

**Epidermal inactivation of the glucocorticoid receptor triggers
skin barrier defects and cutaneous inflammation**

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Abbreviations: GC, glucocorticoid; GR, glucocorticoid receptor; GR^{EKO}, GR epidermal knock out; atopic dermatitis (AD); epidermal differentiation complex (EDC); stratum corneum (SC); K5, K6, K10, keratin 5, 6, 10; E16.5, E18.5, embryonic age in days; P0, P2, etc., postnatal age in days; WT, wild type.

ABSTRACT

The glucocorticoid (GC) receptor (GR) mediates the effects of physiological and pharmacological GC ligands and plays a major role in cutaneous pathophysiology. To dissect the epithelial *vs* mesenchymal contribution of GR in developing and adult skin, we generated mice with keratinocyte-restricted GR inactivation (GR epidermal knock out or GR^{EKO} mice). Developing and early postnatal GR^{EKO} mice exhibited impaired epidermal barrier formation, abnormal keratinocyte differentiation, hyperproliferation, and stratum corneum fragility. At birth, GR^{EKO} epidermis showed altered levels of epidermal differentiation complex genes, proteases and protease inhibitors which participate in stratum corneum maintenance, and innate immunity genes. Many upregulated genes, including *S100a8/a9* and *Tslp*, also have increased expression in inflammatory skin diseases. Infiltration of macrophages and degranulating mast cells were observed in newborn GR^{EKO} skin, hallmarks of atopic dermatitis (AD). In addition to increased ERK activation, GR^{EKO} newborn and adult epidermis had increased levels of phosphorylated STAT3, a feature of psoriasis. While adult GR^{EKO} epidermis had a mild phenotype of increased proliferation, perturbation of skin homeostasis with detergent or phorbol ester triggered an exaggerated proliferative and hyperkeratotic response relative to wild type. Together, our results show that epidermal loss of GR provokes skin barrier defects and cutaneous inflammation.

INTRODUCTION

The glucocorticoid (GC) receptor (GR or *Nr3c1*) is a ligand-activated transcription factor that belongs to the nuclear hormone receptor superfamily and regulates gene expression through DNA-binding-dependent and –independent mechanisms (Nicolaidis et al., 2010; Revollo and Cidlowski, 2009). GR is ubiquitously expressed and mediates the biological and therapeutical effects of endogenous and synthetic GCs (Nicolaidis et al., 2010; Revollo and Cidlowski,

2009). The wide use of GC analogs in clinical practice relies on their great efficacy as anti-inflammatory agents, mostly due to the antagonism between ligand-activated GR and the pro-inflammatory NF- κ B, AP-1 and STAT signaling pathways in many cell types (Clark, 2007; De Bosscher and Haegeman, 2009; Lieberman et al., 2007). GCs are currently used to treat inflammatory skin pathologies, such as atopic dermatitis (AD) and psoriasis, due to their anti-proliferative and anti-inflammatory actions in both immune cells and keratinocytes (Elias, 2010; Schäcke et al., 2002). The mechanisms mediating GR therapeutical actions in skin disease have been widely studied, however, much less is known about the role of GR in skin physiology (Pérez, 2011).

In rodents, classical studies have shown that exogenous GCs promote epidermal barrier formation during development. Conversely, GC treatment of adult animals perturbs permeability barrier homeostasis, suggestive of unique roles for the GR in development and adulthood (Aszterbaum et al., 1993; Hanley et al., 1998; Kao et al., 2003; Sheu et al., 1991). We previously demonstrated that ubiquitous ablation of GR ($GR^{-/-}$) leads to major defects in mouse skin development with impaired keratinocyte differentiation, and augmented proliferation and apoptosis (Bayo et al., 2008). Transcriptional profiling of $GR^{-/-}$ embryonic skin together with studies using cultured primary keratinocytes showed aberrant expression of genes encoding epidermal barrier proteins (Sevilla et al., 2010). However, these analyses did not allow for discrimination of the keratinocyte-specific contribution of GR in skin development and pathophysiology. Moreover, $GR^{-/-}$ mice had alterations in the synthesis and secretion of steroids, which resulted in increased levels of ACTH and circulating corticosterone that may contribute to the skin phenotype (Tronche et al., 1999; Bayo et al., 2008). Above all, perinatal death of $GR^{-/-}$ mice precluded analyzing skin phenotype progression and whether developmental defects result in increased susceptibility to skin inflammation in the adult age, as described for other mouse models featuring epidermal barrier defects (Cork et al., 2009; Elias, 2010; Roberson and Bowcock, 2010; Segre, 2006).

To resolve these issues, we generated a mouse model with constitutive GR inactivation restricted to keratinocytes (GR epidermal knock out or GR^{EKO} mice). In this report, we describe

that GR^{EKO} mice exhibited defects in epidermal development and competence with SC fragility and degranulated mast cells in the dermis. At birth, GR^{EKO} mice showed up-regulation of known markers of cutaneous inflammatory diseases associated with epidermal barrier defects. The changes in gene expression were concomitant with increased ERK and STAT3 activation in GR^{EKO} newborn epidermis. While the skin in adult mice had a milder phenotype than the newborn mice, it was hypersensitive to treatment with detergent (SDS) or phorbol ester (PMA). Our results show that GR is required in keratinocytes for normal skin development and homeostasis and that in its absence mice develop phenotypic and molecular characteristics of inflammatory skin diseases treated by GCs.

RESULTS AND DISCUSSION

Epidermal-specific loss of GR results in impaired barrier formation

GR was absent in the epidermis of newborn and adult GR^{EKO} mice but not in other tissues, as shown by immunoblotting (Fig. 1a). GR was also absent in hair follicles and sebaceous glands, as assessed by immunofluorescence in whole mounts of tail epidermis (Fig. 1b). We investigated whether GR inactivation in keratinocytes affected epidermal barrier formation by assessing the permeability of toluidine blue dye in developing embryos. In WT embryos, the epidermis matured following a dorso-ventral, antero-posterior pattern (Fig. 1c). Dorsal epidermal barrier initiation sites were present at embryonic day (E)16.5 (Fig. 1c, white arrows) and by E17.5 the moving front of the epidermal barrier was evident laterally (Fig. 1c, white line). At E18.5, WT embryos were unstained, consistent with a competent epidermal barrier. In contrast, GR^{EKO} E16.5 and E17.5 embryos showed a delay in barrier formation with initiation sites scattered throughout the dorsal epidermis which did not follow a proper spatio-temporal pattern of development (Fig. 1c, GR^{EKO}, dorsal view, red arrows). Moreover, the moving front of the barrier of E17.5 GR^{EKO} embryos was irregular (Fig. 1c, lateral view, red line) and at E18.5, colored remnants were detected on the ventral side of knockout mice, indicating

epidermal immaturity (Fig. 1a, GR^{EKO}, red arrows). The epidermis of GR^{EKO} E17.5 embryos was much thinner along the dorso-ventral axis compared to WT (Fig. S1a-c), consisting of only a few cell layers in certain areas (Fig. S1b, arrows). Remarkably, the granular layer and SC were greatly diminished and SC detachment was frequent (Fig. S1b, asterisk). Previous reports in rodents in which a role for GR in accelerating epidermal barrier formation was postulated, together with this study (Fig. 1c), strongly suggest that GR plays a major role in regulating the induction of barrier initiation.

Abnormal epidermal differentiation and proliferation in GR^{EKO} newborn mice

After birth, the skin of GR^{EKO} mice featured epidermal hyperplasia (Fig. 2a and 2a'), impaired keratinocyte differentiation (Fig. 2a, arrows) with hyperkeratosis, parakeratosis (Fig. 2d, thin arrows) and extensive areas of SC detachment (Fig. 2a, asterisk). Transmission electron microscopy further illustrated breakages between the granular layer and the first corneocyte layer of the SC (Fig. 2b, asterisks). SC lipids are important modulators of barrier function (Feingold, 2007; Jin et al., 2009; Scharschmidt and Segre, 2008), therefore, we examined epidermal lipids first by electron microscopy, and observed no obvious change in lamellar body extrusion in GR^{EKO} mice (data not shown). However, Nile red staining demonstrated a decreased ratio of polar (red) to nonpolar (green) lipids in GR^{EKO} epidermis (Fig. 2c). Importantly, the observed skin defects improved by P5, coinciding with anagen (Fig. 2a).

We next assessed the expression of epidermal differentiation markers in newborn (P0) GR^{EKO} and control mice. Immunostaining for filaggrin, loricrin and corneodesmosin revealed patches of epidermis negative for these epidermal barrier proteins in GR^{EKO} skin (Fig. 2d). We also detected patchy expression of keratin (K)6, a marker of hyperproliferation commonly seen in skin diseases (Ramot et al., 2009), in GR^{EKO} interfollicular epidermis (Fig. 2d). Consistent with the hyperplasia and K6 staining, we observed a 4-fold increase in keratinocyte proliferation by *in vivo* BrdU labeling (Fig. 2e). TUNEL staining revealed a slight, but not statistically significant, increase in keratinocyte apoptosis in GR^{EKO} epidermis (Fig. S2). Next, we

investigated the processing of pro-filaggrin and observed decreased levels of both precursor and filaggrin monomer in GR^{EKO} skin (Fig. 2f). Furthermore, the activity of the epidermal-specific non-apoptotic caspase-14, which mediates pro-filaggrin processing (Presland, 2009) was reduced, as shown by decreased levels of the active cleaved fragment (Fig. 2f). Decreased filaggrin levels may contribute to epidermal barrier defects as it is critical for the later stages of keratinocyte terminal differentiation as well as for the production of natural moisturizing factor upon its degradation into free amino acids (Hoste et al., 2011). The GR^{EKO} skin phenotype has some similarities to that of GR^{-/-} mice in that both mouse models show defects in epidermal barrier development, indicating keratinocyte autonomous functions of GR (Bayo et al., 2008). However, in contrast to GR^{EKO}, GR^{-/-} had much more dramatic reductions in both the expression of differentiation markers and in the layers of the SC. The different phenotypes may be due to the presence of dermal GR or to the normal levels of ACTH and corticosterone in GR^{EKO} mice (data not shown). Taken together, our data suggest that GR is necessary in both the epidermis and the dermis for proper skin development.

GR^{EKO} epidermis shows up-regulation of gene markers of cutaneous inflammatory diseases associated with epidermal barrier defects

We analyzed the gene expression profile of GR^{EKO} vs WT P0 epidermis by microarrays and identified 293 differentially expressed genes of which 189 were induced and 104 repressed (Table S1). A partial gene list is shown (Fig. 3a) along with validation of a gene subset by RT-QPCR using independent samples (Fig. 3b). GR^{EKO} epidermis showed up-regulation of keratins *Krt6a*, *Krt6b*, and *Krt16*, which are markers of hyperproliferation. Increased *Krt6* transcript levels were consistent with augmented K6 immunostaining in mutant mice (Figs. 3a and 2d). *Krt77* and the epithelial-specific transcription factor *Elf5*, two genes whose expression normally peaks during embryogenesis in early stages of epidermal maturation, were also induced in GR^{EKO} epidermis. We found induction of numerous genes mapping to the EDC, a cluster of related genes involved in epidermal differentiation as well as host defense responses (de Koning

et al., 2011; Hoffjan and Stemmler, 2007; Segre, 2006; Sugiura et al., 2005). Among the 75 most up-regulated genes were EDC members including multiple small proline-rich proteins (*Sprrs*), late cornified envelope proteins (*Lces*), repetin (*Rptn*), peptidoglycan recognition protein 3 (*Pglyrp3*) and S100 calcium binding proteins *S100a8* and *S100a9* (Fig. 3a, b). The up-regulation in group 3 Lce genes is noteworthy as their expression is normally restricted to internal epithelia and is only induced in the epidermis under conditions of stress (De Cid et al, 2009; Jackson et al, 2005). We also found strong induction of proteases and protease inhibitors that participate in the normal maintenance of the SC, such as matrix metalloproteinase *Mmp3*, kallikrein (*Klk*) related peptidases, and secretory leukocyte peptidase inhibitor (*Slpi*). Many genes involved in lipid metabolism and transport had altered expression in GR^{EKO} epidermis, including lipase endothelial (*Lipg*), ATP-binding cassette, sub-family G, member 1 (*Abcg1*) and sub-family A (ABC1), member 12 (*Abca12*), arachidonate 12-lipoxygenase (*Alox12*), and phospholipase A2, group IVE (*Pla2g4e*) (Table S1). GR is a known modulator of lipid metabolism (Elias et al., 2010; Nicolaides et al., 2010; Revollo and Cidlowski, 2009), and the alterations in epidermal lipids in its absence could contribute to the changes in Nile red staining and the observed fragility of the SC.

Importantly, we found up-regulation of genes involved in cutaneous innate immune responses such as thymic stromal lymphopoietin (*Tslp*), interleukin 33 (*Il33*), epiregulin (*Ereg*), and B-cell leukemia 3 (*Bcl3*) (Figs. 3a, b). Almost 50% of the genes up-regulated greater than 2-fold in GR^{EKO} mice were reported markers of inflammatory skin disorders (Roberson and Bowcock, 2010; Sugiura et al., 2005). In fact, a high percentage of the genes induced in GR^{EKO} epidermis have been reported as overexpressed in the skin of AD patients (Cork et al., 2009; Elias, 2010; Sugiura et al., 2005). *Tslp* plays a major role in AD, indeed its overexpression in keratinocytes is sufficient to trigger an AD-like disease in mice (Li et al., 2005; Li et al., 2006; Zhang et al., 2009); importantly, *Tslp* levels in keratinocytes are transcriptionally repressed by ligand-activated GR (Li et al., 2006; Surjit et al., 2011). Together with *Tslp*, the induction of *Bcl3* in GR^{EKO} epidermis suggests alterations in the innate immune response of these animals as it is inducible by Th2 cytokines and is overexpressed in lesional skin of AD patients (Büchau et

al., 2009). While the immune response may contribute to changes in *Bcl3* expression, we found that it was also up-regulated in cultured GR^{EKO} keratinocytes, indicating cell autonomous effects of GR (Fig. S3a). Moreover, treatment with Dex, but not the GR antagonist RU486, inhibited *Bcl3* expression in WT keratinocytes, both in the absence and presence of IL6, a known inducer of *Bcl3* (Fig. S3b).

The list of differentially expressed genes in Table S1 was configured using a cut-off of 1.5 fold change relative to WT, however, we also detected and confirmed by RT-QPCR the induction of the signal transducer and activator of transcription 3 (*Stat3*) gene (1.3-fold by microarray; 3-fold by RT-QPCR) in mutant epidermis (Figs. 3a and b). Remarkably, we detected both overlapping and distinct set of genes in gene expression profiling for GR^{EKO} vs GR^{-/-} mice (Fig. 3, Table 1; Sevilla et al., 2010). There was strong up-regulation of *Krt77* and *Elf5*, as well as down-regulation of known GR target genes such as alcohol dehydrogenase 1 (*Adh1*) and *Fkbp51* (Sevilla et al., 2010); conversely, some EDC genes such as *Sprr2d* and *Rptn*, were oppositely regulated in the GR^{-/-} and GR^{EKO}. Importantly, changes in the expression of genes associated with skin immunity such as *Tslp* and *Bcl3* were detected in GR^{EKO} but not in GR^{-/-} mice. The lack of changes in expression of these genes in GR^{-/-} mice is consistent with the fact that we have not detected immune infiltrates in GR^{-/-} skin (Bayo et al., 2008; Sevilla et al., 2010). However, we can not establish a direct comparison between the gene expression profiles of GR^{EKO} and GR^{-/-} mice since the analyses were performed in newborn mouse epidermis and E18.5 total skin, respectively.

We evaluated macrophages and mast cells, which are increased in AD skin. GR^{EKO} skin had infiltration of macrophages (Fig. 3c) and extensive areas with degranulated mast cells in the upper dermis (Fig. 3c, red arrows). Moreover, there is increased degranulation of mast cells in GR^{EKO} embryonic skin indicating that the observed immune response occurs independently of exposure to the external environment and is driven by changes in communication between immune cells and keratinocytes lacking GR (Fig. S4). The IL-1 family member *Il33*, upregulated 2.6 fold in GR^{EKO} epidermis, activates mast cell degranulation in the presence of IgE, and has increased levels in lesions and blood of AD patients (Liew et al., 2010).

Altogether, the histological characterization of GR^{EKO} mice along with the observed transcriptomic changes suggests that the epidermal-specific loss of GR triggers a skin phenotype resembling key features of AD.

Increased ERK/AKT and STAT3 signaling in GR^{EKO} epidermis

Total GR inactivation results in increased activity of the MAPK ERK in keratinocytes (Bayo et al., 2008). We detected phosphorylated ERK (p-ERK) in the epidermal basal layer of GR^{EKO} late embryos and newborn mice in addition to its normal localization in the upper layers (Fig. 4a). MAPKs propagate inflammatory signaling and ligand-bound GR is known to interfere with the activating phosphorylation of members of this kinase family, including ERK (De Bosscher and Haegeman, 2009). The increase in ERK phosphorylation in GR^{EKO} epidermis likely contributes to the observed inflammation and hyperproliferation and may contribute to the elevated levels of EDC genes and *Krt6/Krt16*, among others, since they are AP-1 targets (Ramot et al., 2009). AKT activity was also elevated in the GR^{EKO} epidermis by approximately 2-fold (Fig. 4b). AKT is critical for proper epidermal development (Peng et al., 2003), and is involved in the initiation of keratinocyte terminal differentiation as well as in the regulation of filaggrin processing and cornified envelope (CE) formation (Calautti et al., 2005; O'Shaughnessy et al., 2005). AKT activity has been shown to transiently increase during barrier acquisition and its inhibition impairs barrier formation (O'Shaughnessy et al., 2009). Given that ligand-bound GR interferes with the phosphatidylinositol-3-kinase signaling pathway and its effector kinase AKT in skin (Leis et al., 2004), the observed defects in epidermal barrier acquisition in GR^{EKO} mice may be at least partially due to misregulation of this pathway.

Cross-talk between GR and STATs plays a role in the regulation of cell proliferation, differentiation, and survival, by modulating gene transcription in a cell-type specific manner (Lieberman et al., 2007). Importantly, STAT3 is activated in epidermal keratinocytes of psoriatic patients (Sano et al., 2008). Given the increased *Stat3* transcript levels in GR^{EKO} epidermis, we analyzed STAT3 protein expression and activity (Fig. 4b). STAT3 protein levels were only

slightly increased in mutant P0 epidermis, however, we detected a 2.5-fold increase of the phosphorylated (p)-STAT3/STAT3 ratio (Fig. 4b). Depending on cellular context, GCs have been shown to inhibit or synergize with the STAT3 transcription factor in terms of its phosphorylation and binding to chromatin (Bertucci et al., 2010; De Bosscher and Haegeman, 2009; Langlais et al., 2008). Our results suggest that in the developing epidermis, STAT3 phosphorylation is negatively regulated by GR, which is particularly relevant as GCs are frequently used to treat psoriatic lesions (Sano et al., 2008). The expression of S100A9, a marker of AD and psoriasis, was also increased in GR^{EKO} relative to WT epidermis (Fig. 4b). Consistent with the *in vivo* data, cultured GR^{EKO} keratinocytes showed relative increases in STAT3 and ERK phosphorylation as compared to WT (Fig. S5).

Adult GR^{EKO} mice show an exacerbated inflammatory response to epidermal challenge

Adult GR^{EKO} skin had a mild phenotype with slightly increased proliferation and patches of epidermis negative for filaggrin and loricrin (Fig. 5a, left panels; Fig. 5b; Fig. S6a). Similar yields of CEs were obtained from GR^{EKO} and WT (data not shown) which were morphologically similar with no changes in fragile/rigid ratios (Fig. S6b and c). These data together with the normal histological appearance suggest that barrier function is intact in adult GR^{EKO} mice. Altogether, these data suggest that GR plays distinct roles in the epidermis during development and in adulthood. Contrary to WT, topical treatment with the GC synthetic analog dexamethasone (Dex) did not cause epidermal atrophy or keratinocyte growth inhibition in GR^{EKO} mice, demonstrating that the anti-proliferative effects of GCs require functional GR in keratinocytes (Fig. 5a, b). Since epidermal defects during development may cause impaired responses in adulthood, we examined the consequences of GR loss-of-function in epidermal barrier repair after injury. Topical treatment of adult WT mice with the detergent SDS, an irritant that mimicks contact dermatitis by disrupting the epidermal barrier, elicited epidermal hyperplasia and hyperkeratosis (Fig. 5c). In GR^{EKO} mice, this response was exaggerated with more pronounced hyperplasia and hyperkeratosis as well as parakeratosis (Fig. 5c). A similar exacerbated response was found in GR^{EKO} mice treated with the tumor promoter PMA (Fig.

5C). In some cases, both SDS and PMA elicited even more severe phenotypes in GR^{EKO} mice, with intraepithelial infiltrates and epidermal destruction (Fig. 5c, lower panels, asterisks). Both SDS and PMA treatments induced elevated levels of K6 (Fig. 5d, upper panels) consistent with its up-regulation in GR^{EKO} developing skin (Figs. 2 and 3). ERK activity was higher in adult GR^{EKO} relative to WT mice either in the absence or presence of topical treatments (Fig. 5d, lower panels). We observed increased SDS-induced nuclear translocation of STAT3 by immunohistochemistry in GR^{EKO} epidermis, especially in the basal layer, compared to WT (Fig. 5E). The levels of p-STAT3 were clearly increased in control and mutant mice after SDS treatment (Fig. 5e'). Collectively, our data reinforce the importance of GR in skin physiology as well as in the pathogenesis of skin diseases and indicate that understanding the transcriptional program by which GR modulates keratinocyte differentiation could contribute to rationale design of therapies for treating cutaneous inflammatory diseases.

MATERIALS AND METHODS

Animal experimentation and treatments

GR^{loxP/loxP} and K5-Cre mice have been reported (Tronche et al., 1999; Ramírez et al., 2004); see Fig. S7 for a diagram of gene targeting strategy. Animal experimentation was conducted according to the current Spanish and European regulations and approved by our institution's ethics committee. When indicated, GR^{EKO} (K5-cre//GR^{loxP/loxP}) and their control littermates (Ocre//GR^{loxP/loxP}) were obtained by cesarean derivation. Topical treatments included Dex (8 µg/mouse; daily for 72h), PMA (8 µg/mouse for 48h) (both from Sigma Chemical Co., St. Louis, MO), and SDS (10%, daily for 5 d) (Merck, Darmstadt, Germany).

Epidermal dye permeability assay was performed with 1% toluidine blue dye (Sigma) as described (Byrne et al., 2010).

Histological and Immunohistochemical analysis

Tail epidermal whole mounts from 8 week old GR^{EKO} and control littermates were prepared and stained as described (Braun et al., 2003), and images collected with a Leica TCS SL confocal microscope. Total embryos (E16.5, E17.5 or E18.5) or dorsal skin samples were collected at postnatal days P0, P1, P2, P5 (n=62), and P56 (n=87), fixed in 4% paraformaldehyde (PFA) or 70% ethanol and embedded in paraffin. Histopathological analysis was performed as described (Bayo et al., 2008). For lipid staining, sections were incubated with 1 mg/mL Nile Red (Sigma) in PBS along with DAPI for 5 min at RT. Mast cells were detected using 0.1% toluidine blue for 3 min.

Epidermal thickness was assessed using images of H&E stained paraffin skin sections from E16.5, E18.5, P0 and P2 mice, counting at least 10 1mm fields per slide using MetaMorph software (Premier Offline 7.0; Molecular Devices, Downingtown, PA). Experiments were performed in at least five individuals of each genotype, and statistical significance was assessed using the Student's t test, ($p < 0.05$).

Analysis of proliferation and apoptosis

BrdU incorporation was assessed by immunohistochemistry (anti-BrdU, biotest, Roche, Indianapolis, IN) in paraffin-embedded sections from mice injected with BrdU 1 hr prior to sacrifice (130 μ g/g of body weight, Roche). Apoptotic cells were labeled in paraffin sections with the In Situ Cell Death Detection kit (Roche), prior to mounting with DAPI and analysis under a fluorescence microscope (Leica DM 1000). Experiments were performed at least in five individuals of each genotype and age, and statistical significance was assessed using the Student's t test, ($p < 0.05$).

Transmission electron microscopy

Skin samples were fixed in 2.5% glutaraldehyde/2.5% PFA/PBS (pH 7.2) for 15 h at 20°C, postfixed with 1% OsO₄/PBS in the dark at 4°C followed by dehydration in an ascending water/acetone series, and embedded in AGAR 100 epoxy resin (Agar Scientific, Stansted, UK). Sections obtained by an ultramicrotome (Reichert Ultracut S; Leica, Wetzlar, Germany) were

stained with 2% uranyl acetate and lead citrate at various concentrations, and examined with a transmission electron microscope (CEM 902A; Zeiss, Oberkochen, Germany) at an acceleration voltage amounting to 80 kV.

Epidermal preparation, RNA isolation, Microarray analysis, and Quantitative RT-PCR

Mouse dorsal epidermis was separated from the dermis following incubation with 1mg/ml dispase II (Roche) for 2h at room temperature and total RNA isolated using Trizol (Invitrogen, Molecular Probes, Eugene, Oregon). RNA was purified by standard procedures (Qiagen, Valencia, CA) and its integrity tested by the Bioanalyzer 2100 (Agilent Technologies). Four microarrays (Affymetrix GeneChip® Mouse Gene 1.0 ST) of GR^{EKO} and WT P0 epidermis were analyzed. Microarray hybridization, data normalization and analysis were carried on the genomic platform at the Centro de Investigación del Cáncer de Salamanca, as described on their webpage (<http://ubioinfo.cicancer.org>). The gene list with the 293 differentially expressed genes with statistical significance (FDR<0.06) in GR^{EKO} vs WT (considering fold-changes of at least 1.5 fold) is in Table S1.

1 µg of total RNA was reverse transcribed by using oligo-dT (Fermentas Inc., Burlington, Canada) followed by quantitative PCR using specific oligonucleotides (Table S2) for each of the genes tested and FastStart Universal SYBR Green Master ROX (Roche) in an Applied Biosystems 7500 Fast real time PCR system. At least three biological replicates were used for each experimental group and technical triplicates were assessed to calculate the mean value ± SD. Statistical significance was calculated using the Student's t test, p < 0.05.

Immunoblotting and Antibodies

Whole cell extracts and immunoblotting were performed as described (Bayo et al. 2008). Experiments were performed in at least three individuals of each genotype.

Polyclonal antibodies to GR (sc-1004), casp-14 (sc-5628), ERK (sc-154), and AKT (sc-1619) and monoclonal antibody for K14 (LL009) were from Santa Cruz Biotechnology, Inc. (Santa Cruz, CA). Antibodies against p-ERK (Thr202/Tyr204; no. #4376), p-AKT (ser-473)

(#9271), STAT3 (#9132), and p-STAT3 (Tyr705 D3A7; #9145) were from Cell Signaling Technology Inc. (Beverly, MA). The anti-keratin K5 (PRB-160P), K6 (PRB-169P), K10 (PRB-159P), loricrin (PRB-145P), and filaggrin (PRB-417P) antibodies were from Covance (Babco, Berkeley, CA). F4/80 antibody (AbD serotec, MorphoSys, Oxford, UK), actin antibody (A-2066, Sigma), and anti-S100A9 (R&D Systems) were used. The monoclonal antibody F28-27 specific for CDSN was a gift from the Serre lab (CNRS; Serre et al., 1991). Secondary peroxidase-conjugated anti-rabbit (Amersham) and anti-goat antibodies (Jackson ImmunoResearch, Inc. West Grove, PA) and secondary biotin-conjugated anti-rabbit or anti-mouse antibodies (Jackson ImmunoResearch) were used.

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Conflict of Interest

The authors declare that they have no conflict of interest.

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FIGURE LEGENDS

Figure 1. Mice with keratinocyte-restricted inactivation of GR (GR^{EKO}) exhibit impaired epidermal barrier formation.

(a) Immunoblotting showing GR loss in epidermis of newborn (NB) and adult mice but not in other tissues. (b) Immunofluorescence of tail epidermal whole mounts showing absence of GR in hair follicles (hf) and sebaceous glands (sg) in addition to interfollicular epidermis (ife). Bar: 100 μ m. (c) Impaired epidermal barrier formation of GR^{EKO} mice. Epidermal maturation assessed by toluidine blue staining in late (E16.5 to E18.5) GR^{EKO} and WT embryos. GR^{EKO} mice showed delayed and altered epidermal barrier formation (red arrows) that did not follow the dorso-ventral, antero-posterior pattern of WT mice (white arrows). Lines indicate the progression of epidermal maturation in WT (white) vs mutant (red) mice.

Figure 2. Abnormal epidermal differentiation and proliferation in GR^{EKO} newborn mice.

(a) H&E stained GR^{EKO} and WT postnatal (P) skin sections. Dotted line: epidermal-dermal border. Arrows: hyperkeratosis. Asterisk: SC detachment. Bar: 100 μ m. (a') Epidermal thickness quantitation; Student's *t* test; *, *p* <0.05; **, *p* <0.005. (b-f) P0 skin samples. (b) Electron microscopy; asterisk: SC detachment. Bar: 20 μ m (left), 3 μ m (right). (c) Nile red staining; polar (red), non-polar (green). Bar: 100 μ m. (d) Immunostaining; FIL, filaggrin; LOR, loricrin; CDSN, corneodesmosin; K6, keratin 6. Black thick arrow: specific staining. White arrows: lack of staining. Thin arrows: parakeratosis. Asterisk: SC detachment. Bar: 100 μ m (H&E), 50 μ m (immunostaining) (e) BrdU-positive keratinocytes (n=12). Mean values \pm SD are shown. Student's *t* test; *, *p* <0.05. (f) Immunoblotting.

Figure 3. Gene expression changes and skin phenotype indicate an intrinsic epidermal stress response of GR^{EKO} mice to barrier disruption.

(a) Selected list of differentially expressed genes in GR^{EKO} relative to WT newborn epidermis grouped by Gene ontology. (b) RT-QPCR validation of selected genes was performed in an independent experiment with at least three individuals of each genotype. (c) Increased degranulation of mast cells and elevated numbers of macrophages indicate an abnormal immune response in GR^{EKO} mice. Normal mast cells in WT dermis (black arrows) and degranulated mast cells in the upper dermis of GR^{EKO} mice (red arrows) are indicated. F480 antibody stained macrophages. Bars: 100 μ m (outer panels), 50 μ m (middle panels).

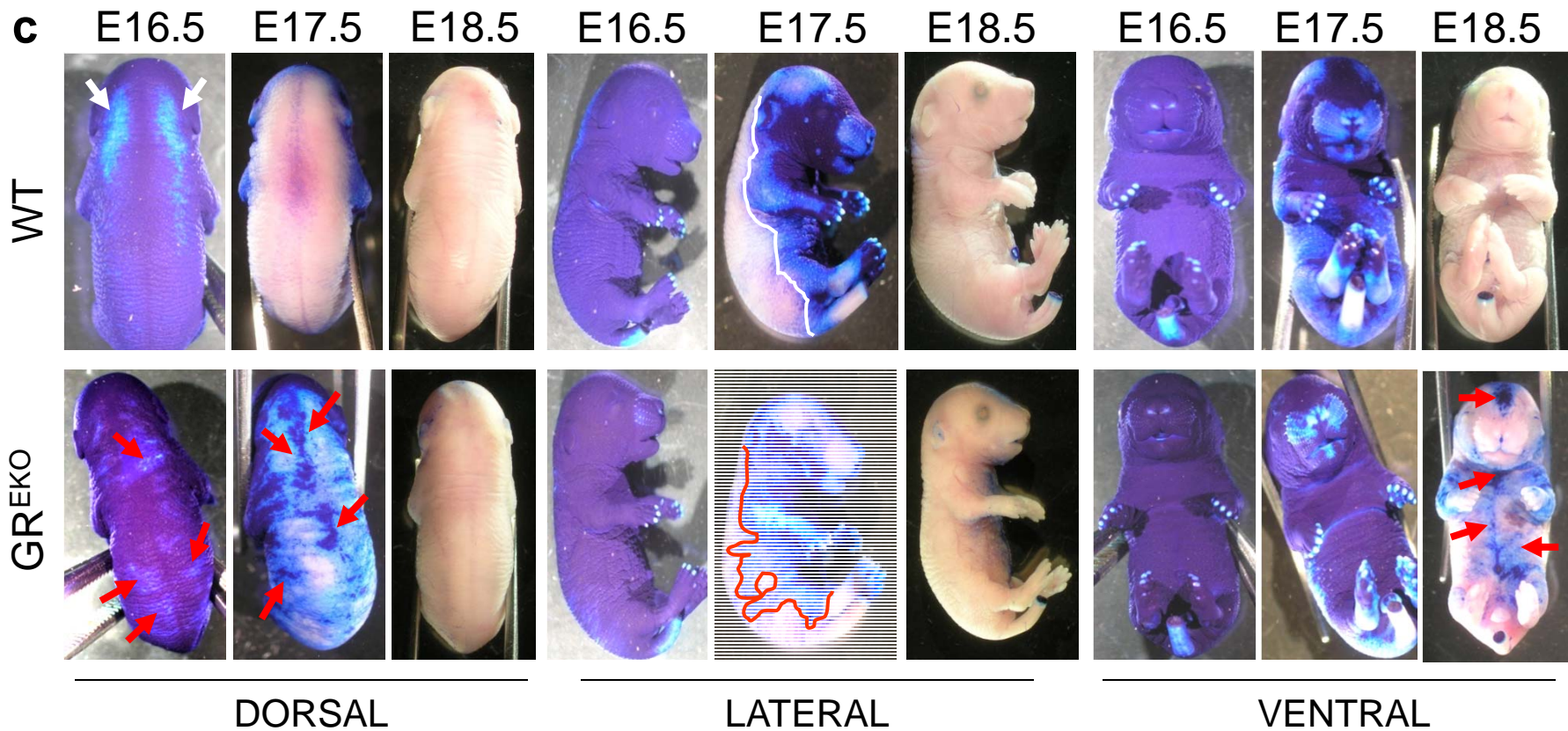
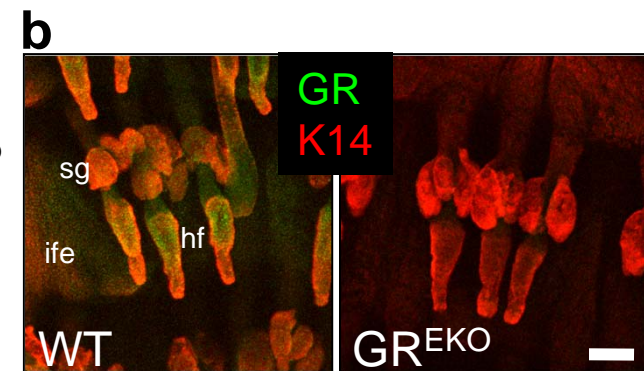
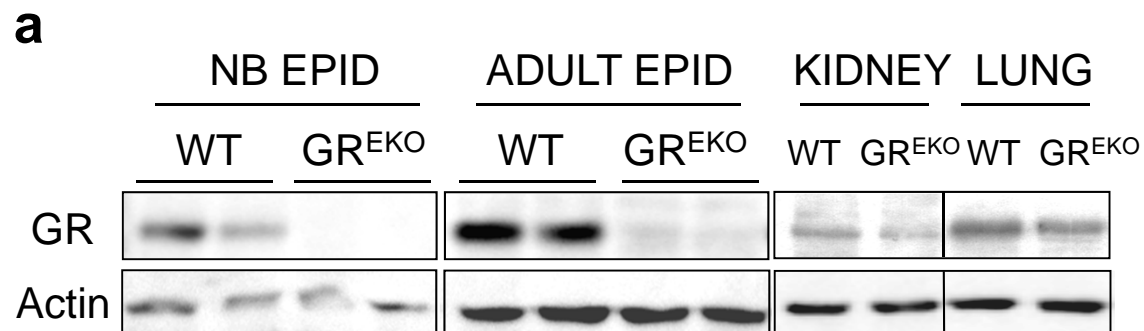
Figure 4. Altered signaling in GR^{EKO} epidermal keratinocytes.

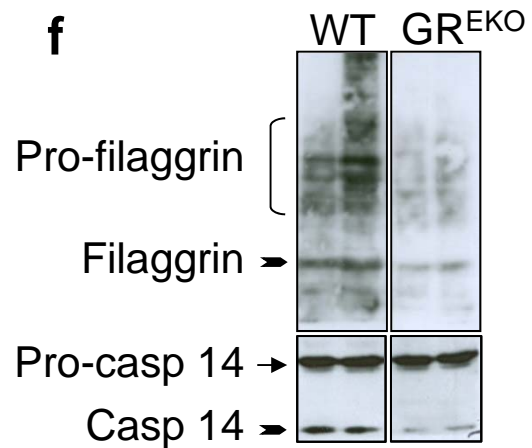
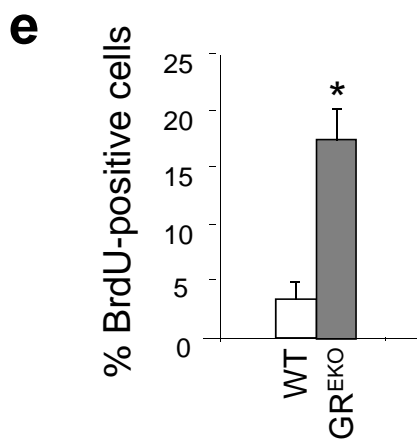
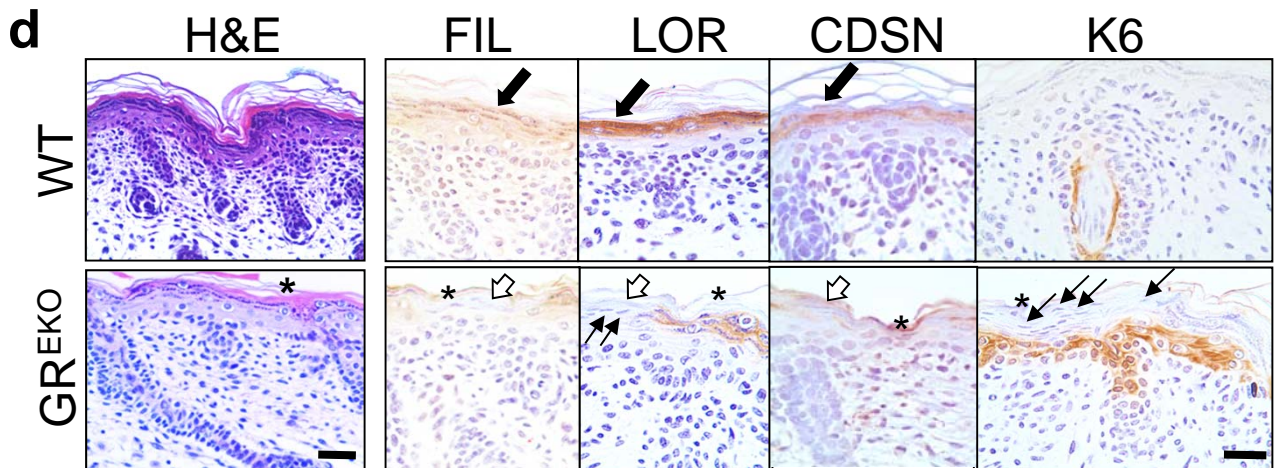
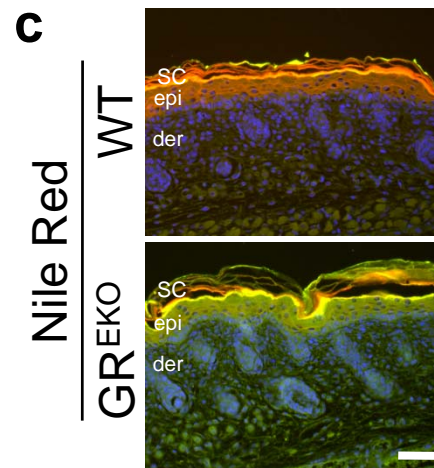
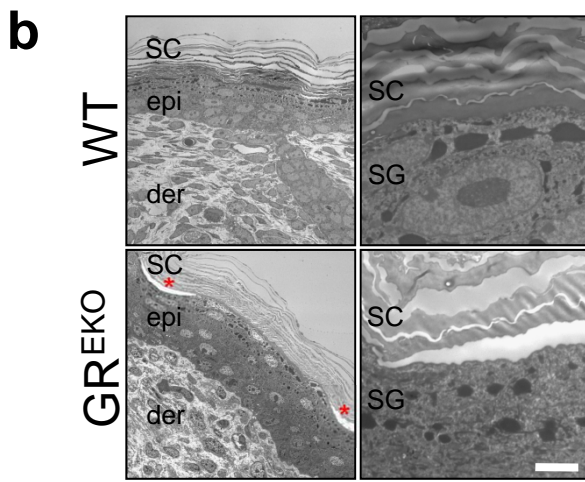
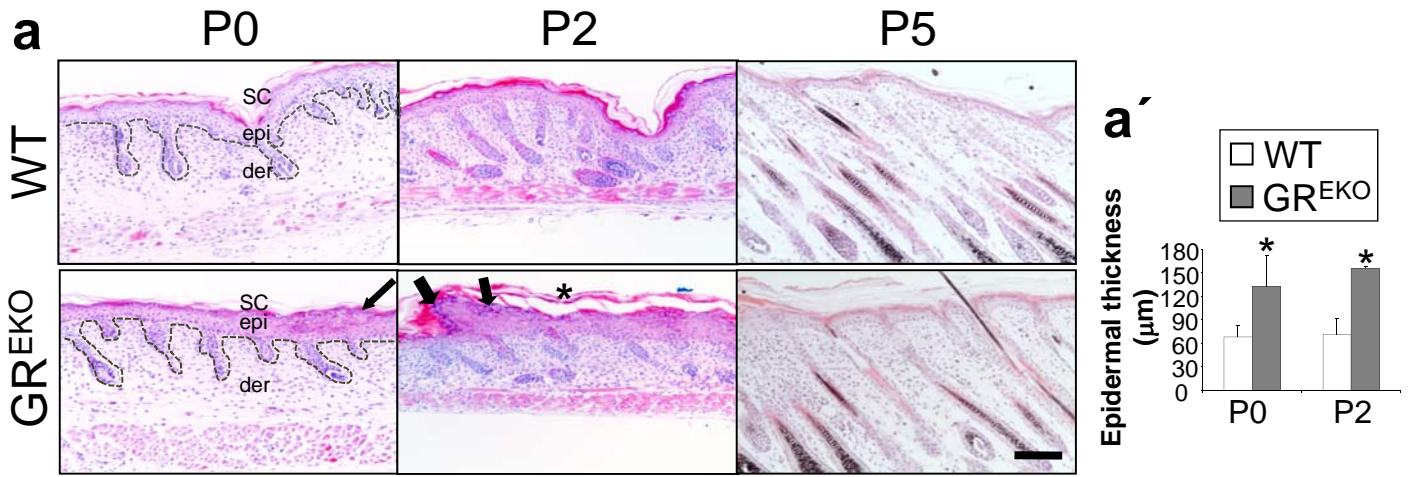
(a) Increased ERK activity in GR^{EKO} epidermis. Immunostaining shows p-ERK in WT and GR^{EKO} suprabasal keratinocytes (arrowheads) and in basal keratinocytes (arrows) of GR^{EKO} epidermis (n=8). Bar: 100 μ m (large panels), 65 μ m (insets). (b) Immunoblotting (left) and quantitation (right) demonstrates increased p-STAT3/STAT-3 and p-AKT/AKT ratios as well as elevated S100A9 levels in GR^{EKO} newborn epidermis (n=12). Actin was used as a loading control. Mean values \pm SD are shown. Asterisks denote statistically significant differences among genotypes, as determined by Student's *t* test (*, $p < 0.05$).

Figure 5. Exacerbated inflammatory responses to epidermal challenge of GR^{EKO} adult mice.

(a) H&E stained skin sections of control (vehicle) and Dex treated GR^{EKO} and WT adult mice (n=8). Bar: 50 μ m. (b) Quantitation of BrdU-positive keratinocytes in (a) (n=8). Mean values \pm SD; Student's *t* test; *, $p < 0.05$. (c) H&E stained skin sections showing exaggerated stress response in GR^{EKO} adult mice upon topical SDS and acute PMA treatment. (n=18). Asterisks: intraepithelial inflammatory infiltrates. Bar: 100 μ m (upper); 60 μ m (lower). (d) Immunostaining of skin sections in (c) using K6 and p-ERK antibodies. Bars: 100 μ m. (e) Immunostaining of skin sections (untreated and SDS-treated) using STAT3. Bar: 100 μ m. (e')

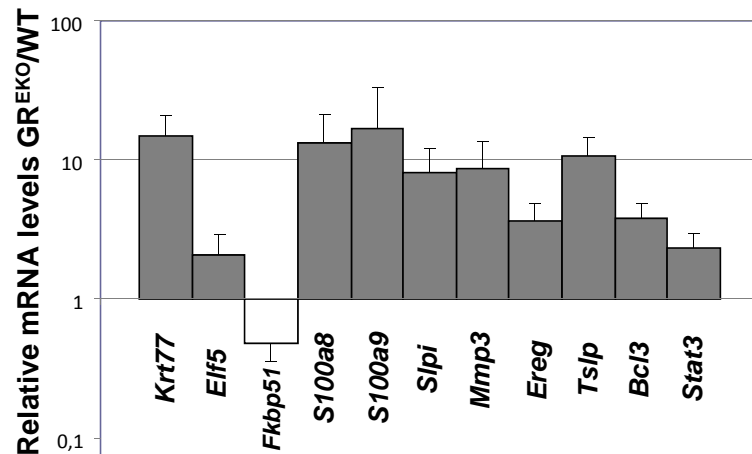
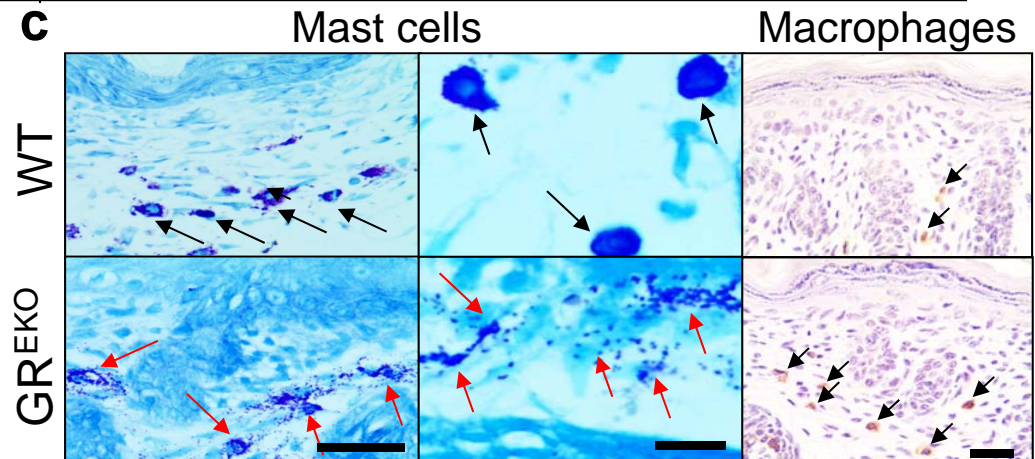
Immunoblotting of skin sections in (e) using STAT3 and p-STAT3 antibodies. Actin, loading control.

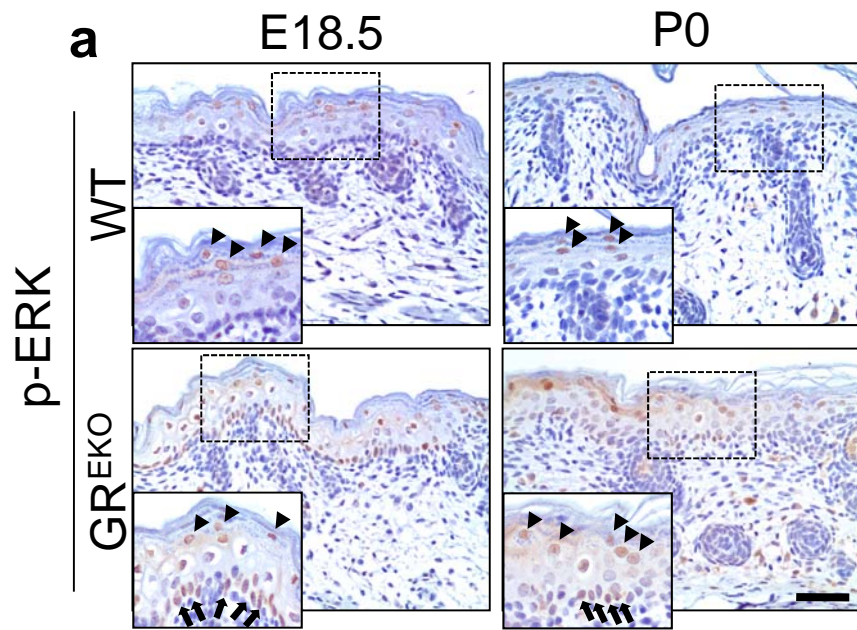




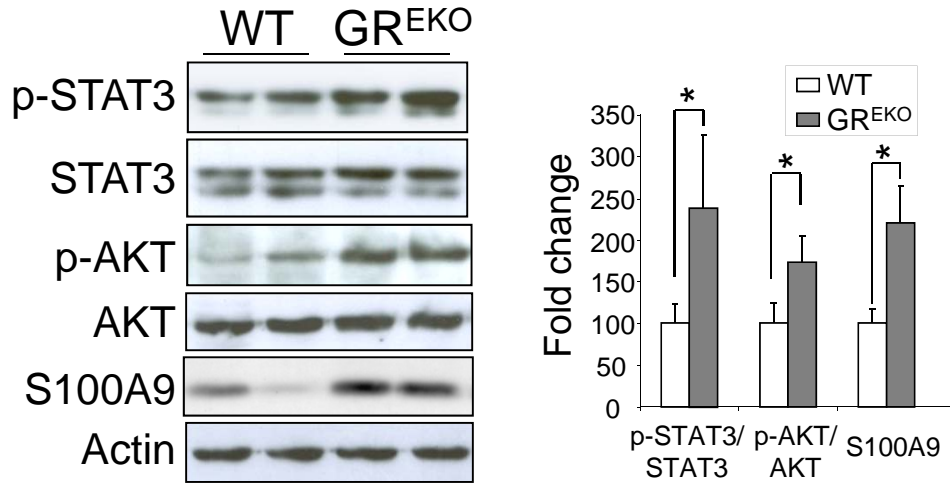
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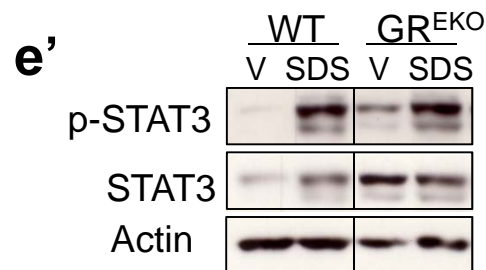
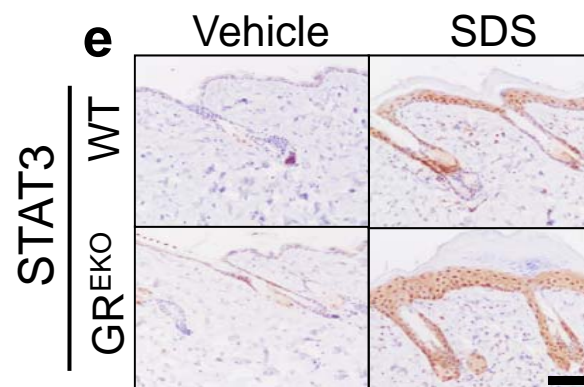
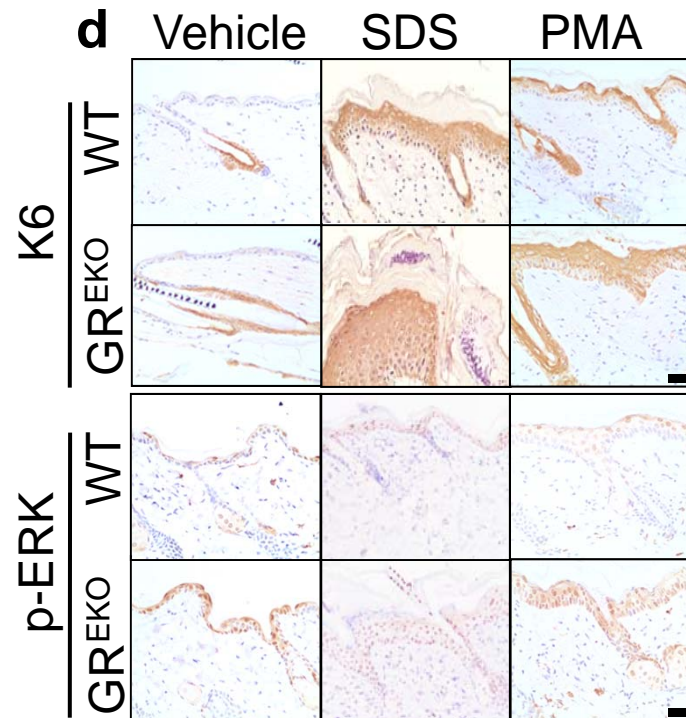
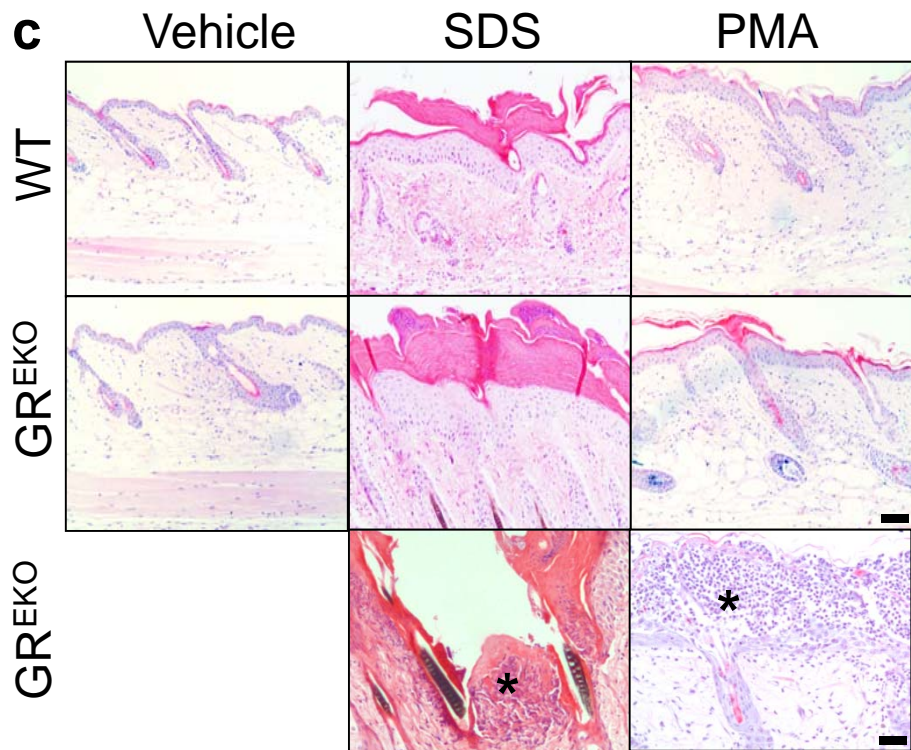
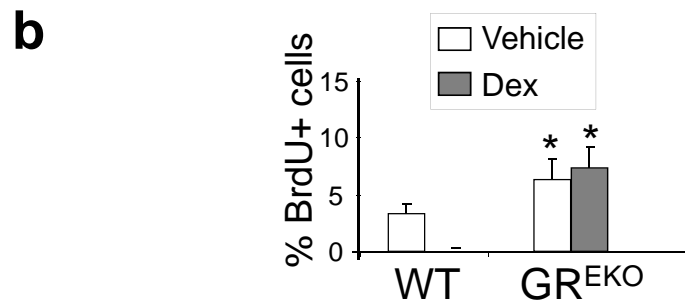
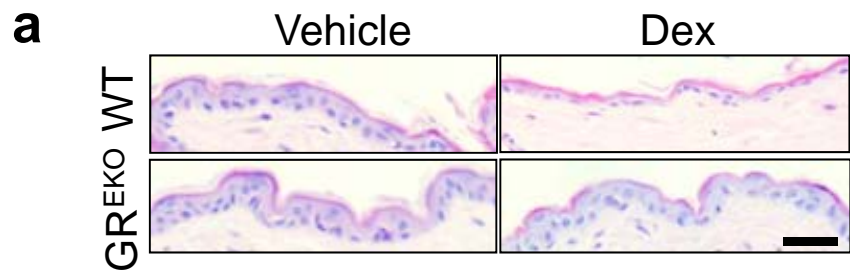
<u>Gene symbol</u>	<u>Gene description</u>	<u>Fold-change</u>	<u>Gene symbol</u>	<u>Gene description</u>	<u>Fold-change</u>
Keratinocyte proliferation/differentiation			Peptidase and peptidase inhibitor activity		
<i>Krt6a</i>	keratin 6A	13	<i>Slpi</i>	secretory leukocyte peptidase inhibitor	3.5
<i>Krt6b</i>	keratin 6B	8	<i>Mmp3</i>	matrix metallopeptidase 3	2.8
<i>Krt16</i>	keratin 16	5.9	<i>Klk6</i>	kallikrein related-peptidase 6	2.9
<i>Krt77</i>	keratin 77	5.2	<i>Klk12</i>	kallikrein related-peptidase 12	2.1
<i>Sprr2e</i>	small proline-rich protein 2E	7.4	<i>Klk9</i>	kallikrein related-peptidase 9	2.0
<i>Sprr2f</i>	small proline-rich protein 2F	6.6	<i>Klk10</i>	kallikrein related-peptidase 10	1.9
<i>Sprr2h</i>	small proline-rich protein 2H	5	<i>Adam8</i>	a disintegrin and metallopeptidase domain 8	1.8
<i>Sprr2b</i>	small proline-rich protein 2B	3.7	<i>Serpina3h</i>	serine peptidase inhibitor, clade A, member 3H	0.5
<i>Sprr2d</i>	small proline-rich protein 2E	3.1	<i>Serpina3c</i>	serine peptidase inhibitor, clade B, member 3C	0.3
<i>Sprr2i</i>	small proline-rich protein 2I	2.6	Immune response		
<i>Sprr1b</i>	small proline-rich protein 1B	2.4	<i>Ifi202b</i>	interferon activated gene 202A	4.7
<i>Sprr1a</i>	small proline-rich protein 1A	2.2	<i>Cxcr2</i>	chemokine (C-X-C motif receptor)	3.7
<i>Sprr3</i>	small proline-rich protein 3	2.2	<i>Psors1c2</i>	psoriasis susceptibility 1 candidate 2	3.3
<i>Sprr2k</i>	small proline-rich protein 2K	1.6	<i>Bcl3</i>	B-cell leukemia 3	3.3
<i>Lce3a</i>	late cornified envelope 3A	8.4	<i>Ereg</i>	epiregulin	2.9
<i>Lce3f</i>	late cornified envelope 3F	6.7	<i>Tslp</i>	thymic stromal lymphopoietin	2.6
<i>Lce3c</i>	late cornified envelope 3C	2.6	<i>Il33</i>	interleukin 33	2.6
<i>S100a9</i>	S100 calcium binding protein A9	3.6	<i>Tnc</i>	tenascin C	2.5
<i>S100a8</i>	S100 calcium binding protein A8	2.1	<i>Cxcl16</i>	chemokine (C-X-C motif) ligand 16	1.8
<i>Rptn</i>	repetin	5.7	<i>Stat3</i>	signal transducer and activator of transcription 3	1.3
<i>Elf5</i>	E74-like factor 5	3.4	<i>Defb1</i>	defensin beta 1	0.6
<i>Pglyrp3</i>	peptidoglycan recognition protein 3	2.6			

b**c**



b





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FIG S1

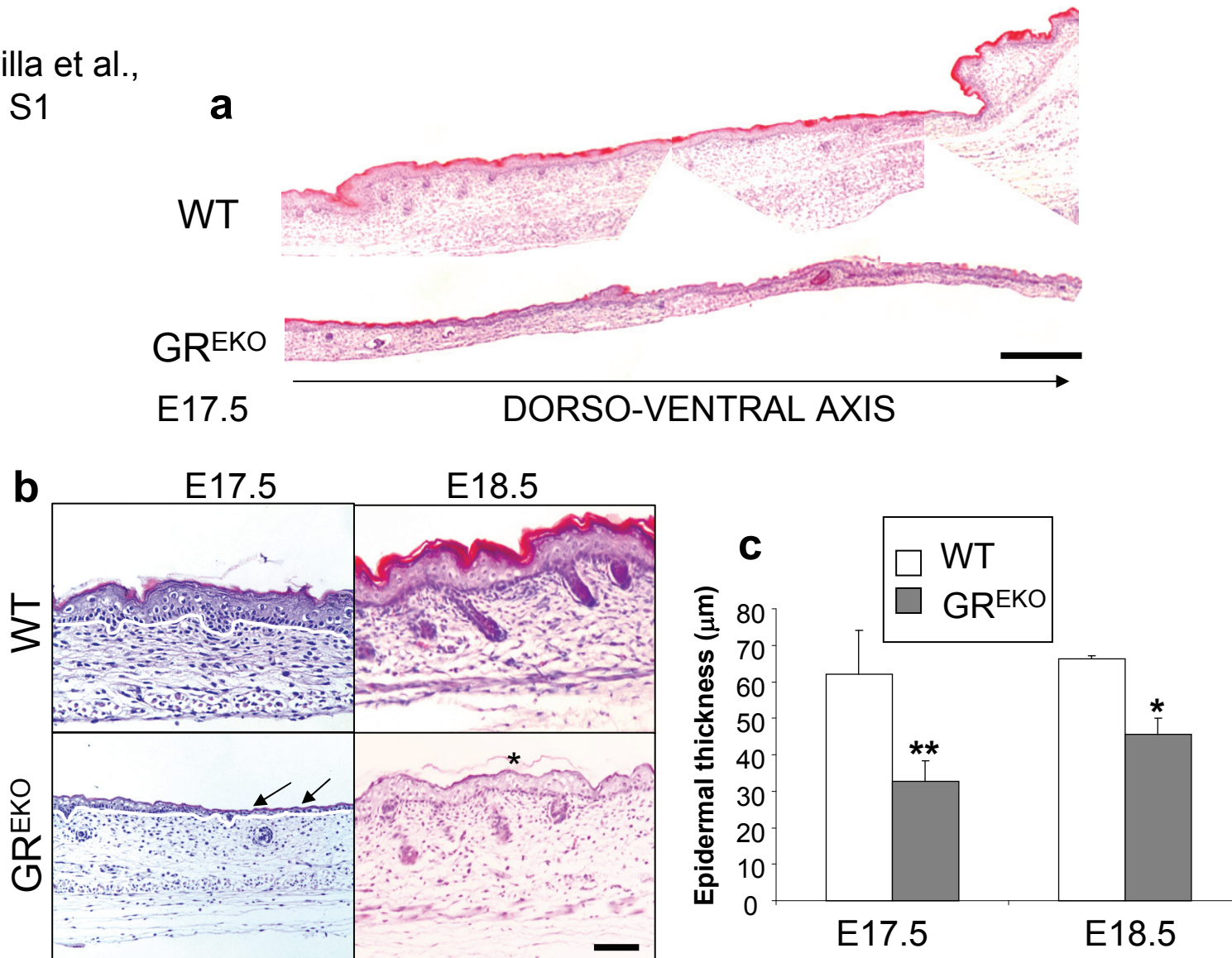


Figure S1. Altered epidermal development of GR^{EKO} mice.

(a) The epidermis of GR^{EKO} E17.5 embryos was much thinner along the dorso-ventral axis as compared to WT. Bar: 200 μm . (b) GR^{EKO} E17.5 skin featured immature thin skin with impaired formation of suprabasal differentiated layers. In certain areas, GR^{EKO} epidermis consisted of only few layers (arrows). GR^{EKO} E18.5 epidermis was more immature relative to WT littermates with areas of SC fragility (asterisk). Bar: 100 μm . (c) Epidermal thickness quantitation showed statistically significant differences (Student's t test; *, $p < 0.05$; **, $p < 0.005$).

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FIG S2

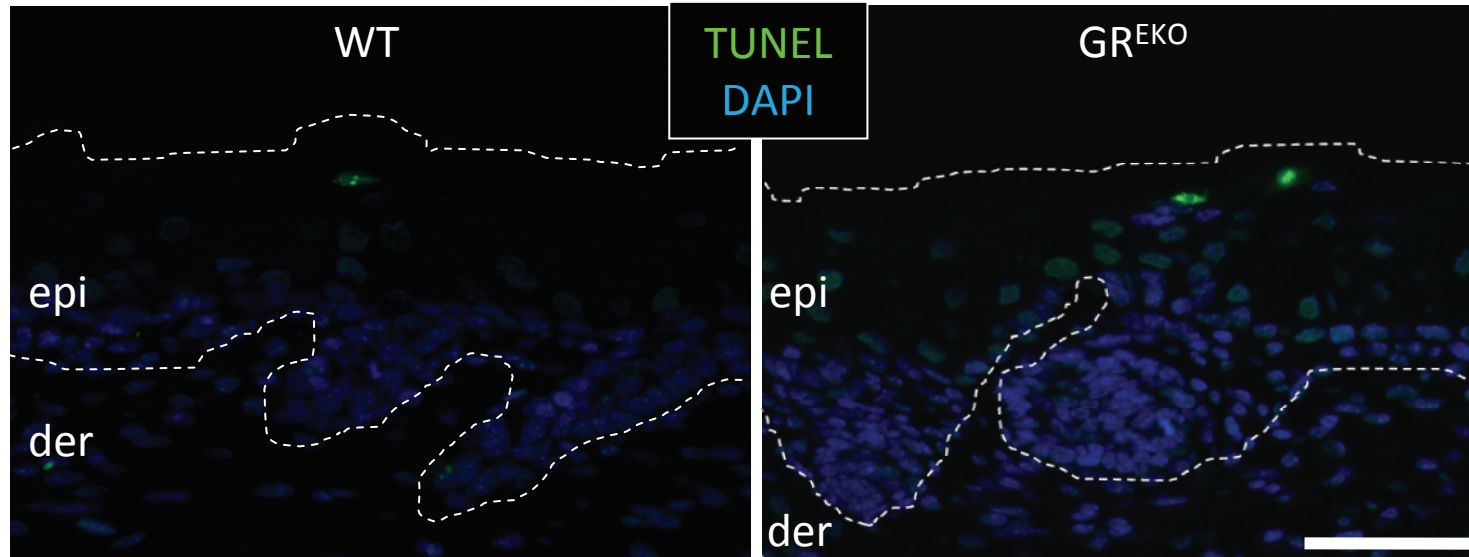


Figure S2. Apoptosis in GR^{EKO} epidermis.

TUNEL staining was performed in paraffin-embedded skin sections from GR^{EKO} and WT P0 mice. Dashed lines delineate the basement membrane. More apoptotic suprabasal keratinocytes (arrows) were found in GR^{EKO} relative to WT epidermis. Bar: 50 μ m.

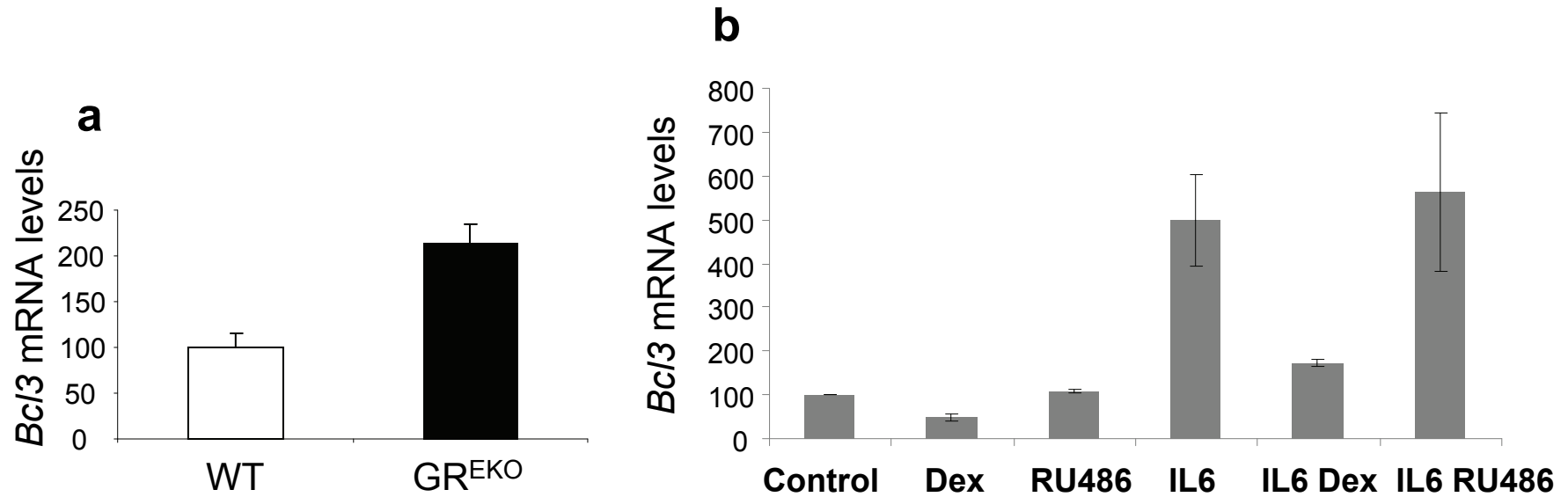


Fig. S3. GR-mediated regulation of *Bcl3* expression.

(a) Relative mRNA levels were assessed in primary keratinocytes isolated from newborn GRE^{EKO} and WT mice by RT-QPCR. (b) Effect of Dex and RU486 on basal and IL6-induced expression of *Bcl3*. Following overnight incubation in media supplemented with 1% charcoal-stripped serum, keratinocytes were treated with either vehicle, Dex (5h), RU486 (5h) and IL6 (ng/ml, 4h), or pre-treated with Dex or RU486 for 1h before addition of IL6 and further incubation (4h). Relative *Bcl3* mRNA levels were determined by RT-QPCR.

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FIG S4

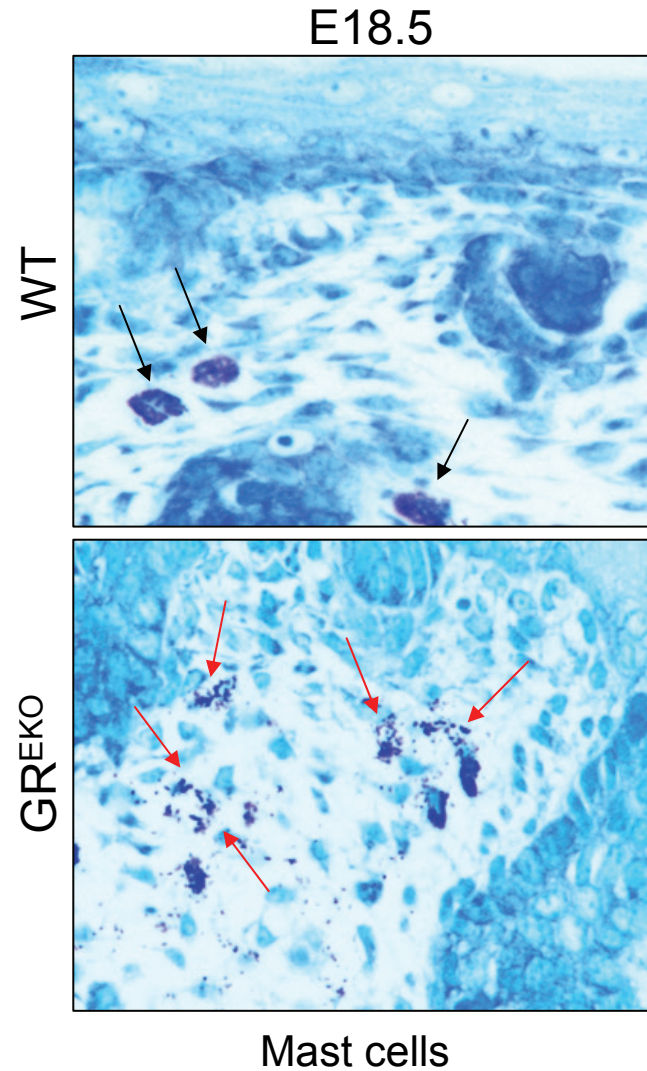


Figure S4. Increased mast cell degranulation in GR^{EKO} developing skin.

Mast cells were visualized by toluidine blue staining in GR^{EKO} and WT E18.5 embryos.

Black arrows: normal mast cells in WT dermis. Red arrows: Degranulated mast cells in GR^{EKO} upper dermis.

Bar: 100 μ m.

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FIG S5

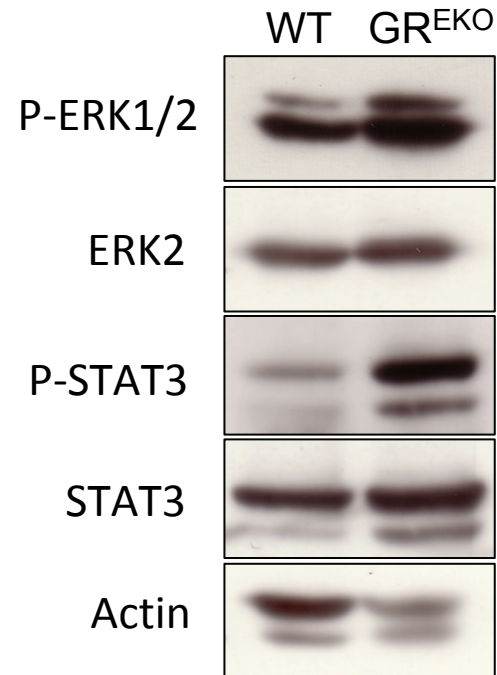


Fig. S5. Altered signaling in GR^{EKO} cultured keratinocytes. Immunoblotting demonstrates increased p-ERK1/2/ERK2 (1.35) and p-STAT3/STAT-3 (2.45) in GR^{EKO} relative to WT keratinocytes. Actin was used as a loading control.

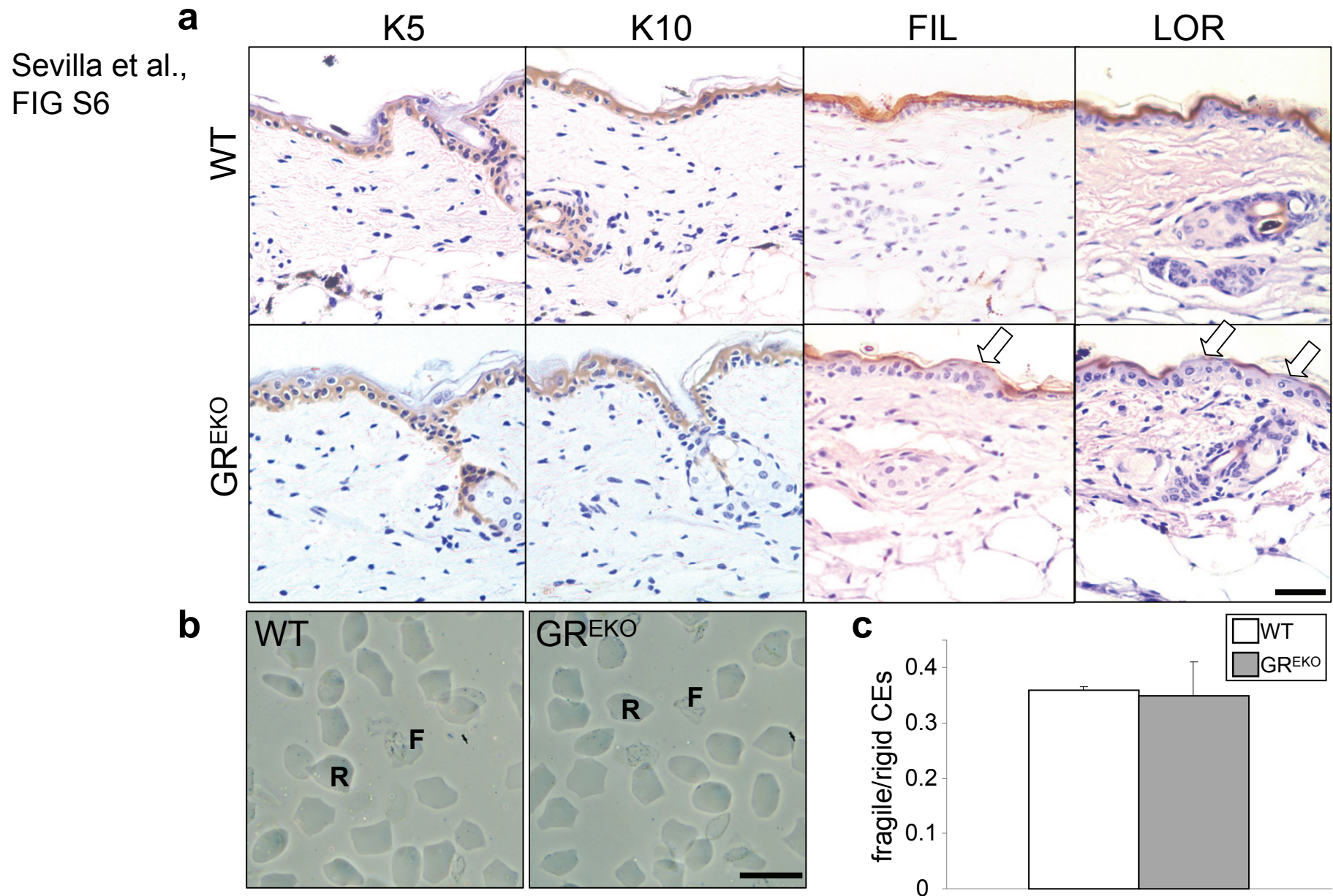


Figure S6. Skin phenotype of adult GR^{EKO} mice.

(a) Immunostaining of GR^{EKO} and WT adult skin sections shows patches of epidermis negative (white arrows) for filaggrin (FIL) and loricrin (LOR). Bar: 50 mm. (b-c) Isolated CEs from adult GR^{EKO} and WT adult mice had similar morphology (b) and fragile (F)/rigid (R) ratios (c). Bar: 60 μ m.

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FIG S7

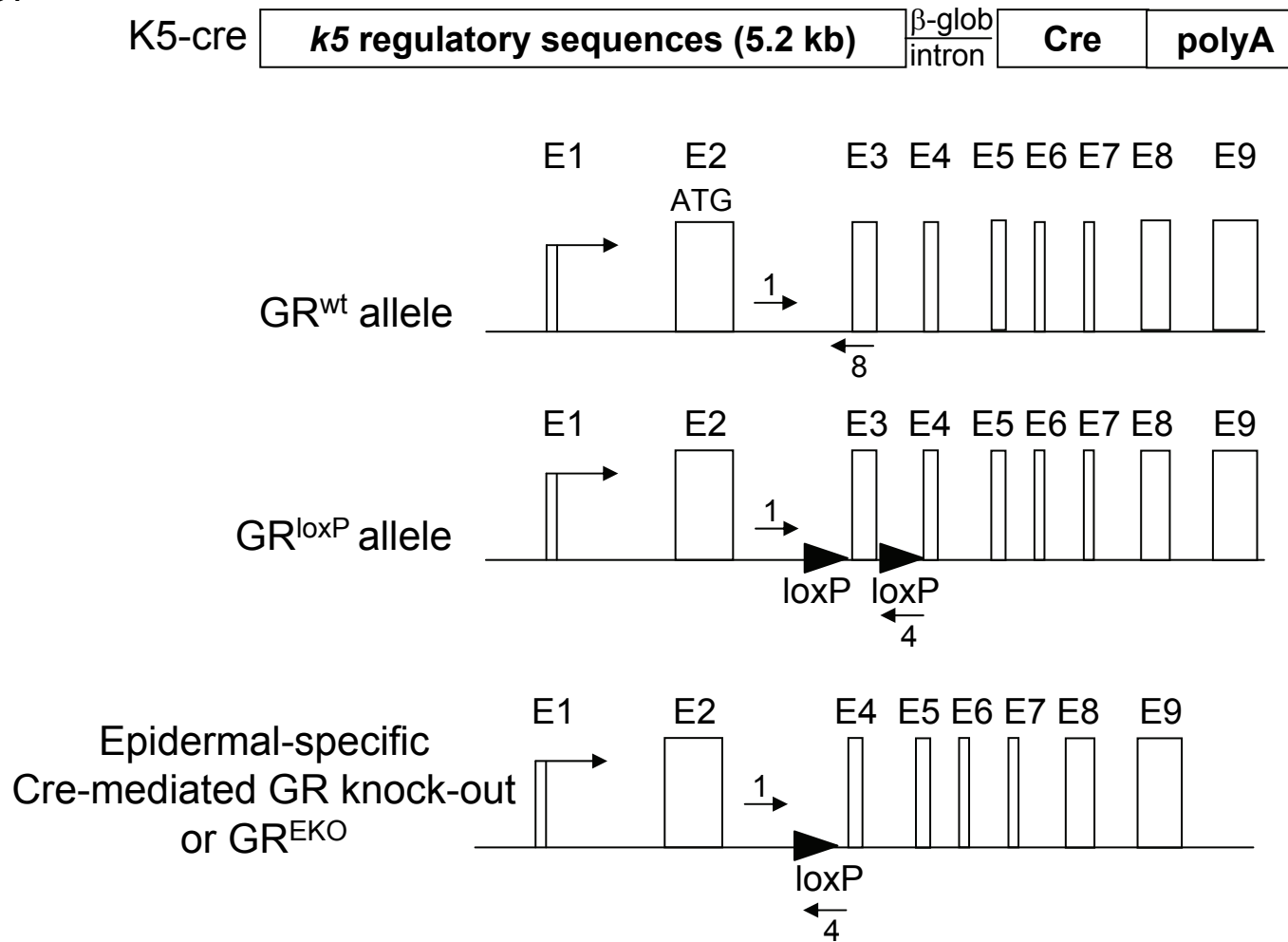


Fig. S7. Scheme depicting generation of GR^{EKO} mice.

The K5-Cre transgene contains the bovine *k5* regulatory sequences (5.2 Kb), the rabbit b-globin intron, Cre, and the SV40 polyadenylation (polyA) signal. The GR^{loxP} allele was generated by introducing two loxP sequences in the second and third introns. In the double transgenic K5-cre//GR^{loxP/loxP} or GR^{EKO}, the recombinase under the control of the K5 promoter deletes the DNA fragment flanked by the loxP sites, rendering an epidermal-specific GR knock-out.

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Up-regulated genes ordered by Fold-change using >1.5 as cutoff

n°	probeset ID	d.value	p.value	q.value	Fold-change	GeneName	Description
14	ENSMUSG00000068320	10,85376	0,00004	0,03733	13,34564	Gm5416	predicted gene 5416 Gene [Source:MGI Symbol;Acc:MGI:3644688]
97	ENSMUSG00000058354	7,51302	0,00030	0,04208	13,01036	Krt6a	keratin 6A Gene [Source:MGI Symbol;Acc:MGI:1100845]
16	ENSMUSG00000027925	10,63428	0,00005	0,03733	8,98522	Sprr2j-ps	small proline-rich protein 2J, pseudogene Pseudogene [Source:MGI Symbol;Acc:MGI:1330345]
110	ENSMUSG00000054325	7,30939	0,00034	0,04208	8,44190	Lce3a	late cornified envelope 3A Gene [Source:MGI Symbol;Acc:MGI:3645650]
853	ENSMUSG00000023041	4,78948	0,00309	0,05065	8,09935	Krt6b	keratin 6B Gene [Source:MGI Symbol;Acc:MGI:1333768]
6	ENSMUSG00000055030	12,24764	0,00002	0,03733	7,38470	Sprr2e	small proline-rich protein 2E Gene [Source:MGI Symbol;Acc:MGI:1330346]
238	ENSMUSG00000068885	6,41558	0,00072	0,04261	6,66251	Lce3f	late cornified envelope 3F Gene [Source:MGI Symbol;Acc:MGI:1916770]
30	ENSMUSG00000050635	9,58083	0,00008	0,03757	6,58943	Sprr2f	small proline-rich protein 2F Gene [Source:MGI Symbol;Acc:MGI:1330349]
25	ENSMUSG00000053797	9,99949	0,00007	0,03755	5,88578	Krt16	keratin 16 Gene [Source:MGI Symbol;Acc:MGI:96690]
177	ENSMUSG00000067594	6,76805	0,00055	0,04208	5,23371	Krt77	keratin 77 Gene [Source:MGI Symbol;Acc:MGI:3588209]
268	ENSMUSG00000041984	6,22400	0,00083	0,04282	5,15223	Rptn	repetin Gene [Source:MGI Symbol;Acc:MGI:1099055]
11	ENSMUSG00000046203	11,61401	0,00003	0,03733	5,10233	AC129296.1	
70	ENSMUSG00000046259	8,16140	0,00019	0,03766	4,97320	Sprr2h	small proline-rich protein 2H Gene [Source:MGI Symbol;Acc:MGI:1330343]
18	ENSMUSG00000074433	10,50667	0,00005	0,03733	4,75214	AC132274.1	
560	ENSMUSG00000026535	5,33715	0,00186	0,04671	4,74335	Ifi202b	interferon activated gene 202A Gene [Source:MGI Symbol;Acc:MGI:1347080]
1118	ENSMUSG00000050092	4,43544	0,00436	0,05482	3,71390	Sprr2b	small proline-rich protein 2B Gene [Source:MGI Symbol;Acc:MGI:1330352]
170	ENSMUSG00000026180	6,79478	0,00054	0,04208	3,68438	Cxcr2	chemokine (C-X-C motif) receptor 2 Gene [Source:MGI Symbol;Acc:MGI:105303]
15	ENSMUSG00000027068	10,80476	0,00004	0,03733	3,67862	Dhrs9	dehydrogenase/reductase (SDR family) member 9 Gene [Source:MGI Symbol;Acc:MGI:2442798]
202	ENSMUSG00000056071	6,65409	0,00061	0,04208	3,60274	S100a9	S100 calcium binding protein A9 (calgranulin B) Gene [Source:MGI Symbol;Acc:MGI:1338947]
305	ENSMUSG00000017002	6,08164	0,00095	0,04282	3,48303	Slpi	secretory leukocyte peptidase inhibitor Gene [Source:MGI Symbol;Acc:MGI:109297]
48	ENSMUSG00000029762	8,72161	0,00014	0,03757	3,46662	Akr1b8	aldo-keto reductase family 1, member B8 Gene [Source:MGI Symbol;Acc:MGI:107673]
188	ENSMUSG00000044294	6,71944	0,00058	0,04208	3,42013	Krt84	keratin 84 Gene [Source:MGI Symbol;Acc:MGI:96700]
32	ENSMUSG00000027186	9,55866	0,00009	0,03757	3,38902	Elf5	E74-like factor 5 Gene [Source:MGI Symbol;Acc:MGI:1335079]
183	ENSMUSG00000024409	6,74567	0,00057	0,04208	3,35155	Psors1c2	psoriasis susceptibility 1 candidate 2 (human) Gene [Source:MGI Symbol;Acc:MGI:1930025]
543	ENSMUSG00000053175	5,37036	0,00179	0,04635	3,28272	Bcl3	B-cell leukemia/lymphoma 3 Gene [Source:MGI Symbol;Acc:MGI:88140]
277	ENSMUSG00000078373	6,20158	0,00086	0,04282	3,11723	2010109K11Rik	RIKEN cDNA 2010109K11 gene Gene [Source:MGI Symbol;Acc:MGI:1919373]
19	ENSMUSG00000042212	10,41697	0,00006	0,03733	3,10809	Sprr2d	small proline-rich protein 2D Gene [Source:MGI Symbol;Acc:MGI:1330347]
894	ENSMUSG00000053846	4,73596	0,00325	0,05114	3,00974	Lipg	lipase, endothelial Gene [Source:MGI Symbol;Acc:MGI:1341803]
181	ENSMUSG00000023885	6,75285	0,00056	0,04208	2,94271	Thbs2	thrombospondin 2 Gene [Source:MGI Symbol;Acc:MGI:98738]
94	ENSMUSG00000029377	7,56179	0,00029	0,04208	2,92150	Ereg	epiregulin Gene [Source:MGI Symbol;Acc:MGI:107508]
414	ENSMUSG00000050063	5,71472	0,00130	0,04394	2,90308	Klk6	kallikrein related-peptidase 6 Gene [Source:MGI Symbol;Acc:MGI:1343166]
335	ENSMUSG00000028479	5,99259	0,00103	0,04326	2,89279	Gne	glucosamine Gene [Source:MGI Symbol;Acc:MGI:1354951]
359	ENSMUSG00000050211	5,87563	0,00114	0,04394	2,87244	Pla2g4e	phospholipase A2, group IVE Gene [Source:MGI Symbol;Acc:MGI:1919144]
117	ENSMUSG00000005667	7,24745	0,00036	0,04208	2,84596	Mthfd2	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methylenetetrahydrofolate cyclohydrolase Gene [Source:MGI Symbol;Acc:MGI:1338850]
91	ENSMUSG00000001473	7,61808	0,00027	0,04199	2,82666	Tubb6	tubulin, beta 6 Gene [Source:MGI Symbol;Acc:MGI:1915201]
300	ENSMUSG00000052353	6,11139	0,00093	0,04282	2,79079	9930013L23Rik	RIKEN cDNA 9930013L23 gene Gene [Source:MGI Symbol;Acc:MGI:2443629]
1106	ENSMUSG00000043613	4,45212	0,00429	0,05461	2,77486	Mmp3	matrix metalloproteinase 3 Gene [Source:MGI Symbol;Acc:MGI:97010]
229	ENSMUSG00000025279	6,46491	0,00070	0,04261	2,75314	Dnase1l3	deoxyribonuclease 1-like 3 Gene [Source:MGI Symbol;Acc:MGI:1314633]
184	ENSMUSG00000036585	6,74398	0,00057	0,04208	2,71379	Fgf1	fibroblast growth factor 1 Gene [Source:MGI Symbol;Acc:MGI:95515]
514	ENSMUSG00000056515	5,43805	0,00166	0,04551	2,70993	Rab31	RAB31, member RAS oncogene family Gene [Source:MGI Symbol;Acc:MGI:1914603]
1239	ENSMUSG00000062991	4,29783	0,00503	0,05708	2,69009	Nrg1	neuregulin 1 Gene [Source:MGI Symbol;Acc:MGI:96083]
56	ENSMUSG00000075582	8,55402	0,00015	0,03757	2,68754	AC119952.1	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3UNM0]
174	ENSMUSG00000022598	6,78811	0,00054	0,04208	2,63344	Pzca	prostate stem cell antigen Gene [Source:MGI Symbol;Acc:MGI:1919623]
760	ENSMUSG00000022665	4,92795	0,00271	0,05019	2,62133	Ccd80	coiled-coil domain containing 80 Gene [Source:MGI Symbol;Acc:MGI:1915146]
205	ENSMUSG00000042157	6,64246	0,00062	0,04208	2,59607	Sprr2i	small proline-rich protein 2E Gene [Source:MGI Symbol;Acc:MGI:1330346]
40	ENSMUSG00000045475	9,14962	0,00011	0,03757	2,59267	Lce3c	late cornified envelope 3C Gene [Source:MGI Symbol;Acc:MGI:2135932]
65	ENSMUSG00000042244	8,27726	0,00018	0,03766	2,58979	Pglyrp3	peptidoglycan recognition protein 3 Gene [Source:MGI Symbol;Acc:MGI:2685266]
341	ENSMUSG00000024810	5,95271	0,00107	0,04394	2,57445	Il33	interleukin 33 Gene [Source:MGI Symbol;Acc:MGI:1924375]
22	ENSMUSG00000037613	10,27208	0,00006	0,03733	2,57206	Tnfrsf23	tumor necrosis factor receptor superfamily, member 23 Gene [Source:MGI Symbol;Acc:MGI:1930269]

n°	probeset ID	d.value	p.value	q.value	Fold-change	Genename	Description
605	ENSMUSG00000024379	5,23525	0,00204	0,04731	2,56484	Tslp	thymic stromal lymphopoietin Gene [Source:MGI Symbol;Acc:MGI:1855696]
1100	ENSMUSG00000032068	4,46428	0,00424	0,05422	2,55456	1600029D21Rik	RIKEN cDNA 1600029D21 gene Gene [Source:MGI Symbol;Acc:MGI:1923759]
432	ENSMUSG00000083500	5,65277	0,00136	0,04420	2,53424	AC162792.1	
288	ENSMUSG00000028364	6,14554	0,00090	0,04282	2,52900	Tnc	tenascin C Gene [Source:MGI Symbol;Acc:MGI:101922]
291	ENSMUSG00000005125	6,14045	0,00091	0,04282	2,52019	Ndrp1	N-myc downstream regulated gene 1 Gene [Source:MGI Symbol;Acc:MGI:1341799]
147	ENSMUSG00000079594	6,97662	0,00046	0,04208	2,50819	BC117090	stefin A1-like protein [Source:RefSeq peptide;Acc:NP_001001332]
759	ENSMUSG00000027737	4,92978	0,00271	0,05019	2,50646	Slc7a11	solute carrier family 7 (cationic amino acid transporter, y+ system), member 11 Gene [Source:MGI Symbol;Acc:MGI:1347355]
314	ENSMUSG00000079434	6,06957	0,00096	0,04282	2,48096	Neu2	neuraminidase 2 Gene [Source:MGI Symbol;Acc:MGI:1344417]
255	ENSMUSG00000026509	6,29658	0,00079	0,04282	2,43978	Capn2	calpain 2 Gene [Source:MGI Symbol;Acc:MGI:88264]
160	ENSMUSG00000029449	6,85259	0,00051	0,04208	2,40487	Rhof	ras homolog gene family, member f Gene [Source:MGI Symbol;Acc:MGI:1345629]
151	ENSMUSG00000025059	6,91392	0,00049	0,04208	2,39301	Gyk	glycerol kinase Gene [Source:MGI Symbol;Acc:MGI:106594]
224	ENSMUSG00000048455	6,49952	0,00068	0,04261	2,36589	Sprp1b	small proline-rich protein 1B Gene [Source:MGI Symbol;Acc:MGI:106659]
491	ENSMUSG00000064232	5,50144	0,00157	0,04479	2,32970	Gm5414	predicted gene 5414 Gene [Source:MGI Symbol;Acc:MGI:3646939]
121	ENSMUSG00000058672	7,21742	0,00038	0,04208	2,31201	Tubb2a	tubulin, beta 2A Gene [Source:MGI Symbol;Acc:MGI:107861]
233	ENSMUSG00000020062	6,44752	0,00071	0,04261	2,30122	Slc5a8	solute carrier family 5 (iodide transporter), member 8 Gene [Source:MGI Symbol;Acc:MGI:2384916]
126	ENSMUSG00000040055	7,17387	0,00039	0,04208	2,25680	Gjb6	gap junction protein, beta 6 Gene [Source:MGI Symbol;Acc:MGI:107588]
222	ENSMUSG00000042268	6,51521	0,00067	0,04261	2,23932	Slc26a9	solute carrier family 26, member 9 Gene [Source:MGI Symbol;Acc:MGI:2444594]
42	ENSMUSG00000050359	9,12689	0,00012	0,03757	2,21438	Sprp1a	small proline-rich protein 1A Gene [Source:MGI Symbol;Acc:MGI:106660]
352	ENSMUSG00000045539	5,89475	0,00112	0,04394	2,18970	Sprp3	small proline-rich protein 3 Gene [Source:MGI Symbol;Acc:MGI:1330237]
187	ENSMUSG00000024030	6,72414	0,00058	0,04208	2,18914	Abcg1	ATP-binding cassette, sub-family G (WHITE), member 1 Gene [Source:MGI Symbol;Acc:MGI:107704]
649	ENSMUSG00000044430	5,13882	0,00221	0,04793	2,14606	Klk12	kallikrein related-peptidase 12 Gene [Source:MGI Symbol;Acc:MGI:1916761]
655	ENSMUSG00000028464	5,12758	0,00223	0,04793	2,14521	Tpm2	tropomyosin 2, beta Gene [Source:MGI Symbol;Acc:MGI:98810]
161	ENSMUSG00000046352	6,85240	0,00051	0,04208	2,13102	Gjb2	gap junction protein, beta 2 Gene [Source:MGI Symbol;Acc:MGI:95720]
1115	ENSMUSG00000056054	4,43714	0,00435	0,05482	2,12704	S100a8	S100 calcium binding protein A8 (calgranulin A) Gene [Source:MGI Symbol;Acc:MGI:88244]
547	ENSMUSG00000023087	5,36105	0,00180	0,04638	2,11506	Ccrn4l	CCR4 carbon catabolite repression 4-like (S. cerevisiae) Gene [Source:MGI Symbol;Acc:MGI:109382]
78	ENSMUSG00000025278	8,04887	0,00021	0,03766	2,11094	Flnb	filamin, beta Gene [Source:MGI Symbol;Acc:MGI:2446089]
34	ENSMUSG00000045136	9,42292	0,00009	0,03757	2,10601	Tubb2b	tubulin, beta 2B Gene [Source:MGI Symbol;Acc:MGI:1920960]
498	ENSMUSG00000061126	5,48642	0,00159	0,04494	2,09641	Cyp4f39	cytochrome P450, family 4, subfamily f, polypeptide 39 Gene [Source:MGI Symbol;Acc:MGI:2445210]
105	ENSMUSG00000029161	7,39332	0,00033	0,04208	2,08800	Cgref1	cell growth regulator with EF hand domain 1 Gene [Source:MGI Symbol;Acc:MGI:1915817]
665	ENSMUSG00000012350	5,09792	0,00228	0,04819	2,07018	Ehf	ets homologous factor Gene [Source:MGI Symbol;Acc:MGI:1270840]
1232	ENSMUSG00000080950	4,30270	0,00500	0,05706	2,06760	AC123613.1	
203	ENSMUSG00000028435	6,65229	0,00062	0,04208	2,04903	Aqp3	aquaporin 3 Gene [Source:MGI Symbol;Acc:MGI:1333777]
104	ENSMUSG00000047884	7,42378	0,00032	0,04208	2,01342	Klk9	kallikrein related-peptidase 9 Gene [Source:MGI Symbol;Acc:MGI:1921082]
469	ENSMUSG00000040511	5,56622	0,00148	0,04420	2,00922	Pvr	poliovirus receptor Gene [Source:MGI Symbol;Acc:MGI:107741]
88	ENSMUSG00000020227	7,78927	0,00025	0,03991	1,96221	Irak3	interleukin-1 receptor-associated kinase 3 Gene [Source:MGI Symbol;Acc:MGI:1921164]
493	ENSMUSG00000078532	5,49644	0,00157	0,04481	1,94542	Nkain1	Na+/K+ transporting ATPase interacting 1 Gene [Source:MGI Symbol;Acc:MGI:1914399]
344	ENSMUSG00000039813	5,93140	0,00108	0,04394	1,92416	Tbc1d2	TBC1 domain family, member 2 Gene [Source:MGI Symbol;Acc:MGI:2652885]
485	ENSMUSG00000011034	5,52032	0,00153	0,04439	1,92339	Slc5a1	solute carrier family 5 (sodium/glucose cotransporter), member 1 Gene [Source:MGI Symbol;Acc:MGI:107678]
306	ENSMUSG00000034751	6,07933	0,00095	0,04282	1,90584	Mast4	microtubule associated serine/threonine kinase family member 4 Gene [Source:MGI Symbol;Acc:MGI:1918885]
436	ENSMUSG00000033852	5,63115	0,00138	0,04420	1,90530	Pla2g4b	phospholipase A2, group IVB (cytosolic) Gene [Source:MGI Symbol;Acc:MGI:2384819]
73	ENSMUSG00000030693	8,14801	0,00020	0,03766	1,89850	Klk10	kallikrein related-peptidase 10 Gene [Source:MGI Symbol;Acc:MGI:1916790]
1235	ENSMUSG00000030666	4,30160	0,00501	0,05706	1,88139	Calcb	calcitonin-related polypeptide, beta Gene [Source:MGI Symbol;Acc:MGI:2151254]
323	ENSMUSG00000028811	6,03491	0,00099	0,04319	1,87372	Yars	tyrosyl-tRNA synthetase Gene [Source:MGI Symbol;Acc:MGI:2147627]
280	ENSMUSG00000037577	6,19640	0,00086	0,04282	1,86995	Ephx3	epoxide hydrolase 3 Gene [Source:MGI Symbol;Acc:MGI:1919182]
318	ENSMUSG00000022468	6,06337	0,00097	0,04282	1,85150	Pp1r	placental protein 11 related Gene [Source:MGI Symbol;Acc:MGI:97746]
1032	ENSMUSG00000028186	4,54369	0,00392	0,05340	1,85065	Uox	urate oxidase Gene [Source:MGI Symbol;Acc:MGI:98907]
221	ENSMUSG00000024812	6,51558	0,00067	0,04261	1,84327	Tjp2	tight junction protein 2 Gene [Source:MGI Symbol;Acc:MGI:1341872]
36	ENSMUSG00000005514	9,26394	0,00010	0,03757	1,83295	Por	P450 (cytochrome) oxidoreductase Gene [Source:MGI Symbol;Acc:MGI:97744]
297	ENSMUSG00000031960	6,11567	0,00092	0,04282	1,82966	Aars	alanyl-tRNA synthetase Gene [Source:MGI Symbol;Acc:MGI:2384560]
553	ENSMUSG00000011632	5,34088	0,00184	0,04671	1,82901	2310033E01Rik	RIKEN cDNA 2310033E01 gene Gene [Source:MGI Symbol;Acc:MGI:3615324]
235	ENSMUSG00000001794	6,42338	0,00072	0,04261	1,82508	Capns1	calpain, small subunit 1 Gene [Source:MGI Symbol;Acc:MGI:88266]
85	ENSMUSG00000025473	7,85706	0,00024	0,03941	1,82438	Adam8	a disintegrin and metalloproteinase domain 8 Gene [Source:MGI Symbol;Acc:MGI:107825]
458	ENSMUSG00000030513	5,59233	0,00144	0,04420	1,82284	Pcsk6	proprotein convertase subtilisin/kexin type 6 Gene [Source:MGI Symbol;Acc:MGI:102897]
173	ENSMUSG00000028430	6,79137	0,00054	0,04208	1,81944	Nol6	nucleolar protein family 6 (RNA-associated) Gene [Source:MGI Symbol;Acc:MGI:2140151]

n°	probeset ID	d.value	p.value	q.value	Fold-change	Genename	Description
67	ENSMUSG00000010830	8,24424	0,00019	0,03766	1,81904	Kdelr3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 Gene [Source:MGI Symbol;Acc:MGI:2145953]
576	ENSMUSG00000038264	5,30193	0,00192	0,04685	1,81749	Sema7a	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A Gene [Source:MGI Symbol;Acc:MGI:1306826]
263	ENSMUSG00000022221	6,25239	0,00082	0,04282	1,81442	Ripk3	receptor-interacting serine-threonine kinase 3 Gene [Source:MGI Symbol;Acc:MGI:2154952]
706	ENSMUSG00000018920	5,02947	0,00244	0,04869	1,81060	Cxcl16	chemokine (C-X-C motif) ligand 16 Gene [Source:MGI Symbol;Acc:MGI:1932682]
969	ENSMUSG00000027293	4,63123	0,00359	0,05217	1,81059	Ehd4	EH-domain containing 4 Gene [Source:MGI Symbol;Acc:MGI:1919619]
841	ENSMUSG00000024952	4,80260	0,00305	0,05065	1,80685	Rps6ka4	ribosomal protein S6 kinase, polypeptide 4 Gene [Source:MGI Symbol;Acc:MGI:1930076]
245	ENSMUSG00000037188	6,35385	0,00075	0,04282	1,78066	Grlh3	grainyhead-like 3 (Drosophila) Gene [Source:MGI Symbol;Acc:MGI:2655333]
388	ENSMUSG00000042195	5,78153	0,00123	0,04394	1,77323	Slc35f2	solute carrier family 35, member F2 Gene [Source:MGI Symbol;Acc:MGI:1919272]
1204	ENSMUSG00000032265	4,33813	0,00481	0,05620	1,76721	AC159809.2	family with sequence similarity 46, member A (Fam46a), transcript variant 2, mRNA [Source:RefSeq DNA;Acc:NM_001160379]
252	ENSMUSG00000035049	6,31932	0,00078	0,04282	1,76509	Rrp12	ribosomal RNA processing 12 homolog (S. cerevisiae) Gene [Source:MGI Symbol;Acc:MGI:2147437]
1061	ENSMUSG00000050762	4,50238	0,00408	0,05401	1,75707	Prss27	protease, serine 27 Gene [Source:MGI Symbol;Acc:MGI:2450123]
860	ENSMUSG00000014444	4,78372	0,00310	0,05065	1,74900	Fam38a	family with sequence similarity 38, member A Gene [Source:MGI Symbol;Acc:MGI:3603204]
600	ENSMUSG00000020075	5,23994	0,00202	0,04731	1,74112	Ddx21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21 Gene [Source:MGI Symbol;Acc:MGI:1860494]
226	ENSMUSG00000026558	6,47508	0,00069	0,04261	1,73342	Uck2	uridine-cytidine kinase 2 Gene [Source:MGI Symbol;Acc:MGI:1931744]
936	ENSMUSG00000023988	4,67939	0,00344	0,05163	1,72958	Bysl	bystin-like Gene [Source:MGI Symbol;Acc:MGI:1858419]
452	ENSMUSG00000020758	5,60421	0,00142	0,04420	1,71275	Itgb4	integrin beta 4 Gene [Source:MGI Symbol;Acc:MGI:96613]
247	ENSMUSG00000036432	6,34754	0,00076	0,04282	1,71127	Siah2	seven in absentia 2 Gene [Source:MGI Symbol;Acc:MGI:108062]
595	ENSMUSG00000060012	5,24945	0,00201	0,04731	1,71087	Kif13b	kinesin family member 13B Gene [Source:MGI Symbol;Acc:MGI:1098265]
437	ENSMUSG00000041313	5,63029	0,00138	0,04420	1,70609	Slc7a1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 Gene [Source:MGI Symbol;Acc:MGI:88117]
893	ENSMUSG00000028893	4,73661	0,00325	0,05114	1,70422	Sesn2	sestrin 2 Gene [Source:MGI Symbol;Acc:MGI:2651874]
627	ENSMUSG00000044813	5,18241	0,00212	0,04757	1,69872	Shb	src homology 2 domain-containing transforming protein B Gene [Source:MGI Symbol;Acc:MGI:98294]
698	ENSMUSG00000022565	5,04733	0,00241	0,04855	1,69796	Plec1	plectin 1 Gene [Source:MGI Symbol;Acc:MGI:1277961]
516	ENSMUSG00000004356	5,43415	0,00167	0,04551	1,69520	Utp20	UTP20, small subunit (SSU) processome component, homolog (yeast) Gene [Source:MGI Symbol;Acc:MGI:1917933]
1175	ENSMUSG00000041025	4,37112	0,00465	0,05559	1,69040	Iffo2	intermediate filament family orphan 2 Gene [Source:MGI Symbol;Acc:MGI:2140675]
1003	ENSMUSG00000032012	4,58222	0,00377	0,05292	1,68877	Pvr1l	poliovirus receptor-related 1 Gene [Source:MGI Symbol;Acc:MGI:1926483]
5	ENSMUSG00000050854	12,44372	0,00002	0,03733	1,67662	Tmem125	transmembrane protein 125 Gene [Source:MGI Symbol;Acc:MGI:1923409]
399	ENSMUSG00000026123	5,75647	0,00126	0,04394	1,67606	Pleckhb2	pleckstrin homology domain containing, family B (evectins) member 2 Gene [Source:MGI Symbol;Acc:MGI:2385825]
935	ENSMUSG00000054321	4,68130	0,00343	0,05163	1,66569	Taf4b	TAF4B RNA polymerase II, TATA box binding protein (TBP)-associated factor Gene [Source:MGI Symbol;Acc:MGI:2152345]
504	ENSMUSG00000051375	5,46225	0,00163	0,04538	1,66389	Pcdh1	protocadherin 1 Gene [Source:MGI Symbol;Acc:MGI:104692]
249	ENSMUSG00000036499	6,33274	0,00077	0,04282	1,66335	Eea1	early endosome antigen 1 Gene [Source:MGI Symbol;Acc:MGI:2442192]
550	ENSMUSG00000030137	5,34570	0,00183	0,04671	1,66276	Tuba8	tubulin, alpha 8 Gene [Source:MGI Symbol;Acc:MGI:1858225]
209	ENSMUSG00000026185	6,62148	0,00063	0,04208	1,66199	Igf1bp5	insulin-like growth factor binding protein 5 Gene [Source:MGI Symbol;Acc:MGI:96440]
761	ENSMUSG00000072812	4,92595	0,00271	0,05019	1,65936	Ahnak2	AHNAK nucleoprotein 2 Gene [Source:MGI Symbol;Acc:MGI:2144831]
137	ENSMUSG00000053819	7,09487	0,00042	0,04208	1,65433	Camk2d	calcium/calmodulin-dependent protein kinase II, delta Gene [Source:MGI Symbol;Acc:MGI:1341265]
175	ENSMUSG00000030835	6,78683	0,00054	0,04208	1,65065	Nomo1	nodal modulator 1 Gene [Source:MGI Symbol;Acc:MGI:2385850]
258	ENSMUSG00000057454	6,27297	0,00080	0,04282	1,64576	Lypd3	Ly6/Plaur domain containing 3 Gene [Source:MGI Symbol;Acc:MGI:1919684]
769	ENSMUSG00000038151	4,91088	0,00275	0,05022	1,64035	Prdm1	PR domain containing 1, with ZNF domain Gene [Source:MGI Symbol;Acc:MGI:99655]
165	ENSMUSG00000001435	6,81809	0,00053	0,04208	1,63589	Col18a1	collagen, type XVIII, alpha 1 Gene [Source:MGI Symbol;Acc:MGI:88451]
687	ENSMUSG00000054215	5,06190	0,00236	0,04839	1,63315	Sprr2k	small proline-rich protein 2K Gene [Source:MGI Symbol;Acc:MGI:1330344]
1089	ENSMUSG00000000320	4,47006	0,00421	0,05422	1,63111	Alox12	arachidonate 12-lipoxygenase Gene [Source:MGI Symbol;Acc:MGI:87998]
478	ENSMUSG00000029752	5,54004	0,00150	0,04420	1,63106	Asns	asparagine synthetase Gene [Source:MGI Symbol;Acc:MGI:1350929]
443	ENSMUSG00000019849	5,61993	0,00140	0,04420	1,62352	Prep	prolyl endopeptidase Gene [Source:MGI Symbol;Acc:MGI:1270863]
699	ENSMUSG00000034485	5,04547	0,00241	0,04855	1,62096	Uaca	uveal autoantigen with coiled-coil domains and ankyrin repeats Gene [Source:MGI Symbol;Acc:MGI:1919815]
865	ENSMUSG00000055491	4,77724	0,00312	0,05065	1,61936	Pprc1	peroxisome proliferative activated receptor, gamma, coactivator-related 1 Gene [Source:MGI Symbol;Acc:MGI:2385096]
824	ENSMUSG00000025081	4,82740	0,00298	0,05065	1,61545	Tdrd1	tudor domain containing 1 Gene [Source:MGI Symbol;Acc:MGI:1933218]
551	ENSMUSG00000029581	5,34416	0,00184	0,04671	1,61212	Fscn1	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus) Gene [Source:MGI Symbol;Acc:MGI:1352745]
427	ENSMUSG00000026773	5,67136	0,00134	0,04399	1,61177	Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3 Gene [Source:MGI Symbol;Acc:MGI:2181202]
9	ENSMUSG00000066441	11,80247	0,00003	0,03733	1,60431	Rdh11	retinol dehydrogenase 11 Gene [Source:MGI Symbol;Acc:MGI:102581]
386	ENSMUSG00000042993	5,78720	0,00123	0,04394	1,60170	Ifnk	interferon kappa Gene [Source:MGI Symbol;Acc:MGI:2683287]
95	ENSMUSG00000025277	7,56144	0,00029	0,04208	1,60059	Abhd6	abhydrolase domain containing 6 Gene [Source:MGI Symbol;Acc:MGI:1913332]
131	ENSMUSG00000005481	7,13732	0,00041	0,04208	1,59399	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39 Gene [Source:MGI Symbol;Acc:MGI:1915528]
463	ENSMUSG00000034112	5,58156	0,00146	0,04420	1,59256	Atp2c2	ATPase, Ca++ transporting, type 2C, member 2 Gene [Source:MGI Symbol;Acc:MGI:1916297]
163	ENSMUSG00000002319	6,83457	0,00052	0,04208	1,59111	Ipo4	importin 4 Gene [Source:MGI Symbol;Acc:MGI:1923001]
449	ENSMUSG00000050244	5,60601	0,00142	0,04420	1,59085	Heatr1	HEAT repeat containing 1 Gene [Source:MGI Symbol;Acc:MGI:2442524]

n°	probeset ID	d.value	p.value	q.value	Fold-change	Genename	Description
239	ENSMUSG00000027895	6,41201	0,00072	0,04261	1,590006	Kcnc4	potassium voltage gated channel, Shaw-related subfamily, member 4 Gene [Source:MGI Symbol;Acc:MGI:96670]
1019	ENSMUSG00000015112	4,55982	0,00385	0,05314	1,58755	Slc25a13	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13 Gene [Source:MGI Symbol;Acc:MGI:1354721]
446	ENSMUSG00000032902	5,61385	0,00141	0,04420	1,58724	Slc16a1	solute carrier family 16 (monocarboxylic acid transporters), member 1 Gene [Source:MGI Symbol;Acc:MGI:106013]
875	ENSMUSG00000026640	4,75853	0,00317	0,05088	1,58708	Plxna2	plexin A2 Gene [Source:MGI Symbol;Acc:MGI:107684]
771	ENSMUSG00000015176	4,90743	0,00277	0,05022	1,58495	Nolc1	nucleolar and coiled-body phosphoprotein 1 Gene [Source:MGI Symbol;Acc:MGI:1918019]
135	ENSMUSG00000028381	7,11424	0,00042	0,04208	1,58339	Ugcg	UDP-glucose ceramide glucosyltransferase Gene [Source:MGI Symbol;Acc:MGI:1332243]
598	ENSMUSG00000033581	5,24024	0,00202	0,04731	1,58268	Igf2bp2	insulin-like growth factor 2 mRNA binding protein 2 Gene [Source:MGI Symbol;Acc:MGI:1890358]
897	ENSMUSG00000031075	4,73321	0,00326	0,05117	1,58177	Ano1	anoctamin 1, calcium activated chloride channel Gene [Source:MGI Symbol;Acc:MGI:2142149]
901	ENSMUSG00000022241	4,72572	0,00328	0,05122	1,57719	Tars	threonyl-tRNA synthetase Gene [Source:MGI Symbol;Acc:MGI:106314]
606	ENSMUSG00000010755	5,23481	0,00204	0,04731	1,57519	Cars	cysteinyln-tRNA synthetase Gene [Source:MGI Symbol;Acc:MGI:1351477]
523	ENSMUSG00000021868	5,41542	0,00170	0,04572	1,57487	Ppif	peptidylprolyl isomerase F (cyclophilin F) Gene [Source:MGI Symbol;Acc:MGI:2145814]
329	ENSMUSG00000038299	6,00039	0,00101	0,04319	1,57178	Wdr36	WD repeat domain 36 Gene [Source:MGI Symbol;Acc:MGI:1917819]
81	ENSMUSG00000020869	7,97011	0,00022	0,03824	1,56439	Lrrc59	leucine rich repeat containing 59 Gene [Source:MGI Symbol;Acc:MGI:2138133]
472	ENSMUSG00000025007	5,55849	0,00149	0,04420	1,56159	Aldh18a1	aldehyde dehydrogenase 18 family, member A1 Gene [Source:MGI Symbol;Acc:MGI:1888908]
261	ENSMUSG00000027463	6,26225	0,00081	0,04282	1,56043	2310046K01Rik	RIKEN cDNA 2310046K01 gene Gene [Source:MGI Symbol;Acc:MGI:1916948]
1038	ENSMUSG00000026827	4,53477	0,00395	0,05354	1,55795	Gpd2	glycerol phosphate dehydrogenase 2, mitochondrial Gene [Source:MGI Symbol;Acc:MGI:99778]
299	ENSMUSG00000030095	6,11401	0,00093	0,04282	1,55680	Tmem43	transmembrane protein 43 Gene [Source:MGI Symbol;Acc:MGI:1921372]
792	ENSMUSG00000033268	4,88196	0,00284	0,05039	1,55379	Duox1	dual oxidase 1 Gene [Source:MGI Symbol;Acc:MGI:2139422]
210	ENSMUSG00000027395	6,60738	0,00063	0,04208	1,55285	Polr1b	polymerase (RNA) I polypeptide B Gene [Source:MGI Symbol;Acc:MGI:108014]
230	ENSMUSG00000021385	6,45899	0,00070	0,04261	1,55040	Ippk	inositol 1,3,4,5,6-pentakisphosphate 2-kinase Gene [Source:MGI Symbol;Acc:MGI:1922928]
927	ENSMUSG00000074923	4,69346	0,00339	0,05149	1,53903	Pak6	p21 protein (Cdc42/Rac)-activated kinase 6 Gene [Source:MGI Symbol;Acc:MGI:2679420]
1132	ENSMUSG00000065444	4,42360	0,00443	0,05496	1,53651	mmu-mir-27a	mmu-mir-27a [Source:miRBase;Acc:MI0000578]
404	ENSMUSG00000032220	5,74382	0,00127	0,04394	1,53253	Myo1e	myosin IE Gene [Source:MGI Symbol;Acc:MGI:106621]
660	ENSMUSG00000035673	5,11178	0,00225	0,04793	1,53154	Sbno2	strawberry notch homolog 2 (Drosophila) Gene [Source:MGI Symbol;Acc:MGI:2448490]
639	ENSMUSG00000037513	5,16108	0,00216	0,04758	1,52983	Samd4b	sterile alpha motif domain containing 4B Gene [Source:MGI Symbol;Acc:MGI:2448542]
1220	ENSMUSG00000023830	4,31452	0,00494	0,05693	1,51927	Igf2r	insulin-like growth factor 2 receptor Gene [Source:MGI Symbol;Acc:MGI:96435]
332	ENSMUSG00000033294	5,99594	0,00102	0,04319	1,51623	Noc4l	nucleolar complex associated 4 homolog (S. cerevisiae) Gene [Source:MGI Symbol;Acc:MGI:2140843]
43	ENSMUSG00000027333	9,01387	0,00012	0,03757	1,51467	Smox	spermine oxidase Gene [Source:MGI Symbol;Acc:MGI:2445356]
530	ENSMUSG00000028645	5,40587	0,00173	0,04583	1,51322	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1 Gene [Source:MGI Symbol;Acc:MGI:95755]
154	ENSMUSG00000039041	6,89743	0,00049	0,04208	1,50340	Adrm1	adhesion regulating molecule 1 Gene [Source:MGI Symbol;Acc:MGI:1929289]
215	ENSMUSG00000050296	6,57470	0,00064	0,04208	1,50313	Abca12	ATP-binding cassette, sub-family A (ABC1), member 12 Gene [Source:MGI Symbol;Acc:MGI:2676312]
326	ENSMUSG00000028854	6,01530	0,00101	0,04319	1,50272	Slc9a1	solute carrier family 9 (sodium/hydrogen exchanger), member 1 Gene [Source:MGI Symbol;Acc:MGI:102462]

Down-regulated genes ordered by Fold-change using <1.5 as cutoff

n°	probeset ID	d.value	p.value	q.value	Fold-change	Genename	Description
1316	ENSMUSG00000023092	-4,17453	0,00571	0,05920	0,66015	Fhl1	four and a half LIM domains 1 Gene [Source:MGI Symbol;Acc:MGI:1298387]
708	ENSMUSG00000058022	-5,02430	0,00246	0,04888	0,65984	9530008L14Rik	RIKEN cDNA 9530008L14 gene Gene [Source:MGI Symbol;Acc:MGI:1924596]
1136	ENSMUSG00000022357	-4,41804	0,00445	0,05510	0,65957	Klhl38	kelch-like 38 (Drosophila) Gene [Source:MGI Symbol;Acc:MGI:3045310]
700	ENSMUSG00000031176	-5,04233	0,00242	0,04855	0,65932	Dynlt3	dynein light chain Tctex-type 3 Gene [Source:MGI Symbol;Acc:MGI:1914367]
1400	ENSMUSG00000026399	-4,03621	0,00658	0,06199	0,65925	Cd55	CD55 antigen Gene [Source:MGI Symbol;Acc:MGI:104850]
333	ENSMUSG00000022450	-5,99533	0,00102	0,04319	0,65818	Ndufa6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14) Gene [Source:MGI Symbol;Acc:MGI:1914380]
593	ENSMUSG00000078135	-5,25415	0,00200	0,04731	0,65768	Eid1	EP300 interacting inhibitor of differentiation 1 Gene [Source:MGI Symbol;Acc:MGI:1889651]
1505	ENSMUSG00000001657	-3,90433	0,00770	0,06463	0,65738	Hoxc8	homeobox C8 Gene [Source:MGI Symbol;Acc:MGI:96198]
837	ENSMUSG00000079317	-4,80984	0,00303	0,05065	0,65716	Trappc2	trafficking protein particle complex 2 Gene [Source:MGI Symbol;Acc:MGI:1913476]
195	ENSMUSG00000025068	-6,68936	0,00060	0,04208	0,65676	Gsto1	glutathione S-transferase omega 1 Gene [Source:MGI Symbol;Acc:MGI:1342273]
920	ENSMUSG00000073664	-4,70307	0,00336	0,05132	0,65598	Nbeal1	neurobeachin like 1 Gene [Source:MGI Symbol;Acc:MGI:2444343]
1506	ENSMUSG00000019437	-3,90232	0,00771	0,06464	0,65285	Tlcd1	TLC domain containing 1 Gene [Source:MGI Symbol;Acc:MGI:1915572]
63	ENSMUSG00000020264	-8,39506	0,00017	0,03766	0,65222	Slc36a2	solute carrier family 36 (proton/amino acid symporter), member 2 Gene [Source:MGI Symbol;Acc:MGI:1891430]
1155	ENSMUSG00000075752	-4,39678	0,00454	0,05523	0,65215	U2	U2 spliceosomal RNA [Source:RFAM;Acc:RF00004]
609	ENSMUSG00000024039	-5,22116	0,00206	0,04731	0,65187	Cbs	cystathionine beta-synthase Gene [Source:MGI Symbol;Acc:MGI:88285]
804	ENSMUSG00000069208	-4,86585	0,00288	0,05039	0,65167	Zfp825	zinc finger protein 825 Gene [Source:MGI Symbol;Acc:MGI:2385315]
763	ENSMUSG00000074558	-4,92168	0,00273	0,05022	0,65149	AC131780.10	
670	ENSMUSG00000036775	-5,09324	0,00230	0,04819	0,65117	Decr2	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal Gene [Source:MGI Symbol;Acc:MGI:1347059]

n°	probeset ID	d.value	p.value	q.value	Fold-change	Genename	Description
1464	ENSMUSG00000030615	-3,95928	0,00722	0,06313	0,65101	Tmem126a	transmembrane protein 126A Gene [Source:MGI Symbol;Acc:MGI:1913521]
1007	ENSMUSG00000021876	-4,57522	0,00381	0,05305	0,65039	Rnase4	ribonuclease, RNase A family 4 Gene [Source:MGI Symbol;Acc:MGI:1926217]
1292	ENSMUSG00000021033	-4,20844	0,00551	0,05882	0,64920	Gstz1	glutathione transferase zeta 1 (maleylacetoacetate isomerase) Gene [Source:MGI Symbol;Acc:MGI:1341859]
1137	ENSMUSG00000026179	-4,41798	0,00445	0,05510	0,64865	Pnkd	paroxysmal nonkinesigenic dyskinesia Gene [Source:MGI Symbol;Acc:MGI:1930773]
330	ENSMUSG00000024646	-6,00011	0,00102	0,04319	0,64810	Cyb5	cytochrome b-5 Gene [Source:MGI Symbol;Acc:MGI:1926952]
102	ENSMUSG00000029735	-7,44892	0,00031	0,04208	0,64794	Tpk1	thiamine pyrophosphokinase Gene [Source:MGI Symbol;Acc:MGI:1352500]
1481	ENSMUSG00000042284	-3,94080	0,00737	0,06356	0,64734	Itga1	integrin alpha 1 Gene [Source:MGI Symbol;Acc:MGI:96599]
369	ENSMUSG00000032067	-5,83565	0,00118	0,04394	0,64493	Pts	6-pyruvoyl-tetrahydropterin synthase Gene [Source:MGI Symbol;Acc:MGI:1338783]
1187	ENSMUSG00000056552	-4,35947	0,00470	0,05566	0,64436	E130120F12Rik	RIKEN cDNA E130120F12 gene Gene [Source:MGI Symbol;Acc:MGI:3612873]
304	ENSMUSG00000031757	-6,08768	0,00094	0,04282	0,64350	Mt4	metallothionein 4 Gene [Source:MGI Symbol;Acc:MGI:99692]
731	ENSMUSG00000030604	-4,97242	0,00257	0,04953	0,64336	4933426I21Rik	RIKEN cDNA 4933426I21 gene Gene [Source:MGI Symbol;Acc:MGI:1918413]
482	ENSMUSG00000020829	-5,52622	0,00152	0,04439	0,64257	Slc46a1	solute carrier family 46, member 1 Gene [Source:MGI Symbol;Acc:MGI:1098733]
236	ENSMUSG00000022122	-6,42072	0,00072	0,04261	0,64221	Ednrb	endothelin receptor type B Gene [Source:MGI Symbol;Acc:MGI:102720]
533	ENSMUSG00000020056	-5,40046	0,00174	0,04583	0,64177	Ccdc53	coiled-coil domain containing 53 Gene [Source:MGI Symbol;Acc:MGI:1914532]
856	ENSMUSG00000001655	-4,78669	0,00309	0,05065	0,64117	Hoxc13	homeobox C13 Gene [Source:MGI Symbol;Acc:MGI:99560]
1454	ENSMUSG00000053070	-3,97220	0,00712	0,06298	0,63829	9230110C19Rik	RIKEN cDNA 9230110C19 gene Gene [Source:MGI Symbol;Acc:MGI:3045346]
1445	ENSMUSG00000028393	-3,98440	0,00702	0,06266	0,63648	Alad	aminolevulinate, delta-, dehydratase Gene [Source:MGI Symbol;Acc:MGI:96853]
185	ENSMUSG00000036062	-6,73814	0,00058	0,04208	0,63635	N28178	Protein KIAA1045 [Source:UniProtKB/Swiss-Prot;Acc:Q80TL4]
107	ENSMUSG00000025912	-7,37672	0,00033	0,04208	0,63502	Myb1	myeloblastosis oncogene-like 1 Gene [Source:MGI Symbol;Acc:MGI:99925]
434	ENSMUSG00000044748	-5,63835	0,00138	0,04420	0,63478	Defb1	defensin beta 1 Gene [Source:MGI Symbol;Acc:MGI:1096878]
266	ENSMUSG00000029530	-6,23964	0,00082	0,04282	0,63388	Ccr9	chemokine (C-C motif) receptor 9 Gene [Source:MGI Symbol;Acc:MGI:1341902]
396	ENSMUSG00000027550	-5,76517	0,00125	0,04394	0,63312	Lrrcc1	leucine rich repeat and coiled-coil domain containing 1 Gene [Source:MGI Symbol;Acc:MGI:1918960]
1417	ENSMUSG00000035831	-4,01451	0,00675	0,06221	0,62934	Krt25	keratin 25 Gene [Source:MGI Symbol;Acc:MGI:1918060]
720	ENSMUSG00000064352	-4,98976	0,00254	0,04946	0,62689	AY172335.2	
554	ENSMUSG00000020492	-5,34050	0,00185	0,04671	0,62680	Fam33a	family with sequence similarity 33, member A Gene [Source:MGI Symbol;Acc:MGI:1913390]
460	ENSMUSG00000032872	-5,58609	0,00145	0,04420	0,62671	Cyb5r4	cytochrome b5 reductase 4 Gene [Source:MGI Symbol;Acc:MGI:2386848]
483	ENSMUSG00000001804	-5,52272	0,00153	0,04439	0,62157	Dsg4	desmoglein 4 Gene [Source:MGI Symbol;Acc:MGI:2661061]
1446	ENSMUSG00000023963	-3,98341	0,00703	0,06271	0,62110	Cyp39a1	cytochrome P450, family 39, subfamily a, polypeptide 1 Gene [Source:MGI Symbol;Acc:MGI:1927096]
507	ENSMUSG00000000579	-5,45820	0,00164	0,04539	0,61745	Dynlt1c	dynein light chain Tctex-type 1D Gene [Source:MGI Symbol;Acc:MGI:98643]
363	ENSMUSG00000075807	-5,86586	0,00116	0,04394	0,61471	SNORD116	Small nucleolar RNA SNORD116 [Source:RFAM;Acc:RF00108]
1368	ENSMUSG00000031214	-4,09380	0,00620	0,06061	0,61438	Ophn1	oligophrenin 1 Gene [Source:MGI Symbol;Acc:MGI:2151070]
367	ENSMUSG00000026989	-5,83779	0,00118	0,04394	0,60733	Dapl1	death associated protein-like 1 Gene [Source:MGI Symbol;Acc:MGI:1923997]
719	ENSMUSG00000020283	-4,99038	0,00254	0,04946	0,60677	Pex13	peroxisomal biogenesis factor 13 Gene [Source:MGI Symbol;Acc:MGI:1919379]
1158	ENSMUSG00000029413	-4,39282	0,00455	0,05527	0,60622	Naaa	N-acyl ethanolamine acid amidase Gene [Source:MGI Symbol;Acc:MGI:1914361]
55	ENSMUSG00000063661	-8,56213	0,00015	0,03757	0,60566	Krt73	keratin 73 Gene [Source:MGI Symbol;Acc:MGI:3607712]
917	ENSMUSG00000033102	-4,70756	0,00334	0,05127	0,60332	Cdc14b	CDC14 cell division cycle 14 homolog B (S. cerevisiae) Gene [Source:MGI Symbol;Acc:MGI:2441808]
1373	ENSMUSG00000049214	-4,07965	0,00629	0,06110	0,60198	Skint7	selection and upkeep of intraepithelial T cells 8 Gene [Source:MGI Symbol;Acc:MGI:3651523]
1507	ENSMUSG00000055725	-3,90210	0,00771	0,06464	0,59661	Paqr3	progesterin and adipoQ receptor family member III Gene [Source:MGI Symbol;Acc:MGI:2679683]
1055	ENSMUSG00000019791	-4,51210	0,00404	0,05388	0,59438	Hint3	histidine triad nucleotide binding protein 3 Gene [Source:MGI Symbol;Acc:MGI:1914097]
732	ENSMUSG00000035967	-4,97154	0,00258	0,04953	0,59215	Ddx26b	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B Gene [Source:MGI Symbol;Acc:MGI:2442593]
863	ENSMUSG00000018570	-4,78012	0,00311	0,05065	0,58904	2810408A11Rik	RIKEN cDNA 2810408A11 gene Gene [Source:MGI Symbol;Acc:MGI:1917669]
505	ENSMUSG00000021482	-5,46154	0,00163	0,04538	0,58894	1110018J18Rik	RIKEN cDNA 1110018J18 gene Gene [Source:MGI Symbol;Acc:MGI:1913379]
462	ENSMUSG00000077583	-5,58214	0,00146	0,04420	0,58662	SCARNA13	Small Cajal body specific RNA 13 [Source:RFAM;Acc:RF00231]
64	ENSMUSG00000032369	-8,35886	0,00018	0,03766	0,58527	Plscr1	phospholipid scramblase 1 Gene [Source:MGI Symbol;Acc:MGI:893575]
948	ENSMUSG00000028551	-4,66469	0,00348	0,05163	0,58501	Cdkn2c	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4) Gene [Source:MGI Symbol;Acc:MGI:105388]
218	ENSMUSG00000067653	-6,55062	0,00065	0,04216	0,58380	Ankrd23	ankyrin repeat domain 23 Gene [Source:MGI Symbol;Acc:MGI:1925571]
1210	ENSMUSG00000032757	-4,32653	0,00487	0,05662	0,58370	Bet1	blocked early in transport 1 homolog (S. cerevisiae) Gene [Source:MGI Symbol;Acc:MGI:1343104]
76	ENSMUSG00000062826	-8,06831	0,00020	0,03766	0,58116	2310038E17Rik	RIKEN cDNA 2310038E17 gene Gene [Source:MGI Symbol;Acc:MGI:1919153]
1479	ENSMUSG00000064348	-3,94315	0,00735	0,06351	0,58027	AY172335.4	
119	ENSMUSG00000003721	-7,23183	0,00037	0,04208	0,57806	Insig2	insulin induced gene 2 Gene [Source:MGI Symbol;Acc:MGI:1920249]
1195	ENSMUSG00000040181	-4,34704	0,00476	0,05602	0,57670	Fmo1	flavin containing monooxygenase 1 Gene [Source:MGI Symbol;Acc:MGI:1310002]
231	ENSMUSG00000027654	-6,45773	0,00071	0,04261	0,57354	Fam83d	family with sequence similarity 83, member D Gene [Source:MGI Symbol;Acc:MGI:1919128]
1341	ENSMUSG00000029270	-4,13682	0,00594	0,05973	0,57262	Fam69a	family with sequence similarity 69, member A Gene [Source:MGI Symbol;Acc:MGI:1914516]
273	ENSMUSG00000023074	-6,20791	0,00085	0,04282	0,56940	Mospd1	motile sperm domain containing 1 Gene [Source:MGI Symbol;Acc:MGI:1917630]

n°	probeset ID	d.value	p.value	q.value	Fold-change	Genename	Description
1345	ENSMUSG00000038332	-4,12455	0,00601	0,06000	0,56646	Sesn1	sestrin 1 Gene [Source:MGI Symbol;Acc:MGI:2155278]
844	ENSMUSG00000074604	-4,80121	0,00305	0,05065	0,56547	Mgst2	microsomal glutathione S-transferase 2 Gene [Source:MGI Symbol;Acc:MGI:2448481]
53	ENSMUSG00000021303	-8,65261	0,00014	0,03757	0,56028	Gng4	guanine nucleotide binding protein (G protein), gamma 4 Gene [Source:MGI Symbol;Acc:MGI:102703]
37	ENSMUSG00000055937	-9,21823	0,00010	0,03757	0,55877	Krt28	keratin 28 Gene [Source:MGI Symbol;Acc:MGI:1918093]
647	ENSMUSG00000024084	-5,13937	0,00221	0,04793	0,55507	Qpct	glutaminyl-peptide cyclotransferase (glutaminyl cyclase) Gene [Source:MGI Symbol;Acc:MGI:1917786]
256	ENSMUSG00000020159	-6,29657	0,00079	0,04282	0,55304	Gabrp	gamma-aminobutyric acid (GABA) A receptor, pi Gene [Source:MGI Symbol;Acc:MGI:2387597]
1027	ENSMUSG00000025993	-4,55043	0,00389	0,05324	0,54768	Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1 Gene [Source:MGI Symbol;Acc:MGI:1315204]
1311	ENSMUSG00000074370	-4,18084	0,00567	0,05913	0,54072	AC165150.2	
156	ENSMUSG00000037348	-6,88879	0,00049	0,04208	0,53619	Paqr7	progesterin and adipoQ receptor family member VII Gene [Source:MGI Symbol;Acc:MGI:1919154]
17	ENSMUSG00000041193	-10,57621	0,00005	0,03733	0,53040	Pla2g5	phospholipase A2, group V Gene [Source:MGI Symbol;Acc:MGI:101899]
1309	ENSMUSG00000038641	-4,18388	0,00566	0,05913	0,52841	Akr1d1	aldo-keto reductase family 1, member D1 Gene [Source:MGI Symbol;Acc:MGI:2384785]
905	ENSMUSG00000033774	-4,72173	0,00330	0,05122	0,51590	Npbwr1	neuropeptides B/W receptor 1 Gene [Source:MGI Symbol;Acc:MGI:891989]
66	ENSMUSG00000018862	-8,24714	0,00019	0,03766	0,51074	Otop3	otopetrin 3 Gene [Source:MGI Symbol;Acc:MGI:1916852]
631	ENSMUSG00000033107	-5,17482	0,00214	0,04758	0,50877	Rnf125	ring finger protein 125 Gene [Source:MGI Symbol;Acc:MGI:1914914]
267	ENSMUSG00000035305	-6,22761	0,00083	0,04282	0,50751	Ror1	receptor tyrosine kinase-like orphan receptor 1 Gene [Source:MGI Symbol;Acc:MGI:1347520]
87	ENSMUSG00000049709	-7,79964	0,00025	0,03991	0,49624	Nlrp10	NLR family, pyrin domain containing 10 Gene [Source:MGI Symbol;Acc:MGI:2444084]
983	ENSMUSG00000067049	-4,61175	0,00367	0,05257	0,49309	Unc93a	unc-93 homolog A (C. elegans) Gene [Source:MGI Symbol;Acc:MGI:1933250]
253	ENSMUSG00000041449	-6,30933	0,00078	0,04282	0,48534	Serpina3h	serine (or cysteine) peptidase inhibitor, clade A, member 3H Gene [Source:MGI Symbol;Acc:MGI:2182839]
424	ENSMUSG00000040170	-5,68086	0,00133	0,04399	0,47833	Fmo2	flavin containing monooxygenase 2 Gene [Source:MGI Symbol;Acc:MGI:1916776]
887	ENSMUSG00000041660	-4,74527	0,00321	0,05094	0,46605	Bbox1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase 1 (gamma-butyrobetaine hydroxylase) Gene [Source:MGI Symbol;Acc:MGI:1891372]
445	ENSMUSG00000029236	-5,61498	0,00141	0,04420	0,46137	Nmu	neuromedin U Gene [Source:MGI Symbol;Acc:MGI:1860476]
2	ENSMUSG00000024431	-19,72859	0,00001	0,03733	0,43727	Nr3c1	nuclear receptor subfamily 3, group C, member 1 Gene [Source:MGI Symbol;Acc:MGI:95824]
1121	ENSMUSG00000074207	-4,43227	0,00437	0,05482	0,43645	Adh1	alcohol dehydrogenase 1 (class I) Gene [Source:MGI Symbol;Acc:MGI:87921]
12	ENSMUSG00000037263	-11,15263	0,00004	0,03733	0,43035	1700055N04Rik	RIKEN cDNA 1700055N04 gene Gene [Source:MGI Symbol;Acc:MGI:1920708]
285	ENSMUSG00000048766	-6,16053	0,00089	0,04282	0,42927	Skint10	selection and upkeep of intraepithelial T cells 10 Gene [Source:MGI Symbol;Acc:MGI:2685416]
623	ENSMUSG00000036322	-5,19093	0,00211	0,04749	0,40166	H2-Ea	histocompatibility 2, class II antigen E alpha Gene [Source:MGI Symbol;Acc:MGI:95900]
1408	ENSMUSG00000028211	-4,02483	0,00666	0,06217	0,36790	Trp53inp1	transformation related protein 53 inducible nuclear protein 1 Gene [Source:MGI Symbol;Acc:MGI:1926609]
270	ENSMUSG00000015665	-6,21326	0,00084	0,04282	0,36304	Awat1	acyl-CoA wax alcohol acyltransferase 1 Gene [Source:MGI Symbol;Acc:MGI:3588200]
1314	ENSMUSG00000024222	-4,17687	0,00570	0,05918	0,33353	Fkbp5	FK506 binding protein 5 Gene [Source:MGI Symbol;Acc:MGI:104670]
279	ENSMUSG00000039760	-6,19748	0,00086	0,04282	0,31931	Il22ra2	interleukin 22 receptor, alpha 2 Gene [Source:MGI Symbol;Acc:MGI:2665114]
47	ENSMUSG00000059606	-8,78391	0,00013	0,03757	0,27939	Ear5	eosinophil-associated, ribonuclease A family, member 5 Gene [Source:MGI Symbol;Acc:MGI:1858598]
287	ENSMUSG00000073601	-6,15084	0,00090	0,04282	0,25035	Serpnb3c	serine (or cysteine) peptidase inhibitor, clade B, member 3C Gene [Source:MGI Symbol;Acc:MGI:1277952]

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Gene Symbol	Description	GenBank	Product (bp)	Forward primer	Reverse primer
<i>Bcl3</i>	B-cell leukemia/lymphoma 3	NM_033601.3	286	CACGCCGTGGAGAACAACAGC	GGTCTGGGGATGGCTCAGGCT
<i>Elf5</i>	E74-like factor 5 (all forms)	NM_001145813.1	315	CGATCTGTTGAGCAATGAAGAC	TGGTCTCTCAGCATCATTGAA
<i>Ereg</i>	epiregulin	NM_007950.2	167	AGACGCTCCCTGCCTCTTGGG	CTGCACCTTGAGCCACACGGGG
<i>Fkbp5</i>	FK506 binding protein 5	NM_010220.3	290	CTTGACCACGCTATGGTTT	AACGACTCTGAGGCTTTGGA
<i>Hprt1</i>	hypoxanthine phosphoribosyl transferase 1	NM_013556	142	TCAGTCAACGGGGGACATAAA	GGGGCTGTACTGCTTAACCAG
<i>Krt77</i>	keratin 77	NM_001003667	200	GAGCAAAGATGAGGCTGAGG	CCTCCGCATCAGAAATCAAT
<i>Mmp3</i>	matrix metalloproteinase 3	NM_010809.1	172	CCAGGTGTTGACTCAAGGGTGGA	ACACAGGATGCCTTCTGGATCTC
<i>S100a8</i>	S100 calcium binding protein A8	NM_013650.2	68	GGAGTTCCTTGCATGGTGAT	TCTGCTACTCCTTGGGCTGTCT
<i>S100a9</i>	S100 calcium binding protein A9	NM_009114.2	60	TGACAGCTGCCCAACCAA	TTCCAGAACAAAGGCCATT
<i>Slpi</i>	secretory leukocyte peptidase inhibitor	NM_011414.3	278	TGGCACCTGGACTGTGAAGG	CCCCTCCTCTGGCAGACAT
<i>Stat3</i>	signal transducer and activator of transcription 3	NM_011486.4	354	CTGGCGGGCTCTTGTGAGC	GACTAAGGGCCGGTCCGGGT
<i>Tslp</i>	thymic stromal lymphopoietin isoform 1	NM_021367.2	125	CCAGGCTACCCTGAAACTGA	TCTGGAGATTGCATGAAGGA

SUPPLEMENTARY MATERIALS AND METHODS

Keratinocyte culture and cornified envelope (CE) isolation

For primary culture, epidermal keratinocytes from newborn mice were isolated as described (Sevilla et al., 2010). Briefly, 10^6 cells of each genotype were plated per 35-mm diameter collagen I-coated tissue culture dish (BD Biosciences, Palo Alto, CA) and cultured at 37° C in standard medium. After 24 h, the medium was replaced with low calcium medium, and cells were grown until subconfluency. The composition of standard medium was: Essential MEM (EMEM; (BioWhittaker, Inc., Walkersville, MD), supplemented with 4% Chelex-treated (Bio-Rad, Hempstead, UK) fetal calf serum (BioWhittaker, Inc.), 0.6 mM CaCl₂ and antibiotics. Low-calcium medium was composed of EMEM supplemented with 4% Chelex treated fetal calf serum, 0.05 mM CaCl₂, 10ng/ml EGF (Sigma) and antibiotics.

For generation of cell lines, keratinocytes were isolated from 8-week-old mouse dorsal skin and cultured on mitomycin C treated J2-3T3 feeders in type I collagen-coated flasks in DMEM-Ham's F12 (3:1) medium supplemented with 1.8×10^{-4} mol/L adenine, 0.35 mM calcium, 10% FCS, insulin, cholera toxin and epidermal growth factor, as described (Romero et al., 1999). Following approximately 10 passages, spontaneously immortalized lines arose.

Keratinocytes were treated with either vehicle, Dex (100 nM), RU486 (1 μ M; BIOMOL Research Laboratories, Inc., Plymouth Meeting, PA), or mouse IL6 (10 ng/ml; eBioscience, San Diego, CA), after incubating cells in charcoal-stripped serum overnight to deplete steroid hormones.

CEs were isolated from adult mouse (8-week-old) ears as described (Sevilla et al., 2007). The type (fragile or rigid) of individual CEs was determined by phase contrast microscopy. CEs from 3 animals per genotype were scored by counting all the envelopes per field on a hemocytometer, corresponding to 819 WT and 783 GR^{EKO} CEs.

References

Romero MR, Carroll JM, Watt FM (1999) Analysis of cultured keratinocytes from a transgenic mouse model of psoriasis: effects of suprabasal integrin expression on keratinocyte adhesion, proliferation and terminal differentiation. *Exp Dermatol* 8:53–67

Sevilla LM, Nachat R, Groot KR *et al.* (2007) Mice deficient in involucrin, envoplakin, and periplakin have a defective epidermal barrier. *J Cell Biol* 179:1599–612

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References

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FIG S1

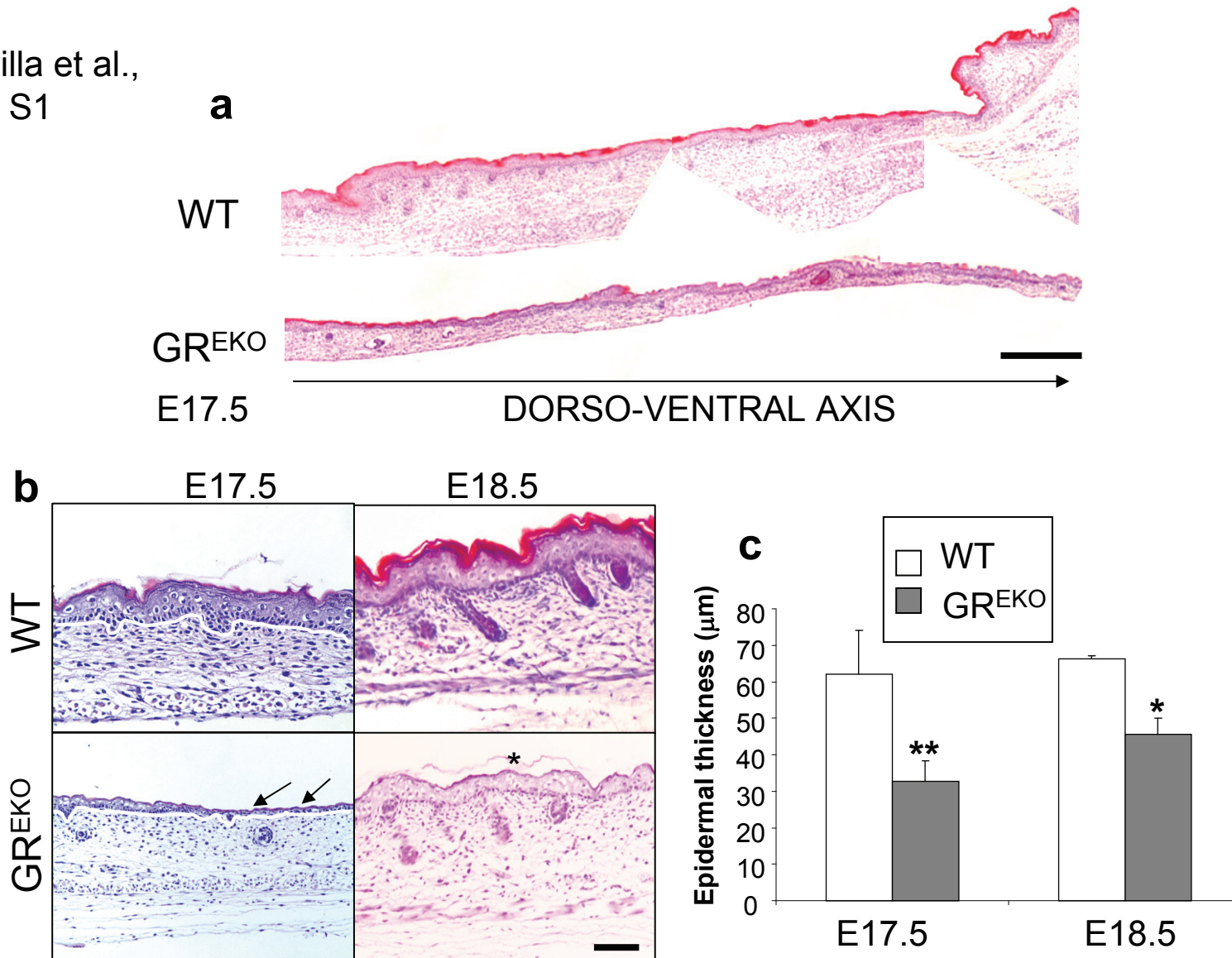


Figure S1. Altered epidermal development of GR^{EKO} mice.

(a) The epidermis of GR^{EKO} E17.5 embryos was much thinner along the dorso-ventral axis as compared to WT. Bar: 200 μm . (b) GR^{EKO} E17.5 skin featured immature thin skin with impaired formation of suprabasal differentiated layers. In certain areas, GR^{EKO} epidermis consisted of only few layers (arrows). GR^{EKO} E18.5 epidermis was more immature relative to WT littermates with areas of SC fragility (asterisk). Bar: 100 μm . (c) Epidermal thickness quantitation showed statistically significant differences (Student's t test; *, $p < 0.05$; **, $p < 0.005$).

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FIG S2

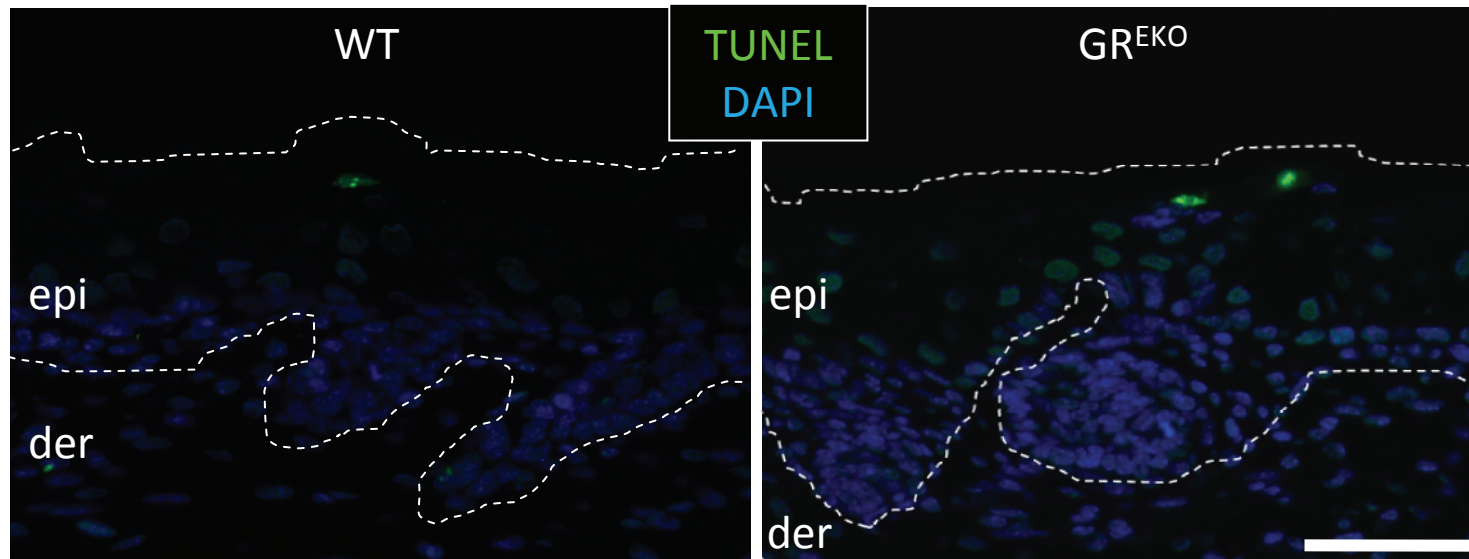


Figure S2. Apoptosis in GR^{EKO} epidermis.

TUNEL staining was performed in paraffin-embedded skin sections from GR^{EKO} and WT P0 mice. Dashed lines delineate the basement membrane. More apoptotic suprabasal keratinocytes (arrows) were found in GR^{EKO} relative to WT epidermis. Bar: 50 μ m.

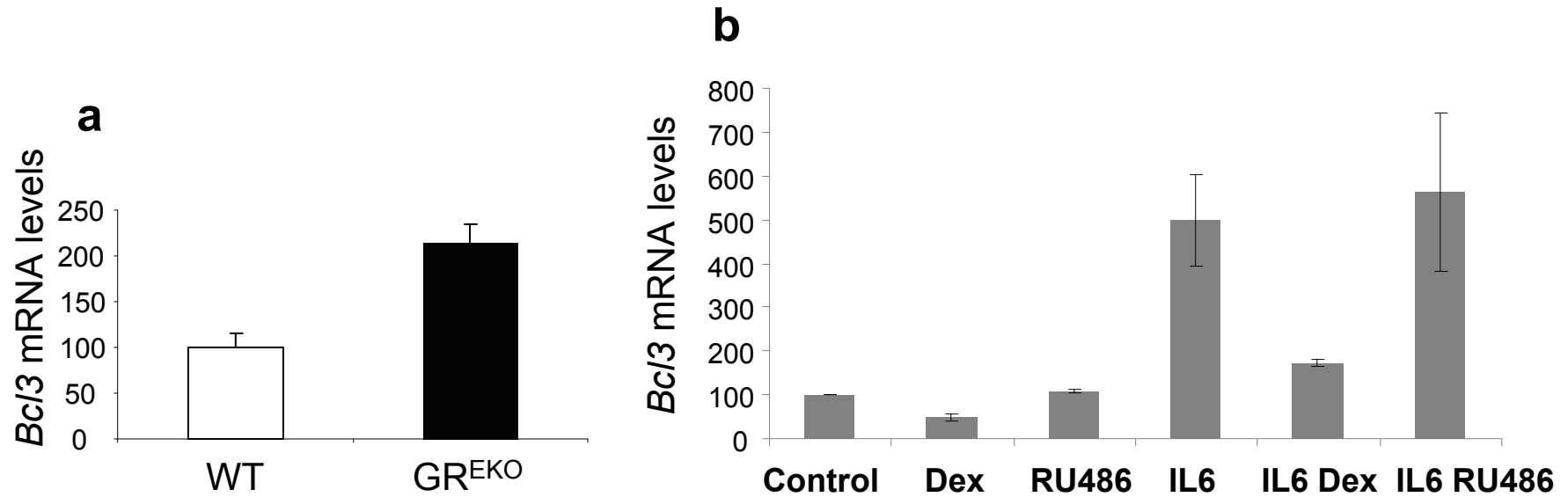


Fig. S3. GR-mediated regulation of *Bcl3* expression.

(a) Relative mRNA levels were assessed in primary keratinocytes isolated from newborn GRE^{EKO} and WT mice by RT-QPCR. (b) Effect of Dex and RU486 on basal and IL6-induced expression of *Bcl3*. Following overnight incubation in media supplemented with 1% charcoal-stripped serum, keratinocytes were treated with either vehicle, Dex (5h), RU486 (5h) and IL6 (ng/ml, 4h), or pre-treated with Dex or RU486 for 1h before addition of IL6 and further incubation (4h). Relative *Bcl3* mRNA levels were determined by RT-QPCR.

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FIG S4

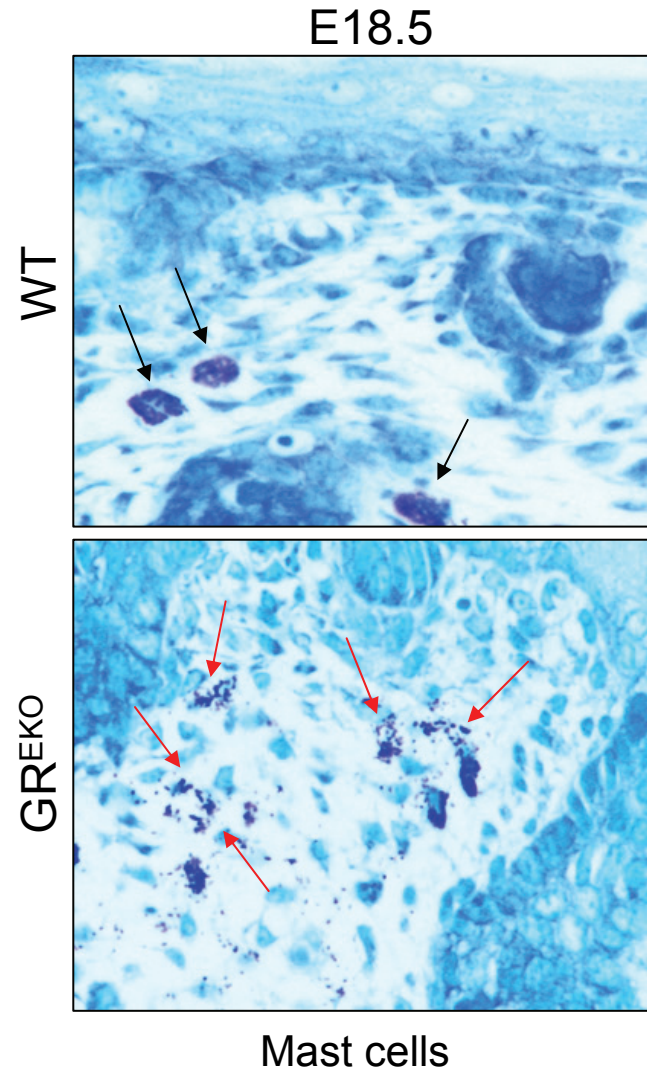


Figure S4. Increased mast cell degranulation in GR^{EKO} developing skin.

Mast cells were visualized by toluidine blue staining in GR^{EKO} and WT E18.5 embryos.

Black arrows: normal mast cells in WT dermis. Red arrows: Degranulated mast cells in GR^{EKO} upper dermis.

Bar: 100 μ m.

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FIG S5

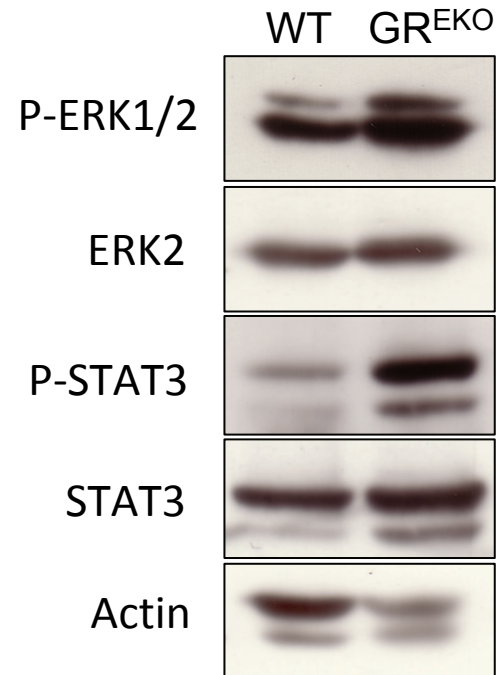


Fig. S5. Altered signaling in GR^{EKO} cultured keratinocytes. Immunoblotting demonstrates increased p-ERK1/2/ERK2 (1.35) and p-STAT3/STAT-3 (2.45) in GR^{EKO} relative to WT keratinocytes. Actin was used as a loading control.

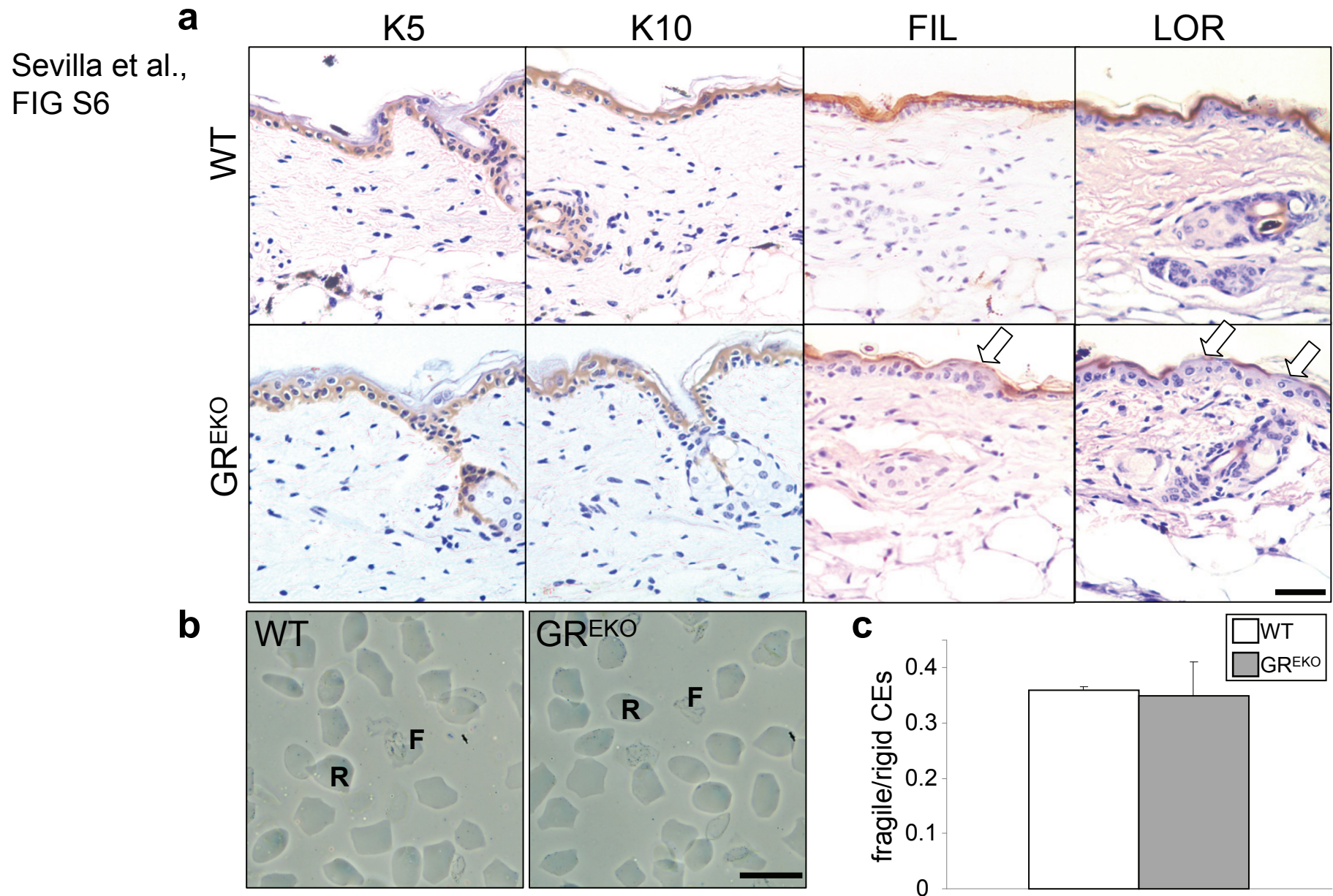


Figure S6. Skin phenotype of adult GR^{EKO} mice.

(a) Immunostaining of GR^{EKO} and WT adult skin sections shows patches of epidermis negative (white arrows) for filaggrin (FIL) and loricrin (LOR). Bar: 50 mm. (b-c) Isolated CEs from adult GR^{EKO} and WT adult mice had similar morphology (b) and fragile (F)/rigid (R) ratios (c). Bar: 60 μ m.

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FIG S7

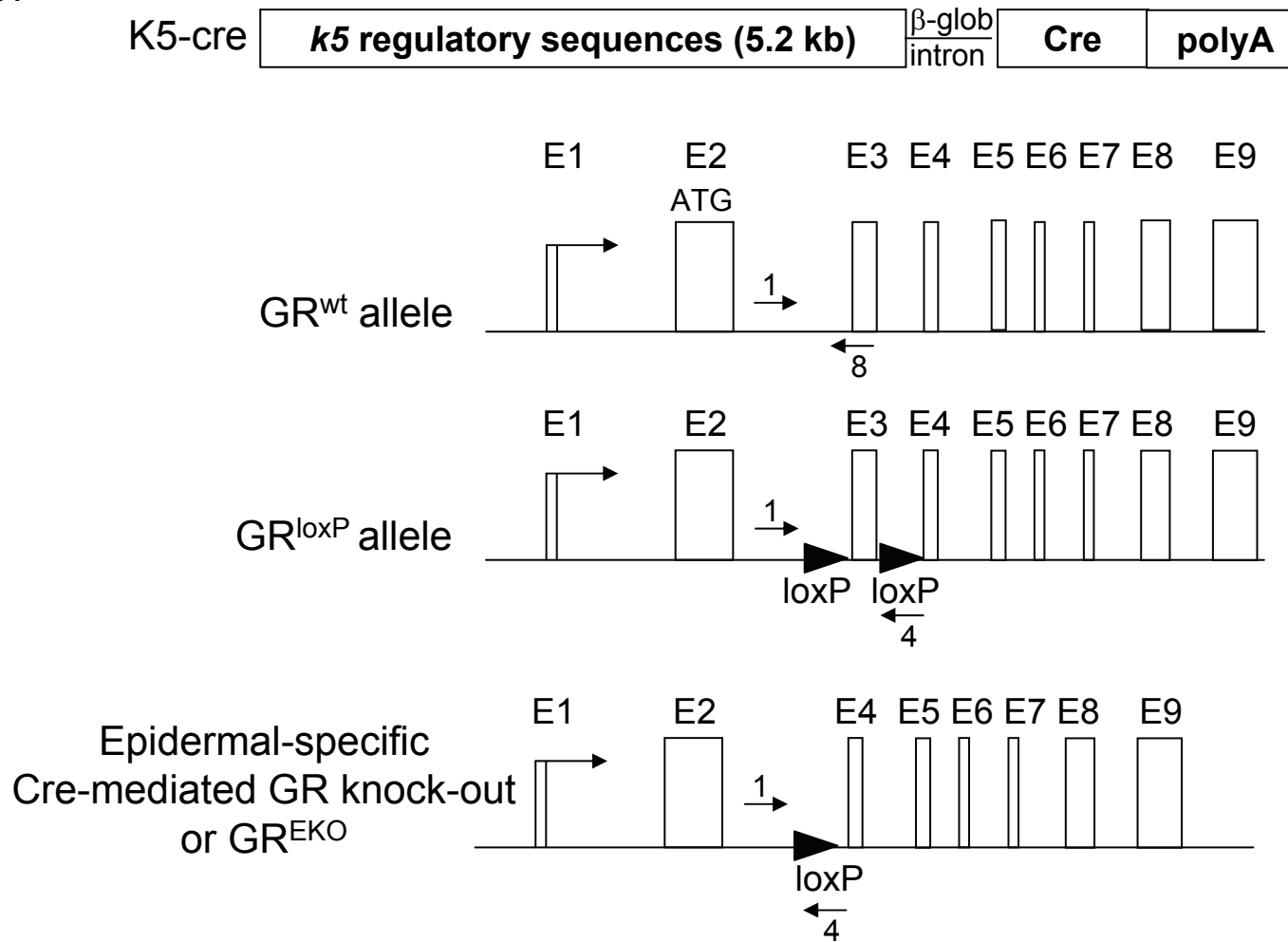


Fig. S7. Scheme depicting generation of GR^{EKO} mice.

The K5-Cre transgene contains the bovine *k5* regulatory sequences (5.2 Kb), the rabbit b-globin intron, Cre, and the SV40 polyadenylation (polyA) signal. The GR^{loxP} allele was generated by introducing two loxP sequences in the second and third introns. In the double transgenic K5-cre//GR^{loxP/loxP} or GR^{EKO}, the recombinase under the control of the K5 promoter deletes the DNA fragment flanked by the loxP sites, rendering an epidermal-specific GR knock-out.

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Up-regulated genes ordered by Fold-change using >1.5 as cutoff

n°	probeset ID	d.value	p.value	q.value	Fold-change	Gene name	Description
14	ENSMUSG00000068320	10,85376	0,00004	0,03733	13,34564	Gm5416	predicted gene 5416 Gene [Source:MGI Symbol;Acc:MGI:3644688]
97	ENSMUSG00000058354	7,51302	0,00030	0,04208	13,01036	Krt6a	keratin 6A Gene [Source:MGI Symbol;Acc:MGI:1100845]
16	ENSMUSG00000027925	10,63428	0,00005	0,03733	8,98522	Sprr2j-ps	small proline-rich protein 2J, pseudogene Pseudogene [Source:MGI Symbol;Acc:MGI:1330345]
110	ENSMUSG00000054325	7,30939	0,00034	0,04208	8,44190	Lce3a	late cornified envelope 3A Gene [Source:MGI Symbol;Acc:MGI:3645650]
853	ENSMUSG00000023041	4,78948	0,00309	0,05065	8,09935	Krt6b	keratin 6B Gene [Source:MGI Symbol;Acc:MGI:1333768]
6	ENSMUSG00000055030	12,24764	0,00002	0,03733	7,38470	Sprr2e	small proline-rich protein 2E Gene [Source:MGI Symbol;Acc:MGI:1330346]
238	ENSMUSG00000068885	6,41558	0,00072	0,04261	6,66251	Lce3f	late cornified envelope 3F Gene [Source:MGI Symbol;Acc:MGI:1916770]
30	ENSMUSG00000050635	9,58083	0,00008	0,03757	6,58943	Sprr2f	small proline-rich protein 2F Gene [Source:MGI Symbol;Acc:MGI:1330349]
25	ENSMUSG00000053797	9,99949	0,00007	0,03755	5,88578	Krt16	keratin 16 Gene [Source:MGI Symbol;Acc:MGI:96690]
177	ENSMUSG00000067594	6,76805	0,00055	0,04208	5,23371	Krt77	keratin 77 Gene [Source:MGI Symbol;Acc:MGI:3588209]
268	ENSMUSG00000041984	6,22400	0,00083	0,04282	5,15223	Rptn	repetin Gene [Source:MGI Symbol;Acc:MGI:1099055]
11	ENSMUSG00000046203	11,61401	0,00003	0,03733	5,10233	AC129296.1	
70	ENSMUSG00000046259	8,16140	0,00019	0,03766	4,97320	Sprr2h	small proline-rich protein 2H Gene [Source:MGI Symbol;Acc:MGI:1330343]
18	ENSMUSG00000074433	10,50667	0,00005	0,03733	4,75214	AC132274.1	
560	ENSMUSG00000026535	5,33715	0,00186	0,04671	4,74335	Ifi202b	interferon activated gene 202A Gene [Source:MGI Symbol;Acc:MGI:1347080]
1118	ENSMUSG00000050092	4,43544	0,00436	0,05482	3,71390	Sprr2b	small proline-rich protein 2B Gene [Source:MGI Symbol;Acc:MGI:1330352]
170	ENSMUSG00000026180	6,79478	0,00054	0,04208	3,68438	Cxcr2	chemokine (C-X-C motif) receptor 2 Gene [Source:MGI Symbol;Acc:MGI:105303]
15	ENSMUSG00000027068	10,80476	0,00004	0,03733	3,67862	Dhrs9	dehydrogenase/reductase (SDR family) member 9 Gene [Source:MGI Symbol;Acc:MGI:2442798]
202	ENSMUSG00000056071	6,65409	0,00061	0,04208	3,60274	S100a9	S100 calcium binding protein A9 (calgranulin B) Gene [Source:MGI Symbol;Acc:MGI:1338947]
305	ENSMUSG00000017002	6,08164	0,00095	0,04282	3,48303	Sipi	secretory leukocyte peptidase inhibitor Gene [Source:MGI Symbol;Acc:MGI:109297]
48	ENSMUSG00000029762	8,72161	0,00014	0,03757	3,46662	Akr1b8	aldo-keto reductase family 1, member B8 Gene [Source:MGI Symbol;Acc:MGI:107673]
188	ENSMUSG00000044294	6,71944	0,00058	0,04208	3,42013	Krt84	keratin 84 Gene [Source:MGI Symbol;Acc:MGI:96700]
32	ENSMUSG00000027186	9,55866	0,00009	0,03757	3,38902	Elf5	E74-like factor 5 Gene [Source:MGI Symbol;Acc:MGI:1335079]
183	ENSMUSG00000024409	6,74567	0,00057	0,04208	3,35155	Psors1c2	psoriasis susceptibility 1 candidate 2 (human) Gene [Source:MGI Symbol;Acc:MGI:1930025]
543	ENSMUSG00000053175	5,37036	0,00179	0,04635	3,28272	Bcl3	B-cell leukemia/lymphoma 3 Gene [Source:MGI Symbol;Acc:MGI:88140]
277	ENSMUSG00000078373	6,20158	0,00086	0,04282	3,11723	2010109K11Rik	RIKEN cDNA 2010109K11 gene Gene [Source:MGI Symbol;Acc:MGI:1919373]
19	ENSMUSG00000042212	10,41697	0,00006	0,03733	3,10809	Sprr2d	small proline-rich protein 2D Gene [Source:MGI Symbol;Acc:MGI:1330347]
894	ENSMUSG00000053846	4,73596	0,00325	0,05114	3,00974	Lipg	lipase, endothelial Gene [Source:MGI Symbol;Acc:MGI:1341803]
181	ENSMUSG00000023885	6,75285	0,00056	0,04208	2,94271	Thbs2	thrombospondin 2 Gene [Source:MGI Symbol;Acc:MGI:98738]
94	ENSMUSG00000029377	7,56179	0,00029	0,04208	2,92150	Ereg	epiregulin Gene [Source:MGI Symbol;Acc:MGI:107508]
414	ENSMUSG00000050063	5,71472	0,00130	0,04394	2,90308	Klk6	kallikrein related-peptidase 6 Gene [Source:MGI Symbol;Acc:MGI:1343166]
335	ENSMUSG00000028479	5,99259	0,00103	0,04326	2,89279	Gne	glucosamine Gene [Source:MGI Symbol;Acc:MGI:1354951]
359	ENSMUSG00000050211	5,87563	0,00114	0,04394	2,87244	Pla2g4e	phospholipase A2, group IVE Gene [Source:MGI Symbol;Acc:MGI:1919144]
117	ENSMUSG00000005667	7,24745	0,00036	0,04208	2,84596	Mthfd2	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methylenetetrahydrofolate cyclohydrolase Gene [Source:MGI Symbol;Acc:MGI:1338850]
91	ENSMUSG00000001473	7,61808	0,00027	0,04199	2,82666	Tubb6	tubulin, beta 6 Gene [Source:MGI Symbol;Acc:MGI:1915201]
300	ENSMUSG00000052353	6,11139	0,00093	0,04282	2,79079	9930013L23Rik	RIKEN cDNA 9930013L23 gene Gene [Source:MGI Symbol;Acc:MGI:2443629]
1106	ENSMUSG00000043613	4,45212	0,00429	0,05461	2,77486	Mmp3	matrix metalloproteinase 3 Gene [Source:MGI Symbol;Acc:MGI:97010]
229	ENSMUSG00000025279	6,46491	0,00070	0,04261	2,75314	Dnase1l3	deoxyribonuclease 1-like 3 Gene [Source:MGI Symbol;Acc:MGI:1314633]
184	ENSMUSG00000036585	6,74398	0,00057	0,04208	2,71379	Fgf1	fibroblast growth factor 1 Gene [Source:MGI Symbol;Acc:MGI:95515]
514	ENSMUSG00000056515	5,43805	0,00166	0,04551	2,70993	Rab31	RAB31, member RAS oncogene family Gene [Source:MGI Symbol;Acc:MGI:1914603]
1239	ENSMUSG00000062991	4,29783	0,00503	0,05708	2,69009	Nrg1	neuregulin 1 Gene [Source:MGI Symbol;Acc:MGI:96083]
56	ENSMUSG00000075582	8,55402	0,00015	0,03757	2,68754	AC119952.1	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3UNM0]
174	ENSMUSG00000022598	6,78811	0,00054	0,04208	2,63344	Pzca	prostate stem cell antigen Gene [Source:MGI Symbol;Acc:MGI:1919623]
760	ENSMUSG00000022665	4,92795	0,00271	0,05019	2,62133	Ccd80	coiled-coil domain containing 80 Gene [Source:MGI Symbol;Acc:MGI:1915146]
205	ENSMUSG00000042157	6,64246	0,00062	0,04208	2,59607	Sprr2i	small proline-rich protein 2E Gene [Source:MGI Symbol;Acc:MGI:1330346]
40	ENSMUSG00000045475	9,14962	0,00011	0,03757	2,59267	Lce3c	late cornified envelope 3C Gene [Source:MGI Symbol;Acc:MGI:2135932]
65	ENSMUSG00000042244	8,27726	0,00018	0,03766	2,58979	Pglyrp3	peptidoglycan recognition protein 3 Gene [Source:MGI Symbol;Acc:MGI:2685266]
341	ENSMUSG00000024810	5,95271	0,00107	0,04394	2,57445	Il33	interleukin 33 Gene [Source:MGI Symbol;Acc:MGI:1924375]
22	ENSMUSG00000037613	10,27208	0,00006	0,03733	2,57206	Tnfrsf23	tumor necrosis factor receptor superfamily, member 23 Gene [Source:MGI Symbol;Acc:MGI:1930269]

n°	probeset ID	d.value	p.value	q.value	Fold-change	Genename	Description
605	ENSMUSG00000024379	5,23525	0,00204	0,04731	2,56484	Tslp	thymic stromal lymphopoietin Gene [Source:MGI Symbol;Acc:MGI:1855696]
1100	ENSMUSG00000032068	4,46428	0,00424	0,05422	2,55456	1600029D21Rik	RIKEN cDNA 1600029D21 gene Gene [Source:MGI Symbol;Acc:MGI:1923759]
432	ENSMUSG00000083500	5,65277	0,00136	0,04420	2,53424	AC162792.1	
288	ENSMUSG00000028364	6,14554	0,00090	0,04282	2,52900	Tnc	tenascin C Gene [Source:MGI Symbol;Acc:MGI:101922]
291	ENSMUSG00000005125	6,14045	0,00091	0,04282	2,52019	Ndrp1	N-myc downstream regulated gene 1 Gene [Source:MGI Symbol;Acc:MGI:1341799]
147	ENSMUSG00000079594	6,97662	0,00046	0,04208	2,50819	BC117090	stefin A1-like protein [Source:RefSeq peptide;Acc:NP_001001332]
759	ENSMUSG00000027737	4,92978	0,00271	0,05019	2,50646	Slc7a11	solute carrier family 7 (cationic amino acid transporter, y+ system), member 11 Gene [Source:MGI Symbol;Acc:MGI:1347355]
314	ENSMUSG00000079434	6,06957	0,00096	0,04282	2,48096	Neu2	neuraminidase 2 Gene [Source:MGI Symbol;Acc:MGI:1344417]
255	ENSMUSG00000026509	6,29658	0,00079	0,04282	2,43978	Capn2	calpain 2 Gene [Source:MGI Symbol;Acc:MGI:88264]
160	ENSMUSG00000029449	6,85259	0,00051	0,04208	2,40487	Rhof	ras homolog gene family, member f Gene [Source:MGI Symbol;Acc:MGI:1345629]
151	ENSMUSG00000025059	6,91392	0,00049	0,04208	2,39301	Gyk	glycerol kinase Gene [Source:MGI Symbol;Acc:MGI:106594]
224	ENSMUSG00000048455	6,49952	0,00068	0,04261	2,36589	Sprp1b	small proline-rich protein 1B Gene [Source:MGI Symbol;Acc:MGI:106659]
491	ENSMUSG00000064232	5,50144	0,00157	0,04479	2,32970	Gm5414	predicted gene 5414 Gene [Source:MGI Symbol;Acc:MGI:3646939]
121	ENSMUSG00000058672	7,21742	0,00038	0,04208	2,31201	Tubb2a	tubulin, beta 2A Gene [Source:MGI Symbol;Acc:MGI:107861]
233	ENSMUSG00000020062	6,44752	0,00071	0,04261	2,30122	Slc5a8	solute carrier family 5 (iodide transporter), member 8 Gene [Source:MGI Symbol;Acc:MGI:2384916]
126	ENSMUSG00000040055	7,17387	0,00039	0,04208	2,25680	Gjb6	gap junction protein, beta 6 Gene [Source:MGI Symbol;Acc:MGI:107588]
222	ENSMUSG00000042268	6,51521	0,00067	0,04261	2,23932	Slc26a9	solute carrier family 26, member 9 Gene [Source:MGI Symbol;Acc:MGI:2444594]
42	ENSMUSG00000050359	9,12689	0,00012	0,03757	2,21438	Sprp1a	small proline-rich protein 1A Gene [Source:MGI Symbol;Acc:MGI:106660]
352	ENSMUSG00000045539	5,89475	0,00112	0,04394	2,18970	Sprp3	small proline-rich protein 3 Gene [Source:MGI Symbol;Acc:MGI:1330237]
187	ENSMUSG00000024030	6,72414	0,00058	0,04208	2,18914	Abcg1	ATP-binding cassette, sub-family G (WHITE), member 1 Gene [Source:MGI Symbol;Acc:MGI:107704]
649	ENSMUSG00000044430	5,13882	0,00221	0,04793	2,14606	Klk12	kallikrein related-peptidase 12 Gene [Source:MGI Symbol;Acc:MGI:1916761]
655	ENSMUSG00000028464	5,12758	0,00223	0,04793	2,14521	Tpm2	tropomyosin 2, beta Gene [Source:MGI Symbol;Acc:MGI:98810]
161	ENSMUSG00000046352	6,85240	0,00051	0,04208	2,13102	Gjb2	gap junction protein, beta 2 Gene [Source:MGI Symbol;Acc:MGI:95720]
1115	ENSMUSG00000056054	4,43714	0,00435	0,05482	2,12704	S100a8	S100 calcium binding protein A8 (calgranulin A) Gene [Source:MGI Symbol;Acc:MGI:88244]
547	ENSMUSG00000023087	5,36105	0,00180	0,04638	2,11506	Ccrn4l	CCR4 carbon catabolite repression 4-like (S. cerevisiae) Gene [Source:MGI Symbol;Acc:MGI:109382]
78	ENSMUSG00000025278	8,04887	0,00021	0,03766	2,11094	Flnb	filamin, beta Gene [Source:MGI Symbol;Acc:MGI:2446089]
34	ENSMUSG00000045136	9,42292	0,00009	0,03757	2,10601	Tubb2b	tubulin, beta 2B Gene [Source:MGI Symbol;Acc:MGI:1920960]
498	ENSMUSG00000061126	5,48642	0,00159	0,04494	2,09641	Cyp4f39	cytochrome P450, family 4, subfamily f, polypeptide 39 Gene [Source:MGI Symbol;Acc:MGI:2445210]
105	ENSMUSG00000029161	7,39332	0,00033	0,04208	2,08800	Cgref1	cell growth regulator with EF hand domain 1 Gene [Source:MGI Symbol;Acc:MGI:1915817]
665	ENSMUSG00000012350	5,09792	0,00228	0,04819	2,07018	Ehf	ets homologous factor Gene [Source:MGI Symbol;Acc:MGI:1270840]
1232	ENSMUSG00000080950	4,30270	0,00500	0,05706	2,06760	AC123613.1	
203	ENSMUSG00000028435	6,65229	0,00062	0,04208	2,04903	Aqp3	aquaporin 3 Gene [Source:MGI Symbol;Acc:MGI:1333777]
104	ENSMUSG00000047884	7,42378	0,00032	0,04208	2,01342	Klk9	kallikrein related-peptidase 9 Gene [Source:MGI Symbol;Acc:MGI:1921082]
469	ENSMUSG00000040511	5,56622	0,00148	0,04420	2,00922	Pvr	poliovirus receptor Gene [Source:MGI Symbol;Acc:MGI:107741]
88	ENSMUSG00000020227	7,78927	0,00025	0,03991	1,96221	Irak3	interleukin-1 receptor-associated kinase 3 Gene [Source:MGI Symbol;Acc:MGI:1921164]
493	ENSMUSG00000078532	5,49644	0,00157	0,04481	1,94542	Nkain1	Na+/K+ transporting ATPase interacting 1 Gene [Source:MGI Symbol;Acc:MGI:1914399]
344	ENSMUSG00000039813	5,93140	0,00108	0,04394	1,92416	Tbc1d2	TBC1 domain family, member 2 Gene [Source:MGI Symbol;Acc:MGI:2652885]
485	ENSMUSG00000011034	5,52032	0,00153	0,04439	1,92339	Slc5a1	solute carrier family 5 (sodium/glucose cotransporter), member 1 Gene [Source:MGI Symbol;Acc:MGI:107678]
306	ENSMUSG00000034751	6,07933	0,00095	0,04282	1,90584	Mast4	microtubule associated serine/threonine kinase family member 4 Gene [Source:MGI Symbol;Acc:MGI:1918885]
436	ENSMUSG00000033852	5,63115	0,00138	0,04420	1,90530	Pla2g4b	phospholipase A2, group IVB (cytosolic) Gene [Source:MGI Symbol;Acc:MGI:2384819]
73	ENSMUSG00000030693	8,14801	0,00020	0,03766	1,89850	Klk10	kallikrein related-peptidase 10 Gene [Source:MGI Symbol;Acc:MGI:1916790]
1235	ENSMUSG00000030666	4,30160	0,00501	0,05706	1,88139	Calcb	calcitonin-related polypeptide, beta Gene [Source:MGI Symbol;Acc:MGI:2151254]
323	ENSMUSG00000028811	6,03491	0,00099	0,04319	1,87372	Yars	tyrosyl-tRNA synthetase Gene [Source:MGI Symbol;Acc:MGI:2147627]
280	ENSMUSG00000037577	6,19640	0,00086	0,04282	1,86995	Ephx3	epoxide hydrolase 3 Gene [Source:MGI Symbol;Acc:MGI:1919182]
318	ENSMUSG00000022468	6,06337	0,00097	0,04282	1,85150	Pp1r	placental protein 11 related Gene [Source:MGI Symbol;Acc:MGI:97746]
1032	ENSMUSG00000028186	4,54369	0,00392	0,05340	1,85065	Uox	urate oxidase Gene [Source:MGI Symbol;Acc:MGI:98907]
221	ENSMUSG00000024812	6,51558	0,00067	0,04261	1,84327	Tjp2	tight junction protein 2 Gene [Source:MGI Symbol;Acc:MGI:1341872]
36	ENSMUSG00000005514	9,26394	0,00010	0,03757	1,83295	Por	P450 (cytochrome) oxidoreductase Gene [Source:MGI Symbol;Acc:MGI:97744]
297	ENSMUSG00000031960	6,11567	0,00092	0,04282	1,82966	Aars	alanyl-tRNA synthetase Gene [Source:MGI Symbol;Acc:MGI:2384560]
553	ENSMUSG00000011632	5,34088	0,00184	0,04671	1,82901	2310033E01Rik	RIKEN cDNA 2310033E01 gene Gene [Source:MGI Symbol;Acc:MGI:3615324]
235	ENSMUSG00000001794	6,42338	0,00072	0,04261	1,82508	Capns1	calpain, small subunit 1 Gene [Source:MGI Symbol;Acc:MGI:88266]
85	ENSMUSG00000025473	7,85706	0,00024	0,03941	1,82438	Adam8	a disintegrin and metallopeptidase domain 8 Gene [Source:MGI Symbol;Acc:MGI:107825]
458	ENSMUSG00000030513	5,59233	0,00144	0,04420	1,82284	Pcsk6	proprotein convertase subtilisin/kexin type 6 Gene [Source:MGI Symbol;Acc:MGI:102897]
173	ENSMUSG00000028430	6,79137	0,00054	0,04208	1,81944	Nol6	nucleolar protein family 6 (RNA-associated) Gene [Source:MGI Symbol;Acc:MGI:2140151]

n°	probeset ID	d.value	p.value	q.value	Fold-change	Genename	Description
67	ENSMUSG00000010830	8,24424	0,00019	0,03766	1,81904	Kdelr3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 Gene [Source:MGI Symbol;Acc:MGI:2145953]
576	ENSMUSG00000038264	5,30193	0,00192	0,04685	1,81749	Sema7a	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A Gene [Source:MGI Symbol;Acc:MGI:1306826]
263	ENSMUSG00000022221	6,25239	0,00082	0,04282	1,81442	Ripk3	receptor-interacting serine-threonine kinase 3 Gene [Source:MGI Symbol;Acc:MGI:2154952]
706	ENSMUSG00000018920	5,02947	0,00244	0,04869	1,81060	Cxcl16	chemokine (C-X-C motif) ligand 16 Gene [Source:MGI Symbol;Acc:MGI:1932682]
969	ENSMUSG00000027293	4,63123	0,00359	0,05217	1,81059	Ehd4	EH-domain containing 4 Gene [Source:MGI Symbol;Acc:MGI:1919619]
841	ENSMUSG00000024952	4,80260	0,00305	0,05065	1,80685	Rps6ka4	ribosomal protein S6 kinase, polypeptide 4 Gene [Source:MGI Symbol;Acc:MGI:1930076]
245	ENSMUSG00000037188	6,35385	0,00075	0,04282	1,78066	Grlh3	grainyhead-like 3 (Drosophila) Gene [Source:MGI Symbol;Acc:MGI:2655333]
388	ENSMUSG00000042195	5,78153	0,00123	0,04394	1,77323	Slc35f2	solute carrier family 35, member F2 Gene [Source:MGI Symbol;Acc:MGI:1919272]
1204	ENSMUSG00000032265	4,33813	0,00481	0,05620	1,76721	AC159809.2	family with sequence similarity 46, member A (Fam46a), transcript variant 2, mRNA [Source:RefSeq DNA;Acc:NM_001160379]
252	ENSMUSG00000035049	6,31932	0,00078	0,04282	1,76509	Rrp12	ribosomal RNA processing 12 homolog (S. cerevisiae) Gene [Source:MGI Symbol;Acc:MGI:2147437]
1061	ENSMUSG00000050762	4,50238	0,00408	0,05401	1,75707	Prss27	protease, serine 27 Gene [Source:MGI Symbol;Acc:MGI:2450123]
860	ENSMUSG00000014444	4,78372	0,00310	0,05065	1,74900	Fam38a	family with sequence similarity 38, member A Gene [Source:MGI Symbol;Acc:MGI:3603204]
600	ENSMUSG00000020075	5,23994	0,00202	0,04731	1,74112	Ddx21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21 Gene [Source:MGI Symbol;Acc:MGI:1860494]
226	ENSMUSG00000026558	6,47508	0,00069	0,04261	1,73342	Uck2	uridine-cytidine kinase 2 Gene [Source:MGI Symbol;Acc:MGI:1931744]
936	ENSMUSG00000023988	4,67939	0,00344	0,05163	1,72958	Bysl	bystin-like Gene [Source:MGI Symbol;Acc:MGI:1858419]
452	ENSMUSG00000020758	5,60421	0,00142	0,04420	1,71275	Itgb4	integrin beta 4 Gene [Source:MGI Symbol;Acc:MGI:96613]
247	ENSMUSG00000036432	6,34754	0,00076	0,04282	1,71127	Siah2	seven in absentia 2 Gene [Source:MGI Symbol;Acc:MGI:108062]
595	ENSMUSG00000060012	5,24945	0,00201	0,04731	1,71087	Kif13b	kinesin family member 13B Gene [Source:MGI Symbol;Acc:MGI:1098265]
437	ENSMUSG00000041313	5,63029	0,00138	0,04420	1,70609	Slc7a1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 Gene [Source:MGI Symbol;Acc:MGI:88117]
893	ENSMUSG00000028893	4,73661	0,00325	0,05114	1,70422	Sesn2	sestrin 2 Gene [Source:MGI Symbol;Acc:MGI:2651874]
627	ENSMUSG00000044813	5,18241	0,00212	0,04757	1,69872	Shb	src homology 2 domain-containing transforming protein B Gene [Source:MGI Symbol;Acc:MGI:98294]
698	ENSMUSG00000022565	5,04733	0,00241	0,04855	1,69796	Plec1	plectin 1 Gene [Source:MGI Symbol;Acc:MGI:1277961]
516	ENSMUSG00000004356	5,43415	0,00167	0,04551	1,69520	Utp20	UTP20, small subunit (SSU) processome component, homolog (yeast) Gene [Source:MGI Symbol;Acc:MGI:1917933]
1175	ENSMUSG00000041025	4,37112	0,00465	0,05559	1,69040	Iffo2	intermediate filament family orphan 2 Gene [Source:MGI Symbol;Acc:MGI:2140675]
1003	ENSMUSG00000032012	4,58222	0,00377	0,05292	1,68877	Pvr1l	poliovirus receptor-related 1 Gene [Source:MGI Symbol;Acc:MGI:1926483]
5	ENSMUSG00000050854	12,44372	0,00002	0,03733	1,67662	Tmem125	transmembrane protein 125 Gene [Source:MGI Symbol;Acc:MGI:1923409]
399	ENSMUSG00000026123	5,75647	0,00126	0,04394	1,67606	Pleckhb2	pleckstrin homology domain containing, family B (evectins) member 2 Gene [Source:MGI Symbol;Acc:MGI:2385825]
935	ENSMUSG00000054321	4,68130	0,00343	0,05163	1,66569	Taf4b	TAF4B RNA polymerase II, TATA box binding protein (TBP)-associated factor Gene [Source:MGI Symbol;Acc:MGI:2152345]
504	ENSMUSG00000051375	5,46225	0,00163	0,04538	1,66389	Pcdh1	protocadherin 1 Gene [Source:MGI Symbol;Acc:MGI:104692]
249	ENSMUSG00000036499	6,33274	0,00077	0,04282	1,66335	Eea1	early endosome antigen 1 Gene [Source:MGI Symbol;Acc:MGI:2442192]
550	ENSMUSG00000030137	5,34570	0,00183	0,04671	1,66276	Tuba8	tubulin, alpha 8 Gene [Source:MGI Symbol;Acc:MGI:1858225]
209	ENSMUSG00000026185	6,62148	0,00063	0,04208	1,66199	Igf1bp5	insulin-like growth factor binding protein 5 Gene [Source:MGI Symbol;Acc:MGI:96440]
761	ENSMUSG00000072812	4,92595	0,00271	0,05019	1,65936	Ahnak2	AHNAK nucleoprotein 2 Gene [Source:MGI Symbol;Acc:MGI:2144831]
137	ENSMUSG00000053819	7,09487	0,00042	0,04208	1,65433	Camk2d	calcium/calmodulin-dependent protein kinase II, delta Gene [Source:MGI Symbol;Acc:MGI:1341265]
175	ENSMUSG00000030835	6,78683	0,00054	0,04208	1,65065	Nomo1	nodal modulator 1 Gene [Source:MGI Symbol;Acc:MGI:2385850]
258	ENSMUSG00000057454	6,27297	0,00080	0,04282	1,64576	Lypd3	Ly6/Plaur domain containing 3 Gene [Source:MGI Symbol;Acc:MGI:1919684]
769	ENSMUSG00000038151	4,91088	0,00275	0,05022	1,64035	Prdm1	PR domain containing 1, with ZNF domain Gene [Source:MGI Symbol;Acc:MGI:99655]
165	ENSMUSG00000001435	6,81809	0,00053	0,04208	1,63589	Col18a1	collagen, type XVIII, alpha 1 Gene [Source:MGI Symbol;Acc:MGI:88451]
687	ENSMUSG00000054215	5,06190	0,00236	0,04839	1,63315	Sprr2k	small proline-rich protein 2K Gene [Source:MGI Symbol;Acc:MGI:1330344]
1089	ENSMUSG00000000320	4,47006	0,00421	0,05422	1,63111	Alox12	arachidonate 12-lipoxygenase Gene [Source:MGI Symbol;Acc:MGI:87998]
478	ENSMUSG00000029752	5,54004	0,00150	0,04420	1,63106	Asns	asparagine synthetase Gene [Source:MGI Symbol;Acc:MGI:1350929]
443	ENSMUSG00000019849	5,61993	0,00140	0,04420	1,62352	Prep	prolyl endopeptidase Gene [Source:MGI Symbol;Acc:MGI:1270863]
699	ENSMUSG00000034485	5,04547	0,00241	0,04855	1,62096	Uaca	uveal autoantigen with coiled-coil domains and ankyrin repeats Gene [Source:MGI Symbol;Acc:MGI:1919815]
865	ENSMUSG00000055491	4,77724	0,00312	0,05065	1,61936	Pprc1	peroxisome proliferative activated receptor, gamma, coactivator-related 1 Gene [Source:MGI Symbol;Acc:MGI:2385096]
824	ENSMUSG00000025081	4,82740	0,00298	0,05065	1,61545	Tdrd1	tudor domain containing 1 Gene [Source:MGI Symbol;Acc:MGI:1933218]
551	ENSMUSG00000029581	5,34416	0,00184	0,04671	1,61212	Fscn1	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus) Gene [Source:MGI Symbol;Acc:MGI:1352745]
427	ENSMUSG00000026773	5,67136	0,00134	0,04399	1,61177	Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3 Gene [Source:MGI Symbol;Acc:MGI:2181202]
9	ENSMUSG00000066441	11,80247	0,00003	0,03733	1,60431	Rdh11	retinol dehydrogenase 11 Gene [Source:MGI Symbol;Acc:MGI:102581]
386	ENSMUSG00000042993	5,78720	0,00123	0,04394	1,60170	Ifnk	interferon kappa Gene [Source:MGI Symbol;Acc:MGI:2683287]
95	ENSMUSG00000025277	7,56144	0,00029	0,04208	1,60059	Abhd6	abhydrolase domain containing 6 Gene [Source:MGI Symbol;Acc:MGI:1913332]
131	ENSMUSG00000005481	7,13732	0,00041	0,04208	1,59399	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39 Gene [Source:MGI Symbol;Acc:MGI:1915528]
463	ENSMUSG00000034112	5,58156	0,00146	0,04420	1,59256	Atp2c2	ATPase, Ca++ transporting, type 2C, member 2 Gene [Source:MGI Symbol;Acc:MGI:1916297]
163	ENSMUSG00000002319	6,83457	0,00052	0,04208	1,59111	Ipo4	importin 4 Gene [Source:MGI Symbol;Acc:MGI:1923001]
449	ENSMUSG00000050244	5,60601	0,00142	0,04420	1,59085	Heatr1	HEAT repeat containing 1 Gene [Source:MGI Symbol;Acc:MGI:2442524]

n°	probeset ID	d.value	p.value	q.value	Fold-change	Genename	Description
239	ENSMUSG00000027895	6,41201	0,00072	0,04261	1,590006	Kcnc4	potassium voltage gated channel, Shaw-related subfamily, member 4 Gene [Source:MGI Symbol;Acc:MGI:96670]
1019	ENSMUSG00000015112	4,55982	0,00385	0,05314	1,58755	Slc25a13	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13 Gene [Source:MGI Symbol;Acc:MGI:1354721]
446	ENSMUSG00000032902	5,61385	0,00141	0,04420	1,58724	Slc16a1	solute carrier family 16 (monocarboxylic acid transporters), member 1 Gene [Source:MGI Symbol;Acc:MGI:106013]
875	ENSMUSG00000026640	4,75853	0,00317	0,05088	1,58708	Plxna2	plexin A2 Gene [Source:MGI Symbol;Acc:MGI:107684]
771	ENSMUSG00000015176	4,90743	0,00277	0,05022	1,58495	Nolc1	nucleolar and coiled-body phosphoprotein 1 Gene [Source:MGI Symbol;Acc:MGI:1918019]
135	ENSMUSG00000028381	7,11424	0,00042	0,04208	1,58339	Ugcg	UDP-glucose ceramide glucosyltransferase Gene [Source:MGI Symbol;Acc:MGI:1332243]
598	ENSMUSG00000033581	5,24024	0,00202	0,04731	1,58268	Igf2bp2	insulin-like growth factor 2 mRNA binding protein 2 Gene [Source:MGI Symbol;Acc:MGI:1890358]
897	ENSMUSG00000031075	4,73321	0,00326	0,05117	1,58177	Ano1	anoctamin 1, calcium activated chloride channel Gene [Source:MGI Symbol;Acc:MGI:2142149]
901	ENSMUSG00000022241	4,72572	0,00328	0,05122	1,57719	Tars	threonyl-tRNA synthetase Gene [Source:MGI Symbol;Acc:MGI:106314]
606	ENSMUSG00000010755	5,23481	0,00204	0,04731	1,57519	Cars	cysteinyln-tRNA synthetase Gene [Source:MGI Symbol;Acc:MGI:1351477]
523	ENSMUSG00000021868	5,41542	0,00170	0,04572	1,57487	Ppif	peptidylprolyl isomerase F (cyclophilin F) Gene [Source:MGI Symbol;Acc:MGI:2145814]
329	ENSMUSG00000038299	6,00039	0,00101	0,04319	1,57178	Wdr36	WD repeat domain 36 Gene [Source:MGI Symbol;Acc:MGI:1917819]
81	ENSMUSG00000020869	7,97011	0,00022	0,03824	1,56439	Lrrc59	leucine rich repeat containing 59 Gene [Source:MGI Symbol;Acc:MGI:2138133]
472	ENSMUSG00000025007	5,55849	0,00149	0,04420	1,56159	Aldh18a1	aldehyde dehydrogenase 18 family, member A1 Gene [Source:MGI Symbol;Acc:MGI:1888908]
261	ENSMUSG00000027463	6,26225	0,00081	0,04282	1,56043	2310046K01Rik	RIKEN cDNA 2310046K01 gene Gene [Source:MGI Symbol;Acc:MGI:1916948]
1038	ENSMUSG00000026827	4,53477	0,00395	0,05354	1,55795	Gpd2	glycerol phosphate dehydrogenase 2, mitochondrial Gene [Source:MGI Symbol;Acc:MGI:99778]
299	ENSMUSG00000030095	6,11401	0,00093	0,04282	1,55680	Tmem43	transmembrane protein 43 Gene [Source:MGI Symbol;Acc:MGI:1921372]
792	ENSMUSG00000033268	4,88196	0,00284	0,05039	1,55379	Duox1	dual oxidase 1 Gene [Source:MGI Symbol;Acc:MGI:2139422]
210	ENSMUSG00000027395	6,60738	0,00063	0,04208	1,55285	Polr1b	polymerase (RNA) I polypeptide B Gene [Source:MGI Symbol;Acc:MGI:108014]
230	ENSMUSG00000021385	6,45899	0,00070	0,04261	1,55040	Ippk	inositol 1,3,4,5,6-pentakisphosphate 2-kinase Gene [Source:MGI Symbol;Acc:MGI:1922928]
927	ENSMUSG00000074923	4,69346	0,00339	0,05149	1,53903	Pak6	p21 protein (Cdc42/Rac)-activated kinase 6 Gene [Source:MGI Symbol;Acc:MGI:2679420]
1132	ENSMUSG00000065444	4,42360	0,00443	0,05496	1,53651	mmu-mir-27a	mmu-mir-27a [Source:miRBase;Acc:MI0000578]
404	ENSMUSG00000032220	5,74382	0,00127	0,04394	1,53253	Myo1e	myosin IE Gene [Source:MGI Symbol;Acc:MGI:106621]
660	ENSMUSG00000035673	5,11178	0,00225	0,04793	1,53154	Sbno2	strawberry notch homolog 2 (Drosophila) Gene [Source:MGI Symbol;Acc:MGI:2448490]
639	ENSMUSG00000037513	5,16108	0,00216	0,04758	1,52983	Samd4b	sterile alpha motif domain containing 4B Gene [Source:MGI Symbol;Acc:MGI:2448542]
1220	ENSMUSG00000023830	4,31452	0,00494	0,05693	1,51927	Igf2r	insulin-like growth factor 2 receptor Gene [Source:MGI Symbol;Acc:MGI:96435]
332	ENSMUSG00000033294	5,99594	0,00102	0,04319	1,51623	Noc4l	nucleolar complex associated 4 homolog (S. cerevisiae) Gene [Source:MGI Symbol;Acc:MGI:2140843]
43	ENSMUSG00000027333	9,01387	0,00012	0,03757	1,51467	Smox	spermine oxidase Gene [Source:MGI Symbol;Acc:MGI:2445356]
530	ENSMUSG00000028645	5,40587	0,00173	0,04583	1,51322	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1 Gene [Source:MGI Symbol;Acc:MGI:95755]
154	ENSMUSG00000039041	6,89743	0,00049	0,04208	1,50340	Adrm1	adhesion regulating molecule 1 Gene [Source:MGI Symbol;Acc:MGI:1929289]
215	ENSMUSG00000050296	6,57470	0,00064	0,04208	1,50313	Abca12	ATP-binding cassette, sub-family A (ABC1), member 12 Gene [Source:MGI Symbol;Acc:MGI:2676312]
326	ENSMUSG00000028854	6,01530	0,00101	0,04319	1,50272	Slc9a1	solute carrier family 9 (sodium/hydrogen exchanger), member 1 Gene [Source:MGI Symbol;Acc:MGI:102462]

Down-regulated genes ordered by Fold-change using <1.5 as cutoff

n°	probeset ID	d.value	p.value	q.value	Fold-change	Genename	Description
1316	ENSMUSG00000023092	-4,17453	0,00571	0,05920	0,66015	Fhl1	four and a half LIM domains 1 Gene [Source:MGI Symbol;Acc:MGI:1298387]
708	ENSMUSG00000058022	-5,02430	0,00246	0,04888	0,65984	9530008L14Rik	RIKEN cDNA 9530008L14 gene Gene [Source:MGI Symbol;Acc:MGI:1924596]
1136	ENSMUSG00000022357	-4,41804	0,00445	0,05510	0,65957	Klhl38	kelch-like 38 (Drosophila) Gene [Source:MGI Symbol;Acc:MGI:3045310]
700	ENSMUSG00000031176	-5,04233	0,00242	0,04855	0,65932	Dynlt3	dynein light chain Tctex-type 3 Gene [Source:MGI Symbol;Acc:MGI:1914367]
1400	ENSMUSG00000026399	-4,03621	0,00658	0,06199	0,65925	Cd55	CD55 antigen Gene [Source:MGI Symbol;Acc:MGI:104850]
333	ENSMUSG00000022450	-5,99533	0,00102	0,04319	0,65818	Ndufa6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14) Gene [Source:MGI Symbol;Acc:MGI:1914380]
593	ENSMUSG00000078135	-5,25415	0,00200	0,04731	0,65768	Eid1	EP300 interacting inhibitor of differentiation 1 Gene [Source:MGI Symbol;Acc:MGI:1889651]
1505	ENSMUSG00000001657	-3,90433	0,00770	0,06463	0,65738	Hoxc8	homeobox C8 Gene [Source:MGI Symbol;Acc:MGI:96198]
837	ENSMUSG00000079317	-4,80984	0,00303	0,05065	0,65716	Trappc2	trafficking protein particle complex 2 Gene [Source:MGI Symbol;Acc:MGI:1913476]
195	ENSMUSG00000025068	-6,68936	0,00060	0,04208	0,65676	Gsto1	glutathione S-transferase omega 1 Gene [Source:MGI Symbol;Acc:MGI:1342273]
920	ENSMUSG00000073664	-4,70307	0,00336	0,05132	0,65598	Nbeal1	neurobeachin like 1 Gene [Source:MGI Symbol;Acc:MGI:2444343]
1506	ENSMUSG00000019437	-3,90232	0,00771	0,06464	0,65285	Tlcd1	TLC domain containing 1 Gene [Source:MGI Symbol;Acc:MGI:1915572]
63	ENSMUSG00000020264	-8,39506	0,00017	0,03766	0,65222	Slc36a2	solute carrier family 36 (proton/amino acid symporter), member 2 Gene [Source:MGI Symbol;Acc:MGI:1891430]
1155	ENSMUSG00000075752	-4,39678	0,00454	0,05523	0,65215	U2	U2 spliceosomal RNA [Source:RFAM;Acc:RF00004]
609	ENSMUSG00000024039	-5,22116	0,00206	0,04731	0,65187	Cbs	cystathionine beta-synthase Gene [Source:MGI Symbol;Acc:MGI:88285]
804	ENSMUSG00000069208	-4,86585	0,00288	0,05039	0,65167	Zfp825	zinc finger protein 825 Gene [Source:MGI Symbol;Acc:MGI:2385315]
763	ENSMUSG00000074558	-4,92168	0,00273	0,05022	0,65149	AC131780.10	
670	ENSMUSG00000036775	-5,09324	0,00230	0,04819	0,65117	Decr2	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal Gene [Source:MGI Symbol;Acc:MGI:1347059]

n°	probeset ID	d.value	p.value	q.value	Fold-change	Genename	Description
1464	ENSMUSG00000030615	-3,95928	0,00722	0,06313	0,65101	Tmem126a	transmembrane protein 126A Gene [Source:MGI Symbol;Acc:MGI:1913521]
1007	ENSMUSG00000021876	-4,57522	0,00381	0,05305	0,65039	Rnase4	ribonuclease, RNase A family 4 Gene [Source:MGI Symbol;Acc:MGI:1926217]
1292	ENSMUSG00000021033	-4,20844	0,00551	0,05882	0,64920	Gstz1	glutathione transferase zeta 1 (maleylacetoacetate isomerase) Gene [Source:MGI Symbol;Acc:MGI:1341859]
1137	ENSMUSG00000026179	-4,41798	0,00445	0,05510	0,64865	Pnkd	paroxysmal nonkinesigenic dyskinesia Gene [Source:MGI Symbol;Acc:MGI:1930773]
330	ENSMUSG00000024646	-6,00011	0,00102	0,04319	0,64810	Cyb5	cytochrome b-5 Gene [Source:MGI Symbol;Acc:MGI:1926952]
102	ENSMUSG00000029735	-7,44892	0,00031	0,04208	0,64794	Tpk1	thiamine pyrophosphokinase Gene [Source:MGI Symbol;Acc:MGI:1352500]
1481	ENSMUSG00000042284	-3,94080	0,00737	0,06356	0,64734	Itga1	integrin alpha 1 Gene [Source:MGI Symbol;Acc:MGI:96599]
369	ENSMUSG00000032067	-5,83565	0,00118	0,04394	0,64493	Pts	6-pyruvoyl-tetrahydropterin synthase Gene [Source:MGI Symbol;Acc:MGI:1338783]
1187	ENSMUSG00000056552	-4,35947	0,00470	0,05566	0,64436	E130120F12Rik	RIKEN cDNA E130120F12 gene Gene [Source:MGI Symbol;Acc:MGI:3612873]
304	ENSMUSG00000031757	-6,08768	0,00094	0,04282	0,64350	Mt4	metallothionein 4 Gene [Source:MGI Symbol;Acc:MGI:99692]
731	ENSMUSG00000030604	-4,97242	0,00257	0,04953	0,64336	4933426I21Rik	RIKEN cDNA 4933426I21 gene Gene [Source:MGI Symbol;Acc:MGI:1918413]
482	ENSMUSG00000020829	-5,52622	0,00152	0,04439	0,64257	Slc46a1	solute carrier family 46, member 1 Gene [Source:MGI Symbol;Acc:MGI:1098733]
236	ENSMUSG00000022122	-6,42072	0,00072	0,04261	0,64221	Ednrb	endothelin receptor type B Gene [Source:MGI Symbol;Acc:MGI:102720]
533	ENSMUSG00000020056	-5,40046	0,00174	0,04583	0,64177	Ccdc53	coiled-coil domain containing 53 Gene [Source:MGI Symbol;Acc:MGI:1914532]
856	ENSMUSG00000001655	-4,78669	0,00309	0,05065	0,64117	Hoxc13	homeobox C13 Gene [Source:MGI Symbol;Acc:MGI:99560]
1454	ENSMUSG00000053070	-3,97220	0,00712	0,06298	0,63829	9230110C19Rik	RIKEN cDNA 9230110C19 gene Gene [Source:MGI Symbol;Acc:MGI:3045346]
1445	ENSMUSG00000028393	-3,98440	0,00702	0,06266	0,63648	Alad	aminolevulinate, delta-, dehydratase Gene [Source:MGI Symbol;Acc:MGI:96853]
185	ENSMUSG00000036062	-6,73814	0,00058	0,04208	0,63635	N28178	Protein KIAA1045 [Source:UniProtKB/Swiss-Prot;Acc:Q80TL4]
107	ENSMUSG00000025912	-7,37672	0,00033	0,04208	0,63502	Myb1	myeloblastosis oncogene-like 1 Gene [Source:MGI Symbol;Acc:MGI:99925]
434	ENSMUSG00000044748	-5,63835	0,00138	0,04420	0,63478	Defb1	defensin beta 1 Gene [Source:MGI Symbol;Acc:MGI:1096878]
266	ENSMUSG00000029530	-6,23964	0,00082	0,04282	0,63388	Ccr9	chemokine (C-C motif) receptor 9 Gene [Source:MGI Symbol;Acc:MGI:1341902]
396	ENSMUSG00000027550	-5,76517	0,00125	0,04394	0,63312	Lrrcc1	leucine rich repeat and coiled-coil domain containing 1 Gene [Source:MGI Symbol;Acc:MGI:1918960]
1417	ENSMUSG00000035831	-4,01451	0,00675	0,06221	0,62934	Krt25	keratin 25 Gene [Source:MGI Symbol;Acc:MGI:1918060]
720	ENSMUSG00000064352	-4,98976	0,00254	0,04946	0,62689	AY172335.2	
554	ENSMUSG00000020492	-5,34050	0,00185	0,04671	0,62680	Fam33a	family with sequence similarity 33, member A Gene [Source:MGI Symbol;Acc:MGI:1913390]
460	ENSMUSG00000032872	-5,58609	0,00145	0,04420	0,62671	Cyb5r4	cytochrome b5 reductase 4 Gene [Source:MGI Symbol;Acc:MGI:2386848]
483	ENSMUSG00000001804	-5,52272	0,00153	0,04439	0,62157	Dsg4	desmoglein 4 Gene [Source:MGI Symbol;Acc:MGI:2661061]
1446	ENSMUSG00000023963	-3,98341	0,00703	0,06271	0,62110	Cyp39a1	cytochrome P450, family 39, subfamily a, polypeptide 1 Gene [Source:MGI Symbol;Acc:MGI:1927096]
507	ENSMUSG00000000579	-5,45820	0,00164	0,04539	0,61745	Dynl1c	dynein light chain Tctex-type 1D Gene [Source:MGI Symbol;Acc:MGI:98643]
363	ENSMUSG00000075807	-5,86586	0,00116	0,04394	0,61471	SNORD116	Small nucleolar RNA SNORD116 [Source:RFAM;Acc:RF00108]
1368	ENSMUSG00000031214	-4,09380	0,00620	0,06061	0,61438	Ophn1	oligophrenin 1 Gene [Source:MGI Symbol;Acc:MGI:2151070]
367	ENSMUSG00000026989	-5,83779	0,00118	0,04394	0,60733	Dapl1	death associated protein-like 1 Gene [Source:MGI Symbol;Acc:MGI:1923997]
719	ENSMUSG00000020283	-4,99038	0,00254	0,04946	0,60677	Pex13	peroxisomal biogenesis factor 13 Gene [Source:MGI Symbol;Acc:MGI:1919379]
1158	ENSMUSG00000029413	-4,39282	0,00455	0,05527	0,60622	Naaa	N-acyl ethanolamine acid amidase Gene [Source:MGI Symbol;Acc:MGI:1914361]
55	ENSMUSG00000063661	-8,56213	0,00015	0,03757	0,60566	Krt73	keratin 73 Gene [Source:MGI Symbol;Acc:MGI:3607712]
917	ENSMUSG00000033102	-4,70756	0,00334	0,05127	0,60332	Cdc14b	CDC14 cell division cycle 14 homolog B (S. cerevisiae) Gene [Source:MGI Symbol;Acc:MGI:2441808]
1373	ENSMUSG00000049214	-4,07965	0,00629	0,06110	0,60198	Skint7	selection and upkeep of intraepithelial T cells 8 Gene [Source:MGI Symbol;Acc:MGI:3651523]
1507	ENSMUSG00000055725	-3,90210	0,00771	0,06464	0,59661	Paqr3	progesterin and adipoQ receptor family member III Gene [Source:MGI Symbol;Acc:MGI:2679683]
1055	ENSMUSG00000019791	-4,51210	0,00404	0,05388	0,59438	Hint3	histidine triad nucleotide binding protein 3 Gene [Source:MGI Symbol;Acc:MGI:1914097]
732	ENSMUSG00000035967	-4,97154	0,00258	0,04953	0,59215	Ddx26b	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B Gene [Source:MGI Symbol;Acc:MGI:2442593]
863	ENSMUSG00000018570	-4,78012	0,00311	0,05065	0,58904	2810408A11Rik	RIKEN cDNA 2810408A11 gene Gene [Source:MGI Symbol;Acc:MGI:1917669]
505	ENSMUSG00000021482	-5,46154	0,00163	0,04538	0,58894	1110018J18Rik	RIKEN cDNA 1110018J18 gene Gene [Source:MGI Symbol;Acc:MGI:1913379]
462	ENSMUSG00000077583	-5,58214	0,00146	0,04420	0,58662	SCARNA13	Small Cajal body specific RNA 13 [Source:RFAM;Acc:RF00231]
64	ENSMUSG00000032369	-8,35886	0,00018	0,03766	0,58527	Plscr1	phospholipid scramblase 1 Gene [Source:MGI Symbol;Acc:MGI:893575]
948	ENSMUSG00000028551	-4,66469	0,00348	0,05163	0,58501	Cdkn2c	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4) Gene [Source:MGI Symbol;Acc:MGI:105388]
218	ENSMUSG00000067653	-6,55062	0,00065	0,04216	0,58380	Ankrd23	ankyrin repeat domain 23 Gene [Source:MGI Symbol;Acc:MGI:1925571]
1210	ENSMUSG00000032757	-4,32653	0,00487	0,05662	0,58370	Bet1	blocked early in transport 1 homolog (S. cerevisiae) Gene [Source:MGI Symbol;Acc:MGI:1343104]
76	ENSMUSG00000062826	-8,06831	0,00020	0,03766	0,58116	2310038E17Rik	RIKEN cDNA 2310038E17 gene Gene [Source:MGI Symbol;Acc:MGI:1919153]
1479	ENSMUSG00000064348	-3,94315	0,00735	0,06351	0,58027	AY172335.4	
119	ENSMUSG00000003721	-7,23183	0,00037	0,04208	0,57806	Insig2	insulin induced gene 2 Gene [Source:MGI Symbol;Acc:MGI:1920249]
1195	ENSMUSG00000040181	-4,34704	0,00476	0,05602	0,57670	Fmo1	flavin containing monooxygenase 1 Gene [Source:MGI Symbol;Acc:MGI:1310002]
231	ENSMUSG00000027654	-6,45773	0,00071	0,04261	0,57354	Fam83d	family with sequence similarity 83, member D Gene [Source:MGI Symbol;Acc:MGI:1919128]
1341	ENSMUSG00000029270	-4,13682	0,00594	0,05973	0,57262	Fam69a	family with sequence similarity 69, member A Gene [Source:MGI Symbol;Acc:MGI:1914516]
273	ENSMUSG00000023074	-6,20791	0,00085	0,04282	0,56940	Mospd1	motile sperm domain containing 1 Gene [Source:MGI Symbol;Acc:MGI:1917630]

n°	probeset ID	d.value	p.value	q.value	Fold-change	Genename	Description
1345	ENSMUSG00000038332	-4,12455	0,00601	0,06000	0,56646	Sesn1	sestrin 1 Gene [Source:MGI Symbol;Acc:MGI:2155278]
844	ENSMUSG00000074604	-4,80121	0,00305	0,05065	0,56547	Mgst2	microsomal glutathione S-transferase 2 Gene [Source:MGI Symbol;Acc:MGI:2448481]
53	ENSMUSG00000021303	-8,65261	0,00014	0,03757	0,56028	Gng4	guanine nucleotide binding protein (G protein), gamma 4 Gene [Source:MGI Symbol;Acc:MGI:102703]
37	ENSMUSG00000055937	-9,21823	0,00010	0,03757	0,55877	Krt28	keratin 28 Gene [Source:MGI Symbol;Acc:MGI:1918093]
647	ENSMUSG00000024084	-5,13937	0,00221	0,04793	0,55507	Qpct	glutaminyl-peptide cyclotransferase (glutaminyl cyclase) Gene [Source:MGI Symbol;Acc:MGI:1917786]
256	ENSMUSG00000020159	-6,29657	0,00079	0,04282	0,55304	Gabrp	gamma-aminobutyric acid (GABA) A receptor, pi Gene [Source:MGI Symbol;Acc:MGI:2387597]
1027	ENSMUSG00000025993	-4,55043	0,00389	0,05324	0,54768	Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1 Gene [Source:MGI Symbol;Acc:MGI:1315204]
1311	ENSMUSG00000074370	-4,18084	0,00567	0,05913	0,54072	AC165150.2	
156	ENSMUSG00000037348	-6,88879	0,00049	0,04208	0,53619	Paqr7	progesterin and adipoQ receptor family member VII Gene [Source:MGI Symbol;Acc:MGI:1919154]
17	ENSMUSG00000041193	-10,57621	0,00005	0,03733	0,53040	Pla2g5	phospholipase A2, group V Gene [Source:MGI Symbol;Acc:MGI:101899]
1309	ENSMUSG00000038641	-4,18388	0,00566	0,05913	0,52841	Akr1d1	aldo-keto reductase family 1, member D1 Gene [Source:MGI Symbol;Acc:MGI:2384785]
905	ENSMUSG00000033774	-4,72173	0,00330	0,05122	0,51590	Npbwr1	neuropeptides B/W receptor 1 Gene [Source:MGI Symbol;Acc:MGI:891989]
66	ENSMUSG00000018862	-8,24714	0,00019	0,03766	0,51074	Otop3	otopetrin 3 Gene [Source:MGI Symbol;Acc:MGI:1916852]
631	ENSMUSG00000033107	-5,17482	0,00214	0,04758	0,50877	Rnf125	ring finger protein 125 Gene [Source:MGI Symbol;Acc:MGI:1914914]
267	ENSMUSG00000035305	-6,22761	0,00083	0,04282	0,50751	Ror1	receptor tyrosine kinase-like orphan receptor 1 Gene [Source:MGI Symbol;Acc:MGI:1347520]
87	ENSMUSG00000049709	-7,79964	0,00025	0,03991	0,49624	Nlrp10	NLR family, pyrin domain containing 10 Gene [Source:MGI Symbol;Acc:MGI:2444084]
983	ENSMUSG00000067049	-4,61175	0,00367	0,05257	0,49309	Unc93a	unc-93 homolog A (C. elegans) Gene [Source:MGI Symbol;Acc:MGI:1933250]
253	ENSMUSG00000041449	-6,30933	0,00078	0,04282	0,48534	Serpina3h	serine (or cysteine) peptidase inhibitor, clade A, member 3H Gene [Source:MGI Symbol;Acc:MGI:2182839]
424	ENSMUSG00000040170	-5,68086	0,00133	0,04399	0,47833	Fmo2	flavin containing monooxygenase 2 Gene [Source:MGI Symbol;Acc:MGI:1916776]
887	ENSMUSG00000041660	-4,74527	0,00321	0,05094	0,46605	Bbox1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase 1 (gamma-butyrobetaine hydroxylase) Gene [Source:MGI Symbol;Acc:MGI:1891372]
445	ENSMUSG00000029236	-5,61498	0,00141	0,04420	0,46137	Nmu	neuromedin U Gene [Source:MGI Symbol;Acc:MGI:1860476]
2	ENSMUSG00000024431	-19,72859	0,00001	0,03733	0,43727	Nr3c1	nuclear receptor subfamily 3, group C, member 1 Gene [Source:MGI Symbol;Acc:MGI:95824]
1121	ENSMUSG00000074207	-4,43227	0,00437	0,05482	0,43645	Adh1	alcohol dehydrogenase 1 (class I) Gene [Source:MGI Symbol;Acc:MGI:87921]
12	ENSMUSG00000037263	-11,15263	0,00004	0,03733	0,43035	1700055N04Rik	RIKEN cDNA 1700055N04 gene Gene [Source:MGI Symbol;Acc:MGI:1920708]
285	ENSMUSG00000048766	-6,16053	0,00089	0,04282	0,42927	Skint10	selection and upkeep of intraepithelial T cells 10 Gene [Source:MGI Symbol;Acc:MGI:2685416]
623	ENSMUSG00000036322	-5,19093	0,00211	0,04749	0,40166	H2-Ea	histocompatibility 2, class II antigen E alpha Gene [Source:MGI Symbol;Acc:MGI:95900]
1408	ENSMUSG00000028211	-4,02483	0,00666	0,06217	0,36790	Trp53inp1	transformation related protein 53 inducible nuclear protein 1 Gene [Source:MGI Symbol;Acc:MGI:1926609]
270	ENSMUSG00000015665	-6,21326	0,00084	0,04282	0,36304	Awat1	acyl-CoA wax alcohol acyltransferase 1 Gene [Source:MGI Symbol;Acc:MGI:3588200]
1314	ENSMUSG00000024222	-4,17687	0,00570	0,05918	0,33353	Fkbp5	FK506 binding protein 5 Gene [Source:MGI Symbol;Acc:MGI:104670]
279	ENSMUSG00000039760	-6,19748	0,00086	0,04282	0,31931	Il22ra2	interleukin 22 receptor, alpha 2 Gene [Source:MGI Symbol;Acc:MGI:2665114]
47	ENSMUSG00000059606	-8,78391	0,00013	0,03757	0,27939	Ear5	eosinophil-associated, ribonuclease A family, member 5 Gene [Source:MGI Symbol;Acc:MGI:1858598]
287	ENSMUSG00000073601	-6,15084	0,00090	0,04282	0,25035	Serpnb3c	serine (or cysteine) peptidase inhibitor, clade B, member 3C Gene [Source:MGI Symbol;Acc:MGI:1277952]

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Gene Symbol	Description	GenBank	Product (bp)	Forward primer	Reverse primer
<i>Bcl3</i>	B-cell leukemia/lymphoma 3	NM_033601.3	286	CACGCCGTGGAGAACAACAGC	GGTCTGGGGATGGCTCAGGCT
<i>Elf5</i>	E74-like factor 5 (all forms)	NM_001145813.1	315	CGATCTGTTGAGCAATGAAGAC	TGGTCTCTCAGCATCATTGAA
<i>Ereg</i>	epiregulin	NM_007950.2	167	AGACGCTCCCTGCCTCTTGGG	CTGCACCTTGAGCCACACGGGG
<i>Fkbp5</i>	FK506 binding protein 5	NM_010220.3	290	CTTGACCACGCTATGGTTT	AACGACTCTGAGGCTTTGGA
<i>Hprt1</i>	hypoxanthine phosphoribosyl transferase 1	NM_013556	142	TCAGTCAACGGGGGACATAAA	GGGGCTGTACTGCTTAACCAG
<i>Krt77</i>	keratin 77	NM_001003667	200	GAGCAAAGATGAGGCTGAGG	CCTCCGCATCAGAAATCAAT
<i>Mmp3</i>	matrix metalloproteinase 3	NM_010809.1	172	CCAGGTGTTGACTCAAGGGTGGA	ACACAGGATGCCTTCTGGATCTC
<i>S100a8</i>	S100 calcium binding protein A8	NM_013650.2	68	GGAGTTCCTTGCATGGTGAT	TCTGCTACTCCTTGTGGCTGTCT
<i>S100a9</i>	S100 calcium binding protein A9	NM_009114.2	60	TGACAGCTGCCCAACCAA	TTCCAGAAACAAAGGCCATT
<i>Slpi</i>	secretory leukocyte peptidase inhibitor	NM_011414.3	278	TGGCACCTGGACTGTGAAGG	CCCCTCCTCTGGCAGACAT
<i>Stat3</i>	signal transducer and activator of transcription 3	NM_011486.4	354	CTGGCGGGCTCTTGTGAGC	GACTAAGGGCCGGTCCGGGT
<i>Tslp</i>	thymic stromal lymphopoietin isoform 1	NM_021367.2	125	CCAGGCTACCCTGAAACTGA	TCTGGAGATTGCATGAAGGA