melting curve analysis for product identification (set according to the LightCycler Operator's Manual version 3.0, Roche Molecular Biochemicals);

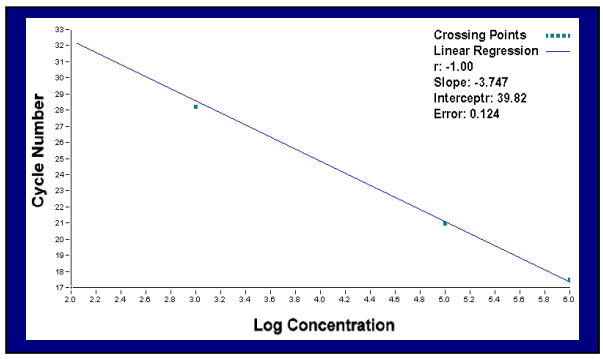
Step 4: Cooling the rotor and thermal chamber and subsequent setting of the fluorescence parameters (set according to the LightCycler Operator's Manual version 3.0, Roche Molecular Biochemicals).

## A. Monitoring of PCR reaction



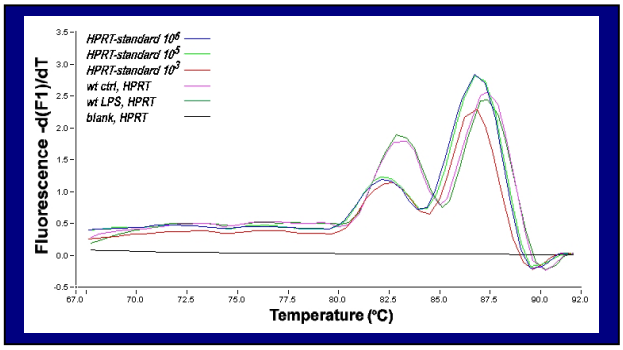

LightCycler PCR reactions are monitored with SYBR Green I and acquisitions are taken once per cycle following extension. The accuracy of measurements during the log-linear phase of PCR indicates that significant variations in the amount of starting material cannot be differentiated by signals measured in the plateau phase. An on-line examination determines the point were the second derivative of the amplification curve is at its maximum. Once the cycle with maximum second derivative is found, a parabola is fit to the region to determine the fractional cycle with the maximum second derivative.

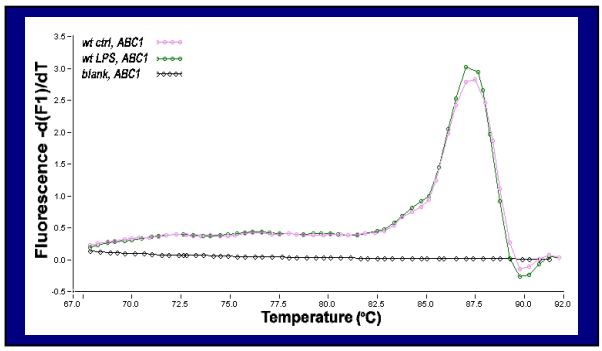
## B. Standard curve




A standard curve is constructed using HPRT as 'external standards'. The crossing points (cycle number) are plotted against the log concentration (copy number) of the HPRT standard DNA

## C. Melting curve analysis




Each peak represents the Tm as it 'melts off' the template DNA. The sample containing only water shows no peak. Melting temperatures of HPRT are between 82-83°C and 87-88°C (indicating gene isomers) and of ABC1 gene between 87°C.

**D. Relative quantification using 'external standards'**

| ***Sample*** | ***HPRT*** | ***crossing point*** |
|---|---|---|
| *standard ($10^6$)* | 9.0 x $10^5$ | 17.51 |
| *standard ($10^5$)* | 1.1 x $10^5$ | 20.97 |
| *standard ($10^4$)* | 1.2 x $10^4$ | 24.23 |
| ***Sample*** | ***HPRT*** | ***crossing point*** |
| wt, ctrl | 999.40 | 28.57 |
| wt, LPS | 917.90 | 28.72 |
| ***Sample*** | ***ABC1*** | ***crossing point*** |
| wt, ctrl | 2326 | 27.20 |
| wt, LPS | 5334 | 25.85 |

| ***ABC1/HPRT*** | ***Fold change (LPS / ctrl)*** |
|---|---|
| 2.33 | 2.5 |
| 5.81 | |

Figure 10. Real-time quantitative PCR analysis (LightCycler)

Real-time PCR run is illustrated for HPRT and ABC1 genes. The measurements by the real-time PCR are performed during the log-linear phase of a PCR and are calculated by LightCycler software (Second Derivative Maximum, Roche) (Figure 10A). As such, the analysis allows a more reliable quantification of mRNA expression, providing that the amplification efficiencies of 'external standard' RNAs and for the RNA being investigated, are equal during the PCR reaction (Figure 10B). The product specificity is controlled during the last segment of the PCR program, where melting of PCR products serves to eliminate non-specific fluorescent signals, since specific PCR products give a single, sharply defined melting curve with a narrow peak (Figure 10C). In contrast, primer-dimers melt at lower temperature and have broader peaks. The quantification of gene abundance/expression is than calculated relative to the expression of HPRT gene (Figure 10D).

### 6. 2. 7. PCR-based automatic sequencing

Sequencing reactions were performed using the Big Dye terminator Cycle sequencing kit (Perkin Elmer Applied Biosystem, cat. # 4303152) according to the manufacturer's introductions. Labelled DNAs were run on a ABI 377 Sequencer (PE Applied Biosystem) and analysed with the 377 DNA Sequencer Data Collection program version 1.1 (ABI Prism) and DNA Sequencing Software version 2.1.1 (ABI Prism). Reactions were performed using the T7 or U-19 primer.

### 6. 2. 8. RNA isolation

Total RNA was isolated using the Qiagen RNeasy kit according to the manufacturer's instruction (Qiagen). Isolated RNA was subjected to DNase I treatment for 30 min at 37°C, follwed by phenol:chloroform extraction. The RNA was precipitated with 2.5 volumes 100% ethanol and 1/10 volume sodium acetate, pH 5.2, resuspended in RNase free water and stored at -70°C.

Poly(A)$^+$ RNA was purified from total RNA using the Oligotex mRNA kit (Qiagen). The concentration and purity of the RNA was determined by $OD_{260/A280}$ reading. The quality of the RNA was assessed by gel electrophoresis and ethidium bromide staining.

### 6. 2. 9. RNase Protection

The *in vitro* transcription system was used for the synthesis of single stranded RNAs [179]. Specifically, plasmid containing DNA-fragments of interest was linearised using the *Eco*RI restriction enzyme which leaves a 5´overhanging end. Linearised DNA was extracted using phenol/chloroform, precipitated and the pellet resuspended in water to 0.5 µg/µl.

cDNA fragments from murine TNF-$\alpha$, IL-6 and cytochrome C genes (379 bp, 471 bp and 110 bp, respectively), cloned into the *Eco*RV site of pT7Blue vector, were used for antisense RNA probe synthesis. The reaction was performed using 250 ng of DNA-template, 1 x T3/T7 transcription buffer (40 mM Tris-Cl pH 8.0, 50 mM NaCl, 8 mM $MgCl_2$, 2 mM spermidin, 10 mM DTT), 5 µM each rATP, rGTP, rCTP, 4 µM UTP, 25 µCi $\alpha^{32}$P-UTP, 0.01 M DTT, 2.5 U of RNasin

(Promega) and 1 U of T7 RNA Polymerase. The reaction was incubated for 30 minutes at 37°C. Digestion of DNA was performed in 1 x DNase buffer (50 mM Tris-Cl pH 7.5, 5 mM $MgCl_2$, 1 mM DTT) in the presence of 20 U of DNase I enzyme and 20 µg of tRNA, for 15 minutes at 37°C. After phenol/chloroform extraction, the reaction was precipitated, centrifuged, the pellet washed once with 75% ethanol/ 25% 0.1 M Na-acetate and finally dissolved in 1 x hybridisation buffer (40 mM Pipes, 0.4 M NaCl, 1 mM EDTA, 80% formamide). The incorporation of radionucleotides was measured as described in section 2. 8.

$\alpha$-$^{32}$P-UTP labelled antisense RNA probes (200,000 cpm) were then subjected to hybridisation against 5 µg of total RNA during overnight at 54°C in 80% formamide. The excess of probe was removed by digestion in RNase buffer (10 mM Tris-Cl pH 7.5, 300 mM NaCl, 5 mM EDTA, 40 µg/ml RNase A, 3.500 U/ml RNase T1). The reaction was stopped by incubation with proteinase K and Tween 20/ NP-40 for 15 min. After phenol/chloroform extraction and precipitation, the pellet was dissolved in sample loading buffer (5 mM EDTA, 50% formamide, brom phenol blue dye). The samples were heat denaturated and loaded onto a denaturing 6% polyacrylamide gel. The protected fragments were analysed after exposure to phosphoimager screen using Analytical Imaging Station (AIS, Imaging Research Inc.).

### 6. 2. 10. Suppressive Subtractive Hybridization

Suppressive subtractive hybridisation (SSH) was performed using the PCR-Select cDNA Subtraction Kit, Clontech, Palo Alto, CA. Briefly, two mRNA populations were converted into *tester* cDNA, which contained differentially expressed transcripts, and *driver*, as the reference cDNA. The *tester* and the *driver* cDNAs were prepared using 2 µg of poly(A)$^+$RNA from LPS-stimulated macrophages (100 ng/ml LPS, 2 h) and 2 µg of poly(A)$^+$RNA from non-treated macrophages, respectively. As a control, 2 µg of skeletal muscle poly(A)$^+$RNA, provided in the kit, was used. All steps were carried out according to the manufacturer's instructions. The quality and efficiency of subtraction was controlled by PCR using two housekeeping genes (G3PDH and $\beta$-actin). The expressison of TNF-$\alpha$ and IL-6 cytokines, which are expected to be enriched by the procedure,

was therefore tested in unsubtracted and subtracted tester and driver samples and their amplification controled on agarose gel electrophoresis as suggested by the manufacturer. Schematical representation of the SSH method is depicted in Figure 11.

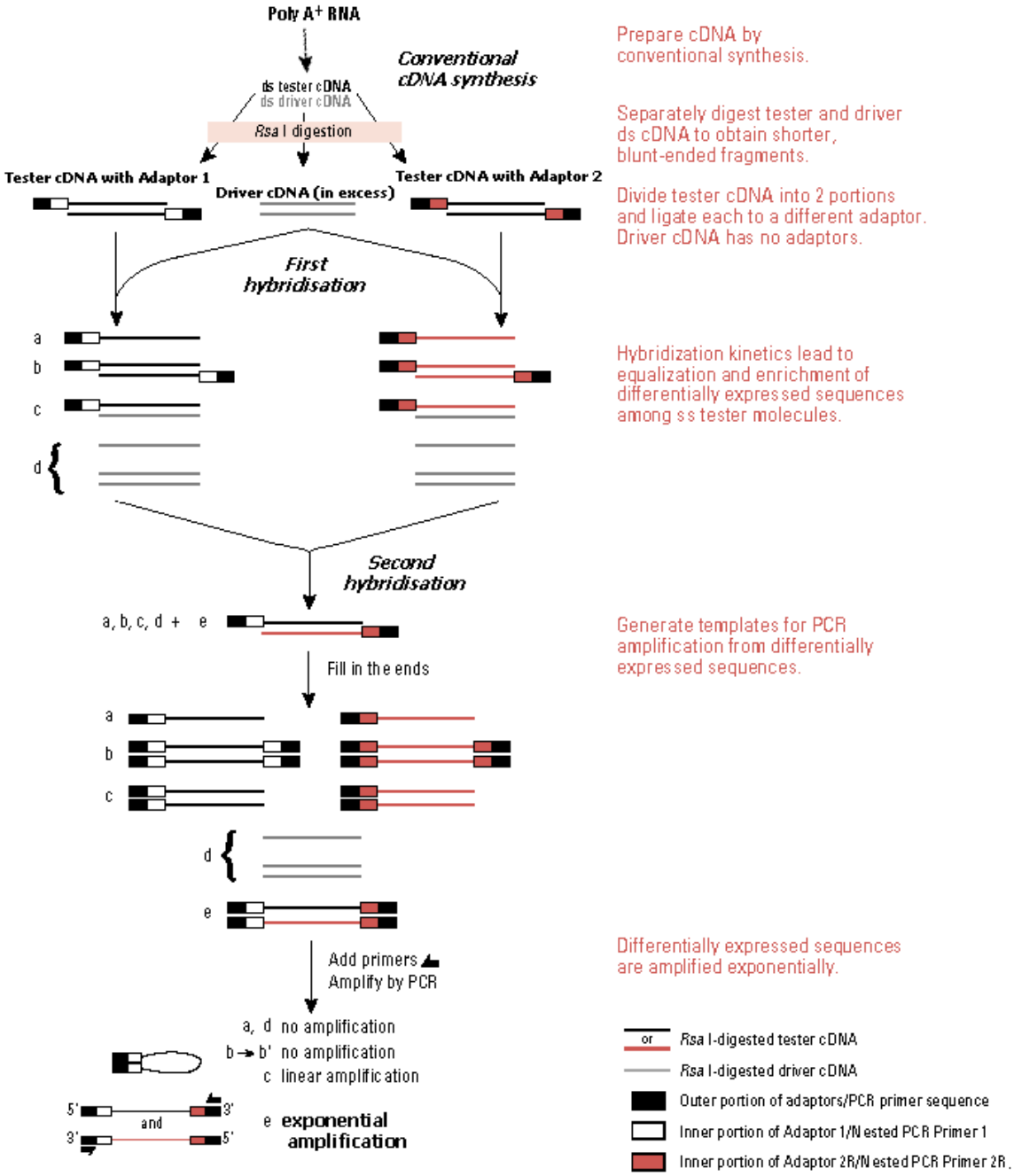



Figure 11. The PCR select cDNA subtraction technique (SSH)

The *tester* and the *driver* cDNAs are digested with *Rsa*I, a four-base-cutting restriction enzyme that yieldes blunt ends. The *tester* cDNA is then subdivided into two portions, and each is ligated with a different cDNA adaptor. Two hybridisations are then performed. In the first, an excess of *driver* is added to each sample of *tester*. Mixtures are heat denaturated and allowed to anneal generating several types of molecules. During the second hybridisation, the two primary hybridisation samples are mixed together without prior denaturation. Here, only the remaining equalised and subtracted single strand *tester* cDNAs can reassociate and form new double stranded hybrids with different ends corresponding to adaptor sequences. The entire population of molecules is then subjected to PCR to amplify the desired differentially expressed sequences. A second PCR is performed using nested primers to further reduce any background PCR products and to enrich for differentially expressed sequences. Taken from *http://www.clontech.com*

### 6. 2. 11. Gene array construction on nylon membranes

The subtracted library was created by cloning the SSH-products using a pT7Blue perfectly blunt cloning kit (Novagen Inc.). The transformation mixture was spread on LB agar plates and, after overnight growth at 37°C, recombinant clones were replica plated on Hybond $N^+$ nylon membranes. Filters were then hybridised with the labelled SSH-products which were used for the initial cloning.

292 SSH-clones were sequenced as described in Section VI 2. 7. Inserts were used for homology search in the GenBank and EMBL database using BLAST algorhythm (available at *http://www.ncbi.nlm.nih.gov/BLAST/*). Inserts of 212 clones were PCR amplified in 50 µl reaction volumes using T7 and U-19 primer under following amplification conditions: 95°C for 5 min; (95°C for 1 min; 57°C for 1 min; 72°C for 1 min) x 35; 72°C for 10 min. Reactions were carried out in the MJ Research Peltier DNA Thermal Cycler 200. The SSH-arrays were generated by spotting 1 µl of amplified PCR products in duplicates, on a Hybond $N^+$ nylon membranes, using robotic workstations. Membranes were pre-treated for 20 minutes in denaturation solution (1.5 M NaCl, 0.5 M NaOH), and after spotting, washed for 1 min in neutralisation solution (1.5 M NaCl, 0.5 M Tris pH 7.2, 0.001 M EDTA), UV cross-linked and stored at -20°C. The SSH-arrays include partial cDNA sequences of 61 known genes, 76 novel ESTs, 9 housekeeping genes and several controls (i.e. cloning vector, empty spot, mouse genomic DNA).

### 6. 2. 12. Probe preparation and Hybridisation of SSH-arrays

100 ng of poly(A)$^+$RNA from unstimulated and LPS-stimulated macrophages from wild type mice, was converted into labelled first strand cDNA using 40 µCi $\alpha^{32}$P dATP (Amersham), 5 µM each dCTP, dGTP, dTTP, 1 µM 10 x CDS primer (Clontech), 1x first-strand buffer (GIBCO, BRL), 0.01 M DTT and 200 U of SuperScript II reverse transcriptase (GIBCO, BRL). After 1 h 30 min incubation at 42°C, 2 µl of 0.5 M EDTA was added to stop the reaction, and the labelled first-strand cDNAs were purified using ProbeQuant G-50 Micro Columns (Amersham). The labelling efficiency was checked by chromatography in Polygram Cel 300 PEI (pre-coated plastic sheets) using 0.75 M

$NaH_2PO_4$ pH 3.5 as a buffer, and the percent of incorporated radionucleotides measured by the Cherenkov method in the scintilation counter. Prior to hybridisation to SSH-arrays, probes were denaturated for 5 min at 95°C.

The SSH-arrays were prehybridized for 30 min in ExpressHyb solution (Clontech) containing 100 µg/ml heat-denaturated salmon sperm DNA (Sigma) at 60°C. The hybridisation was performed at 60°C, using 1.5 x $10^6$ cpm of labelled first-strand cDNA probe. After overnight incubation, SSH-arrays were washed according to the following low- and high-stringency conditions: 3 x 30 min at 60°C in washing solution I (2 x SSC, 1% SDS), 2 x 15 min at 60°C in washing solution II (0.1 x SSC, 0.5 % SDS), and 5 min at room temperature in 2 x SSC. The SSH-arrays were then exposed to a phosphoimager screen (Fujifilm, Japan) and the signals intensities quantitated using a Fuji Phosphoimager.

### 6. 2. 13. Image analysis and data interpretation

The quantitation of the intensity of hybridisation at each position on the nylon-based arrays was calculated using a commertially available Analytical Imaging Station software (Array Vision, Imaging Research Inc.) and the MATLAB version 5.3 (MathWorks Inc.). MATLAB is an interpreted programming environment suited for matrix calculation, available at *http://www.dkfz.de/tbi/services/matlab2web/webdiffs*. The software was run on a Sun Ultra 5 workstation under the Solaris operating system. Both softwares provide a sophisticated grid placement method, tools for background correction, and image filtration. Additionally, scatter plot was obtained for a rapid visualisation of the overall differences between the conditions [127].

Statistical analysis of the hybridisation signals was performed according to the following criteria: a) normalisation of the raw counts obtained after initial analysis of the arrays was assessed using house-keeping genes and/or the set of genes, which did not change during the experiments; b) background correction, performed around each grid's primary element individually and subtracted from the value of each spot using appropriate softwares; c) fold change - candidate

genes were selected if the median hybridisation intensity values was altered by more then two-fold upon treatments.

### 6. 2. 14. Probe preparation and Hybridisation of oligonucleotide chip arrays

200 ng of total RNA from each sample (unstimulated, LPS-, dex+LPS-stimulated macrophages from wild type, $GR^{dim}$ and $GR^{LysCre}$ mice) was used to prepared cDNA according to protocol developed by Baugh LR et al. [120], as illustrated in Figure 12. A single modification was included regarding the temperature at which the reverse transcription reaction was performed (instead of 42°C, incubation at 50°C was used since it resulted in a higher yield of cDNAs). This has been previously verified in experiments using 8 µg vs. 200 or 20 ng of mouse total RNA that were amplified and hybridised to Affymetrix U74Av2 chips with high correlation factor (r = 0.998) observed in intra- and interchip variation (Dr. M. Kenzelmann, personal communication).

Briefly, reverse transcription was performed in 10 µl with 100 ng (dT)-T7 primer, 100 U SuperScript II (Life Technologies), 20 U RNase inhibitor, 0.4 µg T4gp32 (USB), 1 mM dNTPs each, 10 mM DTT, in 1x first-strand buffer (Life Technologies) for 1h at 50°C, in air incubator. Second strand synthesis (SSS) was carried out in the presence of 20 U DNA polymerase I, 1 U *E. coli* RNase H, and 5 U E.coli DNA ligase, 0.1 mM dNTPs each, in 0.5x second-strand buffer (Life Technologies), at 15°C for 2 h. The double stranded (ds) cDNA was polished by adding 10 U T4 DNA polymerase and incubated for further 15 min. cDNA was phenol/chlorophorm purified, ethanol precipitated and transcribed (1° IVT) by adding 40 µl of IVT mix [160 U T7 RNA polymerase (Promega), 7.5 mM each GTP, ATP, UTP, CTP, 10 mM DTT, 60 U RNase inhibitor, 1x buffer (Ampliscribe Epicentre Ampliscribe kit); 9h at 42°C]. Amplified antisense RNA (aRNA) was purified on RNeasy spin columns from Qiagen, 0.5 µg random hexamers (Life Technologies) added and the reverse transcription carried in thermal cycler with a heated lid under following conditions: 20 min at 37°C, 20 min at 42°C, 10 min at 50°C, 10 min at 55°C, 15 min at 65°C. SSS was perfomed ommitting the ligase under the above described conditions. Namely, 1 U RNase H was added to the reaction and incubation continued in thermal cycler for 30 min at 37°C, and then 2 min at 95°C. The reaction

was then chilled on ice, 100 ng (dT)-T7 primer added, and incubation continued for 10 min at 42°C. For the second IVT (2° IVT), modified biotin-11-UTP was included following the instruction of Enzo Diagnostics. The concentration was determined by $OD_{260/A280}$ reading.

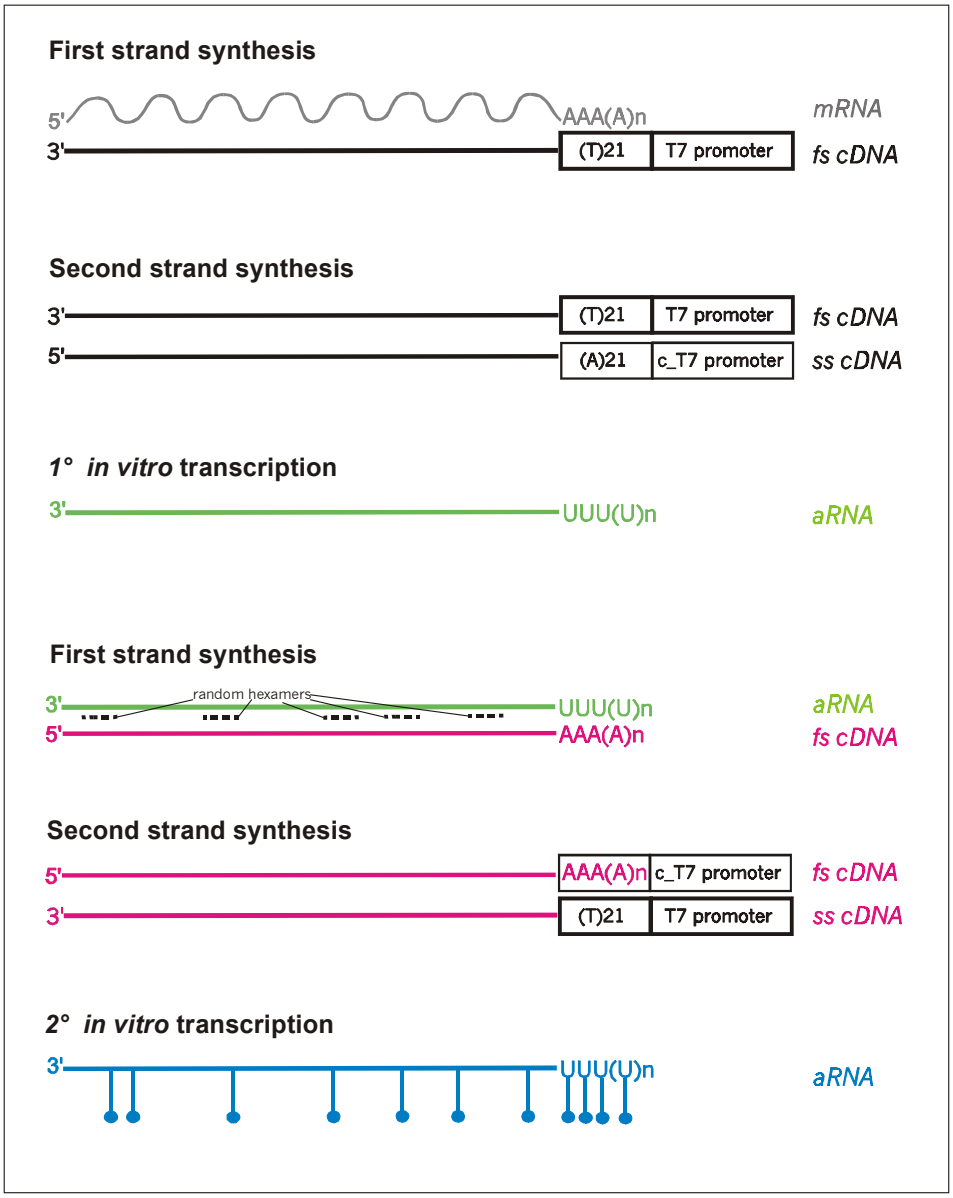



Figure 12. Generation of labelled aRNA probes by *in vitro* transcription (IVT)

Probes were generated according to described amplification protocol by Baugh et al. [120]. The first reverse transcription was performed using 200 ng of total RNA in the presence of T7 primer containing T7 promoter site and $T_{21}$ residues at its 3'end. During the second strand synthesis, antisense RNA (aRNA) was generated which was then used as a templet for the reverse transcription performed with random hexanuleotides. For the second IVT, biotinilated UTP was included to obtained labelled aRNA probes which were subsequently hybridised with oligonucleotide gene chip arrays.
fs cDNA - first strand cDNA
ss cDNA - second strand cDNA
aRNA - antisense RNA
c_T7promoter - antisense T7 promoter
the symbol indicates biotin-11-UTP

9 µg of each biotin-modified product was fragmented to 50- to 150-nt size in 1x fragmentation buffer for 35 min at 95°C, and the quality of unfragmented and fragmented cRNA checked by agarose gel electrophoresis. Five samples were hybridised to Affymetrix Test3 chip which demonstrated that the amplified cRNAs were of good quality. The samples were then hybridised to mouse GeneChip MuU74Av2 Array (Affymetrix) as described in the Affymetrix GeneChip Expression Analysis Technical Manual. After overnight hybridisation, arrays were washed and stained with streptavidin-phycoerythrin (Molecular Probes) and scanned on a HewlettPackard scanner.

Generated array images were reduced to intensity values, average differences (AD) and absolute calls [present (P)/absent (A)/marginal (M)] using GeneChip Software (MicroSuite version 4.0, Affymetrix, Santa Clara, CA). DNAs were considered expressed if their oligonucleotide set results were rated as P by the software. A single raw expression level for each gene was derived from the 16 oligonucleotide pairs representing each gene by using a trimmed mean algorithm. Genes/ESTs with the average difference (AD) less than 200 in all treated samples (i.e. unstimulated, LPS and dex+LPS stimulated cells) were considered unchanged because of their low expression levels. Absolute Calls (AC) from same treatments derived from 2 or 3 experiments, in case of wild type and $GR^{LysCre}$, and $GR^{dim}$ samples), were merged ("concatenated") using functions of Microsoft Excel software. The average (mean value) was calculated from the average difference (AD) values from 2-3 hybridisation experiments for each treatment. These values were than used to calculate the fold change of gene/ESTs expression, given as LPS/ctrl and LPS/dex+LPS, for differentially expressed transcripts Fold change$\geq$ 2 or Fold change$\leq$ 0.5. Filtering and sorting the data were performed with Microsoft Excel.

### 6. 2. 15. Bioinformatics and database development

Sequences from gene expression profile analysis were classified as known genes, ESTs, genomic sequences or novel genes. All the sequences or gene fragments were searched using BLAST algorhythm (available at *http://www.ncbi.nlm.nih.gov/BLAST/*) against GenBank indices. A

databases of genes or ESTs whose expression levels changed during LPS, dex+LPS stimulation was constructed containing information for each one. This included, if available, GenBank matches, Locus link or Unigene clusters, expression patterns, tissue distribution, subcellular localisation, family and superfamily classification, synonym(s) protein name, gene name(s), notation of possible functions, pathways involved, and hyperlinks to the database searches and related references. Supplementary information is available at *http://www.dkfz.de/tbi/macrophage*

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# 8. ABBREVIATIONS

(n)GREs - negative glucocorticoid responsive elements

65 kDa protein - macrophage cytosolic 65-kDa protein

A/P/M - Absent/Present/Marginal

ABC1 - ABC1 transporter

Acc. Num. - Accession Number

AD - Average Difference

AP-1 - Activator Protein 1

aRNA - antisense RNA

B94 - primary response gene B94

BID - BH3-interacting domain death agonist

BLAST - Basic Logical Alignment Search Tool

bp - base pairs

C3 $\alpha$, $\beta$ - complement component 3 $\alpha$, $\beta$ subunit

CBP - cAMP-responsive element binding protein (CREB)-binding protein

CCR - chemokine receptor

cDNA - complementary DNA

CDS - complementary DNA sequence

Clic4 - Chloride intracellular channel 4 (mitochondrial)

COX-2 - Cyclooxygenase

Cre - *Cre* recombinase

cyt-C - cytochrome C

DBD - DNA binding domain

DD - Differential Display

dex - dexamethasone

DNA - Deoxyribonucleic acid

dNTPs - deoxyribonucletide triphosphate

DTT - Dithiothreitol

Egr1 - Early growth response 1

EST - Expressed Sequence Tag

FCS - Foetal calf serum

flox - floxed loxP

fs cDNA - first strand cDNA

GCs - Glucocorticoids

G-CSF - Granulocytes-colony stimulating factor

GM-CSF - Granulocytes/macrophage-colony stimulating factor

GR - Glucocorticoid Receptor

$GR^{dim}$ - $GR^{dim/dim}$

GREs - glucocorticoid responsive elements

$GR^{LysCre}$ - $GR^{flox/flox;LysCre}$

GRO1 - growth factor-inducible immediate early gene (3CH134)

h - hours

HPRT - hypoxanthine phosphoribosyltransferase

hsp90 - heat-shock protein 90

ICAM-1 - Intracellular cell adhesion molecule 1

I-κB - Inhibitor of NF-κB

IL - Interleukin

IPTG - isopropylthio-ß-D-galactosid

Irg1 - Immune-resonsive gene 1

I-TRAF - Inhibitory TRAF

IVT - *in vitro* transcription

JNK - c-jun N-terminal kinase

kDa - kilo Daltons

KDO - 2-keto-2-deoxyoctulosonic acid

LAM - Lipoarabinomannan

LB - Luria broth

LBD - Ligand binding domain

LBP - LPS-binding protein

LPS - Lipopolysaccharide

Lys - Lysozyme

M-CSF - Macrophage-colony stimulating factor

MADP - Myeloid associated differention protein

MAP kinase - mitogen-activated protein kinase

MIP - Macrophage inflammatory protein

mRNA - messenger RNA

muPAR1 - mouse nurokinase-type plasminogen activator receptor, type 1

NF-AT - Nuclear factor of activated T cells

NF-κB - Nuclear factor kappaB

nt - nucleotides

ss DNA - second strand DNA

STAT - Signal transducers and activators of transcription

PAI - Plasminogen activator inhibitor

PAMPs - Pattern-associated molecular patterns

PBS - Phosphate saline buffer

PCR - Polymerase chain reaction

PM/MM - perfect match / mismatch

PMΦ - peritoneal macrophages

Pol - Polymerase

POMC - pro-opiomelanocortin

PRRs - Pattern-recognition receptors

RAP-PCR - RNA fingerprinting by arbitrary primer PCR

RDA - Representation difference analysis

rNTPs - ribonucletide triphosphate

SAGE - Serial Analysis of Gene Expression

SDM - Second Derivative Maximum software

SDS - Sodiumodecylsulphate

SMART II - Switching mechanism at 5' end of RNA template II

Sp1 - SV40 promoter-1

ss cDNA - second strand cDNA

SSH - Suppressive Subtractive Hybridisation

StDev - Standard Deviation

TLR - Toll-like receptor

TNF - Tumour necrosis factor

TNFR - TNF receptor

TRAF - TNFR-associated factor

UBP - ubiquitin binding protein (ubiquitin specific protease)

UTR - untranslated region

VCAM-1 - Vascuolar cell adhesion molecule 1

wt - wild type

X-gal - 5-bromo-4-chloro-3-indolyl-ß-D-galactosidase

Zfp - Zinc-finger protein

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# 10. APPENDIX

## 10. 1. GENE EXPRESSION PROFILES

Gene/ESTs which have been identified by SSH-, oligonucleotide gene array analysis and by real-time PCR, are grouped according to their expression patterns upon LPS- and dex+LPS stimulation of peritoneal macrophages from wild type, $GR^{dim}$ and $GR^{LysCre}$ mice.

Expression level of genes/EST obtained by SSH-array analysis were confirmed by real-time PCR and the values representing the Fold change are shown in orange, whereas those obtained by oligonucleotide gene chip arrays are in green.

Expression profiles of genes/ESTs representing Group 1-A, -B, -C, -D, -E and Group 2-A,-B, -C are shown as normalised values for **ctrl**, **LPS** and **dex+LPS**, obtained by following calculation method:

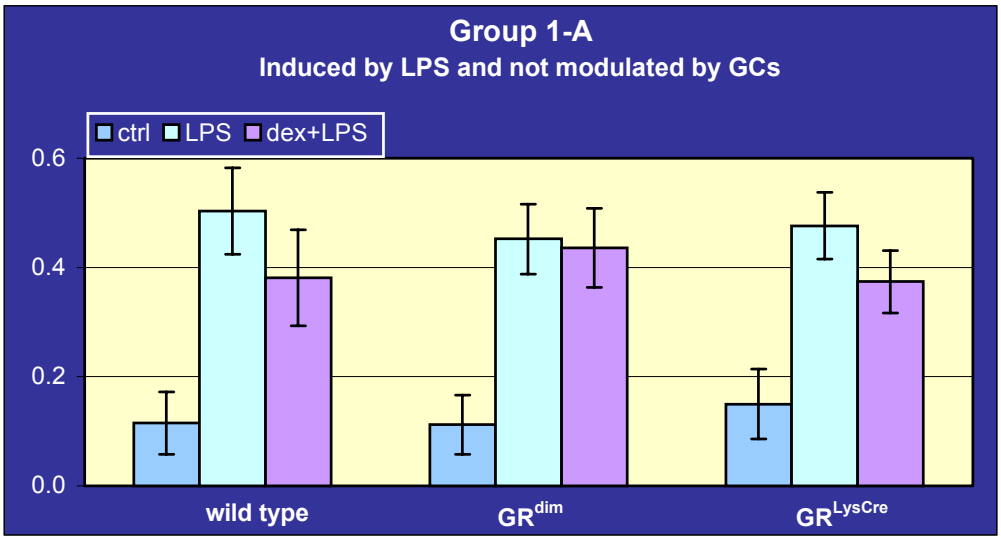
| Gene | expression levels | | | Sum | normalised expression | | |
|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS |
| "1" | $x_1$ | $y_1$ | $z_1$ | $x_1+y_1+z_1$ | $x_1/(x_1+y_1+z_1)$ | $y_1/(x_1+y_1+z_1)$ | $z_1/(x_1+y_1+z_1)$ |
| "2" | $x_2$ | $y_2$ | $z_2$ | $x_2+y_2+z_2$ | $x_2/(x_2+y_2+z_2)$ | $y_2/(x_2+y_2+z_2)$ | $z_2/(x_2+y_2+z_2)$ |
| : | : | : | : | : | : | : | : |
| : | : | : | : | : | : | : | : |
| "n" | $x_n$ | $y_n$ | $z_n$ | $x_n+y_n+z_n$ | $x_n/(x_n+y_n+z_n)$ | $y_n/(x_n+y_n+z_n)$ | $z_n/(x_n+y_n+z_n)$ |

$$\sum_{i=1}^{"n"} x_i/(x_i+y_i+z_i) \qquad \sum_{i=1}^{"n"} y_i/(x_i+y_i+z_i) \qquad \sum_{i=1}^{"n"} z_i/(x_i+y_i+z_i)$$

$$\frac{\sum_{i=1}^{"n"} x_i/(x_i+y_i+z_i)}{K} \qquad \frac{\sum_{i=1}^{"n"} y_i/(x_i+y_i+z_i)}{K} \qquad \frac{\sum_{i=1}^{"n"} z_i/(x_i+y_i+z_i)}{K}$$

*K…total number of genes/ESTs in a Group*

## 10. 2. GROUP 1-A




| | wild type | | | | GR dim | | | | GR LysCre | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS |
| Sum: | **14.65** | **63.91** | **48.43** | Sum: | **13.55** | **54.69** | **52.76** | Sum: | **18.20** | **57.58** | **45.22** |
| Mean: | **0.12** | **0.50** | **0.38** | Mean: | **0.11** | **0.45** | **0.44** | Mean: | **0.15** | **0.48** | **0.37** |
| StDev: | **0.06** | **0.08** | **0.09** | StDev: | **0.05** | **0.06** | **0.07** | StDev: | **0.06** | **0.06** | **0.06** |
| Fold change (LPS/ctrl) | | | **4.4** | Fold change (LPS/ctrl) | | | **4.0** | Fold change (LPS/ctrl) | | | **3.2** |
| Fold change (LPS/dex+LPS) | | | **1.3** | Fold change (LPS/dex+LPS) | | | **1.0** | Fold change (LPS/dex+LPS) | | | **1.3** |

### 10. 2. 1. Expression levels of genes/ESTs representing Group 1-A

| | | | | wild type | | | | Fold change | |
|---|---|---|---|---|---|---|---|---|---|
| Acc. | Gene/EST Name | ctrl | | LPS | | dex+LPS | | LPS | LPS |
| Num. | | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS |
| M62766 | 3-hydroxy-3-methylglutaryl-coenzyme A reductase | 231.05 | AA | 630.1 | PA | 550.55 | PP | 2.7 | 1.1 |
| U20159 | 76 kDa tyrosine phosphoprotein SLP-76 | 2701.2 | PP | 9712.7 | PP | 6870.65 | PP | 3.6 | 1.4 |
| AJ242778 | ABIN1 (A20-binding inhibitor of NF-kappa B activation. large) | 2390 | PP | 11725.2 | PP | 6170.3 | PP | 4.9 | 1.9 |
| AI644801 | Adora2a gene, exon 1 (and joined CDS) | 1783.75 | PP | 5123 | PP | 7213.05 | PP | 2.9 | 0.7 |
| U77630 | Adrenomedullin | 107.7 | AA | 2073.7 | PP | 2802.55 | PP | 19.3 | 0.7 |
| L36829 | alphaA-crystallin-binding protein I (alphaA-CRYBP1) gene | 148.25 | PA | 371.6 | PP | 430.8 | PP | 2.5 | 0.9 |
| L03290 | Amino acid transporter, cationic 2 (low affinity) | 5154.75 | PP | 23862.5 | PP | 13030.1 | PP | 4.6 | 1.8 |
| X82786 | Antigen identified by monoclonal antibody Ki 67 | 585.9 | PP | 7152.8 | PP | 7486.4 | PP | 12.2 | 1.0 |
| AF029215 | Antigen identified by monoclonal antibody MRC OX-2 | 306.3 | PP | 710.95 | PP | 603.25 | PP | 2.3 | 1.2 |
| AJ130975 | Ariadne-2 protein | 102.35 | PP | 566.45 | PP | 350 | PP | 5.5 | 1.6 |
| M61909 | Avian reticuloendotheliosis viral (v-rel) oncogene homolog A | 6859.6 | PP | 14086.2 | PP | 11018.9 | PP | 2.1 | 1.3 |
| U08185 | B lymphocyte induced maturation protein | 504.9 | PP | 1221.3 | PP | 1239.15 | PP | 2.4 | 1.0 |
| M64292 | B-cell translocation gene 2, anti-proliferative | 3849.7 | PP | 10871.1 | PP | 8526.8 | PP | 2.8 | 1.3 |
| AI844806 | Borg4 gene | 458.55 | AA | 1113.25 | PP | 1273.4 | PP | 2.4 | 0.9 |
| D85785 | Brain immunological-like with tyrosine-based motifs | 284.4 | AP | 1204.3 | PP | 629.3 | PP | 4.2 | 1.9 |
| M26071 | Coagulation factor III | 192.65 | PA | 9822.35 | PP | 6442.75 | PP | 51.0 | 1.5 |
| M13926 | Colony stimulating factor, granulocyte | 316.3 | AM | 9303.9 | PP | 7122.55 | PP | 29.4 | 1.3 |
| M63801 | connexin 43 (alpha-1 gap junction) | 147.15 | PA | 1847.15 | PP | 1630.2 | PP | 12.6 | 1.1 |
| U88325 | Cytokine inducible SH2-containing protein 7 | 109.2 | AA | 1036.65 | AP | 663 | PP | 9.5 | 1.6 |
| J04103 | E26 avian leukemia oncogene 2, 3 domain | 2862.45 | PP | 23700.7 | PP | 18098.3 | PP | 8.3 | 1.3 |
| M28845 | Early growth response 1 | 359.2 | PP | 2517.4 | PP | 3165.3 | PP | 7.0 | 0.8 |
| X70764 | ELKL motif kinase | 1977.55 | PP | 4648.7 | PP | 5759.45 | PP | 2.4 | 0.8 |
| D87691 | eRF1 | 3327.8 | PP | 9735.8 | PP | 5704.4 | PP | 2.9 | 1.7 |
| X61399 | F52 mRNA a novel protein | 2084.05 | PP | 20886.3 | PP | 21583.8 | PP | 10.0 | 1.0 |
| Z29532 | follistatin | 256.8 | AA | 1537.1 | PP | 808.05 | PP | 6.0 | 1.9 |
| AF017128 | Fos-like antigen 1 | 51.75 | AA | 382.6 | AP | 291.2 | PP | 7.4 | 1.3 |
| Y11666 | gene encoding hexokinase II, exon 1 (and joined CDS) | 189.6 | AP | 1404 | PP | 943.4 | PP | 7.4 | 1.5 |
| M73696 | Glvr-1 | 1278.25 | PP | 5256.75 | PP | 2671.2 | PP | 4.1 | 2.0 |
| U05265 | Glycoprotein 49 B | 5434.6 | PP | 15302.2 | PP | 7693.1 | PP | 2.8 | 2.0 |
| J04596 | GRO1 oncogene | 6890.65 | PP | 56231.3 | PP | 30771 | PP | 8.2 | 1.8 |
| M59821 | growth factor-inducible protein (pip92) | 657.7 | PP | 2379.25 | PP | 3369.8 | PP | 3.6 | 0.7 |
| U10551 | GTP binding protein (gene overexpressed in skeletal muscle) | 120.3 | PA | 2331.8 | PP | 1564.8 | PP | 19.4 | 1.5 |
| L09737 | GTP cyclohydrolase 1 | 1023.65 | PP | 3814.4 | PP | 2373.2 | PP | 3.7 | 1.6 |
| U23778 | hematopoietic-specific early-response A1-b protein (A1b) gene | 4054.35 | PP | 23670.2 | PP | 18522.6 | PP | 5.8 | 1.3 |
| U23781 | hematopoietic-specific early-response A1-d protein (A1d) gene | 7829.1 | PP | 37784.7 | PP | 22921.1 | PP | 4.8 | 1.6 |
| X57437 | Histidine decarboxylase cluster | 405.35 | AP | 3559.8 | PP | 2487.35 | PP | 8.8 | 1.4 |
| U57524 | I kappa B alpha gene, exons 2-6 | 1202.8 | AP | 7270.55 | PP | 4564.45 | PP | 6.0 | 1.6 |

| | | GR dim | | | | Fold change | | | | GR LysCre | | | | Fold change | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ctrl | | LPS | | dex+LPS | | LPS | LPS | ctrl | | LPS | | dex+LPS | | LPS | LPS | Grid |
| AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | position |
| 204.93 | PAA | 424.07 | PPA | 392.73 | PAA | 2.1 | 1.1 | 153.35 | PA | 408.50 | PP | 242.50 | AA | 2.7 | 1.7 | 104285_at |
| 2217.33 | PPP | 7544.10 | PPP | 7520.20 | PPP | 3.4 | 1.0 | 2767.20 | PP | 5544.60 | PP | 5106.95 | PP | 2.0 | 1.1 | 102957_at |
| 2982.63 | PPP | 11462.53 | PPP | 14349.13 | PPP | 3.8 | 0.8 | 4187.65 | PP | 14819.40 | PP | 11757.55 | PP | 3.5 | 1.3 | 104755_at |
| 1661.40 | PPP | 6391.63 | PPP | 4922.47 | PPP | 3.8 | 1.3 | 1313.30 | PP | 4703.80 | PP | 3686.10 | PP | 3.6 | 1.3 | 101363_at |
| 84.13 | AAA | 1300.93 | PPP | 1240.73 | PPP | 15.5 | 1.0 | 95.60 | AA | 679.85 | PP | 364.75 | PP | 7.1 | 1.9 | 102798_at |
| 163.20 | AAA | 373.30 | PPA | 408.47 | PPA | 2.3 | 0.9 | 112.45 | PA | 325.45 | PP | 252.05 | PA | 2.9 | 1.3 | 92908_at |
| 3324.73 | PAP | 13674.37 | PPP | 19361.53 | PPP | 4.1 | 0.7 | 5364.40 | PP | 14765.40 | PP | 9711.25 | PP | 2.8 | 1.5 | 92736_at |
| 371.93 | AAP | 6162.57 | PPP | 7285.70 | PPP | 16.6 | 0.8 | 553.75 | PP | 4743.60 | PP | 6895.20 | PP | 8.6 | 0.7 | 99457_at |
| 215.23 | PAP | 690.43 | PPP | 272.60 | PAP | 3.2 | 2.5 | 557.20 | PP | 1706.40 | PP | 1187.50 | PP | 3.1 | 1.4 | 101851_at |
| 219.33 | MAP | 570.53 | PPP | 627.70 | PPP | 2.6 | 0.9 | 218.65 | PA | 469.85 | PP | 439.70 | PP | 2.1 | 1.1 | 95600_at |
| 6241.90 | PPP | 14194.93 | PPP | 11763.90 | PPP | 2.3 | 1.2 | 6077.35 | PP | 12957.05 | PP | 10041.80 | PP | 2.1 | 1.3 | 97813_at |
| 483.93 | PPP | 1458.53 | PPP | 1702.03 | PPP | 3.0 | 0.9 | 802.85 | PP | 2008.10 | PP | 2107.65 | PP | 2.5 | 1.0 | 92904_at |
| 3399.20 | PPP | 12374.13 | PPP | 7983.17 | PPP | 3.6 | 1.6 | 4668.00 | PP | 10511.00 | PP | 12683.40 | PP | 2.3 | 0.8 | 101583_at |
| 346.47 | AAA | 1120.70 | PPP | 2239.97 | PPP | 3.2 | 0.5 | 647.45 | AA | 2004.35 | PP | 2129.25 | PP | 3.1 | 0.9 | 94036_at |
| 360.03 | PAA | 1337.60 | PPP | 1126.27 | PPP | 3.7 | 1.2 | 967.45 | PA | 2334.90 | PP | 1178.85 | PP | 2.4 | 2.0 | 95804_g_at |
| 454.10 | AAP | 3999.13 | PPP | 3839.87 | PPP | 8.8 | 1.0 | 479.40 | PA | 6147.40 | PP | 4303.20 | PP | 12.8 | 1.4 | 97689_at |
| 172.93 | MAA | 7244.17 | PPP | 6817.07 | PPP | 41.9 | 1.1 | 600.30 | PA | 7778.10 | PP | 5791.45 | PP | 13.0 | 1.3 | 94142_at |
| 279.67 | AAP | 1451.67 | PPP | 3060.20 | PPP | 5.2 | 0.5 | 819.65 | PP | 3930.95 | PP | 3254.25 | PP | 4.8 | 1.2 | 100064_f_at |
| 110.47 | AAA | 872.97 | PPP | 738.57 | PPP | 7.9 | 1.2 | 329.05 | PA | 1607.90 | PA | 1540.20 | PA | 4.9 | 1.0 | 92832_at |
| 2891.83 | PPP | 21039.80 | PPP | 23990.20 | PPP | 7.3 | 0.9 | 4045.65 | PP | 21848.95 | PP | 18077.15 | PP | 5.4 | 1.2 | 94246_at |
| 675.97 | APP | 3464.57 | PPA | 1950.73 | PPA | 5.1 | 1.8 | 633.50 | PA | 3480.85 | PP | 3210.00 | PP | 5.5 | 1.1 | 98579_at |
| 2278.60 | PPP | 4608.80 | PPP | 4158.43 | PPP | 2.0 | 1.1 | 1506.40 | PP | 3719.40 | PP | 4849.00 | PP | 2.5 | 0.8 | 99458_i_at |
| 2679.77 | PPP | 6340.57 | PPP | 7783.00 | PPP | 2.4 | 0.8 | 3469.95 | PP | 8200.15 | PP | 5922.80 | PP | 2.4 | 1.4 | 160451_at |
| 3207.77 | PPP | 24164.27 | PPP | 21991.37 | PPP | 7.5 | 1.1 | 3970.40 | PP | 20244.75 | PP | 16930.55 | PP | 5.1 | 1.2 | 97203_at |
| 80.60 | APA | 348.03 | PPP | 457.33 | PPP | 4.3 | 0.8 | 652.10 | PP | 2757.45 | PP | 2372.60 | PP | 4.2 | 1.2 | 98817_at |
| 137.20 | AAA | 701.80 | PPP | 578.00 | PPP | 5.1 | 1.2 | 91.30 | AA | 535.65 | PP | 344.15 | MP | 5.9 | 1.6 | 99835_at |
| 607.40 | AAP | 1331.63 | PPP | 1294.33 | PPP | 2.2 | 1.0 | 563.70 | PP | 1496.20 | PP | 885.80 | PP | 2.7 | 1.7 | 94375_at |
| 931.87 | PPP | 3105.70 | PPP | 1788.43 | PPP | 3.3 | 1.7 | 1684.80 | PP | 6240.65 | PP | 4852.95 | PP | 3.7 | 1.3 | 103065_at |
| 6821.97 | PPP | 15567.70 | PPP | 15847.70 | PPP | 2.3 | 1.0 | 7266.90 | PP | 15696.45 | PP | 11262.10 | PP | 2.2 | 1.4 | 92217_s_at |
| 6924.90 | PPP | 56210.63 | PPP | 52517.03 | PPP | 8.1 | 1.1 | 20639.50 | PP | 56899.25 | PP | 57935.25 | PP | 2.8 | 1.0 | 95349_g_at |
| 1080.50 | PPP | 2739.57 | PPP | 2107.33 | PPP | 2.5 | 1.3 | 768.85 | PP | 1879.00 | PP | 1406.10 | PP | 2.4 | 1.3 | 99109_at |
| 103.57 | AAP | 889.57 | PPP | 1292.27 | PPP | 8.6 | 0.7 | 195.10 | PA | 1910.05 | PP | 1684.30 | PP | 9.8 | 1.1 | 92534_at |
| 1142.10 | PPP | 3903.37 | PPP | 3918.20 | PPP | 3.4 | 1.0 | 1589.10 | PP | 5072.75 | PP | 3868.95 | PP | 3.2 | 1.3 | 102313_at |
| 3819.67 | PPP | 23636.97 | PPP | 20781.57 | PPP | 6.2 | 1.1 | 5400.70 | PP | 19754.50 | PP | 15606.45 | PP | 3.7 | 1.3 | 102914_s_at |
| 8233.67 | PAP | 35843.63 | PPP | 30809.93 | PPP | 4.4 | 1.2 | 11645.90 | PP | 30665.70 | PP | 28098.75 | PP | 2.6 | 1.1 | 93869_s_at |
| 597.53 | AAP | 2874.33 | PPP | 4189.03 | PPP | 4.8 | 0.7 | 423.15 | PA | 5058.25 | PP | 2768.25 | PP | 12.0 | 1.8 | 93328_at |
| 1440.57 | APP | 4955.43 | PPP | 5897.30 | PPP | 3.4 | 0.8 | 1112.80 | PP | 4762.35 | PP | 4435.50 | PP | 4.3 | 1.1 | 101554_at |

| | | | | wild type | | | | Fold change | |
|---|---|---|---|---|---|---|---|---|---|
| Acc. | Gene/EST Name | ctrl | | LPS | | dex+LPS | | LPS | LPS |
| Num. | | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS |
| U19799 | IkB-beta | 3073.05 | PP | 9275.15 | PP | 6941 | PP | 3.0 | 1.3 |
| L38281 | Immunoresponsive gene 1 | 493 | AA | 11356.5 | PP | 7864.75 | PP | 23.0 | 1.4 |
| U14135 | Integrin alpha V (Cd51) | 118.85 | PA | 268.45 | MP | 177.2 | PP | 2.3 | 1.5 |
| M90551 | Intercellular adhesion molecule | 3079.7 | PP | 8117.65 | PP | 7277.75 | PP | 2.6 | 1.1 |
| M14639 | Interleukin 1 alpha | 4186.35 | PP | 68021.8 | PP | 40521.1 | PP | 16.2 | 1.7 |
| AV152244 | ISG15 gene | 143 | AP | 2704.95 | AP | 1949.75 | PP | 18.9 | 1.4 |
| AB024717 | macrophage C-type lectin Mincle | 2970.25 | PP | 17033.3 | PP | 11314 | PP | 5.7 | 1.5 |
| AB033887 | mACS4 variant2 mRNA Acyl-CoA synthetase 4 variant2 | 431.45 | PP | 984.2 | PP | 510.55 | PP | 2.3 | 1.9 |
| Y15163 | mrg1 protein | 986.75 | PP | 6929.55 | PP | 5315.25 | PP | 7.0 | 1.3 |
| X62700 | muPAR1 mRNA | 1145.65 | PP | 4277.8 | PP | 4387.1 | PP | 3.7 | 1.0 |
| X54149 | Myeloid differentiation primary response gene 118 | 1722.15 | PP | 14243.3 | PP | 9224.7 | PP | 8.3 | 1.5 |
| AF073882 | myotubularin related protein 7 | 94.15 | AA | 683 | PP | 343.2 | PP | 7.3 | 2.0 |
| AW047899 | NF-kappaB subunit p100 (Nfkb2) | 1490.2 | PP | 6728.3 | PP | 4304.4 | PP | 4.5 | 1.6 |
| M57999 | Nuclear factor of kappa light chain gene enhancer in B-cells 1, p105 | 10189.2 | PP | 41537.4 | PP | 24668.9 | PP | 4.1 | 1.7 |
| X87128 | p75 TNF receptor DNA | 12037.3 | PP | 53911.8 | PP | 30292.9 | PP | 4.5 | 1.8 |
| AI060798 | PGES prostaglandin E synthase | 5694.9 | PP | 16964.5 | PP | 11120.5 | PP | 3.0 | 1.5 |
| AF020313 | proline-rich protein 48 | 4475.85 | PP | 12988.2 | PP | 9174.3 | PP | 2.9 | 1.4 |
| D83484 | protein tyrosine phosphatase epsilon | 3488.75 | PP | 10779.1 | PP | 7296.7 | PP | 3.1 | 1.5 |
| AF030185 | putative beta chemokine receptor (E01) | 1186.55 | PP | 30187.8 | PP | 18011.3 | PP | 25.4 | 1.7 |
| AW047476 | Putative purine nucleotide binding protein | 1787.45 | PP | 5868.85 | PP | 3080.25 | PP | 3.3 | 1.9 |
| AI852608 | RNA 3'-terminal phosphate cyclase like protein (rcl1 gene) | 840.1 | PP | 6134.9 | PP | 7513.5 | PP | 7.3 | 0.8 |
| AF099973 | schlafen2 (Slfn2) | 30655.4 | PP | 68634 | PP | 55098 | PP | 2.2 | 1.2 |
| D78188 | SCID complementing gene 2 | 6877.7 | PP | 13842.9 | PP | 7413.45 | PP | 2.0 | 1.9 |
| U10531 | Ski/sno related | 88.65 | AA | 908.05 | PP | 505.05 | PP | 10.2 | 1.8 |
| J04491 | Small inducible cytokine A3 | 1873.95 | PP | 51543.4 | PP | 36185.8 | PP | 27.5 | 1.4 |
| U88328 | suppressor of cytokine signalling-3 (SOCS-3) | 715.95 | AP | 13336 | PP | 8692.25 | PP | 18.6 | 1.5 |
| L35302 | Tnf receptor-associated factor 1 | 801.55 | PP | 7488.95 | PP | 5576 | PP | 9.3 | 1.3 |
| D78141 | Tnf receptor-associated factor 5 | 2326.9 | PP | 5521.75 | PP | 5381.6 | PP | 2.4 | 1.0 |
| X70956 | TOP gene topoisomerase I, exons 19-21 | 3045.05 | PP | 13531.3 | PP | 10191 | PP | 4.4 | 1.3 |
| U59864 | TRAF-interacting protein I-TRAF | 2182.8 | PP | 8861.45 | PP | 5232.05 | PP | 4.1 | 1.7 |
| X62940 | Transming growth factor beta 1 induced transcript 4 | 518.7 | PP | 4082.15 | PP | 5307.3 | PP | 7.9 | 0.8 |
| L15435 | Tumor necrosis factor (ligand) superfamily, member 9 | 304.15 | AA | 18749.8 | PP | 22043 | PP | 61.6 | 0.9 |
| L24118 | Tumor necrosis factor induced protein 2 | 6218.7 | PP | 40661.2 | PP | 28317.8 | PP | 6.5 | 1.4 |
| M83312 | Tumor necrosis factor receptor superfamily, member 5 | 497.5 | PP | 2801.55 | PP | 1714.1 | PP | 5.6 | 1.6 |
| AI854821 | U8 gene | 2255.25 | PP | 6753.5 | PP | 3551.05 | PP | 3.0 | 1.9 |
| AB030505 | UBE-1c1, UBE-1c2, UBE-1c3 | 1431.65 | PP | 5339.55 | PP | 2817.35 | PP | 3.7 | 1.9 |
| X14678 | Zinc finger protein 36 | 1314.6 | PP | 5459.1 | PP | 3458.55 | PP | 4.2 | 1.6 |

| | | GR dim | | | | Fold change | | | | GR LysCre | | | | Fold change | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ctrl | | LPS | | dex+LPS | | LPS | LPS | ctrl | | LPS | | dex+LPS | | LPS | LPS | Grid |
| AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | position |
| 3912.43 | PPP | 12936.00 | PPP | 14003.63 | PPP | 3.3 | 0.9 | 3811.05 | PP | 10272.75 | PP | 7887.95 | PP | 2.7 | 1.3 | 99982_at |
| 510.73 | AAP | 10347.60 | PPP | 10490.33 | PPP | 20.3 | 1.0 | 770.35 | PA | 7678.05 | PP | 7114.20 | PP | 10.0 | 1.1 | 98774_at |
| 82.63 | AAP | 250.07 | APP | 272.00 | PPP | 3.0 | 0.9 | 57.80 | AA | 321.55 | PA | 137.55 | PA | 5.6 | 2.3 | 98366_at |
| 2207.73 | PPP | 7671.47 | PPP | 9948.17 | PPP | 3.5 | 0.8 | 3226.70 | PP | 9173.00 | PP | 6879.75 | PP | 2.8 | 1.3 | 96752_at |
| 4375.10 | PPP | 53808.60 | PPP | 52001.20 | PPP | 12.3 | 1.0 | 15713.90 | PP | 61153.05 | PP | 56106.20 | PP | 3.9 | 1.1 | 94755_at |
| 98.87 | AAP | 2913.50 | PPP | 2066.17 | PPP | 29.5 | 1.4 | 194.90 | PP | 978.70 | PP | 396.85 | PA | 5.0 | 2.5 | 161511_f_at |
| 4203.20 | PPP | 14740.50 | PPP | 11127.80 | PPP | 3.5 | 1.3 | 6202.55 | PP | 17337.65 | PP | 11685.85 | PP | 2.8 | 1.5 | 96551_at |
| 185.60 | AAP | 449.33 | PPP | 796.87 | PPP | 2.4 | 0.6 | 448.80 | PP | 930.85 | PP | 629.35 | PP | 2.1 | 1.5 | 104017_at |
| 1036.60 | PPP | 3298.97 | PPP | 3363.53 | PPP | 3.2 | 1.0 | 1265.50 | PP | 5223.55 | PP | 3950.80 | PP | 4.1 | 1.3 | 101973_at |
| 2038.87 | PPP | 7393.50 | PPP | 6690.10 | PPP | 3.6 | 1.1 | 1389.90 | PP | 4484.40 | PP | 3258.65 | PP | 3.2 | 1.4 | 102663_at |
| 1653.00 | PPP | 17925.80 | PPP | 17013.07 | PPP | 10.8 | 1.1 | 6706.55 | PP | 19848.70 | PP | 13729.80 | PP | 3.0 | 1.4 | 102779_at |
| 82.10 | AAP | 476.43 | PPP | 632.57 | PPP | 5.8 | 0.8 | 71.90 | AA | 439.40 | PA | 233.00 | PA | 6.1 | 1.9 | 103228_at |
| 2104.97 | PPP | 9363.60 | PPP | 8058.07 | PPP | 4.4 | 1.2 | 2121.90 | PP | 8364.65 | PP | 5363.45 | PP | 3.9 | 1.6 | 103614_at |
| 14055.43 | PPP | 46612.30 | PPP | 39582.90 | PPP | 3.3 | 1.2 | 14866.05 | PP | 35463.75 | PP | 28680.00 | PP | 2.4 | 1.2 | 98427_s_at |
| 11968.90 | PPP | 35488.67 | PPP | 34498.87 | PPP | 3.0 | 1.0 | 15930.70 | PP | 44496.70 | PP | 31629.50 | PP | 2.8 | 1.4 | 94928_at |
| 5259.97 | PPP | 20098.47 | PPP | 17289.70 | PPP | 3.8 | 1.2 | 10599.35 | PP | 21484.65 | PP | 17979.45 | PP | 2.0 | 1.2 | 104406_at |
| 7716.00 | PPP | 16341.43 | PPP | 10733.10 | PPP | 2.1 | 1.5 | 5316.80 | PP | 12791.15 | PP | 10757.95 | PP | 2.4 | 1.2 | 102710_at |
| 3150.83 | PPP | 8572.73 | PPP | 7759.03 | PPP | 2.7 | 1.1 | 3846.35 | PP | 11117.50 | PP | 6242.80 | PP | 2.9 | 1.8 | 101932_at |
| 1602.63 | PPP | 18584.07 | PPP | 18780.93 | PPP | 11.6 | 1.0 | 1502.05 | PP | 15915.50 | PP | 11172.20 | PP | 10.6 | 1.4 | 93617_at |
| 1751.10 | PPP | 8476.17 | PPP | 9062.73 | PPP | 4.8 | 0.9 | 3068.05 | PP | 7955.95 | PP | 5082.75 | PP | 2.6 | 1.6 | 103202_at |
| 1032.97 | PPP | 4794.03 | PPP | 7464.93 | PPP | 4.6 | 0.6 | 2050.55 | PP | 7278.60 | PP | 4685.00 | PP | 3.5 | 1.6 | 98923_at |
| 17892.13 | PPP | 73197.40 | PPP | 79388.67 | PPP | 4.1 | 0.9 | 22527.15 | PP | 64343.15 | PP | 60141.95 | PP | 2.9 | 1.1 | 92471_i_at |
| 8184.07 | PPP | 16897.00 | PPP | 8998.47 | PPP | 2.1 | 1.9 | 7086.70 | PP | 17483.50 | PP | 11702.75 | PP | 2.5 | 1.5 | 160468_at |
| 150.57 | AAA | 427.17 | PPA | 722.37 | PPA | 2.8 | 0.6 | 183.55 | PA | 1086.40 | PP | 522.30 | PP | 5.9 | 2.1 | 94752_s_at |
| 1701.17 | PPP | 41635.97 | PPP | 49390.90 | PPP | 24.5 | 0.8 | 8023.00 | PP | 57805.20 | PP | 44083.20 | PP | 7.2 | 1.3 | 102424_at |
| 1337.53 | AAP | 18737.33 | PPP | 17795.50 | PPP | 14.0 | 1.1 | 1630.95 | PP | 12542.10 | PP | 8808.30 | PP | 7.7 | 1.4 | 92232_at |
| 804.40 | APP | 6553.23 | PPP | 5571.57 | PPP | 8.1 | 1.2 | 2403.50 | PP | 11337.40 | PP | 7759.95 | PP | 4.7 | 1.5 | 94186_at |
| 2313.23 | PPP | 4921.27 | PPP | 4483.07 | PPP | 2.1 | 1.1 | 2323.85 | PP | 6010.15 | PP | 3788.00 | PP | 2.6 | 1.6 | 103255_at |
| 5410.57 | PPP | 12293.83 | PPP | 12071.00 | PPP | 2.3 | 1.0 | 4823.60 | PP | 17435.25 | PP | 13432.70 | PP | 3.6 | 1.3 | 95694_at |
| 1911.63 | PPP | 5623.10 | PPP | 6398.23 | PPP | 2.9 | 0.9 | 3888.60 | PP | 9027.55 | PP | 6836.70 | PP | 2.3 | 1.3 | 103328_at |
| 532.90 | PPP | 4774.47 | PPP | 2240.30 | PPP | 9.0 | 2.1 | 288.85 | PA | 4495.05 | PP | 4487.55 | PP | 15.6 | 1.0 | 93728_at |
| 338.27 | AAA | 20047.70 | PPP | 24029.30 | PPP | 59.3 | 0.8 | 206.95 | AA | 6017.50 | PP | 6381.90 | PP | 29.1 | 0.9 | 92415_at |
| 7113.90 | PPP | 44771.23 | PPP | 34607.13 | PPP | 6.3 | 1.3 | 9218.55 | PP | 31749.40 | PP | 24571.60 | PP | 3.4 | 1.3 | 160489_at |
| 801.50 | PPP | 6357.20 | PPP | 3331.13 | PPP | 7.9 | 1.9 | 976.30 | PP | 3407.75 | PP | 2058.40 | PP | 3.5 | 1.7 | 92962_at |
| 1920.33 | PPP | 5597.93 | PPP | 5668.00 | PPP | 2.9 | 1.0 | 3262.25 | PP | 7520.50 | PP | 5136.65 | PP | 2.3 | 1.5 | 160171_f_at |
| 1192.30 | PPP | 3132.53 | PPP | 2323.00 | PPP | 2.6 | 1.3 | 1595.30 | PP | 4407.15 | PP | 3415.75 | PP | 2.8 | 1.3 | 99592_f_at |
| 1609.90 | PPP | 5432.77 | PPP | 3822.00 | PPP | 3.4 | 1.4 | 2383.65 | PP | 7561.90 | PP | 5417.10 | PP | 3.2 | 1.4 | 92830_s_at |

| | | | | wild type | | | | Fold change | |
|---|---|---|---|---|---|---|---|---|---|
| Acc. | Gene/EST Name | ctrl | | LPS | | dex+LPS | | LPS | LPS |
| Num. | | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS |
| AI323667 | mp96e12.x1 Mus musculus cDNA, 3 end | 5010.1 | PP | 46000.3 | PP | 37691.4 | PP | 9.2 | 1.2 |
| AA168418 | mr29a03.r1 Mus musculus cDNA, 5 end | 173.65 | AA | 534.8 | PA | 451.8 | PP | 3.1 | 1.2 |
| AI592541 | ms93f10.y1 Mus musculus cDNA, 5 end | 533.9 | AA | 2643.75 | PP | 1348.85 | PP | 5.0 | 2.0 |
| AA204579 | mt84d11.r1 Mus musculus cDNA, 5 end | 308.35 | PA | 1470 | PP | 842.4 | PP | 4.8 | 1.7 |
| AV138783 | Mus musculus cDNA | 3748.1 | PP | 23467 | PP | 14877.9 | PP | 6.3 | 1.6 |
| AV374591 | Mus musculus cDNA, 3 end | 35.45 | AA | 3497.35 | PP | 2553.05 | PP | 98.7 | 1.4 |
| C78513 | Mus musculus cDNA, 3 end | 167.3 | AP | 6264.8 | PP | 3931.3 | PP | 37.4 | 1.6 |
| AV374868 | Mus musculus cDNA, 3 end | 2545.45 | PP | 26143.8 | PP | 22029.7 | PP | 10.3 | 1.2 |
| C76063 | Mus musculus cDNA, 3 end | 187.2 | PA | 1026.9 | PP | 772.25 | PP | 5.5 | 1.3 |
| AV309347 | Mus musculus cDNA, 3 end | 655.2 | PP | 2811.35 | PA | 4122.25 | PP | 4.3 | 0.7 |
| AV341518 | Mus musculus cDNA, 3 end | 675.1 | PP | 1952.2 | PP | 1221.9 | PP | 2.9 | 1.6 |
| AA959291 | ua14g10.r1 Mus musculus cDNA, 5 end | 277.95 | MP | 986.2 | PP | 755.1 | PP | 3.5 | 1.3 |
| AI006319 | ua70b05.r1 Mus musculus cDNA, 5 end | 942.75 | PP | 2938.6 | PP | 1905.05 | PP | 3.1 | 1.5 |
| AA833425 | ub58d03.r1 Mus musculus cDNA, 5 end | 2368.2 | PP | 7494.95 | PP | 5159.25 | PP | 3.2 | 1.5 |
| AA960466 | ub58f11.s1 Mus musculus cDNA, 3 end | 1185.6 | PP | 2843.55 | PP | 2048.35 | PP | 2.4 | 1.4 |
| AI462105 | ub70b01.x1 Mus musculus cDNA, 3 end | 929.4 | PP | 3901.15 | PP | 2430.65 | PP | 4.2 | 1.6 |
| AI642048 | ub75b05.x1 Mus musculus cDNA, 3 end | 4457.25 | PP | 21789.6 | PP | 20765.8 | PP | 4.9 | 1.0 |
| AI286698 | ub84b09.r1 Mus musculus cDNA, 5 end | 5214.65 | PP | 12311 | PP | 12468.1 | PP | 2.4 | 1.0 |
| AI837100 | UI-M-AK0-adc-d-02-0-UI.s1 Mus musculus cDNA, 3 end | 673.65 | PP | 3452.55 | PP | 2833.65 | PP | 5.1 | 1.2 |
| AI846304 | UI-M-AK1-aez-g-06-0-UI.s1 Mus musculus cDNA, 3 end | 508.15 | AP | 1758.65 | PP | 1483.1 | PP | 3.5 | 1.2 |
| AI837543 | UI-M-AL0-abs-d-04-0-UI.s1 Mus musculus cDNA, 3 end | 226.35 | PP | 514.45 | PA | 558.45 | PP | 2.3 | 0.9 |
| AI844128 | UI-M-AL1-ahj-d-06-0-UI.s1 Mus musculus cDNA, 3 end | 1304.55 | PP | 4817.7 | PP | 4958.9 | PP | 3.7 | 1.0 |
| AI840446 | UI-M-AN0-aci-b-05-0-UI.s1 Mus musculus cDNA, 3 end | 346.9 | MA | 1039.45 | PP | 619.5 | PP | 3.0 | 1.7 |
| AI845886 | UI-M-AO1-aeg-h-09-0-UI.s1 Mus musculus cDNA, 3 end | 3011.6 | PP | 7897 | PP | 6557.2 | PP | 2.6 | 1.2 |
| AI852645 | UI-M-BH0-aiu-h-04-0-UI.s1 Mus musculus cDNA, 3 end | 233.55 | PP | 596.1 | PP | 461.2 | PP | 2.6 | 1.3 |
| AI852144 | UI-M-BH0-ajb-e-09-0-UI.s1 Mus musculus cDNA, 3 end | 2864.4 | PP | 10106 | PP | 7454.3 | PP | 3.5 | 1.4 |
| AI854506 | UI-M-BH0-ajj-b-09-0-UI.s1 Mus musculus cDNA, 3 end | 436.75 | PA | 3644.9 | PP | 2064.55 | PP | 8.3 | 1.8 |
| AI853712 | UI-M-BH0-ajq-d-05-0-UI.s1 Mus musculus cDNA, 3 end | 420.4 | PP | 1884.55 | PP | 1825.7 | PP | 4.5 | 1.0 |
| AW046627 | UI-M-BH1-ald-c-09-0-UI.s1 Mus musculus cDNA, 3 end | 431.75 | AP | 3521.1 | PP | 3506.35 | PP | 8.2 | 1.0 |
| AW047023 | UI-M-BH1-alp-h-11-0-UI.s1 Mus musculus cDNA, 3 end | 6536.8 | PP | 15083.5 | PP | 10257.9 | PP | 2.3 | 1.5 |
| AW047811 | UI-M-BH1-als-a-04-0-UI.s1 Mus musculus cDNA, 3 end | 3115.4 | PP | 9709.5 | PP | 16104.2 | PP | 3.1 | 0.6 |
| AW048937 | UI-M-BH1-amo-d-08-0-UI.s1 Mus musculus cDNA, 3 end | 2290.8 | PP | 9615.05 | PP | 11651.8 | PP | 4.2 | 0.8 |
| AW049031 | UI-M-BH1-amp-g-08-0-UI.s1 Mus musculus cDNA, 3 end | 8996.3 | PP | 18128.7 | PP | 9698.3 | PP | 2.0 | 1.9 |
| AW124934 | UI-M-BH2.1-apu-g-11-0-UI.s1 Mus musculus cDNA, 3 end | 374.05 | PP | 2095.8 | PP | 2089.75 | PP | 5.6 | 1.0 |
| AW123514 | UI-M-BH2.1-aqb-c-04-0-UI.s1 Mus musculus cDNA, 3 end | 248.1 | AP | 802.6 | PP | 760.15 | PP | 3.2 | 1.1 |
| AW215863 | up02c11.x1 Mus musculus cDNA, 3 end | 209.65 | AP | 812.45 | AP | 1225.75 | PP | 3.9 | 0.7 |
| AA259683 | va36d09.r1 Mus musculus cDNA, 5 end | 222 | PA | 967.05 | PP | 552.35 | PP | 4.4 | 1.8 |

| | | GR dim | | | | Fold change | | | | GR LysCre | | | | Fold change | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ctrl | | LPS | | dex+LPS | | LPS | LPS | ctrl | | LPS | | dex+LPS | | LPS | LPS | Grid |
| AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | position |
| 5989.10 | PPP | 42998.43 | PPP | 42143.97 | PPP | 7.2 | 1.0 | 7242.15 | PP | 39890.75 | PP | 33177.75 | PP | 5.5 | 1.2 | 98773_s_at |
| 183.80 | AAP | 499.37 | PPP | 610.17 | PPP | 2.7 | 0.8 | 328.55 | PA | 684.05 | PP | 600.75 | PP | 2.1 | 1.1 | 93462_at |
| 290.60 | AAA | 2069.03 | PPP | 1468.37 | PPP | 7.1 | 1.4 | 800.65 | PP | 2387.45 | PP | 1808.35 | PP | 3.0 | 1.3 | 103691_at |
| 87.30 | PAA | 3193.47 | PPA | 2482.50 | APA | 36.6 | 1.3 | 188.90 | PA | 48.10 | PA | 113.60 | PA | 0.3 | 0.4 | 104177_at |
| 3797.27 | PPP | 26414.00 | PPP | 24899.60 | PPP | 7.0 | 1.1 | 9512.25 | PP | 30040.85 | PP | 22345.55 | PP | 3.2 | 1.3 | 161666_f_at |
| 170.53 | AAP | 3312.73 | PPP | 2715.23 | PPP | 19.4 | 1.2 | 294.35 | PP | 2439.65 | PP | 2656.10 | PP | 8.3 | 0.9 | 161903_f_at |
| 358.27 | AAP | 9171.23 | PPP | 7693.07 | PPP | 25.6 | 1.2 | 308.45 | PA | 4787.50 | PP | 2971.40 | PP | 15.5 | 1.6 | 97693_at |
| 3609.03 | PPP | 30376.87 | PPP | 28130.87 | PPP | 8.4 | 1.1 | 5176.20 | PP | 25088.95 | PP | 21586.85 | PP | 4.8 | 1.2 | 162206_f_at |
| 308.37 | PPA | 1223.83 | PPP | 822.93 | PPP | 4.0 | 1.5 | 277.60 | PA | 639.35 | PP | 417.90 | PA | 2.3 | 1.5 | 95848_at |
| 561.53 | PPP | 3679.57 | PPP | 3995.10 | PPP | 6.6 | 0.9 | 444.50 | PA | 2719.35 | PP | 4132.65 | PP | 6.1 | 0.7 | 161931_r_at |
| 418.00 | PAP | 1082.70 | PPP | 1098.03 | APP | 2.6 | 1.0 | 1034.75 | PP | 2639.95 | PP | 1998.30 | PP | 2.6 | 1.3 | 162095_f_at |
| 318.80 | PAP | 916.87 | PPP | 604.13 | PPP | 2.9 | 1.5 | 280.40 | PA | 658.95 | PP | 840.85 | PP | 2.4 | 0.8 | 99874_at |
| 1002.97 | PPP | 2606.80 | PPP | 2731.90 | PPP | 2.6 | 1.0 | 1365.35 | PP | 2818.70 | PP | 2166.45 | PP | 2.1 | 1.3 | 94980_at |
| 3174.80 | PPP | 8368.87 | PPP | 6196.70 | PPP | 2.6 | 1.4 | 3243.40 | PP | 7675.55 | PP | 6988.15 | PP | 2.4 | 1.1 | 96135_at |
| 1637.43 | PPP | 4123.80 | PPP | 3479.00 | PPP | 2.5 | 1.2 | 1419.55 | PP | 2936.80 | PP | 2244.15 | PP | 2.1 | 1.3 | 104152_at |
| 702.67 | PPP | 1774.63 | PPP | 3373.23 | PPP | 2.5 | 0.5 | 979.35 | PP | 2601.50 | PP | 2311.10 | PP | 2.7 | 1.1 | 94963_at |
| 5622.53 | PPP | 21709.17 | PPP | 23252.30 | PPP | 3.9 | 0.9 | 6495.10 | PP | 20205.50 | PP | 18592.55 | PP | 3.1 | 1.1 | 104149_at |
| 5186.00 | PPP | 17577.63 | PPP | 22819.60 | PPP | 3.4 | 0.8 | 6132.30 | PP | 13849.35 | PP | 12920.95 | PP | 2.3 | 1.1 | 99992_at |
| 1022.13 | PPA | 9265.10 | PPP | 9256.83 | PPP | 9.1 | 1.0 | 1352.05 | PA | 4269.80 | PP | 2437.45 | PP | 3.2 | 1.8 | 103040_at |
| 580.30 | PPP | 1415.73 | PPP | 1447.83 | PPP | 2.4 | 1.0 | 566.45 | PA | 1322.30 | PP | 1321.15 | PP | 2.3 | 1.0 | 161073_at |
| 159.07 | PAA | 724.53 | PPP | 518.83 | PPA | 4.6 | 1.4 | 229.15 | PA | 825.70 | PP | 548.85 | PA | 3.6 | 1.5 | 98778_at |
| 1593.53 | PPP | 6061.47 | PPP | 5298.07 | PPP | 3.8 | 1.1 | 2362.25 | PP | 5563.20 | PP | 4169.40 | PP | 2.4 | 1.3 | 96930_at |
| 293.50 | PAA | 612.13 | PPP | 699.93 | PPP | 2.1 | 0.9 | 399.70 | PA | 1912.30 | PP | 1383.05 | PP | 4.8 | 1.4 | 160708_at |
| 2796.23 | PPP | 6340.20 | PPP | 6905.90 | PPP | 2.3 | 0.9 | 3396.45 | PP | 7477.20 | PP | 6107.90 | PP | 2.2 | 1.2 | 98608_at |
| 192.30 | PAP | 743.50 | PPP | 572.90 | PPP | 3.9 | 1.3 | 396.55 | PP | 1059.30 | PP | 723.75 | PP | 2.7 | 1.5 | 101372_at |
| 2731.17 | PPP | 8428.73 | PPP | 8234.40 | PPP | 3.1 | 1.0 | 3307.00 | PP | 7384.80 | PP | 5637.90 | PP | 2.2 | 1.3 | 94461_at |
| 1488.40 | APP | 5686.13 | PPP | 4148.03 | PPP | 3.8 | 1.4 | 558.90 | PA | 3745.80 | PP | 2459.60 | PP | 6.7 | 1.5 | 96206_at |
| 229.73 | APP | 2067.03 | PPP | 1304.07 | PPP | 9.0 | 1.6 | 330.55 | PP | 825.75 | PP | 1488.85 | PP | 2.5 | 0.6 | 104645_at |
| 238.87 | PPP | 2156.57 | PPP | 1398.87 | PPP | 9.0 | 1.5 | 650.85 | PP | 4443.00 | PP | 3797.85 | PP | 6.8 | 1.2 | 96841_at |
| 4863.43 | PPP | 13649.00 | PPP | 11554.03 | PPP | 2.8 | 1.2 | 7996.70 | PP | 16212.00 | PP | 10924.60 | PP | 2.0 | 1.5 | 96010_at |
| 3139.70 | PPP | 7695.50 | PPP | 8973.23 | PPP | 2.5 | 0.9 | 3851.00 | PP | 8204.25 | PP | 7485.45 | PP | 2.1 | 1.1 | 98912_at |
| 1499.37 | PPP | 10565.13 | PPP | 6521.97 | PPP | 7.0 | 1.6 | 2910.05 | PP | 6060.05 | PP | 5654.30 | PP | 2.1 | 1.1 | 94881_at |
| 5498.50 | PPP | 12979.17 | PPP | 11566.27 | PPP | 2.4 | 1.1 | 7048.80 | PP | 16548.70 | PP | 11628.25 | PP | 2.3 | 1.4 | 98083_at |
| 567.07 | PPP | 2687.63 | PPP | 2373.87 | PPP | 4.7 | 1.1 | 512.50 | PP | 1043.15 | PP | 1141.80 | PP | 2.0 | 0.9 | 94505_at |
| 329.73 | AAP | 840.20 | PPP | 999.63 | PPP | 2.5 | 0.8 | 250.55 | PA | 1273.55 | PP | 893.70 | PP | 5.1 | 1.4 | 96208_at |
| 254.97 | APM | 1010.50 | PPA | 1073.00 | PPP | 4.0 | 0.9 | 93.75 | AA | 458.40 | PA | 385.70 | PM | 4.9 | 1.2 | 93419_at |
| 158.10 | AAP | 919.17 | PPP | 736.27 | PPP | 5.8 | 1.2 | 328.85 | PP | 817.90 | PP | 511.65 | PP | 2.5 | 1.6 | 95360_at |

| | | | | wild type | | | | Fold change | |
|---|---|---|---|---|---|---|---|---|---|
| Acc. | Gene/EST Name | ctrl | | LPS | | dex+LPS | | LPS | LPS |
| Num. | | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS |
| AA290180 | vb34d04.r1 Mus musculus cDNA, 5 end | 302.3 | PP | 941.15 | PP | 639.45 | PP | 3.1 | 1.5 |
| AA614971 | vo32e09.r1 Mus musculus cDNA, 5 end | 580.6 | PP | 16531.1 | PP | 12015.9 | PP | 28.5 | 1.4 |
| AA815845 | vp71h06.r1 Mus musculus cDNA, 5 end | 235.8 | AP | 631.9 | PP | 472.55 | PP | 2.7 | 1.3 |
| AI506285 | vq56g05.x1 Mus musculus cDNA, 3 end | 5858.2 | PP | 14644.4 | PP | 22000.8 | PP | 2.5 | 0.7 |
| AA656775 | vr50e03.s1 Mus musculus cDNA, 5 end | 1416.85 | PP | 3867.2 | PP | 4699.85 | PP | 2.7 | 0.8 |
| AA690218 | vr79g01.s1 Mus musculus cDNA, 5 end | 414.85 | PP | 2573.2 | PP | 3002 | PP | 6.2 | 0.9 |
| AA764261 | vv49f08.r1 Mus musculus cDNA, 5 end | 2220.85 | PP | 6032.9 | PP | 3945.3 | PP | 2.7 | 1.5 |
| AA738776 | vv67d07.r1 Mus musculus cDNA, 5 end | 514.05 | PP | 1544.95 | PP | 1251.35 | PP | 3.0 | 1.2 |
| AI642662 | vw01d07.x1 Mus musculus cDNA, 3 end | 521.8 | PP | 5751.05 | PP | 7322.85 | PP | 11.0 | 0.8 |
| AA959954 | vw53a09.s1 Mus musculus cDNA, 3 end | 1802.35 | PP | 13540.8 | PP | 17476.4 | PP | 7.5 | 0.8 |
| D37837 | 65 kDa cytosolic protein | 2.21 | | 6.75 | | 4.3 | | 3.1 | 1.6 |
| U19463 | A20 protein | 13.33 | | 86.6 | | 76.8 | | 6.5 | 1.1 |
| X75926 | ABC1 transporter | 2.9 | | 7.98 | | 5.87 | | 2.8 | 1.4 |
| K02782 | C3 alpha, beta subunit | 7.43 | | 25.8 | | 20.1 | | 3.5 | 1.3 |
| M21495 | gamma-actin | 6.99 | | 32.09 | | 16.95 | | 4.6 | 1.9 |
| AF181830 | Pleckstrin | 1.73 | | 7.61 | | 11.8 | | 4.4 | 0.6 |

| | | GR dim | | | | Fold change | | | | GR LysCre | | | | Fold change | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ctrl | | LPS | | dex+LPS | | LPS | LPS | ctrl | | LPS | | dex+LPS | | LPS | LPS | Grid |
| AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | position |
| 262.97 | PMP | 835.23 | PPP | 776.80 | PPP | ***3.2*** | ***1.1*** | 275.85 | PM | 740.25 | PP | 569.85 | PP | ***2.7*** | ***1.3*** | 97111_at |
| 1014.63 | PPP | 11999.57 | PPP | 12947.97 | PPP | ***11.8*** | ***0.9*** | 1884.85 | PP | 14647.95 | PP | 11433.95 | PP | ***7.8*** | ***1.3*** | 98988_at |
| 216.83 | PPP | 586.20 | PPP | 854.23 | PPP | ***2.7*** | ***0.7*** | 163.75 | PA | 348.95 | PA | 253.30 | PA | ***2.1*** | ***1.4*** | 104206_at |
| 3683.77 | PPP | 11144.33 | PPP | 10850.30 | PPP | ***3.0*** | ***1.0*** | 3071.15 | PP | 6163.15 | PP | 4140.20 | PP | ***2.0*** | ***1.5*** | 96501_at |
| 1559.63 | PPP | 4052.00 | PPP | 5150.20 | PPP | ***2.6*** | ***0.8*** | 1872.10 | PP | 3993.75 | PP | 3084.30 | PP | ***2.1*** | ***1.3*** | 96778_at |
| 177.03 | AAP | 1525.03 | PPP | 2202.67 | PPP | ***8.6*** | ***0.7*** | 650.50 | PP | 1728.60 | PP | 1241.75 | PP | ***2.7*** | ***1.4*** | 98569_at |
| 1592.40 | APP | 3758.80 | PPP | 3207.97 | PPP | ***2.4*** | ***1.2*** | 1564.65 | PA | 4208.20 | PP | 3264.30 | PP | ***2.7*** | ***1.3*** | 104533_at |
| 721.30 | PPP | 1640.90 | PPP | 1609.27 | PPP | ***2.3*** | ***1.0*** | 1114.95 | PP | 2246.65 | PP | 1912.70 | PP | ***2.0*** | ***1.2*** | 103393_at |
| 503.33 | AAP | 6121.83 | PPP | 10988.23 | PPP | ***12.2*** | ***0.6*** | 1943.15 | PP | 6215.20 | PP | 5576.20 | PP | ***3.2*** | ***1.1*** | 97740_at |
| 1634.83 | PPP | 20996.47 | PPP | 20782.17 | PPP | ***12.8*** | ***1.0*** | 2756.00 | PP | 6761.75 | PP | 4256.60 | PP | ***2.5*** | ***1.6*** | 103446_at |

### 10. 2. 2. Normalised expression of genes/ESTs representing Group 1-A

| Acc. Num. | Gene/EST Name |
|---|---|
| M62766 | 3-hydroxy-3-methylglutaryl-coenzyme A reductase |
| U20159 | 76 kDa tyrosine phosphoprotein SLP-76 |
| AJ242778 | ABIN1 (A20-binding inhibitor of NF-kappa B activation. large) |
| AI644801 | Adora2a gene, exon 1 (and joined CDS) |
| U77630 | Adrenomedullin |
| L36829 | alphaA-crystallin-binding protein I (alphaA-CRYBP1) gene |
| L03290 | Amino acid transporter, cationic 2 (low affinity) |
| X82786 | Antigen identified by monoclonal antibody Ki 67 |
| AF029215 | Antigen identified by monoclonal antibody MRC OX-2 |
| AJ130975 | Ariadne-2 protein |
| M61909 | Avian reticuloendotheliosis viral (v-rel) oncogene homolog A |
| U08185 | B lymphocyte induced maturation protein |
| M64292 | B-cell translocation gene 2, anti-proliferative |
| AI844806 | Borg4 gene |
| D85785 | Brain immunological-like with tyrosine-based motifs |
| M26071 | Coagulation factor III |
| M13926 | Colony stimulating factor, granulocyte |
| M63801 | connexin 43 (alpha-1 gap junction) |
| U88325 | Cytokine inducible SH2-containing protein 7 |
| J04103 | E26 avian leukemia oncogene 2, 3 domain |
| M28845 | Early growth response 1 |
| X70764 | ELKL motif kinase |
| D87691 | eRF1 |
| X61399 | F52 mRNA a novel protein |
| Z29532 | follistatin |
| AF017128 | Fos-like antigen 1 |
| Y11666 | gene encoding hexokinase II, exon 1 (and joined CDS) |
| M73696 | Glvr-1 |
| U05265 | Glycoprotein 49 B |
| J04596 | GRO1 oncogene |
| M59821 | growth factor-inducible protein (pip92) |
| U10551 | GTP binding protein (gene overexpressed in skeletal muscle) |
| L09737 | GTP cyclohydrolase 1 |
| U23778 | hematopoietic-specific early-response A1-b protein (A1b) gene |
| U23781 | hematopoietic-specific early-response A1-d protein (A1d) gene |
| X57437 | Histidine decarboxylase cluster |
| U57524 | I kappa B alpha gene, exons 2-6 |

| | wild type | | | | GR dim | | | | GR LysCre | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | Grid |
| **Sum** | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | **position** |
| 1411.70 | 0.16 | 0.45 | 0.39 | 1021.73 | 0.20 | 0.42 | 0.38 | 804.35 | 0.19 | 0.51 | 0.30 | 104285_at |
| 19284.55 | 0.14 | 0.50 | 0.36 | 17281.63 | 0.13 | 0.44 | 0.44 | 13418.75 | 0.21 | 0.41 | 0.38 | 102957_at |
| 20285.45 | 0.12 | 0.58 | 0.30 | 28794.30 | 0.10 | 0.40 | 0.50 | 30764.60 | 0.14 | 0.48 | 0.38 | 104755_at |
| 14119.80 | 0.13 | 0.36 | 0.51 | 12975.50 | 0.13 | 0.49 | 0.38 | 9703.20 | 0.14 | 0.48 | 0.38 | 101363_at |
| 4983.95 | 0.02 | 0.42 | 0.56 | 2625.80 | 0.03 | 0.50 | 0.47 | 1140.20 | 0.08 | 0.60 | 0.32 | 102798_at |
| 950.65 | 0.16 | 0.39 | 0.45 | 944.97 | 0.17 | 0.40 | 0.43 | 689.95 | 0.16 | 0.47 | 0.37 | 92908_at |
| 42047.30 | 0.12 | 0.57 | 0.31 | 36360.63 | 0.09 | 0.38 | 0.53 | 29841.05 | 0.18 | 0.49 | 0.33 | 92736_at |
| 15225.10 | 0.04 | 0.47 | 0.49 | 13820.20 | 0.03 | 0.45 | 0.53 | 12192.55 | 0.05 | 0.39 | 0.57 | 99457_at |
| 1620.50 | 0.19 | 0.44 | 0.37 | 1178.27 | 0.18 | 0.59 | 0.23 | 3451.10 | 0.16 | 0.49 | 0.34 | 101851_at |
| 1018.80 | 0.10 | 0.56 | 0.34 | 1417.57 | 0.15 | 0.40 | 0.44 | 1128.20 | 0.19 | 0.42 | 0.39 | 95600_at |
| 31964.60 | 0.21 | 0.44 | 0.34 | 32200.73 | 0.19 | 0.44 | 0.37 | 29076.20 | 0.21 | 0.45 | 0.35 | 97813_at |
| 2965.35 | 0.17 | 0.41 | 0.42 | 3644.50 | 0.13 | 0.40 | 0.47 | 4918.60 | 0.16 | 0.41 | 0.43 | 92904_at |
| 23247.55 | 0.17 | 0.47 | 0.37 | 23756.50 | 0.14 | 0.52 | 0.34 | 27862.40 | 0.17 | 0.38 | 0.46 | 101583_at |
| 2845.20 | 0.16 | 0.39 | 0.45 | 3707.13 | 0.09 | 0.30 | 0.60 | 4781.05 | 0.14 | 0.42 | 0.45 | 94036_at |
| 2118.00 | 0.13 | 0.57 | 0.30 | 2823.90 | 0.13 | 0.47 | 0.40 | 4481.20 | 0.22 | 0.52 | 0.26 | 95804_g_at |
| 16457.75 | 0.01 | 0.60 | 0.39 | 8293.10 | 0.05 | 0.48 | 0.46 | 10930.00 | 0.04 | 0.56 | 0.39 | 97689_at |
| 16742.75 | 0.02 | 0.56 | 0.43 | 14234.17 | 0.01 | 0.51 | 0.48 | 14169.85 | 0.04 | 0.55 | 0.41 | 94142_at |
| 3624.50 | 0.04 | 0.51 | 0.45 | 4791.53 | 0.06 | 0.30 | 0.64 | 8004.85 | 0.10 | 0.49 | 0.41 | 100064_f_at |
| 1808.85 | 0.06 | 0.57 | 0.37 | 1722.00 | 0.06 | 0.51 | 0.43 | 3477.15 | 0.09 | 0.46 | 0.44 | 92832_at |
| 44661.40 | 0.06 | 0.53 | 0.41 | 47921.83 | 0.06 | 0.44 | 0.50 | 43971.75 | 0.09 | 0.50 | 0.41 | 94246_at |
| 6041.90 | 0.06 | 0.42 | 0.52 | 6091.27 | 0.11 | 0.57 | 0.32 | 7324.35 | 0.09 | 0.48 | 0.44 | 98579_at |
| 12385.70 | 0.16 | 0.38 | 0.47 | 11045.83 | 0.21 | 0.42 | 0.38 | 10074.80 | 0.15 | 0.37 | 0.48 | 99458_i_at |
| 18768.00 | 0.18 | 0.52 | 0.30 | 16803.33 | 0.16 | 0.38 | 0.46 | 17592.90 | 0.20 | 0.47 | 0.34 | 160451_at |
| 44554.10 | 0.05 | 0.47 | 0.48 | 49363.40 | 0.06 | 0.49 | 0.45 | 41145.70 | 0.10 | 0.49 | 0.41 | 97203_at |
| 2601.95 | 0.10 | 0.59 | 0.31 | 885.97 | 0.09 | 0.39 | 0.52 | 5782.15 | 0.11 | 0.48 | 0.41 | 98817_at |
| 725.55 | 0.07 | 0.53 | 0.40 | 1417.00 | 0.10 | 0.50 | 0.41 | 971.10 | 0.09 | 0.55 | 0.35 | 99835_at |
| 2537.00 | 0.07 | 0.55 | 0.37 | 3233.37 | 0.19 | 0.41 | 0.40 | 2945.70 | 0.19 | 0.51 | 0.30 | 94375_at |
| 9206.20 | 0.14 | 0.57 | 0.29 | 5826.00 | 0.16 | 0.53 | 0.31 | 12778.40 | 0.13 | 0.49 | 0.38 | 103065_at |
| 28429.85 | 0.19 | 0.54 | 0.27 | 38237.37 | 0.18 | 0.41 | 0.41 | 34225.45 | 0.21 | 0.46 | 0.33 | 92217_s_at |
| 93892.90 | 0.07 | 0.60 | 0.33 | 115652.57 | 0.06 | 0.49 | 0.45 | 135474.00 | 0.15 | 0.42 | 0.43 | 95349_g_at |
| 6406.75 | 0.10 | 0.37 | 0.53 | 5927.40 | 0.18 | 0.46 | 0.36 | 4053.95 | 0.19 | 0.46 | 0.35 | 99109_at |
| 4016.90 | 0.03 | 0.58 | 0.39 | 2285.40 | 0.05 | 0.39 | 0.57 | 3789.45 | 0.05 | 0.50 | 0.44 | 92534_at |
| 7211.25 | 0.14 | 0.53 | 0.33 | 8963.67 | 0.13 | 0.44 | 0.44 | 10530.80 | 0.15 | 0.48 | 0.37 | 102313_at |
| 46247.15 | 0.09 | 0.51 | 0.40 | 48238.20 | 0.08 | 0.49 | 0.43 | 40761.65 | 0.13 | 0.48 | 0.38 | 102914_s_at |
| 68534.90 | 0.11 | 0.55 | 0.33 | 74887.23 | 0.11 | 0.48 | 0.41 | 70410.35 | 0.17 | 0.44 | 0.40 | 93869_s_at |
| 6452.50 | 0.06 | 0.55 | 0.39 | 7660.90 | 0.08 | 0.38 | 0.55 | 8249.65 | 0.05 | 0.61 | 0.34 | 93328_at |
| 13037.80 | 0.09 | 0.56 | 0.35 | 12293.30 | 0.12 | 0.40 | 0.48 | 10310.65 | 0.11 | 0.46 | 0.43 | 101554_at |

| Acc. Num. | Gene/EST Name |
|---|---|
| U19799 | IkB-beta |
| L38281 | Immunoresponsive gene 1 |
| U14135 | Integrin alpha V (Cd51) |
| M90551 | Intercellular adhesion molecule |
| M14639 | Interleukin 1 alpha |
| AV152244 | ISG15 gene |
| AB024717 | macrophage C-type lectin Mincle |
| AB033887 | mACS4 variant2 mRNA Acyl-CoA synthetase 4 variant2 |
| Y15163 | mrg1 protein |
| X62700 | muPAR1 mRNA |
| X54149 | Myeloid differentiation primary response gene 118 |
| AF073882 | myotubularin related protein 7 |
| AW047899 | NF-kappaB subunit p100 (Nfkb2) |
| M57999 | Nuclear factor of kappa light chain gene enhancer in B-cells 1, p105 |
| X87128 | p75 TNF receptor DNA |
| AI060798 | PGES prostaglandin E synthase |
| AF020313 | proline-rich protein 48 |
| D83484 | protein tyrosine phosphatase epsilon |
| AF030185 | putative beta chemokine receptor (E01) |
| AW047476 | Putative purine nucleotide binding protein |
| AI852608 | RNA 3'-terminal phosphate cyclase like protein (rcl1 gene) |
| AF099973 | schlafen2 (Slfn2) |
| D78188 | SCID complementing gene 2 |
| U10531 | Ski/sno related |
| J04491 | Small inducible cytokine A3 |
| U88328 | suppressor of cytokine signalling-3 (SOCS-3) |
| L35302 | Tnf receptor-associated factor 1 |
| D78141 | Tnf receptor-associated factor 5 |
| X70956 | TOP gene topoisomerase I, exons 19-21 |
| U59864 | TRAF-interacting protein I-TRAF |
| X62940 | Transming growth factor beta 1 induced transcript 4 |
| L15435 | Tumor necrosis factor (ligand) superfamily, member 9 |
| L24118 | Tumor necrosis factor induced protein 2 |
| M83312 | Tumor necrosis factor receptor superfamily, member 5 |
| AI854821 | U8 gene |
| AB030505 | UBE-1c1, UBE-1c2, UBE-1c3 |
| X14678 | Zinc finger protein 36 |

| | wild type | | | | GR dim | | | | GR LysCre | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | Grid |
| Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | position |
| 19289.20 | 0.16 | 0.48 | 0.36 | 30852.07 | 0.13 | 0.42 | 0.45 | 21971.75 | 0.17 | 0.47 | 0.36 | 99982_at |
| 19714.20 | 0.03 | 0.58 | 0.40 | 21348.67 | 0.02 | 0.48 | 0.49 | 15562.60 | 0.05 | 0.49 | 0.46 | 98774_at |
| 564.50 | 0.21 | 0.48 | 0.31 | 604.70 | 0.14 | 0.41 | 0.45 | 516.90 | 0.11 | 0.62 | 0.27 | 98366_at |
| 18475.10 | 0.17 | 0.44 | 0.39 | 19827.37 | 0.11 | 0.39 | 0.50 | 19279.45 | 0.17 | 0.48 | 0.36 | 96752_at |
| 112729.25 | 0.04 | 0.60 | 0.36 | 110184.90 | 0.04 | 0.49 | 0.47 | 132973.15 | 0.12 | 0.46 | 0.42 | 94755_at |
| 4797.70 | 0.03 | 0.56 | 0.41 | 5078.53 | 0.02 | 0.57 | 0.41 | 1570.45 | 0.12 | 0.62 | 0.25 | 161511_f_at |
| 31317.50 | 0.09 | 0.54 | 0.36 | 30071.50 | 0.14 | 0.49 | 0.37 | 35226.05 | 0.18 | 0.49 | 0.33 | 96551_at |
| 1926.20 | 0.22 | 0.51 | 0.27 | 1431.80 | 0.13 | 0.31 | 0.56 | 2009.00 | 0.22 | 0.46 | 0.31 | 104017_at |
| 13231.55 | 0.07 | 0.52 | 0.40 | 7699.10 | 0.13 | 0.43 | 0.44 | 10439.85 | 0.12 | 0.50 | 0.38 | 101973_at |
| 9810.55 | 0.12 | 0.44 | 0.45 | 16122.47 | 0.13 | 0.46 | 0.41 | 9132.95 | 0.15 | 0.49 | 0.36 | 102663_at |
| 25190.15 | 0.07 | 0.57 | 0.37 | 36591.87 | 0.05 | 0.49 | 0.46 | 40285.05 | 0.17 | 0.49 | 0.34 | 102779_at |
| 1120.35 | 0.08 | 0.61 | 0.31 | 1191.10 | 0.07 | 0.40 | 0.53 | 744.30 | 0.10 | 0.59 | 0.31 | 103228_at |
| 12522.90 | 0.12 | 0.54 | 0.34 | 19526.63 | 0.11 | 0.48 | 0.41 | 15850.00 | 0.13 | 0.53 | 0.34 | 103614_at |
| 76395.40 | 0.13 | 0.54 | 0.32 | 100250.63 | 0.14 | 0.46 | 0.39 | 79009.80 | 0.19 | 0.45 | 0.36 | 98427_s_at |
| 96241.90 | 0.13 | 0.56 | 0.31 | 81956.43 | 0.15 | 0.43 | 0.42 | 92056.90 | 0.17 | 0.48 | 0.34 | 94928_at |
| 33779.85 | 0.17 | 0.50 | 0.33 | 42648.13 | 0.12 | 0.47 | 0.41 | 50063.45 | 0.21 | 0.43 | 0.36 | 104406_at |
| 26638.30 | 0.17 | 0.49 | 0.34 | 34790.53 | 0.22 | 0.47 | 0.31 | 28865.90 | 0.18 | 0.44 | 0.37 | 102710_at |
| 21564.50 | 0.16 | 0.50 | 0.34 | 19482.60 | 0.16 | 0.44 | 0.40 | 21206.65 | 0.18 | 0.52 | 0.29 | 101932_at |
| 49385.60 | 0.02 | 0.61 | 0.36 | 38967.63 | 0.04 | 0.48 | 0.48 | 28589.75 | 0.05 | 0.56 | 0.39 | 93617_at |
| 10736.55 | 0.17 | 0.55 | 0.29 | 19290.00 | 0.09 | 0.44 | 0.47 | 16106.75 | 0.19 | 0.49 | 0.32 | 103202_at |
| 14488.50 | 0.06 | 0.42 | 0.52 | 13291.93 | 0.08 | 0.36 | 0.56 | 14014.15 | 0.15 | 0.52 | 0.33 | 98923_at |
| 154387.30 | 0.20 | 0.44 | 0.36 | 170478.20 | 0.10 | 0.43 | 0.47 | 147012.25 | 0.15 | 0.44 | 0.41 | 92471_i_at |
| 28134.00 | 0.24 | 0.49 | 0.26 | 34079.53 | 0.24 | 0.50 | 0.26 | 36272.95 | 0.20 | 0.48 | 0.32 | 160468_at |
| 1501.75 | 0.06 | 0.60 | 0.34 | 1300.10 | 0.12 | 0.33 | 0.56 | 1792.25 | 0.10 | 0.61 | 0.29 | 94752_s_at |
| 89603.10 | 0.02 | 0.58 | 0.40 | 92728.03 | 0.02 | 0.45 | 0.53 | 109911.40 | 0.07 | 0.53 | 0.40 | 102424_at |
| 22744.15 | 0.03 | 0.59 | 0.38 | 37870.37 | 0.04 | 0.49 | 0.47 | 22981.35 | 0.07 | 0.55 | 0.38 | 92232_at |
| 13866.50 | 0.06 | 0.54 | 0.40 | 12929.20 | 0.06 | 0.51 | 0.43 | 21500.85 | 0.11 | 0.53 | 0.36 | 94186_at |
| 13230.25 | 0.18 | 0.42 | 0.41 | 11717.57 | 0.20 | 0.42 | 0.38 | 12122.00 | 0.19 | 0.50 | 0.31 | 103255_at |
| 26767.25 | 0.11 | 0.51 | 0.38 | 29775.40 | 0.18 | 0.41 | 0.41 | 35691.55 | 0.14 | 0.49 | 0.38 | 95694_at |
| 16276.30 | 0.13 | 0.54 | 0.32 | 13932.97 | 0.14 | 0.40 | 0.46 | 19752.85 | 0.20 | 0.46 | 0.35 | 103328_at |
| 9908.15 | 0.05 | 0.41 | 0.54 | 7547.67 | 0.07 | 0.63 | 0.30 | 9271.45 | 0.03 | 0.48 | 0.48 | 93728_at |
| 41096.90 | 0.01 | 0.46 | 0.54 | 44415.27 | 0.01 | 0.45 | 0.54 | 12606.35 | 0.02 | 0.48 | 0.51 | 92415_at |
| 75197.65 | 0.08 | 0.54 | 0.38 | 86492.27 | 0.08 | 0.52 | 0.40 | 65539.55 | 0.14 | 0.48 | 0.37 | 160489_at |
| 5013.15 | 0.10 | 0.56 | 0.34 | 10489.83 | 0.08 | 0.61 | 0.32 | 6442.45 | 0.15 | 0.53 | 0.32 | 92962_at |
| 12559.80 | 0.18 | 0.54 | 0.28 | 13186.27 | 0.15 | 0.42 | 0.43 | 15919.40 | 0.20 | 0.47 | 0.32 | 160171_f_at |
| 9588.55 | 0.15 | 0.56 | 0.29 | 6647.83 | 0.18 | 0.47 | 0.35 | 9418.20 | 0.17 | 0.47 | 0.36 | 99592_f_at |
| 10232.25 | 0.13 | 0.53 | 0.34 | 10864.67 | 0.15 | 0.50 | 0.35 | 15362.65 | 0.16 | 0.49 | 0.35 | 92830_s_at |

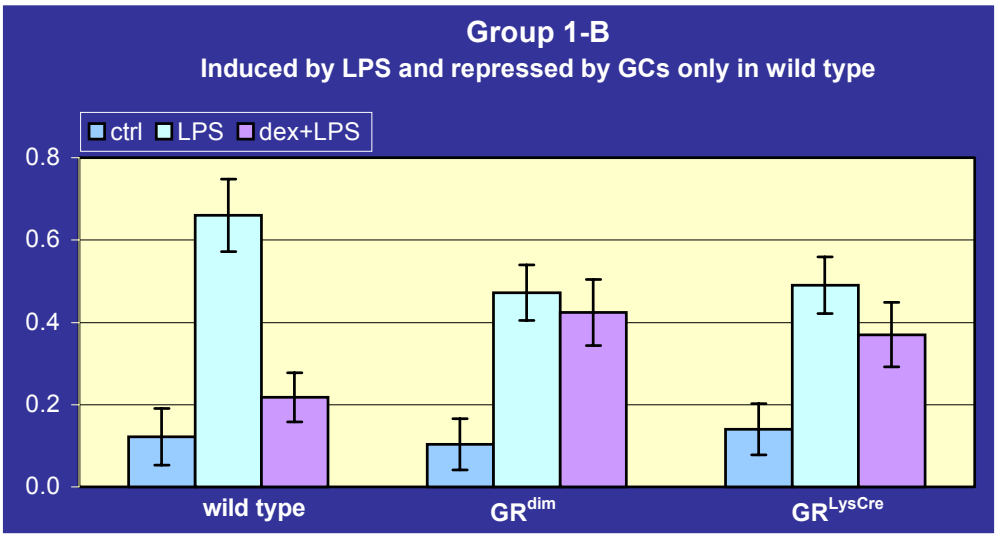
| Acc. Num. | Gene/EST Name |
|---|---|
| AI323667 | mp96e12.x1 Mus musculus cDNA, 3 end |
| AA168418 | mr29a03.r1 Mus musculus cDNA, 5 end |
| AI592541 | ms93f10.y1 Mus musculus cDNA, 5 end |
| AA204579 | mt84d11.r1 Mus musculus cDNA, 5 end |
| AV138783 | Mus musculus cDNA |
| AV374591 | Mus musculus cDNA, 3 end |
| C78513 | Mus musculus cDNA, 3 end |
| AV374868 | Mus musculus cDNA, 3 end |
| C76063 | Mus musculus cDNA, 3 end |
| AV309347 | Mus musculus cDNA, 3 end |
| AV341518 | Mus musculus cDNA, 3 end |
| AA959291 | ua14g10.r1 Mus musculus cDNA, 5 end |
| AI006319 | ua70b05.r1 Mus musculus cDNA, 5 end |
| AA833425 | ub58d03.r1 Mus musculus cDNA, 5 end |
| AA960466 | ub58f11.s1 Mus musculus cDNA, 3 end |
| AI462105 | ub70b01.x1 Mus musculus cDNA, 3 end |
| AI642048 | ub75b05.x1 Mus musculus cDNA, 3 end |
| AI286698 | ub84b09.r1 Mus musculus cDNA, 5 end |
| AI837100 | UI-M-AK0-adc-d-02-0-UI.s1 Mus musculus cDNA, 3 end |
| AI846304 | UI-M-AK1-aez-g-06-0-UI.s1 Mus musculus cDNA, 3 end |
| AI837543 | UI-M-AL0-abs-d-04-0-UI.s1 Mus musculus cDNA, 3 end |
| AI844128 | UI-M-AL1-ahj-d-06-0-UI.s1 Mus musculus cDNA, 3 end |
| AI840446 | UI-M-AN0-aci-b-05-0-UI.s1 Mus musculus cDNA, 3 end |
| AI845886 | UI-M-AO1-aeg-h-09-0-UI.s1 Mus musculus cDNA, 3 end |
| AI852645 | UI-M-BH0-aiu-h-04-0-UI.s1 Mus musculus cDNA, 3 end |
| AI852144 | UI-M-BH0-ajb-e-09-0-UI.s1 Mus musculus cDNA, 3 end |
| AI854506 | UI-M-BH0-ajj-b-09-0-UI.s1 Mus musculus cDNA, 3 end |
| AI853712 | UI-M-BH0-ajq-d-05-0-UI.s1 Mus musculus cDNA, 3 end |
| AW046627 | UI-M-BH1-ald-c-09-0-UI.s1 Mus musculus cDNA, 3 end |
| AW047023 | UI-M-BH1-alp-h-11-0-UI.s1 Mus musculus cDNA, 3 end |
| AW047811 | UI-M-BH1-als-a-04-0-UI.s1 Mus musculus cDNA, 3 end |
| AW048937 | UI-M-BH1-amo-d-08-0-UI.s1 Mus musculus cDNA, 3 end |
| AW049031 | UI-M-BH1-amp-g-08-0-UI.s1 Mus musculus cDNA, 3 end |
| AW124934 | UI-M-BH2.1-apu-g-11-0-UI.s1 Mus musculus cDNA, 3 end |
| AW123514 | UI-M-BH2.1-aqb-c-04-0-UI.s1 Mus musculus cDNA, 3 end |
| AW215863 | up02c11.x1 Mus musculus cDNA, 3 end |
| AA259683 | va36d09.r1 Mus musculus cDNA, 5 end |

| | wild type | | | | GR dim | | | | GR LysCre | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | Grid |
| Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | position |
| 88701.75 | 0.06 | 0.52 | 0.42 | 91131.50 | 0.07 | 0.47 | 0.46 | 80310.65 | 0.09 | 0.50 | 0.41 | 98773_s_at |
| 1160.25 | 0.15 | 0.46 | 0.39 | 1293.33 | 0.14 | 0.39 | 0.47 | 1613.35 | 0.20 | 0.42 | 0.37 | 93462_at |
| 4526.50 | 0.12 | 0.58 | 0.30 | 3828.00 | 0.08 | 0.54 | 0.38 | 4996.45 | 0.16 | 0.48 | 0.36 | 103691_at |
| 2620.75 | 0.12 | 0.56 | 0.32 | 5763.27 | 0.02 | 0.55 | 0.43 | 350.60 | 0.54 | 0.14 | 0.32 | 104177_at |
| 42092.95 | 0.09 | 0.56 | 0.35 | 55110.87 | 0.07 | 0.48 | 0.45 | 61898.65 | 0.15 | 0.49 | 0.36 | 161666_f_at |
| 6085.85 | 0.01 | 0.57 | 0.42 | 6198.50 | 0.03 | 0.53 | 0.44 | 5390.10 | 0.05 | 0.45 | 0.49 | 161903_f_at |
| 10363.40 | 0.02 | 0.60 | 0.38 | 17222.57 | 0.02 | 0.53 | 0.45 | 8067.35 | 0.04 | 0.59 | 0.37 | 97693_at |
| 50718.95 | 0.05 | 0.52 | 0.43 | 62116.77 | 0.06 | 0.49 | 0.45 | 51852.00 | 0.10 | 0.48 | 0.42 | 162206_f_at |
| 1986.35 | 0.09 | 0.52 | 0.39 | 2355.13 | 0.13 | 0.52 | 0.35 | 1334.85 | 0.21 | 0.48 | 0.31 | 95848_at |
| 7588.80 | 0.09 | 0.37 | 0.54 | 8236.20 | 0.07 | 0.45 | 0.49 | 7296.50 | 0.06 | 0.37 | 0.57 | 161931_r_at |
| 3849.20 | 0.18 | 0.51 | 0.32 | 2598.73 | 0.16 | 0.42 | 0.42 | 5673.00 | 0.18 | 0.47 | 0.35 | 162095_f_at |
| 2019.25 | 0.14 | 0.49 | 0.37 | 1839.80 | 0.17 | 0.50 | 0.33 | 1780.20 | 0.16 | 0.37 | 0.47 | 99874_at |
| 5786.40 | 0.16 | 0.51 | 0.33 | 6341.67 | 0.16 | 0.41 | 0.43 | 6350.50 | 0.21 | 0.44 | 0.34 | 94980_at |
| 15022.40 | 0.16 | 0.50 | 0.34 | 17740.37 | 0.18 | 0.47 | 0.35 | 17907.10 | 0.18 | 0.43 | 0.39 | 96135_at |
| 6077.50 | 0.20 | 0.47 | 0.34 | 9240.23 | 0.18 | 0.45 | 0.38 | 6600.50 | 0.22 | 0.44 | 0.34 | 104152_at |
| 7261.20 | 0.13 | 0.54 | 0.33 | 5850.53 | 0.12 | 0.30 | 0.58 | 5891.95 | 0.17 | 0.44 | 0.39 | 94963_at |
| 47012.55 | 0.09 | 0.46 | 0.44 | 50584.00 | 0.11 | 0.43 | 0.46 | 45293.15 | 0.14 | 0.45 | 0.41 | 104149_at |
| 29993.75 | 0.17 | 0.41 | 0.42 | 45583.23 | 0.11 | 0.39 | 0.50 | 32902.60 | 0.19 | 0.42 | 0.39 | 99992_at |
| 6959.85 | 0.10 | 0.50 | 0.41 | 19544.07 | 0.05 | 0.47 | 0.47 | 8059.30 | 0.17 | 0.53 | 0.30 | 103040_at |
| 3749.90 | 0.14 | 0.47 | 0.40 | 3443.87 | 0.17 | 0.41 | 0.42 | 3209.90 | 0.18 | 0.41 | 0.41 | 161073_at |
| 1299.25 | 0.17 | 0.40 | 0.43 | 1402.43 | 0.11 | 0.52 | 0.37 | 1603.70 | 0.14 | 0.51 | 0.34 | 98778_at |
| 11081.15 | 0.12 | 0.43 | 0.45 | 12953.07 | 0.12 | 0.47 | 0.41 | 12094.85 | 0.20 | 0.46 | 0.34 | 96930_at |
| 2005.85 | 0.17 | 0.52 | 0.31 | 1605.57 | 0.18 | 0.38 | 0.44 | 3695.05 | 0.11 | 0.52 | 0.37 | 160708_at |
| 17465.80 | 0.17 | 0.45 | 0.38 | 16042.33 | 0.17 | 0.40 | 0.43 | 16981.55 | 0.20 | 0.44 | 0.36 | 98608_at |
| 1290.85 | 0.18 | 0.46 | 0.36 | 1508.70 | 0.13 | 0.49 | 0.38 | 2179.60 | 0.18 | 0.49 | 0.33 | 101372_at |
| 20424.70 | 0.14 | 0.49 | 0.36 | 19394.30 | 0.14 | 0.43 | 0.42 | 16329.70 | 0.20 | 0.45 | 0.35 | 94461_at |
| 6146.20 | 0.07 | 0.59 | 0.34 | 11322.57 | 0.13 | 0.50 | 0.37 | 6764.30 | 0.08 | 0.55 | 0.36 | 96206_at |
| 4130.65 | 0.10 | 0.46 | 0.44 | 3600.83 | 0.06 | 0.57 | 0.36 | 2645.15 | 0.12 | 0.31 | 0.56 | 104645_at |
| 7459.20 | 0.06 | 0.47 | 0.47 | 3794.30 | 0.06 | 0.57 | 0.37 | 8891.70 | 0.07 | 0.50 | 0.43 | 96841_at |
| 31878.10 | 0.21 | 0.47 | 0.32 | 30066.47 | 0.16 | 0.45 | 0.38 | 35133.30 | 0.23 | 0.46 | 0.31 | 96010_at |
| 28929.10 | 0.11 | 0.34 | 0.56 | 19808.43 | 0.16 | 0.39 | 0.45 | 19540.70 | 0.20 | 0.42 | 0.38 | 98912_at |
| 23557.60 | 0.10 | 0.41 | 0.49 | 18586.47 | 0.08 | 0.57 | 0.35 | 14624.40 | 0.20 | 0.41 | 0.39 | 94881_at |
| 36823.30 | 0.24 | 0.49 | 0.26 | 30043.93 | 0.18 | 0.43 | 0.38 | 35225.75 | 0.20 | 0.47 | 0.33 | 98083_at |
| 4559.60 | 0.08 | 0.46 | 0.46 | 5628.57 | 0.10 | 0.48 | 0.42 | 2697.45 | 0.19 | 0.39 | 0.42 | 94505_at |
| 1810.85 | 0.14 | 0.44 | 0.42 | 2169.57 | 0.15 | 0.39 | 0.46 | 2417.80 | 0.10 | 0.53 | 0.37 | 96208_at |
| 2247.85 | 0.09 | 0.36 | 0.55 | 2338.47 | 0.11 | 0.43 | 0.46 | 937.85 | 0.10 | 0.49 | 0.41 | 93419_at |
| 1741.40 | 0.13 | 0.56 | 0.32 | 1813.53 | 0.09 | 0.51 | 0.41 | 1658.40 | 0.20 | 0.49 | 0.31 | 95360_at |

| Acc. Num. | Gene/EST Name |
|---|---|
| AA290180 | vb34d04.r1 Mus musculus cDNA, 5 end |
| AA614971 | vo32e09.r1 Mus musculus cDNA, 5 end |
| AA815845 | vp71h06.r1 Mus musculus cDNA, 5 end |
| AI506285 | vq56g05.x1 Mus musculus cDNA, 3 end |
| AA656775 | vr50e03.s1 Mus musculus cDNA, 5 end |
| AA690218 | vr79g01.s1 Mus musculus cDNA, 5 end |
| AA764261 | vv49f08.r1 Mus musculus cDNA, 5 end |
| AA738776 | vv67d07.r1 Mus musculus cDNA, 5 end |
| AI642662 | vw01d07.x1 Mus musculus cDNA, 3 end |
| AA959954 | vw53a09.s1 Mus musculus cDNA, 3 end |
| D37837 | 65 kDa cytosolic protein |
| U19463 | A20 protein |
| X75926 | ABC1 transporter |
| K02782 | C3 alpha, beta subunit |
| M21495 | gamma-actin |
| AF181830 | Pleckstrin |

| | wild type | | | | GR dim | | | | GR LysCre | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | Grid |
| Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | position |
| 1882.90 | 0.16 | 0.50 | 0.34 | 1875.00 | 0.14 | 0.45 | 0.41 | 1585.95 | 0.17 | 0.47 | 0.36 | 97111_at |
| 29127.55 | 0.02 | 0.57 | 0.41 | 25962.17 | 0.04 | 0.46 | 0.50 | 27966.75 | 0.07 | 0.52 | 0.41 | 98988_at |
| 1340.25 | 0.18 | 0.47 | 0.35 | 1657.27 | 0.13 | 0.35 | 0.52 | 766.00 | 0.21 | 0.46 | 0.33 | 104206_at |
| 42503.35 | 0.14 | 0.34 | 0.52 | 25678.40 | 0.14 | 0.43 | 0.42 | 13374.50 | 0.23 | 0.46 | 0.31 | 96501_at |
| 9983.90 | 0.14 | 0.39 | 0.47 | 10761.83 | 0.14 | 0.38 | 0.48 | 8950.15 | 0.21 | 0.45 | 0.34 | 96778_at |
| 5990.05 | 0.07 | 0.43 | 0.50 | 3904.73 | 0.05 | 0.39 | 0.56 | 3620.85 | 0.18 | 0.48 | 0.34 | 98569_at |
| 12199.05 | 0.18 | 0.49 | 0.32 | 8559.17 | 0.19 | 0.44 | 0.37 | 9037.15 | 0.17 | 0.47 | 0.36 | 104533_at |
| 3310.35 | 0.16 | 0.47 | 0.38 | 3971.47 | 0.18 | 0.41 | 0.41 | 5274.30 | 0.21 | 0.43 | 0.36 | 103393_at |
| 13595.70 | 0.04 | 0.42 | 0.54 | 17613.40 | 0.03 | 0.35 | 0.62 | 13734.55 | 0.14 | 0.45 | 0.41 | 97740_at |
| 32819.50 | 0.05 | 0.41 | 0.53 | 43413.47 | 0.04 | 0.48 | 0.48 | 13774.35 | 0.20 | 0.49 | 0.31 | 103446_at |
| 13.26 | 0.17 | 0.51 | 0.32 | | | | | | | | | |
| 176.73 | 0.08 | 0.49 | 0.43 | | | | | | | | | |
| 16.75 | 0.17 | 0.48 | 0.35 | | | | | | | | | |
| 53.33 | 0.14 | 0.48 | 0.38 | | | | | | | | | |
| 56.03 | 0.12 | 0.57 | 0.30 | | | | | | | | | |
| 21.14 | 0.08 | 0.36 | 0.56 | | | | | | | | | |

## 10. 3. GROUP 1-B




| | wild type | | | | GR dim | | | | GR LysCre | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS |
| Sum: | 5.75 | 31.03 | 10.23 | Sum: | 4.88 | 22.18 | 19.94 | Sum: | 6.59 | 23.03 | 17.39 |
| Mean: | 0.12 | 0.66 | 0.22 | Mean: | 0.10 | 0.47 | 0.42 | Mean: | 0.14 | 0.49 | 0.37 |
| StDev: | 0.07 | 0.09 | 0.06 | StDev: | 0.06 | 0.07 | 0.08 | StDev: | 0.06 | 0.07 | 0.08 |
| Fold change (LPS/ctrl) | | | 5.4 | Fold change (LPS/ctrl) | | | 4.5 | Fold change (LPS/ctrl) | | | 3.5 |
| Fold change (LPS/dex+LPS) | | | 3.0 | Fold change (LPS/dex+LPS) | | | 1.1 | Fold change (LPS/dex+LPS) | | | 1.3 |

### 10. 3. 1. Expression levels of genes/ESTs representing Group 1-B

| | | | | wild type | | | | Fold change | |
|---|---|---|---|---|---|---|---|---|---|
| Acc. | Gene/EST Name | ctrl | | LPS | | dex+LPS | | LPS | LPS |
| Num. | | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS |
| U05673 | Balb/C clone R13 adenosine receptor subtype mRNA | 24.5 | AA | 1052.05 | PP | 398.8 | PP | 42.9 | 2.6 |
| AF059213 | cholesterol 25-hydroxylase mRNA | 104.35 | AA | 2067.4 | PP | 641.3 | PP | 19.8 | 3.2 |
| X78445 | Cyp1-b-1 mRNA for cytochrome P450 | 4890 | PP | 17777.3 | PP | 3123.4 | PP | 3.6 | 5.7 |
| D89613 | Cytokine inducible SH2-containing protein | 468.15 | AA | 2284.3 | PP | 632.3 | PP | 4.9 | 3.6 |
| D30782 | epiregulin | 20.85 | AA | 12690.2 | PP | 620.5 | PP | >100 | 20.5 |
| AA182189 | Ets-protein Spi-C | 406.65 | PA | 1348.55 | PP | 436.05 | PP | 3.3 | 3.1 |
| X14961 | Fatty acid binding protein heart 1 | 206.75 | PP | 604.05 | PP | 301.35 | PP | 2.9 | 2.0 |
| U00937 | GADD45 protein (gadd45) gene | 4283.1 | PP | 35013.3 | PP | 8438.75 | PP | 8.2 | 4.1 |
| L32838 | germline interleukin 1 receptor antagonist (IL-1rn) gene | 21684.1 | PP | 75172 | PP | 35693.5 | PP | 3.5 | 2.1 |
| M88242 | glucocortoid-regulated inflammatory prostaglandin G/H synthase | 337.05 | PA | 29481.3 | PP | 7016.65 | PP | 87.5 | 4.2 |
| X67644 | gly96 mRNA | 8260.6 | PP | 35366.7 | PP | 11560.7 | PP | 4.3 | 3.1 |
| L07924 | guanine nucleotide dissociation stimulator for a ras-related GTPase | 2995.85 | PP | 8353.7 | PP | 3533.05 | PP | 2.8 | 2.4 |
| X69619 | Inhibin beta-A | 584.9 | MP | 11589.7 | PP | 3939.7 | PP | 19.8 | 2.9 |
| AF077861 | Inhibitor of DNA binding 2 | 6011.7 | PP | 23077.6 | PP | 7493.3 | PP | 3.8 | 3.1 |
| X04725 | Insulin I | 1426.25 | PP | 5745.45 | PP | 1745.75 | PP | 4.0 | 3.3 |
| M86672 | Interleukin 12a | 142.6 | AA | 891.95 | PP | 263.1 | PP | 6.3 | 3.4 |
| L16956 | Janus kinase 2 | 2244.95 | PP | 10135.6 | PP | 4992.25 | PP | 4.5 | 2.0 |
| X66473 | Matrix metalloproteinase 1 | 1084.15 | PP | 5503.8 | PP | 444.45 | PP | 5.1 | 12.4 |
| X62502 | MIP-1b | 230.25 | AP | 35888.1 | PP | 24462.6 | PP | >100 | 1.5 |
| AB026569 | MSSP | 3417.65 | PP | 9653.55 | PP | 3521.2 | PP | 2.8 | 2.7 |
| M60474 | Myristoylated alanine rich protein kinase C substrate | 990.55 | PP | 4823.7 | PP | 2157.2 | PP | 4.9 | 2.2 |
| X86000 | N-glycan alpha 2,8-sialyltransferase | 4723.4 | PP | 15825 | PP | 7267.85 | PP | 3.4 | 2.2 |
| M73748 | OTS-8 mRNA | 739.55 | PP | 2195 | PP | 664.95 | PP | 3.0 | 3.3 |
| U90926 | putative TNF-resistance related protein mRNA | 723.3 | AA | 3539.15 | PP | 834.35 | PP | 4.9 | 4.2 |
| M19681 | Small inducible cytokine A2 | 861.95 | PA | 11712.3 | PP | 4024.1 | PP | 13.6 | 2.9 |
| U27267 | Small inducible cytokine B subfamily, member 5 | 2516.35 | PP | 21524.5 | PP | 4174.45 | PP | 8.6 | 5.2 |
| M22998 | Solute carrier family 2 (facilitated glucose transporter), member 1 | 232.75 | PA | 1678.95 | PP | 587.4 | PP | 7.2 | 2.9 |
| U44088 | TDAG51 (TDAG51) mRNA | 40.2 | AA | 2981.6 | PP | 763.8 | PP | 74.2 | 3.9 |
| U20735 | transcription factor junB (junB) gene, 5 region and cds | 716.8 | PP | 4118.5 | PP | 1659 | PP | 5.7 | 2.5 |
| D44464 | uridine phosphorylase | 252.25 | AA | 2055.9 | PP | 744.85 | PP | 8.2 | 2.8 |
| M84487 | Vascular cell adhesion molecule 1 | 112.15 | AA | 2110.15 | PP | 437.6 | PP | 18.8 | 4.8 |

| | | GR dim | | | | Fold change | | | | GR LysCre | | | | Fold change | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ctrl | | LPS | | dex+LPS | | LPS | LPS | ctrl | | LPS | | dex+LPS | | LPS | LPS | Grid |
| AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | position |
| 110.47 | AAP | 944.17 | PPP | 1485.47 | PPP | 8.5 | 0.6 | 325.10 | PP | 1916.65 | PP | 1387.80 | PP | 5.9 | 1.4 | 97733_at |
| 901.93 | AAP | 7928.07 | PPP | 6854.10 | PPP | 8.8 | 1.2 | 490.55 | PA | 3362.25 | PP | 1738.80 | PP | 6.9 | 1.9 | 104509_at |
| 1615.93 | PAP | 7293.30 | PAP | 4295.93 | PAP | 4.5 | 1.7 | 8158.40 | PP | 17267.30 | PP | 11968.90 | PP | 2.1 | 1.4 | 99979_at |
| 375.27 | AAA | 2177.97 | PPP | 1492.07 | PPP | 5.8 | 1.5 | 367.00 | PA | 1618.65 | PP | 1091.80 | PP | 4.4 | 1.5 | 100022_at |
| 180.57 | AAP | 6258.00 | PPP | 3200.53 | PPP | 34.7 | 2.0 | 132.90 | PA | 10976.85 | PP | 8727.70 | PP | 82.6 | 1.3 | 98802_at |
| 262.10 | PAP | 652.83 | PAP | 865.40 | PPP | 2.5 | 0.8 | 232.75 | AA | 583.70 | PP | 490.65 | PP | 2.5 | 1.2 | 103454_at |
| 125.40 | AAP | 480.17 | PPP | 714.17 | PPP | 3.8 | 0.7 | 84.85 | AA | 342.35 | PP | 228.80 | PP | 4.0 | 1.5 | 94214_at |
| 3912.87 | PPP | 20761.87 | PPP | 18333.63 | PPP | 5.3 | 1.1 | 10079.15 | PP | 39827.35 | PP | 26299.85 | PP | 4.0 | 1.5 | 102292_at |
| 16479.77 | PPP | 59681.37 | PPP | 53195.00 | PPP | 3.6 | 1.1 | 27167.80 | PP | 60056.10 | PP | 48697.05 | PP | 2.2 | 1.2 | 93871_at |
| 200.10 | AAP | 15051.93 | PPP | 12226.23 | PPP | 75.2 | 1.2 | 1610.60 | PP | 17450.35 | PP | 16302.20 | PP | 10.8 | 1.1 | 104647_at |
| 6332.23 | PPP | 26809.87 | PPP | 24985.63 | PPP | 4.2 | 1.1 | 5987.35 | PP | 33877.15 | PP | 23024.50 | PP | 5.7 | 1.5 | 94384_at |
| 2673.47 | PPP | 5919.20 | PPP | 5560.00 | PPP | 2.2 | 1.1 | 2866.25 | PP | 11405.70 | PP | 8642.25 | PP | 4.0 | 1.3 | 100530_at |
| 376.60 | AAP | 3952.77 | PPP | 3695.60 | PPP | 10.5 | 1.1 | 1182.50 | PP | 8966.20 | PP | 7068.75 | PP | 7.6 | 1.3 | 100277_at |
| 8088.70 | PPP | 16251.23 | PPP | 18729.37 | PPP | 2.0 | 0.9 | 8706.65 | PP | 20571.15 | PP | 16117.95 | PP | 2.4 | 1.3 | 93013_at |
| 794.50 | PPP | 6722.47 | PPP | 3513.40 | PPP | 8.5 | 1.9 | 1731.15 | PP | 3723.25 | PP | 3064.50 | PP | 2.2 | 1.2 | 97659_r_at |
| 88.47 | AAP | 741.10 | PPP | 512.23 | PAA | 8.4 | 1.4 | 1379.35 | PP | 6137.60 | PP | 4109.05 | PP | 4.4 | 1.5 | 100773_at |
| 1841.07 | PPP | 9687.73 | PPP | 9124.00 | PPP | 5.3 | 1.1 | 3939.15 | PP | 8373.85 | PP | 5956.25 | PP | 2.1 | 1.4 | 101457_at |
| 540.43 | PPP | 2121.03 | PPP | 1738.23 | PPP | 3.9 | 1.2 | 2112.80 | PA | 6896.50 | PP | 4692.20 | PP | 3.3 | 1.5 | 100484_at |
| 135.03 | AAP | 41623.40 | PPP | 35773.60 | PPP | >100 | 1.2 | 3397.60 | PP | 26442.50 | PP | 20423.90 | PP | 7.8 | 1.3 | 94146_at |
| 1322.20 | PAP | 5336.63 | PPP | 4106.00 | PPP | 4.0 | 1.3 | 2395.20 | PP | 5512.25 | PP | 4027.20 | PP | 2.3 | 1.4 | 94972_at |
| 1679.40 | PPP | 5200.60 | PPP | 5662.97 | PPP | 3.1 | 0.9 | 1564.80 | PP | 3378.30 | PP | 3805.30 | PP | 2.2 | 0.9 | 96865_at |
| 4791.87 | PPP | 12622.47 | PPP | 6378.53 | PPP | 2.6 | 2.0 | 6609.50 | PP | 15890.55 | PP | 11088.45 | PP | 2.4 | 1.4 | 102318_at |
| 470.87 | PPP | 982.30 | PPP | 763.33 | PPP | 2.1 | 1.3 | 638.45 | PP | 1334.10 | PP | 836.10 | PP | 2.1 | 1.6 | 104469_at |
| 716.00 | MAM | 3046.27 | PPP | 1847.77 | PPP | 4.3 | 1.6 | 2939.65 | PP | 12115.45 | PP | 5911.55 | PP | 4.1 | 2.0 | 100717_at |
| 603.97 | PAP | 7705.83 | PPP | 14460.07 | PPP | 12.8 | 0.5 | 3232.05 | PP | 9796.50 | PP | 4012.70 | PP | 3.0 | 2.4 | 102736_at |
| 2868.93 | PAP | 10644.40 | PPP | 8354.63 | PPP | 3.7 | 1.3 | 12302.60 | PP | 25242.00 | PP | 22028.15 | PP | 2.1 | 1.1 | 98772_at |
| 466.67 | PAP | 934.40 | PAP | 1252.67 | PPP | 2.0 | 0.7 | 843.45 | PA | 1982.10 | PP | 1036.20 | PP | 2.3 | 1.9 | 93738_at |
| 273.40 | AAP | 2445.50 | PPP | 2434.20 | PPP | 8.9 | 1.0 | 188.95 | PP | 4588.30 | PP | 3664.90 | PP | 24.3 | 1.3 | 160829_at |
| 476.53 | PAP | 2312.90 | PPP | 1638.40 | PPP | 4.9 | 1.4 | 515.45 | PP | 1705.30 | PP | 1597.00 | PP | 3.3 | 1.1 | 102363_r_a |
| 356.47 | AAA | 1078.80 | PPP | 593.80 | PAP | 3.0 | 1.8 | 687.50 | PP | 2197.45 | PP | 1116.25 | PP | 3.2 | 2.0 | 100030_at |
| 6.43 | AAA | 1715.50 | PPP | 1539.87 | PPP | 266.7 | 1.1 | 132.30 | PA | 2734.75 | PP | 1352.40 | PA | 20.7 | 2.0 | 92558_at |

| | | | | wild type | | | | Fold change | |
|---|---|---|---|---|---|---|---|---|---|
| Acc. | Gene/EST Name | ctrl | | LPS | | dex+LPS | | LPS | LPS |
| Num. | | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS |
| AI327518 | mb43a09.y1 Mus musculus cDNA, 5 end | 3370.2 | PP | 9505.95 | PP | 3475.85 | PP | 2.8 | 2.7 |
| AV292869 | Mus musculus cDNA, 3 end | 178.6 | AP | 1971.8 | PP | 467.45 | PP | 11.0 | 4.2 |
| D18865 | MUSGS01047 Mus musculus cDNA, 3 end | 216.7 | PP | 447.4 | PA | 203.3 | PP | 2.1 | 2.2 |
| AI121305 | uc30b06.r1 Mus musculus cDNA, 5 end | 61.25 | AA | 2046.45 | PP | 439.75 | PP | 33.4 | 4.7 |
| AI047791 | uh83e04.r1 Mus musculus cDNA, 5 end | 764.1 | PP | 3948.15 | PP | 1676.85 | PP | 5.2 | 2.4 |
| AI842065 | UI-M-AN1-afg-a-10-0-UI.s1 Mus musculus cDNA, 3 end | 2011.6 | PP | 5860.35 | PP | 1684.05 | PP | 2.9 | 3.5 |
| AI853996 | UI-M-BH0-aiv-g-11-0-UI.s1 Mus musculus cDNA, 3 end | 469.75 | PA | 1136.6 | PP | 539.15 | PP | 2.4 | 2.1 |
| AI853531 | UI-M-BH0-ajd-f-01-0-UI.s1 Mus musculus cDNA, 3 end | 281.25 | PA | 1854.75 | PP | 873.9 | PP | 6.6 | 2.1 |
| AI852314 | UI-M-BH0-aje-g-07-0-UI.s1 Mus musculus cDNA, 3 end | 794.7 | PP | 2863.2 | PP | 904.95 | PP | 3.6 | 3.2 |
| AA608277 | vn61g12.r1 Mus musculus cDNA, 5 end | 202.65 | PA | 10431.9 | PP | 3955.35 | PP | 51.5 | 2.6 |
| AA681998 | vr45a06.s1 Mus musculus cDNA, 5 end | 260.8 | PA | 1202.45 | PP | 577.35 | PP | 4.6 | 2.1 |
| AA717740 | vt98b12.r1 Mus musculus cDNA, 5 end | 412.95 | PP | 1594.35 | PP | 381 | PP | 3.9 | 4.2 |
| AA823202 | vw41h10.r1 Mus musculus cDNA, 5 end | 982.95 | PP | 5842.7 | PP | 2840.35 | PP | 5.9 | 2.1 |
| M34510 | CD14 | 11.58 | | 45.51 | | 15.43 | | 3.9 | 2.9 |
| NM_013885 | Clic4 | 3.03 | | 11.16 | | 4.60 | | 3.7 | 2.4 |
| X16490 | PAI-2 | 35.69 | | 114.43 | | 35.56 | | 3.2 | 3.2 |

| | | GR dim | | | | Fold change | | | | GR LysCre | | | | Fold change | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ctrl | | LPS | | dex+LPS | | LPS | LPS | ctrl | | LPS | | dex+LPS | | LPS | LPS | Grid |
| AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | position |
| 1410.17 | PPP | 4273.60 | PPP | 3446.40 | PPP | ***3.0*** | ***1.2*** | 7995.40 | PP | 16108.50 | PP | 9589.95 | PP | ***2.0*** | ***1.7*** | 103219_at |
| 252.03 | APP | 1295.10 | PPP | 1188.93 | PPP | ***5.1*** | ***1.1*** | 146.75 | AA | 1536.10 | PP | 1282.05 | PP | ***10.5*** | ***1.2*** | 161281_f_a |
| 212.03 | APA | 456.23 | PAP | 292.93 | PPP | ***2.2*** | ***1.6*** | 130.15 | AP | 363.05 | PP | 346.10 | PP | ***2.8*** | ***1.0*** | 101217_at |
| 101.97 | AAP | 1676.23 | PPP | 1637.13 | PPP | ***16.4*** | ***1.0*** | 104.95 | AA | 725.20 | PA | 331.35 | PA | ***6.9*** | ***2.2*** | 97413_at |
| 763.10 | PPP | 3522.10 | PPP | 2721.97 | PPP | ***4.6*** | ***1.3*** | 872.15 | PP | 2760.15 | PP | 2683.30 | PP | ***3.2*** | ***1.0*** | 160588_at |
| 2240.20 | PPP | 6827.57 | PPP | 6869.17 | PPP | ***3.0*** | ***1.0*** | 2719.95 | PP | 6042.05 | PP | 4578.80 | PP | ***2.2*** | ***1.3*** | 104735_at |
| 426.83 | PAP | 956.50 | PPP | 907.07 | PPP | ***2.2*** | ***1.1*** | 283.50 | PA | 706.25 | PP | 460.10 | PA | ***2.5*** | ***1.5*** | 96238_at |
| 365.30 | AAP | 3844.30 | PPP | 6581.90 | PPP | ***10.5*** | ***0.6*** | 1035.65 | PP | 3912.15 | PP | 2672.85 | PP | ***3.8*** | ***1.5*** | 93975_at |
| 457.80 | PPP | 1585.07 | PPP | 1695.53 | PPP | ***3.5*** | ***0.9*** | 851.35 | PP | 1836.15 | PP | 1350.50 | PP | ***2.2*** | ***1.4*** | 94970_at |
| 571.73 | AAP | 7720.43 | PPP | 8690.83 | PPP | ***13.5*** | ***0.9*** | 1499.80 | PA | 12826.00 | PP | 9632.50 | PP | ***8.6*** | ***1.3*** | 99864_at |
| 264.53 | PAP | 878.47 | PPP | 860.90 | PPP | ***3.3*** | ***1.0*** | 390.30 | PP | 1117.80 | PP | 1418.00 | PP | ***2.9*** | ***0.8*** | 97527_at |
| 372.73 | PAA | 835.27 | PPP | 526.43 | PPA | ***2.2*** | ***1.6*** | 622.55 | PP | 1627.75 | PP | 1559.20 | PP | ***2.6*** | ***1.0*** | 95655_at |
| 1055.30 | PPP | 3524.90 | PPP | 3327.83 | PPP | ***3.3*** | ***1.1*** | 1449.65 | PP | 4707.15 | PP | 3714.35 | PP | ***3.2*** | ***1.3*** | 98917_at |
| 8.46 | | 116.12 | | 100.35 | | ***13.7*** | ***1.2*** | 18.04 | | 182.11 | | 575.58 | | ***10.1*** | ***0.3*** | |
| 0.75 | | 5.20 | | 5.71 | | ***6.9*** | ***0.9*** | 9.11 | | 27.95 | | 29.39 | | ***3.1*** | ***1.0*** | |
| 3.36 | | 90.80 | | 99.94 | | ***27.0*** | ***0.9*** | 60.98 | | 228.08 | | 151.37 | | ***3.7*** | ***1.5*** | |

### 10. 3. 2. Normalised expression of genes/ESTs representing Group 1-B

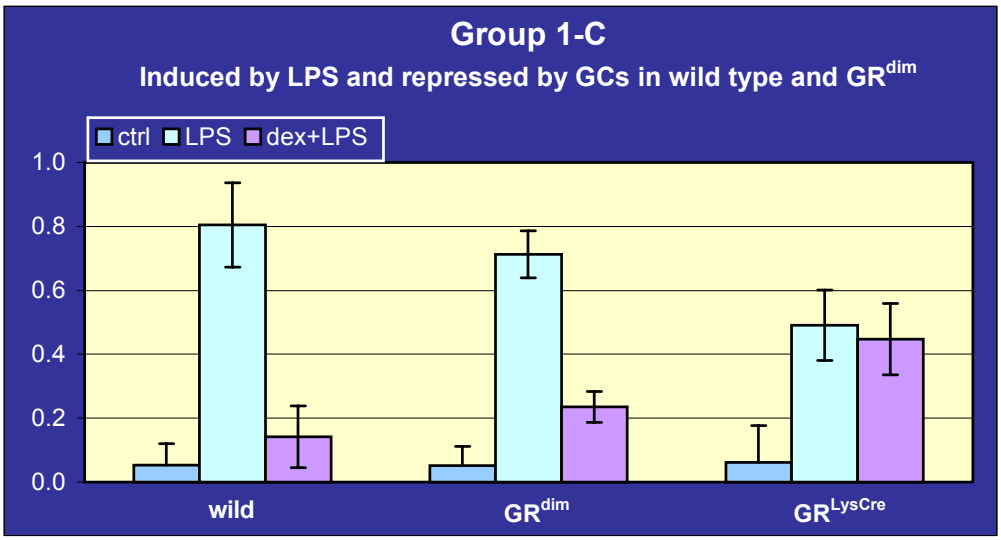
| Acc. Num. | Gene/EST Name |
|---|---|
| U05673 | Balb/C clone R13 adenosine receptor subtype mRNA |
| AF059213 | cholesterol 25-hydroxylase mRNA |
| X78445 | Cyp1-b-1 mRNA for cytochrome P450 |
| D89613 | Cytokine inducible SH2-containing protein |
| D30782 | epiregulin |
| AA182189 | Ets-protein Spi-C |
| X14961 | Fatty acid binding protein heart 1 |
| U00937 | GADD45 protein (gadd45) gene |
| L32838 | germline interleukin 1 receptor antagonist (IL-1rn) gene |
| M88242 | glucocortoid-regulated inflammatory prostaglandin G/H synthase |
| X67644 | gly96 mRNA |
| L07924 | guanine nucleotide dissociation stimulator for a ras-related GTPase |
| X69619 | Inhibin beta-A |
| AF077861 | Inhibitor of DNA binding 2 |
| X04725 | Insulin I |
| M86672 | Interleukin 12a |
| L16956 | Janus kinase 2 |
| X66473 | Matrix metalloproteinase 1 |
| X62502 | MIP-1b |
| AB026569 | MSSP |
| M60474 | Myristoylated alanine rich protein kinase C substrate |
| X86000 | N-glycan alpha 2,8-sialyltransferase |
| M73748 | OTS-8 mRNA |
| U90926 | putative TNF-resistance related protein mRNA |
| M19681 | Small inducible cytokine A2 |
| U27267 | Small inducible cytokine B subfamily, member 5 |
| M22998 | Solute carrier family 2 (facilitated glucose transporter), member 1 |
| U44088 | TDAG51 (TDAG51) mRNA |
| U20735 | transcription factor junB (junB) gene, 5 region and complete cds |
| D44464 | uridine phosphorylase |
| M84487 | Vascular cell adhesion molecule 1 |

| | wild type | | | | GR dim | | | | GR LysCre | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | Grid |
| Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | position |
| 1475.35 | 0.02 | 0.71 | 0.27 | 2540.10 | 0.04 | 0.37 | 0.58 | 3629.55 | 0.09 | 0.53 | 0.38 | 97733_at |
| 2813.05 | 0.04 | 0.73 | 0.23 | 15684.10 | 0.06 | 0.51 | 0.44 | 5591.60 | 0.09 | 0.60 | 0.31 | 104509_at |
| 25790.70 | 0.19 | 0.69 | 0.12 | 13205.17 | 0.12 | 0.55 | 0.33 | 37394.60 | 0.22 | 0.46 | 0.32 | 99979_at |
| 3384.75 | 0.14 | 0.67 | 0.19 | 4045.30 | 0.09 | 0.54 | 0.37 | 3077.45 | 0.12 | 0.53 | 0.35 | 100022_at |
| 13331.50 | 0.00 | 0.95 | 0.05 | 9639.10 | 0.02 | 0.65 | 0.33 | 19837.45 | 0.01 | 0.55 | 0.44 | 98802_at |
| 2191.25 | 0.19 | 0.62 | 0.20 | 1780.33 | 0.15 | 0.37 | 0.49 | 1307.10 | 0.18 | 0.45 | 0.38 | 103454_at |
| 1112.15 | 0.19 | 0.54 | 0.27 | 1319.73 | 0.10 | 0.36 | 0.54 | 656.00 | 0.13 | 0.52 | 0.35 | 94214_at |
| 47735.15 | 0.09 | 0.73 | 0.18 | 43008.37 | 0.09 | 0.48 | 0.43 | 76206.35 | 0.13 | 0.52 | 0.35 | 102292_at |
| 132549.55 | 0.16 | 0.57 | 0.27 | 129356.13 | 0.13 | 0.46 | 0.41 | 135920.95 | 0.20 | 0.44 | 0.36 | 93871_at |
| 36835.00 | 0.01 | 0.80 | 0.19 | 27478.27 | 0.01 | 0.55 | 0.44 | 35363.15 | 0.05 | 0.49 | 0.46 | 104647_at |
| 55188.00 | 0.15 | 0.64 | 0.21 | 58127.73 | 0.11 | 0.46 | 0.43 | 62889.00 | 0.10 | 0.54 | 0.37 | 94384_at |
| 14882.60 | 0.20 | 0.56 | 0.24 | 14152.67 | 0.19 | 0.42 | 0.39 | 22914.20 | 0.13 | 0.50 | 0.38 | 100530_at |
| 16114.30 | 0.04 | 0.72 | 0.24 | 8024.97 | 0.05 | 0.49 | 0.46 | 17217.45 | 0.07 | 0.52 | 0.41 | 100277_at |
| 36582.60 | 0.16 | 0.63 | 0.20 | 43069.30 | 0.19 | 0.38 | 0.43 | 45395.75 | 0.19 | 0.45 | 0.36 | 93013_at |
| 8917.45 | 0.16 | 0.64 | 0.20 | 11030.37 | 0.07 | 0.61 | 0.32 | 8518.90 | 0.20 | 0.44 | 0.36 | 97659_r_at |
| 1297.65 | 0.11 | 0.69 | 0.20 | 1341.80 | 0.07 | 0.55 | 0.38 | 11626.00 | 0.12 | 0.53 | 0.35 | 100773_at |
| 17372.75 | 0.13 | 0.58 | 0.29 | 20652.80 | 0.09 | 0.47 | 0.44 | 18269.25 | 0.22 | 0.46 | 0.33 | 101457_at |
| 7032.40 | 0.15 | 0.78 | 0.06 | 4399.70 | 0.12 | 0.48 | 0.40 | 13701.50 | 0.15 | 0.50 | 0.34 | 100484_at |
| 60580.85 | 0.00 | 0.59 | 0.40 | 77532.03 | 0.00 | 0.54 | 0.46 | 50264.00 | 0.07 | 0.53 | 0.41 | 94146_at |
| 16592.40 | 0.21 | 0.58 | 0.21 | 10764.83 | 0.12 | 0.50 | 0.38 | 11934.65 | 0.20 | 0.46 | 0.34 | 94972_at |
| 7971.45 | 0.12 | 0.61 | 0.27 | 12542.97 | 0.13 | 0.41 | 0.45 | 8748.40 | 0.18 | 0.39 | 0.43 | 96865_at |
| 27816.25 | 0.17 | 0.57 | 0.26 | 23792.87 | 0.20 | 0.53 | 0.27 | 33588.50 | 0.20 | 0.47 | 0.33 | 102318_at |
| 3599.50 | 0.21 | 0.61 | 0.18 | 2216.50 | 0.21 | 0.44 | 0.34 | 2808.65 | 0.23 | 0.47 | 0.30 | 104469_at |
| 5096.80 | 0.14 | 0.69 | 0.16 | 5610.03 | 0.13 | 0.54 | 0.33 | 20966.65 | 0.14 | 0.58 | 0.28 | 100717_at |
| 16598.30 | 0.05 | 0.71 | 0.24 | 22769.87 | 0.03 | 0.34 | 0.64 | 17041.25 | 0.19 | 0.57 | 0.24 | 102736_at |
| 28215.30 | 0.09 | 0.76 | 0.15 | 21867.97 | 0.13 | 0.49 | 0.38 | 59572.75 | 0.21 | 0.42 | 0.37 | 98772_at |
| 2499.10 | 0.09 | 0.67 | 0.24 | 2653.73 | 0.18 | 0.35 | 0.47 | 3861.75 | 0.22 | 0.51 | 0.27 | 93738_at |
| 3785.60 | 0.01 | 0.79 | 0.20 | 5153.10 | 0.05 | 0.47 | 0.47 | 8442.15 | 0.02 | 0.54 | 0.43 | 160829_at |
| 6494.30 | 0.11 | 0.63 | 0.26 | 4427.83 | 0.11 | 0.52 | 0.37 | 3817.75 | 0.14 | 0.45 | 0.42 | 102363_r_at |
| 3053.00 | 0.08 | 0.67 | 0.24 | 2029.07 | 0.18 | 0.53 | 0.29 | 4001.20 | 0.17 | 0.55 | 0.28 | 100030_at |
| 2659.90 | 0.04 | 0.79 | 0.16 | 3261.80 | 0.00 | 0.53 | 0.47 | 4219.45 | 0.03 | 0.65 | 0.32 | 92558_at |

| Acc. Num. | Gene/EST Name |
|---|---|
| AI327518 | mb43a09.y1 Mus musculus cDNA, 5 end |
| AV292869 | Mus musculus cDNA, 3 end |
| D18865 | MUSGS01047 Mus musculus cDNA, 3 end |
| AI121305 | uc30b06.r1 Mus musculus cDNA, 5 end |
| AI047791 | uh83e04.r1 Mus musculus cDNA, 5 end |
| AI842065 | UI-M-AN1-afg-a-10-0-UI.s1 Mus musculus cDNA, 3 end |
| AI853996 | UI-M-BH0-aiv-g-11-0-UI.s1 Mus musculus cDNA, 3 end |
| AI853531 | UI-M-BH0-ajd-f-01-0-UI.s1 Mus musculus cDNA, 3 end |
| AI852314 | UI-M-BH0-aje-g-07-0-UI.s1 Mus musculus cDNA, 3 end |
| AA608277 | vn61g12.r1 Mus musculus cDNA, 5 end |
| AA681998 | vr45a06.s1 Mus musculus cDNA, 5 end |
| AA717740 | vt98b12.r1 Mus musculus cDNA, 5 end |
| AA823202 | vw41h10.r1 Mus musculus cDNA, 5 end |
| M34510 | CD14 |
| NM_013885 | Clic4 |
| X16490 | PAI-2 |

| | wild type | | | | $GR^{dim}$ | | | | $GR^{LysCre}$ | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | Grid |
| Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | position |
| 16352.00 | 0.21 | 0.58 | 0.21 | 9130.17 | 0.15 | 0.47 | 0.38 | 33693.85 | 0.24 | 0.48 | 0.28 | 103219_at |
| 2617.85 | 0.07 | 0.75 | 0.18 | 2736.07 | 0.09 | 0.47 | 0.43 | 2964.90 | 0.05 | 0.52 | 0.43 | 161281_f_at |
| 867.40 | 0.25 | 0.52 | 0.23 | 961.20 | 0.22 | 0.47 | 0.30 | 839.30 | 0.16 | 0.43 | 0.41 | 101217_at |
| 2547.45 | 0.02 | 0.80 | 0.17 | 3415.33 | 0.03 | 0.49 | 0.48 | 1161.50 | 0.09 | 0.62 | 0.29 | 97413_at |
| 6389.10 | 0.12 | 0.62 | 0.26 | 7007.17 | 0.11 | 0.50 | 0.39 | 6315.60 | 0.14 | 0.44 | 0.42 | 160588_at |
| 9556.00 | 0.21 | 0.61 | 0.18 | 15936.93 | 0.14 | 0.43 | 0.43 | 13340.80 | 0.20 | 0.45 | 0.34 | 104735_at |
| 2145.50 | 0.22 | 0.53 | 0.25 | 2290.40 | 0.19 | 0.42 | 0.40 | 1449.85 | 0.20 | 0.49 | 0.32 | 96238_at |
| 3009.90 | 0.09 | 0.62 | 0.29 | 10791.50 | 0.03 | 0.36 | 0.61 | 7620.65 | 0.14 | 0.51 | 0.35 | 93975_at |
| 4562.85 | 0.17 | 0.63 | 0.20 | 3738.40 | 0.12 | 0.42 | 0.45 | 4038.00 | 0.21 | 0.45 | 0.33 | 94970_at |
| 14589.90 | 0.01 | 0.72 | 0.27 | 16983.00 | 0.03 | 0.45 | 0.51 | 23958.30 | 0.06 | 0.54 | 0.40 | 99864_at |
| 2040.60 | 0.13 | 0.59 | 0.28 | 2003.90 | 0.13 | 0.44 | 0.43 | 2926.10 | 0.13 | 0.38 | 0.48 | 97527_at |
| 2388.30 | 0.17 | 0.67 | 0.16 | 1734.43 | 0.21 | 0.48 | 0.30 | 3809.50 | 0.16 | 0.43 | 0.41 | 95655_at |
| 9666.00 | 0.10 | 0.60 | 0.29 | 7908.03 | 0.13 | 0.45 | 0.42 | 9871.15 | 0.15 | 0.48 | 0.38 | 98917_at |
| 72.52 | 0.16 | 0.63 | 0.21 | 224.93 | 0.04 | 0.52 | 0.45 | 775.73 | 0.02 | 0.23 | 0.74 | |
| 18.79 | 0.16 | 0.59 | 0.24 | 11.66 | 0.06 | 0.45 | 0.49 | 66.45 | 0.14 | 0.42 | 0.44 | |
| 185.68 | 0.19 | 0.62 | 0.19 | 194.10 | 0.02 | 0.47 | 0.51 | 440.43 | 0.14 | 0.52 | 0.34 | |

## 10. 4. GROUP 1-C




| | wild type | | | | GR dim | | | | GR LysCre | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS |
| Sum: | **0.33** | **4.71** | **0.96** | Sum: | **0.33** | **4.40** | **1.27** | Sum: | **0.42** | **2.65** | **2.92** |
| Mean: | **0.06** | **0.78** | **0.16** | Mean: | **0.05** | **0.73** | **0.21** | Mean: | **0.07** | **0.44** | **0.49** |
| StDev: | **0.07** | **0.11** | **0.06** | StDev: | **0.07** | **0.08** | **0.04** | StDev: | **0.15** | **0.10** | **0.11** |
| Fold change (LPS/ctrl) | | | **14.2** | Fold change (LPS/ctrl) | | | **13.3** | Fold change (LPS/ctrl) | | | **6.3** |
| Fold change (LPS/dex+LPS) | | | **4.9** | Fold change (LPS/dex+LPS) | | | **3.5** | Fold change (LPS/dex+LPS) | | | **0.9** |

### 10. 4. 1. Expression levels of genes/ESTs representing Group 1-C

| | | | | wild type | | | | Fold change | |
|---|---|---|---|---|---|---|---|---|---|
| Acc. | Gene/EST Name | ctrl | | LPS | | dex+LPS | | LPS | LPS |
| Num. | | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS |
| L41352 | Amphiregulin | 43.05 | AA | 5595.05 | PP | 150.7 | PP | >100 | 37.1 |
| X03020 | Granulocyte-macrophage colony stimulating factor (GM-CSF) | 18.6 | AA | 4496.5 | PP | 24.95 | AA | >100 | >100 |
| X56602 | Interferon-induced 15-KDa protein | 375.45 | AP | 6924.65 | PP | 3458.55 | PP | 18.4 | 2.0 |
| AI848841 | UI-M-AJ1-ahb-c-08-0-UI.s1 Mus musculus cDNA, 3 end | 121.25 | AP | 579.35 | AP | 87.6 | PP | 4.8 | 6.6 |
| M94967 | COX-2 | 0.03 | | 14.80 | | 2.22 | | > 100 | 6.7 |
| G198293 | IL-1beta * | 1.93 | | 9.56 | | 1.83 | | 5.0 | 5.2 |
| J03783 | IL-6 * | 0.02 | | 9.84 | | 2.03 | | > 100 | 4.8 |
| X53798 | MIP-2 * | 4.26 | | 92.45 | | 23.92 | | 21.7 | 3.9 |
| M38296 | TNF-alpha * | 0.04 | | 17.33 | | 1.48 | | > 100 | 11.7 |
| AF069502 | UBP43 | 2.30 | | 9.67 | | 3.88 | | 4.2 | 2.5 |
| M15131 | IL-1beta * | 3565.65 | PP | 86212 | PP | 50257 | PP | 24.2 | 1.7 |
| X54542 | IL-6 * | 69.1 | AA | 27738.9 | PP | 9667.75 | PP | >100 | 2.9 |
| X53798 | MIP-2 * | 5567.7 | PP | 48481.6 | PP | 35722 | PP | 8.7 | 1.4 |
| D84196 | TNF-alpha * | 685.05 | PP | 67676.6 | PP | 27160.2 | PP | 98.8 | 2.5 |

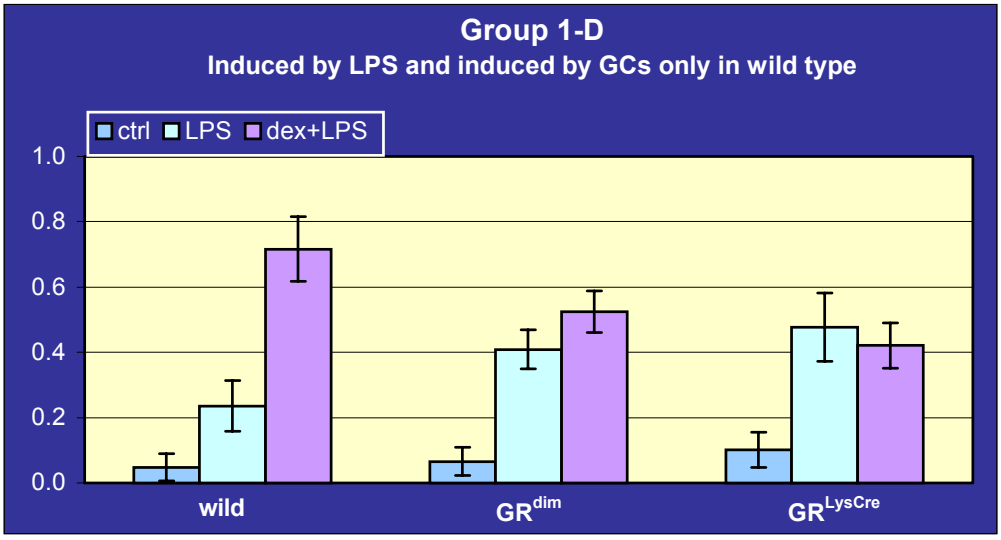
| | | GR dim | | | | Fold change | | | | GR LysCre | | | | Fold change | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ctrl | | LPS | | dex+LPS | | LPS | LPS | ctrl | | LPS | | dex+LPS | | LPS | LPS | Grid |
| AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | position |
| 55.70 | AAA | 2385.13 | PPP | 849.50 | PPP | **42.8** | **2.8** | 39.35 | AA | 931.95 | PP | 746.30 | PP | **23.7** | **1.2** | 99915_at |
| 247.90 | AAA | 7137.80 | PPA | 2354.97 | APA | **28.8** | **3.0** | 52.20 | AA | 2598.00 | PP | 1217.15 | PP | **49.8** | **2.1** | 92948_at |
| 238.20 | AAP | 7374.77 | PPP | 3585.43 | PPP | **31.0** | **2.1** | 409.90 | PP | 2090.40 | PP | 1024.35 | PP | **5.1** | **2.0** | 98822_at |
| 104.00 | PPM | 531.67 | PAP | 228.13 | PPP | **5.1** | **2.3** | 25.65 | AA | 329.95 | PA | 379.60 | PA | **12.9** | **0.9** | 104030_at |
| 0.003 | | 5.75 | | 2.15 | | **> 100** | **2.7** | 0.72 | | 15.50 | | 17.80 | | **21.5** | **0.9** | |
| 0.09 | | 9.81 | | 2.68 | | **> 100** | **3.7** | 0.16 | | 8.54 | | 5.52 | | **53.4** | **1.5** | |
| 1.07 | | 7.41 | | 1.75 | | **6.9** | **4.2** | 0.03 | | 4.45 | | 6.38 | | **> 100** | **0.7** | |
| 2.90 | | 53.17 | | 16.37 | | **18.3** | **3.2** | 0.0005 | | 13.350 | | 16.020 | | **> 100** | **0.8** | |
| 0.02 | | 13.84 | | 2.62 | | **> 100** | **5.3** | 0.57 | | 21.74 | | 28.20 | | **38.1** | **0.8** | |
| 2.71 | | 9.16 | | 3.49 | | **3.4** | **2.6** | 2.25 | | 1.81 | | 1.93 | | **0.8** | **0.9** | |
| 8497.60 | APP | 83023.03 | PPP | 73836.73 | PPP | *9.8* | *1.1* | 22622.25 | PP | 76487.45 | PP | 77784.35 | PP | *3.4* | *1.0* | 103486_at |
| 65.77 | AAP | 18572.87 | PPP | 13893.30 | PPP | *>100* | *1.3* | 478.75 | PP | 17948.70 | PP | 15379.65 | PP | *37.5* | *1.2* | 102218_at |
| 5074.97 | PPP | 40017.53 | PPP | 40120.00 | PPP | *7.9* | *1.0* | 17759.40 | PP | 43285.65 | PP | 41961.90 | PP | *2.4* | *1.0* | 101160_at |
| 989.43 | AAP | 63700.63 | PPP | 37811.60 | PPP | *64.4* | *1.7* | 2331.45 | PP | 50744.60 | PP | 35286.30 | PP | *21.8* | *1.4* | 102629_at |

### 10. 4. 2. Normalised expression of genes/ESTs representing Group 1-C

| Acc. Num. | Gene/EST Name |
|---|---|
| L41352 | Amphiregulin |
| X03020 | Granulocyte-macrophage colony stimulating factor (GM-CSF) |
| X56602 | Interferon-induced 15-KDa protein |
| AI848841 | UI-M-AJ1-ahb-c-08-0-UI.s1 Mus musculus cDNA, 3 end |
| M94967 | COX-2 |
| G198293 | IL-1beta |
| J03783 | IL-6 |
| X53798 | MIP-2 |
| M38296 | TNF-alpha |
| AF069502 | UBP43 |

| | wild type | | | | GR dim | | | | GR LysCre | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | Grid |
| **Sum** | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | **position** |
| 5788.80 | 0.01 | 0.97 | 0.03 | 3290.33 | 0.02 | 0.72 | 0.26 | 1717.60 | 0.02 | 0.54 | 0.43 | 99915_at |
| 4540.05 | 0.00 | 0.99 | 0.01 | 9740.67 | 0.03 | 0.73 | 0.24 | 3867.35 | 0.01 | 0.67 | 0.31 | 92948_at |
| 10758.65 | 0.03 | 0.64 | 0.32 | 11198.40 | 0.02 | 0.66 | 0.32 | 3524.65 | 0.12 | 0.59 | 0.29 | 98822_at |
| 788.20 | 0.15 | 0.74 | 0.11 | 863.80 | 0.12 | 0.62 | 0.26 | 735.20 | 0.03 | 0.45 | 0.52 | 104030_at |
| 17.05 | 0.00 | 0.87 | 0.13 | 7.90 | 0.00 | 0.73 | 0.27 | 34.02 | 0.02 | 0.46 | 0.52 | |
| 13.32 | 0.14 | 0.72 | 0.14 | 12.58 | 0.01 | 0.78 | 0.21 | 14.22 | 0.01 | 0.60 | 0.39 | |
| 11.89 | 0.00 | 0.83 | 0.17 | 10.23 | 0.10 | 0.72 | 0.17 | 10.86 | 0.00 | 0.41 | 0.59 | |
| 120.63 | 0.04 | 0.77 | 0.20 | 72.44 | 0.04 | 0.73 | 0.23 | 29.37 | 0.00 | 0.45 | 0.55 | |
| 18.85 | 0.00 | 0.92 | 0.08 | 16.48 | 0.00 | 0.84 | 0.16 | 50.51 | 0.01 | 0.43 | 0.56 | |
| 15.85 | 0.15 | 0.61 | 0.24 | 15.36 | 0.18 | 0.60 | 0.23 | 5.99 | 0.38 | 0.30 | 0.32 | |

## 10. 5. GROUP 1-D




| | wild type | | | | GR dim | | | | GR LysCre | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS |
| Sum: | **0.24** | **1.18** | **3.58** | Sum: | **0.33** | **2.04** | **2.62** | Sum: | **0.51** | **2.38** | **2.10** |
| Mean: | **0.05** | **0.24** | **0.72** | Mean: | **0.07** | **0.41** | **0.52** | Mean: | **0.10** | **0.48** | **0.42** |
| StDev: | **0.04** | **0.08** | **0.10** | StDev: | **0.04** | **0.06** | **0.06** | StDev: | **0.05** | **0.10** | **0.07** |
| Fold change (LPS/ctrl) | | | **4.9** | Fold change (LPS/ctrl) | | | **6.2** | Fold change (LPS/ctrl) | | | **4.7** |
| Fold change (LPS/dex+LPS) | | | **0.3** | Fold change (LPS/dex+LPS) | | | **0.8** | Fold change (LPS/dex+LPS) | | | **1.1** |

### 10. 5. 1. Expression levels of genes/ESTs representing Group 1-D

| | | | | wild type | | | | Fold change | |
|---|---|---|---|---|---|---|---|---|---|
| Acc. | Gene/EST Name | ctrl | | LPS | | dex+LPS | | LPS | LPS |
| Num. | | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS |
| M33960 | plasminogen activator inhibitor (PAI-1) mRNA, complete cds | 67.9 | AA | 4102.95 | PP | 9294.4 | PP | 60.4 | 0.4 |
| D89571 | ryudocan core protein, complete cds | 208.85 | PA | 1952.1 | PP | 16660.8 | PP | 9.3 | 0.1 |
| AI647003 | ub68e09.x1 Mus musculus cDNA, 3 end | 1240.15 | PP | 3247.2 | PP | 8304.9 | PP | 2.6 | 0.4 |
| AI849939 | UI-M-BG0-ahz-g-03-0-UI.s1 Mus musculus cDNA, 3 end | 582.4 | AP | 3463.6 | AP | 10134.8 | PP | 5.9 | 0.3 |
| AW121294 | UI-M-BH2.3-aog-d-09-0-UI.s1 Mus musculus cDNA, 3 end | 167 | AA | 531.35 | AP | 1251.2 | PP | 3.2 | 0.4 |

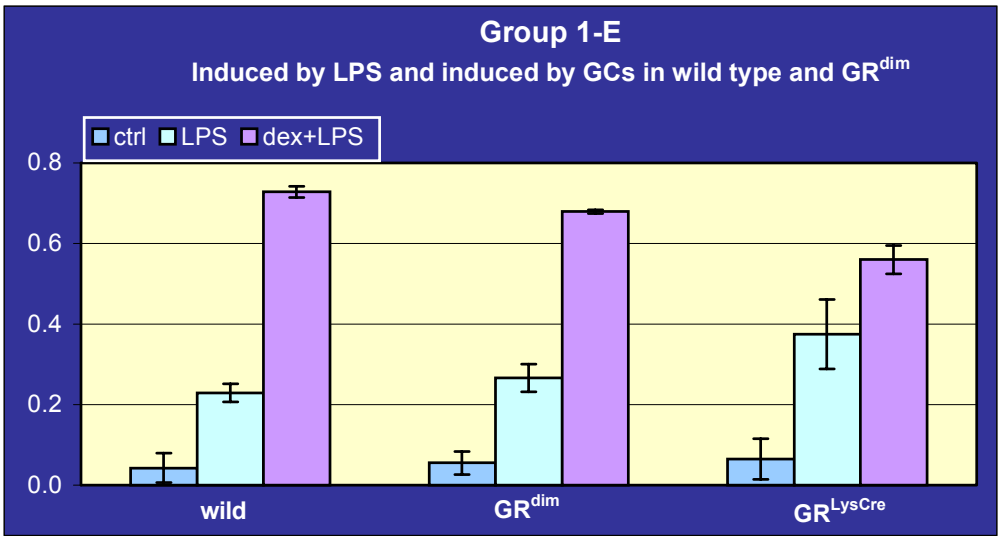
| | | GR dim | | | | Fold change | | | | GR LysCre | | | | Fold change | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ctrl | | LPS | | dex+LPS | | LPS | LPS | ctrl | | LPS | | dex+LPS | | LPS | LPS | Grid |
| AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | position |
| 1169.90 | APP | 9978.30 | PPP | 10027.37 | PPP | **8.5** | **1.0** | 224.15 | PM | 2164.85 | PP | 1227.45 | PP | **9.7** | **1.8** | 94147_at |
| 229.77 | PAA | 4284.33 | PPP | 7036.00 | PPP | **18.6** | **0.6** | 206.30 | PA | 2382.60 | PP | 1910.20 | PP | **11.5** | **1.2** | 98590_at |
| 1581.00 | PPP | 4031.00 | PPP | 6023.30 | PPP | **2.5** | **0.7** | 1893.40 | PP | 3976.70 | PP | 6557.75 | PP | **2.1** | **0.6** | 100958_at |
| 470.50 | PPP | 3207.13 | PPP | 3071.00 | PPP | **6.8** | **1.0** | 1379.60 | PP | 7736.90 | PP | 6844.10 | PP | **5.6** | **1.1** | 103460_at |
| 188.60 | AAA | 1422.83 | PPP | 2123.13 | PPP | **7.5** | **0.7** | 311.90 | PP | 847.60 | PP | 722.00 | PP | **2.7** | **1.2** | 96747_at |

### 10. 5. 2. Normalised expression of genes/ESTs representing Group 1-D

| Acc. Num. | Gene/EST Name |
|---|---|
| M33960 | plasminogen activator inhibitor (PAI-1) mRNA, complete cds |
| D89571 | ryudocan core protein, complete cds |
| AI647003 | ub68e09.x1 Mus musculus cDNA, 3 end |
| AI849939 | UI-M-BG0-ahz-g-03-0-UI.s1 Mus musculus cDNA, 3 end |
| AW121294 | UI-M-BH2.3-aog-d-09-0-UI.s1 Mus musculus cDNA, 3 end |

| | wild type | | | | GR dim | | | | GR LysCre | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | Grid |
| Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | position |
| 13465.25 | 0.01 | 0.30 | 0.69 | 21175.57 | 0.06 | 0.47 | 0.47 | 3616.45 | 0.06 | 0.60 | 0.34 | 94147_at |
| 18821.75 | 0.01 | 0.10 | 0.89 | 11550.10 | 0.02 | 0.37 | 0.61 | 4499.10 | 0.05 | 0.53 | 0.42 | 98590_at |
| 12792.25 | 0.10 | 0.25 | 0.65 | 11635.30 | 0.14 | 0.35 | 0.52 | 12427.85 | 0.15 | 0.32 | 0.53 | 100958_at |
| 14180.80 | 0.04 | 0.24 | 0.71 | 6748.63 | 0.07 | 0.48 | 0.46 | 15960.60 | 0.09 | 0.48 | 0.43 | 103460_at |
| 1949.55 | 0.09 | 0.27 | 0.64 | 3734.57 | 0.05 | 0.38 | 0.57 | 1881.50 | 0.17 | 0.45 | 0.38 | 96747_at |

# 10. 6. GROUP 1-E




| | wild type | | | | GR dim | | | | GR LysCre | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS |
| Sum: | **0.09** | **0.46** | **1.46** | Sum: | **0.11** | **0.53** | **1.36** | Sum: | **0.13** | **0.75** | **1.12** |
| Mean: | **0.04** | **0.23** | **0.73** | Mean: | **0.05** | **0.27** | **0.68** | Mean: | **0.07** | **0.37** | **0.56** |
| StDev: | **0.04** | **0.02** | **0.01** | StDev: | **0.03** | **0.03** | **0.00** | StDev: | **0.05** | **0.09** | **0.04** |
| Fold change (LPS/ctrl) | | | **5.4** | Fold change (LPS/ctrl) | | | **4.9** | Fold change (LPS/ctrl) | | | **5.7** |
| Fold change (LPS/dex+LPS) | | | **0.3** | Fold change (LPS/dex+LPS) | | | **0.4** | Fold change (LPS/dex+LPS) | | | **0.7** |

### 10. 6. 1. Expression levels of genes/ESTs representing Group 1-E

| | | | | wild type | | | | Fold change | |
|---|---|---|---|---|---|---|---|---|---|
| Acc. | Gene/EST Name | ctrl | | LPS | | dex+LPS | | LPS | LPS |
| Num. | | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS |
| U35233 | Endothelin 1 | 93.65 | AA | 1335.65 | PP | 4029 | PP | 14.3 | 0.3 |
| X61940 | Growth factor-inducible immediate early gene (3CH134) | 1434.9 | PP | 4527 | PP | 15175.8 | PP | 3.2 | 0.3 |

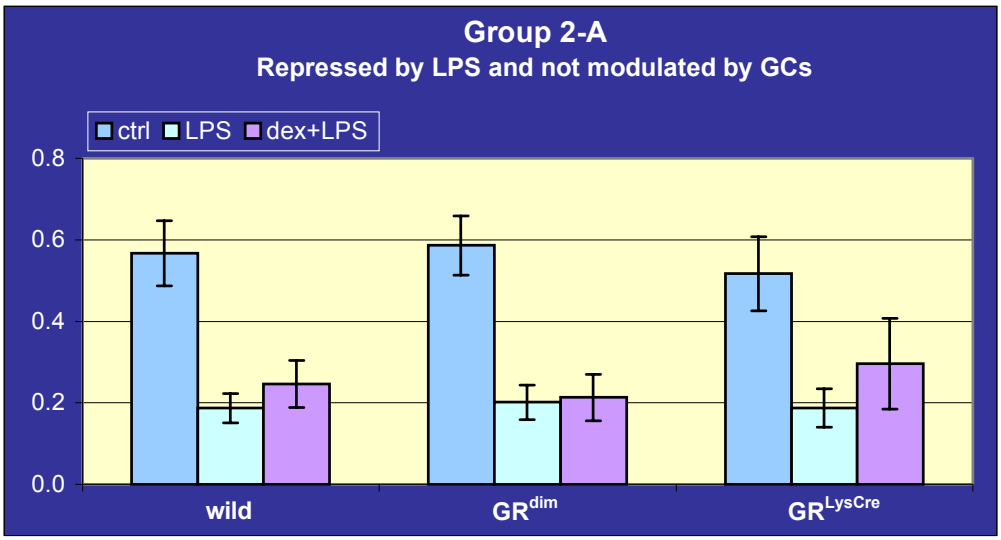
| | | GR dim | | | | Fold change | | | | GR LysCre | | | | Fold change | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ctrl | | LPS | | dex+LPS | | LPS | LPS | ctrl | | LPS | | dex+LPS | | LPS | LPS | Grid |
| AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | position |
| 191.30 | PAA | 1630.57 | PPP | 3800.67 | PPP | ***8.5*** | ***0.4*** | 69.55 | AA | 1021.00 | PA | 1253.50 | PP | ***14.7*** | ***0.8*** | 102737_at |
| 1035.07 | PPP | 3324.27 | PPP | 9385.00 | PPP | ***3.2*** | ***0.4*** | 1902.70 | PP | 5914.20 | PP | 11011.65 | PP | ***3.1*** | ***0.5*** | 104598_at |

### 10. 6. 2. Normalised expression of genes/ESTs representing Group 1-E

| Acc. Num. | Gene/EST Name |
|---|---|
| U35233 | Endothelin 1 |
| X61940 | Growth factor-inducible immediate early gene (3CH134) |

| | wild type | | | | GR dim | | | | GR LysCre | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | Grid |
| **Sum** | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | **position** |
| 5458.30 | 0.02 | 0.24 | 0.74 | 5622.53 | 0.03 | 0.29 | 0.68 | 2344.05 | 0.03 | 0.44 | 0.53 | 102737_at |
| 21137.65 | 0.07 | 0.21 | 0.72 | 13744.33 | 0.08 | 0.24 | 0.68 | 18828.55 | 0.10 | 0.31 | 0.58 | 104598_at |

## 10. 7. GROUP 2-A




| | wild type | | | | GR dim | | | | GR LysCre | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS |
| Sum: | **58.97** | **19.50** | **25.54** | Sum: | **60.97** | **20.88** | **22.15** | Sum: | **53.80** | **19.43** | **30.76** |
| Mean: | **0.57** | **0.19** | **0.25** | Mean: | **0.59** | **0.20** | **0.21** | Mean: | **0.52** | **0.19** | **0.30** |
| StDev: | **0.08** | **0.04** | **0.06** | StDev: | **0.07** | **0.04** | **0.06** | StDev: | **0.09** | **0.05** | **0.11** |
| Fold change (LPS/ctrl) | | | **0.3** | Fold change (LPS/ctrl) | | | **0.3** | Fold change (LPS/ctrl) | | | **0.4** |
| Fold change (LPS/dex+LPS) | | | **0.8** | Fold change (LPS/dex+LPS) | | | **0.9** | Fold change (LPS/dex+LPS) | | | **0.6** |

### 10. 7. 1. Expression levels of genes/ESTs representing Group 2-A

| | | | | wild type | | | | Fold change | |
|---|---|---|---|---|---|---|---|---|---|
| Acc. | Gene/EST Name | ctrl | | LPS | | dex+LPS | | LPS | LPS |
| Num. | | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS |
| M28489 | (clone Mu6a) ribosomal protein S6 kinase (rsk) mRNA | 2563.35 | PP | 1110 | AP | 1491 | PP | 0.4 | 0.7 |
| U22262 | Apolipoprotein B editing complex 1 | 13807.8 | PP | 3699 | PP | 4558.5 | PP | 0.3 | 0.8 |
| AF017085 | BAP-135 homolog (Diws1t) mRNA | 5105.55 | PP | 2547.05 | PP | 4579.15 | PP | 0.5 | 0.6 |
| U75506 | BH3 interacting domain death agonist | 360.65 | PP | 156.7 | AA | 177.2 | PP | 0.4 | 0.9 |
| AF076156 | Catechol-O-methyltransferase | 3347.95 | PP | 744.7 | AP | 1319.05 | PP | 0.2 | 0.6 |
| U53455 | chloride ion current inducer protein (CLCI) mRNA | 4235.4 | PP | 1286.7 | PP | 1173.2 | PP | 0.3 | 1.1 |
| X55663 | Cytoplasmic tyrosine kinase, Dscr28C related (Drosophila) | 2948.95 | PP | 1030.2 | PP | 1323.75 | PP | 0.3 | 0.8 |
| AB001990 | Dcra | 3817.7 | PP | 1655 | PP | 2276.45 | PP | 0.4 | 0.7 |
| U78818 | Downstream of tyrosine kinase 1 | 1348.55 | PP | 479.45 | AP | 660.35 | PP | 0.4 | 0.7 |
| D10475 | Epimorphin | 2204.45 | PP | 532.5 | AP | 455.3 | PP | 0.2 | 1.2 |
| L00919 | Erythrocyte protein band 4.1 | 1106.55 | PP | 473.7 | PP | 599.45 | PP | 0.4 | 0.8 |
| V00727 | FBJ osteosarcoma oncogene | 2287.1 | PP | 335.1 | AP | 309.9 | PP | 0.1 | 1.1 |
| U67187 | G protein signaling regulator RGS2 (rgs2) mRNA | 1231.65 | PP | 235.4 | AP | 175.55 | PP | 0.2 | 1.3 |
| M96265 | galactose-1-phosphate uridyl transferase (GALT) mRNA | 442.65 | PP | 106.1 | AA | 180.4 | PA | 0.2 | 0.6 |
| L07508 | Golli-mpb mRNA (alternate transcript from clone BG21) | 2799.4 | PP | 701.3 | PP | 1035.55 | PP | 0.3 | 0.7 |
| M98036 | guanine nucleotide exchange factor delta subunit (JGR1A) mRNA | 744.7 | PP | 342.7 | MA | 528.3 | PP | 0.5 | 0.6 |
| AW122990 | Hagoromo | 1126.9 | PP | 526.2 | AP | 560.1 | PP | 0.5 | 0.9 |
| M32489 | Interferon concensus sequence binding protein | 5456.35 | PP | 1534.35 | PP | 1948.05 | PP | 0.3 | 0.8 |
| AF042487 | intermediate conductance potassium channel mIK1 mRNA | 558.4 | PP | 172 | AP | 312.95 | PP | 0.3 | 0.5 |
| X57687 | LYL gene (clone L6) | 5826 | PP | 1737.1 | PP | 1875.8 | PP | 0.3 | 0.9 |
| AB028921 | NAKAP95 | 813.65 | PP | 373.8 | AP | 478.9 | PP | 0.5 | 0.8 |
| AI853802 | Phosphofructokinase-1 C isozyme | 1075.9 | PP | 502.9 | PP | 591.1 | PP | 0.5 | 0.9 |
| M34141 | Prostaglandin-endoperoxide synthase 1 | 1966 | PP | 902.4 | PP | 956.8 | PP | 0.5 | 0.9 |
| X95281 | retinal short-chain dehydrogenase/reductase | 1729.3 | PP | 284.7 | AP | 446.15 | PP | 0.2 | 0.6 |
| U05245 | T-cell lymphoma invasion and metastasis 1 | 788.05 | PP | 293.1 | PA | 348.7 | PP | 0.4 | 0.8 |
| X64361 | vav mRNA | 3159 | PP | 919.65 | PP | 1360 | PP | 0.3 | 0.7 |
| D83266 | vav-T | 4363 | PP | 1496.15 | PP | 2022.25 | PP | 0.3 | 0.7 |
| U27398 | Xeroderma pigmentosum, complementation group C | 620.2 | PP | 183.1 | AP | 250.15 | PP | 0.3 | 0.7 |
| D43643 | YL-1 mRNA for YL-1 protein (nuclear protein with DNA-binding ability) | 607.45 | AP | 242.6 | AP | 289.3 | PP | 0.4 | 0.8 |
| AA980810 | ua45h04.r1 Mus musculus cDNA, 5 end | 754.95 | PP | 120.95 | AA | 147.6 | PP | 0.2 | 0.8 |
| AI462312 | ub62c01.x1 Mus musculus cDNA, 3 end | 602 | PP | 260.35 | PP | 304.5 | PP | 0.4 | 0.9 |
| AI882440 | uc01f05.r1 Mus musculus cDNA, 5 end | 2728.95 | PP | 367.75 | AP | 583.05 | PP | 0.1 | 0.6 |
| AI154249 | ud30f12.r1 Mus musculus cDNA, 5 end | 4947.6 | PP | 2377.05 | AP | 1584.55 | PP | 0.5 | 1.5 |
| AI115399 | uh85b06.r1 Mus musculus cDNA, 5 end | 1011.1 | PP | 366.85 | PP | 443.3 | PP | 0.4 | 0.8 |
| AI841137 | UI-M-AH0-acz-g-06-0-UI.s1 Mus musculus cDNA, 3 end | 8690.15 | PP | 3206.4 | PP | 4219.35 | PP | 0.4 | 0.8 |
| AI848207 | UI-M-AH1-agq-g-08-0-UI.s1 Mus musculus cDNA, 3 end | 2025.6 | PP | 544.5 | PP | 955.25 | PP | 0.3 | 0.6 |
| AI849587 | UI-M-AH1-agr-e-02-0-UI.s1 Mus musculus cDNA, 3 end | 2225.8 | PP | 990.4 | PP | 1679.9 | PP | 0.4 | 0.6 |

| | | GR dim | | | | Fold change | | | | GR LysCre | | | | Fold change | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ctrl | | LPS | | dex+LPS | | LPS | LPS | ctrl | | LPS | | dex+LPS | | LPS | LPS | Grid |
| AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | position |
| 2686.20 | PPP | 1055.00 | PPP | 1377.37 | PPP | 0.4 | 0.8 | 2069.70 | PP | 919.75 | PP | 1040.25 | PP | 0.4 | 0.9 | 97405_at |
| 14127.83 | PPP | 2273.20 | PPP | 2305.83 | PPP | 0.2 | 1.0 | 12858.10 | PP | 4488.85 | PP | 3226.80 | PP | 0.3 | 1.4 | 98398_s_at |
| 5713.57 | PPP | 2535.40 | PPP | 2440.60 | PPP | 0.4 | 1.0 | 3605.05 | PP | 1767.00 | PP | 5630.05 | PP | 0.5 | 0.3 | 94295_at |
| 381.83 | PPP | 121.30 | APA | 71.27 | AAA | 0.3 | 1.7 | 233.50 | PP | 88.70 | PA | 138.50 | PA | 0.4 | 0.6 | 98433_at |
| 2576.33 | PPP | 827.37 | PPP | 882.90 | PPP | 0.3 | 0.9 | 1754.55 | PP | 595.30 | PP | 686.30 | PP | 0.3 | 0.9 | 98535_at |
| 2656.20 | PPP | 949.57 | PAP | 1785.90 | PPP | 0.4 | 0.5 | 4645.15 | PP | 2125.25 | PP | 2014.55 | PP | 0.5 | 1.1 | 93812_at |
| 3380.97 | PPP | 1115.33 | PPP | 1495.50 | PPP | 0.3 | 0.7 | 2582.00 | PP | 993.65 | PP | 1529.60 | PP | 0.4 | 0.6 | 103539_at |
| 4232.17 | PPP | 1349.27 | PPP | 2040.90 | PPP | 0.3 | 0.7 | 3826.40 | PP | 1706.10 | PP | 1730.95 | PP | 0.4 | 1.0 | 101104_at |
| 1771.40 | PPP | 499.27 | PPP | 690.10 | PPP | 0.3 | 0.7 | 1157.30 | PP | 469.85 | PP | 367.55 | PP | 0.4 | 1.3 | 102896_at |
| 3154.37 | PPP | 486.43 | PAP | 689.43 | PPP | 0.2 | 0.7 | 1527.25 | PP | 409.45 | PP | 361.45 | PA | 0.3 | 1.1 | 104482_at |
| 794.47 | PPA | 278.00 | PPA | 427.70 | PPA | 0.3 | 0.6 | 539.85 | PP | 200.65 | AA | 1186.80 | PA | 0.4 | 0.2 | 160379_at |
| 2836.30 | PPP | 478.33 | PPP | 493.13 | PPP | 0.2 | 1.0 | 1058.50 | PP | 284.55 | PP | 499.90 | PP | 0.3 | 0.6 | 160901_at |
| 2557.07 | PPP | 200.47 | PMA | 357.53 | PPA | 0.1 | 0.6 | 2592.50 | PP | 315.15 | PP | 458.75 | PP | 0.1 | 0.7 | 97844_at |
| 515.00 | PPP | 155.77 | MAA | 163.03 | PPM | 0.3 | 1.0 | 490.35 | AP | 122.55 | PA | 335.45 | PM | 0.2 | 0.4 | 104616_g_at |
| 2121.43 | PPP | 700.40 | PPP | 533.77 | PPP | 0.3 | 1.3 | 3230.80 | PP | 891.60 | PP | 1647.05 | PP | 0.3 | 0.5 | 96310_at |
| 856.63 | PPP | 398.23 | PPP | 376.00 | PPP | 0.5 | 1.1 | 760.55 | PP | 358.00 | PA | 589.70 | PA | 0.5 | 0.6 | 95046_s_at |
| 1434.43 | PPP | 709.47 | PAP | 500.63 | PPP | 0.5 | 1.4 | 923.55 | PP | 374.60 | PP | 531.45 | PP | 0.4 | 0.7 | 102478_f_at |
| 7594.57 | PPP | 3521.63 | PPP | 2679.07 | PPP | 0.5 | 1.3 | 6909.60 | PP | 1937.70 | PP | 1151.00 | PP | 0.3 | 1.7 | 98002_at |
| 660.97 | PPP | 315.50 | PPP | 502.23 | PPP | 0.5 | 0.6 | 943.20 | PM | 260.10 | PA | 1268.65 | PA | 0.3 | 0.2 | 102198_at |
| 8838.63 | PPP | 3105.17 | PPP | 1295.97 | PPP | 0.4 | 2.4 | 5545.50 | PP | 1873.95 | PP | 1065.70 | PP | 0.3 | 1.8 | 100468_g_at |
| 832.77 | PPP | 311.47 | PPA | 326.73 | PPA | 0.4 | 1.0 | 836.10 | PP | 295.60 | PP | 492.25 | PA | 0.4 | 0.6 | 101947_at |
| 1253.57 | PPP | 532.50 | PPP | 633.63 | PPP | 0.4 | 0.8 | 1735.85 | PP | 775.35 | PP | 733.50 | PP | 0.4 | 1.1 | 97834_g_at |
| 1092.73 | PPP | 450.67 | PPP | 508.83 | PPP | 0.4 | 0.9 | 2655.55 | PP | 1168.50 | PP | 1205.60 | PP | 0.4 | 1.0 | 95597_at |
| 2326.00 | PPP | 909.43 | PPP | 568.37 | PPP | 0.4 | 1.6 | 1423.35 | PP | 442.85 | PP | 775.10 | PP | 0.3 | 0.6 | 102797_at |
| 511.60 | APP | 192.63 | PAA | 262.87 | APP | 0.4 | 0.7 | 736.40 | PP | 282.45 | AP | 497.35 | PP | 0.4 | 0.6 | 102283_at |
| 2710.03 | PPP | 919.40 | PPP | 1265.50 | PPP | 0.3 | 0.7 | 3086.90 | PP | 1200.45 | PP | 1424.90 | PP | 0.4 | 0.8 | 99799_at |
| 3934.03 | PPP | 1426.93 | PPP | 2130.93 | PPP | 0.4 | 0.7 | 3956.25 | PP | 1947.80 | PP | 1983.40 | PP | 0.5 | 1.0 | 96511_s_at |
| 635.17 | PPP | 207.10 | PPA | 169.83 | APA | 0.3 | 1.2 | 454.20 | PP | 73.75 | PA | 477.55 | PA | 0.2 | 0.2 | 95626_at |
| 825.80 | PPP | 269.53 | PAA | 265.63 | APP | 0.3 | 1.0 | 756.70 | PP | 354.90 | AP | 517.90 | PP | 0.5 | 0.7 | 160363_at |
| 487.93 | PPP | 31.90 | AAP | 127.10 | APP | 0.1 | 0.3 | 438.85 | PP | 107.00 | PP | 208.85 | PP | 0.2 | 0.5 | 160922_at |
| 595.73 | PPP | 213.63 | APP | 373.43 | PPP | 0.4 | 0.6 | 685.40 | PP | 221.60 | PA | 1967.70 | PP | 0.3 | 0.1 | 161076_at |
| 2076.53 | PPP | 280.27 | PPP | 565.20 | PPP | 0.1 | 0.5 | 2483.65 | PP | 523.15 | PA | 547.70 | PA | 0.2 | 1.0 | 104293_at |
| 3430.63 | PPP | 1613.73 | PPM | 847.27 | PPA | 0.5 | 1.9 | 2165.35 | PP | 539.15 | PP | 4584.35 | PP | 0.2 | 0.1 | 100511_at |
| 775.83 | PPP | 331.63 | PPP | 282.37 | PPP | 0.4 | 1.2 | 970.45 | PP | 381.10 | PP | 312.65 | PP | 0.4 | 1.2 | 103711_at |
| 10443.30 | PPP | 3885.53 | PPP | 3168.73 | PPP | 0.4 | 1.2 | 6150.05 | PP | 2990.35 | PP | 2469.15 | PP | 0.5 | 1.2 | 160311_at |
| 1873.50 | PPP | 574.20 | PPP | 679.37 | PPP | 0.3 | 0.8 | 1980.75 | PP | 697.85 | PP | 799.05 | PP | 0.4 | 0.9 | 103852_at |
| 4425.23 | PPP | 1306.40 | PPP | 2768.27 | PPP | 0.3 | 0.5 | 1791.65 | PP | 799.95 | AP | 708.70 | MP | 0.4 | 1.1 | 95465_s_at |

| | | | | wild type | | | | Fold change | |
|---|---|---|---|---|---|---|---|---|---|
| Acc. | Gene/EST Name | ctrl | | LPS | | dex+LPS | | LPS | LPS |
| Num. | | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS |
| AI849497 | UI-M-AH1-agt-d-06-0-UI.s1 Mus musculus cDNA, 3 end | 444.55 | MP | 172.9 | AA | 223.45 | PP | 0.4 | 0.8 |
| AI835963 | UI-M-AI0-aao-h-06-0-UI.s1 Mus musculus cDNA, 3 end | 627.4 | PP | 140.8 | AA | 224.1 | PA | 0.2 | 0.6 |
| AI842242 | UI-M-AI1-afp-d-07-0-UI.s1 Mus musculus cDNA, 3 end | 2476.9 | PP | 600.6 | AA | 922.95 | PP | 0.2 | 0.7 |
| AI837229 | UI-M-AK0-ade-e-06-0-UI.s1 Mus musculus cDNA, 3 end | 1549.15 | PP | 437.4 | AP | 499.8 | PP | 0.3 | 0.9 |
| AI837679 | UI-M-AK0-adj-b-10-0-UI.s1 Mus musculus cDNA, 3 end | 1889.45 | PP | 646.85 | AP | 1146.9 | PP | 0.3 | 0.6 |
| AI843884 | UI-M-AK1-aeu-e-10-0-UI.s1 Mus musculus cDNA, 3 end | 7502.15 | PP | 1053.6 | PP | 1505.55 | PP | 0.1 | 0.7 |
| AI845902 | UI-M-AK1-aex-b-07-0-UI.s1 Mus musculus cDNA, 3 end | 1362.05 | PP | 600.95 | PP | 684.1 | PP | 0.4 | 0.9 |
| AI849679 | UI-M-AL1-ahl-e-09-0-UI.s1 Mus musculus cDNA, 3 end | 970.5 | PP | 312.7 | AP | 309.45 | PP | 0.3 | 1.0 |
| AI849743 | UI-M-AL1-ahn-d-06-0-UI.s1 Mus musculus cDNA, 3 end | 440.05 | PP | 130.95 | PP | 234.35 | PP | 0.3 | 0.6 |
| AI844739 | UI-M-AL1-ahq-d-01-0-UI.s1 Mus musculus cDNA, 3 end | 1842.05 | PP | 663.95 | MP | 854.7 | PP | 0.4 | 0.8 |
| AI846531 | UI-M-AN1-aff-f-08-0-UI.s1 Mus musculus cDNA, 3 end | 816.2 | PP | 289.15 | PA | 304.55 | AA | 0.4 | 0.9 |
| AI846534 | UI-M-AN1-aff-f-11-0-UI.s1 Mus musculus cDNA, 3 end | 865.55 | PP | 388.2 | PA | 420.15 | PP | 0.4 | 0.9 |
| AI838655 | UI-M-AO0-aca-c-08-0-UI.s1 Mus musculus cDNA, 3 end | 3072.75 | PP | 808.75 | AP | 974.15 | PP | 0.3 | 0.8 |
| AI838702 | UI-M-AO0-aca-h-06-0-UI.s1 Mus musculus cDNA, 3 end | 1873.85 | PP | 75.25 | AA | 108.5 | PA | 0.0 | 0.7 |
| AI840137 | UI-M-AO0-acc-b-07-0-UI.s1 Mus musculus cDNA, 3 end | 4511.85 | PP | 1778.25 | PP | 2251.65 | PP | 0.4 | 0.8 |
| AI841579 | UI-M-AP0-abn-e-04-0-UI.s1 Mus musculus cDNA, 3 end | 1275.25 | PP | 543.55 | MP | 414.15 | PP | 0.4 | 1.3 |
| AI846994 | UI-M-AP1-agj-c-06-0-UI.s1 Mus musculus cDNA, 3 end | 1864.75 | PP | 648.6 | AP | 1130.55 | PP | 0.3 | 0.6 |
| AI836322 | UI-M-AQ0-aag-a-02-0-UI.s2 Mus musculus cDNA, 3 end | 1185.95 | PP | 544.95 | AP | 990.4 | PP | 0.5 | 0.6 |
| AI843384 | UI-M-AQ1-adz-f-07-0-UI.s1 Mus musculus cDNA, 3 end | 1269.95 | PP | 453.05 | AP | 668.95 | PP | 0.4 | 0.7 |
| AI845183 | UI-M-BG0-aht-a-12-0-UI.s1 Mus musculus cDNA, 3 end | 2226.9 | PP | 738.6 | AP | 849.85 | PP | 0.3 | 0.9 |
| AI850087 | UI-M-BG0-aia-f-10-0-UI.s1 Mus musculus cDNA, 3 end | 1164.6 | PP | 363.2 | AP | 333.6 | PP | 0.3 | 1.1 |
| AI851750 | UI-M-BH0-aim-c-02-0-UI.s1 Mus musculus cDNA, 3 end | 934.3 | PP | 461.4 | AP | 501.55 | PP | 0.5 | 0.9 |
| AI853960 | UI-M-BH0-aiv-d-02-0-UI.s1 Mus musculus cDNA, 3 end | 564.8 | PP | 281.75 | AA | 420.2 | PA | 0.5 | 0.7 |
| AI852087 | UI-M-BH0-aja-g-04-0-UI.s1 Mus musculus cDNA, 3 end | 3158.5 | PP | 543.45 | AP | 830.5 | PP | 0.2 | 0.7 |
| AI852741 | UI-M-BH0-aji-h-09-0-UI.s1 Mus musculus cDNA, 3 end | 664.7 | PP | 196.1 | PA | 223.95 | PP | 0.3 | 0.9 |
| AI851064 | UI-M-BH0-ajv-h-03-0-UI.s1 Mus musculus cDNA, 3 end | 4313.55 | PP | 1853.75 | PP | 2270.5 | PP | 0.4 | 0.8 |
| AI851207 | UI-M-BH0-ajx-f-06-0-UI.s1 Mus musculus cDNA, 3 end | 607.7 | PP | 214 | PA | 230.25 | PA | 0.4 | 0.9 |
| AI850953 | UI-M-BH0-akd-e-11-0-UI.s1 Mus musculus cDNA, 3 end | 7710.55 | PP | 3208.45 | PP | 3888.05 | PP | 0.4 | 0.8 |
| AW046438 | UI-M-BH1-akp-d-11-0-UI.s1 Mus musculus cDNA, 3 end | 397.95 | PP | 167.7 | AA | 181.7 | PP | 0.4 | 0.9 |
| AW045753 | UI-M-BH1-akt-a-10-0-UI.s1 Mus musculus cDNA, 3 end | 1018.35 | PP | 498.4 | PP | 560.8 | PP | 0.5 | 0.9 |
| AW046027 | UI-M-BH1-alc-h-08-0-UI.s1 Mus musculus cDNA, 3 end | 1293.3 | PP | 369.9 | AP | 420 | PP | 0.3 | 0.9 |
| AW047450 | UI-M-BH1-all-e-01-0-UI.s1 Mus musculus cDNA, 3 end | 609.7 | PP | 143.05 | AA | 221.6 | PP | 0.2 | 0.6 |
| AW047874 | UI-M-BH1-als-g-02-0-UI.s1 Mus musculus cDNA, 3 end | 2836.35 | PP | 627.5 | PP | 862.25 | PP | 0.2 | 0.7 |
| AW047978 | UI-M-BH1-alv-d-06-0-UI.s1 Mus musculus cDNA, 3 end | 5815.75 | PP | 1856.4 | PP | 2263.8 | PP | 0.3 | 0.8 |
| AW047237 | UI-M-BH1-amb-g-05-0-UI.s1 Mus musculus cDNA, 3 end | 1354.3 | PP | 462.15 | MP | 549.3 | PP | 0.3 | 0.8 |
| AW047237 | UI-M-BH1-amb-g-05-0-UI.s1 Mus musculus cDNA, 3 end | 1409.45 | PP | 391.85 | AP | 557.45 | PP | 0.3 | 0.7 |
| AW048989 | UI-M-BH1-amp-b-07-0-UI.s1 Mus musculus cDNA, 3 end | 450.45 | PP | 124.3 | AA | 89 | PA | 0.3 | 1.4 |

| | | GR dim | | | | Fold change | | | | GR LysCre | | | | Fold change | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ctrl | | LPS | | dex+LPS | | LPS | LPS | ctrl | | LPS | | dex+LPS | | LPS | LPS | Grid |
| AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | position |
| 884.33 | PPP | 217.93 | PAA | 154.47 | PAA | 0.2 | 1.4 | 637.40 | PP | 135.45 | AA | 250.05 | PP | 0.2 | 0.5 | 160161_at |
| 630.47 | APP | 260.10 | AAA | 209.37 | AAA | 0.4 | 1.2 | 624.90 | PP | 258.40 | AP | 237.35 | PA | 0.4 | 1.1 | 160615_at |
| 2134.27 | PPP | 608.47 | PAM | 735.23 | PAP | 0.3 | 0.8 | 2797.05 | PP | 604.80 | PA | 1143.15 | PA | 0.2 | 0.5 | 104332_at |
| 1292.03 | PPP | 333.83 | PPP | 422.37 | PPP | 0.3 | 0.8 | 1206.40 | PP | 583.30 | PP | 532.65 | PP | 0.5 | 1.1 | 94241_at |
| 1785.80 | PPP | 700.50 | PPP | 719.40 | PPP | 0.4 | 1.0 | 2217.35 | PP | 900.15 | PP | 1007.85 | PP | 0.4 | 0.9 | 98065_at |
| 8813.77 | PPP | 1238.47 | PPP | 940.00 | PPP | 0.1 | 1.3 | 5730.95 | PP | 1539.10 | PP | 1098.50 | PP | 0.3 | 1.4 | 95618_at |
| 2403.70 | PPP | 1032.33 | PPP | 806.20 | PPP | 0.4 | 1.3 | 1422.35 | PP | 547.50 | PP | 1767.00 | PA | 0.4 | 0.3 | 92787_at |
| 683.53 | APP | 165.43 | AAA | 423.57 | PAA | 0.2 | 0.4 | 896.45 | PA | 236.35 | AA | 628.05 | PA | 0.3 | 0.4 | 99151_at |
| 391.50 | PAA | 185.33 | PPA | 199.77 | PPA | 0.5 | 0.9 | 382.70 | PM | 121.25 | PA | 336.80 | PP | 0.3 | 0.4 | 103760_at |
| 1603.33 | PPP | 749.27 | MAA | 470.97 | PPA | 0.5 | 1.6 | 1516.40 | PP | 602.60 | PA | 768.50 | PP | 0.4 | 0.8 | 160747_at |
| 1146.67 | APP | 425.90 | PPA | 352.03 | PPP | 0.4 | 1.2 | 622.80 | PA | 286.95 | PA | 292.15 | PP | 0.5 | 1.0 | 160351_at |
| 1095.13 | PPP | 415.83 | PPP | 521.77 | PPP | 0.4 | 0.8 | 1463.15 | PP | 727.00 | PP | 593.20 | PP | 0.5 | 1.2 | 160846_at |
| 5882.07 | PPP | 1882.33 | PPP | 2845.80 | PPP | 0.3 | 0.7 | 3756.50 | PP | 1103.65 | PP | 665.80 | PP | 0.3 | 1.7 | 94504_at |
| 1616.43 | APA | 533.40 | MAP | 583.47 | AAA | 0.3 | 0.9 | 1834.60 | AP | 436.60 | AA | 314.15 | PA | 0.2 | 1.4 | 97012_f_at |
| 5151.83 | PPP | 2280.03 | PPP | 1417.33 | PPP | 0.4 | 1.6 | 4151.40 | PP | 1749.75 | PP | 2855.20 | PP | 0.4 | 0.6 | 96615_at |
| 1072.20 | PPP | 462.83 | PPA | 417.07 | PPP | 0.4 | 1.1 | 1339.50 | PP | 651.40 | PA | 650.80 | PA | 0.5 | 1.0 | 160713_at |
| 1986.50 | PPP | 920.40 | APP | 882.77 | PPP | 0.5 | 1.0 | 1069.65 | PP | 431.95 | PA | 916.95 | PP | 0.4 | 0.5 | 93838_at |
| 1159.53 | PPA | 540.27 | PPA | 544.70 | PPP | 0.5 | 1.0 | 1119.90 | PP | 485.50 | PA | 662.90 | PA | 0.4 | 0.7 | 101929_at |
| 1318.60 | PPP | 543.83 | PPP | 357.83 | APA | 0.4 | 1.5 | 919.55 | PP | 262.45 | PA | 466.05 | PA | 0.3 | 0.6 | 101356_at |
| 2201.03 | PPP | 905.23 | PPP | 764.87 | PAP | 0.4 | 1.2 | 1918.60 | PP | 876.00 | PP | 1838.70 | PP | 0.5 | 0.5 | 99635_at |
| 1277.00 | PPP | 342.40 | PPA | 319.80 | PAA | 0.3 | 1.1 | 1240.50 | PP | 200.25 | AA | 798.25 | PA | 0.2 | 0.3 | 104032_at |
| 937.10 | PPP | 436.30 | AMA | 361.33 | APA | 0.5 | 1.2 | 1010.85 | PP | 444.95 | PP | 538.20 | PA | 0.4 | 0.8 | 100473_at |
| 663.00 | PPA | 305.00 | PAA | 293.23 | PPA | 0.5 | 1.0 | 555.20 | PA | 207.00 | MM | 191.00 | AA | 0.4 | 1.1 | 92857_at |
| 3773.43 | PPP | 696.57 | PPP | 817.97 | PAP | 0.2 | 0.9 | 1868.85 | PP | 824.70 | PP | 755.65 | PP | 0.4 | 1.1 | 95665_at |
| 714.77 | PPP | 189.53 | PPP | 306.80 | PPP | 0.3 | 0.6 | 557.55 | PP | 241.30 | PA | 368.25 | PA | 0.4 | 0.7 | 160824_at |
| 4927.77 | PPP | 2155.23 | PPP | 2542.37 | PPP | 0.4 | 0.8 | 4241.15 | PP | 1880.60 | PP | 2420.55 | PP | 0.4 | 0.8 | 92622_at |
| 705.53 | PPP | 326.10 | PMA | 356.90 | PPP | 0.5 | 0.9 | 674.80 | PP | 271.95 | PM | 348.05 | PA | 0.4 | 0.8 | 94509_at |
| 7094.57 | PPP | 2042.13 | PPP | 2030.40 | PPP | 0.3 | 1.0 | 5308.45 | PP | 2570.70 | PP | 2203.10 | PP | 0.5 | 1.2 | 97485_at |
| 502.10 | PPP | 155.00 | AAM | 101.77 | PAA | 0.3 | 1.5 | 300.85 | PP | 141.75 | PA | 264.10 | PA | 0.5 | 0.5 | 97514_at |
| 903.07 | PPP | 381.00 | PPP | 369.43 | MPP | 0.4 | 1.0 | 1109.95 | PP | 498.00 | PP | 1236.05 | PP | 0.4 | 0.4 | 104217_at |
| 1363.03 | PPP | 390.10 | PPP | 564.53 | PPP | 0.3 | 0.7 | 897.25 | PP | 219.45 | PP | 461.15 | PA | 0.2 | 0.5 | 93777_at |
| 530.63 | PPP | 224.57 | APA | 335.83 | PPA | 0.4 | 0.7 | 775.15 | PP | 178.75 | PA | 275.25 | PA | 0.2 | 0.6 | 160597_at |
| 2924.97 | PPP | 697.00 | PPP | 584.90 | PAP | 0.2 | 1.2 | 3326.95 | PP | 945.55 | PP | 715.00 | PP | 0.3 | 1.3 | 103773_at |
| 5700.17 | PPP | 2042.07 | PPP | 1506.13 | PPP | 0.4 | 1.4 | 5017.90 | PP | 1744.45 | PP | 1768.85 | PP | 0.3 | 1.0 | 104102_at |
| 1394.03 | PPP | 305.47 | PPA | 266.70 | PAA | 0.2 | 1.1 | 1319.35 | PP | 288.55 | PP | 1397.90 | PP | 0.2 | 0.2 | 95940_f_at |
| 1300.90 | PPA | 445.33 | PPA | 212.07 | APA | 0.3 | 2.1 | 1121.45 | PP | 255.95 | AP | 1266.65 | PA | 0.2 | 0.2 | 95939_i_at |
| 410.00 | PAP | 81.53 | AAA | 93.20 | AAA | 0.2 | 0.9 | 183.75 | PA | 65.85 | AA | 130.50 | PA | 0.4 | 0.5 | 99360_at |

| | | | | wild type | | | | Fold change | |
|---|---|---|---|---|---|---|---|---|---|
| Acc. | Gene/EST Name | ctrl | | LPS | | dex+LPS | | LPS | LPS |
| Num. | | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS |
| AW049351 | UI-M-BH1-amr-h-10-0-UI.s1 Mus musculus cDNA, 3 end | 3959 | PP | 1826.8 | PP | 1959.95 | PP | 0.5 | 0.9 |
| AW060270 | UI-M-BH1-amv-g-11-0-UI.s1 Mus musculus cDNA, 3 end | 2087.7 | PP | 767.1 | PA | 1420.5 | PP | 0.4 | 0.5 |
| AW049376 | UI-M-BH1-ane-c-05-0-UI.s1 Mus musculus cDNA, 3 end | 613.8 | PP | 207.9 | PA | 170.2 | PP | 0.3 | 1.2 |
| AW050342 | UI-M-BH1-ang-c-10-0-UI.s1 Mus musculus cDNA, 3 end | 720.65 | PP | 192.9 | AA | 323.35 | PA | 0.3 | 0.6 |
| AW049730 | UI-M-BH1-ani-g-03-0-UI.s1 Mus musculus cDNA, 3 end | 479.4 | PP | 181.45 | PP | 224.25 | PP | 0.4 | 0.8 |
| AW122831 | UI-M-BH2.1-aoz-d-08-0-UI.s1 Mus musculus cDNA, 3 end | 6325.1 | PP | 2214.95 | PP | 3154.05 | PP | 0.4 | 0.7 |
| AW122914 | UI-M-BH2.1-apa-f-12-0-UI.s1 Mus musculus cDNA, 3 end | 369.25 | PP | 156.4 | AA | 238.35 | PP | 0.4 | 0.7 |
| AW123154 | UI-M-BH2.1-apd-c-06-0-UI.s1 Mus musculus cDNA, 3 end | 632.1 | PP | 248.45 | AP | 392.85 | PP | 0.4 | 0.6 |
| AW123396 | UI-M-BH2.1-apf-h-12-0-UI.s1 Mus musculus cDNA, 3 end | 1497.35 | PP | 429.65 | PP | 629.55 | PP | 0.3 | 0.7 |
| AW124836 | UI-M-BH2.1-apk-e-10-0-UI.s1 Mus musculus cDNA, 3 end | 5823.95 | PP | 2346.55 | PP | 4352.05 | PP | 0.4 | 0.5 |
| AW123783 | UI-M-BH2.1-apm-d-01-0-UI.s1 Mus musculus cDNA, 3 end | 1277.1 | PP | 440.4 | PP | 563.45 | PP | 0.3 | 0.8 |
| AW124359 | UI-M-BH2.1-apq-h-06-0-UI.s1 Mus musculus cDNA, 3 end | 1196.5 | PP | 460.8 | AP | 515.1 | PP | 0.4 | 0.9 |
| AW125010 | UI-M-BH2.1-apv-g-03-0-UI.s1 Mus musculus cDNA, 3 end | 1508 | PP | 503.65 | AP | 853.2 | PP | 0.3 | 0.6 |
| AW125314 | UI-M-BH2.1-apy-d-10-0-UI.s1 Mus musculus cDNA, 3 end | 2006.05 | PP | 662.1 | PP | 552.45 | PP | 0.3 | 1.2 |
| AW125333 | UI-M-BH2.1-apy-f-04-0-UI.s1 Mus musculus cDNA, 3 end | 1776.85 | PP | 566.45 | AP | 553.65 | PP | 0.3 | 1.0 |
| AW121453 | UI-M-BH2.2-aon-e-02-0-UI.s1 Mus musculus cDNA, 3 end | 2976.35 | PP | 1008.7 | PP | 1490.25 | PP | 0.3 | 0.7 |
| AW122114 | UI-M-BH2.2-aor-a-11-0-UI.s1 Mus musculus cDNA, 3 end | 2639.55 | PP | 643.4 | AA | 951.9 | PP | 0.2 | 0.7 |
| AW122766 | UI-M-BH2.2-aot-h-10-0-UI.s1 Mus musculus cDNA, 3 end | 475.45 | PA | 204.65 | AA | 205.75 | PM | 0.4 | 1.0 |
| AW122419 | UI-M-BH2.2-aow-f-09-0-UI.s1 Mus musculus cDNA, 3 end | 728.75 | PP | 300.9 | AP | 342.25 | PP | 0.4 | 0.9 |
| AW125822 | UI-M-BH2.2-aqk-b-05-0-UI.s1 Mus musculus cDNA, 3 end | 800.7 | PP | 356.35 | PP | 696.6 | PP | 0.4 | 0.5 |
| AW120628 | UI-M-BH2.3-anz-a-04-0-UI.s1 Mus musculus cDNA, 3 end | 4673.4 | PP | 1489.35 | AP | 2027.55 | PP | 0.3 | 0.7 |
| AW121695 | UI-M-BH2.3-aoc-f-07-0-UI.s1 Mus musculus cDNA, 3 end | 3514.25 | PP | 1394.35 | PP | 2351.05 | PP | 0.4 | 0.6 |
| AW121162 | UI-M-BH2.3-aoh-g-10-0-UI.s1 Mus musculus cDNA, 3 end | 1456.5 | PP | 513.95 | AP | 814.1 | PP | 0.4 | 0.6 |
| AW121972 | UI-M-BH2.3-aoj-a-09-0-UI.s1 Mus musculus cDNA, 3 end | 2008 | PP | 735.25 | PP | 1157.95 | PP | 0.4 | 0.6 |
| AI315698 | uj34a01.x1 Mus musculus cDNA, 3 end | 1540.4 | PP | 693.2 | PA | 1291.25 | PP | 0.5 | 0.5 |
| AI987835 | um07f07.x1 Mus musculus cDNA, 3 end | 6562.65 | PP | 2586.15 | PP | 2748 | PP | 0.4 | 0.9 |
| AA681764 | vt61b04.r1 Mus musculus cDNA, 5 end | 876.55 | PP | 266.35 | AA | 416 | PP | 0.3 | 0.6 |
| AA790056 | vt78h04.r1 Mus musculus cDNA, 5 end | 857.25 | PP | 259 | AP | 398.35 | PP | 0.3 | 0.7 |
| AA914734 | vy91g08.r1 Mus musculus cDNA, 5 end | 1708.1 | PP | 539.25 | PP | 560.7 | PP | 0.3 | 1.0 |
| AA939571 | vz51d08.r1 Mus musculus cDNA, 5 end | 6283.75 | PP | 2095.15 | PP | 4099.4 | PP | 0.3 | 0.5 |

| | | GR dim | | | | Fold change | | | | GR LysCre | | | | Fold change | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ctrl | | LPS | | dex+LPS | | LPS | LPS | ctrl | | LPS | | dex+LPS | | LPS | LPS | Grid |
| AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | position |
| 4170.43 | PPP | 1689.60 | PPP | 1257.20 | PPP | 0.4 | 1.3 | 2049.40 | PP | 918.85 | PP | 803.50 | PP | 0.4 | 1.1 | 100948_at |
| 2150.90 | PPP | 1068.33 | PPP | 1327.60 | PPP | 0.5 | 0.8 | 2292.15 | PP | 956.00 | PP | 1035.25 | PP | 0.4 | 0.9 | 97868_at |
| 546.00 | PPP | 223.10 | PAA | 196.73 | PPP | 0.4 | 1.1 | 620.50 | PP | 220.20 | PP | 345.15 | PP | 0.4 | 0.6 | 93056_g_at |
| 574.70 | MAP | 237.43 | AAP | 333.67 | AAP | 0.4 | 0.7 | 532.95 | PP | 194.05 | MA | 356.65 | PA | 0.4 | 0.5 | 95027_at |
| 243.07 | PPP | 79.57 | AAA | 141.90 | PAA | 0.3 | 0.6 | 312.90 | PP | 49.25 | AA | 130.60 | PA | 0.2 | 0.4 | 100597_at |
| 8044.97 | PPP | 2598.33 | PPP | 2551.13 | PPP | 0.3 | 1.0 | 6805.30 | PP | 2447.10 | PP | 3323.15 | PP | 0.4 | 0.7 | 103404_at |
| 422.17 | PPP | 181.37 | PAA | 168.23 | PAA | 0.4 | 1.1 | 336.60 | PA | 96.65 | PA | 237.70 | PA | 0.3 | 0.4 | 160135_at |
| 569.50 | PPP | 181.57 | AAP | 259.33 | APA | 0.3 | 0.7 | 495.00 | PP | 192.70 | PA | 408.20 | PA | 0.4 | 0.5 | 160783_at |
| 1589.17 | PPP | 456.60 | PPP | 388.70 | PPP | 0.3 | 1.2 | 1063.75 | PP | 338.30 | PP | 373.85 | PP | 0.3 | 0.9 | 100565_at |
| 6700.77 | PPP | 1893.77 | PPP | 1335.90 | PPP | 0.3 | 1.4 | 8637.10 | PP | 3814.55 | PP | 3374.55 | PP | 0.4 | 1.1 | 160671_at |
| 1196.90 | PPP | 461.60 | PMP | 552.57 | PPP | 0.4 | 0.8 | 1379.55 | PP | 683.65 | PP | 922.40 | PP | 0.5 | 0.7 | 99139_at |
| 1228.63 | PPP | 552.03 | PPA | 372.63 | PPA | 0.4 | 1.5 | 1006.65 | PP | 365.75 | PP | 514.15 | PP | 0.4 | 0.7 | 103866_at |
| 1616.53 | PPP | 609.53 | PPP | 784.27 | PPP | 0.4 | 0.8 | 1100.45 | PP | 383.85 | PM | 1115.80 | PP | 0.3 | 0.3 | 97446_at |
| 1609.97 | PPP | 674.43 | PPP | 351.40 | PPA | 0.4 | 1.9 | 1468.35 | PP | 697.80 | PP | 531.35 | PP | 0.5 | 1.3 | 102936_at |
| 2261.43 | PPP | 621.50 | PPP | 754.73 | PPP | 0.3 | 0.8 | 1371.85 | PP | 548.20 | PP | 1878.85 | PA | 0.4 | 0.3 | 101426_at |
| 3006.83 | PPP | 627.03 | PPA | 962.93 | PPP | 0.2 | 0.7 | 2523.15 | PP | 1254.70 | PP | 1419.65 | PP | 0.5 | 0.9 | 160242_at |
| 2148.37 | PAP | 757.67 | PAA | 865.40 | PAA | 0.4 | 0.9 | 1883.40 | PP | 530.40 | AA | 606.35 | AA | 0.3 | 0.9 | 92525_i_at |
| 443.13 | PAP | 214.97 | MPA | 244.67 | PPA | 0.5 | 0.9 | 546.45 | PA | 267.00 | AA | 159.40 | PA | 0.5 | 1.7 | 97257_at |
| 741.27 | PPP | 287.90 | PPP | 409.63 | PPP | 0.4 | 0.7 | 758.30 | PP | 325.30 | PA | 767.30 | PP | 0.4 | 0.4 | 94490_at |
| 996.07 | PPP | 374.80 | PPP | 461.83 | PPP | 0.4 | 0.8 | 770.00 | PP | 330.90 | PP | 861.85 | PP | 0.4 | 0.4 | 103251_at |
| 5646.93 | PPP | 1763.70 | PPP | 1465.33 | PPP | 0.3 | 1.2 | 5506.35 | PP | 1443.15 | PP | 4137.05 | PP | 0.3 | 0.3 | 95161_at |
| 3519.90 | PPP | 1752.53 | PPP | 1981.97 | PPP | 0.5 | 0.9 | 3983.90 | PP | 1918.70 | PP | 2287.65 | PP | 0.5 | 0.8 | 160307_at |
| 1445.43 | PPP | 471.20 | PPP | 641.53 | PPP | 0.3 | 0.7 | 1113.85 | PP | 509.20 | PP | 1278.25 | PP | 0.5 | 0.4 | 98057_at |
| 2080.13 | PPP | 804.23 | PPP | 652.77 | PPP | 0.4 | 1.2 | 1925.00 | PP | 697.50 | PP | 1096.15 | PP | 0.4 | 0.6 | 104602_at |
| 1487.60 | PPP | 640.77 | PPP | 904.23 | PPP | 0.4 | 0.7 | 1104.30 | PP | 456.40 | PP | 1036.25 | PP | 0.4 | 0.4 | 104670_at |
| 7530.17 | PPP | 2685.37 | PPP | 2406.07 | PPP | 0.4 | 1.1 | 4929.55 | PP | 2179.90 | PP | 2745.45 | PP | 0.4 | 0.8 | 98461_at |
| 1007.73 | PPP | 370.07 | PPP | 397.00 | PPP | 0.4 | 0.9 | 848.00 | PP | 277.85 | PP | 420.65 | PP | 0.3 | 0.7 | 94459_at |
| 928.33 | PPP | 428.87 | PPP | 274.80 | PPP | 0.5 | 1.6 | 956.80 | PP | 386.45 | PP | 840.35 | PP | 0.4 | 0.5 | 103467_g_at |
| 1394.50 | PPP | 489.03 | PPP | 504.73 | PPP | 0.4 | 1.0 | 1067.50 | PP | 413.10 | PP | 902.00 | PP | 0.4 | 0.5 | 104263_at |
| 7598.17 | PPP | 3068.70 | PPP | 3903.03 | PPP | 0.4 | 0.8 | 5339.95 | PP | 2088.65 | PP | 3165.55 | PP | 0.4 | 0.7 | 104148_at |

### 10. 7. 2. Normalised expression of genes/ESTs representing Group 2-A

| Acc. Num. | Gene/EST Name |
|---|---|
| M28489 | (clone Mu6a) ribosomal protein S6 kinase (rsk) mRNA |
| U22262 | Apolipoprotein B editing complex 1 |
| AF017085 | BAP-135 homolog (Diws1t) mRNA |
| U75506 | BH3 interacting domain death agonist |
| AF076156 | Catechol-O-methyltransferase |
| U53455 | chloride ion current inducer protein (CLCI) mRNA, partial cds |
| X55663 | Cytoplasmic tyrosine kinase, Dscr28C related (Drosophila) |
| AB001990 | Dcra |
| U78818 | Downstream of tyrosine kinase 1 |
| D10475 | Epimorphin |
| L00919 | Erythrocyte protein band 4.1 |
| V00727 | FBJ osteosarcoma oncogene |
| U67187 | G protein signaling regulator RGS2 (rgs2) mRNA |
| M96265 | galactose-1-phosphate uridyl transferase (GALT) mRNA |
| L07508 | Golli-mpb mRNA (alternate transcript from clone BG21) |
| M98036 | guanine nucleotide exchange factor delta subunit (JGR1A) mRNA |
| AW122990 | Hagoromo |
| M32489 | Interferon concensus sequence binding protein |
| AF042487 | intermediate conductance potassium channel mIK1 mRNA |
| X57687 | LYL gene (clone L6) |
| AB028921 | NAKAP95 |
| AI853802 | Phosphofructokinase-1 C isozyme |
| M34141 | Prostaglandin-endoperoxide synthase 1 |
| X95281 | retinal short-chain dehydrogenase/reductase |
| U05245 | T-cell lymphoma invasion and metastasis 1 |
| X64361 | vav mRNA |
| D83266 | vav-T |
| U27398 | Xeroderma pigmentosum, complementation group C |
| D43643 | YL-1 mRNA for YL-1 protein (nuclear protein with DNA-binding ability) |
| AA980810 | ua45h04.r1 Mus musculus cDNA, 5 end |
| AI462312 | ub62c01.x1 Mus musculus cDNA, 3 end |
| AI882440 | uc01f05.r1 Mus musculus cDNA, 5 end |
| AI154249 | ud30f12.r1 Mus musculus cDNA, 5 end |
| AI115399 | uh85b06.r1 Mus musculus cDNA, 5 end |
| AI841137 | UI-M-AH0-acz-g-06-0-UI.s1 Mus musculus cDNA, 3 end |
| AI848207 | UI-M-AH1-agq-g-08-0-UI.s1 Mus musculus cDNA, 3 end |
| AI849587 | UI-M-AH1-agr-e-02-0-UI.s1 Mus musculus cDNA, 3 end |

| | wild type | | | | GR dim | | | | GR LysCre | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | Grid |
| Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | position |
| 5164.35 | 0.50 | 0.21 | 0.29 | 5118.57 | 0.52 | 0.21 | 0.27 | 4029.70 | 0.51 | 0.23 | 0.26 | 97405_at |
| 22065.25 | 0.63 | 0.17 | 0.21 | 18706.87 | 0.76 | 0.12 | 0.12 | 20573.75 | 0.62 | 0.22 | 0.16 | 98398_s_at |
| 12231.75 | 0.42 | 0.21 | 0.37 | 10689.57 | 0.53 | 0.24 | 0.23 | 11002.10 | 0.33 | 0.16 | 0.51 | 94295_at |
| 694.55 | 0.52 | 0.23 | 0.26 | 574.40 | 0.66 | 0.21 | 0.12 | 460.70 | 0.51 | 0.19 | 0.30 | 98433_at |
| 5411.70 | 0.62 | 0.14 | 0.24 | 4286.60 | 0.60 | 0.19 | 0.21 | 3036.15 | 0.58 | 0.20 | 0.23 | 98535_at |
| 6695.30 | 0.63 | 0.19 | 0.18 | 5391.67 | 0.49 | 0.18 | 0.33 | 8784.95 | 0.53 | 0.24 | 0.23 | 93812_at |
| 5302.90 | 0.56 | 0.19 | 0.25 | 5991.80 | 0.56 | 0.19 | 0.25 | 5105.25 | 0.51 | 0.19 | 0.30 | 103539_at |
| 7749.15 | 0.49 | 0.21 | 0.29 | 7622.33 | 0.56 | 0.18 | 0.27 | 7263.45 | 0.53 | 0.23 | 0.24 | 101104_at |
| 2488.35 | 0.54 | 0.19 | 0.27 | 2960.77 | 0.60 | 0.17 | 0.23 | 1994.70 | 0.58 | 0.24 | 0.18 | 102896_at |
| 3192.25 | 0.69 | 0.17 | 0.14 | 4330.23 | 0.73 | 0.11 | 0.16 | 2298.15 | 0.66 | 0.18 | 0.16 | 104482_at |
| 2179.70 | 0.51 | 0.22 | 0.28 | 1500.17 | 0.53 | 0.19 | 0.29 | 1927.30 | 0.28 | 0.10 | 0.62 | 160379_at |
| 2932.10 | 0.78 | 0.11 | 0.11 | 3807.77 | 0.74 | 0.13 | 0.13 | 1842.95 | 0.57 | 0.15 | 0.27 | 160901_at |
| 1642.60 | 0.75 | 0.14 | 0.11 | 3115.07 | 0.82 | 0.06 | 0.11 | 3366.40 | 0.77 | 0.09 | 0.14 | 97844_at |
| 729.15 | 0.61 | 0.15 | 0.25 | 833.80 | 0.62 | 0.19 | 0.20 | 948.35 | 0.52 | 0.13 | 0.35 | 104616_g_at |
| 4536.25 | 0.62 | 0.15 | 0.23 | 3355.60 | 0.63 | 0.21 | 0.16 | 5769.45 | 0.56 | 0.15 | 0.29 | 96310_at |
| 1615.70 | 0.46 | 0.21 | 0.33 | 1630.87 | 0.53 | 0.24 | 0.23 | 1708.25 | 0.45 | 0.21 | 0.35 | 95046_s_at |
| 2213.20 | 0.51 | 0.24 | 0.25 | 2644.53 | 0.54 | 0.27 | 0.19 | 1829.60 | 0.50 | 0.20 | 0.29 | 102478_f_at |
| 8938.75 | 0.61 | 0.17 | 0.22 | 13795.27 | 0.55 | 0.26 | 0.19 | 9998.30 | 0.69 | 0.19 | 0.12 | 98002_at |
| 1043.35 | 0.54 | 0.16 | 0.30 | 1478.70 | 0.45 | 0.21 | 0.34 | 2471.95 | 0.38 | 0.11 | 0.51 | 102198_at |
| 9438.90 | 0.62 | 0.18 | 0.20 | 13239.77 | 0.67 | 0.23 | 0.10 | 8485.15 | 0.65 | 0.22 | 0.13 | 100468_g_at |
| 1666.35 | 0.49 | 0.22 | 0.29 | 1470.97 | 0.57 | 0.21 | 0.22 | 1623.95 | 0.51 | 0.18 | 0.30 | 101947_at |
| 2169.90 | 0.50 | 0.23 | 0.27 | 2419.70 | 0.52 | 0.22 | 0.26 | 3244.70 | 0.53 | 0.24 | 0.23 | 97834_g_at |
| 3825.20 | 0.51 | 0.24 | 0.25 | 2052.23 | 0.53 | 0.22 | 0.25 | 5029.65 | 0.53 | 0.23 | 0.24 | 95597_at |
| 2460.15 | 0.70 | 0.12 | 0.18 | 3803.80 | 0.61 | 0.24 | 0.15 | 2641.30 | 0.54 | 0.17 | 0.29 | 102797_at |
| 1429.85 | 0.55 | 0.20 | 0.24 | 967.10 | 0.53 | 0.20 | 0.27 | 1516.20 | 0.49 | 0.19 | 0.33 | 102283_at |
| 5438.65 | 0.58 | 0.17 | 0.25 | 4894.93 | 0.55 | 0.19 | 0.26 | 5712.25 | 0.54 | 0.21 | 0.25 | 99799_at |
| 7881.40 | 0.55 | 0.19 | 0.26 | 7491.90 | 0.53 | 0.19 | 0.28 | 7887.45 | 0.50 | 0.25 | 0.25 | 96511_s_at |
| 1053.45 | 0.59 | 0.17 | 0.24 | 1012.10 | 0.63 | 0.20 | 0.17 | 1005.50 | 0.45 | 0.07 | 0.47 | 95626_at |
| 1139.35 | 0.53 | 0.21 | 0.25 | 1360.97 | 0.61 | 0.20 | 0.20 | 1629.50 | 0.46 | 0.22 | 0.32 | 160363_at |
| 1023.50 | 0.74 | 0.12 | 0.14 | 646.93 | 0.75 | 0.05 | 0.20 | 754.70 | 0.58 | 0.14 | 0.28 | 160922_at |
| 1166.85 | 0.52 | 0.22 | 0.26 | 1182.80 | 0.50 | 0.18 | 0.32 | 2874.70 | 0.24 | 0.08 | 0.68 | 161076_at |
| 3679.75 | 0.74 | 0.10 | 0.16 | 2922.00 | 0.71 | 0.10 | 0.19 | 3554.50 | 0.70 | 0.15 | 0.15 | 104293_at |
| 8909.20 | 0.56 | 0.27 | 0.18 | 5891.63 | 0.58 | 0.27 | 0.14 | 7288.85 | 0.30 | 0.07 | 0.63 | 100511_at |
| 1821.25 | 0.56 | 0.20 | 0.24 | 1389.83 | 0.56 | 0.24 | 0.20 | 1664.20 | 0.58 | 0.23 | 0.19 | 103711_at |
| 16115.90 | 0.54 | 0.20 | 0.26 | 17497.57 | 0.60 | 0.22 | 0.18 | 11609.55 | 0.53 | 0.26 | 0.21 | 160311_at |
| 3525.35 | 0.57 | 0.15 | 0.27 | 3127.07 | 0.60 | 0.18 | 0.22 | 3477.65 | 0.57 | 0.20 | 0.23 | 103852_at |
| 4896.10 | 0.45 | 0.20 | 0.34 | 8499.90 | 0.52 | 0.15 | 0.33 | 3300.30 | 0.54 | 0.24 | 0.21 | 95465_s_at |

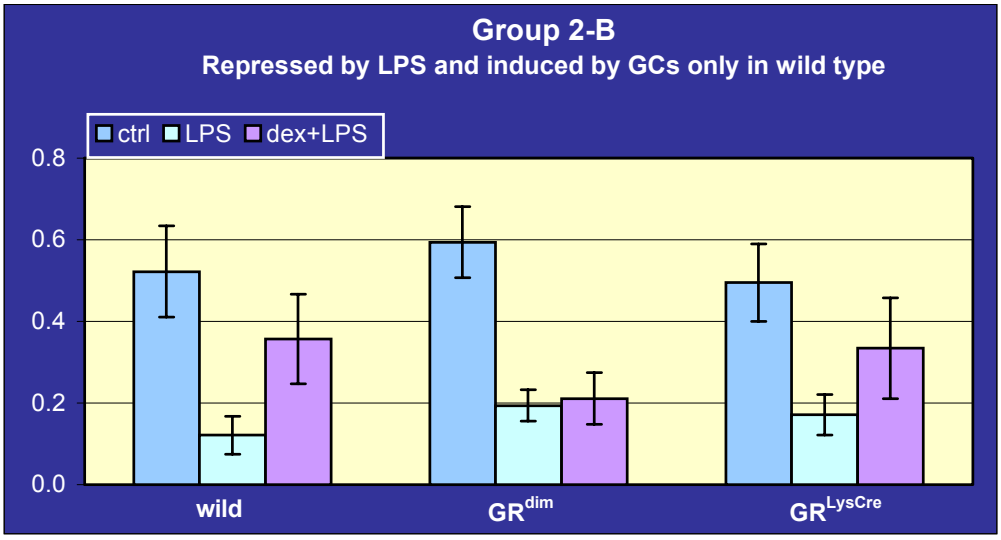
| Acc. Num. | Gene/EST Name |
|---|---|
| AI849497 | UI-M-AH1-agt-d-06-0-UI.s1 Mus musculus cDNA, 3 end |
| AI835963 | UI-M-AI0-aao-h-06-0-UI.s1 Mus musculus cDNA, 3 end |
| AI842242 | UI-M-AI1-afp-d-07-0-UI.s1 Mus musculus cDNA, 3 end |
| AI837229 | UI-M-AK0-ade-e-06-0-UI.s1 Mus musculus cDNA, 3 end |
| AI837679 | UI-M-AK0-adj-b-10-0-UI.s1 Mus musculus cDNA, 3 end |
| AI843884 | UI-M-AK1-aeu-e-10-0-UI.s1 Mus musculus cDNA, 3 end |
| AI845902 | UI-M-AK1-aex-b-07-0-UI.s1 Mus musculus cDNA, 3 end |
| AI849679 | UI-M-AL1-ahl-e-09-0-UI.s1 Mus musculus cDNA, 3 end |
| AI849743 | UI-M-AL1-ahn-d-06-0-UI.s1 Mus musculus cDNA, 3 end |
| AI844739 | UI-M-AL1-ahq-d-01-0-UI.s1 Mus musculus cDNA, 3 end |
| AI846531 | UI-M-AN1-aff-f-08-0-UI.s1 Mus musculus cDNA, 3 end |
| AI846534 | UI-M-AN1-aff-f-11-0-UI.s1 Mus musculus cDNA, 3 end |
| AI838655 | UI-M-AO0-aca-c-08-0-UI.s1 Mus musculus cDNA, 3 end |
| AI838702 | UI-M-AO0-aca-h-06-0-UI.s1 Mus musculus cDNA, 3 end |
| AI840137 | UI-M-AO0-acc-b-07-0-UI.s1 Mus musculus cDNA, 3 end |
| AI841579 | UI-M-AP0-abn-e-04-0-UI.s1 Mus musculus cDNA, 3 end |
| AI846994 | UI-M-AP1-agj-c-06-0-UI.s1 Mus musculus cDNA, 3 end |
| AI836322 | UI-M-AQ0-aag-a-02-0-UI.s2 Mus musculus cDNA, 3 end |
| AI843384 | UI-M-AQ1-adz-f-07-0-UI.s1 Mus musculus cDNA, 3 end |
| AI845183 | UI-M-BG0-aht-a-12-0-UI.s1 Mus musculus cDNA, 3 end |
| AI850087 | UI-M-BG0-aia-f-10-0-UI.s1 Mus musculus cDNA, 3 end |
| AI851750 | UI-M-BH0-aim-c-02-0-UI.s1 Mus musculus cDNA, 3 end |
| AI853960 | UI-M-BH0-aiv-d-02-0-UI.s1 Mus musculus cDNA, 3 end |
| AI852087 | UI-M-BH0-aja-g-04-0-UI.s1 Mus musculus cDNA, 3 end |
| AI852741 | UI-M-BH0-aji-h-09-0-UI.s1 Mus musculus cDNA, 3 end |
| AI851064 | UI-M-BH0-ajv-h-03-0-UI.s1 Mus musculus cDNA, 3 end |
| AI851207 | UI-M-BH0-ajx-f-06-0-UI.s1 Mus musculus cDNA, 3 end |
| AI850953 | UI-M-BH0-akd-e-11-0-UI.s1 Mus musculus cDNA, 3 end |
| AW046438 | UI-M-BH1-akp-d-11-0-UI.s1 Mus musculus cDNA, 3 end |
| AW045753 | UI-M-BH1-akt-a-10-0-UI.s1 Mus musculus cDNA, 3 end |
| AW046027 | UI-M-BH1-alc-h-08-0-UI.s1 Mus musculus cDNA, 3 end |
| AW047450 | UI-M-BH1-all-e-01-0-UI.s1 Mus musculus cDNA, 3 end |
| AW047874 | UI-M-BH1-als-g-02-0-UI.s1 Mus musculus cDNA, 3 end |
| AW047978 | UI-M-BH1-alv-d-06-0-UI.s1 Mus musculus cDNA, 3 end |
| AW047237 | UI-M-BH1-amb-g-05-0-UI.s1 Mus musculus cDNA, 3 end |
| AW047237 | UI-M-BH1-amb-g-05-0-UI.s1 Mus musculus cDNA, 3 end |
| AW048989 | UI-M-BH1-amp-b-07-0-UI.s1 Mus musculus cDNA, 3 end |

| | wild type | | | | GR dim | | | | GR LysCre | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | Grid |
| Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | position |
| 840.90 | 0.53 | 0.21 | 0.27 | 1256.73 | 0.70 | 0.17 | 0.12 | 1022.90 | 0.62 | 0.13 | 0.24 | 160161_at |
| 992.30 | 0.63 | 0.14 | 0.23 | 1099.93 | 0.57 | 0.24 | 0.19 | 1120.65 | 0.56 | 0.23 | 0.21 | 160615_at |
| 4000.45 | 0.62 | 0.15 | 0.23 | 3477.97 | 0.61 | 0.17 | 0.21 | 4545.00 | 0.62 | 0.13 | 0.25 | 104332_at |
| 2486.35 | 0.62 | 0.18 | 0.20 | 2048.23 | 0.63 | 0.16 | 0.21 | 2322.35 | 0.52 | 0.25 | 0.23 | 94241_at |
| 3683.20 | 0.51 | 0.18 | 0.31 | 3205.70 | 0.56 | 0.22 | 0.22 | 4125.35 | 0.54 | 0.22 | 0.24 | 98065_at |
| 10061.30 | 0.75 | 0.10 | 0.15 | 10992.23 | 0.80 | 0.11 | 0.09 | 8368.55 | 0.68 | 0.18 | 0.13 | 95618_at |
| 2647.10 | 0.51 | 0.23 | 0.26 | 4242.23 | 0.57 | 0.24 | 0.19 | 3736.85 | 0.38 | 0.15 | 0.47 | 92787_at |
| 1592.65 | 0.61 | 0.20 | 0.19 | 1272.53 | 0.54 | 0.13 | 0.33 | 1760.85 | 0.51 | 0.13 | 0.36 | 99151_at |
| 805.35 | 0.55 | 0.16 | 0.29 | 776.60 | 0.50 | 0.24 | 0.26 | 840.75 | 0.46 | 0.14 | 0.40 | 103760_at |
| 3360.70 | 0.55 | 0.20 | 0.25 | 2823.57 | 0.57 | 0.27 | 0.17 | 2887.50 | 0.53 | 0.21 | 0.27 | 160747_at |
| 1409.90 | 0.58 | 0.21 | 0.22 | 1924.60 | 0.60 | 0.22 | 0.18 | 1201.90 | 0.52 | 0.24 | 0.24 | 160351_at |
| 1673.90 | 0.52 | 0.23 | 0.25 | 2032.73 | 0.54 | 0.20 | 0.26 | 2783.35 | 0.53 | 0.26 | 0.21 | 160846_at |
| 4855.65 | 0.63 | 0.17 | 0.20 | 10610.20 | 0.55 | 0.18 | 0.27 | 5525.95 | 0.68 | 0.20 | 0.12 | 94504_at |
| 2057.60 | 0.91 | 0.04 | 0.05 | 2733.30 | 0.59 | 0.20 | 0.21 | 2585.35 | 0.71 | 0.17 | 0.12 | 97012_f_at |
| 8541.75 | 0.53 | 0.21 | 0.26 | 8849.20 | 0.58 | 0.26 | 0.16 | 8756.35 | 0.47 | 0.20 | 0.33 | 96615_at |
| 2232.95 | 0.57 | 0.24 | 0.19 | 1952.10 | 0.55 | 0.24 | 0.21 | 2641.70 | 0.51 | 0.25 | 0.25 | 160713_at |
| 3643.90 | 0.51 | 0.18 | 0.31 | 3789.67 | 0.52 | 0.24 | 0.23 | 2418.55 | 0.44 | 0.18 | 0.38 | 93838_at |
| 2721.30 | 0.44 | 0.20 | 0.36 | 2244.50 | 0.52 | 0.24 | 0.24 | 2268.30 | 0.49 | 0.21 | 0.29 | 101929_at |
| 2391.95 | 0.53 | 0.19 | 0.28 | 2220.27 | 0.59 | 0.24 | 0.16 | 1648.05 | 0.56 | 0.16 | 0.28 | 101356_at |
| 3815.35 | 0.58 | 0.19 | 0.22 | 3871.13 | 0.57 | 0.23 | 0.20 | 4633.30 | 0.41 | 0.19 | 0.40 | 99635_at |
| 1861.40 | 0.63 | 0.20 | 0.18 | 1939.20 | 0.66 | 0.18 | 0.16 | 2239.00 | 0.55 | 0.09 | 0.36 | 104032_at |
| 1897.25 | 0.49 | 0.24 | 0.26 | 1734.73 | 0.54 | 0.25 | 0.21 | 1994.00 | 0.51 | 0.22 | 0.27 | 100473_at |
| 1266.75 | 0.45 | 0.22 | 0.33 | 1261.23 | 0.53 | 0.24 | 0.23 | 953.20 | 0.58 | 0.22 | 0.20 | 92857_at |
| 4532.45 | 0.70 | 0.12 | 0.18 | 5287.97 | 0.71 | 0.13 | 0.15 | 3449.20 | 0.54 | 0.24 | 0.22 | 95665_at |
| 1084.75 | 0.61 | 0.18 | 0.21 | 1211.10 | 0.59 | 0.16 | 0.25 | 1167.10 | 0.48 | 0.21 | 0.32 | 160824_at |
| 8437.80 | 0.51 | 0.22 | 0.27 | 9625.37 | 0.51 | 0.22 | 0.26 | 8542.30 | 0.50 | 0.22 | 0.28 | 92622_at |
| 1051.95 | 0.58 | 0.20 | 0.22 | 1388.53 | 0.51 | 0.23 | 0.26 | 1294.80 | 0.52 | 0.21 | 0.27 | 94509_at |
| 14807.05 | 0.52 | 0.22 | 0.26 | 11167.10 | 0.64 | 0.18 | 0.18 | 10082.25 | 0.53 | 0.25 | 0.22 | 97485_at |
| 747.35 | 0.53 | 0.22 | 0.24 | 758.87 | 0.66 | 0.20 | 0.13 | 706.70 | 0.43 | 0.20 | 0.37 | 97514_at |
| 2077.55 | 0.49 | 0.24 | 0.27 | 1653.50 | 0.55 | 0.23 | 0.22 | 2844.00 | 0.39 | 0.18 | 0.43 | 104217_at |
| 2083.20 | 0.62 | 0.18 | 0.20 | 2317.67 | 0.59 | 0.17 | 0.24 | 1577.85 | 0.57 | 0.14 | 0.29 | 93777_at |
| 974.35 | 0.63 | 0.15 | 0.23 | 1091.03 | 0.49 | 0.21 | 0.31 | 1229.15 | 0.63 | 0.15 | 0.22 | 160597_at |
| 4326.10 | 0.66 | 0.15 | 0.20 | 4206.87 | 0.70 | 0.17 | 0.14 | 4987.50 | 0.67 | 0.19 | 0.14 | 103773_at |
| 9935.95 | 0.59 | 0.19 | 0.23 | 9248.37 | 0.62 | 0.22 | 0.16 | 8531.20 | 0.59 | 0.20 | 0.21 | 104102_at |
| 2365.75 | 0.57 | 0.20 | 0.23 | 1966.20 | 0.71 | 0.16 | 0.14 | 3005.80 | 0.44 | 0.10 | 0.47 | 95940_f_at |
| 2358.75 | 0.60 | 0.17 | 0.24 | 1958.30 | 0.66 | 0.23 | 0.11 | 2644.05 | 0.42 | 0.10 | 0.48 | 95939_i_at |
| 663.75 | 0.68 | 0.19 | 0.13 | 584.73 | 0.70 | 0.14 | 0.16 | 380.10 | 0.48 | 0.17 | 0.34 | 99360_at |

| Acc. Num. | Gene/EST Name |
|---|---|
| AW049351 | UI-M-BH1-amr-h-10-0-UI.s1 Mus musculus cDNA, 3 end |
| AW060270 | UI-M-BH1-amv-g-11-0-UI.s1 Mus musculus cDNA, 3 end |
| AW049376 | UI-M-BH1-ane-c-05-0-UI.s1 Mus musculus cDNA, 3 end |
| AW050342 | UI-M-BH1-ang-c-10-0-UI.s1 Mus musculus cDNA, 3 end |
| AW049730 | UI-M-BH1-ani-g-03-0-UI.s1 Mus musculus cDNA, 3 end |
| AW122831 | UI-M-BH2.1-aoz-d-08-0-UI.s1 Mus musculus cDNA, 3 end |
| AW122914 | UI-M-BH2.1-apa-f-12-0-UI.s1 Mus musculus cDNA, 3 end |
| AW123154 | UI-M-BH2.1-apd-c-06-0-UI.s1 Mus musculus cDNA, 3 end |
| AW123396 | UI-M-BH2.1-apf-h-12-0-UI.s1 Mus musculus cDNA, 3 end |
| AW124836 | UI-M-BH2.1-apk-e-10-0-UI.s1 Mus musculus cDNA, 3 end |
| AW123783 | UI-M-BH2.1-apm-d-01-0-UI.s1 Mus musculus cDNA, 3 end |
| AW124359 | UI-M-BH2.1-apq-h-06-0-UI.s1 Mus musculus cDNA, 3 end |
| AW125010 | UI-M-BH2.1-apv-g-03-0-UI.s1 Mus musculus cDNA, 3 end |
| AW125314 | UI-M-BH2.1-apy-d-10-0-UI.s1 Mus musculus cDNA, 3 end |
| AW125333 | UI-M-BH2.1-apy-f-04-0-UI.s1 Mus musculus cDNA, 3 end |
| AW121453 | UI-M-BH2.2-aon-e-02-0-UI.s1 Mus musculus cDNA, 3 end |
| AW122114 | UI-M-BH2.2-aor-a-11-0-UI.s1 Mus musculus cDNA, 3 end |
| AW122766 | UI-M-BH2.2-aot-h-10-0-UI.s1 Mus musculus cDNA, 3 end |
| AW122419 | UI-M-BH2.2-aow-f-09-0-UI.s1 Mus musculus cDNA, 3 end |
| AW125822 | UI-M-BH2.2-aqk-b-05-0-UI.s1 Mus musculus cDNA, 3 end |
| AW120628 | UI-M-BH2.3-anz-a-04-0-UI.s1 Mus musculus cDNA, 3 end |
| AW121695 | UI-M-BH2.3-aoc-f-07-0-UI.s1 Mus musculus cDNA, 3 end |
| AW121162 | UI-M-BH2.3-aoh-g-10-0-UI.s1 Mus musculus cDNA, 3 end |
| AW121972 | UI-M-BH2.3-aoj-a-09-0-UI.s1 Mus musculus cDNA, 3 end |
| AI315698 | uj34a01.x1 Mus musculus cDNA, 3 end |
| AI987835 | um07f07.x1 Mus musculus cDNA, 3 end |
| AA681764 | vt61b04.r1 Mus musculus cDNA, 5 end |
| AA790056 | vt78h04.r1 Mus musculus cDNA, 5 end |
| AA914734 | vy91g08.r1 Mus musculus cDNA, 5 end |
| AA939571 | vz51d08.r1 Mus musculus cDNA, 5 end |

| | wild type | | | | GR dim | | | | GR LysCre | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | Grid |
| Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | position |
| 7745.75 | 0.51 | 0.24 | 0.25 | 7117.23 | 0.59 | 0.24 | 0.18 | 3771.75 | 0.54 | 0.24 | 0.21 | 100948_at |
| 4275.30 | 0.49 | 0.18 | 0.33 | 4546.83 | 0.47 | 0.23 | 0.29 | 4283.40 | 0.54 | 0.22 | 0.24 | 97868_at |
| 991.90 | 0.62 | 0.21 | 0.17 | 965.83 | 0.57 | 0.23 | 0.20 | 1185.85 | 0.52 | 0.19 | 0.29 | 93056_g_at |
| 1236.90 | 0.58 | 0.16 | 0.26 | 1145.80 | 0.50 | 0.21 | 0.29 | 1083.65 | 0.49 | 0.18 | 0.33 | 95027_at |
| 885.10 | 0.54 | 0.21 | 0.25 | 464.53 | 0.52 | 0.17 | 0.31 | 492.75 | 0.64 | 0.10 | 0.27 | 100597_at |
| 11694.10 | 0.54 | 0.19 | 0.27 | 13194.43 | 0.61 | 0.20 | 0.19 | 12575.55 | 0.54 | 0.19 | 0.26 | 103404_at |
| 764.00 | 0.48 | 0.20 | 0.31 | 771.77 | 0.55 | 0.24 | 0.22 | 670.95 | 0.50 | 0.14 | 0.35 | 160135_at |
| 1273.40 | 0.50 | 0.20 | 0.31 | 1010.40 | 0.56 | 0.18 | 0.26 | 1095.90 | 0.45 | 0.18 | 0.37 | 160783_at |
| 2556.55 | 0.59 | 0.17 | 0.25 | 2434.47 | 0.65 | 0.19 | 0.16 | 1775.90 | 0.60 | 0.19 | 0.21 | 100565_at |
| 12522.55 | 0.47 | 0.19 | 0.35 | 9930.43 | 0.67 | 0.19 | 0.13 | 15826.20 | 0.55 | 0.24 | 0.21 | 160671_at |
| 2280.95 | 0.56 | 0.19 | 0.25 | 2211.07 | 0.54 | 0.21 | 0.25 | 2985.60 | 0.46 | 0.23 | 0.31 | 99139_at |
| 2172.40 | 0.55 | 0.21 | 0.24 | 2153.30 | 0.57 | 0.26 | 0.17 | 1886.55 | 0.53 | 0.19 | 0.27 | 103866_at |
| 2864.85 | 0.53 | 0.18 | 0.30 | 3010.33 | 0.54 | 0.20 | 0.26 | 2600.10 | 0.42 | 0.15 | 0.43 | 97446_at |
| 3220.60 | 0.62 | 0.21 | 0.17 | 2635.80 | 0.61 | 0.26 | 0.13 | 2697.50 | 0.54 | 0.26 | 0.20 | 102936_at |
| 2896.95 | 0.61 | 0.20 | 0.19 | 3637.67 | 0.62 | 0.17 | 0.21 | 3798.90 | 0.36 | 0.14 | 0.49 | 101426_at |
| 5475.30 | 0.54 | 0.18 | 0.27 | 4596.80 | 0.65 | 0.14 | 0.21 | 5197.50 | 0.49 | 0.24 | 0.27 | 160242_at |
| 4234.85 | 0.62 | 0.15 | 0.22 | 3771.43 | 0.57 | 0.20 | 0.23 | 3020.15 | 0.62 | 0.18 | 0.20 | 92525_i_at |
| 885.85 | 0.54 | 0.23 | 0.23 | 902.77 | 0.49 | 0.24 | 0.27 | 972.85 | 0.56 | 0.27 | 0.16 | 97257_at |
| 1371.90 | 0.53 | 0.22 | 0.25 | 1438.80 | 0.52 | 0.20 | 0.28 | 1850.90 | 0.41 | 0.18 | 0.41 | 94490_at |
| 1853.65 | 0.43 | 0.19 | 0.38 | 1832.70 | 0.54 | 0.20 | 0.25 | 1962.75 | 0.39 | 0.17 | 0.44 | 103251_at |
| 8190.30 | 0.57 | 0.18 | 0.25 | 8875.97 | 0.64 | 0.20 | 0.17 | 11086.55 | 0.50 | 0.13 | 0.37 | 95161_at |
| 7259.65 | 0.48 | 0.19 | 0.32 | 7254.40 | 0.49 | 0.24 | 0.27 | 8190.25 | 0.49 | 0.23 | 0.28 | 160307_at |
| 2784.55 | 0.52 | 0.18 | 0.29 | 2558.17 | 0.57 | 0.18 | 0.25 | 2901.30 | 0.38 | 0.18 | 0.44 | 98057_at |
| 3901.20 | 0.51 | 0.19 | 0.30 | 3537.13 | 0.59 | 0.23 | 0.18 | 3718.65 | 0.52 | 0.19 | 0.29 | 104602_at |
| 3524.85 | 0.44 | 0.20 | 0.37 | 3032.60 | 0.49 | 0.21 | 0.30 | 2596.95 | 0.43 | 0.18 | 0.40 | 104670_at |
| 11896.80 | 0.55 | 0.22 | 0.23 | 12621.60 | 0.60 | 0.21 | 0.19 | 9854.90 | 0.50 | 0.22 | 0.28 | 98461_at |
| 1558.90 | 0.56 | 0.17 | 0.27 | 1774.80 | 0.57 | 0.21 | 0.22 | 1546.50 | 0.55 | 0.18 | 0.27 | 94459_at |
| 1514.60 | 0.57 | 0.17 | 0.26 | 1632.00 | 0.57 | 0.26 | 0.17 | 2183.60 | 0.44 | 0.18 | 0.38 | 103467_g_at |
| 2808.05 | 0.61 | 0.19 | 0.20 | 2388.27 | 0.58 | 0.20 | 0.21 | 2382.60 | 0.45 | 0.17 | 0.38 | 104263_at |
| 12478.30 | 0.50 | 0.17 | 0.33 | 14569.90 | 0.52 | 0.21 | 0.27 | 10594.15 | 0.50 | 0.20 | 0.30 | 104148_at |

## 10. 8. GROUP 2-B




| | wild type | | | | GR dim | | | | GR LysCre | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS |
| Sum: | **19.83** | **4.59** | **13.58** | Sum: | **22.59** | **7.38** | **8.03** | Sum: | **18.82** | **6.49** | **12.69** |
| Mean: | **0.52** | **0.12** | **0.36** | Mean: | **0.59** | **0.19** | **0.21** | Mean: | **0.50** | **0.17** | **0.33** |
| StDev: | **0.11** | **0.05** | **0.11** | StDev: | **0.09** | **0.04** | **0.06** | StDev: | **0.10** | **0.05** | **0.12** |
| Fold change (LPS/ctrl) | | | **0.2** | Fold change (LPS/ctrl) | | | **0.3** | Fold change (LPS/ctrl) | | | **0.3** |
| Fold change (LPS/dex+LPS) | | | **0.3** | Fold change (LPS/dex+LPS) | | | **0.9** | Fold change (LPS/dex+LPS) | | | **0.5** |

### 10. 8. 1. Expression levels of genes/ESTs representing Group 2-B

| | | | | wild type | | | | Fold change | |
|---|---|---|---|---|---|---|---|---|---|
| Acc. | Gene/EST Name | ctrl | | LPS | | dex+LPS | | LPS | LPS |
| Num. | | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS |
| X13586 | 2,3-bisphosphoglycerate mutase (BPGM; EC 5.4.2.4) | 359.15 | PP | 31.25 | AA | 212.55 | PP | 0.1 | 0.1 |
| M62362 | CCAAT enhancer binding protein (CEBP), alpha | 2916.35 | PP | 672.55 | PP | 1352.5 | PP | 0.2 | 0.5 |
| U43512 | Dystroglycan 1 | 2204.05 | PP | 138.75 | MP | 1154.25 | PP | 0.1 | 0.1 |
| U11680 | glycerol-3-phosphate acyltransferase gene | 472.25 | PP | 77 | MA | 164.05 | PP | 0.2 | 0.5 |
| AB012808 | mBOCT | 921.05 | PP | 245.8 | AM | 514.5 | PP | 0.3 | 0.5 |
| U39827 | putative G protein-coupled receptor TDAG8 (TDAG8) mRNA | 1423.65 | PP | 379.3 | AP | 804.15 | PP | 0.3 | 0.5 |
| Z14132 | Sphingomyelin phosphodiesterase 1, acid lysosomal | 2581.7 | PP | 863 | AP | 1944.35 | PP | 0.3 | 0.4 |
| M26270 | Stearoyl-coenzyme A desaturase 2 | 2997.9 | PP | 920.5 | PP | 2006.45 | PP | 0.3 | 0.5 |
| U86137 | Telomerase associated protein 1 | 724.05 | PP | 7.6 | AA | 244.85 | PP | 0.0 | 0.0 |
| D86344 | Topoisomerase-inhibitor suppressed | 514.1 | PP | 161.05 | AA | 2547.15 | PP | 0.3 | 0.1 |
| AI414025 | ma02g05.x1 Mus musculus cDNA, 3 end | 1234.1 | AP | 434.8 | PP | 1111.8 | PP | 0.4 | 0.4 |
| AI596360 | me60c05.x1 Mus musculus cDNA, 3 end | 897.65 | PP | 195.7 | AA | 561.6 | PP | 0.2 | 0.3 |
| AA014745 | mh18b05.r1 Mus musculus cDNA, 5 end | 886.75 | PP | 317.2 | PP | 797.45 | PP | 0.4 | 0.4 |
| AA048058 | mj24a07.r1 Mus musculus cDNA, 5 end | 651.25 | PP | 70.15 | AA | 417.05 | PP | 0.1 | 0.2 |
| AV265258 | Mus musculus cDNA, 3 end | 1736.75 | PP | 770.95 | PP | 1610.9 | PP | 0.4 | 0.5 |
| AV244370 | Mus musculus cDNA, 3 end | 1445 | PP | 489.15 | PP | 1193.35 | PP | 0.3 | 0.4 |
| AV376312 | Mus musculus cDNA, 3 end | 805.95 | PP | 182.9 | PA | 442.5 | PP | 0.2 | 0.4 |
| AI226158 | ue85d06.y1 Mus musculus cDNA, 5 end | 1044.2 | PP | 213.35 | AA | 754.9 | PP | 0.2 | 0.3 |
| AI839899 | UI-M-AH0-acw-d-06-0-UI.s1 Mus musculus cDNA, 3 end | 621.25 | PP | 209.7 | AP | 424.85 | PP | 0.3 | 0.5 |
| AI847490 | UI-M-AI1-afs-g-11-0-UI.s1 Mus musculus cDNA, 3 end | 2368.75 | PP | 542.05 | PP | 1443.15 | PP | 0.2 | 0.4 |
| AI835989 | UI-M-AJ0-abb-a-04-0-UI.s1 Mus musculus cDNA, 3 end | 1025.55 | PP | 266.7 | AA | 540.4 | PP | 0.3 | 0.5 |
| AI839232 | UI-M-AK0-adh-d-11-0-UI.s1 Mus musculus cDNA, 3 end | 1780.2 | PP | 769.95 | PP | 1605.35 | PP | 0.4 | 0.5 |
| AI843106 | UI-M-AK1-aes-e-01-0-UI.s1 Mus musculus cDNA, 3 end | 3499.7 | PP | 750.45 | PP | 4430.65 | PP | 0.2 | 0.2 |
| AI841364 | UI-M-AM0-adv-f-01-0-UI.s1 Mus musculus cDNA, 3 end | 1062.6 | PM | 153.95 | AM | 1088.25 | PP | 0.1 | 0.1 |
| AI841777 | UI-M-AN0-acl-d-07-0-UI.s1 Mus musculus cDNA, 3 end | 5888.7 | PP | 1979.9 | PP | 4324.05 | PP | 0.3 | 0.5 |
| AI847661 | UI-M-AP1-agm-a-04-0-UI.s1 Mus musculus cDNA, 3 end | 1298.2 | PP | 199.2 | AA | 607.15 | PP | 0.2 | 0.3 |
| AI847699 | UI-M-AP1-agm-d-10-0-UI.s1 Mus musculus cDNA, 3 end | 861.1 | PP | 164.15 | AA | 361.75 | PP | 0.2 | 0.5 |
| AI842544 | UI-M-AQ1-aea-e-05-0-UI.s1 Mus musculus cDNA, 3 end | 1011.9 | PP | 116.6 | AA | 273.55 | PP | 0.1 | 0.4 |
| AI845735 | UI-M-AQ1-aeb-b-07-0-UI.s1 Mus musculus cDNA, 3 end | 296.3 | PP | 43.85 | AA | 123.5 | AP | 0.1 | 0.4 |
| AI850202 | UI-M-BG1-aie-b-01-0-UI.s1 Mus musculus cDNA, 3 end | 1973.3 | PP | 411.55 | AP | 925.5 | PP | 0.2 | 0.4 |
| AI851901 | UI-M-BH0-aix-d-03-0-UI.s1 Mus musculus cDNA, 3 end | 752.8 | PP | 191.05 | PP | 385.75 | PP | 0.3 | 0.5 |
| AW049360 | UI-M-BH1-ane-a-10-0-UI.s1 Mus musculus cDNA, 3 end | 1114.55 | PP | 215.45 | MP | 2517.3 | PP | 0.2 | 0.1 |
| AW124250 | UI-M-BH2.1-aph-f-11-0-UI.s1 Mus musculus cDNA, 3 end | 5326.4 | PP | 2583.9 | PP | 5823.95 | PP | 0.5 | 0.4 |
| AW123746 | UI-M-BH2.1-apl-h-09-0-UI.s1 Mus musculus cDNA, 3 end | 591.1 | PP | 66.75 | AA | 269.55 | PP | 0.1 | 0.2 |
| AW121330 | UI-M-BH2.2-aom-b-01-0-UI.s1 Mus musculus cDNA, 3 end | 1597.7 | PP | 534.5 | PP | 1320.45 | PP | 0.3 | 0.4 |
| AW125438 | UI-M-BH2.3-aqh-g-08-0-UI.s1 Mus musculus cDNA, 3 end | 4040.05 | PP | 1559.95 | PP | 3414.9 | PP | 0.4 | 0.5 |
| AW107702 | um33b01.x1 Mus musculus cDNA, 3 end | 559.65 | PP | 131.55 | PA | 265.55 | PP | 0.2 | 0.5 |
| AA960603 | vw64d05.s1 Mus musculus cDNA, 3 end | 7621 | PP | 2327.7 | PP | 6599.65 | PP | 0.3 | 0.4 |

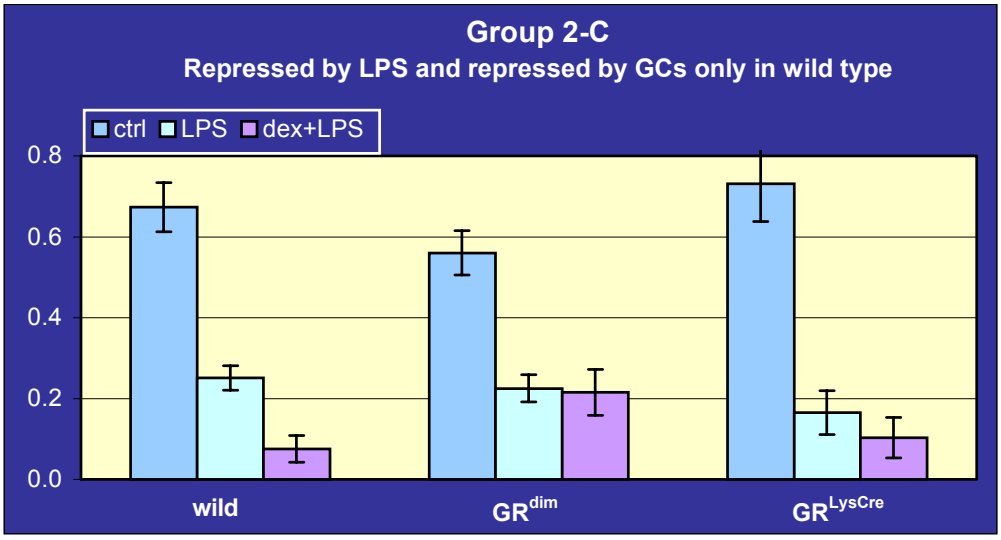
| | | GR dim | | | | Fold change | | | | GR LysCre | | | | Fold change | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ctrl | | LPS | | dex+LPS | | LPS | LPS | ctrl | | LPS | | dex+LPS | | LPS | LPS | Grid |
| AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | position |
| 326.27 | PAP | 126.27 | APA | 119.87 | APA | 0.4 | 1.1 | 393.45 | PP | 146.40 | AA | 699.65 | PA | 0.4 | 0.2 | 94815_at |
| 6596.03 | PPP | 1152.27 | PPP | 1773.13 | PPP | 0.2 | 0.6 | 3602.95 | PP | 1039.95 | PP | 766.60 | PP | 0.3 | 1.4 | 98447_at |
| 1580.53 | PPP | 475.43 | AAP | 544.73 | PAP | 0.3 | 0.9 | 1015.95 | PP | 504.15 | AA | 1014.75 | PA | 0.5 | 0.5 | 101109_at |
| 505.60 | PPP | 185.30 | APP | 149.40 | MPP | 0.4 | 1.2 | 533.95 | PP | 95.85 | AA | 308.85 | PP | 0.2 | 0.3 | 101867_at |
| 902.43 | PPP | 306.40 | AAA | 299.30 | PMA | 0.3 | 1.0 | 534.55 | AP | 206.05 | AA | 214.10 | AA | 0.4 | 1.0 | 95012_at |
| 2707.40 | PPP | 723.30 | PPP | 626.37 | PPA | 0.3 | 1.2 | 1712.30 | PP | 813.15 | AP | 823.90 | PP | 0.5 | 1.0 | 96553_at |
| 2525.80 | PPP | 1026.07 | PPP | 819.03 | PPP | 0.4 | 1.3 | 2018.90 | PP | 661.55 | PP | 778.70 | PP | 0.3 | 0.8 | 100099_at |
| 2164.67 | PPP | 834.17 | PAA | 865.93 | PPP | 0.4 | 1.0 | 2723.95 | PP | 676.70 | PP | 3981.35 | PP | 0.2 | 0.2 | 95758_at |
| 739.27 | PPM | 165.27 | PAA | 237.20 | PMA | 0.2 | 0.7 | 552.85 | PP | 199.10 | AA | 140.90 | AA | 0.4 | 1.4 | 93367_at |
| 657.70 | PPP | 310.47 | PPA | 319.10 | PPA | 0.5 | 1.0 | 719.80 | PP | 335.00 | PP | 1926.30 | PA | 0.5 | 0.2 | 103029_at |
| 1442.37 | APP | 557.20 | AAP | 451.93 | AAA | 0.4 | 1.2 | 1137.00 | AP | 401.05 | AP | 1397.60 | PA | 0.4 | 0.3 | 104502_f_at |
| 1768.03 | PPP | 402.60 | PPP | 354.47 | PPP | 0.2 | 1.1 | 923.95 | PP | 209.95 | PP | 522.00 | PP | 0.2 | 0.4 | 161013_f_at |
| 703.40 | PPP | 327.27 | PAP | 348.37 | PPP | 0.5 | 0.9 | 1291.50 | PP | 260.30 | PP | 535.50 | PM | 0.2 | 0.5 | 98855_r_at |
| 602.83 | PPP | 169.33 | AAA | 159.63 | PAA | 0.3 | 1.1 | 325.05 | PP | 134.45 | AA | 948.85 | PA | 0.4 | 0.1 | 160625_f_at |
| 1991.43 | PPP | 880.37 | PPP | 1343.30 | PPP | 0.4 | 0.7 | 1591.05 | PP | 564.90 | PP | 1068.70 | PP | 0.4 | 0.5 | 161214_r_at |
| 1369.97 | PPP | 613.97 | PPP | 556.73 | PPP | 0.4 | 1.1 | 937.90 | PP | 419.30 | PP | 514.35 | PP | 0.4 | 0.8 | 161183_at |
| 1227.93 | PPP | 337.67 | APP | 207.07 | PAP | 0.3 | 1.6 | 684.50 | PP | 136.20 | AA | 443.15 | PP | 0.2 | 0.3 | 161817_f_at |
| 833.63 | PMP | 236.87 | AAA | 449.53 | PAA | 0.3 | 0.5 | 950.30 | PM | 309.50 | AA | 899.10 | PA | 0.3 | 0.3 | 102412_at |
| 792.33 | PPP | 389.17 | PPP | 473.80 | PPP | 0.5 | 0.8 | 836.25 | PP | 392.05 | PP | 305.00 | PP | 0.5 | 1.3 | 160654_at |
| 2337.07 | PPP | 940.37 | PPP | 1049.23 | PPP | 0.4 | 0.9 | 2636.95 | PP | 1193.90 | PP | 1619.30 | PP | 0.5 | 0.7 | 160282_at |
| 864.83 | PPP | 137.47 | APP | 78.17 | PPA | 0.2 | 1.8 | 799.80 | PA | 300.25 | PP | 409.35 | PP | 0.4 | 0.7 | 103447_at |
| 1937.10 | PPP | 813.57 | PPP | 1057.67 | PPP | 0.4 | 0.8 | 3090.85 | PP | 1310.30 | PP | 2967.60 | PP | 0.4 | 0.4 | 103685_at |
| 5076.80 | PPP | 453.80 | PPA | 481.47 | PPA | 0.1 | 0.9 | 3056.20 | PP | 376.85 | PP | 2760.80 | PP | 0.1 | 0.1 | 95731_at |
| 779.80 | PPA | 277.17 | PAA | 529.10 | PPA | 0.4 | 0.5 | 1258.85 | PP | 567.75 | PA | 411.95 | PA | 0.5 | 1.4 | 95556_at |
| 4222.73 | PPP | 1482.23 | PPP | 1860.50 | PPP | 0.4 | 0.8 | 3105.10 | PP | 1144.20 | PP | 1769.80 | PP | 0.4 | 0.6 | 104320_at |
| 1416.07 | PPP | 379.60 | PAP | 282.93 | PAP | 0.3 | 1.3 | 1134.25 | PP | 346.20 | PP | 641.10 | PA | 0.3 | 0.5 | 102374_at |
| 440.00 | PPA | 182.93 | PAP | 143.87 | PAA | 0.4 | 1.3 | 522.15 | PP | 208.60 | PP | 348.80 | PA | 0.4 | 0.6 | 104699_at |
| 1044.60 | PPP | 289.37 | PPP | 296.23 | PPP | 0.3 | 1.0 | 747.10 | PP | 175.40 | PA | 419.35 | PA | 0.2 | 0.4 | 104298_at |
| 361.50 | APP | 92.00 | PAA | 63.40 | AAA | 0.3 | 1.5 | 177.00 | PA | 68.90 | AA | 85.15 | PA | 0.4 | 0.8 | 93325_at |
| 1896.40 | PPP | 819.53 | PPP | 966.53 | PPP | 0.4 | 0.8 | 1907.20 | PP | 728.75 | PP | 1088.90 | PP | 0.4 | 0.7 | 95468_at |
| 955.53 | PPP | 292.13 | PPA | 469.97 | PPP | 0.3 | 0.6 | 947.30 | PP | 340.25 | PP | 268.50 | PP | 0.4 | 1.3 | 94382_at |
| 1652.93 | PPP | 395.00 | PPP | 534.67 | PPP | 0.2 | 0.7 | 1403.10 | PP | 413.60 | PP | 640.60 | PP | 0.3 | 0.6 | 104389_at |
| 6422.53 | PPP | 3122.60 | PPP | 2366.37 | PPP | 0.5 | 1.3 | 7056.05 | PP | 2959.85 | PP | 5119.95 | PP | 0.4 | 0.6 | 101072_at |
| 636.60 | PPP | 228.53 | PAA | 268.00 | PPP | 0.4 | 0.9 | 660.65 | PP | 233.20 | PP | 620.90 | PA | 0.4 | 0.4 | 95759_at |
| 1765.27 | PPP | 614.80 | PPP | 694.87 | PPP | 0.3 | 0.9 | 1339.95 | PP | 547.60 | PP | 954.20 | PP | 0.4 | 0.6 | 94403_at |
| 3041.57 | PPP | 1370.70 | PPP | 2098.97 | PPP | 0.5 | 0.7 | 5009.85 | PP | 2404.70 | PP | 3103.00 | PP | 0.5 | 0.8 | 101070_at |
| 378.20 | APP | 166.17 | AAP | 191.40 | PPA | 0.4 | 0.9 | 257.80 | PP | 59.75 | AA | 192.80 | PA | 0.2 | 0.3 | 102883_at |
| 8610.47 | PPP | 1992.07 | PPP | 2208.93 | PPP | 0.2 | 0.9 | 6860.35 | PP | 1953.45 | PP | 4732.20 | PP | 0.3 | 0.4 | 160273_at |

### 10. 8. 2. Normalised expression of genes/ESTs representing Group 2-B

| Acc. Num. | Gene/EST Name |
|---|---|
| X13586 | 2,3-bisphosphoglycerate mutase (BPGM; EC 5.4.2.4) |
| M62362 | CCAAT enhancer binding protein (CEBP), alpha |
| U43512 | Dystroglycan 1 |
| U11680 | glycerol-3-phosphate acyltransferase gene, nuclear gene for mitochondrial protein |
| AB012808 | mBOCT |
| U39827 | putative G protein-coupled receptor TDAG8 (TDAG8) mRNA |
| Z14132 | Sphingomyelin phosphodiesterase 1, acid lysosomal |
| M26270 | Stearoyl-coenzyme A desaturase 2 |
| U86137 | Telomerase associated protein 1 |
| D86344 | Topoisomerase-inhibitor suppressed |
| AI414025 | ma02g05.x1 Mus musculus cDNA, 3 end |
| AI596360 | me60c05.x1 Mus musculus cDNA, 3 end |
| AA014745 | mh18b05.r1 Mus musculus cDNA, 5 end |
| AA048058 | mj24a07.r1 Mus musculus cDNA, 5 end |
| AV265258 | Mus musculus cDNA, 3 end |
| AV244370 | Mus musculus cDNA, 3 end |
| AV376312 | Mus musculus cDNA, 3 end |
| AI226158 | ue85d06.y1 Mus musculus cDNA, 5 end |
| AI839899 | UI-M-AH0-acw-d-06-0-UI.s1 Mus musculus cDNA, 3 end |
| AI847490 | UI-M-AI1-afs-g-11-0-UI.s1 Mus musculus cDNA, 3 end |
| AI835989 | UI-M-AJ0-abb-a-04-0-UI.s1 Mus musculus cDNA, 3 end |
| AI839232 | UI-M-AK0-adh-d-11-0-UI.s1 Mus musculus cDNA, 3 end |
| AI843106 | UI-M-AK1-aes-e-01-0-UI.s1 Mus musculus cDNA, 3 end |
| AI841364 | UI-M-AM0-adv-f-01-0-UI.s1 Mus musculus cDNA, 3 end |
| AI841777 | UI-M-AN0-acl-d-07-0-UI.s1 Mus musculus cDNA, 3 end |
| AI847661 | UI-M-AP1-agm-a-04-0-UI.s1 Mus musculus cDNA, 3 end |
| AI847699 | UI-M-AP1-agm-d-10-0-UI.s1 Mus musculus cDNA, 3 end |
| AI842544 | UI-M-AQ1-aea-e-05-0-UI.s1 Mus musculus cDNA, 3 end |
| AI845735 | UI-M-AQ1-aeb-b-07-0-UI.s1 Mus musculus cDNA, 3 end |
| AI850202 | UI-M-BG1-aie-b-01-0-UI.s1 Mus musculus cDNA, 3 end |
| AI851901 | UI-M-BH0-aix-d-03-0-UI.s1 Mus musculus cDNA, 3 end |
| AW049360 | UI-M-BH1-ane-a-10-0-UI.s1 Mus musculus cDNA, 3 end |
| AW124250 | UI-M-BH2.1-aph-f-11-0-UI.s1 Mus musculus cDNA, 3 end |
| AW123746 | UI-M-BH2.1-apl-h-09-0-UI.s1 Mus musculus cDNA, 3 end |
| AW121330 | UI-M-BH2.2-aom-b-01-0-UI.s1 Mus musculus cDNA, 3 end |
| AW125438 | UI-M-BH2.3-aqh-g-08-0-UI.s1 Mus musculus cDNA, 3 end |
| AW107702 | um33b01.x1 Mus musculus cDNA, 3 end |
| AA960603 | vw64d05.s1 Mus musculus cDNA, 3 end |

| | wild type | | | | GR dim | | | | GR LysCre | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | Grid |
| Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | position |
| 602.95 | 0.60 | 0.05 | 0.35 | 572.40 | 0.57 | 0.22 | 0.21 | 1239.50 | 0.32 | 0.12 | 0.56 | 94815_at |
| 4941.40 | 0.59 | 0.14 | 0.27 | 9521.43 | 0.69 | 0.12 | 0.19 | 5409.50 | 0.67 | 0.19 | 0.14 | 98447_at |
| 3497.05 | 0.63 | 0.04 | 0.33 | 2600.70 | 0.61 | 0.18 | 0.21 | 2534.85 | 0.40 | 0.20 | 0.40 | 101109_at |
| 713.30 | 0.66 | 0.11 | 0.23 | 840.30 | 0.60 | 0.22 | 0.18 | 938.65 | 0.57 | 0.10 | 0.33 | 101867_at |
| 1681.35 | 0.55 | 0.15 | 0.31 | 1508.13 | 0.60 | 0.20 | 0.20 | 954.70 | 0.56 | 0.22 | 0.22 | 95012_at |
| 2607.10 | 0.55 | 0.15 | 0.31 | 4057.07 | 0.67 | 0.18 | 0.15 | 3349.35 | 0.51 | 0.24 | 0.25 | 96553_at |
| 5389.05 | 0.48 | 0.16 | 0.36 | 4370.90 | 0.58 | 0.23 | 0.19 | 3459.15 | 0.58 | 0.19 | 0.23 | 100099_at |
| 5924.85 | 0.51 | 0.16 | 0.34 | 3864.77 | 0.56 | 0.22 | 0.22 | 7382.00 | 0.37 | 0.09 | 0.54 | 95758_at |
| 976.50 | 0.74 | 0.01 | 0.25 | 1141.73 | 0.65 | 0.14 | 0.21 | 892.85 | 0.62 | 0.22 | 0.16 | 93367_at |
| 3222.30 | 0.16 | 0.05 | 0.79 | 1287.27 | 0.51 | 0.24 | 0.25 | 2981.10 | 0.24 | 0.11 | 0.65 | 103029_at |
| 2780.70 | 0.44 | 0.16 | 0.40 | 2451.50 | 0.59 | 0.23 | 0.18 | 2935.65 | 0.39 | 0.14 | 0.48 | 104502_f_at |
| 1654.95 | 0.54 | 0.12 | 0.34 | 2525.10 | 0.70 | 0.16 | 0.14 | 1655.90 | 0.56 | 0.13 | 0.32 | 161013_f_at |
| 2001.40 | 0.44 | 0.16 | 0.40 | 1379.03 | 0.51 | 0.24 | 0.25 | 2087.30 | 0.62 | 0.12 | 0.26 | 98855_r_at |
| 1138.45 | 0.57 | 0.06 | 0.37 | 931.80 | 0.65 | 0.18 | 0.17 | 1408.35 | 0.23 | 0.10 | 0.67 | 160625_f_at |
| 4118.60 | 0.42 | 0.19 | 0.39 | 4215.10 | 0.47 | 0.21 | 0.32 | 3224.65 | 0.49 | 0.18 | 0.33 | 161214_r_at |
| 3127.50 | 0.46 | 0.16 | 0.38 | 2540.67 | 0.54 | 0.24 | 0.22 | 1871.55 | 0.50 | 0.22 | 0.27 | 161183_at |
| 1431.35 | 0.56 | 0.13 | 0.31 | 1772.67 | 0.69 | 0.19 | 0.12 | 1263.85 | 0.54 | 0.11 | 0.35 | 161817_f_at |
| 2012.45 | 0.52 | 0.11 | 0.38 | 1520.03 | 0.55 | 0.16 | 0.30 | 2158.90 | 0.44 | 0.14 | 0.42 | 102412_at |
| 1255.80 | 0.49 | 0.17 | 0.34 | 1655.30 | 0.48 | 0.24 | 0.29 | 1533.30 | 0.55 | 0.26 | 0.20 | 160654_at |
| 4353.95 | 0.54 | 0.12 | 0.33 | 4326.67 | 0.54 | 0.22 | 0.24 | 5450.15 | 0.48 | 0.22 | 0.30 | 160282_at |
| 1832.65 | 0.56 | 0.15 | 0.29 | 1080.47 | 0.80 | 0.13 | 0.07 | 1509.40 | 0.53 | 0.20 | 0.27 | 103447_at |
| 4155.50 | 0.43 | 0.19 | 0.39 | 3808.33 | 0.51 | 0.21 | 0.28 | 7368.75 | 0.42 | 0.18 | 0.40 | 103685_at |
| 8680.80 | 0.40 | 0.09 | 0.51 | 6012.07 | 0.84 | 0.08 | 0.08 | 6193.85 | 0.49 | 0.06 | 0.45 | 95731_at |
| 2304.80 | 0.46 | 0.07 | 0.47 | 1586.07 | 0.49 | 0.17 | 0.33 | 2238.55 | 0.56 | 0.25 | 0.18 | 95556_at |
| 12192.65 | 0.48 | 0.16 | 0.35 | 7565.47 | 0.56 | 0.20 | 0.25 | 6019.10 | 0.52 | 0.19 | 0.29 | 104320_at |
| 2104.55 | 0.62 | 0.09 | 0.29 | 2078.60 | 0.68 | 0.18 | 0.14 | 2121.55 | 0.53 | 0.16 | 0.30 | 102374_at |
| 1387.00 | 0.62 | 0.12 | 0.26 | 766.80 | 0.57 | 0.24 | 0.19 | 1079.55 | 0.48 | 0.19 | 0.32 | 104699_at |
| 1402.05 | 0.72 | 0.08 | 0.20 | 1630.20 | 0.64 | 0.18 | 0.18 | 1341.85 | 0.56 | 0.13 | 0.31 | 104298_at |
| 463.65 | 0.64 | 0.09 | 0.27 | 516.90 | 0.70 | 0.18 | 0.12 | 331.05 | 0.53 | 0.21 | 0.26 | 93325_at |
| 3310.35 | 0.60 | 0.12 | 0.28 | 3682.47 | 0.51 | 0.22 | 0.26 | 3724.85 | 0.51 | 0.20 | 0.29 | 95468_at |
| 1329.60 | 0.57 | 0.14 | 0.29 | 1717.63 | 0.56 | 0.17 | 0.27 | 1556.05 | 0.61 | 0.22 | 0.17 | 94382_at |
| 3847.30 | 0.29 | 0.06 | 0.65 | 2582.60 | 0.64 | 0.15 | 0.21 | 2457.30 | 0.57 | 0.17 | 0.26 | 104389_at |
| 13734.25 | 0.39 | 0.19 | 0.42 | 11911.50 | 0.54 | 0.26 | 0.20 | 15135.85 | 0.47 | 0.20 | 0.34 | 101072_at |
| 927.40 | 0.64 | 0.07 | 0.29 | 1133.13 | 0.56 | 0.20 | 0.24 | 1514.75 | 0.44 | 0.15 | 0.41 | 95759_at |
| 3452.65 | 0.46 | 0.15 | 0.38 | 3074.93 | 0.57 | 0.20 | 0.23 | 2841.75 | 0.47 | 0.19 | 0.34 | 94403_at |
| 9014.90 | 0.45 | 0.17 | 0.38 | 6511.23 | 0.47 | 0.21 | 0.32 | 10517.55 | 0.48 | 0.23 | 0.30 | 101070_at |
| 956.75 | 0.58 | 0.14 | 0.28 | 735.77 | 0.51 | 0.23 | 0.26 | 510.35 | 0.51 | 0.12 | 0.38 | 102883_at |
| 16548.35 | 0.46 | 0.14 | 0.40 | 12811.47 | 0.67 | 0.16 | 0.17 | 13546.00 | 0.51 | 0.14 | 0.35 | 160273_at |

## 10. 9. GROUP 2-C




| | wild type | | | | GR dim | | | | GR LysCre | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS |
| Sum: | **2.69** | **1.01** | **0.30** | Sum: | **2.24** | **0.90** | **0.86** | Sum: | **2.93** | **0.66** | **0.41** |
| Mean: | **0.67** | **0.25** | **0.08** | Mean: | **0.56** | **0.22** | **0.21** | Mean: | **0.73** | **0.17** | **0.10** |
| StDev: | **0.06** | **0.03** | **0.03** | StDev: | **0.06** | **0.03** | **0.06** | StDev: | **0.09** | **0.05** | **0.05** |
| Fold change (LPS/ctrl) | | | **0.4** | Fold change (LPS/ctrl) | | | **0.4** | Fold change (LPS/ctrl) | | | **0.2** |
| Fold change (LPS/dex+LPS) | | | **3.3** | Fold change (LPS/dex+LPS) | | | **1.0** | Fold change (LPS/dex+LPS) | | | **1.6** |

### 10. 9. 1. Expression levels of genes/ESTs representing Group 2-C

| | | | | wild type | | | | Fold change | |
|---|---|---|---|---|---|---|---|---|---|
| Acc. | Gene/EST Name | ctrl | | LPS | | dex+LPS | | LPS | LPS |
| Num. | | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS |
| AF022990 | CC chemokine receptor-5 (CCR5) gene, complete cds | 1505.6 | PP | 421.7 | PP | 57.75 | PA | 0.3 | 7.3 |
| U29678 | Chemokine (C-C) receptor 1 | 5883.55 | PP | 2162.35 | PP | 796.05 | PP | 0.4 | 2.7 |
| AV370035 | Mus musculus cDNA, 3 end | 1088.55 | PP | 445.25 | PP | 125.85 | AP | 0.4 | 3.5 |
| AW046775 | UI-M-BH1-alt-h-01-0-UI.s1 Mus musculus cDNA, 3 end | 1998.75 | PP | 913.35 | PP | 349 | PP | 0.5 | 2.6 |

| | | GR dim | | | | Fold change | | | | GR LysCre | | | | Fold change | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ctrl | | LPS | | dex+LPS | | LPS | LPS | ctrl | | LPS | | dex+LPS | | LPS | LPS | Grid |
| AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | AD | AC | AD | AC | AD | AC | ctrl | dex+LPS | position |
| 639.13 | PPP | 270.93 | PPP | 270.83 | APA | 0.4 | 1.0 | 2279.35 | PP | 339.70 | PP | 232.90 | AA | 0.1 | 1.5 | 102718_at |
| 3597.03 | PPP | 1557.43 | PPP | 2079.10 | PPP | 0.4 | 0.7 | 9514.40 | PP | 3762.45 | PP | 2228.40 | PP | 0.4 | 1.7 | 99413_at |
| 1486.03 | PPP | 697.10 | APP | 410.87 | APP | 0.5 | 1.7 | 678.55 | PP | 119.85 | AA | 35.25 | AA | 0.2 | 3.4 | 161968_f_at |
| 1325.60 | PPP | 392.93 | PAP | 388.43 | PPP | 0.3 | 1.0 | 1498.50 | PP | 334.85 | PP | 312.65 | PA | 0.2 | 1.1 | 104744_at |

### 10. 9. 2. Normalised expression of genes/ESTs representing Group 2-C

| Acc. Num. | Gene/EST Name |
|---|---|
| AF022990 | CC chemokine receptor-5 (CCR5) gene, complete cds |
| U29678 | Chemokine (C-C) receptor 1 |
| AV370035 | Mus musculus cDNA, 3 end |
| AW046775 | UI-M-BH1-alt-h-01-0-UI.s1 Mus musculus cDNA, 3 end |

| | wild type | | | | GR dim | | | | GR LysCre | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | | ctrl | LPS | dex+LPS | Grid |
| Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | Sum | position |
| 1985.05 | 0.76 | 0.21 | 0.03 | 1180.90 | 0.54 | 0.23 | 0.23 | 2851.95 | 0.80 | 0.12 | 0.08 | 102718_at |
| 8841.95 | 0.67 | 0.24 | 0.09 | 7233.57 | 0.50 | 0.22 | 0.29 | 15505.25 | 0.61 | 0.24 | 0.14 | 99413_at |
| 1659.65 | 0.66 | 0.27 | 0.08 | 2594.00 | 0.57 | 0.27 | 0.16 | 833.65 | 0.81 | 0.14 | 0.04 | 161968_f_at |
| 3261.10 | 0.61 | 0.28 | 0.11 | 2106.97 | 0.63 | 0.19 | 0.18 | 2146.00 | 0.70 | 0.16 | 0.15 | 104744_at |